US012384828B2

(12) **United States Patent**
Pentecost et al.

(10) **Patent No.: US 12,384,828 B2**
(45) **Date of Patent: Aug. 12, 2025**

(54) **ENGINEERED EXTRACELLULAR VESICLES COMPRISING FUSION PROTEINS**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 67 days.

(21) Appl. No.: **18/056,029**

(22) Filed: **Nov. 16, 2022**

(65) **Prior Publication Data**

US 2023/0312678 A1 Oct. 5, 2023

Related U.S. Application Data

(60) Division of application No. 17/377,550, filed on Jul. 16, 2021, now Pat. No. 11,578,116, which is a continuation of application No. PCT/US2021/016949, filed on Feb. 5, 2021.

(60) Provisional application No. 62/970,374, filed on Feb. 5, 2020.

(51) **Int. Cl.**

C07K 14/705	(2006.01)
A61K 35/17	(2025.01)
A61K 47/54	(2017.01)
A61K 47/58	(2017.01)
A61K 47/62	(2017.01)
A61K 47/69	(2017.01)
A61P 27/02	(2006.01)
A61P 37/06	(2006.01)
C07K 14/75	(2006.01)
C12N 9/14	(2006.01)
A61K 38/00	(2006.01)

(52) **U.S. Cl.**

CPC ***C07K 14/70532*** (2013.01); ***A61K 35/17*** (2013.01); ***A61K 47/544*** (2017.08); ***A61K 47/605*** (2017.08); ***A61K 47/62*** (2017.08); ***A61K 47/69*** (2017.08); ***A61K 47/6901*** (2017.08); ***A61K 47/6911*** (2017.08); ***A61K 47/6917*** (2017.08); ***A61P 27/02*** (2018.01); ***A61P 37/06*** (2018.01); ***C07K 14/705*** (2013.01); ***C07K 14/70521*** (2013.01); ***C07K 14/7056*** (2013.01); ***C07K 14/70596*** (2013.01); ***C07K 14/75*** (2013.01); ***C12N 9/14*** (2013.01); *A61K 38/00* (2013.01); *C07K 14/70503* (2013.01); *C07K 2319/01* (2013.01); *C07K 2319/02* (2013.01); *C07K 2319/035* (2013.01); *C07K 2319/055* (2013.01); *C07K 2319/30* (2013.01); *C07K 2319/74* (2013.01); *C07K 2319/75* (2013.01); *C07K 2319/912* (2013.01); *C07K 2319/915* (2013.01); *C12Y 304/24081* (2013.01)

(58) **Field of Classification Search**

CPC C07K 14/70532; C07K 14/70521; C07K 14/70596; C07K 2319/035; C07K 2319/055; C07K 2319/30; C07K 2319/75; C07K 2319/92; C07K 2319/915; A61K 47/6917; A61K 38/00; C12Y 304/24081

See application file for complete search history.

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(57) **ABSTRACT**

Described herein are compositions and techniques related to generation and therapeutic application of artificial synapses. Artificial synapses are engineered extracellular vesicles, including exosomes, which incorporate sticky binders on their surface to anchor signaling domains against biological targets, such as receptors. These engineered additives can be organized in genetic vector constructs, expressed in mammalian cells, wherein the sticky binders attach to extracellular vesicles such as exosomes, thereby presenting their joined signaling domains which are rapidly taken up by recipient cells. Artificial synapses adopt the hallmark biophysical and biochemical features of extracellular vesicles, allowing for rapid deployment and scale-up. Importantly, this strategy can allow for kinetically favorable signal generation and signal propagation. This includes, for example, increasing density of agonist presentation to support receptor clustering—an onerous barrier for traditional receptor targeting strategies.

23 Claims, 102 Drawing Sheets

Specification includes a Sequence Listing.

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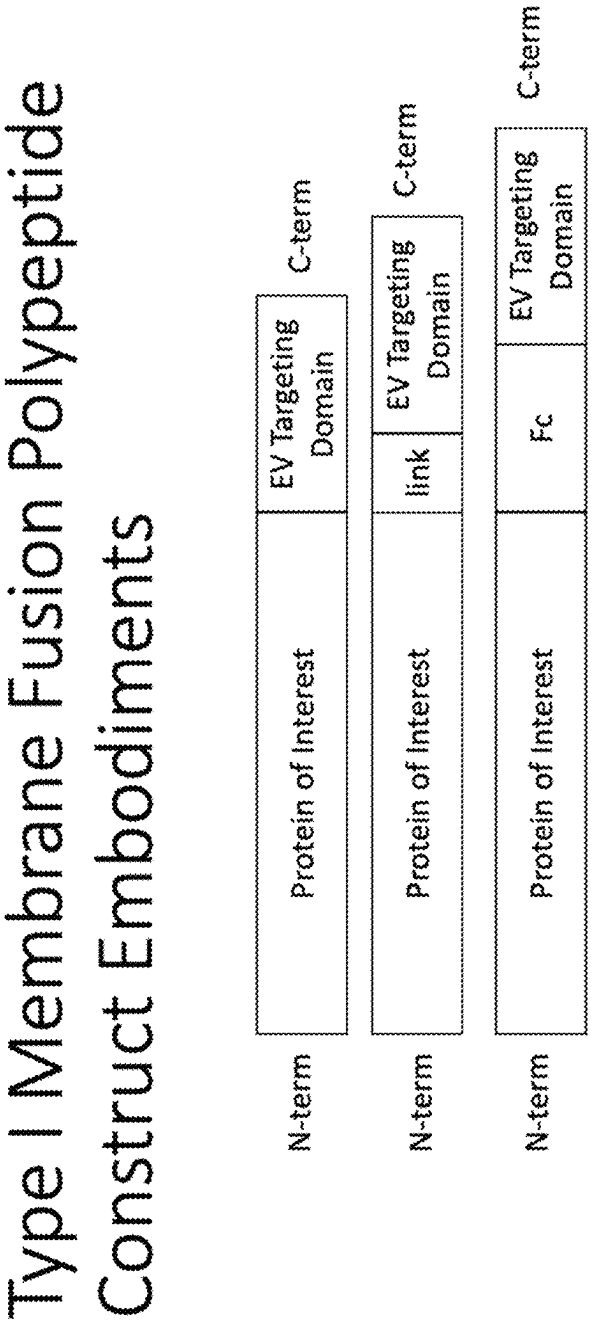

Type I Membrane Fusion Polypeptide Construct Embodiments
N-term
Protein of Interest
EV Targeting Domain
C-term
N-term
Protein of Interest
link
EV Targeting Domain
C-term
N-term
Protein of Interest
Fc
EV Targeting Domain
C-term

FIG. 1

Phosphatidylserine binding: Lactadherin (MFGE8) C1C2

>NM_005928.4 Homo sapiens milk fat globule-EGF factor 8 protein (MFGE8), transcript variant 1, mRNA
AGAACCCCGCGGGGTCTGAGCAGCCCAGCGTGCCCATTCCAGCGCCCGCGTCCCCGCAGCATGCCGCGCCCCCGCCTGCTGGCCGCGCTGTGCGGCGCGCTGCTCTG
CGCCCCCAGCCTCCTCGTCGCCCTGGATATCTGTTCCAAAAACCCCTGCCACAACGGTGGTTTATGCGAGGAGATTTCCCAAGAAGTGCGAGGAGATGTCTTCCCCTC
GTACACCTGCACGTGCCTTAAGGGCTACGCGGGCAACCACTGTGAGACGAAATGT**GTCGAGCCACTGGGCCTGGAGAATGGGAACATTGCCAACTCACAGATCGCC**
GCCTCGTCTGTGCGTGTGACCTTCTTGGGTTTGCAGCATTGGGTCCCGGAGCTGGCCCGCCTGAACCGCGCAGGCATGGTCAATGCCTGGACACCCAGCAGCAATG
ACGATAACCCCTGGATCCAGGTGAACCTGCTGCGGAGGATGTGGGTAACAGGTGTGGTGACGCAGGGTGCCAGCCGCTTGGCCAGTCATGAGTACCTGAAGGCC
TTCAAGGTGGCCTACAGCCTTAATGGACACGAATTCGATTTCATCCATGATGTTAATAAAAAACACAAGGAGTTTGTGGGTAACTGGAACAAAAACGCGGTGCAT
GTCAACCTGTTTGAGACCCCTGTGGAGGCTCAGTACGTGAGATTGTACCCCACGAGCTGCCACACGGCCTGCACTCTGCGCTTTGAGCTACTGGGCTGTGAGCTGA
ACGGATGCGCCAATCCCCTGGGCCTGAAGAATAACAGCATCCCTGACAAGCAGATCACGGCCTCCAGCAGCTACAAGACCTGGGGCTTGCATCTCTTCAGCTGGAA
CCCCTCCTATGCACGGCTGGACAAGCAGGGCAACTTCAACGCCTGGGTTGCGGGGAGCTACGGTAACGATCAGTGGCTGCAGGTGGACCTGGGCTCCTCGAAGGA
GGTGACAGGCATCATCACCCAGGGGGCCCGTAACTTTGGCTCTGTCCAGTTTGTGGCATCCTACAAGGTTGCCTACAGTAATGACAGTGCGAACTGGACTGAGTAC
CAGGACCCCAGGACTGGCAGCAGTAAGATCTTCCCTGGCAACTGGGACAACCACTCCCACAAGAAGAACTTGTTTGAGACGCCCATCCTGGCTCGCTATGTGCGCA
TCCTGCCTGTAGCCTGGCACAACCGCATCGCCCTGCGCCTGGAGCTGCTGGGCTGTTAGTGGCCACCTGCCACCCCCAGGTCTTCCTGCTTTCCATGGGCCCGCTGCC
TCTTGGCTTCTCAGCCCCTTTAAATCACCATAGGGCTGGGGACTGGGGAAGGGGAGGGTGTTCAGAGGCAGCACCACCACACAGTCACCCCTCCCTCCCTCTTTCCCA
CCCTCCACCTCTCACGGGCCCTGCCCCAGCCCCTAAGCCCCGTCCCCTAACCCCCAGTCCTCACTGTCCTGTTTTCTTAGGCACTGAGGGATCTGAGTAGGTCTGGGAT
GGACAGGAAAGGGCAAAGTAGGGCGTGTGGTTTCCCTGCCCCTGTCCGGACCGCCGATCCCAGGTGCGTGTGTCTCTGTCTCTCCTAGCCCCTCTCTCACACATCACA
TTCCCATGGTGGCCTCAAGAAAGGCCCGGAAGCGCCAGGCTGGAGATAACAGCCTCTTGCCCGTCGGCCCTGCGTCGGCCCTGGGGTACCATGTGGCCACAACTGCT
GTGGCCCCCTGTCCCCAAGACACTTCCCCTTGTCTCCCTGGTTGCCTCTCTTGCCCCTTGTCCTGAAGCCCAGCGACACAGAAGGGGGTGGGGCGGGTCTATGGGGA
GAAAGGGAGCGAGGTCAGAGGAGGGCATGGGTTGGCAGGGTGGGCGTTTGGGGCCCTCTATGCTGGCTTTTCACCCCAGAGGACACAGGCAGCTTCCAAAATATA
TTTATCTTCTTCACGGGAA

>NP_005919.2 lactadherin isoform a preproprotein [Homo sapiens]
MPRPRLLAALCGALLCAPSLLVALDICSKNPCHNGGLCEEISQEVRGDVFPSYTCTCLKGYAGNHCETKC**VEPLGLENGNIANSQIAASSVRVTFLGLQHWVPELARLNRAG**
MVNAWTPSSNDDNPWIQVNLLRRMWVTGVVTQGASRLASHEYLKAFKVAYSLNGHEFDFIHDVNKKHKEFVGNWNKNAVHVNLFETPVEAQYVRLYPTSCHTACT
LRFELLGCELNGCANPLGLKNNSIPDKQITASSSYKTWGLHLFSWNPSYARLDKQGNFNAWVAGSYGNDQWLQVDLGSSKEVTGIITQGARNFGSVQFVASYKVAYSN
DSANWTEYQDPRTGSSKIFPGNWDNHSHKKNLFETPILARYVRILPVAWHNRIALRLELLGC

FIG. 2A

Lipid binding: CD55 (DAF) Glycosylphosphatidylinositol (GPI) Anchor

>NM_000574.5 Homo sapiens CD55 molecule (Cromer blood group) (CD55), transcript variant 1, mRNA
CTGCTTACTGCAACTCGCTCCGGCCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCG
TGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATG
CCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCC
TTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTT
TCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAA
TTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGT
ACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATT
GACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACT
GTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA
ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA
CAACC**CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTG**
CTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCA
TTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGA
ACAACTTGCAGAATTGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTT
CCACAAGATCTGTAATGTTATTTCCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCTCTTCTAAGCAAAATTGC
TAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAACCAGGGGTG
TTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTAA
AAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTTATTTATATT
TATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTGGT
ATCATGTAGTATGTGAAATTTATTCTTAAACGTGACTACTTTATTTCTAAATAAGAAATTCCCTACCTGCTTCCTACAAGCAGTTCAGAATGCCATGCCTTGGTTGTCCTAGTG
TGAATAATTTTCAGCTACTTTAAAATTATATTGTACTTTCTCAAGCATGTCATATCCTTTCCTATTAGAGTATCTATATTACTTGTTACTGATTTACCTGAAGGCAATCTGATTA
ATTTCTAGGTTTTTACCATATTCTTGTCATCTTGCCAATTACATTTTAAGTGTTAGACTAGACTAAGATGTACTAGTTGTATAGAATATAACTAGA
TTTATTATGGCAATGTTTATTTTGTCATTTTGCTTCATCTGTTTTGTTGTTGAAGTACTTTAAATTTCATACGTTCATGGCATTTCACTGTAAAGACTTTAATGTGTATTTCTTAA
AATAAAACTTTTTTTCCTCCTTAA

>NP_000565.1 complement decay-accelerating factor isoform 1 preproprotein [Homo sapiens]
MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPEDTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPTRLNSASLKQPYITQNYFP
VGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGERD
HYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVSRTTKHFHETT**PNKGSGTTSGTTRL**
LSGHTCFTLTGLLGTLVTMGLLT

FIG. 2B

Fc Linker

>KY053479.1 Synthetic construct Fc-adiponectin gene, complete cds
ATGTACAGGATGCAACTCCTGTCTTGCATTGCACTAAGTCTTGCACTTGTCACGAACTCGATATCGGCCA
TGGTTAGATCT**GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA**
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA
AGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG
GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGA
TGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGA
CCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
CACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGCCAGCGGAAGTGGCGGAGGAGGCGGTCCTGGAGAAGGTGCCTATGTAT
ACCGCTCAGCATTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAGATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACT
GGTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTCT
TCACCTATGATCAGTACCAGGAAAATAATGTGGACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAGGTGTATGGGGAAGGA
GAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTCACAGGCTTTCTTCTCTACCATGACACCAACTCTAGAAAGCTTCCTGGAGAAGGTGCCTATGTATA
CCGCTCAGCATTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAGATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTG
GTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTCTT
CACCTATGATCAGTACCAGGAAAATAATGTGGACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAGGTGTATGGGGAAGGAG
AGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTCACAGGCTTTCTTCTCTACCATGACACCAACACTAGTCCTGGAGAAGGTGCCTATGTATACCGCTCA
GCATTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAGATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATT
CCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTAT
GATCAGTACCAGGAAAATAATGTGGACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTA
ATGGACTCTATGCTGATAATGACAATGACTCCACCTTCACAGGCTTTCTTCTCTACCATGACACCAACTAA

>Fc Translation
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
SLSLSPGK

FIG. 3

Human PD-L1 extracellular domains

>NM_014143.4 Homo sapiens CD274 molecule (CD274), transcript variant 1, mRNA
AGTTCTGCGCAGCTTCCCGAGGCTCCGCACCAGCCGCGCTTCTGTCCGCCTGCAGGGCATTCCAGAAAG**ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTAC**
TGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGAT
AAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATCACA
GATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAACAAAATCAACCAAAGAATTTTGGTTG
TGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAA
GAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATC
CCAGAACTACCTCTGGCACATCCTCCAAATGAAAGGACTCACTTGGTAATTCTGGGAGCCATCTTATTATGCCTTGGTGTAGCACTGACATTCATCTTCCGTTTAAGAAAAGGGAGAATGATGGA
TGTGAAAAAATGTGGCATCCAAGATACAAACTCAAAGAAGCAAAGTGATACACATTTGGAGGAGACGTAATCCAGCATTGGAACTTCTGATCTTCAAGCAGGGATTCTCAACCTGTGGTTTAGGG
GTTCATCGGGGCTGAGCGTGACAAGAGGAAGGAATGGGCCCGTGGGATGCAGGCAATGTGGGACTTAAAAGGCCCAAGCACTGAAAATGGAACCTGGCGAAAGCAGAGGAGGAGAATGAAGAA
AGATGGAGTCAAACAGGGAGCCTGGAGGGAGACCTTGATACTTTCAAATGCCTGAGGGGCTCATCGACGCCTGTGACAGGGAGAAAGGATACTTCTGAACAAGGAGCCTCCAAGCAAATCATCCAT
TGCTCATCCTAGGAAGACGGGTTGAGAATCCCTAATTTGAGGGTCAGTTCCTGCAGAAGTGCCCTTTGCCTCCACTCAATGCCTCAATTTGTTTTCTGCATGACTGAGAGTCTCAGTGTTGGAACGGGA
CAGTATTTATGTATGAGTTTTTCCTATTTATTTTGAGTCTGTGAGGTCTTCTTGTCATGTGAGTGTGGTTGTGAATGATTTCTTTTGAAGATATATTGTAGTAGATGTTACAATTTTGTCGCCAAACTAAA
CTTGCTGCTTAATGATTTGCTCACATCTAGTAAAACATGGAGTATTTGTAAGGTGCTTGGTCTCCTCTATAACTACAAGTATACATTGGAAGCATAAAGATCAAACCGTTGGTTGCATAGGATGTCACCT
TTATTTAACCCATTAATACTCTGGTTGACCTAATCTTATTCTCAGACCTCAAGTGTCTGTGCAGTATCTGTTCCATTTAAATATCAGCTTTACAATTATGTGGTAGCCTACACACATAATCTCATTTCATCG
CTGTAACCACCCTGTTGTGATAACCACTATTATTTTACCCATCGTACAGCTGAGGAAGCAAACAGATTAAGTAACTTGCCCAAACCAGTAAATAGCAGACCTCAGACTGCCACCCACTGTCCTTTTATAA
TACAATTTACAGCTATATTTTACTTTAAGCAATTCTTTTATTCAAAAACCATTTATTAAGTGCCCTTGCAATATCAATCGCTGTGCCAGGCATTGAATCTACAGATGTGAGCAAGACAAAGTACCTGTCCT
CAAGGAGCTCATAGTATAATGAGGAGATTAACAAGAAAATGTATTATTACAATTTAGTCCAGTGTCATAGCATAAGGATGATGCGAGGGGAAAACCCGAGCAGTGTTGCCAAGAGGAGGAAATAGG
CCAATGTGGTCTGGGACGGTTGGATATACTTAAACATCTTAATAATCAGAGTAATTTTCATTTACAAAGAGAGGTCGGTACTTAAAATAACCCTGAAAAATAACACTGGAATTCCTTTTCTAGCATTAT
ATTTATTCCTGATTTGCCTTTGCCATATAATCTAATGCTTGTTTATATAGTGTCTGGTATTGTTTAACAGTTCTGTCTTTTCTATTTAAATGCCACTAAATTTTAAATTCATACCTTTCCATGATTCAAAATTC
AAAAGATCCCATGGGAGATGGTTGGAAAATCTCCACTTCATCCTCCAAGCCATTCAAGTTTCCTTTCCAGAAGCAACTGCTACTGCCTTTCATTCATATGTTCTTCTAAAGATAGTCTACATTTGGAAAT
GTATGTTAAAAGCACGTATTTTTAAAATTTTTTTCCTAAATAGTAACACATTGTATGTCTGCTGTGTACTTTGCTATTTTTATTTATTTTAGTGTTTCTTATATAGCAGATGGAATGAATTTGAAGTTCCCA
GGGCTGAGGATCCATGCCTTCTTTGTTTCTAAGTTATCTTTCCCATAGCTTTTCATTATCTTTCATATGATCCAGTATATGTTAAATATGTCCTACATATACATTTAGACAACCACCATTTGTTAAGTATTT
GCTCTAGGACAGAGTTTGGATTTGTTTATGTTTGCTCAAAAGGAGACCCATGGGCTCTCCAGGGTGCACTGAGTCAATCTAGTCCTAAAAAGCAATCTTATTATTAACTCTGTATGACAGAATCATGTC
TGGAACTTTTGTTTTCTGCTTTCTGTCAAGTATAAACTTCACTTTGATGCTGTACTTGCAAAATCACATTTTCTTTCTGGAAATTCCGGCAGTGTACCTTGACTGCTAGCTACCCTGTGCCAGAAAAGCCT
CATTCGTTGTGCTTGAACCCTTGAATGCCACCAGCTGTCATCACTACACAGCCCTCCTAAGAGGCTTCCTGGAGGTTTCGAGATTCAGATGCCCTGGGAGATCCCAGAGTTTCCTTTCCCTCTTGGCCAT
ATTCTGGTGTCAATGACAAGGAGTACCTTGGCTTTGCCACATGTCAAGGCTGAAGAAACAGTGTCTCCAACAGAGCTCCTTGTGTTATCTGTTTGTACATGTGCATTTGTACAGTAATTGGTGTGACAG
TGTTCTTTGTGTGAATTACAGGCAAGAATTGTGGCTGAGCAAGGCACATAGTCTACTCAGTCTATTCCTAAGTCCTAACTCCTCCTTGTGGTGTTGGATTTGTAAGGCACTTTATCCCTTTTGTCTCATGT
TTCATCGTAAATGGCATAGGCAGAGATGATACCTAATTCTGCATTTGATTGTCACTTTTTGTACCTGCATTAATTTAATAAAATATTCTTATTTATTTTGTTACTTGGTACACCAGCATGTCCATTTTCTTG
TTTATTTTGTGTTTAATAAAATGTTCAGTTTAACATCCCA

>NP_054862.1 programmed cell death 1 ligand 1 isoform a precursor [Homo sapiens]
MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRCMISYGGADYKRITVKV
NAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPELPLAHPPNERTHLVILGAILLCLGVALTFIFRLRKGRM
MDVKKCGIQDTNSKKQSDTHLEET

FIG. 4A

Human PD-L2 extracellular domains

>NM_025239.4 Homo sapiens programmed cell death 1 ligand 2 (PDCD1LG2), mRNA
ACTCTCATGTTACGGCAAACCTTAAGCTGAATGAACAACTTTTCTTCTCTTGAATATATCTTAACGCCAAATTTTGAGTGCTTTTTTGTTACCCATCCTCATATGTCCCAGCTA
GAAAGAATCCTGGGTTGGAGCTACTGCATGTTGATTGTTTTGTTTTTCCTTTTGGCTGTTCATTTTGGTGGCTACTATAAGGAAATCTAACACAAACAGCAACTGTTTTTTG
TTGTTTACTTTTGCATCTTTACTTGTGGAGCTGTGGCAAGTCCTCATATCAAATACAGAAC**ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGATA**
GCAGCTTTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGCATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCATGTGAACCTTGGA
GCAATAACAGCCAGTTTGCAAAAGGTGGAAAATGATACATCCCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCCTAGGGAAGGCCTCGTTCCACAT
ACCTCAAGTCCAAGTGAGGGACGAAGGACAGTACCAATGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAAAGCTTCCTACAGGA
AAATAAACACTCACATCCTAAAGGTTCCAGAAACAGATGAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAAGTATCCTGGCCAAACGTCAGCGTTC
CTGCCAACACCAGCCACTCCAGGACCCCTGAAGGCCTCTACCAGGTCACCAGTGTTCTGCGCCTAAAGCCACCCCCTGGCAGAAACTTCAGCTGTGTGTTCTGGAATAC
TCACGTGAGGGAACTTACTTTGGCCAGCATTGACCTTCAAAGTCAGATGGAACCCAGGACCCATCCAACTTGGCTGCTTCACATTTTCATCCCCTTCTGCATCATTGCTT
TCATTTTCATAGCCACAGTGATAGCCCTAAGAAAACAACTCTGTCAAAAGCTGTATTCTTCAAAAGACACAACAAAAAGACCTGTCACCACAACAAAGAGGGAAGTGA
ACAGTGCTATCTGAACCTGTGGTCTTGGGAGCCAGGGTGACCTGATATGACATCTAAAGAAGCTTCTGGACTCTGAACAAGAATTCGGTGGCCTGCAGAGCTTGCCATTT
GCACTTTTCAAATGCCTTTGGATGACCCAGCACTTTAATCTGAAACCTGCAACAAGACTAGCCAACACCTGGCCATGAAACTTGCCCCTTCACTGATCTGGACTCACCTCTG
GAGCCTATGGCTTTAAGCAAGCACTACTGCACTTTACAGAATTACCCCACTGGATCCTGGACCCACAGAATTCCTTCAGGATCCTTCTTGCTGCCAGACTGAAAGCAAAAG
GAATTATTTCCCCTCAAGTTTTCTAAGTGATTTCCAAAAGCAGAGGTGTGTGGAAATTTCCAGTAACAGAAACAGATGGGTTGCCAATAGAGTTATTTTTTATCTATAGCTT
CCTCTGGGTACTAGAAGAGGCTATTGAGACTATGAGCTCACAGACAGGGCTTCGCACAAACTCAAATCATAATTGACATGTTTTATGGATTACTGGAATCTTGATAGCAT
AATGAAGTTGTTCTAATTAACAGAGAGCATTTAAATATACACTAAGTGCACAAATTGTGGAGTAAAGTCATCAAGCTCTGTTTTTGAGGTCTAAGTCACAAAGCATTTGTT
TTAACCTGTAATGGCACCATGTTTAATGGTGGTTTTTTTTTTGAACTACATCTTTCCTTTAAAAATTATTGGTTTCTTTTTATTTGTTTTTACCTTAGAAATCAATTATATACAG
TCAAAAATATTTGATATGCTCATACGTTGTATCTGCAGCAATTTCAGATAAGTAGCTAAAATGGCCAAAGCCCCAAACTAAGCCTCCTTTTCTGGCCCTCAATATGACTTTA
AATTTGACTTTTCAGTGCCTCAGTTTGCACATCTGTAATACAGCAATGCTAAGTAGTCAAGGCCTTTGATAATTGGCACTATGGAAATCCTGCAAGATCCCACTACATATGT
GTGGAGCAGAAGGGTAACTCGGCTACAGTAACAGCTTAATTTTGTTAAATTTGTTCTTTATACTGGAGCCATGAAGCTCAGAGCATTAGCTGACCCTTGAACTATTCAAAT
GGGCACATTAGCTAGTATAACAGACTTACATAGGTGGGCCTAAAGCAAGCTCCTTAACTGAGCAAAATTTGGGGCTTATGAGAATGAAAGGGTGTGAAATTGACTAACA
GACAAATCATACATCTCAGTTTCTCAATTCTCATGTAAATCAGAGAATGCCTTTAAAGAATAAAACTCAATTGTTATTCTTCAACGTTCTTTATATATTCTACTTTTGGGTA

>NP_079515.2 programmed cell death 1 ligand 2 precursor [Homo sapiens]
MIFLLLMLSLELQLHQIAALFTVTVPKELYIIEHGSNVTLECNFDTGSHVNLGAITASLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQYQCIIIYGVAWDYKYLTL
KVKASYRKINTHILKVPETDEVELTCQATGYPLAEVSWPNVSVPANTSHSRTPEGLYQVTSVLRLKPPPGRNFSCVFWNTHVRELTLASIDLQSQMEPRTHPTWLLHIFIPFCII
AFIFIATVIALRKQLCQKLYSSKDTTKRPVTTTKREVNSAI

FIG. 4B

Human CTLA-4 (CD152) extracellular domains

>NM_005214.5 Homo sapiens cytotoxic T-lymphocyte associated protein 4 (CTLA4), transcript variant 1, mRNA
GCTTTCTATTCAAGTGCCTTCTGTGTGTGCACATGTGTAATACATATCTGGGATCAAAGCTATCTATATAAAGTCCTTGATTCTGTGTGGGTTCAAACACATTTCAAAGCTT
CAGGATCCTGAAAGGTTTTGCTCTACTTCCTGAAGACCTGAACACCGCTCCCATAAAGCC**ATGGCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTA**
CCAGGACCTGGCCCTGCACTCTCCTGTTTTTTCTTCTCTTCATCCCTGTCTTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGTGGTACTGGCCAGCAGCCGAGGCATC
GCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAAGCCACTGAGGTCCGGGTGACAGTGCTTCGGCAGGCTGACAGCCAGGTGACTGAAGTCTGTGCGGCAACCTA
CATGATGGGGAATGAGTTGACCTTCCTAGATGATTCCATCTGCACGGGCACCTCCAGTGGAAATCAAGTGAACCTCACTATCCAAGGACTGAGGGCCATGGACACGG
GACTCTACATCTGCAAGGTGGAGCTCATGTACCCACCGCCATACTACCTGGGCATAGGCAACGGAACCCAGATTTATGTAATTGATCCAGAACCGTGCCCAGATTCTG
ACTTCCTCCTCTGGATCCTTGCAGCAGTTAGTTCGGGGTTGTTTTTTTATAGCTTTCTCCTCACAGCTGTTTCTTTGAGCAAAATGCTAAAGAAAAGAAGCCCTCTTACA
ACAGGGGTCTATGTGAAAATGCCCCCAACAGAGCCAGAATGTGAAAAGCAATTTCAGCCTTATTTTATTCCCATCAATTGAGAAACCATTATGAAGAAGAGAGTCCAT
ATTTCAATTTCCAAGAGCTGAGGCAATTCTAACTTTTTTGCTATCCAGCTATTTTTATTTGTTTGTGCATTTGGGGGGAATTCATCTCTCTTTAATATAAAGTTGGATGCGG
AACCCAAATTACGTGTACTACAATTTAAAGCAAAGGAGTAGAAAGACAGAGCTGGGATGTTTCTGTCACATCAGCTCCACTTTCAGTGAAAGCATCACTTGGGATTAATA
TGGGGATGCAGCATTATGATGTGGGTCAAGGAATTAAGTTAGGGAATGGCACAGCCCAAAGAAGGAAAAGGCAGGGAGCGAGGGAGAAGACTATATTGTACACACC
TTATATTTACGTATGAGACGTTTATAGCCGAAATGATCTTTTCAAGTTAAATTTTATGCCTTTTATTTCTTAAACAAATGTATGATTACATCAAGGCTTCAAAAATACTCACA
TGGCTATGTTTTAGCCAGTGATGCTAAAGGTTGTATTGCATATATACATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATTTTAATTTGA
TAGTATTGTGCATAGAGCCACGTATGTTTTTGTGTATTTGTTAATGGTTTGAATATAAACACTATATGGCAGTGTCTTTCCACCTTGGGTCCCAGGGAAGTTTTGTGGAGG
AGCTCAGGACACTAATACACCAGGTAGAACACAAGGTCATTTGCTAACTAGCTTGGAAACTGGATGAGGTCATAGCAGTGCTTGATTGCGTGGAATTGTGCTGAGTTGG
TGTTGACATGTGCTTTGGGGCTTTTACACCAGTTCCTTTCAATGGTTTGCAAGGAAGCCACAGCTGGTGGTATCTGAGTTGACTTGACAGAACACTGTCTTGAAGACAAT
GGCTTACTCCAGGAGACCCACAGGTATGACCTTCTAGGAAGCTCCAGTTCGATGGGCCCAATTCTTACAAACATGTGGTTAATGCCATGGACAGAAGAAGGCAGCAGGT
GGCAGAATGGGGTGCATGAAGGTTTCTGAAAATTAACACTGCTTGTGTTTTTAACTCAATATTTTCCATGAAAATGCAACAACATGTATAATATTTTTAATTAAATAAAAA
TCTGTGGTGGTCGTTTTCCGGA

>NP_005205.2 cytotoxic T-lymphocyte protein 4 isoform CTLA4-TM precursor [Homo sapiens]
MACLGFQRHKAQLNLATRTWPCTLLFFLLFIPVFCKAMHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSSGNQ
VNLTIQGLRAMDTGLYICKVELMYPPPYYLGIGNGTQIYVIDPEPCPDSDFLLWILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKMPPTEPECEKQFQPYFIPIN

FIG. 4C

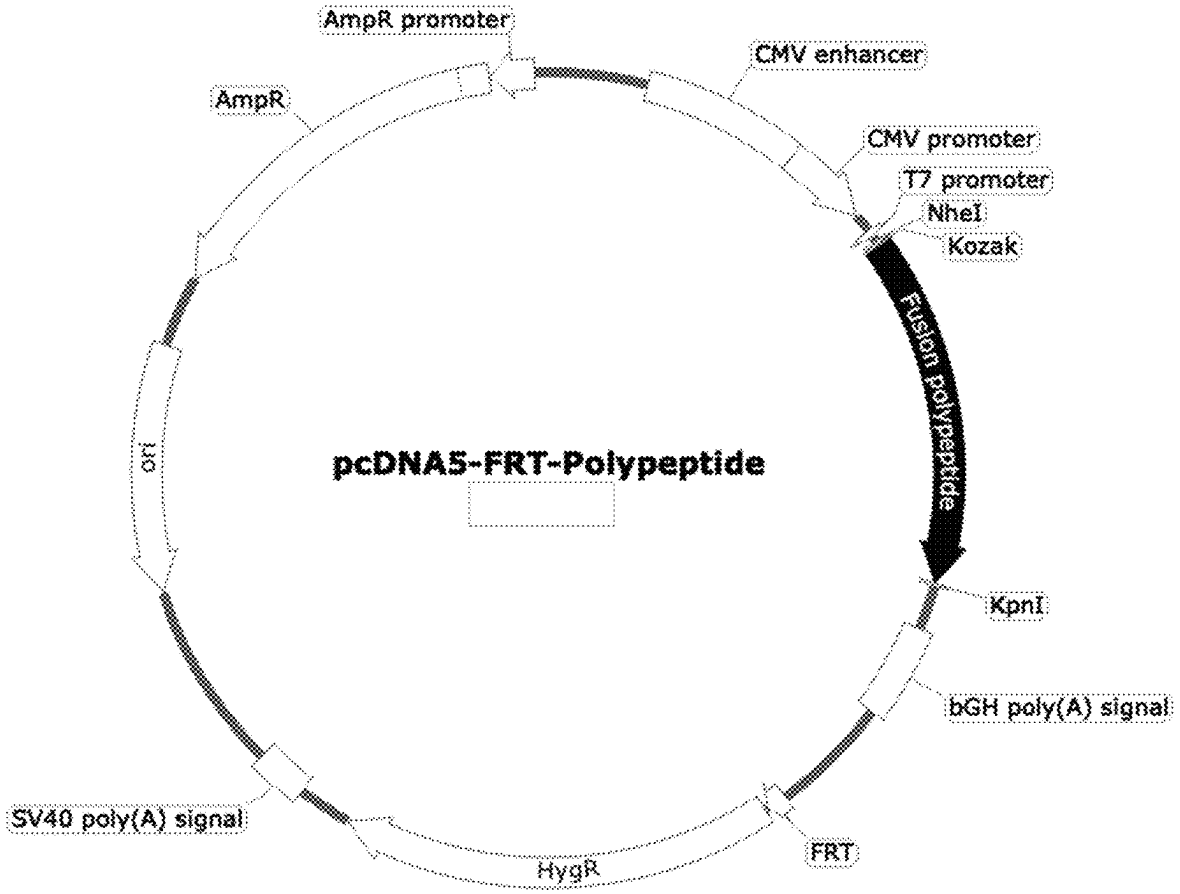

AmpR promoter
CMV enhancer
AmpR
CMV promoter
T7 promoter
NheI
Kozak
Fusion polypeptide
ori
pcDNA5-FRT-Polypeptide
KpnI
bGH poly(A) signal
SV40 poly(A) signal
FRT
HygR

FIG. 5A

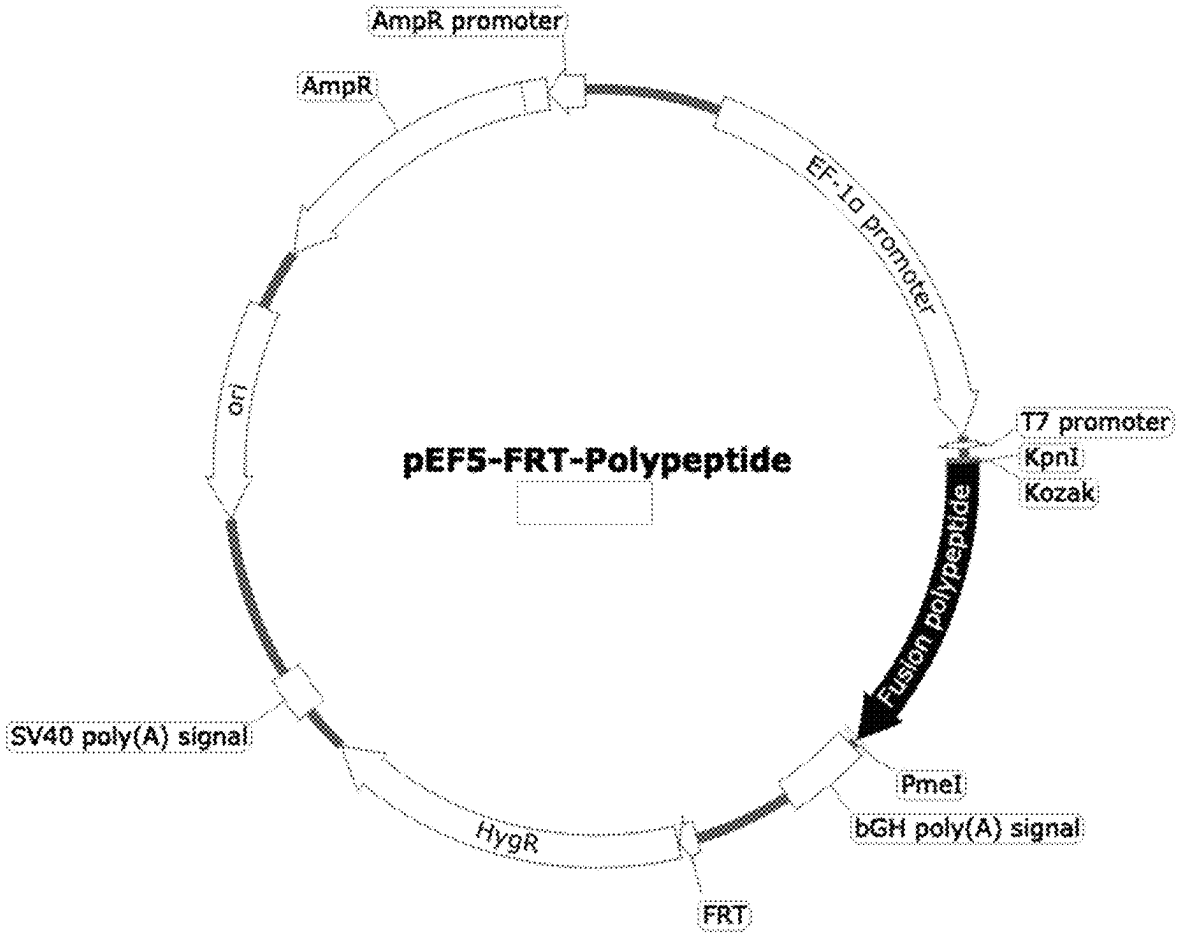

AmpR promoter
AmpR
EF-1α promoter
ori
pEF5-FRT-Polypeptide
T7 promoter
KpnI
Kozak
Fusion polypeptide
SV40 poly(A) signal
PmeI
bGH poly(A) signal
HygR
FRT

FIG. 5B

hCTLA4-Fc-*GPI*

ATGGCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTACCAGGACCTGGCCCTGCACTCTCCTGTTTTTTCTTCTCTTCATCCCT
GTCTTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGTGGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAG
GCAAAGCCACTGAGGTCCGGGTGACAGTGCTTCGGCAGGCTGACAGCCAGGTGACTGAAGTCTGTGCGGCAACCTACATGATGGGGAATGAG
TTGACCTTCCTAGATGATTCCATCTGCACGGGCACCTCCAGTGGAAATCAAGTGAACCTCACTATCCAAGGACTGAGGGCCATGGACACGGGAC
TCTACATCTGCAAGGTGGAGCTCATGTACCCACCGCCATACTACCTGGGCATAGGCAACGGAACCCAGATTTATGTAATTGATCCAGAACCGTGC
CCAGATTCTGACATCGATGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA
ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTC
CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCA
AAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCAC
AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCT*
GGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MACLGFQRHKAQLNLATRTWPCTLLFFLLFIPVFCKAMHVAQPAVVLASSRGIASFV
CEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSSGNQVNL
TIQGLRAMDTGLYICKVELMYPPPYYLGIGNGTQIYVIDPEPCPDSDIDDKTHTCPP
CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*PNKGSGT*
TSGTTRLLSGHTCFTLTGLLGTLVTMGLLT

FIG. 5C

hPDL1-*GPI*-P2A-hHVEM-*GPI*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAG
CAATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTG
TGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATC
ACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAA
CAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAA
GCAGTGACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACA
ACTAATGAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAA
TGAAAGG*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAA*
*CCATGGGCTTGCTGACT*GGAAGCGGAGCTACTAACTTCAGCCTGCTGAAGCAGGCTGGCGACGTGGAGGAGAACCCTGGACCT**ATGGAGCCTCCTGGAGAC**
TGGGGGCCTCCTCCCTGGAGATCCACCCCCAAAACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGAGCCCCCTGCTACGCCCCAGCTCTGCC
GTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAG
TGTGTGAACCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGCG
AGCCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTA
CGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGTCAGAACTGCCCCCCGGGGACCTTCTCTCCCAATGGGA
CCCTGGAGGAATGTCAGCACCAGACCAAGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGCAGCTCCCACTGGGTA*CCAAATAAAGGAAGTGGA*
ACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQI
TDVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTT
TNEIFYCTFRRLDPEENHTAELVIPELPLAHPPNER*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*GSGATNFSLLKQAGDVEENPGP**MEPPGD**
WGPPPWRSTPKTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRA
SRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQHQTKCSWLVTKAGAGTSSSHWV*PNKGSG*
TTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT

FIG. 5D

hPDL1-*GPI*-P2A-FGL1-*GPI*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGC
AATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTGTG
CATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATCACA
GATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAACAAA
ATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGT
GACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAAT
GAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAATGAAAGG
CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGC
*TTGCTGACT*GGAAGCGGAGCTACTAACTTCAGCCTGCTGAAGCAGGCTGGCGACGTGGAGGAGAACCCTGGACCTATGGCAAAGGTGTTCAGTTTCATCCTT
GTTACCACCGCTCTGACAATGGGCAGGGAAATTTCGGCGCTCGAGGACTGTGCCCAGGAGCAGATGCGGCTCAGAGCCCAGGTGCGCCTGCTTGAGACCCGG
GTCAAACAGCAACAGGTCAAGATCAAGCAGCTTTTGCAGGAGAATGAAGTCCAGTTCCTTGATAAAGGAGATGAGAATACTGTCATTGATCTTGGAAGCAAG
AGGCAGTATGCAGATTGTTCAGAGATTTTCAATGATGGGTATAAGCTCAGTGGATTTTACAAAATCAAACCTCTCCAGAGCCCAGCAGAATTTTCTGTTTAT
TGTGACATGTCCGATGGAGGAGGATGGACTGTAATTCAGAGACGATCTGATGGCAGTGAAAACTTTAACAGAGGATGGAAAGACTATGAAAATGGCTTTGGA
AATTTTGTCCAAAAACATGGTGAATATTGGCTGGGCAATAAAAATCTTCACTTCTTGACCACTCAAGAAGACTACACTTTAAAAATCGACCTTGCAGATTTT
GAAAAAAATAGCCGTTATGCACAATATAAGAATTTCAAAGTTGGAGATGAAAAGAATTTCTACGAGTTGAATATTGGGGAATATTCTGGAACAGCTGGAGAT
TCCCTTGCGGGGAATTTTCATCCTGAGGTGCAGTGGTGGGCTAGTCACCAAAGAATGAAATTCAGCACGTGGGACAGAGATCATGACAACTATGAAGGGAAC
TGCGCAGAAGAAGATCAGTCTGGCTGGTGGTTTAACAGGTGTCACTCTGCAAACCTGAATGGTGTATACTACAGCGGCCCCTACACGGCTAAAACAGACAAT
GGGATTGTCTGGTACACCTGGCATGGGTGGTGGTATTCTCTGAAATCTGTGGTTATGAAAATTAGGCCAAATGATTTTATTCCAAATGTAATT*CCAAATAAA*
GGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACT
TAG

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQIT
DVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTTTN
EIFYCTFRRLDPEENHTAELVIPELPLAHPPNER*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*GSGATNFSLLKQAGDVEENPGPMAKVFSFIL
VTTALTMGREISALEDCAQEQMRLRAQVRLLETRVKQQQVKIKQLLQENEVQFLDKGDENTVIDLGSKRQYADCSEIFNDGYKLSGFYKIKPLQSPAEFSVY
CDMSDGGGWTVIQRRSDGSENFNRGWKDYENGFGNFVQKHGEYWLGNKNLHFLTTQEDYTLKIDLADFEKNSRYAQYKNFKVGDEKNFYELNIGEYSGTAGD
SLAGNFHPEVQWWASHQRMKFSTWDRDHDNYEGNCAEEDQSGWWFNRCHSANLNGVYYSGPYTAKTDNGIVWYTWHGWWYSLKSVVMKIRPNDFIPNVI*PNK*
GSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT

FIG. 5E

hPDL1-*GPI*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAG
TATGGTAGCAATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAG
AACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCC
CTGGGAAATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAG
CGAATTACTGTGAAAGTCAATGCCCCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGT
CAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGA
GAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAG
GAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAATGAAAGG*CCAAATAAAGGAAGTGGAACCACTTCAGGT*
ACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLS
LGNAALQITDVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKR
EEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPELPLAHPPNER*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5F

hPDL1-Fc-*GPI*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAG
CAATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTG
TGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATC
ACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAA
CAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAA
GCAGTGACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACA
ACTAATGAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAA
TGAAAGGATCGATGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA
CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG
GTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA
GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCC
TGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT
GGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
GCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATA*
AAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTG
ACTTAG

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQI
TDVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTT
TNEIFYCTFRRLDPEENHTAELVIPELPLAHPPNERIDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLL*
T

FIG. 5G

hPDL2-Fc-*GPI*

ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGATAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGCAT
GGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCATGTGAACCTTGGAGCAATAACAGCCAGTTTGCAAAAGGTGGAAAATGATACATCCCCA
CACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCCTAGGGAAGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGGGACGAAGGACAGTACCAATGC
ATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAAAGCTTCCTACAGGAAAATAAACACTCACATCCTAAAGGTTCCAGAAACA
GATGAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAAGTATCCTGGCCAAACGTCAGCGTTCCTGCCAACACCAGCCACTCCAGGACCCCT
GAAGGCCTCTACCAGGTCACCAGTGTTCTGCGCCTAAAGCCACCCCCTGGCAGAAACTTCAGCTGTGTGTTCTGGAATACTCACGTGAGGGAACTTACTTTG
GCCAGCATTGACCTTCAAAGTCAGATGGAACCCAGGACCCATCCAACTATCGATGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGG
GGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC
TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC
TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGC
CTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGT*
TTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MIFLLLMLSLELQLHQIAALFTVTVPKELYIIEHGSNVTLECNFDTGSHVNLGAITASLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQYQC
IIIYGVAWDYKYLTLKVKASYRKINTHILKVPETDEVELTCQATGYPLAEVSWPNVSVPANTSHSRTPEGLYQVTSVLRLKPPPGRNFSCVFWNTHVRELTL
ASIDLQSQMEPRTHPTIDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5H

hPDL1-*C1C2*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAG
CAATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTG
TGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATC
ACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAA
CAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAA
GCAGTGACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACA
ACTAATGAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAA
TGAAAGGATCGAT*GTCGAGCCACTGGGCATGGAGAATGGGAACATTGCCAACTCACAGATCGCCGCCTCATCTGTGCGTGTGACCTTCTTGGGTTTGCAGC*
ATTGGGTCCCGGAGCTGGCCCGCCTGAACCGCGCAGGCATGGTCAATGCCTGGACACCCAGCAGCAATGACGATAACCCCTGGATCCAGGTGAACCTGCTG
CGGAGGATGTGGGTAACAGGTGTGGTGACGCAGGGTGCCAGCCGCTTGGCCAGTCATGAGTACCTGAAGGCCTTCAAGGTGGCCTACAGCCTTAATGGACA
CGAATTCGATTTCATCCATGATGTTAATAAAAAACACAAGGAGTTTGTGGGTAACTGGAACAAAAACGCGGTGCATGTCAACCTGTTTGAGACCCCTGTGG
AGGCTCAGTACGTGAGATTGTACCCCACGAGCTGCCACACGGCCTGCACTCTGCGCTTTGAGCTACTGGGCTGTGAGCTGAACGGATGCGCCAATCCCCTG
GGCCTGAAGAATAACAGCATCCCTGACAAGCAGATCACGGCCTCCAGCAGCTACAAGACCTGGGGCTTGCATCTCTTCAGCTGGAACCCCTCCTATGCACG
GCTGGACAAGCAGGGCAACTTCAACGCCTGGGTTGCGGGGAGCTACGGTAACGATCAGTGGCTGCAGATCTTCCCTGGCAACTGGGACAACCACTCCCACA
AGAAGAACTTGTTTGAGACGCCCATCCTGGCTCGCTATGTGCGCATCCTGCCTGTAGCCTGGCACAACCGCATCGCCCTGCGCCTGGAGCTGCTGGGCTGT
TAG

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQI
TDVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTT
TNEIFYCTFRRLDPEENHTAELVIPELPLAHPPNERIDVEPLGMENGNIANSQIAASSVRVTFLGLQHWVPELARLNRAGMVNAWTPSSNDDNPWIQVNLL
RRMWVTGVVTQGASRLASHEYLKAFKVAYSLNGHEFDFIHDVNKKHKEFVGNWNKNAVHVNLFETPVEAQYVRLYPTSCHTACTLRFELLGCELNGCANPL
GLKNNSIPDKQITASSSYKTWGLHLFSWNPSYARLDKQGNFNAWVAGSYGNDQWLQIFPGNWDNHSHKKNLFETPILARYVRILPVAWHNRIALRLELLGC

FIG. 5I

hPDL2-*C1C2*

ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGATAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGCA
TGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCATGTGAACCTTGGAGCAATAACAGCCAGTTTGCAAAAGGTGGAAAATGATACATCCC
CACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCCTAGGGAAGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGGGACGAAGGACAGTACCAA
TGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAAAGCTTCCTACAGGAAAATAAACACTCACATCCTAAAGGTTCCAGA
AACAGATGAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAAGTATCCTGGCCAAACGTCAGCGTTCCTGCCAACACCAGCCACTCCAGGA
CCCCTGAAGGCCTCTACCAGGTCACCAGTGTTCTGCGCCTAAAGCCACCCCCTGGCAGAAACTTCAGCTGTGTGTTCTGGAATACTCACGTGAGGGAACTT
ACTTTGGCCAGCATTGACCTTCAAAGTCAGATGGAACCCAGGACCCATCCAACTATCGAT*GTCGAGCCACTGGGCATGGAGAATGGGAACATTGCCAACTC*
ACAGATCGCCGCCTCATCTGTGCGTGTGACCTTCTTGGGTTTGCAGCATTGGGTCCCGGAGCTGGCCCGCCTGAACCGCGCAGGCATGGTCAATGCCTGGA
CACCCAGCAGCAATGACGATAACCCCTGGATCCAGGTGAACCTGCTGCGGAGGATGTGGGTAACAGGTGTGGTGACGCAGGGTGCCAGCCGCTTGGCCAGT
CATGAGTACCTGAAGGCCTTCAAGGTGGCCTACAGCCTTAATGGACACGAATTCGATTTCATCCATGATGTTAATAAAAAACACAAGGAGTTTGTGGGTAA
CTGGAACAAAAACGCGGTGCATGTCAACCTGTTTGAGACCCCTGTGGAGGCTCAGTACGTGAGATTGTACCCCACGAGCTGCCACACGGCCTGCACTCTGC
GCTTTGAGCTACTGGGCTGTGAGCTGAACGGATGCGCCAATCCCCTGGGCCTGAAGAATAACAGCATCCCTGACAAGCAGATCACGGCCTCCAGCAGCTAC
AAGACCTGGGGCTTGCATCTCTTCAGCTGGAACCCCTCCTATGCACGGCTGGACAAGCAGGGCAACTTCAACGCCTGGGTTGCGGGGAGCTACGGTAACGA
TCAGTGGCTGCAGATCTTCCCTGGCAACTGGGACAACCACTCCCACAAGAAGAACTTGTTTGAGACGCCCATCCTGGCTCGCTATGTGCGCATCCTGCCTG
TAGCCTGGCACAACCGCATCGCCCTGCGCCTGGAGCTGCTGGGCTGTTAG

MIFLLLMLSLELQLHQIAALFTVTVPKELYIIEHGSNVTLECNFDTGSHVNLGAITASLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQYQ
CIIIYGVAWDYKYLTLKVKASYRKINTHILKVPETDEVELTCQATGYPLAEVSWPNVSVPANTSHSRTPEGLYQVTSVLRLKPPPGRNFSCVFWNTHVREL
TLASIDLQSQMEPRTHPTIDVEPLGMENGNIANSQIAASSVRVTFLGLQHWVPELARLNRAGMVNAWTPSSNDDNPWIQVNLLRRMWVTGVVTQGASRLAS
HEYLKAFKVAYSLNGHEFDFIHDVNKKHKEFVGNWNKNAVHVNLFETPVEAQYVRLYPTSCHTACTLRFELLGCELNGCANPLGLKNNSIPDKQITASSSY
KTWGLHLFSWNPSYARLDKQGNFNAWVAGSYGNDQWLQIFPGNWDNHSHKKNLFETPILARYVRILPVAWHNRIALRLELLGC

FIG. 5J

4F2-h41BBL

ATGAGCCAGGACACCGAGGTGGATATGAAGGAGGTGGAGCTGAATGAGTTAGAGCCCGAGAAGCAGCCGATGAACGCGGCGTCTGGGGCGGCCATGTCCCTG
GCGGGAGCCGAGAAGAATGGTCTGGTGAAGATCAAGGTGGCGGAAGACGAGGCGGAGGCGGCAGCCGCGGCTAAGTTCACGGGCCTGTCCAAGGAGGAGCTG
CTGAAGGTGGCAGGCAGCCCCGGCTGGGTACGCACCCGCTGGGCACTGCTGCTGCTCTTCTGGCTCGGCTGGCTCGGCATGCTTGCTGGTGCCGTGGTCATA
*ATCGTG***GCCTGCCCCTGGGCCGTGTCCGGGGCTCGCGCCTCGCCCGGCTCCGCGGCCAGCCCGAGACTCCGCGAGGGTCCCGAGCTTTCGCCCGACGATCCC**
GCCGGCCTCTTGGACCTGCGGCAGGGCATGTTTGCGCAGCTGGTGGCCCAAAATGTTCTGCTGATCGATGGGCCCCTGAGCTGGTACAGTGACCCAGGCCTG
GCAGGCGTGTCCCTGACGGGGGGCCTGAGCTACAAAGAGGACACGAAGGAGCTGGTGGTGGCCAAGGCTGGAGTCTACTATGTCTTCTTTCAACTAGAGCTG
CGGCGCGTGGTGGCCGGCGAGGGCTCAGGCTCCGTTTCACTTGCGCTGCACCTGCAGCCACTGCGCTCTGCTGCTGGGGCCGCCGCCCTGGCTTTGACCGTG
GACCTGCCACCCGCCTCCTCCGAGGCTCGGAACTCGGCCTTCGGTTTCCAGGGCCGCTTGCTGCACCTGAGTGCCGGCCAGCGCCTGGGCGTCCATCTTCAC
ACTGAGGCCAGGGCACGCCATGCCTGGCAGCTTACCCAGGGCGCCACAGTCTTGGGACTCTTCCGGGTGACCCCCGAAATCCCAGCCGGACTCCCTTCACCG
AGGTCGGAATAA

MSQDTEVDMKEVELNELEPEKQPMNAASGAAMSLAGAEKNGLVKIKVAEDEAEAAAAAKFTGLSKEELLKVAGSPGWVRTRWALLLLFWLGWLGMLAGAVVI
*IV***ACPWAVSGARASPGSAASPRLREGPELSPDDPAGLLDLRQGMFAQLVAQNVLLIDGPLSWYSDPGLAGVSLTGGLSYKEDTKELVVAKAGVYYVFFQLEL**
RRVVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTPEIPAGLPSP
RSE

FIG. 5K

hPDL1-4Fc-*GPI*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAG
CAATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTG
TGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATC
ACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAA
CAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAA
GCAGTGACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACA
ACTAATGAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAA
TGAAAGGGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGCACCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACA
CTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAG
GTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGGGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGTAA
GGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCC
TGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT
GGGCAGCCGGAGGACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCA
GGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA*CCAAATAAAGGAA*
GTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQI
TDVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTT
TNEIFYCTFRRLDPEENHTAELVIPELPLAHPPNERESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE
VHNAKTKPREEQFNSTYRVVRVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPEDNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5L

Myr-NanoLuc Luciferase

*ATGGGTTGCTGTTTCTCCAAGACC*GGCTCGAGCGGC**GTCTTCACACTCGAAGATTTCGTTGGGGACTGGCGACAGACAGCCGGCTACAACC**
TGGACCAAGTCCTTGAACAGGGAGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACTCCGATCCAAAGGATTGTCCTGAGCGG
TGAAAATGGGCTGAAGATCGACATCCATGTCATCATCCCGTATGAAGGTCTGAGCGGCGACCAAATGGGCCAGATCGAAAAAATTTTTAAG
GTGGTGTACCCTGTGGATGATCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGATCGACT
ATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACAGGGACCCTGTGGAACGGCAACAAAATTATCGA
CGAGCGCCTGATCAACCCCGACGGCTCCCTGCTGTTCCGAGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAACGCATTCTGGCG
TAA

*MGCCFSKT*GSSGVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFK
VVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

FIG. 5M

Myr-mScarlet

*ATGGGTTGCTGTTTCTCCAAGACC*GGCTCGAGCGGC**GTGAGCAAGGGCGAGGCAGTGATCAAGGAGTTCATGCGGTTCAAGGTGCACATGGAG**
GGCTCCATGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCACCCAGACCGCCAAGCTGAAGGTGACCAAG
GGTGGCCCCCTGCCCTTCTCCTGGGACATCCTGTCCCCTCAGTTCATGTACGGCTCCAGGGCCTTCACCAAGCACCCCGCCGACATCCCCGAC
TACTATAAGCAGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGCCGTGACCGTGACCCAGGACACCTCC
CTGGAGGACGGCACCCTGATCTACAAGGTGAAGCTCCGCGGCACCAACTTCCCTCCTGACGGCCCCGTAATGCAGAAGAAGACAATGGGCTGG
GAAGCGTCCACCGAGCGGTTGTACCCCGAGGACGGCGTGCTGAAGGGCGACATTAAGATGGCCCTGCGCCTGAAGGACGGCGGCCGCTACCTG
GCGGACTTCAAGACCACCTACAAGGCCAAGAAGCCCGTGCAGATGCCCGGCGCCTACAACGTCGACCGCAAGTTGGACATCACCTCCCACAAC
GAGGACTACACCGTGGTGGAACAGTACGAACGCTCCGAGGGCCGCCACTCCACCGGCGGCATGGACGAGCTGTACAAG

*MGCCFSKT*GSSG**VSKGEAVIKEFMRFKVHMEGSMNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFSWDILSPQFMYGSRAFTKHPADIPD**
YYKQSFPEGFKWERVMNFEDGGAVTVTQDTSLEDGTLIYKVKLRGTNFPPDGPVMQKKTMGWEASTERLYPEDGVLKGDIKMALRLKDGGRYL
ADFKTTYKAKKPVQMPGAYNVDRKLDITSHNEDYTVVEQYERSEGRHSTGGMDELYK

FIG. 5N

hSecPDL1-*GPI*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGC
AATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTGTG
CATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATCACA
GATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAACAAA
ATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGT
GACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAAT
GAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGGTAATATTCTGAATGTGTCCATTAAAATATGT
CTAACACTGTCCCCTAGCACC*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTT*
GGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQIT
DVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTTTN
EIFYCTFRRLDPEENHTAELVIPGNILNVSIKICLTLSPST*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5O

Tfr2-h41BBL

ATGGAGCGGCTTTGGGGTCTATTCCAGAGAGCGCAACAACTGTCCCCAAGATCCTCTCAGACCGTCTACCAGCGTGTGGAAGGCCCCCGGAAAGGGCACCTGG
AGGAGGAAGAGGAAGACGGGGAGGAGGGGGCGGAGACATTGGCCCACTTCTGCCCCATGGAGCTGAGGGGCCCTGAGCCCCTGGGCTCTAGACCCAGGCAGCC
AAACCTCATTCCCTGGGCGGCAGCAGGACGGAGGGCTGCCCCCTACCTGGTCCTGACGGCCCTGCTGATCTTCACTGGGGCCTTCCTACTGGGCTACGTCGCC
*TTCCGAGGGTCC**GCCTGCCCCTGGGCCGTGTCCGGGGCTCGCGCCTCGCCCGGCTCCGCGGCCAGCCCGAGACTCCGCGAGGGTCCCGAGCTTTCGCCCGACG***
ATCCCGCCGGCCTCTTGGACCTGCGGCAGGGCATGTTTGCGCAGCTGGTGGCCCAAAATGTTCTGCTGATCGATGGGCCCCTGAGCTGGTACAGTGACCCAGG
CCTGGCAGGCGTGTCCCTGACGGGGGGCCTGAGCTACAAAGAGGACACGAAGGAGCTGGTGGTGGCCAAGGCTGGAGTCTACTATGTCTTCTTTCAACTAGAG
CTGCGGCGCGTGGTGGCCGGCGAGGGCTCAGGCTCCGTTTCACTTGCGCTGCACCTGCAGCCACTGCGCTCTGCTGCTGGGGCCGCCGCCCTGGCTTTGACCG
TGGACCTGCCACCCGCCTCCTCCGAGGCTCGGAACTCGGCCTTCGGTTTCCAGGGCCGCTTGCTGCACCTGAGTGCCGGCCAGCGCCTGGGCGTCCATCTTCA
CACTGAGGCCAGGGCACGCCATGCCTGGCAGCTTACCCAGGGCGCCACAGTCTTGGGACTCTTCCGGGTGACCCCCGAAATCCCAGCCGGACTCCCTTCACCG
AGGTCGGAATAA

MERLWGLFQRAQQLSPRSSQTVYQRVEGPRKGHLEEEEEDGEEGAETLAHFCPMELRGPEPLGSRPRQPNLIPWAAAGRRAAPYLVLTALLIFTGAFLLGYVA
*FRGS***ACPWAVSGARASPGSAASPRLRGPELSPDDPAGLLDLRQGMFAQLVAQNVLLIDGPLSWYSDPGLAGVSLTGGLSYKEDTKELVVAKAGVYYVFFQLEL**
RRVVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTPEIPAGLPSPR
SE

FIG. 5P

CD9tm3-h41BBL

ATGGGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGCATGCTGGGACTGTTCTTCGGCTTCCTCTTGGTGATATTCGCCATTGAAATAGCT
*GCGGCCATCTGGGGATATTCCCACAAGGATGAG***GCCTGCCCCTGGGCCGTGTCCGGGGCTCGCGCCTCGCCCGGCTCCGCGGCCAGCCCG**
AGACTCCGCGAGGGTCCCGAGCTTTCGCCCGACGATCCCGCCGGCCTCTTGGACCTGCGGCAGGGCATGTTTGCGCAGCTGGTGGCCCAA
AATGTTCTGCTGATCGATGGGCCCCTGAGCTGGTACAGTGACCCAGGCCTGGCAGGCGTGTCCCTGACGGGGGGCCTGAGCTACAAAGAG
GACACGAAGGAGCTGGTGGTGGCCAAGGCTGGAGTCTACTATGTCTTCTTTCAACTAGAGCTGCGGCGCGTGGTGGCCGGCGAGGGCTCA
GGCTCCGTTTCACTTGCGCTGCACCTGCAGCCACTGCGCTCTGCTGCTGGGGCCGCCGCCCTGGCTTTGACCGTGGACCTGCCACCCGCC
TCCTCCGAGGCTCGGAACTCGGCCTTCGGTTTCCAGGGCCGCTTGCTGCACCTGAGTGCCGGCCAGCGCCTGGGCGTCCATCTTCACACT
GAGGCCAGGGCACGCCATGCCTGGCAGCTTACCCAGGGCGCCACAGTCTTGGGACTCTTCCGGGTGACCCCCGAAATCCCAGCCGGACTC
CCTTCACCGAGGTCGGAATAA

*MGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDE***ACPWAVSGARASPGSAASPRLREGPELSPDDPAGLLDLRQGMFAQLVAQ**
NVLLIDGPLSWYSDPGLAGVSLTGGLSYKEDTKELVVAKAGVYYVFFQLELRRVVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPPA
SSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTPEIPAGLPSPRSE

FIG. 5Q

Myr/Palm-*4F2*-h41BBL

*ATGGGTTGCTGTTTCTCCAAGACC*GGCTCGAGCGGC*AGCCAGGACACCGAGGTGGATATGAAGGAGGTGGAGCTGAATGAGTTAGAGCCCGAGAAGCAGCCGA*
TGAACGCGGCGTCTGGGGCGGCCATGTCCCTGGCGGGAGCCGAGAAGAATGGTCTGGTGAAGATCAAGGTGGCGGAAGACGAGGCGGAGGCGGCAGCCGCGGC
TAAGTTCACGGGCCTGTCCAAGGAGGAGCTGCTGAAGGTGGCAGGCAGCCCCGGCTGGGTACGCACCCGCTGGGCACTGCTGCTGCTCTTCTGGCTCGGCTGG
*CTCGGCATGCTTGCTGGTGCCGTGGTCATAATCGTG***GCCTGCCCCTGGGCCGTGTCCGGGGCTCGCGCCTCGCCCGGCTCCGCGGCCAGCCCGAGACTCCGCG**
AGGGTCCCGAGCTTTCGCCCGACGATCCCGCCGGCCTCTTGGACCTGCGGCAGGGCATGTTTGCGCAGCTGGTGGCCCAAAATGTTCTGCTGATCGATGGGCC
CCTGAGCTGGTACAGTGACCCAGGCCTGGCAGGCGTGTCCCTGACGGGGGGCCTGAGCTACAAAGAGGACACGAAGGAGCTGGTGGTGGCCAAGGCTGGAGTC
TACTATGTCTTCTTTCAACTAGAGCTGCGGCGCGTGGTGGCCGGCGAGGGCTCAGGCTCCGTTTCACTTGCGCTGCACCTGCAGCCACTGCGCTCTGCTGCTG
GGGCCGCCGCCCTGGCTTTGACCGTGGACCTGCCACCCGCCTCCTCCGAGGCTCGGAACTCGGCCTTCGGTTTCCAGGGCCGCTTGCTGCACCTGAGTGCCGG
CCAGCGCCTGGGCGTCCATCTTCACACTGAGGCCAGGGCACGCCATGCCTGGCAGCTTACCCAGGGCGCCACAGTCTTGGGACTCTTCCGGGTGACCCCCGAA
ATCCCAGCCGGACTCCCTTCACCGAGGTCGGAATAA

*MGCCFSKT*GSSGSQDTEVDMKEVELNELEPEKQPMNAASGAAMSLAGAEKNGLVKIKVAEDEAEAAAAAKFTGLSKEELLKVAGSPGWVRTRWALLLLFWLGW
*LGMLAGAVVIIV***ACPWAVSGARASPGSAASPRLREGPELSPDDPAGLLDLRQGMFAQLVAQNVLLIDGPLSWYSDPGLAGVSLTGGLSYKEDTKELVVAKAGV**
YYVFFQLELRRVVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTPE
IPAGLPSPRSE

FIG. 5R

Myr/Palm-Link-41BBL

*ATGGGTTGCTGTTTCTCCAAGACC*GGCTCGAGCGGCTGGGCCCTGGTCGCGGGGCTGCTGCTGCTGCTGCTGCTCGCTGCCGCCTGCGCCGTCTTCCTCGCC
TGCCCCTGGGCCGTGTCCGGGGCTCGCGCCTCGCCCGGCTCCGCGGCCAGCCCGAGACTCCGCGAGGGTCCCGAGCTTTCGCCCGACGATCCCGCCGGCCTC
TTGGACCTGCGGCAGGGCATGTTTGCGCAGCTGGTGGCCCAAAATGTTCTGCTGATCGATGGGCCCCTGAGCTGGTACAGTGACCCAGGCCTGGCAGGCGTG
TCCCTGACGGGGGGCCTGAGCTACAAAGAGGACACGAAGGAGCTGGTGGTGGCCAAGGCTGGAGTCTACTATGTCTTCTTTCAACTAGAGCTGCGGCGCGTG
GTGGCCGGCGAGGGCTCAGGCTCCGTTTCACTTGCGCTGCACCTGCAGCCACTGCGCTCTGCTGCTGGGGCCGCCGCCCTGGCTTTGACCGTGGACCTGCCA
CCCGCCTCCTCCGAGGCTCGGAACTCGGCCTTCGGTTTCCAGGGCCGCTTGCTGCACCTGAGTGCCGGCCAGCGCCTGGGCGTCCATCTTCACACTGAGGCC
AGGGCACGCCATGCCTGGCAGCTTACCCAGGGCGCCACAGTCTTGGGACTCTTCCGGGTGACCCCCGAAATCCCAGCCGGACTCCCTTCACCGAGGTCGGAA
TAA

*MGCCFSKT*GSSG***WALVAGLLLLLLLAAACAVFLACPWAVSGARASPGSAASPRLREGPELSPDDPAGLLDLRQGMFAQLVAQNVLLIDGPLSWYSDPGLAGV***
SLTGGLSYKEDTKELVVAKAGVYYVFFQLELRRVVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEA
RARHAWQLTQGATVLGLFRVTPEIPAGLPSPRSE

FIG. 5S

hPDL1-Link-*GPI*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGA
GTATGGTAGCAATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATA
AGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTC
TCCCTGGGAAATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTA
CAAGCGAATTACTGTGAAAGTCAATGCCCCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGA
CATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCC
AAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGCACTTTTAGGAGATTAGA
TCCTGAGGAAAACCATACAGCTGAATTGGGCTCGAGCGGC*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGC*
ACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQL
SLGNAALQITDVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNS
KREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELGSSG*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5T

hSecPDL1-*CD9tm2*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTA
GCAATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATT
TGTGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAG
ATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCAT
ACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTG
GACAAGCAGTGACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAAC
ACAACAACTAATGAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGGTAATATTCTGAATGTGT
CCATTAAAATATGTCTAACACTGTCCCCTAGCACC*TTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGG*
CTGCTGCGGGGCTGTGCAGGAGTCCCAGTGCTAG

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQ
ITDVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRIN
TTTNEIFYCTFRRLDPEENHTAELVIPGNILNVSIKICLTLSPST*FYTGVYILIGAGALMMLVGFLGCCGAVQESQC*

FIG. 5U

hSecPDL1-*CD9tm2*-*KRAS*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGC
AATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTGTG
CATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATCACA
GATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAACAAA
ATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGT
GACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAAT
GAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGGTAATATTCTGAATGTGTCCATTAAAATATGT
CTAACACTGTCCCCTAGCACC*TTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTG*
CAGGAGTCCCAGTGC<u>*AAAAAGAAGAAAAAGAAGTCAAAGACAAAGTGTGTAATTATGTAA*</u>

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQIT
DVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTTTN
EIFYCTFRRLDPEENHTAELVIPGNILNVSIKICLTLSPST*FYTGVYILIGAGALMMLVGFLGCCGAVQESQC*<u>*KKKKKKKSKTKCVIM*</u>

FIG. 5V

hSecPDL1-*CD9tm4*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAG
CAATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTG
TGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATC
ACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAA
CAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAA
GCAGTGACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACA
ACTAATGAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGGTAATATTCTGAATGTGTCCATTAA
AATATGTCTAACACTGTCCCCTAGCACC*ATCGGCGCAGTGGGCATCGGCATTGCCGTGGTCATGATATTTGGCATGATCTTCAGTATGATCTTGTGCTGTG*
CTATCCGCAGGAACCGCGAGATGGTCTAG

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQI
TDVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTT
TNEIFYCTFRRLDPEENHTAELVIPGNILNVSIKICLTLSPST*IGAVGIGIAVVMIFGMIFSMILCCAIRRNREMV*

FIG. 5W

hSecPDL1-*CD81*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATAT
GACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGG
AAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATCACAGATGTGAAATTGCAG
GATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAACAAAATCAACCAAAGAATTTTGGT
TGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAAGTCCTGAGTGGTAAGA
CCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGCACTTTTAGGAGATTA
GATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGGTAATATTCTGAATGTGTCCATTAAAATATGTCTAACACTGTCCCCTAGCACC*CTGTACCTCATCGG*
CATTGCTGCCATCGTGGTCGCTGTGATCATGATCTTCGAGATGATCCTGAGCATGGTGCTGTGCTGTGGCATCCGGAACAGCTCCGTGTACTGA

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQ
DAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRL
DPEENHTAELVIPGNILNVSIKICLTLSPST*LYLIGIAAIVVAVIMIFEMILSMVLCCGIRNSSVY*

FIG. 5X

hCD200-Fc-*GPI*

ATGGAGAGGCTGGTGATCAGGATGCCCTTCTCTCATCTGTCTACCTACAGCCTGGTTTGGGTCATGGCAGCAGTGGTGCTGTGCACAGCACAAGTGCAAGTGGTGAC
CCAGGATGAAAGAGAGCAGCTGTACACACCTGCTTCCTTAAAATGCTCTCTGCAAAATGCCCAGGAAGCCCTCATTGTGACATGGCAGAAAAAGAAAGCTGTAAGCC
CAGAAAACATGGTCACCTTCAGCGAGAACCATGGGGTGGTGATCCAGCCTGCCTATAAGGACAAGATAAACATTACCCAGCTGGGACTCCAAAACTCAACCATCACC
TTCTGGAATATCACCCTGGAGGATGAAGGGTGTTACATGTGTCTCTTCAATACCTTTGGTTTTGGGAAGATCTCAGGAACGGCCTGCCTCACCGTCTATGTACAGCC
CATAGTATCCCTTCACTACAAATTCTCTGAAGACCACCTAAATATCACTTGCTCTGCCACTGCCCGCCCAGCCCCCATGGTCTTCTGGAAGGTCCCTCGGTCAGGGA
TTGAAAATAGTACAGTGACTCTGTCTCACCCAAATGGGACCACGTCTGTTACCAGCATCCTCCATATCAAAGACCCTAAGAATCAGGTGGGGAAGGAGGTGATCTGC
CAGGTGCTGCACCTGGGGACTGTGACCGACTTTAAGCAAACCGTCAACAAAGGCATCGATGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGG
GGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTG
AGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACC
GTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCC
CCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CC*
AAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGA
CTTAG

MERLVIRMPFSHLSTYSLVWVMAAVVLCTAQVQVVTQDEREQLYTPASLKCSLQNAQEALIVTWQKKKAVSPENMVTFSENHGVVIQPAYKDKINITQLGLQNSTIT
FWNITLEDEGCYMCLFNTFGFGKISGTACLTVYVQPIVSLHYKFSEDHLNITCSATARPAPMVFWKVPRSGIENSTVTLSHPNGTTSVTSILHIKDPKNQVGKEVIC
QVLHLGTVTDFKQTVNKGIDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5Y

hFGL1-*GPI*

ATGGCAAAGGTGTTCAGTTTCATCCTTGTTACCACCGCTCTGACAATGGGCAGGGAAATTTCGGCGCTCGAGGACTGTGCCCAGGAGCAGATGCGGCTCA
GAGCCCAGGTGCGCCTGCTTGAGACCCGGGTCAAACAGCAACAGGTCAAGATCAAGCAGCTTTTGCAGGAGAATGAAGTCCAGTTCCTTGATAAAGGAGA
TGAGAATACTGTCATTGATCTTGGAAGCAAGAGGCAGTATGCAGATTGTTCAGAGATTTTCAATGATGGGTATAAGCTCAGTGGATTTTACAAAATCAAA
CCTCTCCAGAGCCCAGCAGAATTTTCTGTTTATTGTGACATGTCCGATGGAGGAGGATGGACTGTAATTCAGAGACGATCTGATGGCAGTGAAAACTTTA
ACAGAGGATGGAAAGACTATGAAAATGGCTTTGGAAATTTTGTCCAAAAACATGGTGAATATTGGCTGGGCAATAAAAATCTTCACTTCTTGACCACTCA
AGAAGACTACACTTTAAAAATCGACCTTGCAGATTTTGAAAAAAATAGCCGTTATGCACAATATAAGAATTTCAAAGTTGGAGATGAAAAGAATTTCTAC
GAGTTGAATATTGGGGAATATTCTGGAACAGCTGGAGATTCCCTTGCGGGGAATTTTCATCCTGAGGTGCAGTGGTGGGCTAGTCACCAAAGAATGAAAT
TCAGCACGTGGGACAGAGATCATGACAACTATGAAGGGAACTGCGCAGAAGAAGATCAGTCTGGCTGGTGGTTTAACAGGTGTCACTCTGCAAACCTGAA
TGGTGTATACTACAGCGGCCCCTACACGGCTAAAACAGACAATGGGATTGTCTGGTACACCTGGCATGGGTGGTGGTATTCTCTGAAATCTGTGGTTATG
AAAATTAGGCCAAATGATTTTATTCCAAATGTAATT*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCA*
CGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MAKVFSFILVTTALTMGREISALEDCAQEQMRLRAQVRLLETRVKQQQVKIKQLLQENEVQFLDKGDENTVIDLGSKRQYADCSEIFNDGYKLSGFYKIK
PLQSPAEFSVYCDMSDGGGWTVIQRRSDGSENFNRGWKDYENGFGNFVQKHGEYWLGNKNLHFLTTQEDYTLKIDLADFEKNSRYAQYKNFKVGDEKNFY
ELNIGEYSGTAGDSLAGNFHPEVQWWASHQRMKFSTWDRDHDNYEGNCAEEDQSGWWFNRCHSANLNGVYYSGPYTAKTDNGIVWYTWHGWWYSLKSVVM
KIRPNDFIPNVI*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5Z

hGal9-Fc-*GPI*

ATGGCCTTCAGCGGTTCCCAGGCTCCCTACCTGAGTCCAGCTGTCCCCTTTTCTGGGACTATTCAAGGAGGTCTCCAGGACGGACTTCAGATCACTGTCAATGGGACC
GTTCTCAGCTCCAGTGGAACCAGGTTTGCTGTGAACTTTCAGACTGGCTTCAGTGGAAATGACATTGCCTTCCACTTCAACCCTCGGTTTGAAGATGGAGGGTACGTG
GTGTGCAACACGAGGCAGAACGGAAGCTGGGGGCCCGAGGAGAGGAAGACACACATGCCTTTCCAGAAGGGGATGCCCTTTGACCTCTGCTTCCTGGTGCAGAGCTCA
GATTTCAAGGTGATGGTGAACGGGATCCTCTTCGTGCAGTACTTCCACCGCGTGCCCTTCCACCGTGTGGACACCATCTCCGTCAATGGCTCTGTGCAGCTGTCCTAC
ATCAGCTTCCAGAACCCCCGCACAGTCCCTGTTCAGCCTGCCTTCTCCACGGTGCCGTTCTCCCAGCCTGTCTGTTTCCCACCCAGGCCCAGGGGGCGCAGACAAAAA
CCTCCCGGCGTGTGGCCTGCCAACCCGGCTCCCATTACCCAGACAGTCATCCACACAGTGCAGAGCGCCCCTGGACAGATGTTCTCTACTCCCGCCATCCCACCTATG
ATGTACCCCCACCCCGCCTATCCGATGCCTTTCATCACCACCATTCTGGGAGGGCTGTACCCATCCAAGTCCATCCTCCTGTCAGGCACTGTCCTGCCCAGTGCTCAG
AGGTTCCACATCAACCTGTGCTCTGGGAACCACATCGCCTTCCACCTGAACCCCCGTTTTGATGAGAATGCTGTGGTCCGCAACACCCAGATCGACAACTCCTGGGGG
TCTGAGGAGCGAAGTCTGCCCCGAAAAATGCCCTTCGTCCGTGGCCAGAGCTTCTCAGTGTGGATCTTGTGTGAAGCTCACTGCCTCAAGGTGGCCGTGGATGGTCAG
CACCTGTTTGAATACTACCATCGCCTGAGGAACCTGCCCACCATCAACAGACTGGAAGTGGGGGGCGACATCCAGCTGACCCATGTGCAGACAATCGATGACAAAACT
CACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC
ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGC
CTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAG
AGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTG*
CTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAFHFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSS
DFKVMVNGILFVQYFHRVPFHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQKPPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPM
MYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQ
HLFEYYHRLRNLPTINRLEVGGDIQLTHVQTIDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5AA

hCD200-*GPI*

ATGGAGAGGCTGGTGATCAGGATGCCCTTCTCTCATCTGTCTACCTACAGCCTGGTTTGGGTCATGGCAGCAGTGGTGCTGTGCACAGCACAAGTGCAAGT
GGTGACCCAGGATGAAAGAGAGCAGCTGTACACACCTGCTTCCTTAAAATGCTCTCTGCAAAATGCCCAGGAAGCCCTCATTGTGACATGGCAGAAAAAGA
AAGCTGTAAGCCCAGAAAACATGGTCACCTTCAGCGAGAACCATGGGGTGGTGATCCAGCCTGCCTATAAGGACAAGATAAACATTACCCAGCTGGGACTC
CAAAACTCAACCATCACCTTCTGGAATATCACCCTGGAGGATGAAGGGTGTTACATGTGTCTCTTCAATACCTTTGGTTTTGGGAAGATCTCAGGAACGGC
CTGCCTCACCGTCTATGTACAGCCCATAGTATCCCTTCACTACAAATTCTCTGAAGACCACCTAAATATCACTTGCTCTGCCACTGCCCGCCCAGCCCCCA
TGGTCTTCTGGAAGGTCCCTCGGTCAGGGATTGAAAATAGTACAGTGACTCTGTCTCACCCAAATGGGACCACGTCTGTTACCAGCATCCTCCATATCAAA
GACCCTAAGAATCAGGTGGGGAAGGAGGTGATCTGCCAGGTGCTGCACCTGGGGACTGTGACCGACTTTAAGCAAACCGTCAACAAAGGC*CCAAATAAAGG*
AAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTT
AG

MERLVIRMPFSHLSTYSLVWVMAAVVLCTAQVQVVTQDEREQLYTPASLKCSLQNAQEALIVTWQKKKAVSPENMVTFSENHGVVIQPAYKDKINITQLGL
QNSTITFWNITLEDEGCYMCLFNTFGFGKISGTACLTVYVQPIVSLHYKFSEDHLNITCSATARPAPMVFWKVPRSGIENSTVTLSHPNGTTSVTSILHIK
DPKNQVGKEVICQVLHLGTVTDFKQTVNKG*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5BB

hGal9-*GPI*

ATGGCCTTCAGCGGTTCCCAGGCTCCCTACCTGAGTCCAGCTGTCCCCTTTTCTGGGACTATTCAAGGAGGTCTCCAGGACGGACTTCAGATCACTGTCAATGGGACC
GTTCTCAGCTCCAGTGGAACCAGGTTTGCTGTGAACTTTCAGACTGGCTTCAGTGGAAATGACATTGCCTTCCACTTCAACCCTCGGTTTGAAGATGGAGGGTACGTG
GTGTGCAACACGAGGCAGAACGGAAGCTGGGGGCCCGAGGAGAGGAAGACACACATGCCTTTCCAGAAGGGGATGCCCTTTGACCTCTGCTTCCTGGTGCAGAGCTCA
GATTTCAAGGTGATGGTGAACGGGATCCTCTTCGTGCAGTACTTCCACCGCGTGCCCTTCCACCGTGTGGACACCATCTCCGTCAATGGCTCTGTGCAGCTGTCCTAC
ATCAGCTTCCAGAACCCCCGCACAGTCCCTGTTCAGCCTGCCTTCTCCACGGTGCCGTTCTCCCAGCCTGTCTGTTTCCCACCCAGGCCCAGGGGGCGCAGACAAAAA
CCTCCCGGCGTGTGGCCTGCCAACCCGGCTCCCATTACCCAGACAGTCATCCACACAGTGCAGAGCGCCCCTGGACAGATGTTCTCTACTCCCGCCATCCCACCTATG
ATGTACCCCCACCCCGCCTATCCGATGCCTTTCATCACCACCATTCTGGGAGGGCTGTACCCATCCAAGTCCATCCTCCTGTCAGGCACTGTCCTGCCCAGTGCTCAG
AGGTTCCACATCAACCTGTGCTCTGGGAACCACATCGCCTTCCACCTGAACCCCCGTTTTGATGAGAATGCTGTGGTCCGCAACACCCAGATCGACAACTCCTGGGGG
TCTGAGGAGCGAAGTCTGCCCCGAAAAATGCCCTTCGTCCGTGGCCAGAGCTTCTCAGTGTGGATCTTGTGTGAAGCTCACTGCCTCAAGGTGGCCGTGGATGGTCAG
CACCTGTTTGAATACTACCATCGCCTGAGGAACCTGCCCACCATCAACAGACTGGAAGTGGGGGGCGACATCCAGCTGACCCATGTGCAGACA*CCAAATAAAGGAAGT*
GGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAFHFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSS
DFKVMVNGILFVQYFHRVPFHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQKPPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPM
MYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQ
HLFEYYHRLRNLPTINRLEVGGDIQLTHVQT*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5CC

hHVEM-*GPI*

ATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGGAGATCCACCCCCAAAACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGG
AGCCCCCTGCTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTTATC
GTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAG
TGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGCGAGCCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGCTGCAGCCC
AGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAGGGAG
GCACCGAGAGTCAGGACACCCTGTGTCAGAACTGCCCCCCGGGGACCTTCTCTCCCAATGGGACCCTGGAGGAATGTCAGCACCAGACCAAG
TGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGCAGCTCCCACTGGGTA*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCG*
TCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MEPPGDWGPPPWRSTPKTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSK
CLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQHQTK
CSWLVTKAGAGTSSSHWV*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5DD

hPDL2-*GPI*

ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGATAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAACTGTACATAA
TAGAGCATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCATGTGAACCTTGGAGCAATAACAGCCAGTTTGCAAAAGGTGGA
AAATGATACATCCCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCCTAGGGAAGGCCTCGTTCCACATACCTCAAGTCCAAGTG
AGGGACGAAGGACAGTACCAATGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAAAGCTTCCTACAGGAAAA
TAAACACTCACATCCTAAAGGTTCCAGAAACAGATGAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAAGTATCCTGGCCAAA
CGTCAGCGTTCCTGCCAACACCAGCCACTCCAGGACCCCTGAAGGCCTCTACCAGGTCACCAGTGTTCTGCGCCTAAAGCCACCCCCTGGCAGA
AACTTCAGCTGTGTGTTCTGGAATACTCACGTGAGGGAACTTACTTTGGCCAGCATTGACCTTCAAAGTCAGATGGAACCCAGGACCCATCCAA
CT*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGT*
AACCATGGGCTTGCTGACTTAG

MIFLLLMLSLELQLHQIAALFTVTVPKELYIIEHGSNVTLECNFDTGSHVNLGAITASLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQV
RDEGQYQCIIIYGVAWDYKYLTLKVKASYRKINTHILKVPETDEVELTCQATGYPLAEVSWPNVSVPANTSHSRTPEGLYQVTSVLRLKPPPGR
NFSCVFWNTHVRELTLASIDLQSQMEPRTHPT*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5EE

hTSG6-*GPI*

ATGATCATCTTAATTTACTTATTTCTCTTGCTATGGGAAGACACTCAAGGATGGGGATTCAAGGATGGAATTTTTCATAACTCCATATGGC
TTGAACGAGCAGCCGGTGTGTACCACAGAGAAGCACGGTCTGGCAAATACAAGCTCACCTACGCAGAAGCTAAGGCGGTGTGTGAATTTGA
AGGCGGCCATCTCGCAACTTACAAGCAGCTAGAGGCAGCCAGAAAAATTGGATTTCATGTCTGTGCTGCTGGATGGATGGCTAAGGGCAGA
GTTGGATACCCCATTGTGAAGCCAGGGCCCAACTGTGGATTTGGAAAAACTGGCATTATTGATTATGGAATCCGTCTCAATAGGAGTGAAA
GATGGGATGCCTATTGCTACAACCCACACGCAAAGGAGTGTGGTGGCGTCTTTACAGATCCAAAGCAAATTTTTAAATCTCCAGGCTTCCC
AAATGAGTACGAAGATAACCAAATCTGCTACTGGCACATTAGACTCAAGTATGGTCAGCGTATTCACCTGAGTTTTTTAGATTTTGACCTT
GAAGATGACCCAGGTTGCTTGGCTGATTATGTTGAAATATATGACAGTTACGATGATGTCCATGGCTTTGTGGGAAGATACTGTGGAGATG
AGCTTCCAGATGACATCATCAGTACAGGAAATGTCATGACCTTGAAGTTTCTAAGTGATGCTTCAGTGACAGCTGGAGGTTTCCAAATCAA
ATATGTTGCAATGGATCCTGTATCCAAATCCAGTCAAGGAAAAAATACAAGTACTACTTCTACTGGAAATAAAAACTTTTTAGCTGGAAGA
TTTAGCCACTTAATCGAT*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAG*
GTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MIILIYLFLLLWEDTQGWGFKDGIFHNSIWLERAAGVYHREARSGKYKLTYAEAKAVCEFEGGHLATYKQLEAARKIGFHVCAAGWMAKGR
VGYPIVKPGPNCGFGKTGIIDYGIRLNRSERWDAYCYNPHAKECGGVFTDPKQIFKSPGFPNEYEDNQICYWHIRLKYGQRIHLSFLDFDL
EDDPGCLADYVEIYDSYDDVHGFVGRYCGDELPDDIISTGNVMTLKFLSDASVTAGGFQIKYVAMDPVSKSSQGKNTSTTSTGNKNFLAGR
FSHLID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5FF

hHVEM-Fc-*GPI*

ATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGGAGATCCACCCCCAAAACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGAGCCCCCTGCTACGCC
CCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGC
ACAGTGTGTGAACCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGCGAGC
CGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCC
AGCCCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGTCAGAACTGCCCCCCGGGGACCTTCTCTCCCAATGGGACCCTGGAGGAATGTCAG
CACCAGACCAAGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGCAGCTCCCACTGGGTAATCGATGACAAAACTCACACATGCCCACCGTGCCCAGCACCT
GAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAC
GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA
GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATC
GAT*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTG*
CTGACTTAG

MEPPGDWGPPPWRSTPKTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRAS
RNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQHQTKCSWLVTKAGAGTSSSHWVIDDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKI
D*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5GG

mCTLA4-Fc-*GPI*

ATGGCTTGTCTTGGACTCCGGAGGTACAAAGCTCAACTGCAGCTGCCTTCTAGGACTTGGCCTTTTGTAGCCCTGCTCACTCTTCTTTTCATCCCAGTCTTC
TCTGAAGCCATACAGGTGACCCAACCTTCAGTGGTGTTGGCTAGCAGCCATGGTGTCGCCAGCTTTCCATGTGAATATTCACCATCACACAACACTGATGAG
GTCCGGGTGACTGTGCTGCGGCAGACAAATGACCAAATGACTGAGGTCTGTGCCACGACATTCACAGAGAAGAATACAGTGGGCTTCCTAGATTACCCCTTC
TGCAGTGGTACCTTTAATGAAAGCAGAGTGAACCTCACCATCCAAGGACTGAGAGCTGTTGACACGGGACTGTACCTCTGCAAGGTGGAACTCATGTACCCA
CCGCCATACTTTGTGGGCATGGGCAACGGGACGCAGATTTATGTCATTGATCCAGAACCATGCCCGGATTCTGAATCGATGACAAAACTCACACATGCCCAC
CGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCG
TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT
ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAG
CCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCA
GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGC
TGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTC
TGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTG*
GGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MACLGLRRYKAQLQLPSRTWPFVALLTLLFIPVFSEAIQVTQPSVVLASSHGVASFPCEYSPSHNTDEVRVTVLRQTNDQMTEVCATTFTEKNTVGFLDYPF
CSGTFNESRVNLTIQGLRAVDTGLYLCKVELMYPPPYFVGMGNGTQIYVIDPEPCPDSDIDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC
VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*PNKGSGTTSGTTRLLS*
GHTCFTLTGLLGTLVTMGLLT

FIG. 5HH

mPDL1-*C1C2*

ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTTACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGC
AACGTCACGATGGAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGGGAAAAGGAAGATGAGCAAGTGATTCAGTTTGTG
GCAGGAGAGGAGGACCTTAAGCCTCAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGAAATGCTGCCCTTCAGATCACA
GACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGCATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCATACCGCAAA
ATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTAATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGAC
CACCAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGACAGAGGGGATGCTTCTCAATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGAT
GTTTTCTACTGTACGTTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTGCCTGCAACACATCCTCCACAGAACAGGACT
ATCGATGTCGAGCCACTGGGCATGGAGAATGGGAACATTGCCAACTCACAGATCGCCGCCTCATCTGTGCGTGTGACCTTCTTGGGTTTGCAGCATTGGGTC
CCGGAGCTGGCCCGCCTGAACCGCGCAGGCATGGTCAATGCCTGGACACCCAGCAGCAATGACGATAACCCCTGGATCCAGGTGAACCTGCTGCGGAGGATG
TGGGTAACAGGTGTGGTGACGCAGGGTGCCAGCCGCTTGGCCAGTCATGAGTACCTGAAGGCCTTCAAGGTGGCCTACAGCCTTAATGGACACGAATTCGAT
TTCATCCATGATGTTAATAAAAAACACAAGGAGTTTGTGGGTAACTGGAACAAAAACGCGGTGCATGTCAACCTGTTTGAGACCCCTGTGGAGGCTCAGTAC
GTGAGATTGTACCCCACGAGCTGCCACACGGCCTGCACTCTGCGCTTTGAGCTACTGGGCTGTGAGCTGAACGGATGCGCCAATCCCCTGGGCCTGAAGAAT
AACAGCATCCCTGACAAGCAGATCACGGCCTCCAGCAGCTACAAGACCTGGGGCTTGCATCTCTTCAGCTGGAACCCCTCCTATGCACGGCTGGACAAGCAG
GGCAACTTCAACGCCTGGGTTGCGGGGAGCTACGGTAACGATCAGTGGCTGCAGATCTTCCCTGGCAACTGGGACAACCACTCCCACAAGAAGAACTTGTTT
GAGACGCCCATCCTGGCTCGCTATGTGCGCATCCTGCCTGTAGCCTGGCACAACCGCATCGCCCTGCGCCTGGAGCTGCTGGGCTGTTAG

MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYWEKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQIT
DVKLQDAGVYCCIISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDHQPVSGKRSVTTSRTEGMLLNVTSSLRVNATAND
VFYCTFWRSQPGQNHTAELIIPELPATHPPQNRTI*DVEPLGMENGNIANSQIAASSVRVTFLGLQHWVPELARLNRAGMVNAWTPSSNDDNPWIQVNLLRRM*
WVTGVVTQGASRLASHEYLKAFKVAYSLNGHEFDFIHDVNKKHKEFVGNWNKNAVHVNLFETPVEAQYVRLYPTSCHTACTLRFELLGCELNGCANPLGLKN
NSIPDKQITASSSYKTWGLHLFSWNPSYARLDKQGNFNAWVAGSYGNDQWLQIFPGNWDNHSHKKNLFETPILARYVRILPVAWHNRIALRLELLGC

FIG. 5II

mPDL1-Fc-*GPI*

ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTTACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGC
AACGTCACGATGGAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGGGAAAAGGAAGATGAGCAAGTGATTCAGTTTGTG
GCAGGAGAGGAGGACCTTAAGCCTCAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGAAATGCTGCCCTTCAGATCACA
GACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGCATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCATACCGCAAA
ATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTAATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGAC
CACCAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGACAGAGGGGATGCTTCTCAATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGAT
GTTTTCTACTGTACGTTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTGCCTGCAACACATCCTCCACAGAACAGGACT
ATCGATGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATG
ATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT
GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
CGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG
AACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
TTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGTGGAACC*
ACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYWEKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQIT
DVKLQDAGVYCCIISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDHQPVSGKRSVTTSRTEGMLLNVTSSLRVNATAND
VFYCTFWRSQPGQNHTAELIIPELPATHPPQNRTIDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5JJ

mPDL1-*GPI*

ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTTACTATCACGGCTCCAAAGGACTTGTACGTGGTGGA
GTATGGCAGCAACGTCACGATGGAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGGGAAAAGGAAGATG
AGCAAGTGATTCAGTTTGTGGCAGGAGAGGAGGACCTTAAGCCTCAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTT
TTGAAGGGAAATGCTGCCCTTCAGATCACAGACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGCATAATCAGCTACGGTGGTGCGGACTA
CAAGCGAATCACGCTGAAAGTCAATGCCCCATACCGCAAAATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTAATAT
GTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGACCACCAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGG
ACAGAGGGGATGCTTCTCAATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGATGTTTTCTACTGTACGTTTTGGAGATCACAGCC
AGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTGCCTGCAACACATCCTCCACAGAACAGGACT*CCAAATAAAGGAAGTGGAACCA*
CTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYWEKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQL
LKGNAALQITDVKLQDAGVYCCIISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDHQPVSGKRSVTTSR
TEGMLLNVTSSLRVNATANDVFYCTFWRSQPGQNHTAELIIPELPATHPPQNRT*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5KK

mPDL2-*C1C2*

ATGCTGCTCCTGCTGCCGATACTGAACCTGAGCTTACAACTTCATCCTGTAGCAGCTTTATTCACCGTGACAGCCCCTAAAGAAGTGTACACCGTAGACGTC
GGCAGCAGTGTGAGCCTGGAGTGCGATTTTGACCGCAGAGAATGCACTGAACTGGAAGGGATAAGAGCCAGTTTGCAGAAGGTAGAAAATGATACGTCTCTG
CAAAGTGAAAGAGCCACCCTGCTGGAGGAGCAGCTGCCCCTGGGAAAGGCTTTGTTCCACATCCCTAGTGTCCAAGTGAGAGATTCCGGGCAGTACCGTTGC
CTGGTCATCTGCGGGGCCGCCTGGGACTACAAGTACCTGACGGTGAAAGTCAAAGCTTCTTACATGAGGATAGACACTAGGATCCTGGAGGTTCCAGGTACA
GGGGAGGTGCAGCTTACCTGCCAGGCTAGAGGTTATCCCCTAGCAGAAGTGTCCTGGCAAAATGTCAGTGTTCCTGCCAACACCAGCCACATCAGGACCCCC
GAAGGCCTCTACCAGGTCACCAGTGTTCTGCGCCTCAAGCCTCAGCCTAGCAGAAACTTCAGCTGCATGTTCTGGAATGCTCACATGAAGGAGCTGACTTCA
GCCATCATTGACCCTCTGAGTCGGATGGAACCCAAAGTCCCCAGAACGATCGATGTCGAGCCACTGGGCATGGAGAATGGGAACATTGCCAACTCACAGATC
GCCGCCTCATCTGTGCGTGTGACCTTCTTGGGTTTGCAGCATTGGGTCCCGGAGCTGGCCCGCCTGAACCGCGCAGGCATGGTCAATGCCTGGACACCCAGC
AGCAATGACGATAACCCCTGGATCCAGGTGAACCTGCTGCGGAGGATGTGGGTAACAGGTGTGGTGACGCAGGGTGCCAGCCGCTTGGCCAGTCATGAGTAC
CTGAAGGCCTTCAAGGTGGCCTACAGCCTTAATGGACACGAATTCGATTTCATCCATGATGTTAATAAAAAACACAAGGAGTTTGTGGGTAACTGGAACAAA
AACGCGGTGCATGTCAACCTGTTTGAGACCCCTGTGGAGGCTCAGTACGTGAGATTGTACCCCACGAGCTGCCACACGGCCTGCACTCTGCGCTTTGAGCTA
CTGGGCTGTGAGCTGAACGGATGCGCCAATCCCCTGGGCCTGAAGAATAACAGCATCCCTGACAAGCAGATCACGGCCTCCAGCAGCTACAAGACCTGGGGC
TTGCATCTCTTCAGCTGGAACCCCTCCTATGCACGGCTGGACAAGCAGGGCAACTTCAACGCCTGGGTTGCGGGGAGCTACGGTAACGATCAGTGGCTGCAG
ATCTTCCCTGGCAACTGGGACAACCACTCCCACAAGAAGAACTTGTTTGAGACGCCCATCCTGGCTCGCTATGTGCGCATCCTGCCTGTAGCCTGGCACAAC
CGCATCGCCCTGCGCCTGGAGCTGCTGGGCTGTTAG

MLLLLPILNLSLQLHPVAALFTVTAPKEVYTVDVGSSVSLECDFDRRECTELEGIRASLQKVENDTSLQSERATLLEEQLPLGKALFHIPSVQVRDSGQYRC
LVICGAAWDYKYLTVKVKASYMRIDTRILEVPGTGEVQLTCQARGYPLAEVSWQNVSVPANTSHIRTPEGLYQVTSVLRLKPQPSRNFSCMFWNAHMKELTS
AIIDPLSRMEPKVPRTIDVEPLGMENGNIANSQIAASSVRVTFLGLQHWVPELARLNRAGMVNAWTPSSNDDNPWIQVNLLRRMWVTGVVTQGASRLASHEY
LKAFKVAYSLNGHEFDFIHDVNKKHKEFVGNWNKNAVHVNLFETPVEAQYVRLYPTSCHTACTLRFELLGCELNGCANPLGLKNNSIPDKQITASSSYKTWG
LHLFSWNPSYARLDKQGNFNAWVAGSYGNDQWLQIFPGNWDNHSHKKNLFETPILARYVRILPVAWHNRIALRLELLGC

FIG. 5LL

mPDL2-Fc-*GPI*

ATGCTGCTCCTGCTGCCGATACTGAACCTGAGCTTACAACTTCATCCTGTAGCAGCTTTATTCACCGTGACAGCCCCTAAAGAAGTGTACACCGTAGACGTCGGCAG
CAGTGTGAGCCTGGAGTGCGATTTTGACCGCAGAGAATGCACTGAACTGGAAGGGATAAGAGCCAGTTTGCAGAAGGTAGAAAATGATACGTCTCTGCAAAGTGAAA
GAGCCACCCTGCTGGAGGAGCAGCTGCCCCTGGGAAAGGCTTTGTTCCACATCCCTAGTGTCCAAGTGAGAGATTCCGGGCAGTACCGTTGCCTGGTCATCTGCGGG
GCCGCCTGGGACTACAAGTACCTGACGGTGAAAGTCAAAGCTTCTTACATGAGGATAGACACTAGGATCCTGGAGGTTCCAGGTACAGGGGAGGTGCAGCTTACCTG
CCAGGCTAGAGGTTATCCCCTAGCAGAAGTGTCCTGGCAAAATGTCAGTGTTCCTGCCAACACCAGCCACATCAGGACCCCCGAAGGCCTCTACCAGGTCACCAGTG
TTCTGCGCCTCAAGCCTCAGCCTAGCAGAAACTTCAGCTGCATGTTCTGGAATGCTCACATGAAGGAGCTGACTTCAGCCATCATTGACCCTCTGAGTCGGATGGAA
CCCAAAGTCCCCAGAACGATCGATGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAA
GGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG
TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG
GGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACT
ACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
GTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCG*
TCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MLLLLPILNLSLQLHPVAALFTVTAPKEVYTVDVGSSVSLECDFDRRECTELEGIRASLQKVENDTSLQSERATLLEEQLPLGKALFHIPSVQVRDSGQYRCLVICG
AAWDYKYLTVKVKASYMRIDTRILEVPGTGEVQLTCQARGYPLAEVSWQNVSVPANTSHIRTPEGLYQVTSVLRLKPQPSRNFSCMFWNAHMKELTSAIIDPLSRME
PKVPRTIDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGKID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5MM

mPDL1-mFc-*GPI*

ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTTACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGC
AACGTCACGATGGAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGGGAAAAGGAAGATGAGCAAGTGATTCAGTTTGTG
GCAGGAGAGGAGGACCTTAAGCCTCAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGAAATGCTGCCCTTCAGATCACA
GACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGCATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCATACCGCAAA
ATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTAATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGAC
CACCAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGACAGAGGGGATGCTTCTCAATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGAT
GTTTTCTACTGTACGTTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTGCCTGCAACACATCCTCCACAGAACAGGACT
GGTTGTAAGCCTTGCATATGTACAGTCCCAGAAGTATCATCTGTCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTC
ACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCCCGGGAG
GAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGCAGCT
TTCCCTGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCGAAGGCTCCACAGGTGTACACCATTCCACCTCCCAAGGAGCAGATGGCCAAGGAT
AAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGAATGGGCAGCCAGCGGAGAACTACAAGAACACTCAG
CCCATCATGGACACAGATGGCTCTTACTTCGTCTACAGCAAGCTCAATGTGCAGAAGAGCAACTGGGAGGCAGGAAATACTTTCACCTGCTCTGTGTTACAT
GAGGGCCTGCACAACCACCATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCT*
GGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYWEKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQIT
DVKLQDAGVYCCIISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDHQPVSGKRSVTTSRTEGMLLNVTSSLRVNATAND
VFYCTFWRSQPGQNHTAELIIPELPATHPPQNRTGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPRE
EQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQ
PIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5NN

mPDL2-*GPI*

ATGCTGCTCCTGCTGCCGATACTGAACCTGAGCTTACAACTTCATCCTGTAGCAGCTTTATTCACCGTGACAGCCCCTAAAGAAGTGTACACCGTAGACG
TCGGCAGCAGTGTGAGCCTGGAGTGCGATTTTGACCGCAGAGAATGCACTGAACTGGAAGGGATAAGAGCCAGTTTGCAGAAGGTAGAAAATGATACGTC
TCTGCAAAGTGAAAGAGCCACCCTGCTGGAGGAGCAGCTGCCCCTGGGAAAGGCTTTGTTCCACATCCCTAGTGTCCAAGTGAGAGATTCCGGGCAGTAC
CGTTGCCTGGTCATCTGCGGGGCCGCCTGGGACTACAAGTACCTGACGGTGAAAGTCAAAGCTTCTTACATGAGGATAGACACTAGGATCCTGGAGGTTC
CAGGTACAGGGGAGGTGCAGCTTACCTGCCAGGCTAGAGGTTATCCCCTAGCAGAAGTGTCCTGGCAAAATGTCAGTGTTCCTGCCAACACCAGCCACAT
CAGGACCCCCGAAGGCCTCTACCAGGTCACCAGTGTTCTGCGCCTCAAGCCTCAGCCTAGCAGAAACTTCAGCTGCATGTTCTGGAATGCTCACATGAAG
GAGCTGACTTCAGCCATCATTGACCCTCTGAGTCGGATGGAACCCAAAGTCCCCAGAACG*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTC*
TTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG

MLLLLPILNLSLQLHPVAALFTVTAPKEVYTVDVGSSVSLECDFDRRECTELEGIRASLQKVENDTSLQSERATLLEEQLPLGKALFHIPSVQVRDSGQY
RCLVICGAAWDYKYLTVKVKASYMRIDTRILEVPGTGEVQLTCQARGYPLAEVSWQNVSVPANTSHIRTPEGLYQVTSVLRLKPQPSRNFSCMFWNAHMK
ELTSAIIDPLSRMEPKVPRT*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 50O

mPDL1-*GPI*-P2A-mHVEM-*GPI*

ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTTACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGCAACGTC
ACGATGGAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGGGAAAAGGAAGATGAGCAAGTGATTCAGTTTGTGGCAGGAGAGGAG
GACCTTAAGCCTCAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGAAATGCTGCCCTTCAGATCACAGACGTCAAGCTGCAGGAC
GCAGGCGTTTACTGCTGCATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCATACCGCAAAATCAACCAGAGAATTTCCGTGGAT
CCAGCCACTTCTGAGCATGAACTAATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGACCACCAACCCGTGAGTGGGAAGAGAAGTGTC
ACCACTTCCCGGACAGAGGGGATGCTTCTCAATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGATGTTTTCTACTGTACGTTTTGGAGATCACAGCCAGGG
CAAAACCACACAGCGGAGCTGATCATCCCAGAACTGCCTGCAACACATCCTCCACAGAACAGGACT*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTT*
CTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTGGAAGCGGAGCTACTAACTTCAGCCTGCTGAAGCAGGCT
GGCGACGTGGAGGAGAACCCTGGACCT**ATGGAACCTCTCCCAGGATGGGGGTCGGCACCCTGGAGCCAGGCCCCTACAGACAACACCTTCAGGCTGGTGCCTTGTGTC**
TTCCTTTTGAACTTGCTGCAGCGCATCTCTGCCCAGCCCTCATGCAGACAGGAGGAGTTCCTTGTGGGAGACGAGTGCTGCCCCATGTGCAACCCAGGTTACCATGTG
AAGCAGGTCTGCAGTGAGCATACAGGCACAGTGTGTGCCCCCTGTCCCCCACAGACATATACCGCCCATGCAAATGGCCTGAGCAAGTGTCTGCCCTGCGGAGTCTGT
GATCCAGACATGGGCCTGCTGACCTGGCAGGAGTGCTCCAGCTGGAAGGACACTGTGTGCAGATGCATCCCAGGCTACTTCTGTGAGAACCAGGATGGGAGCCACTGT
TCCACATGCTTGCAGCACACCACCTGCCCTCCAGGGCAGAGGGTAGAGAAGAGAGGGACTCACGACCAGGACACTGTATGTGCTGACTGCCTAACAGGGACCTTCTCA
CTTGGAGGGACTCAGGAGGAATGCCTGCCCTGGACCAACTGCAGTGCATTTCAACAGGAAGTAAGACGTGGGACCAACAGCACAGACACCACCTGCTCCTCCCAG*CCA*
AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACT
TAG

MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYWEKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQITDVKLQD
AGVYCCIISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDHQPVSGKRSVTTSRTEGMLLNVTSSLRVNATANDVFYCTFWRSQPG
QNHTAELIIPELPATHPPQNRT*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLTGSGATNFSLLKQAGDVEENPGP***MEPLPGWGSAPWSQAPTDNTFRLVPCV**
FLLNLLQRISAQPSCRQEEFLVGDECCPMCNPGYHVKQVCSEHTGTVCAPCPPQTYTAHANGLSKCLPCGVCDPDMGLLTWQECSSWKDTVCRCIPGYFCENQDGSHC
STCLQHTTCPPGQRVEKRGTHDQDTVCADCLTGTFSLGGTQEECLPWTNCSAFQQEVRRGTNSTDTTCSSQ*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*

FIG. 5PP

hPDL1-*ADAM10*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGC
AATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTGTG
CATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATCACA
GATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAACAAA
ATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGT
GACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAAT
GAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAATGAAAGG
TGTGGAAATGGAATGGTAGAACAAGGTGAAGAATGTGATTGTGGCTATAGTGACCAGTGTAAAGATGAATGCTGCTTCGATGCAAATCAACCAGAGGGAAGA
AAATGCAAACTGAAACCTGGGAAACAGTGCAGTCCAAGTCAAGGTCCTTGTTGTACAGCACAGTGTGCATTCAAGTCAAAGTCTGAGAAGTGTCGGGATGAT
TCAGACTGTGCAAGGGAAGGAATATGTAATGGCTTCACAGCTCTCTGCCCAGCATCTGACCCTAAACCAAACTTCACAGACTGTAATAGGCATACACAAGTG
TGCATTAATGGGCAATGTGCAGGTTCTATCTGTGAGAAATATGGCTTAGAGGAGTGTACGTGTGCCAGTTCTGATGGCAAAGATGATAAAGAATTATGCCAT
GTATGCTGTATGAAGAAAATGGACCCATCAACTTGTGCCAGTACAGGGTCTGTGCAGTGGAGTAGGCACTTCAGTGGTCGAACCATCACCCTGCAACCTGGA
TCCCCTTGCAACGATTTTAGAGGTTACTGTGATGTTTTCATGCGGTGCAGATTAGTAGATGCTGATGGTCCTCTAGCTAGGCTTAAAAAAGCAATTTTTAGT
CCAGAGCTCTATGAAAACATTGCTGAATGGATTGTGGCTCATTGGTGGGCAGTATTACTTATGGGAATTGCTCTGATCATGCTAATGGCTGGATTTATTAAG
ATATGCAGTGTTCATACTCCAAGTAGTAATCCAAAGTTGCCTCCTCCTAAACCACTTCCAGGCACTTTAAAGAGGAGGAGACCTCCACAGCCCATTCAGCAA
CCCCAGCGTCAGCGGCCCCGAGAGAGTTATCAAATGGGACACATGAGACGCTAA

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQIT
DVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTTTN
EIFYCTFRRLDPEENHTAELVIPELPLAHPPNER*CGNGMVEQGEECDCGYSDQCKDECCFDANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDD*
SDCAREGICNGFTALCPASDPKPNFTDCNRHTQVCINGQCAGSICEKYGLEECTCASSDGKDDKELCHVCCMKKMDPSTCASTGSVQWSRHFSGRTITLQPG
SPCNDFRGYCDVFMRCRLVDADGPLARLKKAIFSPELYENIAEWIVAHWWAVLLMGIALIMLMAGFIKICSVHTPSSNPKLPPPKPLPGTLKRRRPPQPIQQ
PQRQRPRESYQMGHMRR

FIG. 5QQ

hPDL1-4Fc-*CD9tm2*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATAT
GACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGG
AAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATCACAGATGTGAAATTGCAG
GATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAACAAAATCAACCAAAGAATTTTGGT
TGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAAGTCCTGAGTGGTAAGA
CCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGCACTTTTAGGAGATTA
GATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAATGAAAGGGAGTCCAAATATGGTCCCCCATGCCCATCATGCCC
AGCACCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACG
TGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACGTACCGT
GTGGTCAGGGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGTAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTC
CAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT
ACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGGACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGC
AGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTC
TCCGGGTAAA*TTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGC*

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQ
DAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRL
DPEENHTAELVIPELPLAHPPNERESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR
VVRVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEDNYKTTPPVLDSDGSFFLYS
RLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK*FYTGVYILIGAGALMMLVGFLGCCGAVQESQCVIM*

FIG. 5RR

hPDL1-4Fc-*CD9tm2*-*KRAS*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATAT
GACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGG
AAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATCACAGATGTGAAATTGCAG
GATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAACAAAATCAACCAAAGAATTTTGGT
TGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAAGTCCTGAGTGGTAAGA
CCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGCACTTTTAGGAGATTA
GATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAATGAAAGGGAGTCCAAATATGGTCCCCCATGCCCATCATGCCC
AGCACCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACG
TGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACGTACCGT
GTGGTCAGGGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGTAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTC
CAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT
ACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGGACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGC
AGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTC
TCCGGGTAAA*TTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGCA*
AAAAGAAGAAAAAGAAGAAGAAGACAAAGTGTGTAATTATGTAA

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQ
DAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRL
DPEENHTAELVIPELPLAHPPNERESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR
VVRVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEDNYKTTPPVLDSDGSFFLYS
RLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK*FYTGVYILIGAGALMMLVGFLGCCGAVQESQCKKKKKKKKTKCVIM*

FIG. 5SS

hPDL1-Fc-*CD9tm2*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGC
AATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTGTG
CATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAGATCACA
GATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAACAAA
ATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGT
GACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAAT
GAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAATGAAAGG
ATCGATGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATG
ATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT
GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
CGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG
AACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
TTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*TTCTACACAGGAGTCTATATT*
CTGATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGCGTAATTATGTAA

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQIT
DVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRINTTTN
EIFYCTFRRLDPEENHTAELVIPELPLAHPPNERIDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*FYTGVYILIGAGALMMLVGFLGCCGAVQESQCVIM*

FIG. 5TT

hPDL1-Fc-*CD9tm2*-*KRAS*

ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGT
AGCAATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAA
TTTGTGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTT
CAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCC
CCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTC
ATCTGGACAAGCAGTGACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGA
ATCAACACAACAACTAATGAGATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTG
GCACATCCTCCAAATGAAAGGATCGATGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCC
CCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC
CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG
CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCC
CTGTCTCCGGGTAAAATCGAT*TTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCT*
GTGCAGGAGTCCCAGTGCAAAAAGAAGAAAAAGAAGAAGAAGACAAAGTGTGTAATTATGTAA

MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAAL
QITDVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLR
INTTTNEIFYCTFRRLDPEENHTAELVIPELPLAHPPNERIDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*FYTGVYILIGAGALMMLVGFLGCCGA*
VQESQCKKKKKKKKTKCVIM

FIG. 5UU

mPDL1-mFc-*CD9tm2*

ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTTACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAG
CAACGTCACGATGGAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGGGAAAAGGAAGATGAGCAAGTGATTCAGTTTG
TGGCAGGAGAGGAGGACCTTAAGCCTCAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGAAATGCTGCCCTTCAGATC
ACAGACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGCATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCATACCG
CAAAATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTAATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACA
GTGACCACCAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGACAGAGGGGATGCTTCTCAATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCG
AATGATGTTTTCTACTGTACGTTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTGCCTGCAACACATCCTCCACAGAA
CAGGACTGGTTGTAAGCCTTGCATATGTACAGTCCCAGAAGTATCATCTGTCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTC
CTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAA
CCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAA
CAGTGCAGCTTTCCCTGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCGAAGGCTCCACAGGTGTACACCATTCCACCTCCCAAGGAGCAGA
TGGCCAAGGATAAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGAATGGGCAGCCAGCGGAGAACTAC
AAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTTCGTCTACAGCAAGCTCAATGTGCAGAAGAGCAACTGGGAGGCAGGAAATACTTTCACCTG
CTCTGTGTTACATGAGGGCCTGCACAACCACCATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA*TTCTACACAGGAGTCTATATTCTGATCGGAGCCG*
GCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGCGTAATTATGTAA

MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYWEKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQI
TDVKLQDAGVYCCIISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDHQPVSGKRSVTTSRTEGMLLNVTSSLRVNATA
NDVFYCTFWRSQPGQNHTAELIIPELPATHPPQNRTGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQ
PREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENY
KNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK*FYTGVYILIGAGALMMLVGFLGCCGAVQESQCVIM*

FIG. 5VV

mPDL1-mFc-*CD9tm2*-*KRAS*

ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTTACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGC
AACGTCACGATGGAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGGGAAAAGGAAGATGAGCAAGTGATTCAGTTTGTG
GCAGGAGAGGAGGACCTTAAGCCTCAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGAAATGCTGCCCTTCAGATCACA
GACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGCATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCATACCGCAAA
ATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTAATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGAC
CACCAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGACAGAGGGGATGCTTCTCAATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGAT
GTTTTCTACTGTACGTTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTGCCTGCAACACATCCTCCACAGAACAGGACT
GGTTGTAAGCCTTGCATATGTACAGTCCCAGAAGTATCATCTGTCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTC
ACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCCCGGGAG
GAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGCAGCT
TTCCCTGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCGAAGGCTCCACAGGTGTACACCATTCCACCTCCCAAGGAGCAGATGGCCAAGGAT
AAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGAATGGGCAGCCAGCGGAGAACTACAAGAACACTCAG
CCCATCATGGACACAGATGGCTCTTACTTCGTCTACAGCAAGCTCAATGTGCAGAAGAGCAACTGGGAGGCAGGAAATACTTTCACCTGCTCTGTGTTACAT
GAGGGCCTGCACAACCACCATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA*TTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATGATG*
CTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGCAAAAAGAAGAAAAAGAAGAAGAAGACAAAGTGTGTAATTATGTAA

MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYWEKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQIT
DVKLQDAGVYCCIISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDHQPVSGKRSVTTSRTEGMLLNVTSSLRVNATAND
VFYCTFWRSQPGQNHTAELIIPELPATHPPQNRTGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPRE
EQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQ
PIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK*FYTGVYILIGAGALMMLVGFLGCCGAVQESQCKKKKKKKKTKCVIM*

FIG. 5WW

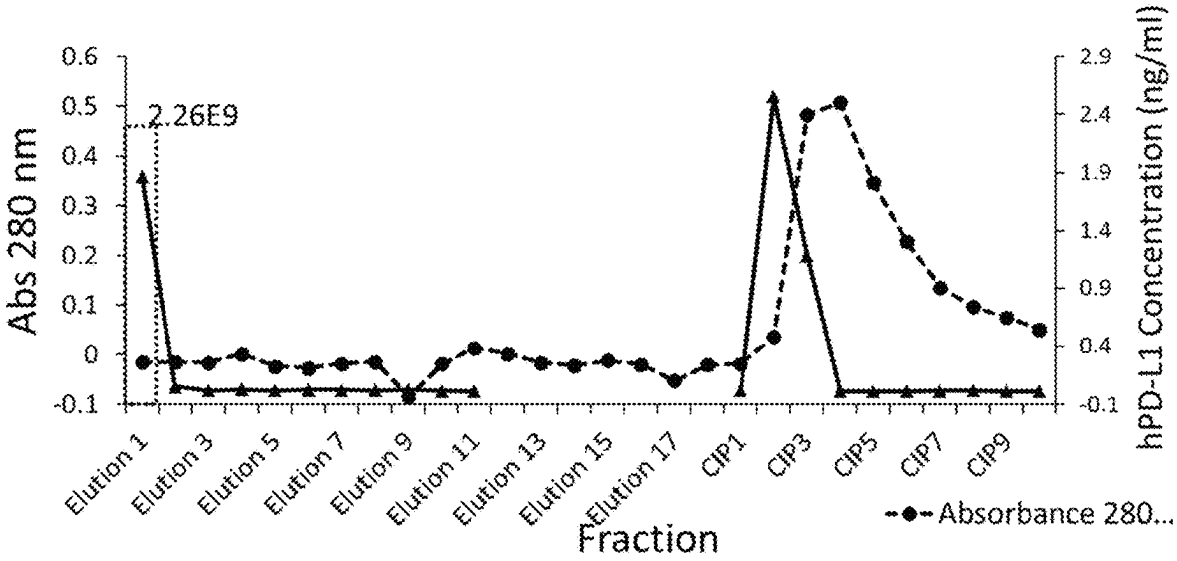

Abs 280 nm
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
2.26E9
hPD-L1 Concentration (ng/ml)
2.9
2.4
1.9
1.4
0.9
0.4
-0.1
Elution 1
Elution 3
Elution 5
Elution 7
Elution 9
Elution 11
Elution 13
Elution 15
Elution 17
CIP1
CIP3
CIP5
CIP7
CIP9
Fraction
Absorbance 280...

FIG. 6

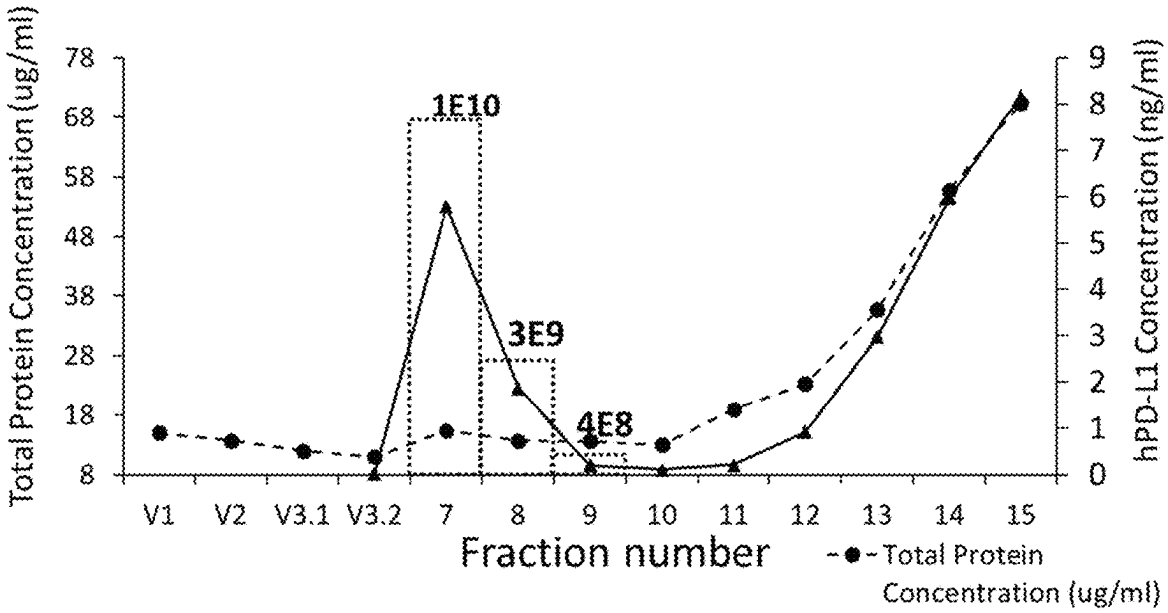
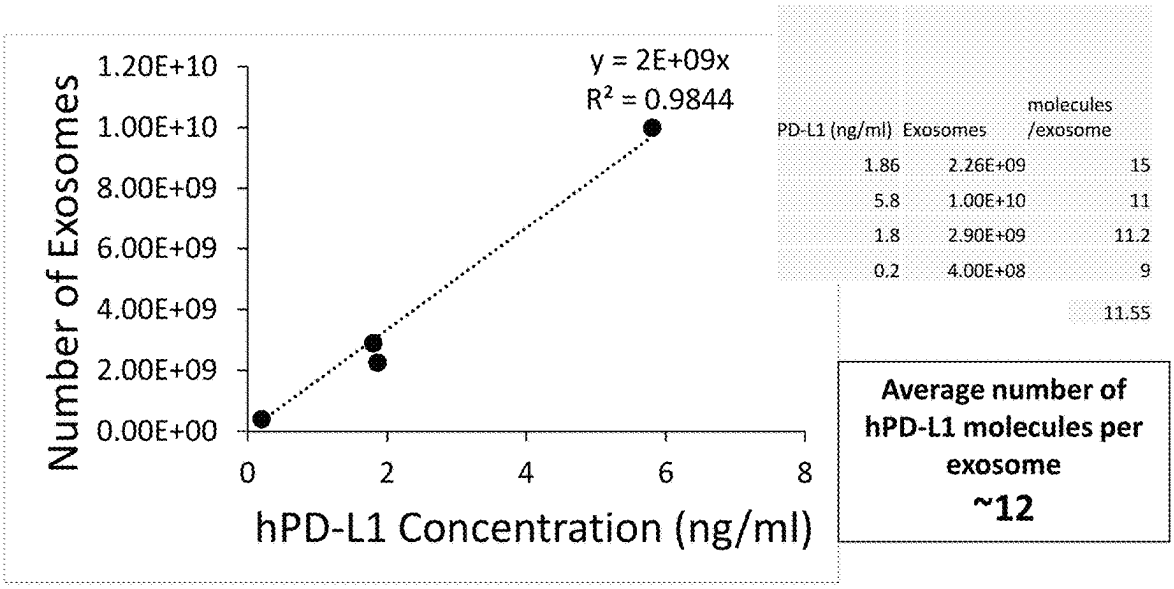

Total Protein Concentration (ug/ml)
78
68
58
48
38
28
18
8
1E10
3E9
4E8
hPD-L1 Concentration (ng/ml)
9
8
7
6
5
4
3
2
1
0
V1
V2
V3.1
V3.2
7
8
9
10
11
12
13
14
15
Fraction number
Total Protein Concentration (ug/ml)

FIG. 7



PD-L1 (ng/ml)	Exosomes	molecules /exosome
1.86	2.26E+09	15
5.8	1.00E+10	11
1.8	2.90E+09	11.2
0.2	4.00E+08	9
		11.55

FIG. 8

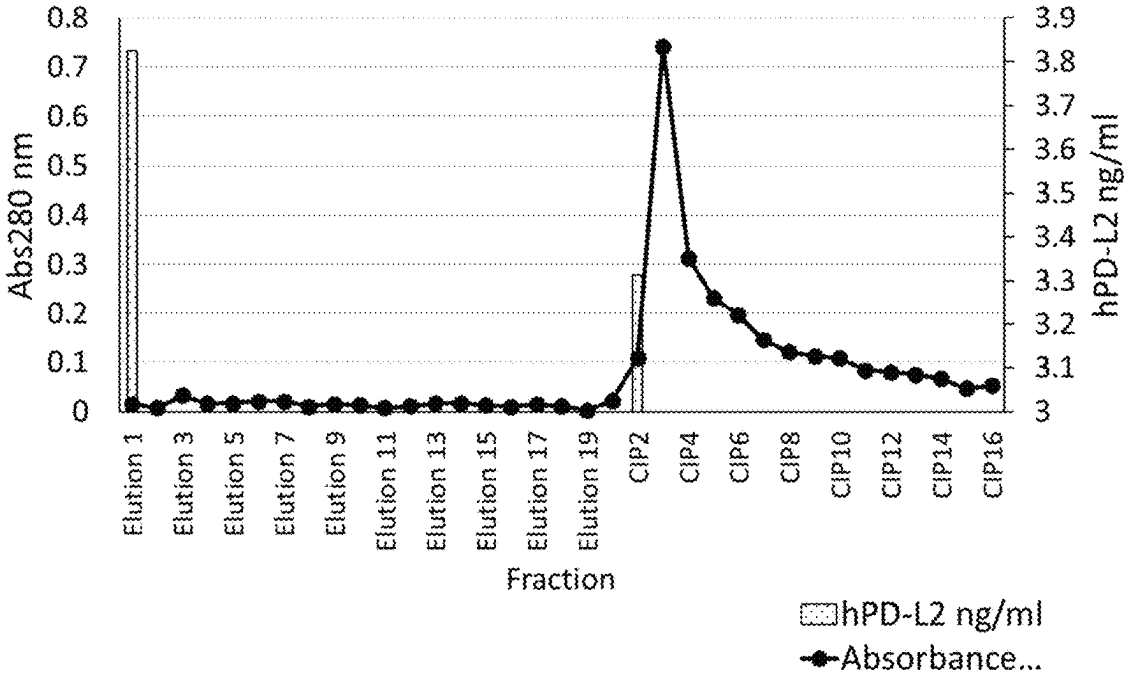


FIG. 9

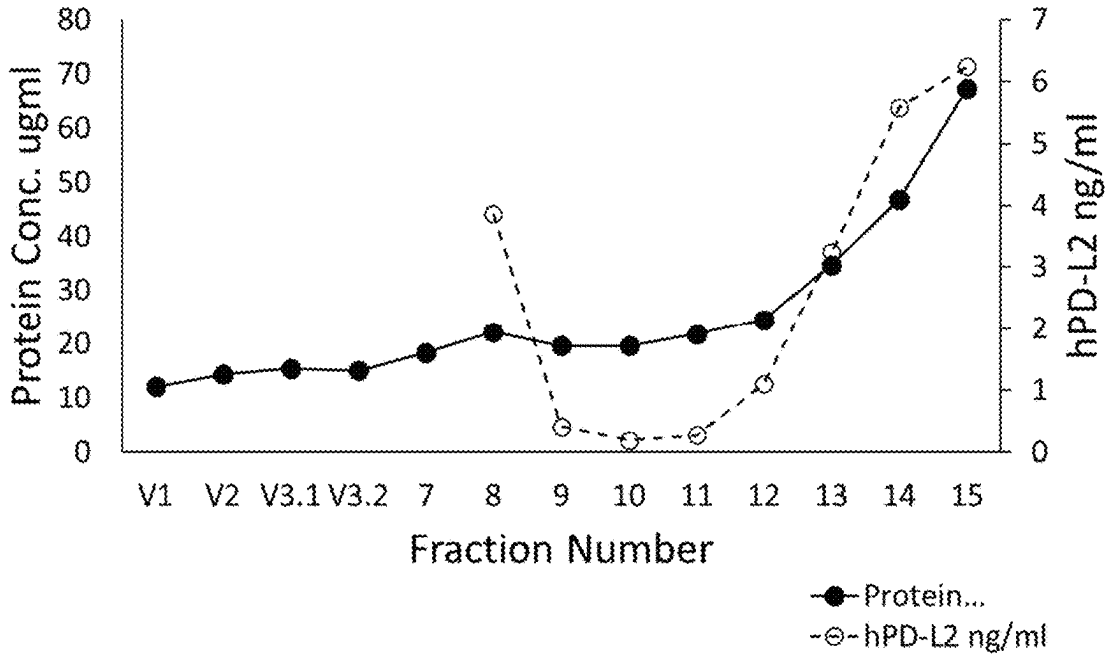

Protein Conc. ugml
hPD-L2 ng/ml
Fraction Number
V1 V2 V3.1 V3.2 7 8 9 10 11 12 13 14 15
Protein...
hPD-L2 ng/ml

FIG. 10

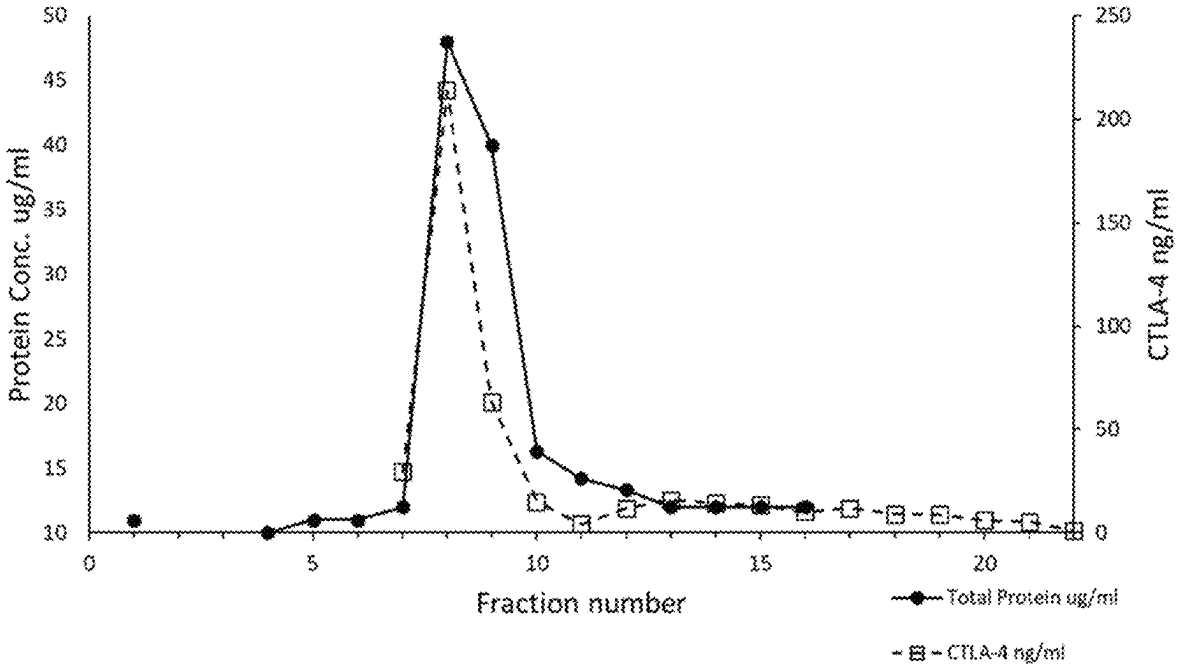

Protein Conc. ug/ml
CTLA-4 ng/ml
Fraction number
Total Protein ug/ml
CTLA-4 ng/ml

FIG. 11

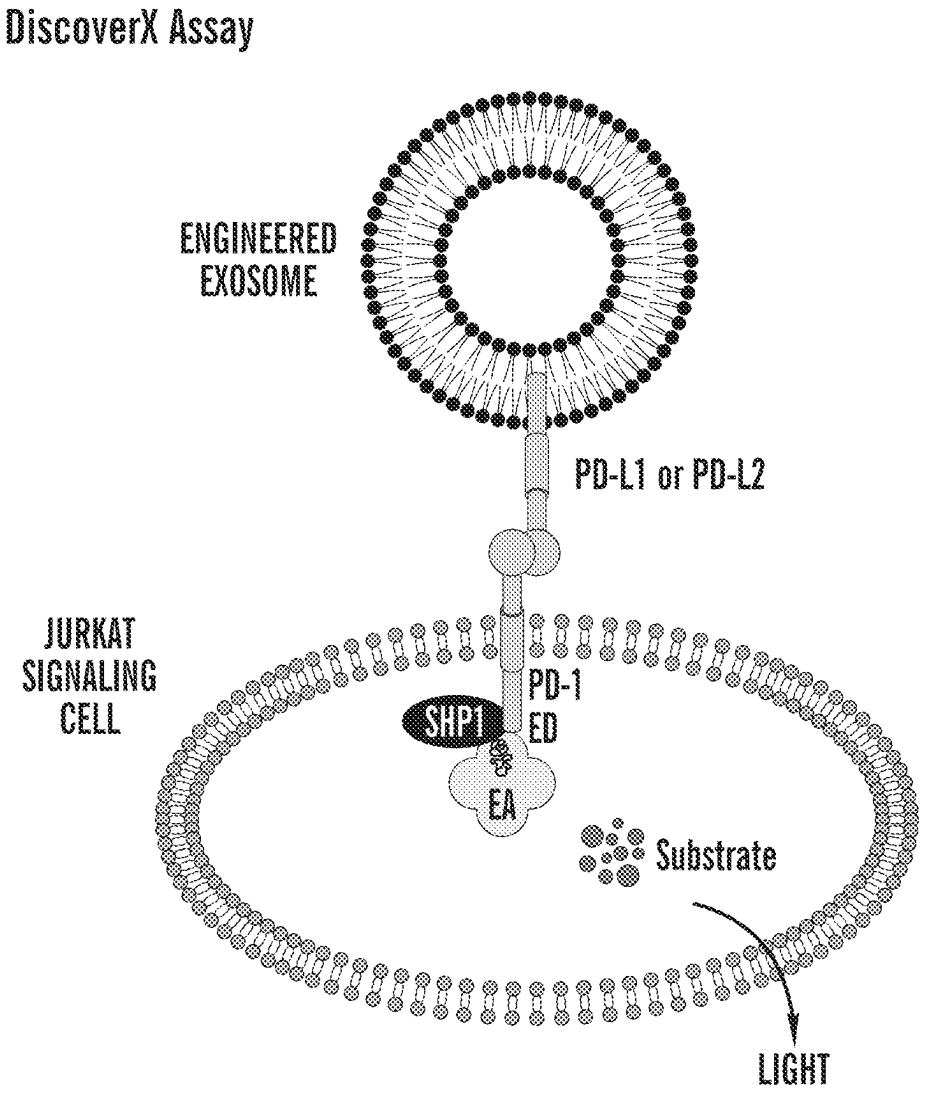

DiscoverX Assay
ENGINEERED EXOSOME
PD-L1 or PD-L2
JURKAT SIGNALING CELL
PD-1
SHP1
ED
EA
Substrate
LIGHT

FIG. 12A

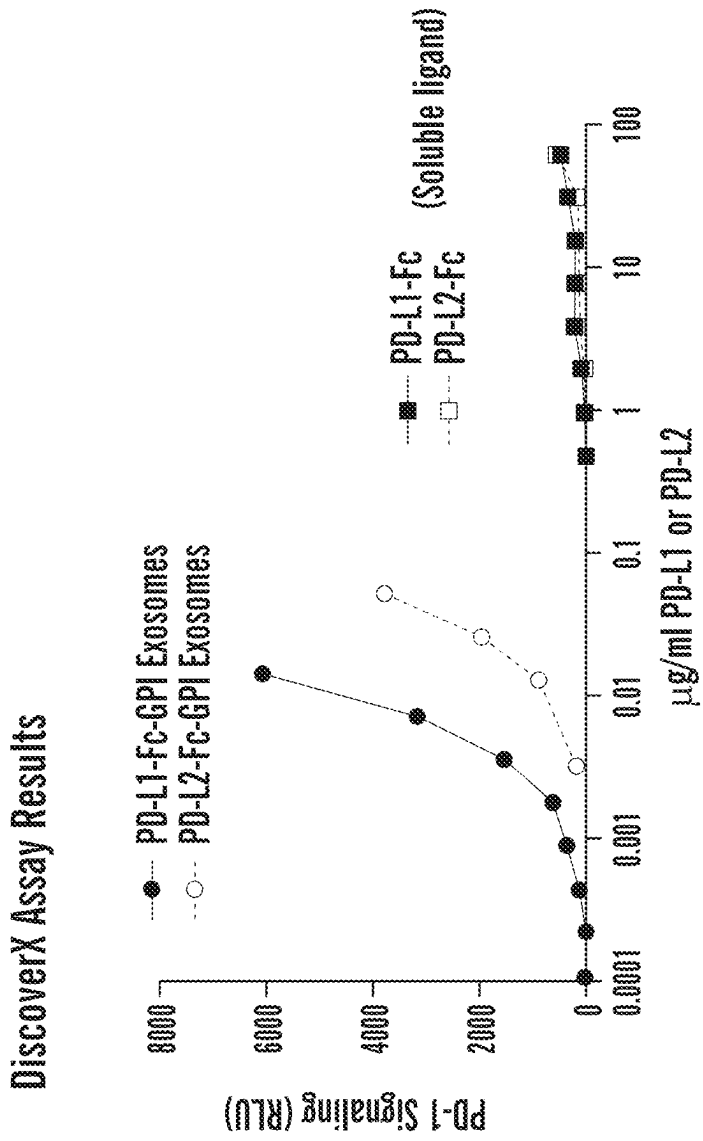

DiscoverX Assay Results
PD-L1-Fc-GPI Exosomes
PD-L2-Fc-GPI Exosomes
PD-L1-Fc
PD-L2-Fc
(Soluble ligand)
PD-1 Signaling (RLU)
8000
6000
4000
2000
0
0.0001
0.001
0.01
0.1
1
10
100
μg/ml PD-L1 or PD-L2

FIG. 12B

EAU Dosing Test Articles

	Unmodified Exosomes (IVT)	mPD-L1-Fc-GPI Exosomes 1X (IVT)	mPD-L1-Fc-GPI Exosomes 10X (IVT)	mPD-L1 Exosomes (IV)
Dose	2 μl	2 μl	2 μl	5ml/kg
Total protein concentration	40 μg/ml	40 μg/ml	400 μg/ml	40 μg/ml
Total protein administered	80 ng/eye	80 ng/eye	800 ng/eye	50 μg/ animal (~200 μg/kg)
Exosome concentration	5.7×10^{10}/ml	2.34×10^{10}/ml	2.34×10^{11}/ml	2.34×10^{10}/ml
Total exosomes administered	4.7×10^{7}	4.7×10^{7}	4.7×10^{8}	2.93×10^{10}

EAU Dosing Schedule

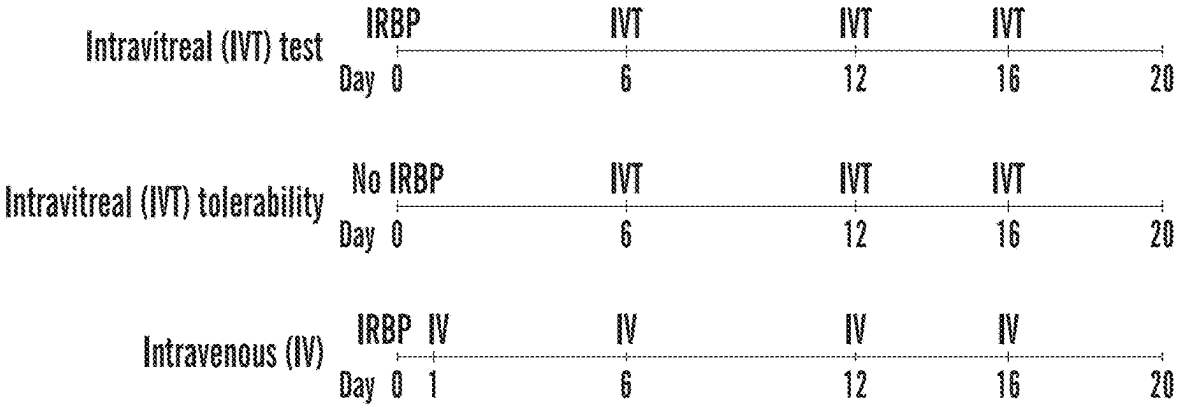


FIG. 13A

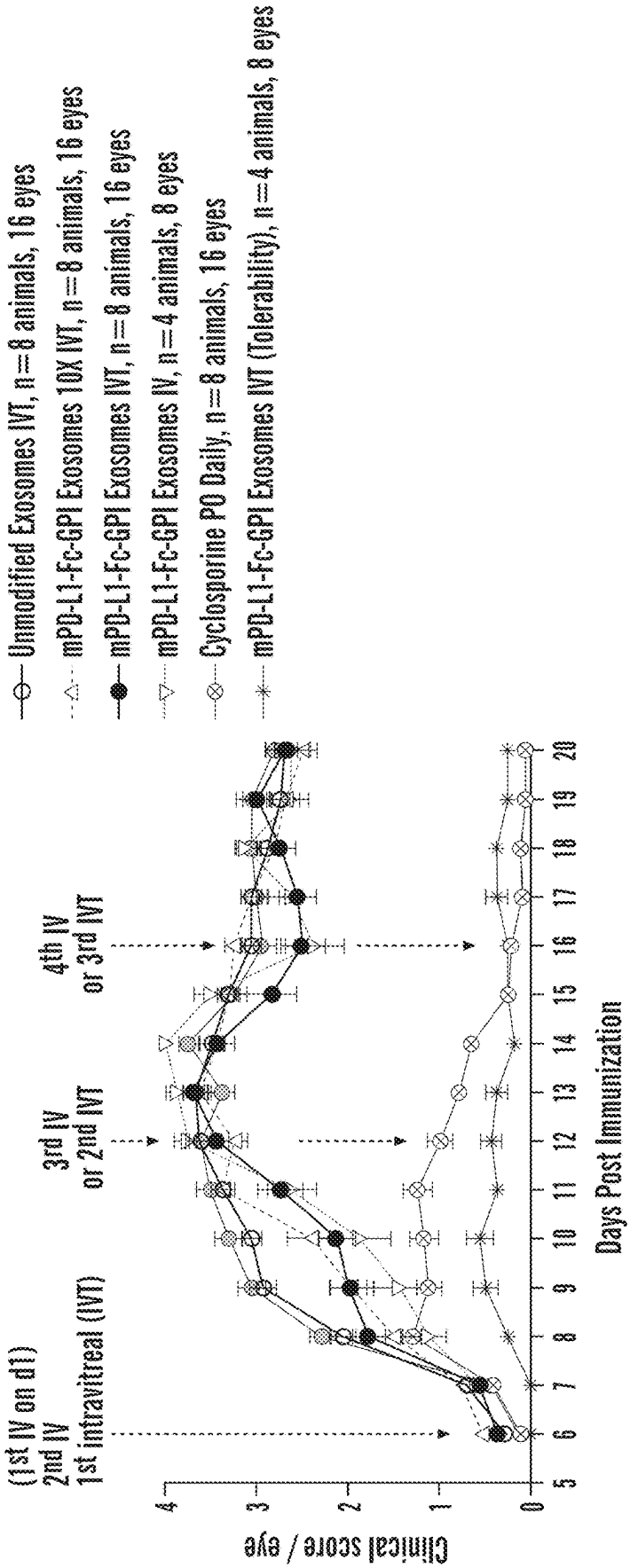

Vehicle IVT, n = 8 animals, 16 eyes
Unmodified Exosomes IVT, n = 8 animals, 16 eyes
mPD-L1-Fc-GPI Exosomes 10X IVT, n = 8 animals, 16 eyes
mPD-L1-Fc-GPI Exosomes IVT, n = 8 animals, 16 eyes
mPD-L1-Fc-GPI Exosomes IV, n = 4 animals, 8 eyes
Cyclosporine PO Daily, n = 8 animals, 16 eyes
mPD-L1-Fc-GPI Exosomes IVT (Tolerability), n = 4 animals, 8 eyes
(1st IV on d1)
2nd IV
1st intravitreal (IVT)
3rd IV
or 2nd IVT
4th IV
or 3rd IVT
Clinical score / eye
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
Days Post Immunization

FIG. 13B

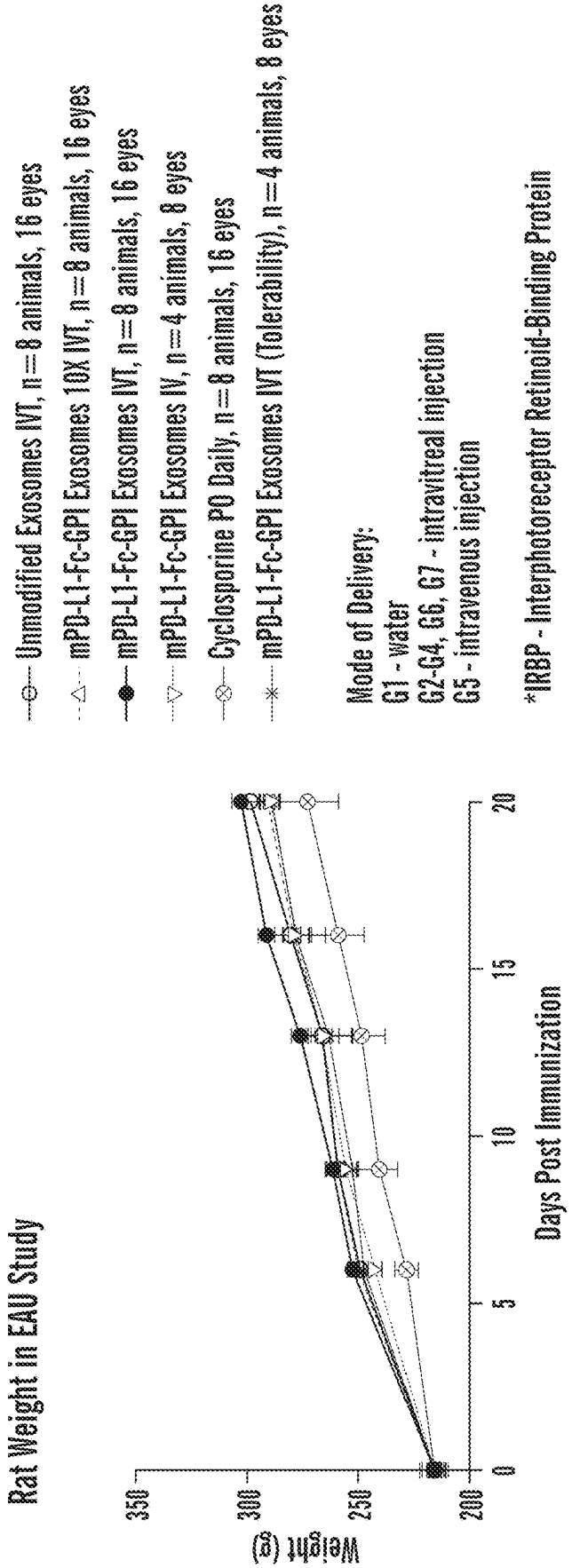

Rat Weight in EAU Study
Weight (g)
350
300
250
200
0
5
10
15
20
Days Post Immunization
Vehicle IVT, n=8 animals, 16 eyes
Unmodified Exosomes IVT, n=8 animals, 16 eyes
mPD-L1-Fc-GPI Exosomes 10X IVT, n=8 animals, 16 eyes
mPD-L1-Fc-GPI Exosomes IVT, n=8 animals, 16 eyes
mPD-L1-Fc-GPI Exosomes IV, n=4 animals, 8 eyes
Cyclosporine PO Daily, n=8 animals, 16 eyes
mPD-L1-Fc-GPI Exosomes IVT (Tolerability), n=4 animals, 8 eyes
Mode of Delivery:
G1 - water
G2-G4, G6, G7 - intravitreal injection
G5 - intravenous injection
*IRBP - Interphotoreceptor Retinoid-Binding Protein

FIG. 13C

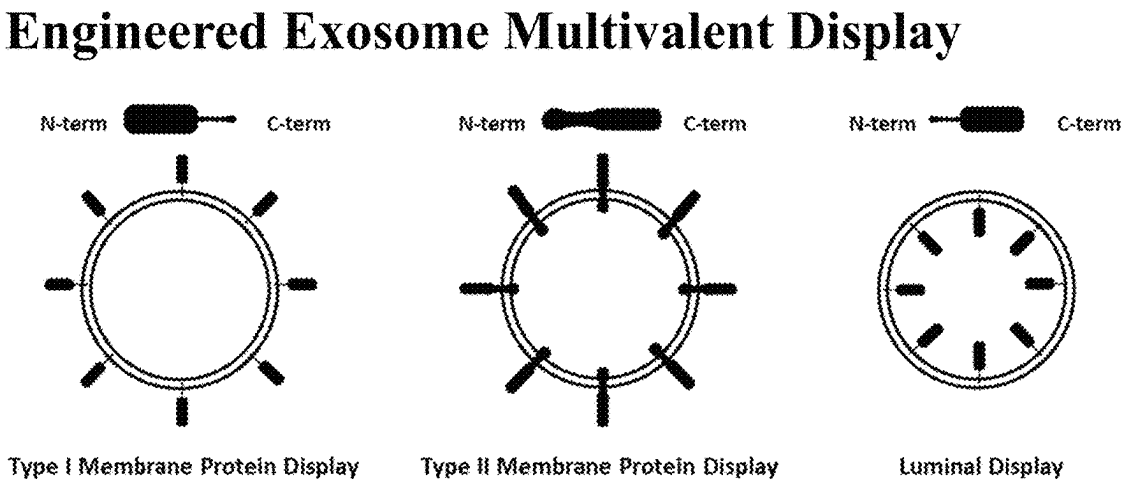

Engineered Exosome Multivalent Display
N-term
C-term
N-term
C-term
N-term
C-term
Type I Membrane Protein Display
Type II Membrane Protein Display
Luminal Display

FIG. 14

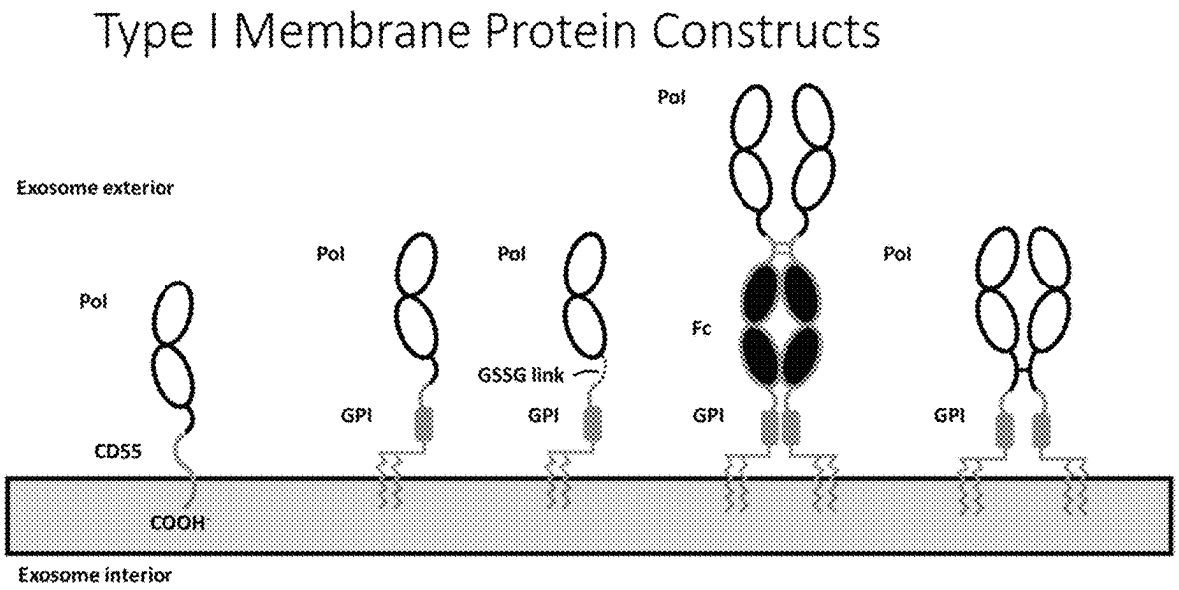

Type I Membrane Protein Constructs
Exosome exterior
Pol
Pol
Pol
Pol
Pol
Fc
GSSG link
GPI
GPI
GPI
GPI
CD55
COOH
Exosome interior

FIG. 15

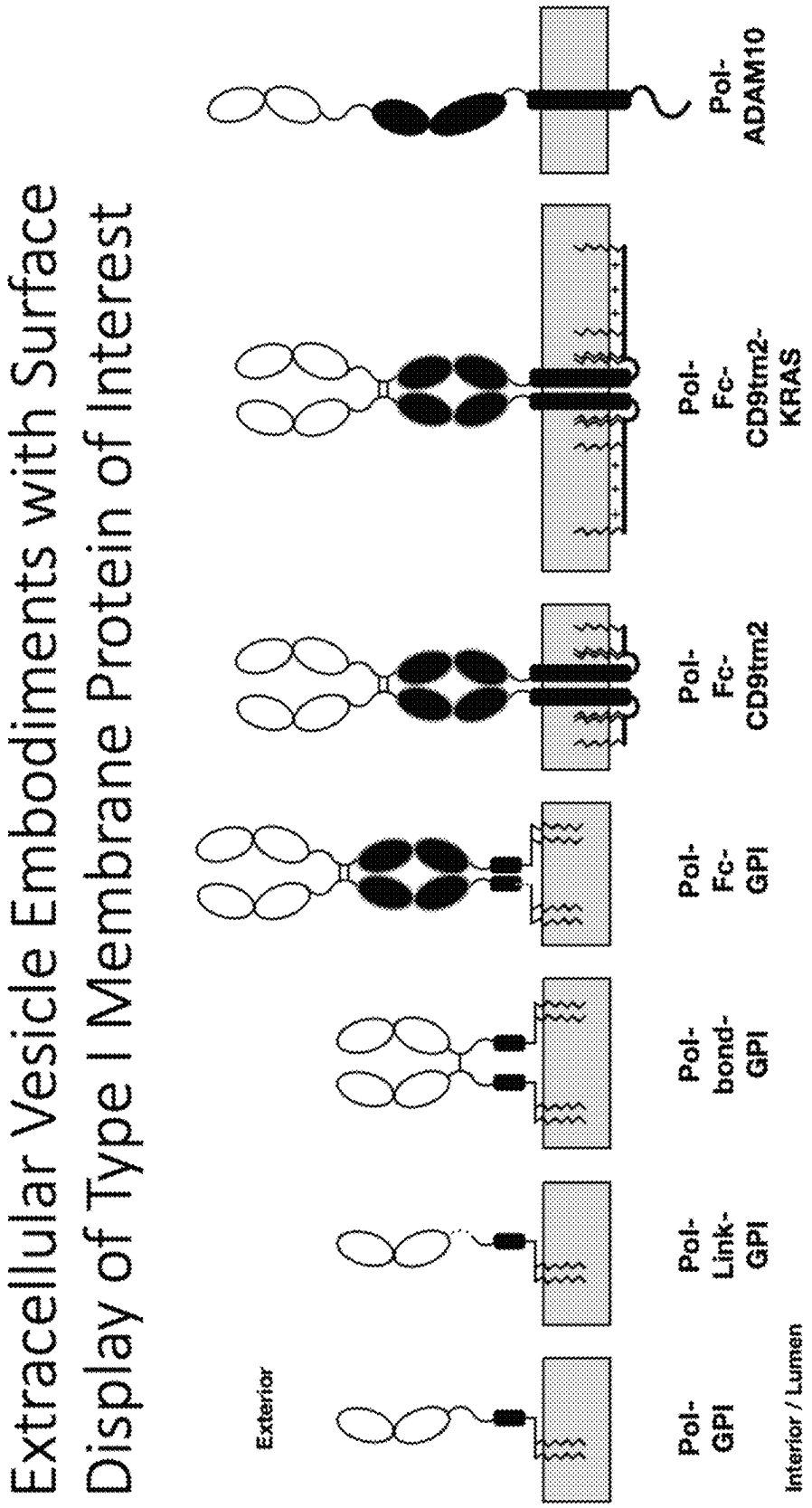

Extracellular Vesicle Embodiments with Surface Display of Type I Membrane Protein of Interest
Exterior
Interior / Lumen
Pol-GPI
Pol-Link-GPI
Pol-bond-GPI
Pol-Fc-GPI
Pol-Fc-CD9tm2
Pol-Fc-CD9tm2-KRAS
Pol-ADAM10

FIG. 16

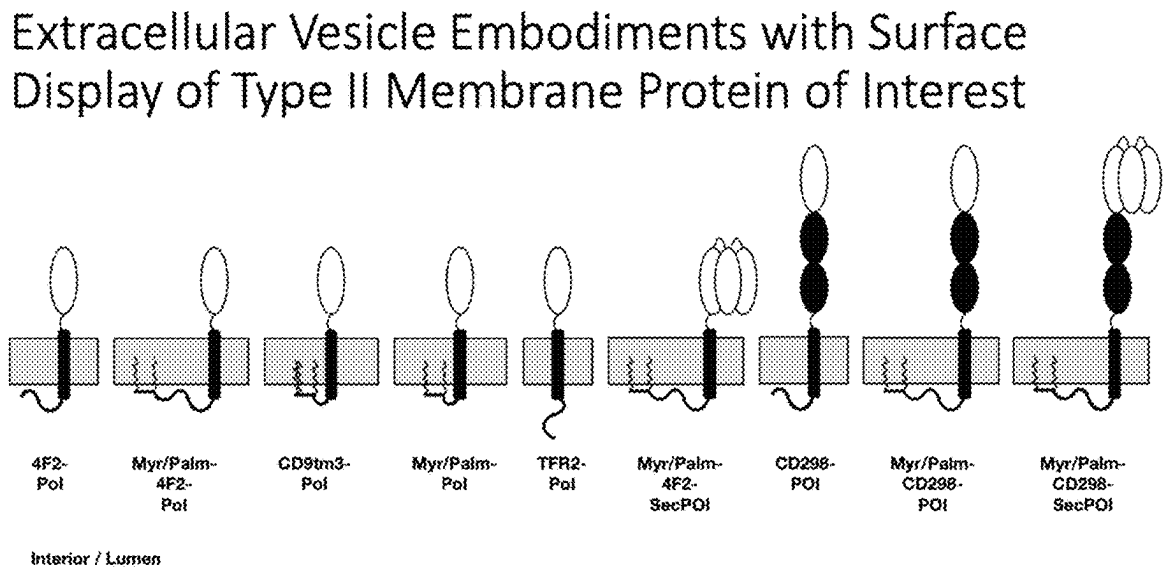

Extracellular Vesicle Embodiments with Surface Display of Type II Membrane Protein of Interest
4F2-Pol
Myr/Palm-4F2-Pol
CD9tm3-Pol
Myr/Palm-Pol
TFR2-Pol
Myr/Palm-4F2-SecPOI
CD298-POI
Myr/Palm-CD298-POI
Myr/Palm-CD298-SecPOI
Interior / Lumen

FIG. 17

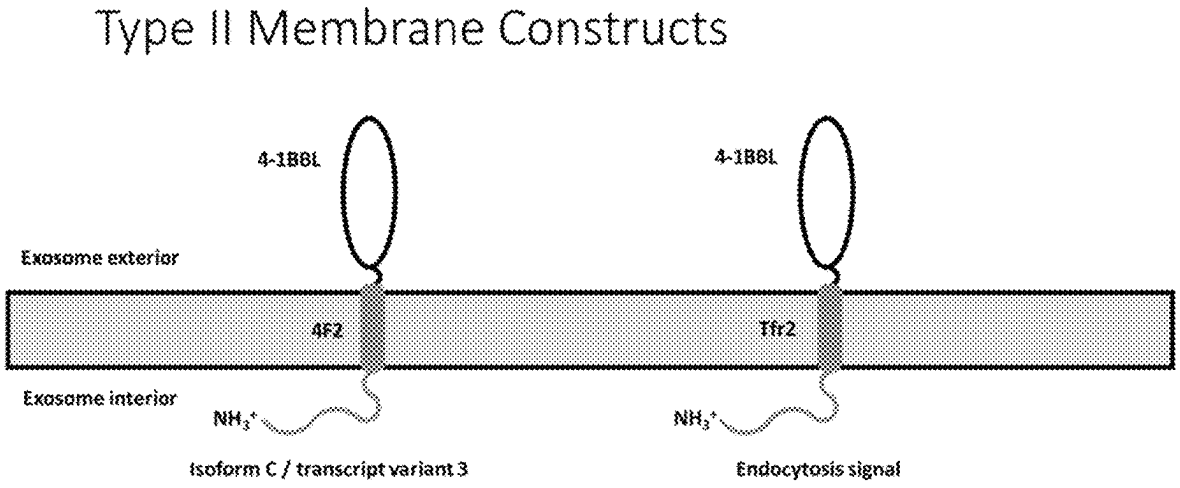

Type II Membrane Constructs
4-1BBL
4-1BBL
Exosome exterior
4F2
Tfr2
Exosome interior
NH3+
NH3+
Isoform C / transcript variant 3
Endocytosis signal

FIG. 18

Type II Membrane Protein Constructs

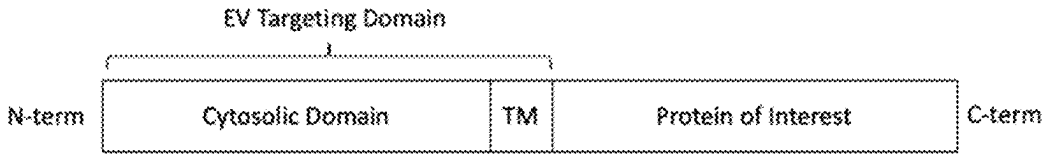


FIG. 19

Multiple Protein Display

FIG. 20

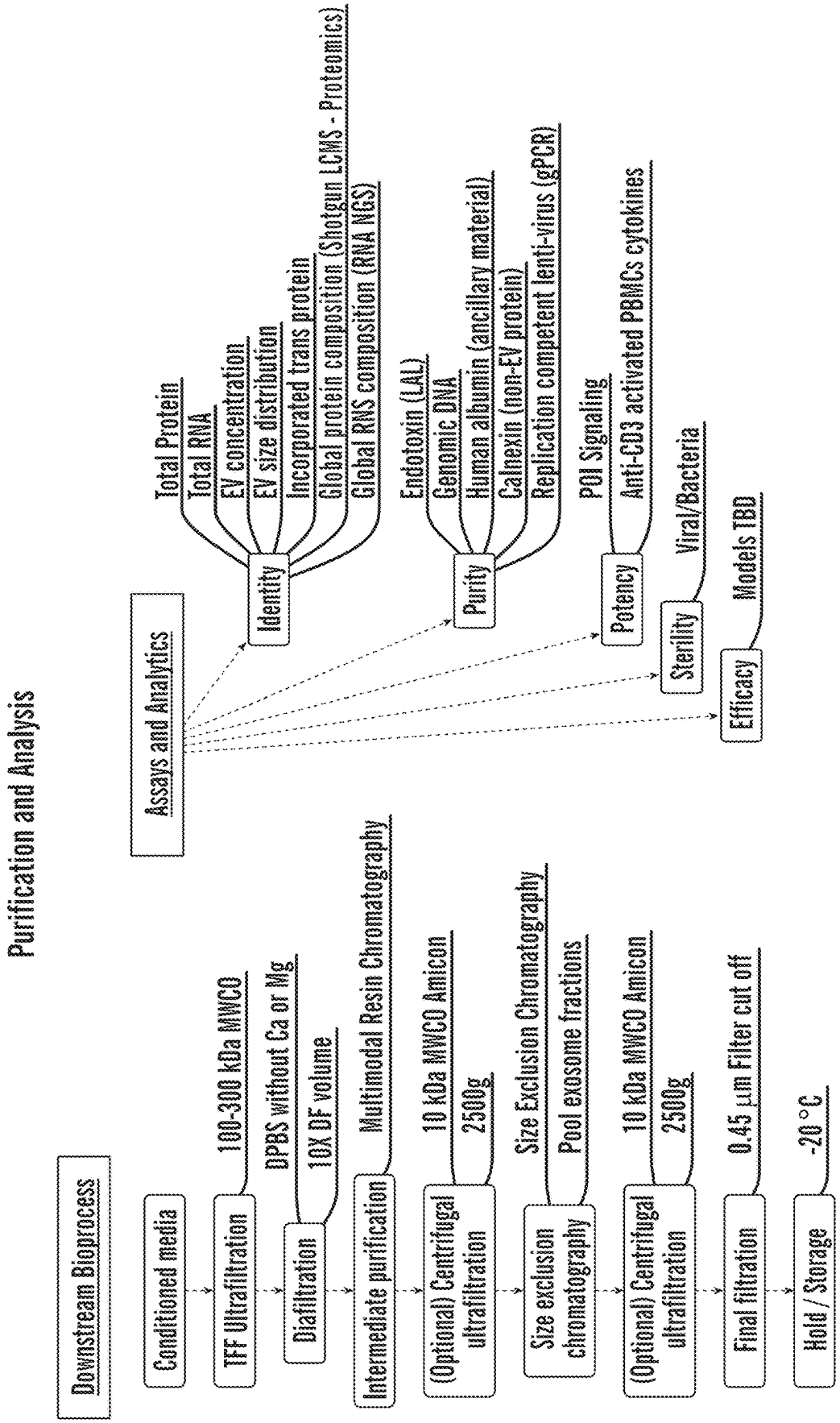

Purification and Analysis
Downstream Bioprocess
Conditioned media
TFF Ultrafiltration
100-300 kDa MWCO
Diafiltration
DPBS without Ca or Mg
10X DF volume
Intermediate purification
Multimodal Resin Chromatography
(Optional) Centrifugal ultrafiltration
10 kDa MWCO Amicon
2500g
Size exclusion chromatography
Size Exclusion Chromatography
Pool exosome fractions
(Optional) Centrifugal ultrafiltration
10 kDa MWCO Amicon
2500g
Final filtration
0.45 µm Filter cut off
Hold / Storage
-20 °C
Assays and Analytics
Identity
Total Protein
Total RNA
EV concentration
EV size distribution
Incorporated trans protein
Global protein composition (Shotgun LCMS - Proteomics)
Global RNS composition (RNA NGS)
Purity
Endotoxin (LAL)
Genomic DNA
Human albumin (ancillary material)
Calnexin (non-EV protein)
Replication competent lenti-virus (gPCR)
Potency
POI Signaling
Anti-CD3 activated PBMCs cytokines
Sterility
Viral/Bacteria
Efficacy
Models TBD

FIG. 21

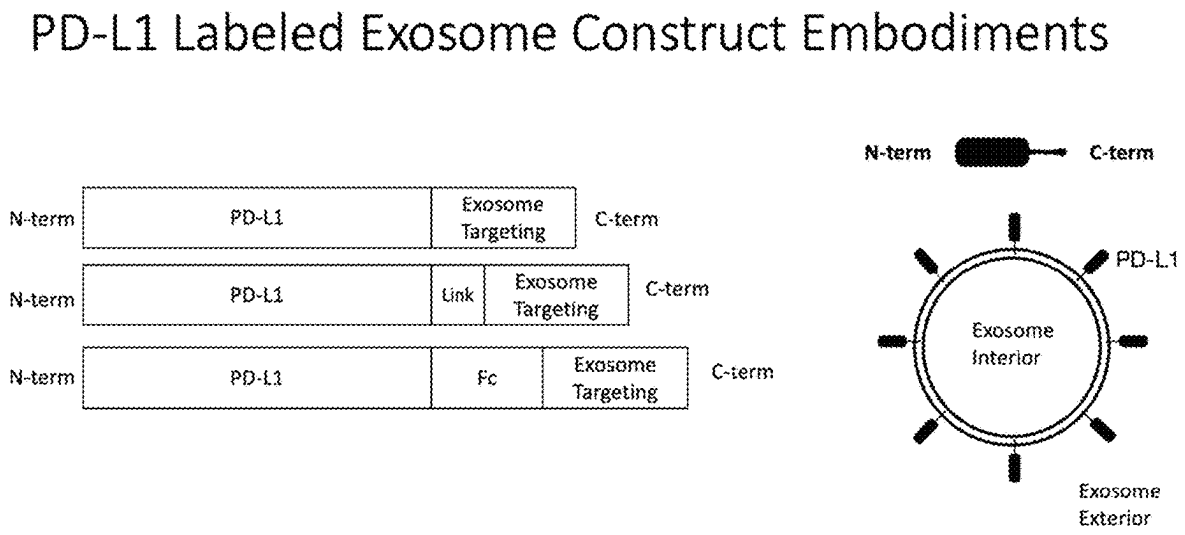

PD-L1 Labeled Exosome Construct Embodiments
N-term
PD-L1
Exosome Targeting
C-term
N-term
PD-L1
Link
Exosome Targeting
C-term
N-term
PD-L1
Fc
Exosome Targeting
C-term
N-term
C-term
PD-L1
Exosome Interior
Exosome Exterior

FIG. 22

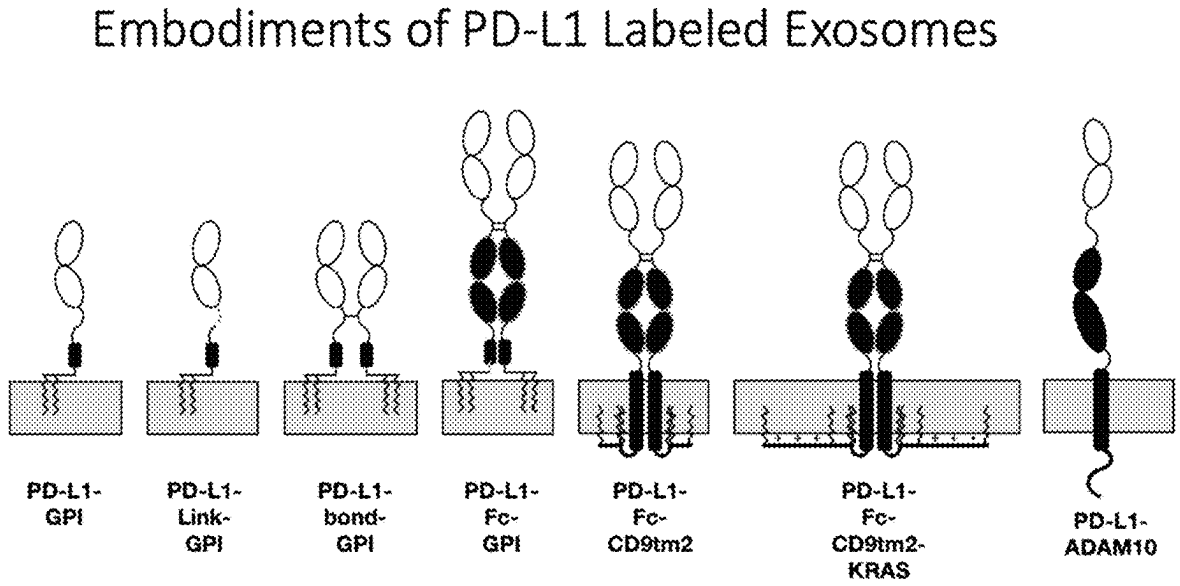

Embodiments of PD-L1 Labeled Exosomes
PD-L1-GPI
PD-L1-Link-GPI
PD-L1-bond-GPI
PD-L1-Fc-GPI
PD-L1-Fc-CD9tm2
PD-L1-Fc-CD9tm2-KRAS
PD-L1-ADAM10

FIG. 23

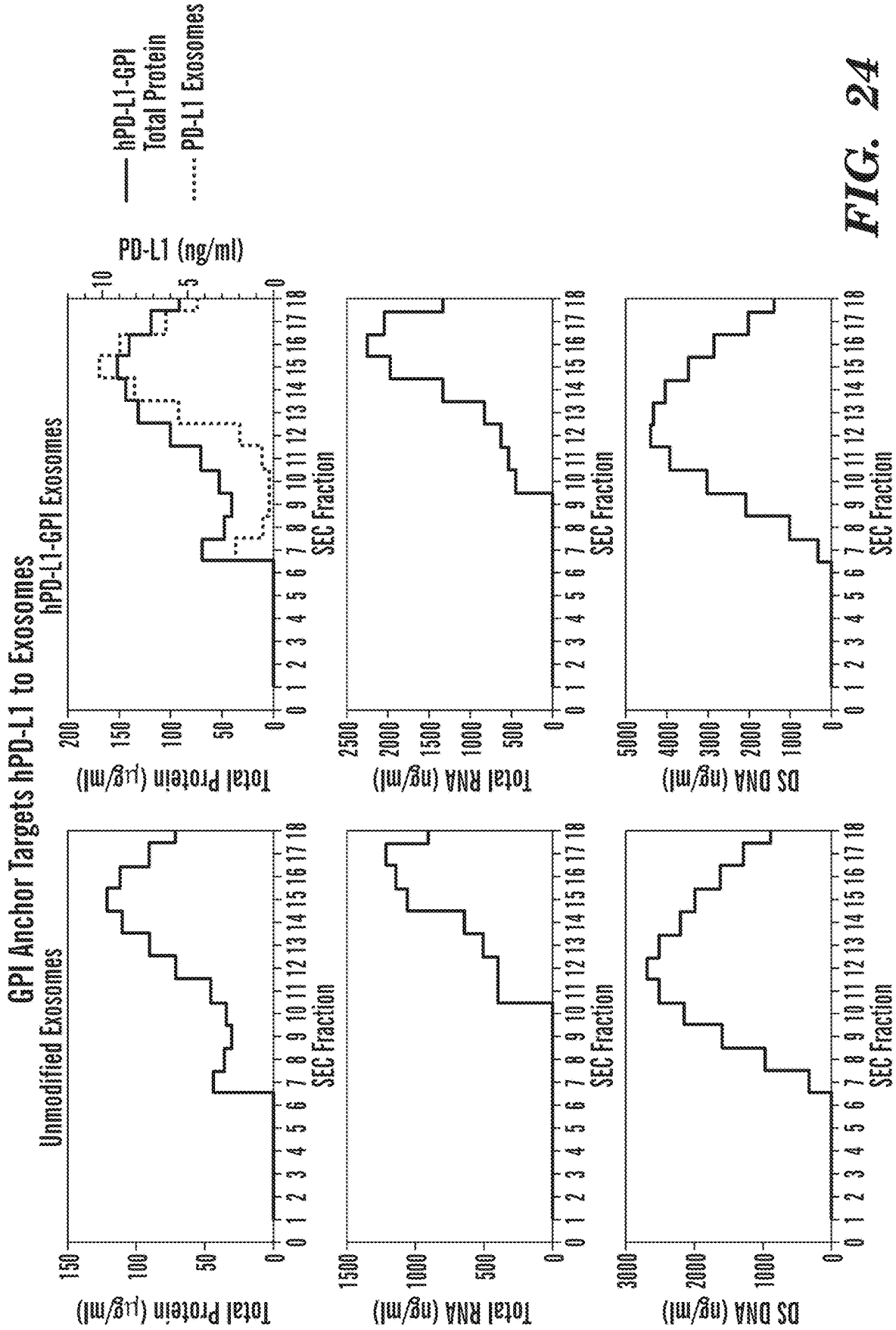

GPI Anchor Targets hPD-L1 to Exosomes
Unmodified Exosomes
hPD-L1-GPI Exosomes
hPD-L1-GPI
Total Protein
PD-L1 Exosomes
PD-L1 (ng/ml)
Total Protein (μg/ml)
Total RNA (ng/ml)
DS DNA (ng/ml)
SEC Fraction

FIG. 24

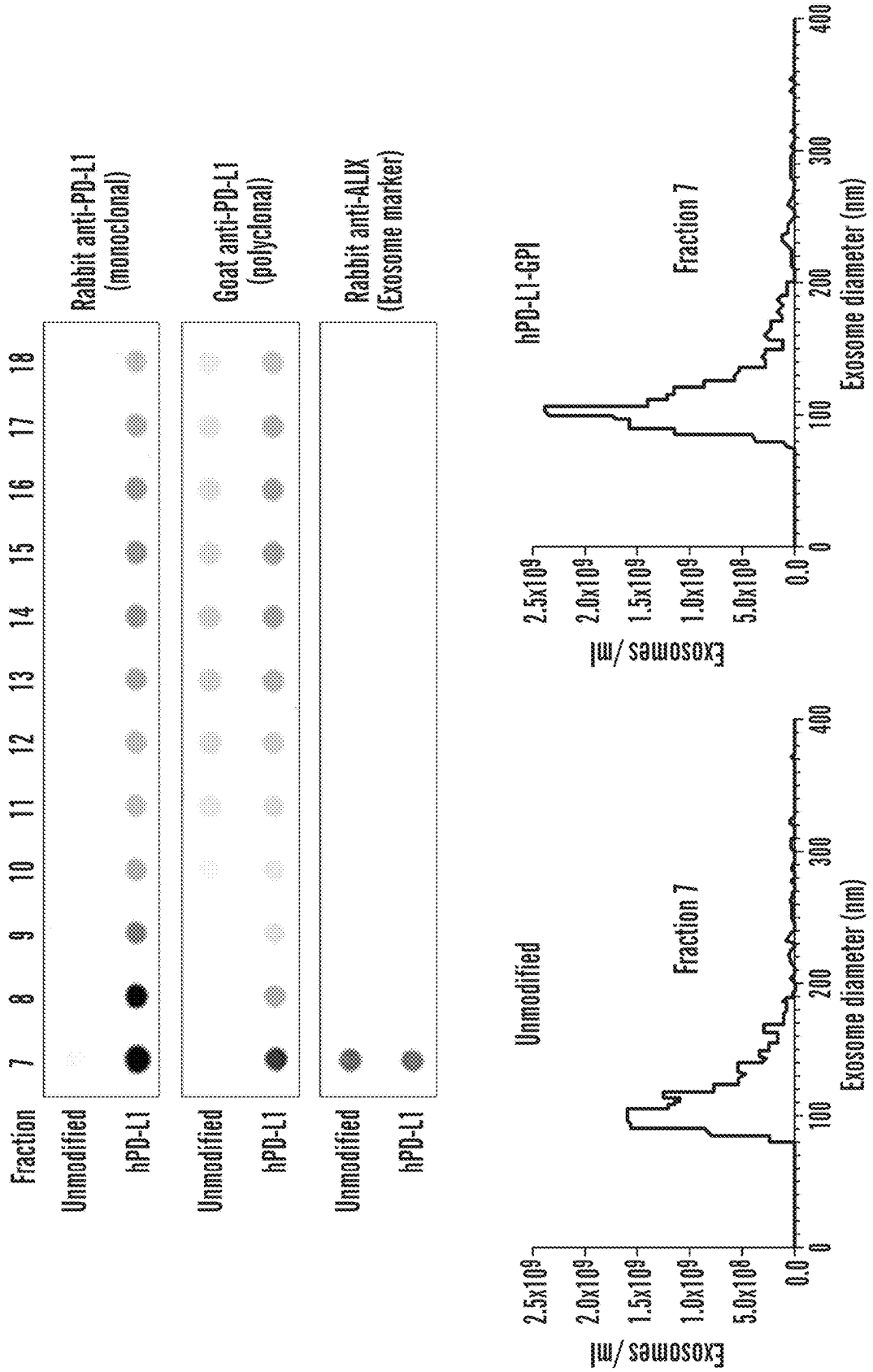

Fraction
7
8
9
10
11
12
13
14
15
16
17
18
Unmodified
hPD-L1
Rabbit anti-PD-L1 (monoclonal)
Unmodified
hPD-L1
Goat anti-PD-L1 (polyclonal)
Unmodified
hPD-L1
Rabbit anti-ALIX (Exosome marker)
Unmodified
Fraction 7
Exosomes /ml
2.5x10^9
2.0x10^9
1.5x10^9
1.0x10^9
5.0x10^8
0.0
0
100
200
300
400
Exosome diameter (nm)
hPD-L1-GPI
Fraction 7
Exosomes /ml
2.5x10^9
2.0x10^9
1.5x10^9
1.0x10^9
5.0x10^8
0.0
0
100
200
300
400
Exosome diameter (nm)

FIG. 24 (cont.)

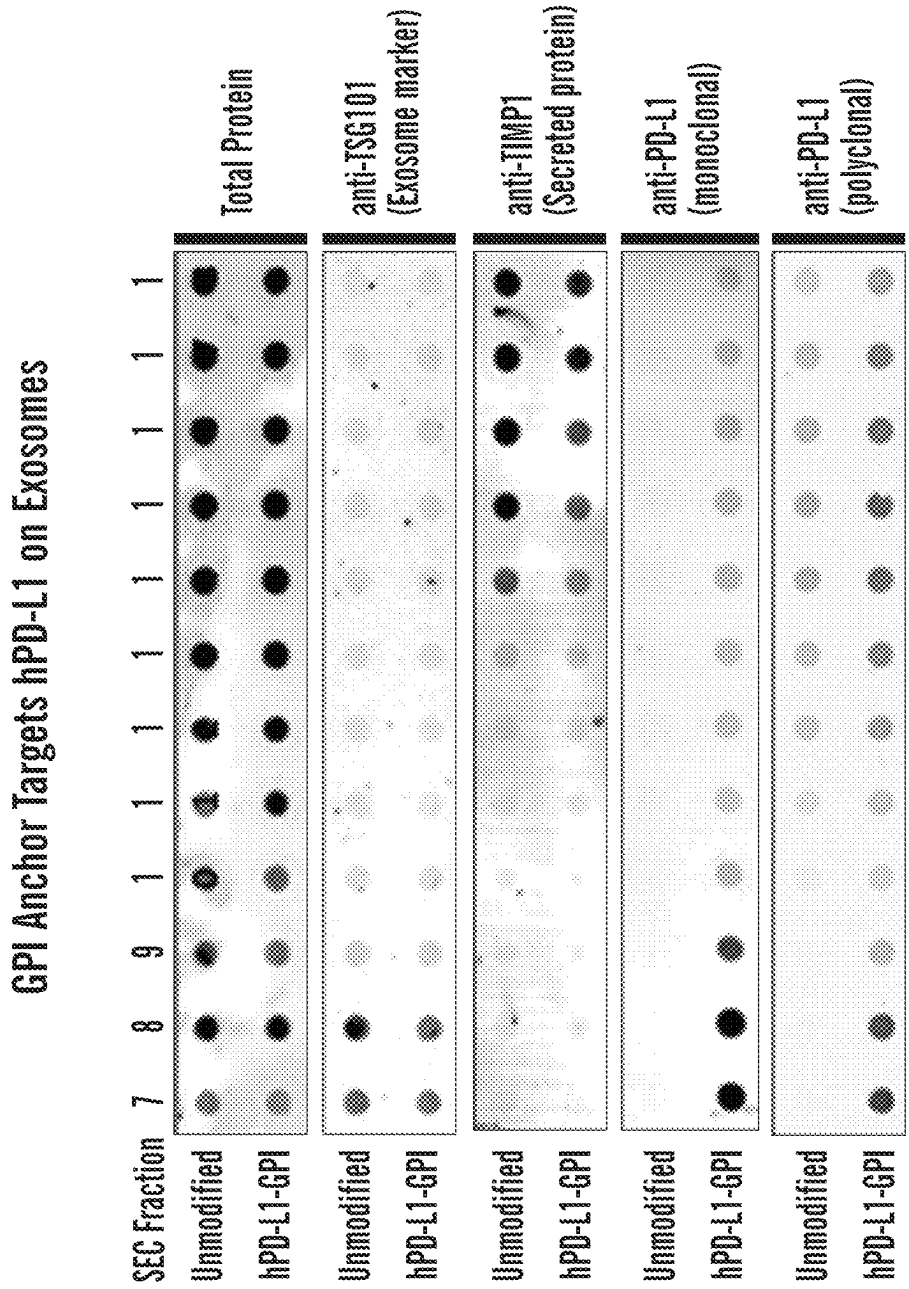

GPI Anchor Targets hPD-L1 on Exosomes
SEC Fraction
7
8
9
1
1
1
1
1
1
1
1
Unmodified
hPD-L1-GPI
Total Protein
anti-TSG101 (Exosome marker)
anti-TIMP1 (Secreted protein)
anti-PD-L1 (monoclonal)
anti-PD-L1 (polyclonal)

FIG. 25

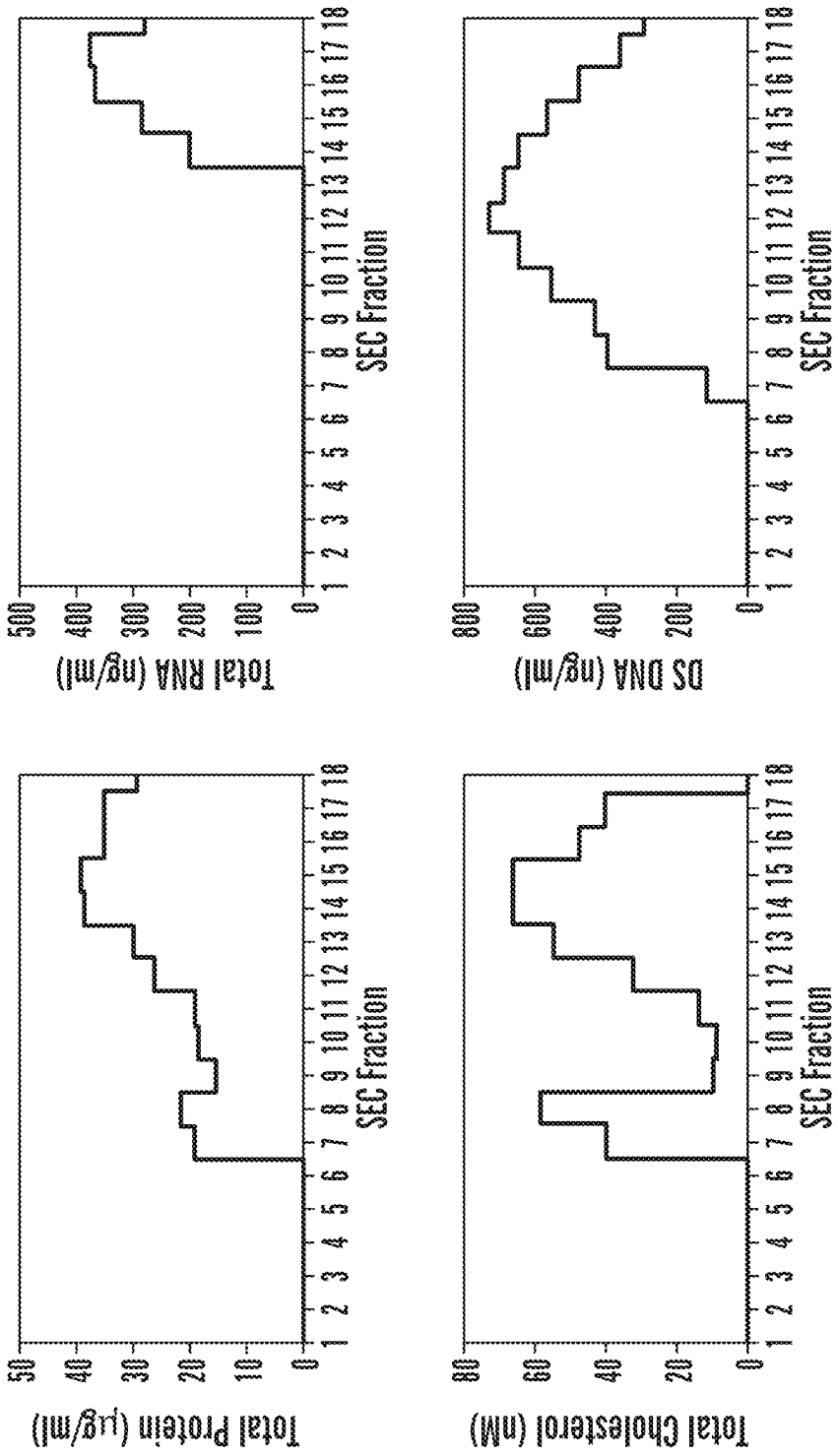

Total Protein (μg/ml)
50
40
30
20
10
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
SEC Fraction
Total RNA (ng/ml)
500
400
300
200
100
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
SEC Fraction
Total Cholesterol (nM)
80
60
40
20
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
SEC Fraction
DS DNA (ng/ml)
800
600
400
200
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
SEC Fraction

FIG. 25 (cont.)

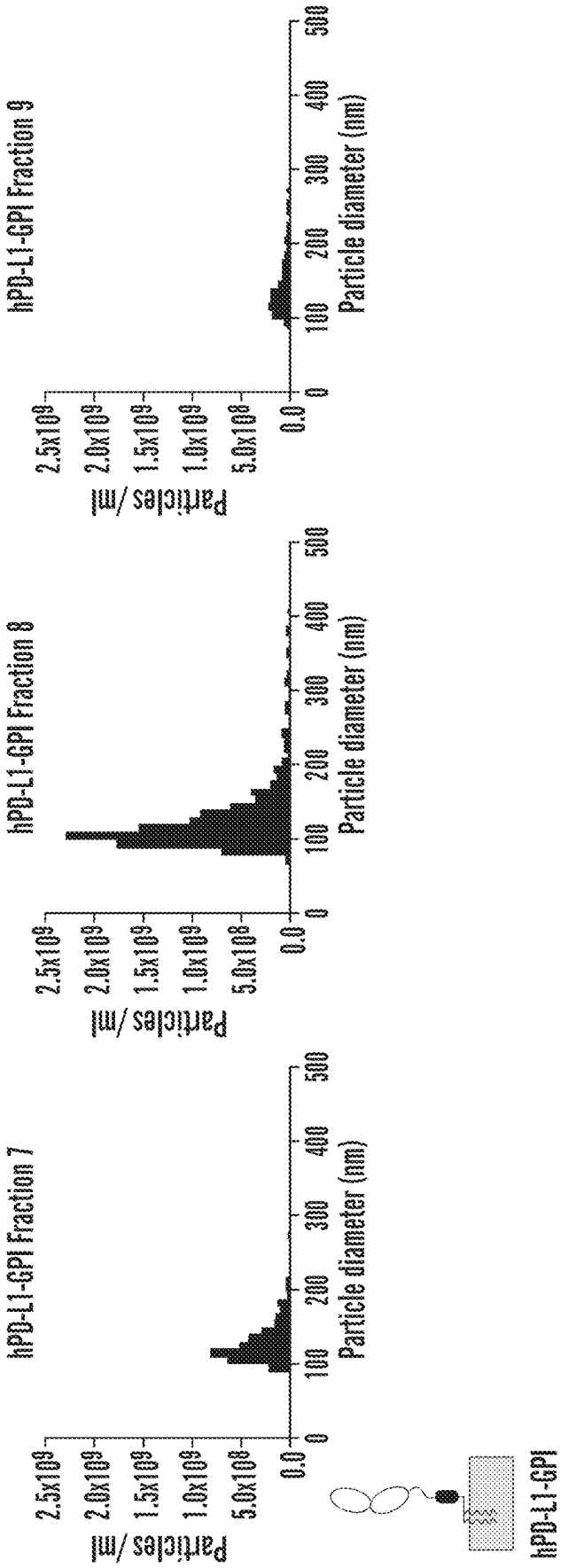

hPD-L1-GPI Fraction 7
hPD-L1-GPI Fraction 8
hPD-L1-GPI Fraction 9
Particles /ml
2.5x10^9
2.0x10^9
1.5x10^9
1.0x10^9
5.0x10^8
0.0
0
100
200
300
400
500
Particle diameter (nm)
hPD-L1-GPI

FIG. 25 (cont.)

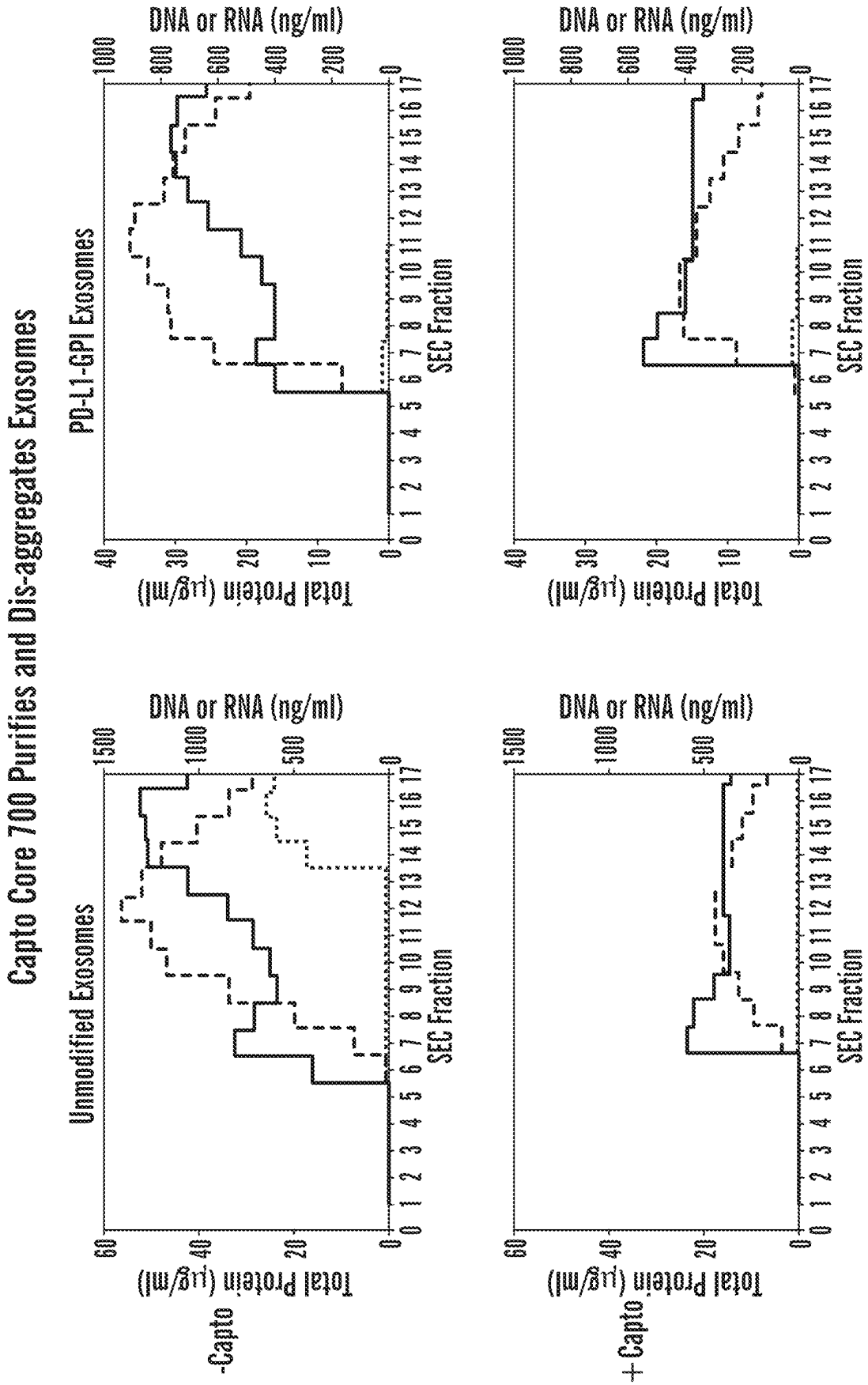

Capto Core 700 Purifies and Dis-aggregates Exosomes
Unmodified Exosomes
PD-L1-GPI Exosomes
-Capto
+Capto
Total Protein (µg/ml)
DNA or RNA (ng/ml)
SEC Fraction

FIG. 26

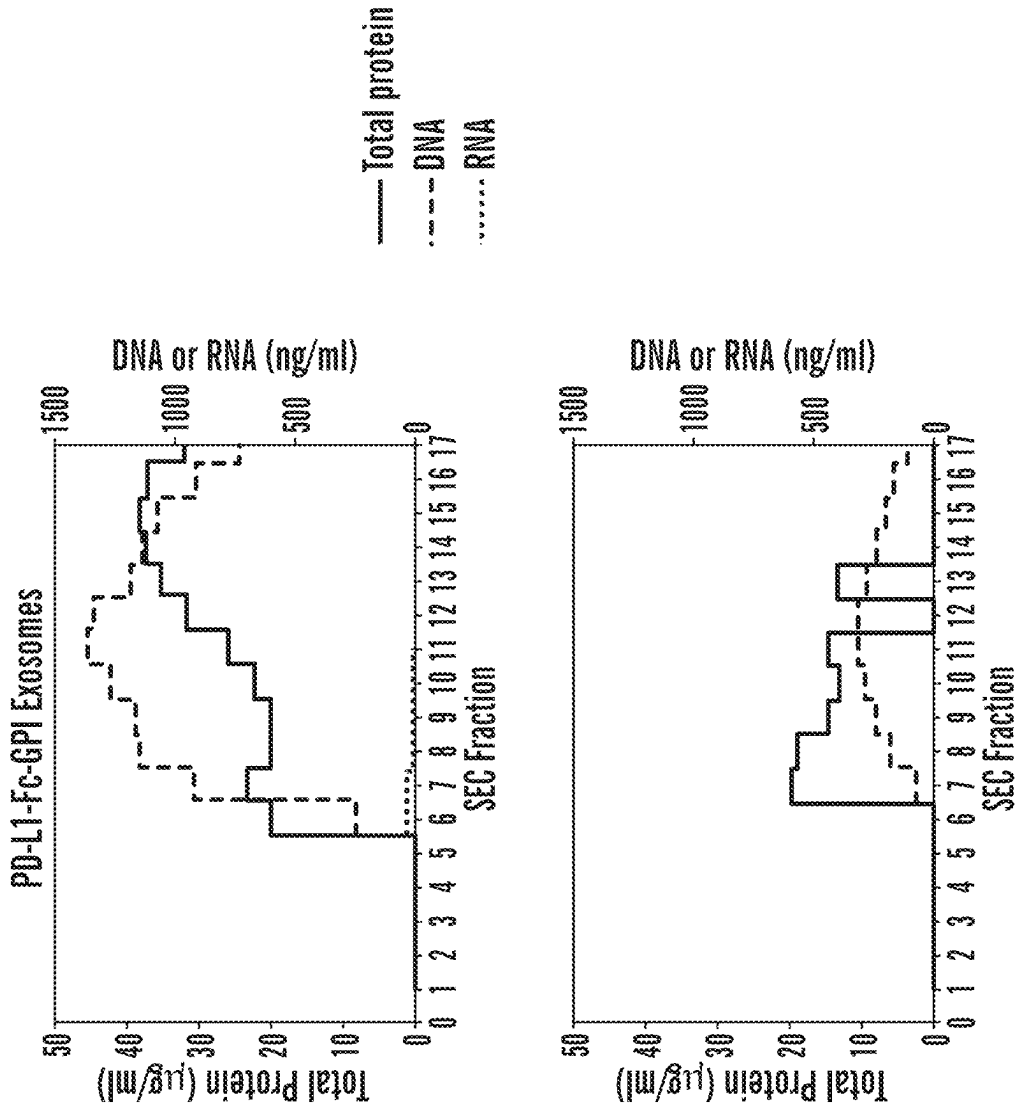

Total protein
DNA
RNA
PD-L1-Fc-GPI Exosomes
DNA or RNA (ng/ml)
1500
1000
500
0
Total Protein (µg/ml)
50
40
30
20
10
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17
SEC Fraction
DNA or RNA (ng/ml)
1500
1000
500
0
Total Protein (µg/ml)
50
40
30
20
10
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17
SEC Fraction

FIG. 26 (cont.)

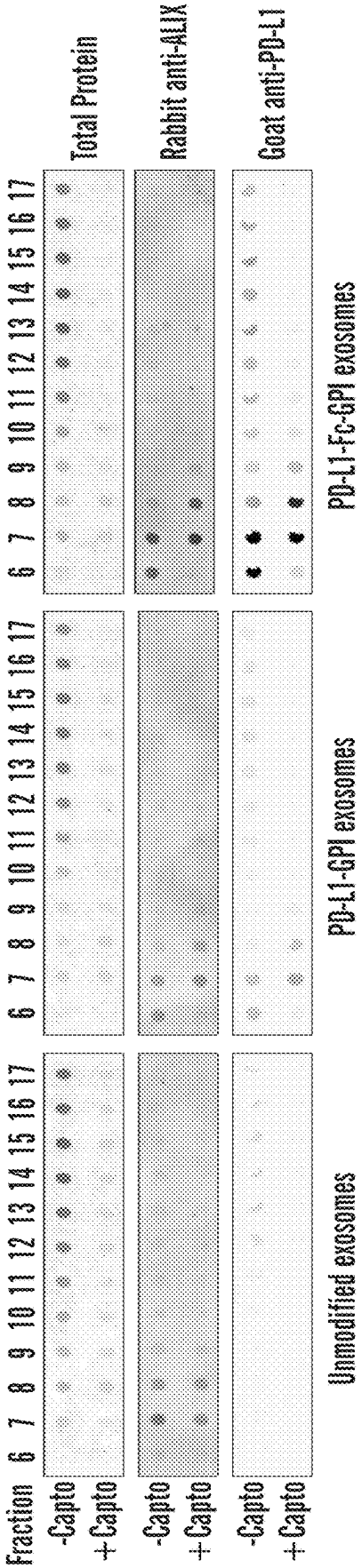

Fraction
6 7 8 9 10 11 12 13 14 15 16 17
-Capto
+Capto
Unmodified exosomes
PD-L1-GPI exosomes
PD-L1-Fc-GPI exosomes
Total Protein
Rabbit anti-ALIX
Goat anti-PD-L1

FIG. 26 (cont.)

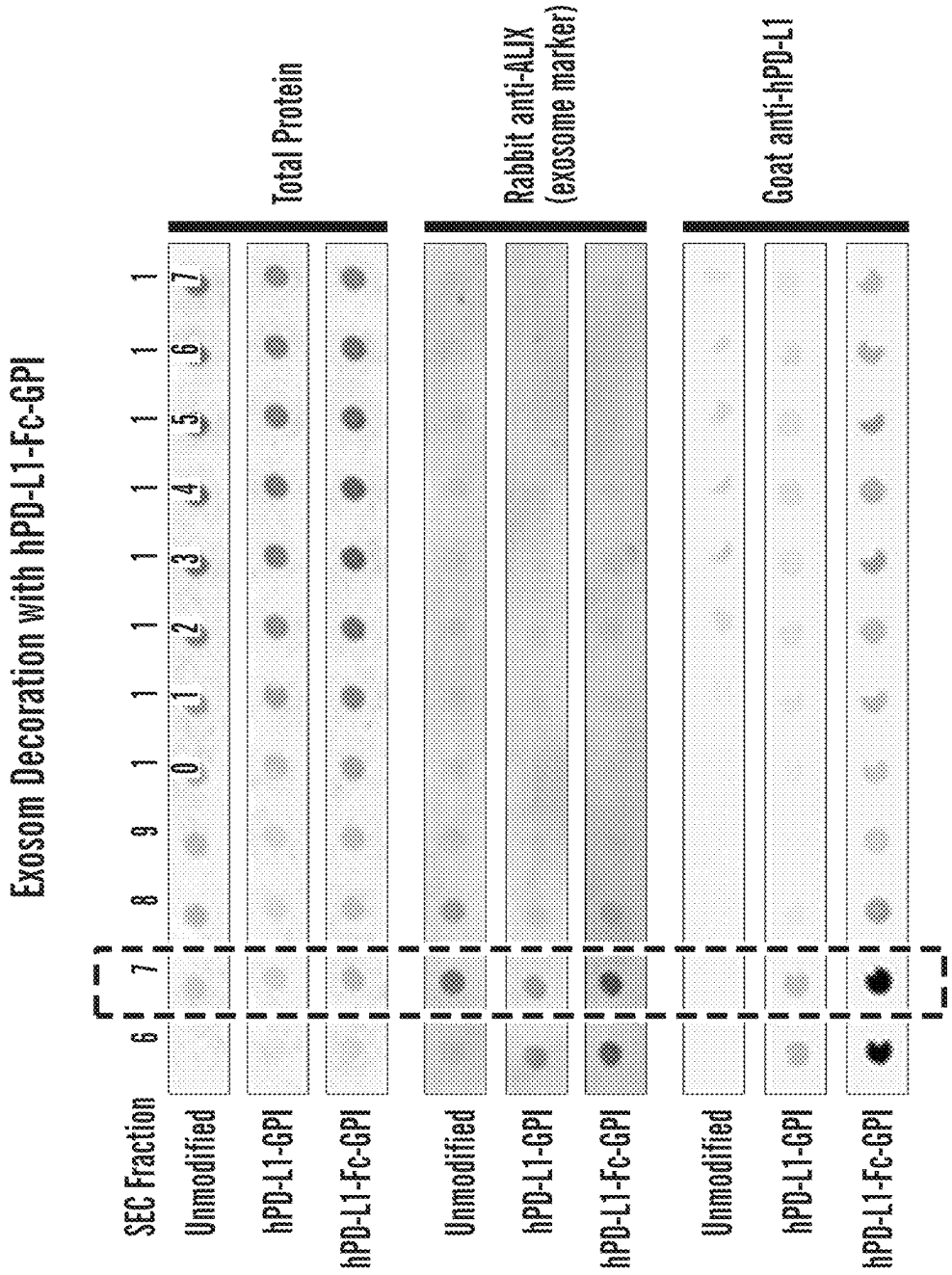

Exosom Decoration with hPD-L1-Fc-GPI
SEC Fraction
6
7
8
9
10
11
12
13
14
15
16
17
Unmodified
hPD-L1-GPI
hPD-L1-Fc-GPI
Total Protein
Rabbit anti-ALIX (exosome marker)
Goat anti-hPD-L1

FIG. 27

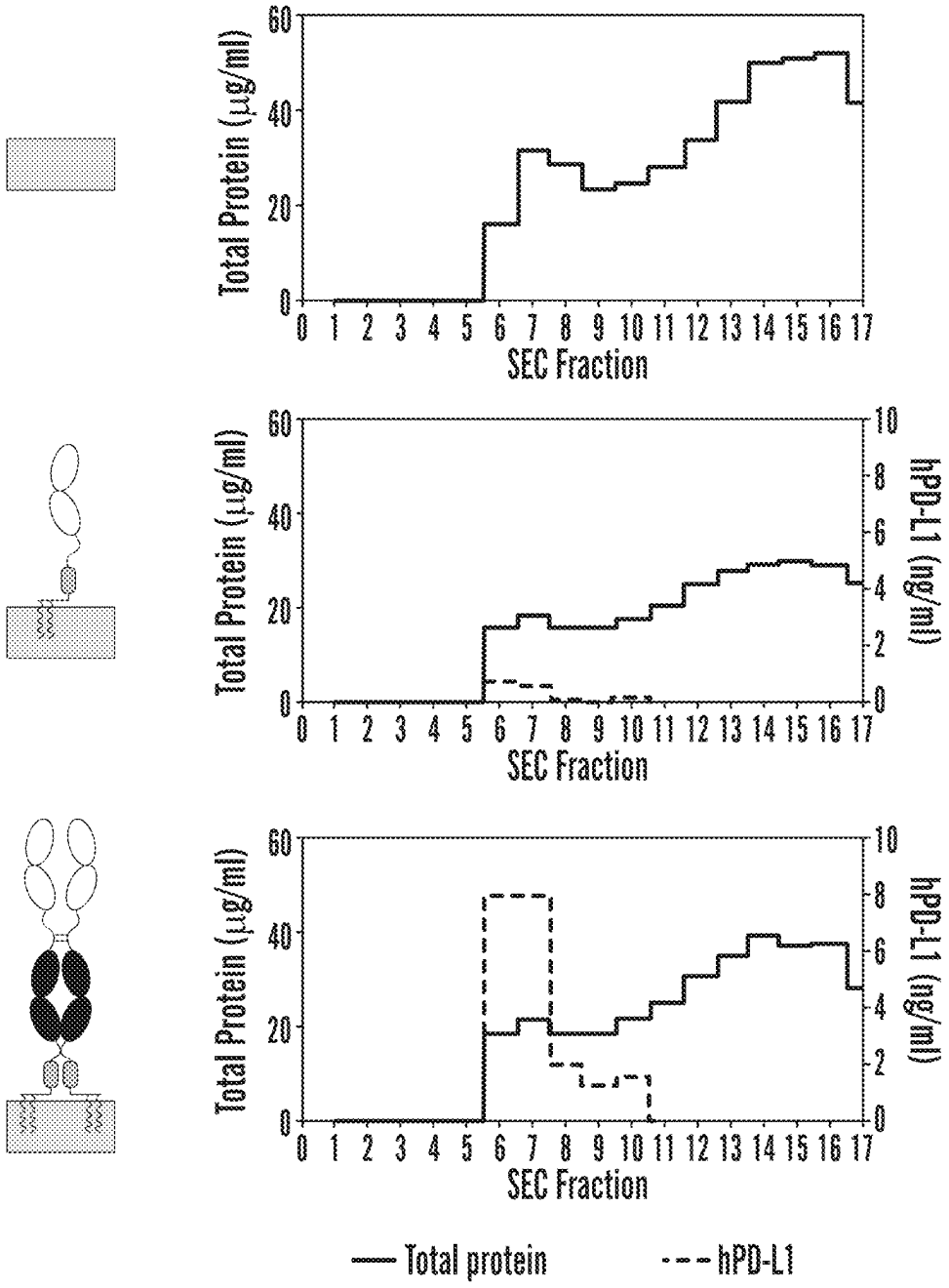

Total Protein (μg/ml)
SEC Fraction
hPD-L1 (ng/ml)
Total protein
hPD-L1

FIG. 27 (cont.)

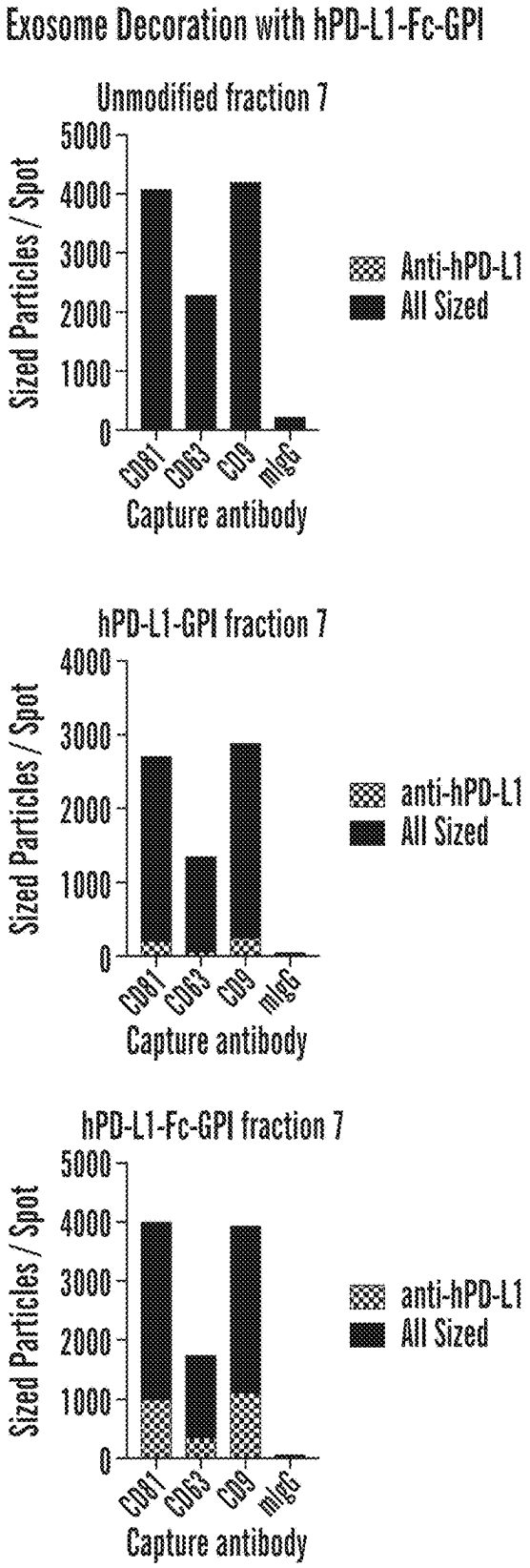

Exosome Decoration with hPD-L1-Fc-GPI
Unmodified fraction 7
Sized Particles / Spot
5000
4000
3000
2000
1000
0
CD81
CD63
CD9
mIgG
Capture antibody
Anti-hPD-L1
All Sized
hPD-L1-GPI fraction 7
Sized Particles / Spot
4000
3000
2000
1000
0
CD81
CD63
CD9
mIgG
Capture antibody
anti-hPD-L1
All Sized
hPD-L1-Fc-GPI fraction 7
Sized Particles / Spot
5000
4000
3000
2000
1000
0
CD81
CD63
CD9
mIgG
Capture antibody
anti-hPD-L1
All Sized

FIG. 28A

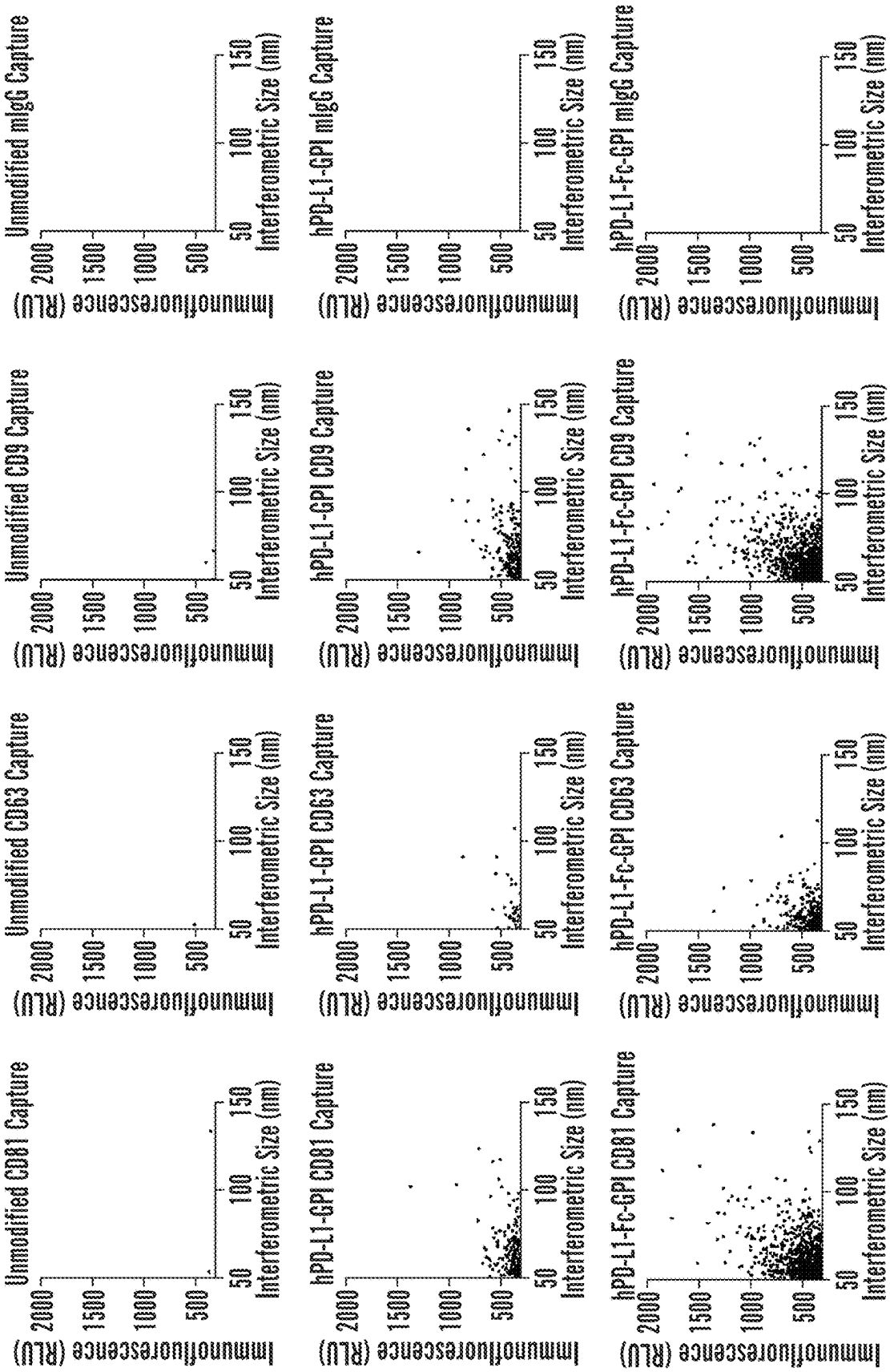

Unmodified CD81 Capture
hPD-L1-GPI CD81 Capture
hPD-L1-Fc-GPI CD81 Capture
Unmodified CD63 Capture
hPD-L1-GPI CD63 Capture
hPD-L1-Fc-GPI CD63 Capture
Unmodified CD9 Capture
hPD-L1-GPI CD9 Capture
hPD-L1-Fc-GPI CD9 Capture
Unmodified mIgG Capture
hPD-L1-GPI mIgG Capture
hPD-L1-Fc-GPI mIgG Capture
Immunofluorescence (RLU)
2000
1500
1000
500
50
100
150
Interferometric Size (nm)

FIG. 28A (cont.)

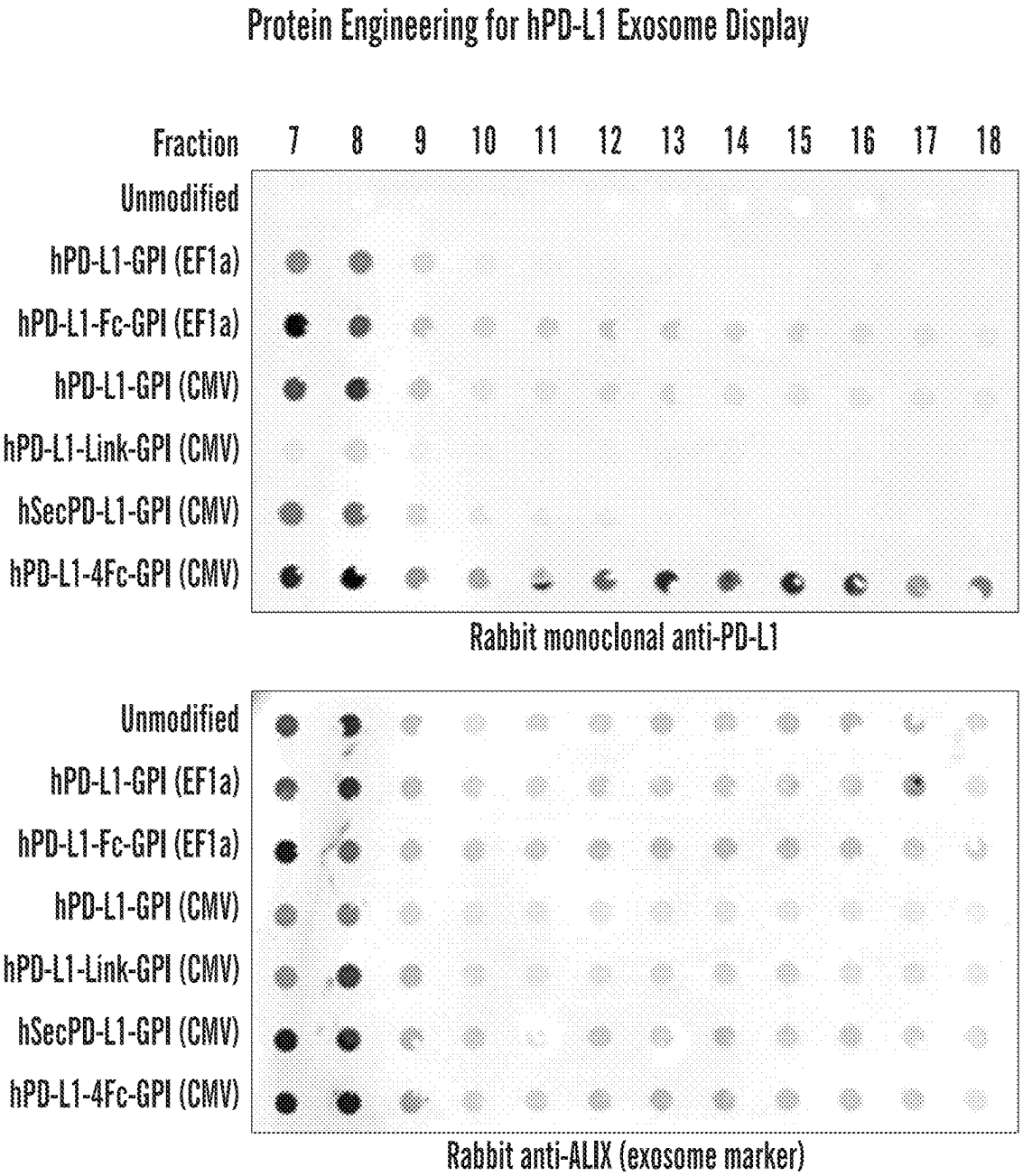

Protein Engineering for hPD-L1 Exosome Display
Fraction
7
8
9
10
11
12
13
14
15
16
17
18
Unmodified
hPD-L1-GPI (EF1a)
hPD-L1-Fc-GPI (EF1a)
hPD-L1-GPI (CMV)
hPD-L1-Link-GPI (CMV)
hSecPD-L1-GPI (CMV)
hPD-L1-4Fc-GPI (CMV)
Rabbit monoclonal anti-PD-L1
Unmodified
hPD-L1-GPI (EF1a)
hPD-L1-Fc-GPI (EF1a)
hPD-L1-GPI (CMV)
hPD-L1-Link-GPI (CMV)
hSecPD-L1-GPI (CMV)
hPD-L1-4Fc-GPI (CMV)
Rabbit anti-ALIX (exosome marker)

FIG. 28B

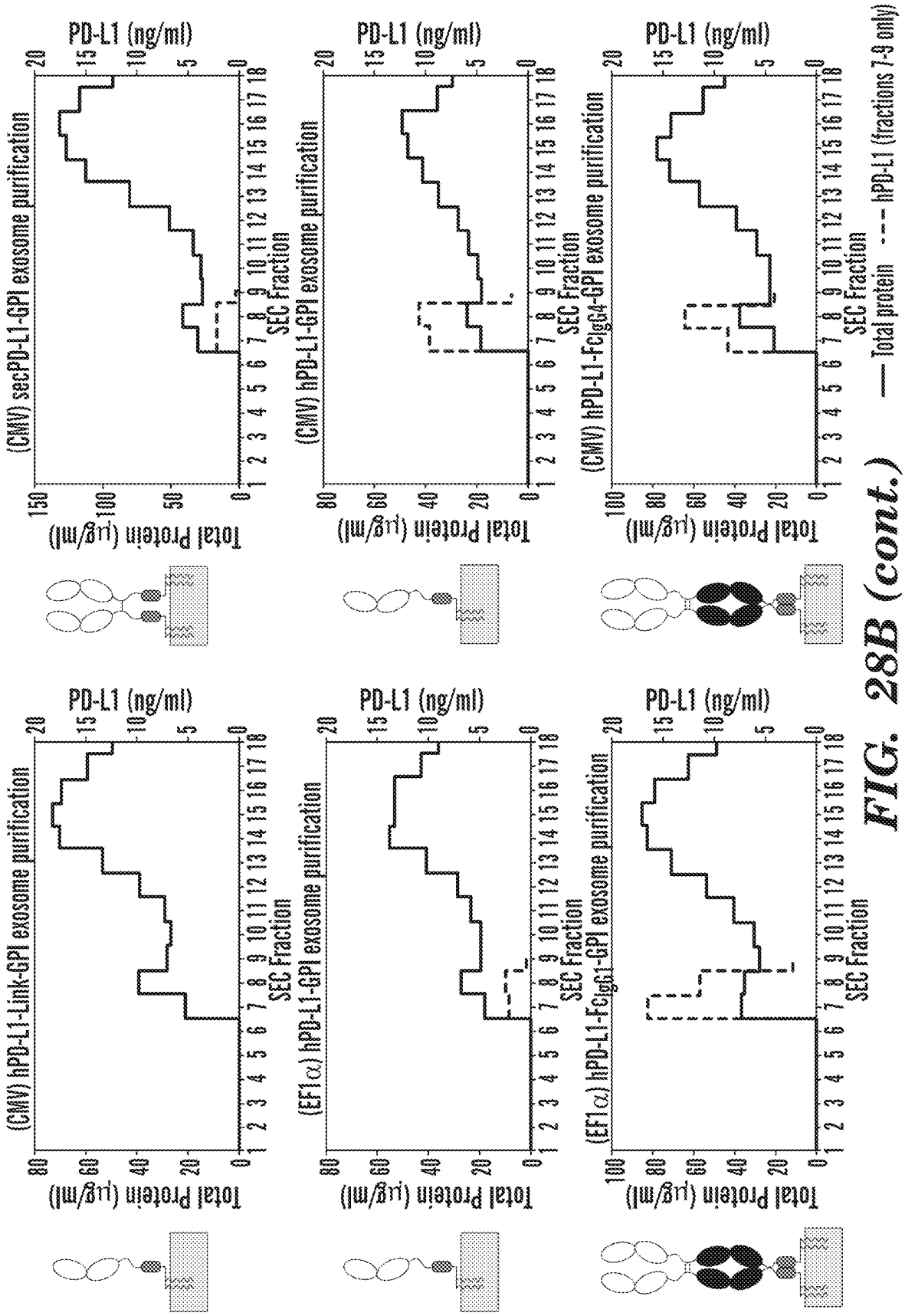

(CMV) hPD-L1-Link-GPI exosome purification
(EF1α) hPD-L1-GPI exosome purification
(EF1α) hPD-L1-FcIgG1-GPI exosome purification
(CMV) secPD-L1-GPI exosome purification
(CMV) hPD-L1-GPI exosome purification
(CMV) hPD-L1-FcIgG4-GPI exosome purification
Total Protein (μg/ml)
PD-L1 (ng/ml)
SEC Fraction
— Total protein
--- hPD-L1 (fractions 7-9 only)

FIG. 28B (cont.)

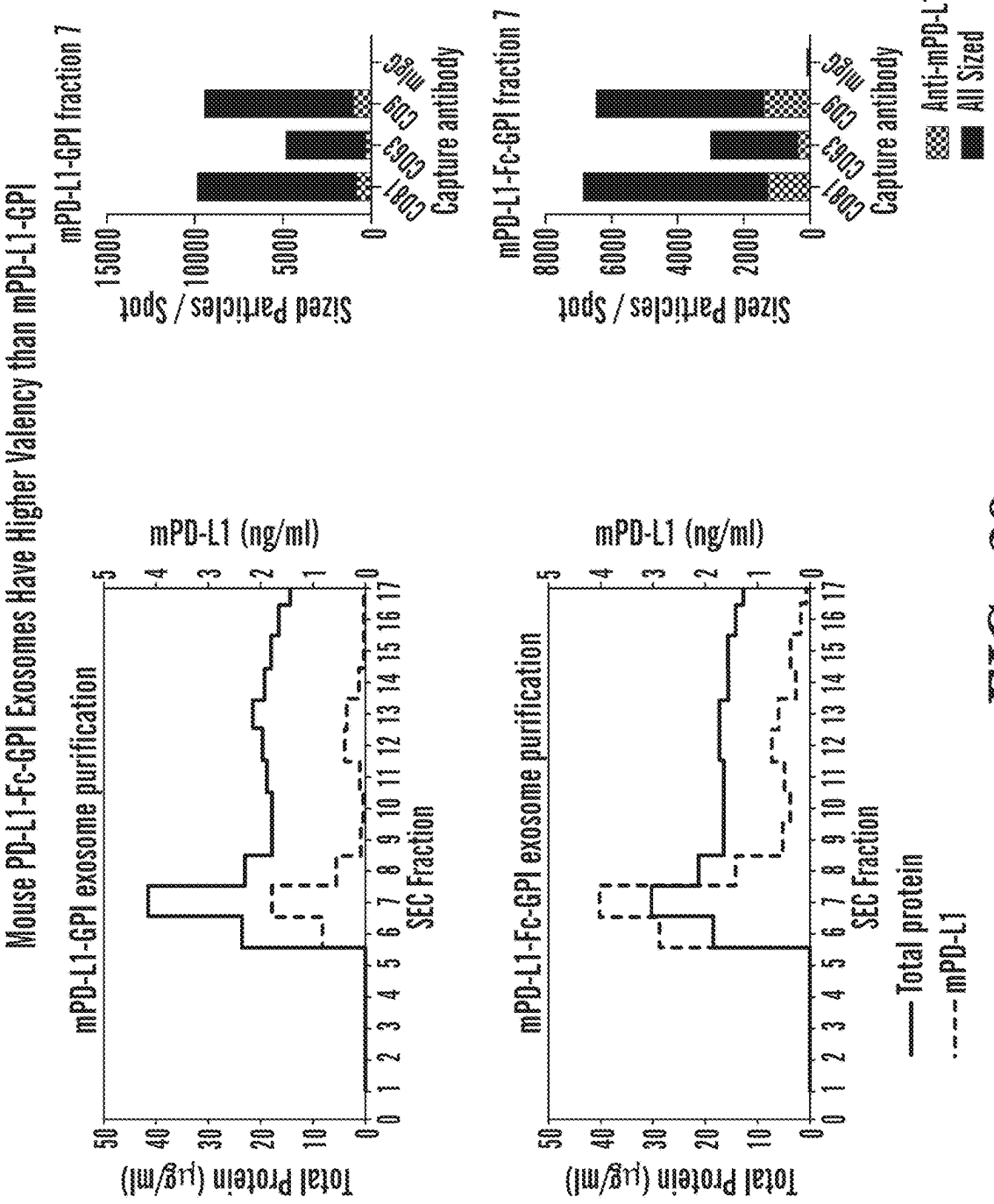

Mouse PD-L1-Fc-GPI Exosomes Have Higher Valency than mPD-L1-GPI
mPD-L1-GPI exosome purification
mPD-L1 (ng/ml)
Total Protein (µg/ml)
SEC Fraction
mPD-L1-Fc-GPI exosome purification
mPD-L1-GPI fraction 7
mPD-L1-Fc-GPI fraction 7
Sized Particles / Spot
Capture antibody
CD81
CD63
CD9
mIgG
Anti-mPD-L1
All Sized
Total protein
mPD-L1

FIG. 29

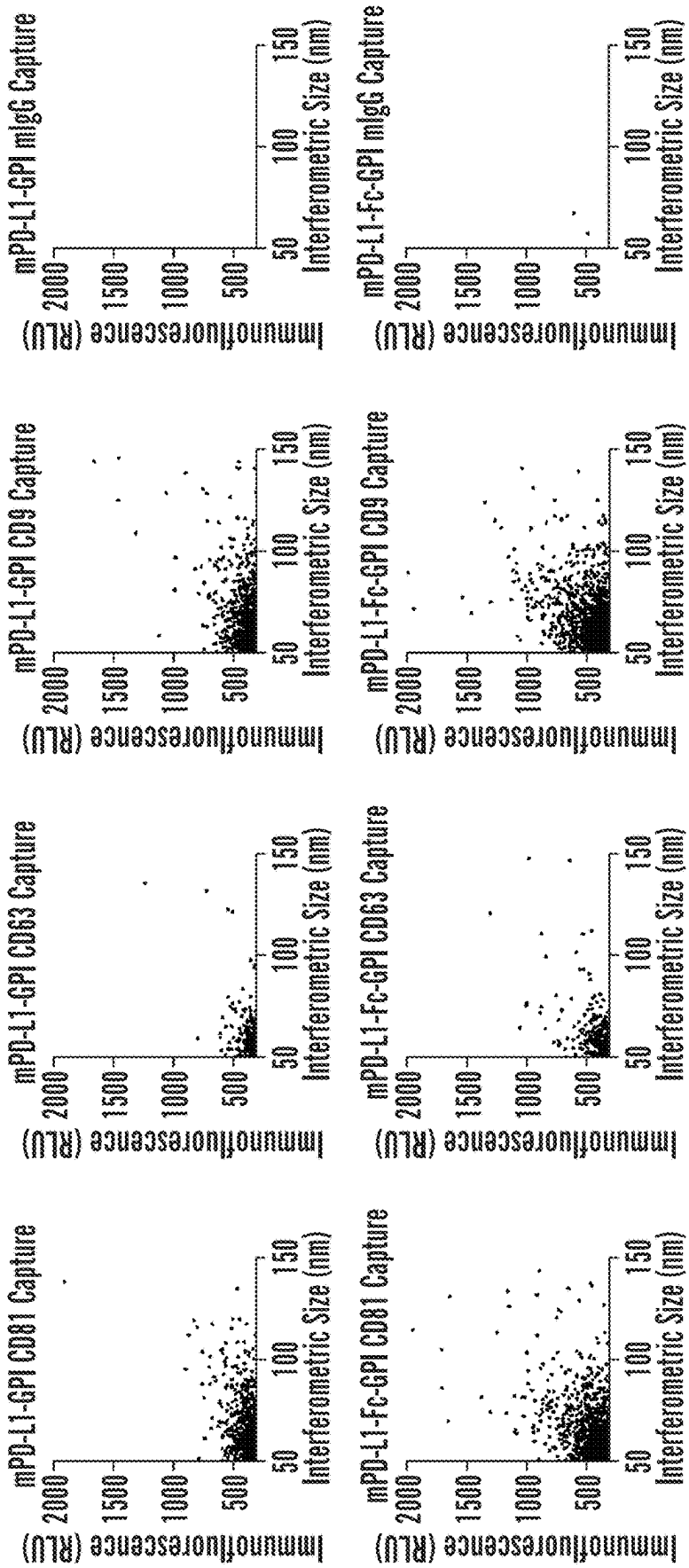

mPD-L1-GPI CD81 Capture
mPD-L1-Fc-GPI CD81 Capture
mPD-L1-GPI CD63 Capture
mPD-L1-Fc-GPI CD63 Capture
mPD-L1-GPI CD9 Capture
mPD-L1-Fc-GPI CD9 Capture
mPD-L1-GPI mIgG Capture
mPD-L1-Fc-GPI mIgG Capture
Immunofluorescence (RLU)
2000
1500
1000
500
50
100
150
Interferometric Size (nm)

FIG. 29 (cont.)

Comparative Proteomics

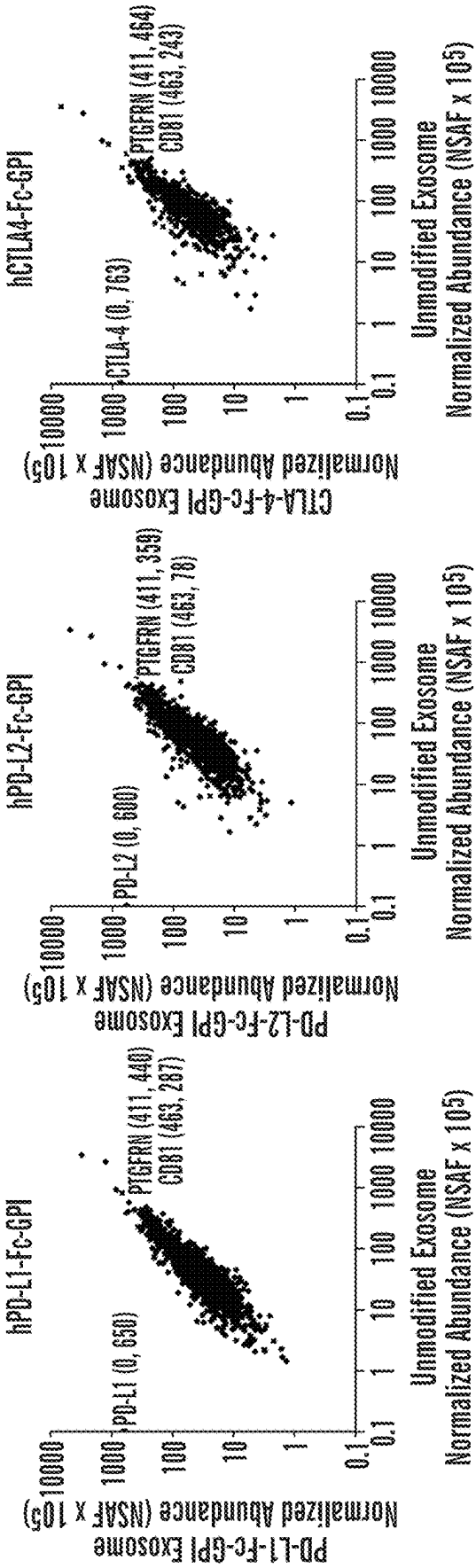
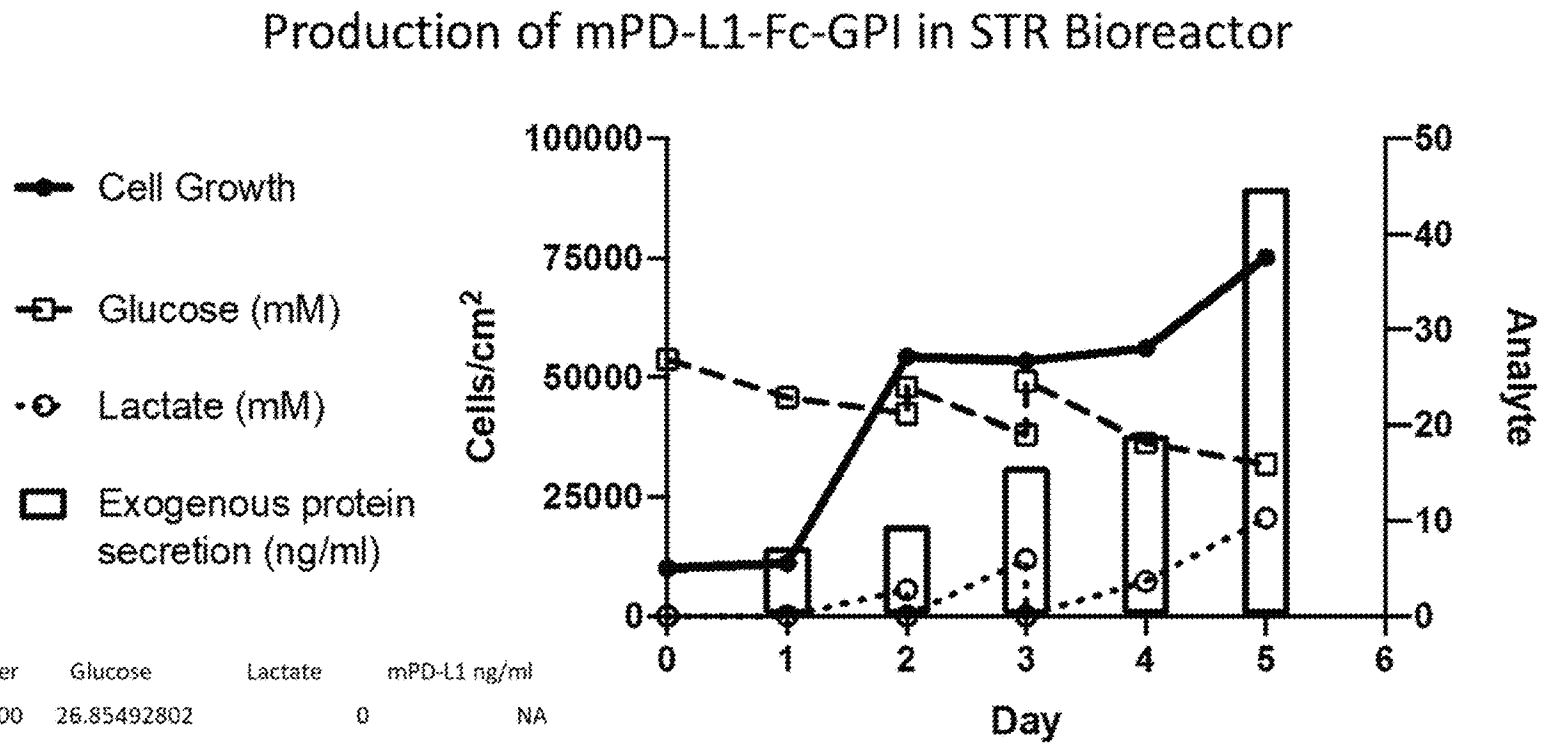


FIG. 30A

FIG. 30B

FIG. 30C



	Cell number	Glucose	Lactate	mPD-L1 ng/ml
Day 0	10,000	26.85492802	0	NA
Day 1	1.11E+04	22.86821705	0	7.33
Day 2	5.43E+04	21.20708749	2.775310835	
Day 2 Post	5.43E+04	23.97563677	0	9.61
Day 3	5.34E+04	18.99224806	5.994671403	
Day 3 Post	5.34E+04	24.58471761	0	15.77
Day 4	5.60E+04	18.16168328	3.663410302	19.05
Day 5	7.51E+04	15.94684385	10.32415631	44.89

FIG. 31

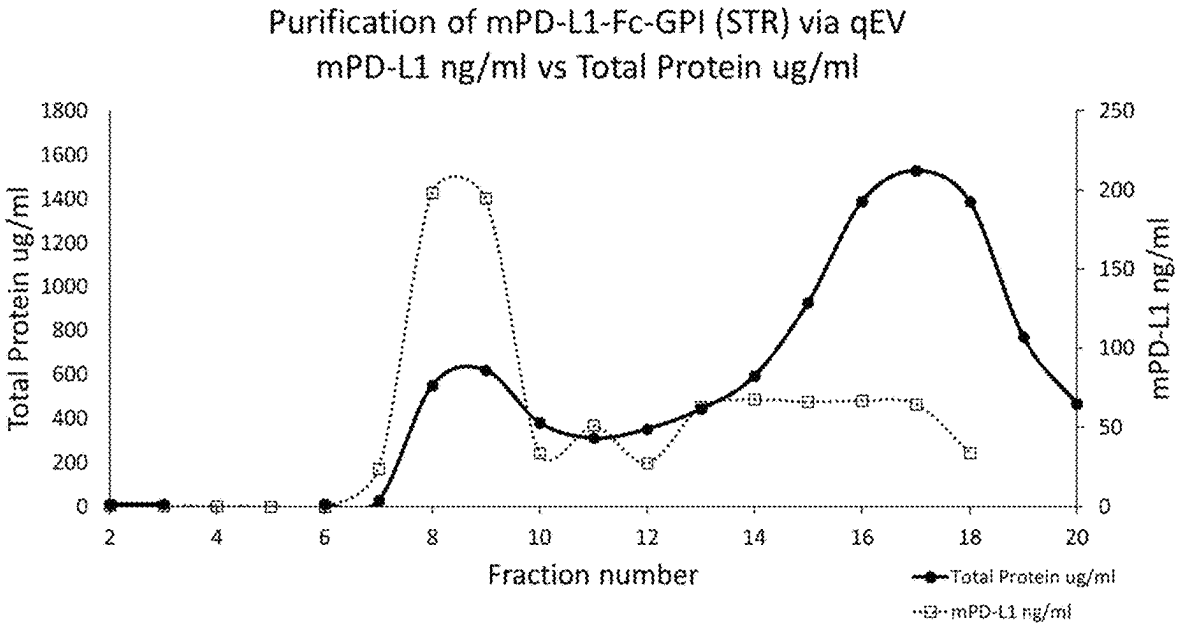


FIG. 32

Purification of mPDL1-Fc-GPI

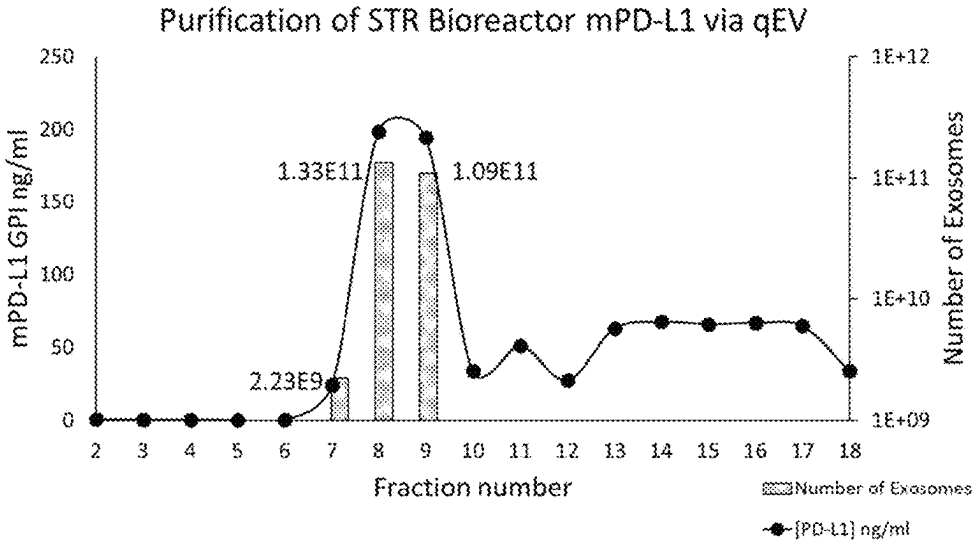


FIG. 33

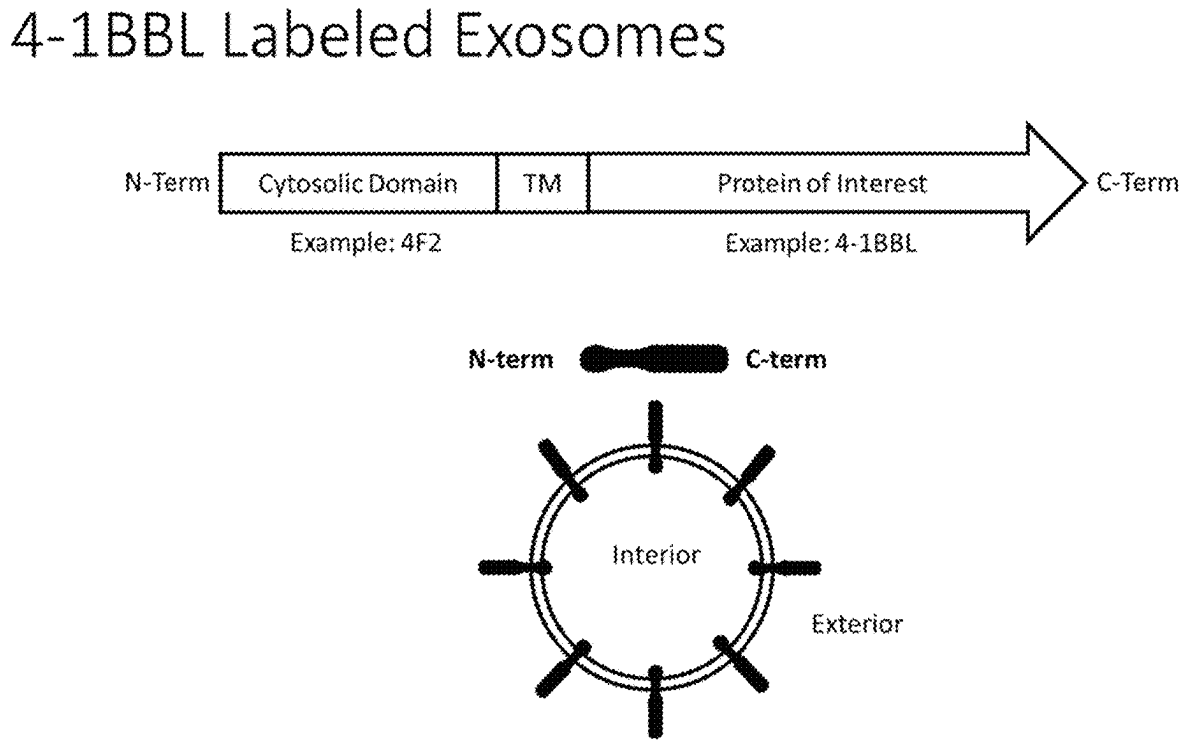

4-1BBL Labeled Exosomes
N-Term
Cytosolic Domain
TM
Protein of Interest
C-Term
Example: 4F2
Example: 4-1BBL
N-term
C-term
Interior
Exterior

FIG. 34

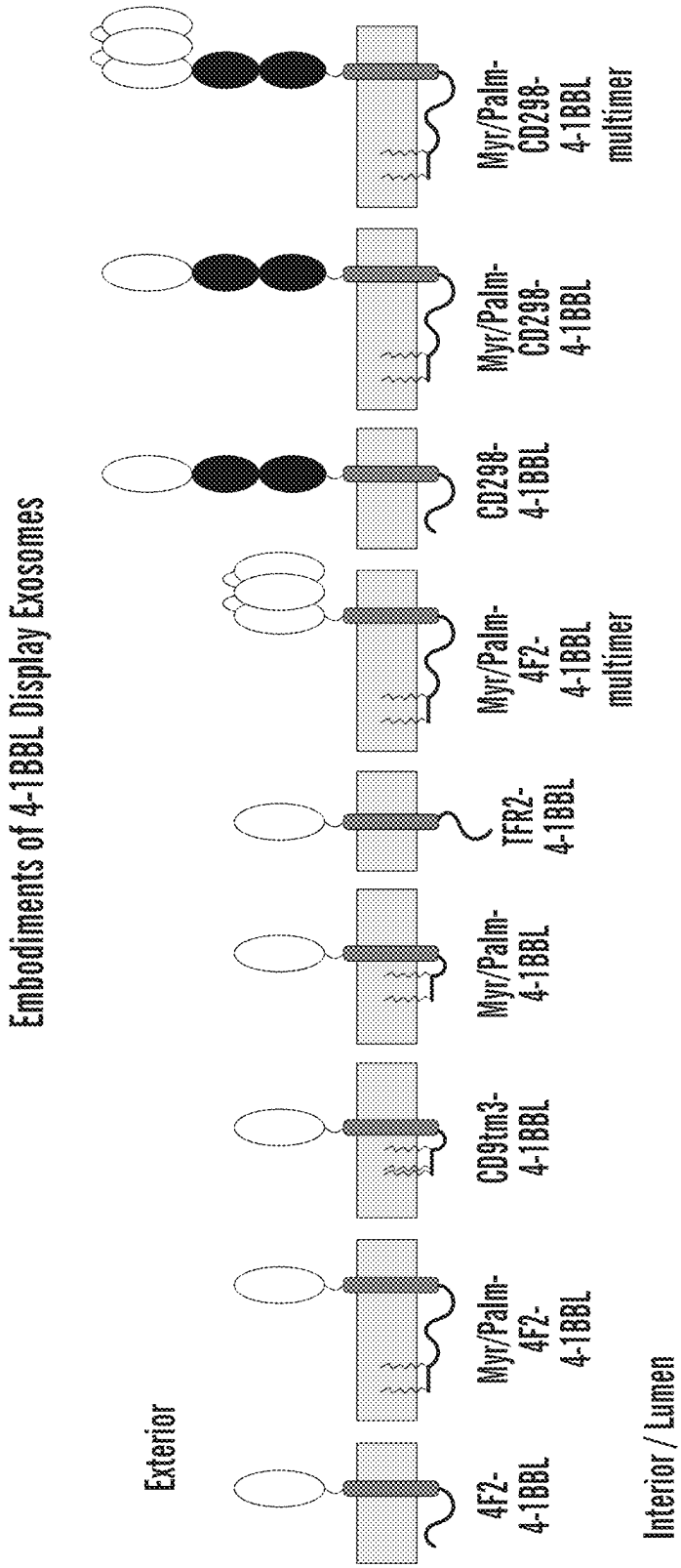

Embodiments of 4-1BBL Display Exosomes
Exterior
4F2-4-1BBL
Myr/Palm-4F2-4-1BBL
CD9tm3-4-1BBL
Myr/Palm-4-1BBL
TFR2-4-1BBL
Myr/Palm-4F2-4-1BBL multimer
CD298-4-1BBL
Myr/Palm-CD298-4-1BBL
Myr/Palm-CD298-4-1BBL multimer
Interior / Lumen

FIG. 35

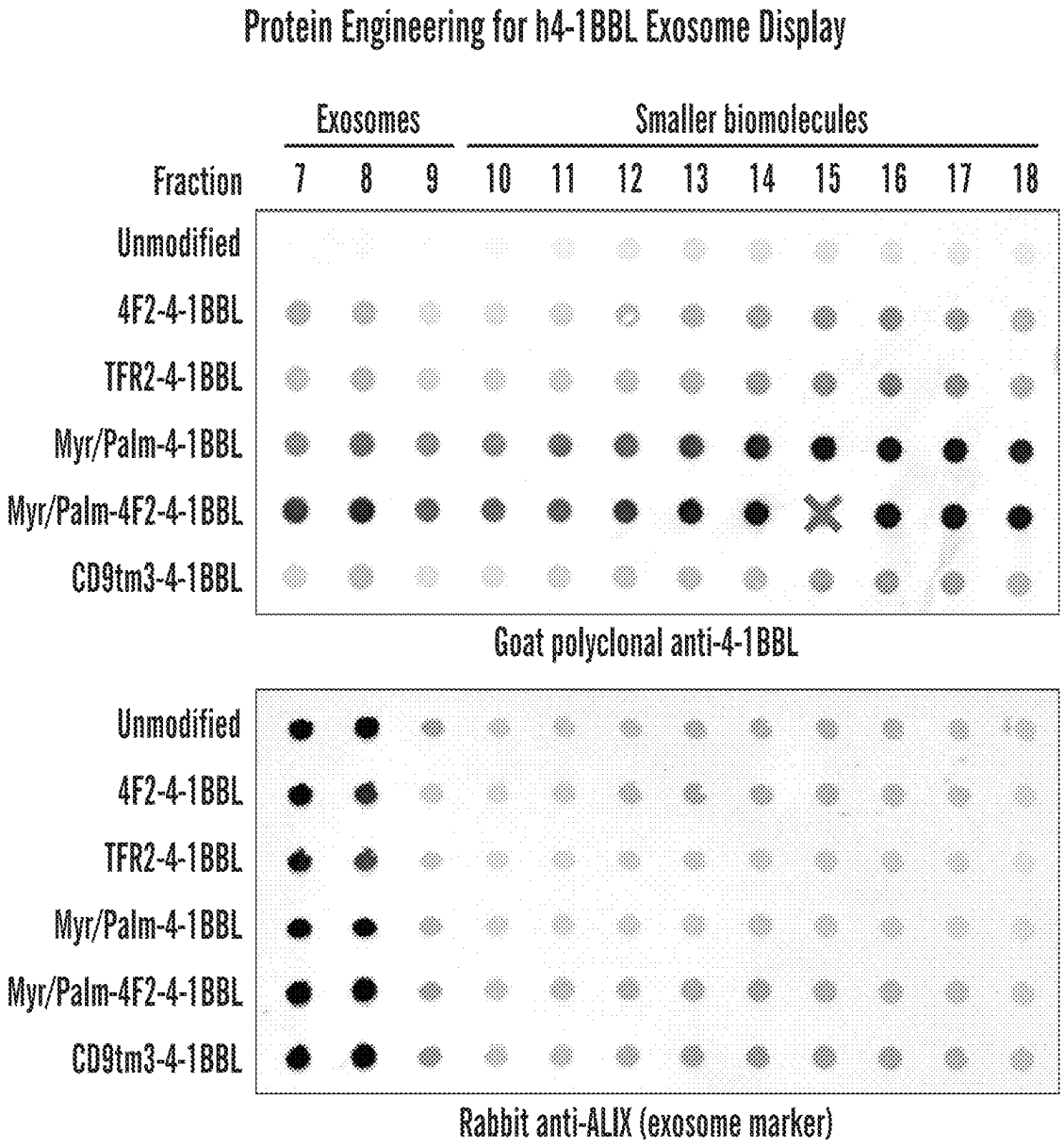

Protein Engineering for h4-1BBL Exosome Display
Exosomes
Smaller biomolecules
Fraction
7
8
9
10
11
12
13
14
15
16
17
18
Unmodified
4F2-4-1BBL
TFR2-4-1BBL
Myr/Palm-4-1BBL
Myr/Palm-4F2-4-1BBL
CD9tm3-4-1BBL
Goat polyclonal anti-4-1BBL
Unmodified
4F2-4-1BBL
TFR2-4-1BBL
Myr/Palm-4-1BBL
Myr/Palm-4F2-4-1BBL
CD9tm3-4-1BBL
Rabbit anti-ALIX (exosome marker)

FIG. 36A

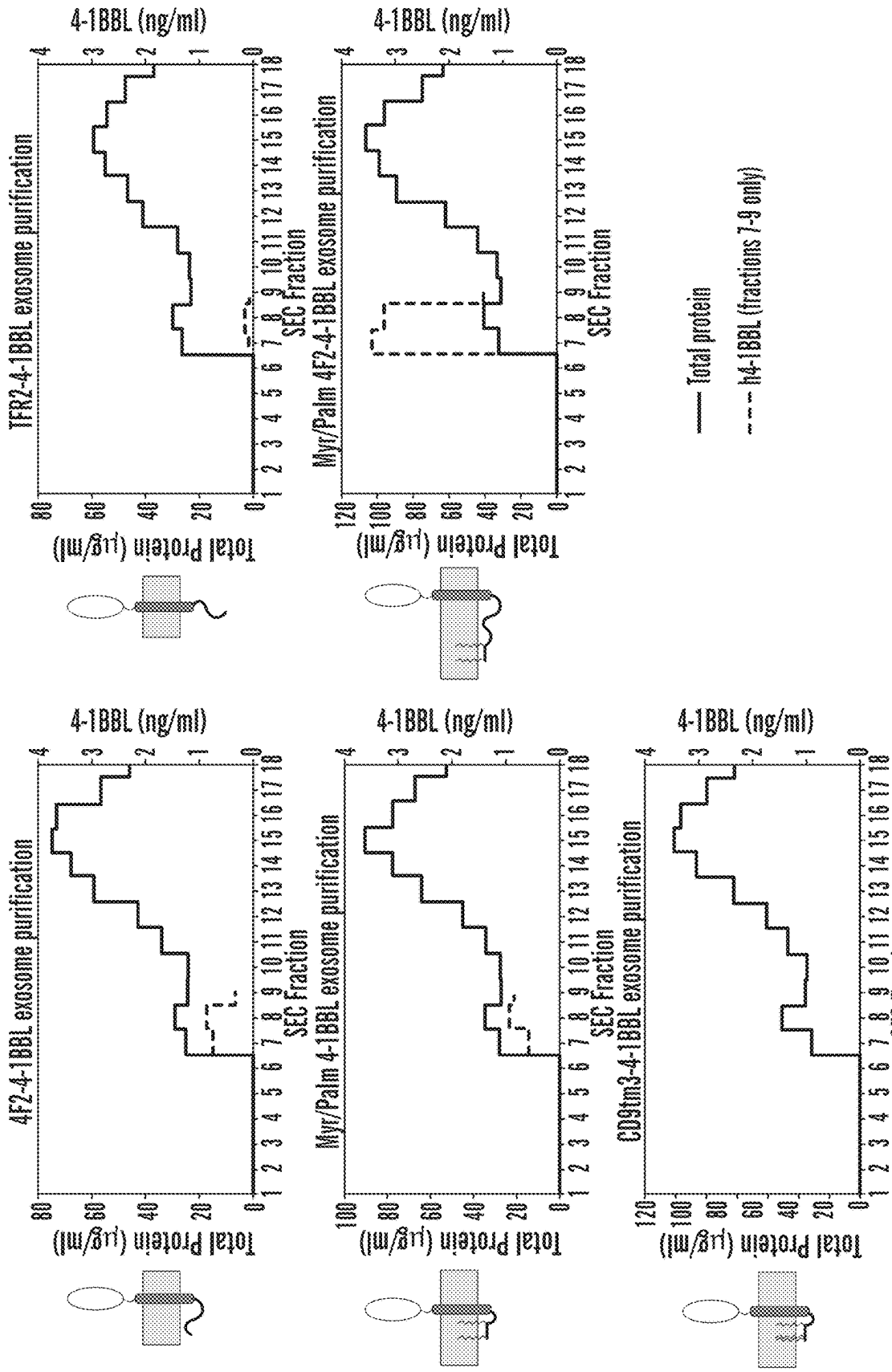
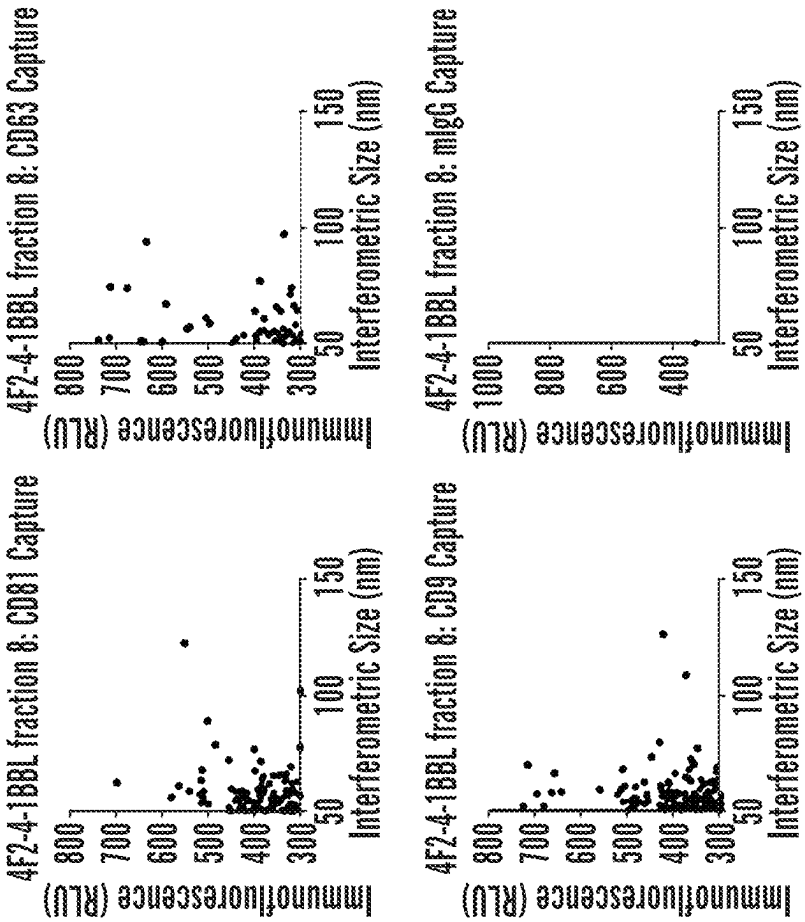

TFR2-4-1BBL exosome purification
Myr/Palm 4F2-4-1BBL exosome purification
4F2-4-1BBL exosome purification
Myr/Palm 4-1BBL exosome purification
CD9tm3-4-1BBL exosome purification
4-1BBL (ng/ml)
Total Protein (µg/ml)
SEC Fraction
Total protein
h4-1BBL (fractions 7-9 only)

FIG. 36A (cont.)

h4-1BBL is Displayed on Exosomes



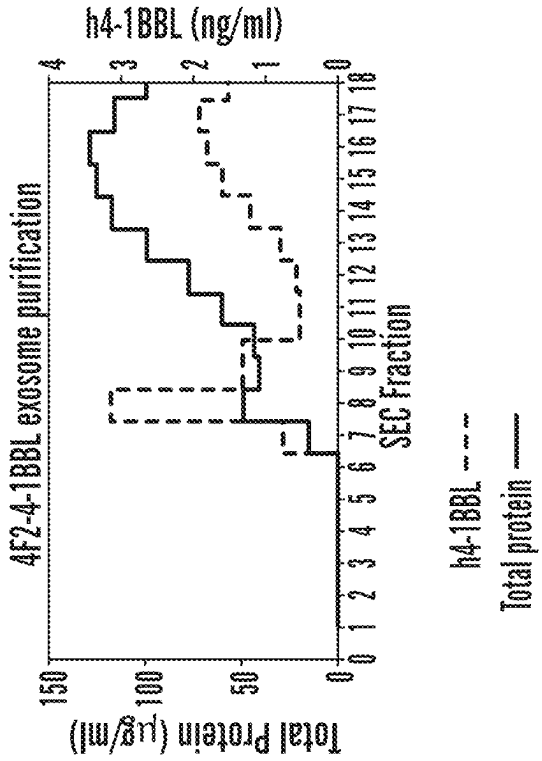


FIG. 36B

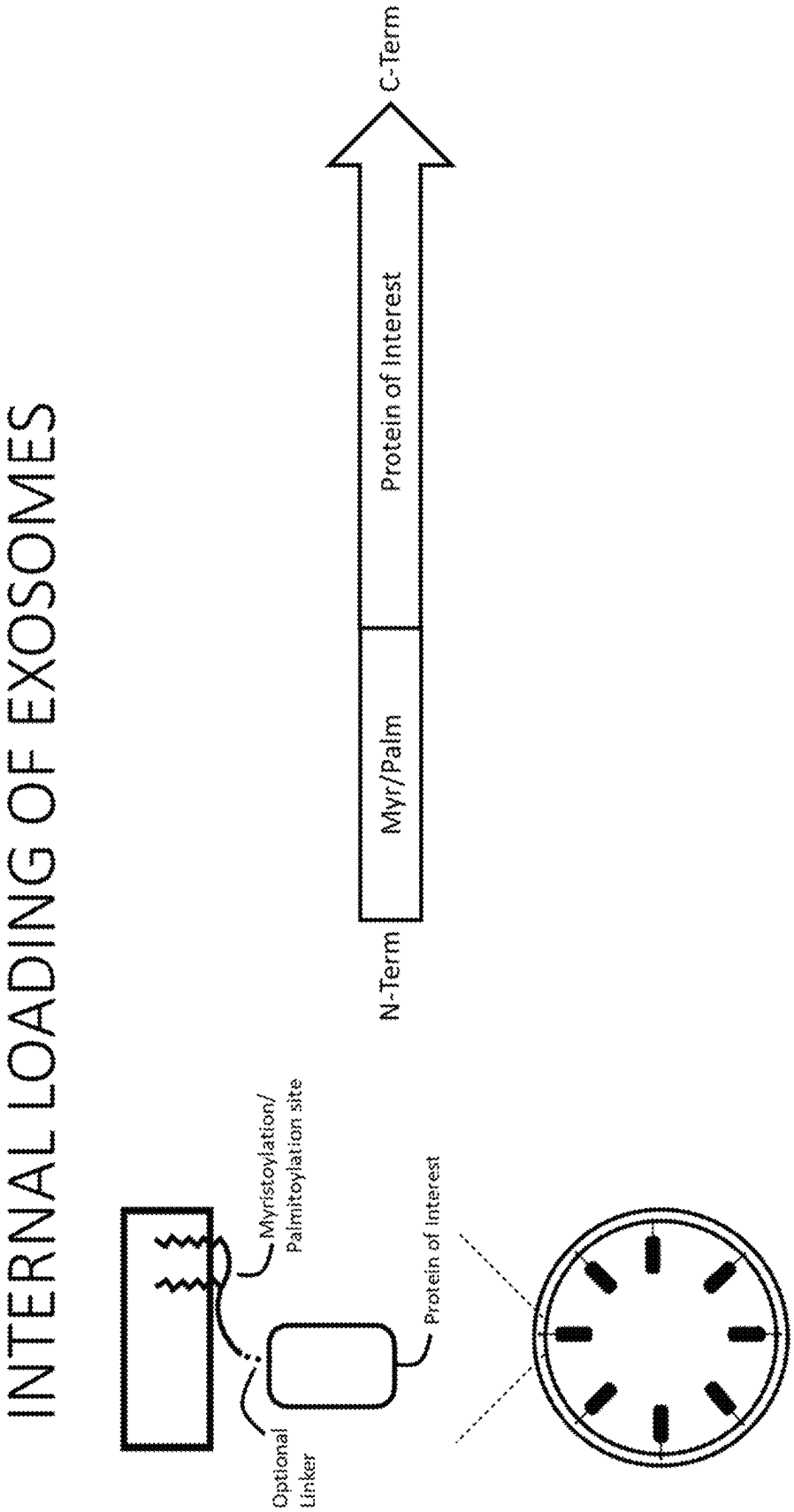

INTERNAL LOADING OF EXOSOMES
N-Term
Myr/Palm
Protein of Interest
C-Term
Myristoylation/
Palmitoylation site
Optional
Linker
Protein of Interest

FIG. 37

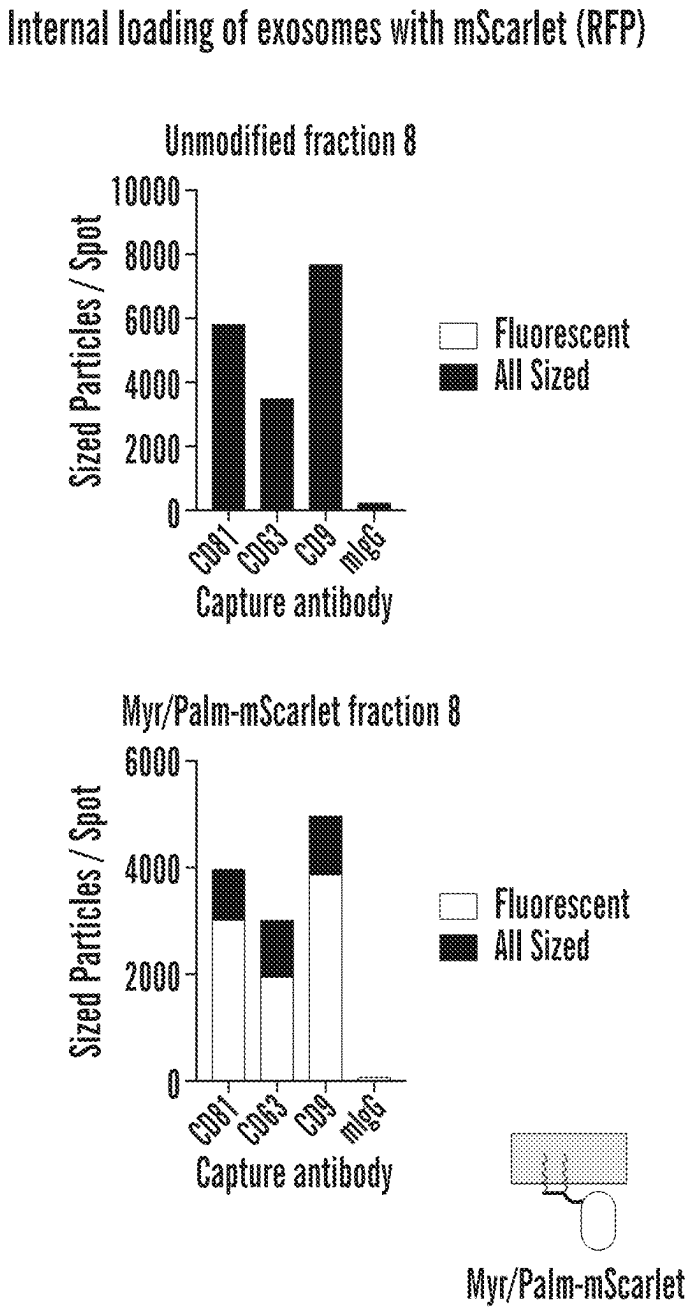

Internal loading of exosomes with mScarlet (RFP)
Unmodified fraction 8
Sized Particles / Spot
10000
8000
6000
4000
2000
0
CD81
CD63
CD9
mIgG
Capture antibody
Fluorescent
All Sized
Myr/Palm-mScarlet fraction 8
Sized Particles / Spot
6000
4000
2000
0
CD81
CD63
CD9
mIgG
Capture antibody
Fluorescent
All Sized
Myr/Palm-mScarlet

FIG. 38

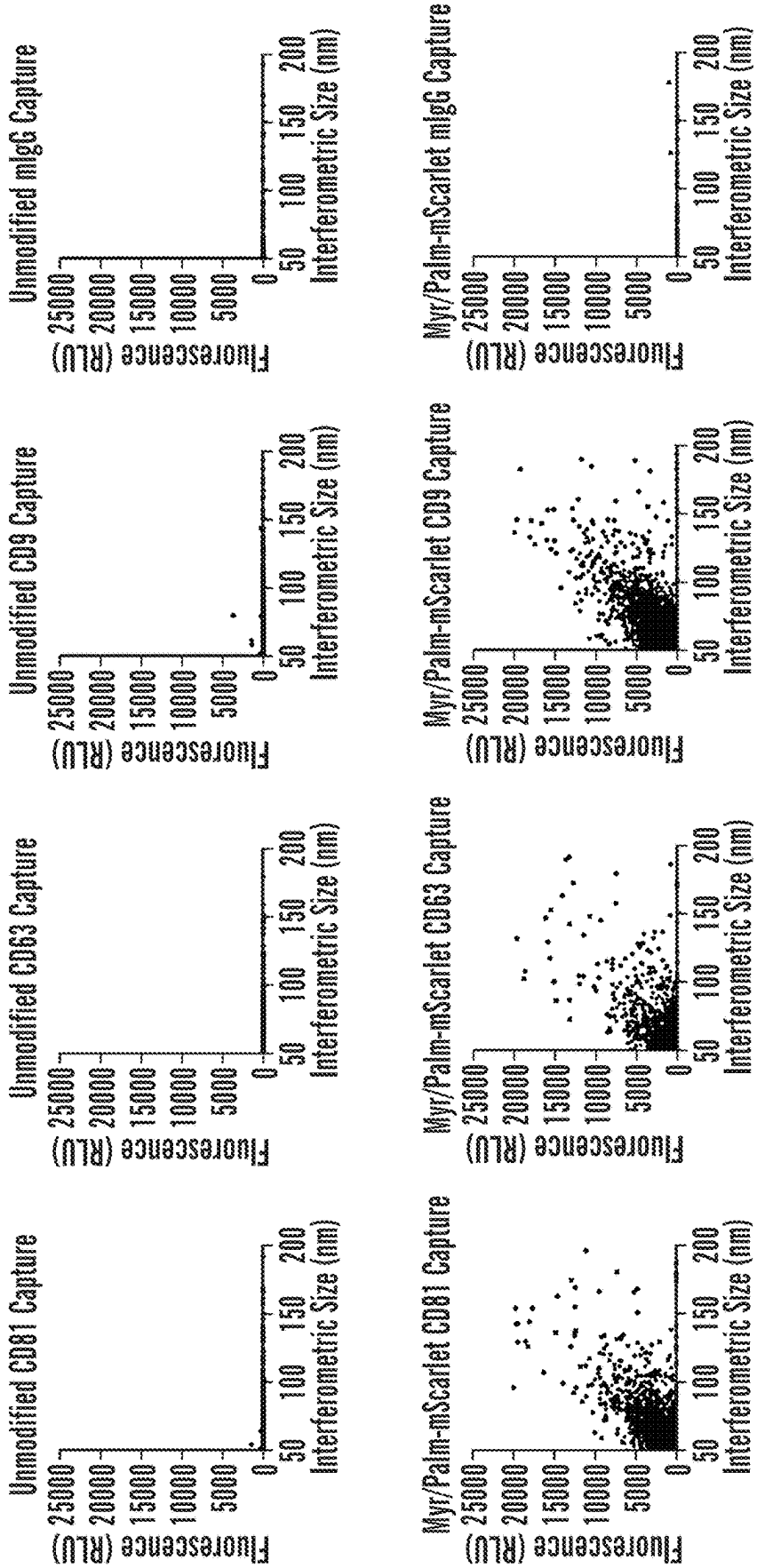

Unmodified CD81 Capture
Unmodified CD63 Capture
Unmodified CD9 Capture
Unmodified mIgG Capture
Myr/Palm-mScarlet CD81 Capture
Myr/Palm-mScarlet CD63 Capture
Myr/Palm-mScarlet CD9 Capture
Myr/Palm-mScarlet mIgG Capture
Fluorescence (RLU)
25000
20000
15000
10000
5000
0
50
100
150
200
Interferometric Size (nm)

FIG. 38 (cont.)

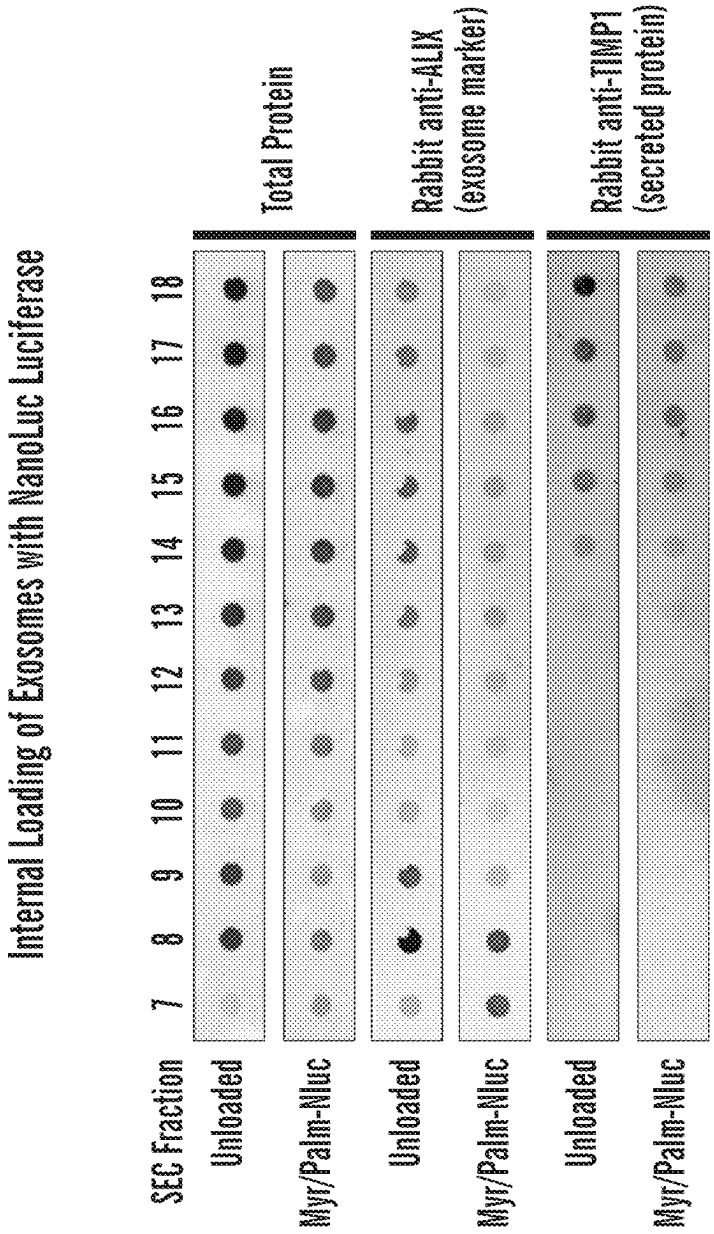

Internal Loading of Exosomes with NanoLuc Luciferase
SEC Fraction
7
8
9
10
11
12
13
14
15
16
17
18
Unloaded
Myr/Palm-Nluc
Unloaded
Myr/Palm-Nluc
Unloaded
Myr/Palm-Nluc
Total Protein
Rabbit anti-ALIX
(exosome marker)
Rabbit anti-TIMP1
(secreted protein)

FIG. 39A

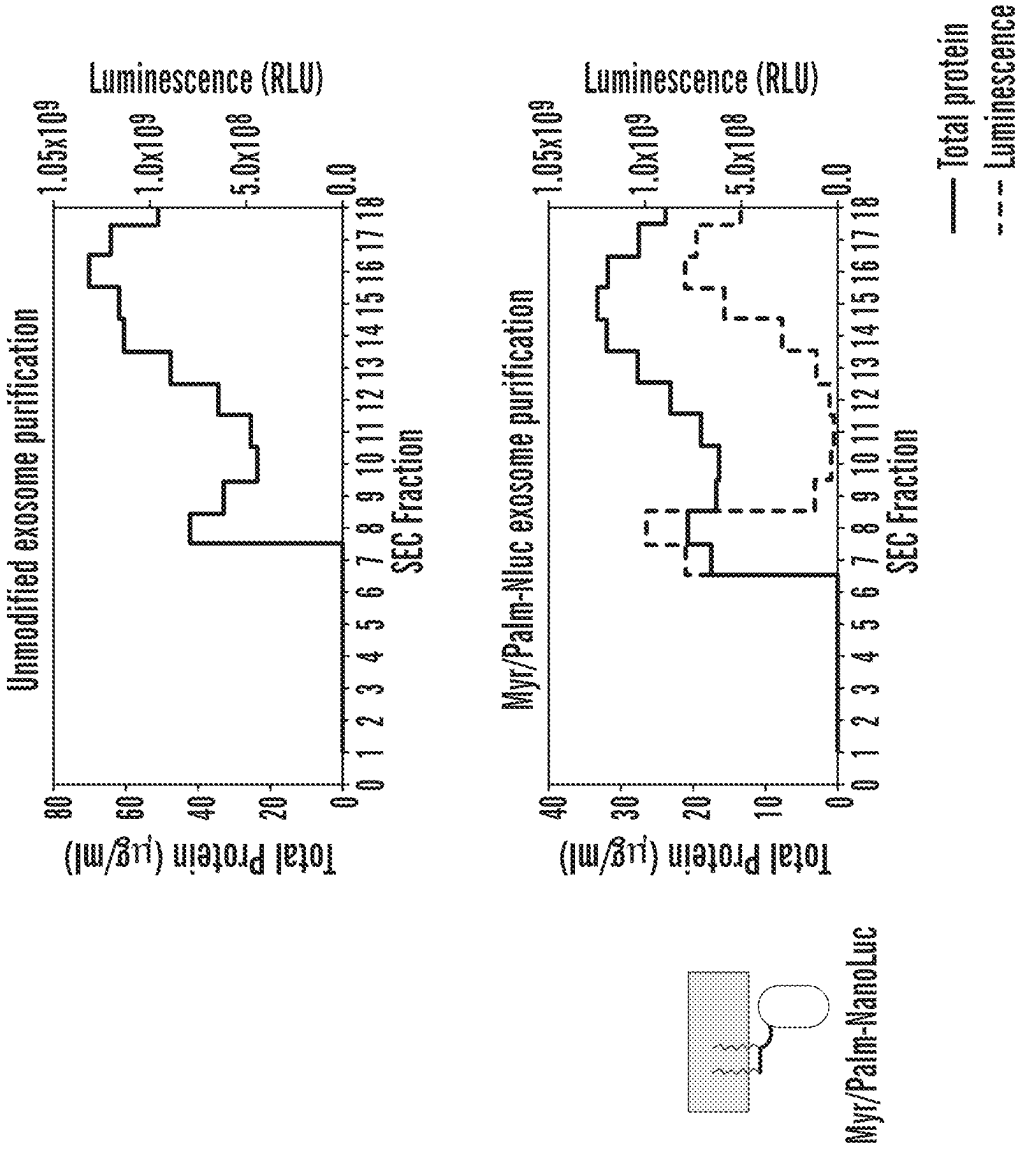

Unmodified exosome purification
Luminescence (RLU)
1.05x10^9
1.0x10^9
5.0x10^8
0.0
Total Protein (µg/ml)
80
60
40
20
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
SEC Fraction
Myr/Palm-Nluc exosome purification
Luminescence (RLU)
1.05x10^9
1.0x10^9
5.0x10^8
0.0
Total Protein (µg/ml)
40
30
20
10
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
SEC Fraction
Total protein
Luminescence
Myr/Palm-NanoLuc

FIG. 39A (cont.)

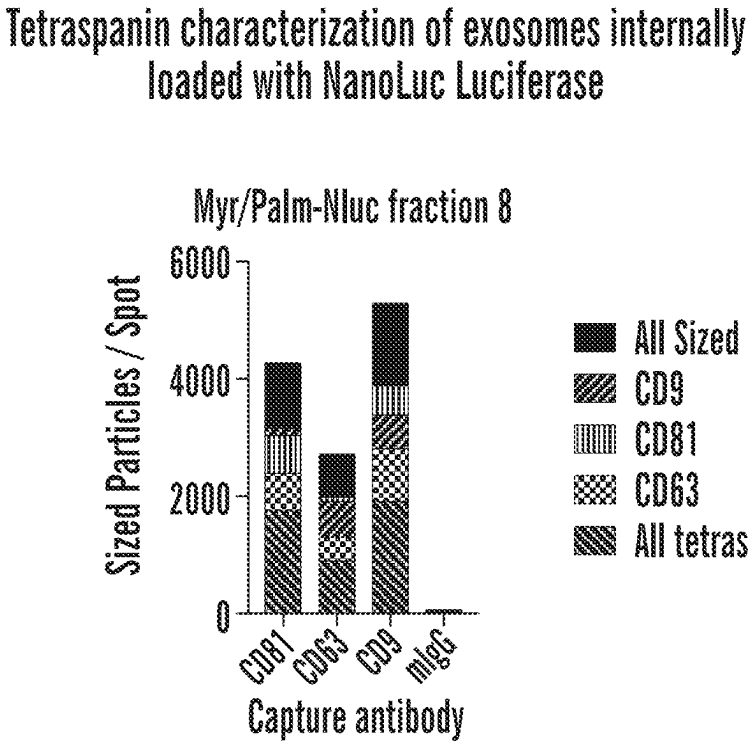

Tetraspanin characterization of exosomes internally loaded with NanoLuc Luciferase
Myr/Palm-Nluc fraction 8
Sized Particles / Spot
6000
4000
2000
0
CD81
CD63
CD9
mIgG
Capture antibody
All Sized
CD9
CD81
CD63
All tetras

FIG. 39B

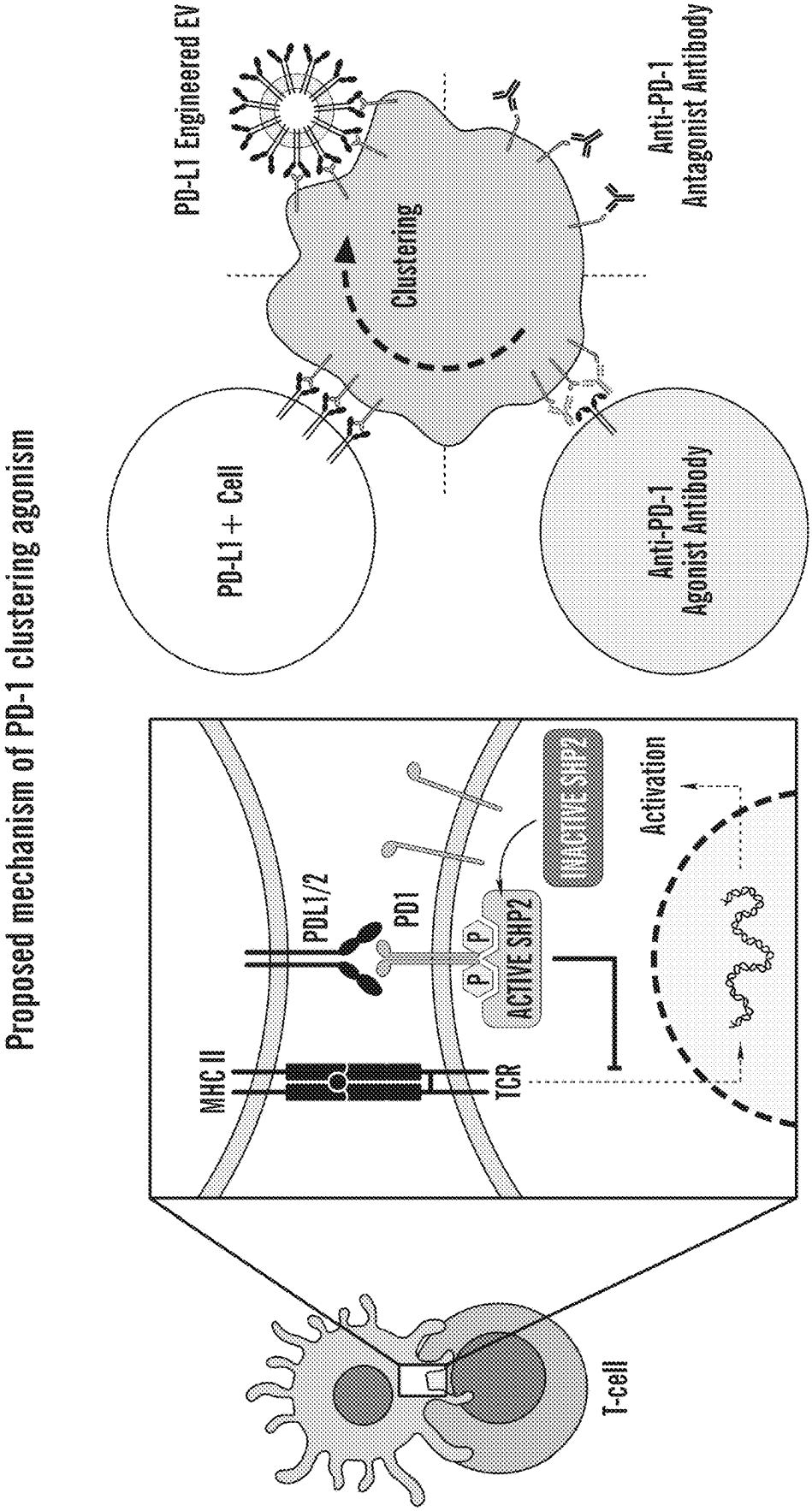

Proposed mechanism of PD-1 clustering agonism
PD-L1 Engineered EV
Clustering
Anti-PD-1
Antagonist Antibody
PD-L1 + Cell
Anti-PD-1
Agonist Antibody
MHC II
PDL1/2
PD1
TCR
P
P
ACTIVE SHP2
INACTIVE SHP2
Activation
T-cell

FIG. 40A

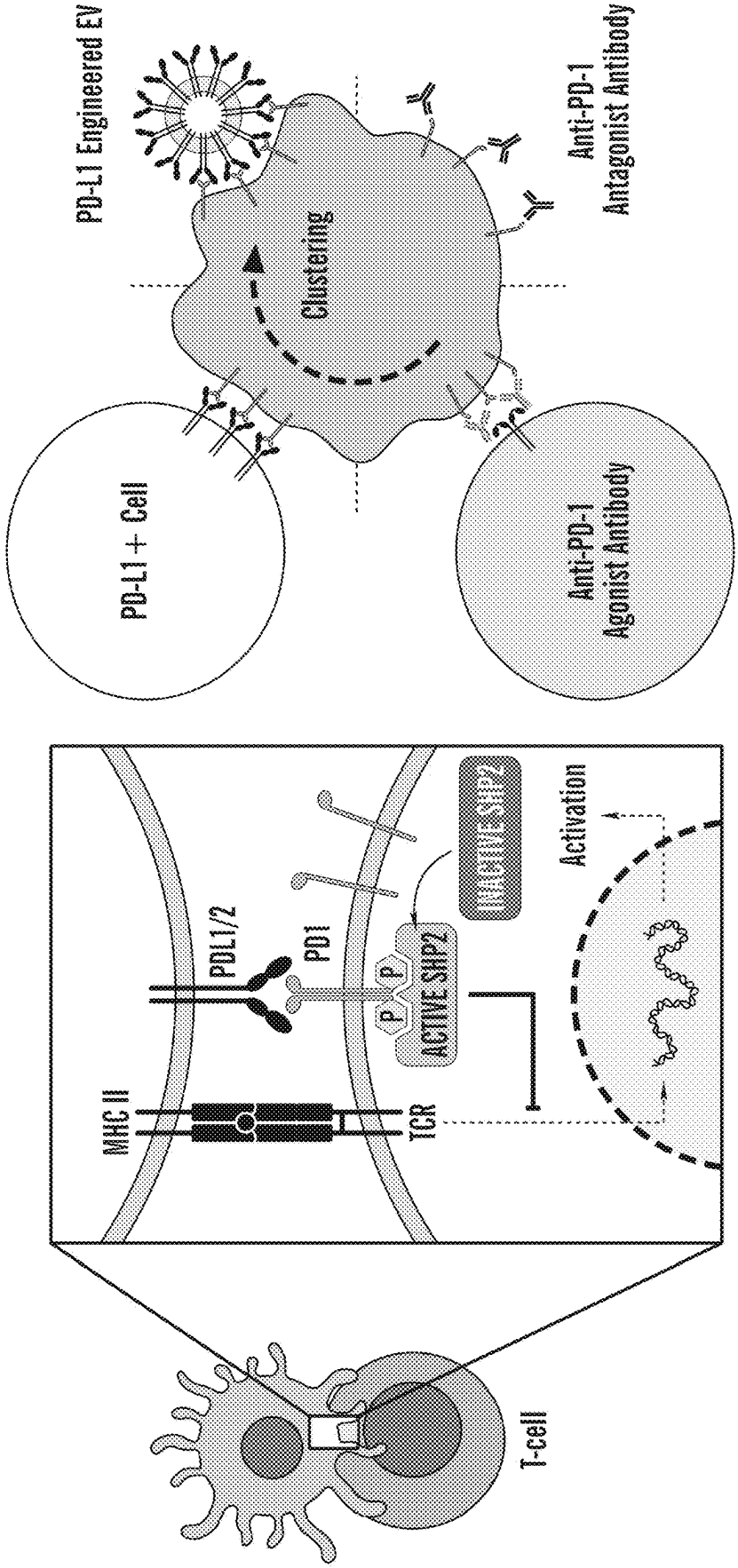

Proposed mechanism of 4-1BBL clustering agonism
PD-L1 Engineered EV
Clustering
Anti-PD-1
Antagonist Antibody
PD-L1 + Cell
Anti-PD-1
Agonist Antibody
MHC II
PDL1/2
PD1
TCR
P
P
ACTIVE SHP2
INACTIVE SHP2
Activation
T-cell

FIG. 40B

ENGINEERED EXTRACELLULAR VESICLES COMPRISING FUSION PROTEINS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a division of U.S. application Ser. No. 17/377,550, filed Jul. 16, 2021, now U.S. Pat. No. 11,578,116, which is a continuation of International Application No. PCT/US2021/016949, filed Feb. 5, 2021, which designated the U.S., and also claims the benefit of priority under 35 U.S.C. § 119(e) of U.S. Provisional Application No. 62/970,374, filed Feb. 5, 2020, the contents of each of which are incorporated herein by reference in their entirety.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in XML format and is hereby incorporated by reference in its entirety. Said XML copy, created on Nov. 9, 2022, is named 085172_000001USD1_ST.26.xml and is 724,326 bytes in size.

FIELD OF THE INVENTION

This invention relates to the generation of artificial synapses or extracellular vesicles, including features of extracellular vesicles engineered to deliver signaling, for therapeutic use, including treatment of immune diseases and cancer.

BACKGROUND

Extracellular vesicles (EVs) play a critical role in intercellular communication by transferring microRNAs, lipids, and proteins to neighboring cells. The delivery of encapsulated molecules within EVs is a highly promising strategy as a therapeutic platform in many contexts, exploiting the unique biophysical and biochemical characteristics of extracellular vesicles (EVs). However, there remains a great need in the art for a flexible and dynamic platform, where specific biological signals can be reliably targeted without off-target effects and that provide a robust cellular response to achieve a therapeutic effect, such as modulating inflammation.

SUMMARY

The compositions and methods provided herein are based, in part, on the discovery that extracellular vesicles can be used to express engineered fusion polypeptides that can modulate biological signal generation. These engineered vesicles, also termed artificial synapses, adopt the hallmark biophysical and biochemical features of extracellular vesicles, but are further engineered with vesicle targeting domains (e.g., sticky binders) and signaling domains, optionally joined by a linker with specific functions. The fusion polypeptides provided herein are designed and produced as nucleic acid constructs (e.g., vectors) and expressed in cells, such as mammalian cells. In particular, the vesicle targeting domain of each fusion polypeptide anchors the polypeptide to the extracellular vesicle lipid membrane, thereby presenting the signaling domain(s) of the polypeptide. The signaling domains on or within the vesicle membrane can make contact with recipient cells via target polypeptides (e.g., receptors on the extracellular surface of the recipient cell). Importantly, this strategy can allow for kinetically favorable signal generation and signal propagation. This includes, for example, increasing density of agonist presentation to support receptor clustering of a target receptor located on a target cell—an onerous barrier for traditional receptor targeting strategies.

This strategy was applied to alter immune checkpoint signaling, by engineering artificial synapses through genetic constructs with lipid binding glycosylphosphatidylinositol (GPI) sticky binders joined with programmed death-ligand 1 (PD-L1) signaling domain, e.g., human programmed death-ligand 1 (hPD-L1), expressed in cells and capable of attachment to exosomes. Isolation, purification, and analysis of artificial synapses revealed a high density of signaling domains of the hPD-L1-GPI fusion polypeptide. The hPD-L1 artificial synapse exosomes further demonstrated enhanced agonist signaling than soluble PD-L1 ligand alone, supporting receptor clustering on a target cell. When applied to a model of experimental autoimmune uveoretinitis (EAU), a statistically significant reduction in EAU symptoms was observed.

Thus, in one aspect, provided herein is an engineered extracellular vesicle or artificial vesicle comprising: at least one fusion polypeptide comprising: at least one protein of interest (POI) domain; and at least one vesicle targeting domain. In some embodiments of any of the aspects, the engineered extracellular vesicle is an exosome. In some embodiments, of any of the aspects, the fusion protein further comprises at least one linker. In some embodiments of any of the aspects, the POI domain can substantially bind to a target polypeptide.

In another aspect, provided herein is an engineered extracellular vesicle comprising: at least one fusion polypeptide comprising:

(i) at least one protein of interest (POI) domain or a fragment thereof; and

(ii) at least one vesicle targeting domain,

wherein the POI domain is in an extracellular position relative to a lipid membrane of the extracellular vesicle.

In another aspect, provided herein is an engineered extracellular vesicle comprising:

(a) a first fusion polypeptide comprising:

(i) at least one protein of interest (POI) domain or a fragment thereof; and

(ii) at least one vesicle targeting domain,

wherein the at least one POI domain is in an extracellular position relative to a lipid membrane of the extracellular vesicle,

(b) a second fusion polypeptide comprising:

(i) at least one protein of interest (POI) domain or a fragment thereof; and

(ii) at least one vesicle targeting domain,

wherein the POI domain is in an extracellular position relative to a lipid membrane of the extracellular vesicle,

and wherein the at least one vesicle targeting domain is within a lipid membrane of the extracellular vesicle.

In another aspect, provided herein is an extracellular vesicle composition comprising: a plurality of artificial synapses, wherein each artificial synapse comprises (i) an extracellular vesicle; (ii) one or more sticky binders; and (iii) one or more signaling domains.

In another aspect, provided herein is a composition comprising a plurality of the engineered extracellular vesicles provided herein.

In another aspect, provided herein is a composition comprising two or more of the engineered extracellular vesicles provided herein.

In another aspect, provided herein is a composition comprising three or more of the engineered extracellular vesicles provided herein.

In another aspect, provided herein is a method of producing the engineered extracellular vesicle or the compositions provided herein, comprising:

(a) providing a population of cells expressing a vector construct encoding one or more sticky binder and one or more signaling domains; and

(b) isolating a plurality of artificial synapses from the population of cells.

In another aspect, provided herein is a method of producing the engineered extracellular vesicle or the compositions provided herein, comprising:

(a) providing a population of cells expressing a vector construct encoding one or more sticky binder and one or more signaling domains; and

(b) isolating a plurality of artificial synapses from the population of cells; and

(c) purifying the plurality of artificial synapses from the population of cells.

In another aspect, provided herein is a method of modulating inflammation in a subject, the method comprising:

administering a composition comprising a plurality of engineered extracellular vesicles to a subject in need thereof,

wherein the engineered extracellular vesicles comprise at least one fusion polypeptide comprising:

(i) at least one protein of interest (POI) domain or a fragment thereof; and

(ii) at least one vesicle targeting domain.

In another aspect, provided herein is a use of a composition or engineered extracellular vesicle provided herein for the treatment of an inflammatory disease or condition.

In another aspect, provided herein is a use of a composition or engineered extracellular vesicle provided herein for the treatment of an autoimmune disease or condition.

In another aspect, provided herein is a use of a composition or engineered extracellular vesicle provided herein for the treatment of cancer.

In one embodiment of any of the aspects, the engineered extracellular vesicle is an exosome.

In another embodiment of any of the aspects, the protein of interest (POI) domain or a fragment thereof is a N-terminal domain of the fusion polypeptide. In another embodiment of any of the aspects, the POI domain is selected from the group consisting of: Table 1. In another embodiment of any of the aspects, the POI domain is PD-L1 or a fragment thereof. In another embodiment of any of the aspects, the POI domain is PD-L2 or a fragment thereof. In another embodiment of any of the aspects, the POI domain is FGL1 or a fragment thereof. In another embodiment of any of the aspects, the POI domain is 4-1BBL or a fragment thereof. In another embodiment of any of the aspects, the POI domain is CTLA-4 or a fragment thereof. In another embodiment of any of the aspects, the protein of interest (POI) domain is HVEM or a fragment thereof.

In another embodiment of any of the aspects, the vesicle targeting domain is a C-terminal domain of the fusion polypeptide. In another embodiment of any of the aspects, the vesicle targeting domain is in a luminal position relative to the lipid membrane of the extracellular vesicle. In another embodiment of any of the aspects, the vesicle targeting domain in an exterior position relative to the lipid membrane of the extracellular vesicle. In another embodiment of any of the aspects, the vesicle targeting domain is selected from the group consisting of: Table 3. In another embodiment of any of the aspects, the vesicle targeting domain is selected from the group consisting of: a Glycosylphosphatidylinositol (GPI) anchor, a fatty acylation site, and a prenylation site. In another embodiment of any of the aspects, the vesicle targeting domain is C1C2. In another embodiment of any of the aspects, the vesicle targeting domain is a GPI anchor.

In another embodiment of any of the aspects, the fusion polypeptide comprises at least two POI domains and/or at least two exosome targeting domains.

In another embodiment of any of the aspects, the POI domain substantially binds to one or more of a target polypeptide. In another embodiment of any of the aspects, the target polypeptide is selected from the group consisting of: Table 2.

In another embodiment of any of the aspects, the fusion polypeptide further comprises a peptide linker. In another embodiment of any of the aspects, the fusion polypeptide further comprises a fragment crystallizable region (Fc) domain. In another embodiment of any of the aspects, the linker is in an exterior position relative to the lipid membrane of the extracellular vesicle. In another embodiment of any of the aspects, the linker is a transmembrane linker. In another embodiment of any of the aspects, the linker is in a luminal position relative to the lipid membrane of the extracellular vesicle.

In another embodiment of any of the aspects, the engineered extracellular vesicle does not comprise an endogenous POI polypeptide.

In another embodiment of any of the aspects, the composition further comprises a pharmaceutically acceptable carrier.

In another embodiment of any of the aspects, the one or more sticky binders or the vesicle targeting domain is selected from the group consisting of: a GPI anchor, a fatty acylation site, and a prenylation site.

In another embodiment of any of the aspects, the signaling domain or the protein of interest comprises one or more of: PD-L1, PD-L2, CTLA-4 (CD152), 4-1BBL (CD137L), HVEM (CD270), FGL1, OX-2 (CD200), Galectin-9, PVR (CD155), Nectin-2 (CD112) isoform alpha, Nectin-2 (CD112) isoform beta, Nectin-2 (CD112) isoform delta, IL-10, TSG-6, B7-H3 (CD276), B7-H4 (VTCN1), B7-H5 (VISTA), B7-H7 (HHLA2), BTNL1, VSIG8, VSIG3 (IGSF11), VSIG4, TIM-3 (HAVCR2), TIM-4 (TIMD4), CEACAM1, BTN3A1, BTN3A2, BTN2A1, BTNL8, BTN2A2, BTN1A1, TIGIT, CD27L (CD70), CD30L (CD153), GITRL, CD40L (CD154), LIGHT (CD258), TL1, CD80, CD86, LFA-3 (CD58), SLAM (CD150), CD40, CD28, CD28H, CD2, LFA-3 (CD58), CD48, CD226, DR3, DcR3, FasL, TIM-1 (CD365), PD-1, or active fragment thereof.

In another embodiment of any of the aspects, the isolating is via size exclusion chromatography. In another embodiment of any of the aspects, the purifying is via multimodal chromatography. In another embodiment of any of the aspects, the method further comprises performing an assay for POI binding to a target polypeptide.

In another embodiment of any of the aspects, the vector construct further encodes a promoter. In another embodiment of any of the aspects, the promoter is a tissue-specific promoter or an inducible promotor.

In one embodiment of any of the aspects, the method further comprises selecting a subject that has or is suspected of having an autoimmune disease or an inflammatory disease or condition. In another embodiment of any of the aspects, the inflammatory disease and/or condition is acute.

In another embodiment of any of the aspects, the inflammatory related disease and/or condition is chronic.

In another embodiment of any of the aspects, administering the composition provided herein comprises injection, topical administration, or inhalation.

A BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** shows construct representation of fusion polypeptides for labeling an exosome surface with Type I membrane proteins.

FIG. **2**A shows nucleic acid and translated protein sequences of full-length Phosphatidylserine binding: Lactadherin (MFGE8) C1C2. Underlined nucleic acid sequence highlights the sequence translated to the C1C2 protein. Bold and underlined text highlights the C1C2 domain used to anchor signaling domains of interest (i.e., PD-L1 extracellular domain) onto the surface of the Inventors' artificial synapses. FIG. **2**B shows nucleic acid and translated protein sequences of full length CD55 (DAF) Glycosylphosphatidylinositol (GPI) anchor. Bold and underlined text highlights the GPI anchor domain used to anchor signaling domains of interest (i.e., PD-L1 extracellular domain) onto the surface of the Inventors' artificial synapses engineered from exosomes. FIGS. **2**A-**2**B disclose SEQ ID NOS: 199-200, and 196-197, respectively, in order of appearance.

FIG. **3** demonstrates the nucleic acid and translated protein sequence for the Fc linker used in genetically engineered constructs is shown in bold and underlined. FIG. **3** discloses SEQ ID NOS: 219-220, respectively, in order of appearance.

FIG. **4**A demonstrates nucleic acid and translated protein sequence of human PD-L1 (CD274). Bold and underlined sequence highlights the PD-L1 extracellular domain used in the Inventors' artificial synapses engineered from exosomes. FIG. **4**B demonstrates nucleic acid and protein sequence of human PD-L2. Bold and underlined sequence highlights the PD-L2 extracellular domain used in the Inventors' artificial synapses engineered from exosomes. FIG. **4**C shows mRNA and protein sequence of human CTLA-4 (CD152). Bold and underlined sequence highlights the CTLA-4 extracellular domain used in the Inventors' artificial synapses. FIGS. **4**A-**4**C disclose SEQ ID NOS: 1-2, 5-6, and 9-10, respectively, in order of appearance.

FIG. **5**A shows an exemplary embodiment of pcDNA5-FRT cloning vector with a gene sequence coding for a fusion polypeptide inserted into a multiple cloning site. FIG. **5**B shows an exemplary embodiment of the Gateway® destination vector pEF5-FRT-V5-DEST with a gene sequence coding for a fusion polypeptide inserted into a multiple cloning site. The vectors were used for constitutive high-level expression of fusion polypeptide described herein in mammalian cells. FIG. **5**C shows the nucleic acid and protein sequence for the hCTLA4-Fc-GPI fusion polypeptide wherein the text for the signaling domain is bolded, Fc linker is underlined, and sticky binder is italicized. FIG. **5**D shows the nucleic acid and protein sequence for the hPDL1-GPI-P2A-hHVEM-GPI fusion polypeptide wherein the text for the signaling domain hPDL1 and hHVEM are bolded, P2A sequence is underlined, and sticky binder GPI is italicized. With P2A included, a self-cleaving peptide sequence, artificial synapses with this feature will have both hPDL1-GPI and hHVEM-GPI loaded onto the surface. FIG. **5**E shows the nucleic acid and protein sequence for the hPDL1-GPI-P2A-hFGL1-GPI fusion polypeptide wherein the text for the signaling domain hPDL1 and hFGL1 are bolded, P2A sequence is underlined, and sticky binder GPI is italicized. With P2A included, a self-cleaving peptide sequence, artificial synapses with this feature will have both hPDL1-GPI and FGL1-GPI loaded onto the surface. FIG. **5**F shows the nucleic acid and protein sequence for the hPDL1-GPI fusion polypeptide wherein the text for the signaling domain hPDL1 is bolded and sticky binder GPI is italicized. FIG. **5**G shows the nucleic acid and protein sequence for the hPDL1-Fc-GPI fusion polypeptide wherein the text for the signaling domain hPDL1 is bolded, Fc is underlined, and sticky binder GPI is italicized. FIG. **5**H shows the nucleic acid and protein sequence for the hPDL2-Fc-GPI fusion polypeptide wherein the text for the signaling domain hPDL2 is bolded, Fc is underlined, and sticky binder GPI is italicized. FIG. **5**I shows the nucleic acid and protein sequence for the hPDL1-C1C2 fusion polypeptide wherein the text for the signaling domain hPDL1 is bolded and sticky binder C1C2 is italicized. FIG. **5**J shows the nucleic acid and protein sequence for the hPDL2-C1C2 fusion polypeptide wherein the text for the signaling domain hPDL2 is bolded and sticky binder C1C2 is italicized. FIG. **5**K shows the nucleic acid and protein sequence for the 4F2-h41BBL fusion polypeptide wherein the text for the signaling domain h41BBL is bolded and sticky binder 4F2 is italicized. FIG. **5**L shows the nucleic acid and protein sequence for the hPDL1-4Fc-GPI fusion polypeptide wherein the text for the signaling domain hPDL1 is bolded, 4Fc is underlined, and sticky binder GPI is italicized. FIG. **5**M shows the nucleic acid and protein sequence for the Myr-NanoLuc® Luciferase fusion polypeptide wherein the text for the signaling domain NanoLuc® Luciferase is bolded, and sticky binder Myr is italicized. FIG. **5**N shows the nucleic acid and protein sequence for the Myr-mScarlet fusion polypeptide wherein the text for the signaling domain mScarlet is bolded, and sticky binder Myr is italicized. FIG. **5**O shows the nucleic acid and protein sequence for the secreted isoform of hPDL1 (SecPDL1) fusion polypeptide hSecPDL1-GPI wherein the text for the signaling domain hSecPDL1 is bolded and sticky binder GPI is italicized. FIG. **5**P shows the nucleic acid and protein sequence for the Tfr2-h41BBL fusion polypeptide wherein the text for the signaling domain h41BBL is bolded and sticky binder Tfr2 is italicized. FIG. **5**Q shows the nucleic acid and protein sequence for the CD9tm3-h41BBL fusion polypeptide wherein the text for the signaling domain h41BBL is bolded and sticky binder CD9tm3 is italicized. FIG. **5**R shows the nucleic acid and protein sequence for the Myr/Palm-4F2-h41BBL fusion polypeptide wherein the text for the signaling domain h41BBL is bolded, sticky binder Myr/Palm is underlined, and sticky binder 4F2 is italicized. FIG. **5**S shows the nucleic acid and protein sequence for the Myr/Palm-Link-h41BBL fusion polypeptide wherein the text for the signaling domain h41BBL is bolded, sticky binder Myr/Palm is italicized and underlined, and sticky binder Link (in this embodiment a GSSG linker (SEQ ID NO: 319)) is in regular text (not underlined and not italicized). FIG. **5**T shows the nucleic acid and protein sequence for the hPDL1-Link-GPI fusion polypeptide wherein the text for the signaling domain hPDL1 is bolded, Link is underlined (in this embodiment a GSSG linker (SEQ ID NO: 319)), and sticky binder GPI is italicized. FIG. **5**U shows the nucleic acid and protein sequence for the secreted isoform of hPDL1 (SecPDL1) fusion polypeptide hSecPDL1-CD9tm2 wherein the text for the signaling domain hSecPDL1 is bolded and sticky binder CD9tm2 is italicized. FIG. **5**V shows the nucleic acid and protein sequence for the secreted isoform of hPDL1 (SecPDL1) fusion polypeptide hSecPDL1-CD9tm2-KRAS wherein the text for the signal-

ing domain hSecPDL1 is bolded, sticky binder CD9tm2 is italicized, and sticky binder KRAS is italicized and underlined. FIG. **5**W shows the nucleic acid and protein sequence for the secreted isoform of hPDL1 (SecPDL1) fusion polypeptide hSecPDL1-CD9tm4 wherein the text for the signaling domain hSecPDL1 is bolded and sticky binder CD9tm4 is italicized. FIG. **5**X shows the nucleic acid and protein sequence for the secreted isoform of hPDL1 (SecPDL1) fusion polypeptide hSecPDL1-CD81 wherein the text for the signaling domain hSecPDL1 is bolded and sticky binder CD81 is italicized. FIG. **5**Y shows the nucleic acid and protein sequence for the hCD200-Fc-GPI fusion polypeptide wherein the text for the signaling domain hCD200 is bolded, Fc is underlined, and sticky binder GPI is italicized, a spacer sequence domain (regular text, not underlined and not italicized) separates hCD200 sequence from the Fc domain, a spacer sequence domain (regular text, not underlined and not italicized) separates Fc sequence from the GPI. FIG. **5**Z shows the nucleic acid and protein sequence for the hFGL1-GPI fusion polypeptide wherein the text for the signaling domain hFGL1 is bolded, and sticky binder GPI is italicized. FIG. **5**AA shows the nucleic acid and protein sequence for the hGal9-Fc-GPI fusion polypeptide wherein the text for the signaling domain hGal9 is bolded, Fc is underlined, and sticky binder GPI is italicized. FIG. **5**BB shows the nucleic acid and protein sequence for the hCD200-GPI fusion polypeptide wherein the text for the signaling domain hCD200 is bolded, and sticky binder GPI is italicized. FIG. **5**CC shows the nucleic acid and protein sequence for the hGal9-GPI fusion polypeptide wherein the text for the signaling domain hGal9 is bolded, and sticky binder GPI is italicized. FIG. **5**DD shows the nucleic acid and protein sequence for the hHVEM-GPI fusion polypeptide wherein the text for the signaling domain hHVEM is bolded, and sticky binder GPI is italicized. FIG. **5**EE shows the nucleic acid and protein sequence for the hPDL2-GPI fusion polypeptide wherein the text for the signaling domain hPDL2 is bolded, and sticky binder GPI is italicized. FIG. **5**FF shows the nucleic acid and protein sequence for the hTSG6-GPI fusion polypeptide wherein the text for the signaling domain hTSG6 is bolded, and sticky binder GPI is italicized. FIG. **5**GG shows the nucleic acid and protein sequence for the hHVEM-Fc-GPI fusion polypeptide wherein the text for the signaling domain hHVEM is bolded, Fc is underlined, and sticky binder GPI is italicized. FIG. **5**HH shows the nucleic acid and protein sequence for the mCTLA4-Fc-GPI fusion polypeptide wherein the text for the signaling domain mCTLA4 is bolded, Fc is underlined, and sticky binder GPI is italicized. FIG. **5**II shows the nucleic acid and protein sequence for the mPDL1-C1C2 fusion polypeptide wherein the text for the signaling domain mPDL1 is bolded and sticky binder C1C2 is italicized. FIG. **5**JJ shows the nucleic acid and protein sequence for the mPDL1-Fc-GPI fusion polypeptide wherein the text for the signaling domain mPDL1 is bolded, Fc is underlined, and sticky binder GPI is italicized. FIG. **5**KK shows the nucleic acid and protein sequence for the mPDL1-GPI fusion polypeptide wherein the text for the signaling domain mPDL1 is bolded and sticky binder GPI is italicized. FIG. **5**LL shows the nucleic acid and protein sequence for the mPDL2-C1C2 fusion polypeptide wherein the text for the signaling domain mPDL2 is bolded and sticky binder C1C2 is italicized. FIG. **5**MM shows the nucleic acid and protein sequence for the mPDL2-Fc-GPI fusion polypeptide wherein the text for the signaling domain mPDL2 is bolded, Fc is underlined, and sticky binder GPI is italicized. FIG. **5**NN shows the nucleic acid and protein sequence for the mPDL1-mFc-GPI fusion polypeptide wherein the text for the signaling domain mPDL2 is bolded, mFc is underlined, and sticky binder GPI is italicized. FIG. **5**OO shows the nucleic acid and protein sequence for the mPDL2-GPI fusion polypeptide wherein the text for the signaling domain mPDL2 is bolded and sticky binder GPI is italicized. FIG. **5**PP shows the nucleic acid and protein sequence for the mPDL1-GPI-P2A-mHVEM-GPI fusion polypeptide wherein the text for the signaling domain mPDL1 and mHVEM are bolded, P2A sequence is underlined, and sticky binder GPI is italicized. With P2A included, a self-cleaving peptide sequence, artificial synapses with this feature will have both mPDL1-GPI and mHVEM-GPI loaded onto the surface. FIG. **5**QQ shows the nucleic acid and protein sequence for the hPDL1-ADAM10 fusion polypeptide wherein the text for the signaling domain mPDL1 is bolded and sticky binder ADAM10 is italicized. FIG. **5**RR shows the nucleic acid and protein sequence for the hPDL1-4Fc-CD9tm2 fusion polypeptide wherein the text for the signaling domain hPDL1 is bolded, 4Fc is underlined, and sticky binder CD9tm2 is italicized. FIG. **5**SS shows the nucleic acid and protein sequence for the fusion polypeptide hPDL1-4Fc-CD9tm2-KRAS wherein the text for the signaling domain hPDL1 is bolded, sticky binder 4Fc is underlined, sticky binder CD9tm2 is italicized, and sticky binder KRAS is italicized and underlined. FIG. **5**TT shows the nucleic acid and protein sequence for the hPDL1-Fc-CD9tm2 fusion polypeptide wherein the text for the signaling domain hPDL1 is bolded, Fc is underlined, and sticky binder CD9tm2 is italicized. FIG. **5**UU shows the nucleic acid and protein sequence for the fusion polypeptide hPDL1-Fc-CD9tm2-KRAS wherein the text for the signaling domain hPDL1 is bolded, sticky binder Fc is underlined, sticky binder CD9tm2 is italicized, and sticky binder KRAS is italicized and underlined. FIG. **5**VV shows the nucleic acid and protein sequence for the mPDL1-mFc-CD9tm2 fusion polypeptide wherein the text for the signaling domain mouse PDL1 (mPDL1) is bolded, mouse mFc (mFc) is underlined, and sticky binder CD9tm2 is italicized. FIG. **5**WW shows the nucleic acid and protein sequence for the fusion polypeptide mPDL1-mFc-CD9tm2-KRAS wherein the text for the signaling domain mPDL1 is bolded, sticky binder mFc is underlined, sticky binder CD9tm2 is italicized, and sticky binder KRAS is italicized and underlined. Wherein mPDL1 and mFc are mouse PDL1 and mouse Fc, respectively. FIGS. **5**C-**5**WW disclose SEQ ID NOS: 223-224, 283-284, 239-240, 225-226, 229-230, 233-234, 227-228, 231-232, 235-238, 243-244, 241-242, 245-282, and 285-316, respectively, in order of appearance.

FIG. **6** shows hPD-L1-Fc-GPI artificial synapse purification via a multimodal resin marketed for exosome purification. Large MW artificial synapses elute in the first fraction as shown by the high hPD-L1 concentration and artificial synapse quantity (2.26E9 synapses/ml) in elution 1. Clean in place (CIP) fractions show bound and eliminated proteins from the Inventors' artificial synapse elution.

FIG. **7** shows hPDL1-Fc-GPI exosome purification via size exclusion chromatography using a resin marketed for exosome purification. Artificial synapses engineered from exosomes eluted from via a multimodal resin may be further purified via size exclusion chromatography using a resin marketed for exosome purification as shown here. Using a size exclusion chromatography, artificial synapses elute in fractions 7-9. Total protein (determined by Qubit™) and hPD-L1 ng/ml (determined by ELISA) of each fraction is shown in the graph. Bars show exosome number per ml (i.e., 1E10 exosomes/ml etc.). Fractions 7-9 contain >99% purified artificial synapses. Fractions 7-9 are pooled and may be

concentrated using a filtration device, for example a 10K MWCO Amicon® centrifugal filter. Final purified product may be filtered through a low protein binding filter, for example a 0.2 μm or 0.45 μm PES filter.

FIG. **8** shows hPD-L1 Expression on exosomes, quantity and hPD-L1 concentration was determined in size exclusion chromatography fractions 7-9. Knowing the molecular weight of engineered hPD-L1, the Inventors can determine the number of hPD-L1 molecules per exosome to be approximately between 12 and 40 hPD-L1/exosome. This value is consistent between different purification runs and constructs.

FIG. **9** shows the purification of hPD-L2-Fc-GPI artificial synapses engineered from exosomes via multimodal resin marketed for exosome purification. This graph shows Abs 280 of fractions and quantity of hPDL2 in indicated fractions. Exosomes eluted in Elution 1. Clean in place (CIP) fractions show bound and eliminated proteins from the Inventors' artificial synapse elution.

FIG. **10** shows purification of hPD-L2-Fc-GPI labeled exosomes via size exclusion column as shown here using size exclusion resin marketed for exosome purification. Fractions containing large molecular weight exosomes (Fractions 7-9) showed high hPD-L2 concentration indicating that the purified exosomes contain hPD-L2-Fc-GPI. Total protein (determined by Qubit™) and hPD-L1 ng/ml (determined by ELISA) of each fraction is shown in the graph. Lower molecular weight unbound hPD-L2-Fc-GPI eluted at later fractions.

FIG. **11** shows hCTLA4-Fc-GPI exosome purification via size exclusion column as shown here using size exclusion resin marketed for exosome purification. Using size exclusion chromatography, exosomes elute in fractions 7-9. Total protein (determined by Qubit™) and hCTLA4 ng/ml (determined by ELISA) of each fraction is shown in the graph. Fractions 7-9 are pooled and contain >99% purified exosomes. Pooled exosome fractions may then be concentrated using a filtration device, for example a 10K MWCO Amicon® centrifugal filter. Final purified product may be filtered through a low protein binding filter, for example a 0.2 μm or 0.45 μm PES filter. Knowing the molecular weight of engineered hCTLA-4, the Inventors can determine the number of hCTLA-4 molecules per exosome to be approximately 233 hCTLA-4/exosome.

FIG. **12**A shows PD-1 Signaling Bioassay Method. The Inventors established a method to validate that PD-L1 and PD-L2 artificial synapses engineered from exosomes can bind to cells expressing PD-1 ligand. To perform this validation method, the Inventors modified the PathHunter® PD-1 Signaling Bioassay from DISCOVERX® Briefly, the PathHunter® PD-1 Signaling Bioassay relies on the well-established PathHunter® Enzyme Fragment Complementation (EFC) technology to interrogate receptor activity. EFC consists of a split-galactosidase (β-gal) enzyme: the Enzyme Donor (ED) and Enzyme Acceptor (EA) fragments which independently have no β-gal activity. However, when forced to complement they form an active β-gal enzyme that will hydrolyze substrate to produce a chemiluminescent signal. The PathHunter® PD-1 Signaling Bioassay consists of human cells engineered to stably express an ED-tagged PD-1 receptor, while EA is fused to the phosphotyrosine-binding SH2 domain of the intracellular signaling protein, SHP1. Ligand or antibody-induced activation of the receptor results in phosphorylation of the receptor's cytosolic tail. Ligand engagement, through addition of ligand-presenting artificial synapses engineered from exosomes, results in phosphorylation of PD-1, leading to the recruitment of SHP1-EA. This forces complementation of the EFC components to create an active β-gal enzyme. This active enzyme hydrolyzes substrate to create chemiluminescence as a measure of receptor activity. Addition of an antagonist (e.g., antibody to PD-L1) blocks PD-1 signaling, and will prevent complementation, resulting in a loss of signal. FIG. **12**B shows that the Inventors obtained approximately 10,000× higher increase in Relative Light Units (RLU) in Jurkat signaling cells treated with PD-L1 or PD-L2 labeled artificial synapses when compared to soluble PD-L1-Fc or PD-L2-Fc ligand, respectively. Meaning, it took 10,000× less μg/ml of PD-L1 or PD-L2 on artificial synapses than solubilized PD-L1-Fc or PD-L2 ligand to achieve the same RLU signaling. Shown is a dose-response curve for the PD-L1 and PD-L2 artificial synapses engineered from exosomes vs soluble PD-L1 and PD-L2 signaling bioassay.

FIG. **13**A-**13**C shows experimental EAU outline Test Agent A—unmodified exosomes, Test Agent B—mPDL1-Fc-GPI artificial synapses engineered from exosomes 40 μg/ml, Test Agent C—mPDL1-Fc-GPI artificial synapses engineered from exosomes 400 μg/ml, IRBP-interphotoreceptor retinoid-binding protein (IRBP) peptide, BID-Bis in die (2× daily) p.o.—Per os (orally) (FIG. **13**B) EAU symptoms appear at day 6. 1st intravitreal injection and 2nd intravenous injections are performed on Day 6. There is a statistically significant initial reduction in EAU in mouse PD-L1 (mPD-L1) artificial synapses engineered from exosomes treated rats via either the intravitreal and intravenous delivery modes. 2nd intravitreal and 3rd intravenous injections are performed on Day 12. There appears to be a more rapid rate of resolution in the 1× intravitreal and intravenous groups. (FIG. **13**C) Weight of rats was monitored throughout the study. 3rd intravitreal and 4th intravenous injections are performed on Day 16. There does not appear to be any significant change in EAU in any of the test groups. The aforementioned results provide proof of principle of successfully treating an autoimmune condition (i.e., EAU) with human cell derived artificial synapses with PD-L1.

FIG. **14** shows 2 types of ligands displayed on the exosome surface (Type I and Type II membrane proteins). Type I membrane proteins wherein the N-Terminus is on the luminal (interior) side of the exosome membrane and the C-Terminus is on the exterior of the exosome.

Type II membrane proteins wherein the N-Terminus is on the exterior while the C-Terminus is on the interior.

FIG. **15** shows a schematic representation of several embodiments of Type I membrane protein constructs, which include but are not limited to: PD-L1, PD-L2, FGL1, OX40L. FIG. **15** discloses "GSSG link" as SEQ ID NO: 319.

FIG. **16** shows a schematic representation of several embodiments of the surface of an extracellular vesicle engineered with a Type I membrane protein of interest (POI) with a variable membrane anchor. Vesicle targeting sequences such as select sequences from 4F2 (CD98), ADAM10, CD298, TFR2, transmembrane portions of CD9, MARCKS, KRAS, and GPI from CD55. Proteins engineered to include a targeting sequence domain may include one or more linkers between the sticky binder and signaling domain (e.g., an Fc linker or a bond sequence wherein the bond sequence may be dimerization or multimerization sequence).

FIG. **17** shows a schematic representation of the surface of an exosome engineered with an extracellular portion of the Type II membrane protein of interest (POI) with transmembrane/exosome targeting domains.

FIG. **18** shows a schematic representation of an exosome engineered with an extracellular portion of the Type II membrane protein 4-1BB.

FIG. **19** demonstrates a construct design for labeling an exosome surface with Type II membrane proteins.

FIG. **20** shows a schematic representation of a construct design for labeling an exosome surface with multiple POI domains operably linked by a cleavable (e.g., P2A) linker.

FIG. **21** shows a flow chart of purification and analytical processes provided herein.

FIG. **22** shows a PD-L1 labeled exosome constructs.

FIG. **23** shows several embodiments of the surface of an exosome engineered with PD-L1. The PD-L1 can be the membrane-bound PD-L1 isotype or secreted PD-L1 (SecPD-L1).

FIG. **24** demonstrates size exclusion chromatography for purifying human PD-L1-GPI (no Fc) exosomes. Left panel: Protein, RNA and DNA measurements in SEC fractions are shown. Invitrogen Qubit™ fluorometric assays were used to measure biomolecules from unmodified concentrated cell media SEC fractions or hPD-L1-Exo-Tag concentrated cell media SEC fractions. PD-L1 was measured using an R&D systems PD-L1 ELISA kit. Right panel shows dot-blot immunoblot analysis of SEC fractions. A 96-well dot blot apparatus was used to immobilize 50 μl of each SEC fraction onto PVDF. Right bottom figures: Exosome size and concentration was measured in fraction 7 by tunable resistive pulse sensing (TRPS).

FIG. **25** demonstrates that GPI anchors hPD-L1 on exosomes.

FIG. **26** demonstrates that a multimodal resin marketed for exosome purification purifies and disaggregates exosomes.

FIG. **27** shows the exosome decoration with hPD-L1-Fc-GPI.

FIG. **28**A shows the exosome decoration with hPD-L1-Fc-GPI. Fraction 7 contained the purified hPD-L1-Fc-GPI vesicles. FIG. **28**B shows size exclusion chromatography (SEC) purification results of various embodiments of human PD-L1 displayed on the surface of extracellular vesicles.

FIG. **29** shows that mouse PD-L1-Fc-GPI exosomes have higher valency than mPD-L1-GPI.

FIG. **30**A-**30**C demonstrates comparison proteomics of transprotein expression and shows that surface labeling on the engineered extracellular vesicles provided herein do not affect the relative expression of native and associated exosome proteins. FIG. **30**A shows hPD-L1-Fc-GPI. FIG. **30**B shows hPD-L2-FcGPI. FIG. **30**C shows hCTLA4-Fc-GPI.

FIG. **31** shows production of mPD-L1-Fc-GPI in STR Bioreactor.

FIG. **32** shows purification of mPD-L1-Fc-GPI (STR) via SEC. Graph shows mPD-L1 ng/ml vs Total Protein μg/ml.

FIG. **33** shows purification mPDL1-Fc-GPI (STR bioreactor).

FIG. **34** shows a schematic representation of the 4-1BBL labeled exosomes. Top: Vector map showing the N-terminal cystolic domain, a transmembrane (TM) domain, and the POI domain at the C-terminus. Bottom: An embodiment of an engineered EV with a type-II membrane display of the fusion protein.

FIG. **35** shows embodiments of a 4-1BBL display exosome.

FIG. **36**A-**36**B show the protein engineering and purification of 4F2-4-1BBL labeled exosomes. FIG. **36**B confirms that h4-1BBL is displayed on the engineered exosomes.

FIG. **37** shows internal fusion protein loading of exosomes.

FIG. **38** shows internal loading of exosomes with mScarlet (RFP).

FIG. **39**A shows internal loading of exosomes with NanoLuc® luciferase. FIG. **39**B shows tetraspanin characterization of exosomes internally loaded with NanoLuc® luciferase.

FIG. **40**A shows the mechanism of PD-L1 engineered extracellular vesicles induce membrane clustering and receptor agonism on a target cell. An exemplary model of proposed mechanism of extracellular vesicles with a Type I membrane protein signaling domain (PD-L1) promoting receptor clustering on a target cell, wherein receptor clustering promotes increased potency of signal transduction of the target receptor. Antagonist antibodies function well at blocking receptors. Antibodies are poor agonist modalities due to their general inability to cluster receptors. Ligands on a membrane surface are potent agonists, however the cost and cold chain logistics of cell therapies makes commercialization difficult and expensive. Extracellular vesicles engineered with Type I membrane protein are able to induce receptor clustering of target receptors and initiate and propagate a potent signal response on a target cell.

FIG. **40**B shows the mechanism of 4-1BBL engineered extracellular vesicles induce membrane clustering and receptor agonism on a target cell. An exemplary model of proposed mechanism of extracellular vesicles with a Type II membrane protein signaling domain (4-1BBL) promoting receptor clustering on a target cell, wherein receptor clustering promotes increased potency of signal transduction of the target receptor. Soluble ligands are often poor agonist modalities due to their general inability to cluster receptors. Ligands displayed on a membrane surface are potent agonists, however the cost and cold chain logistics of cell therapies makes commercialization difficult and expensive. Extracellular vesicles engineered with Type II membrane protein are able to induce receptor clustering of target receptors and initiate and propagate a potent signal response on a target cell.

DETAILED DESCRIPTION

The compositions and methods provided herein are based, in part, on the discovery that engineered extracellular vesicles (e.g., exosomes) expressing an engineered fusion protein (e.g., PD-L1) reduces inflammation in an animal model of experimental autoimmune uveoretinitis (EAU), an autoimmune disorder. The compositions and methods provided herein are further based, in part, on the discovery that engineered extracellular vesicles produce enhanced signaling compared to an equal quantity of recombinant ligand. Since some cellular receptors, (e.g., PD-1) require clustering or super-clustering to promote a signaling response, it stands to reason that extracellular vesicles engineered to express ligands on their surface wherein the ligands may engage target receptors on target cells and promote clustering of said target receptors thereby promoting a signal response on said target cell.

In one aspect, provided herein is an engineered extracellular vesicle comprising: at least one fusion polypeptide comprising: at least one protein of interest (POI) domain; and at least one vesicle targeting domain. In some embodiments of any of the aspects, the engineered extracellular vesicle is an exosome. In some embodiments, of any of the aspects, the fusion protein further comprises at least one linker. In some embodiments of any of the aspects, the POI domain can substantially bind to a target polypeptide. In

some embodiments of any of the aspects provided herein, the engineered extracellular vesicle is an artificial synapse.

Generally, the extracellular vesicles (e.g., exosomes) provided herein are produced by contacting a population of cells with a nucleic acid construct encoding the fusion proteins provided herein and isolating a plurality of extracellular vesicles. The extracellular vesicles can then be purified by methods provided herein and are formulated for therapeutic use, including but not limited to, for the treatment of autoimmune diseases, cancer, or modulating inflammation in a subject.

The compositions and methods provided herein are specifically designed to exploit the membrane trafficking mechanisms of extracellular vesicles and rely on the hallmark biophysical and biochemical properties of extracellular vesicles, such as exosomes. The vesicles/artificial synapses provided herein are specifically engineered to induce/agonize and propagate biological signaling via a target polypeptide (e.g., by activating a receptor or enzyme or agonizing said receptor or enzyme). Alternatively, the engineered extracellular vesicles provided herein can act as cellular decoys or to reduce or antagonize biological signaling, e.g., by blocking an endogenous ligand from binding to a target cellular receptor and preventing activation of the receptor.

Engineering of the extracellular vesicles provided herein extends these capabilities significantly by incorporating sticky binders attaching to extracellular vesicles such as exosomes, further coupled with signaling domains of choice. For example, attachment of sticky binders to exosomes, along with their linked signaling domains, allows for receptor clustering for biological signal induction/agonism and propagation not otherwise possible. In this aspect, the aforementioned design achieves the aim of an engineered extracellular vesicle by inducing the desired biological signaling in a target recipient cell.

Various aspects and embodiments of the compositions and methods are provided herein in detail below.

Engineered Extracellular Vesicle (EV) Compositions

The compositions provided herein comprises at least one extracellular vesicle (also termed artificial synapse or abbrv: EV), wherein the extracellular vesicle comprises at least one fusion polypeptide or a plurality of fusion polypeptides comprising: at least one vesicle targeting domain (e.g., sticky binders); and at least one protein of interest domain or a fragment thereof (also termed signaling domains).

Extracellular vesicles (EVs) are lipid particles that are released from various cell types that function to transfer "cargo" such as nucleic acids and proteins to other cells. EVs are not able to replicate but serve as cell messengers. EV-mediated signals can be transmitted by all the different biomolecule categories-protein, lipids, nucleic acids and sugars—and the unique package of this information provides both protection and the option of simultaneous delivery of multiple different messengers even to sites remote to the vesicular origin. See, e.g., Yáñez-Mó M, Siljander P R, Andreu Z, et al. Biological properties of extracellular vesicles and their physiological functions. J Extracell Vesicles. 2015; 4:27066. Published 2015 May 14. doi: 10.3402/jev.v4.27066, which is incorporated herein by reference in its entirety. Furthermore, there is an increasing amount of evidence that shows that EVs can modulate a milieu of cellular signaling processes. See, e.g., Yadid et al. *Science Translation Medicine* (2020); Cerqueira de Abreu et al. *Nature Reviews Cardiology* (2020); Zhang W. et al. *Protein J.* (2019); Zha Q B et al. *Tumor Biology*. February 2017; Tan et al. (2016) Recent advances of exosomes in immune modulation and autoimmune diseases, *Autoimmunity,* 49:6, 357-365; Kalluri R, LeBleu V S. et al. The biology, function, and biomedical applications of exosomes. Science. 2020 Feb. 7; 367(6478); which is incorporated herein by reference in its entirety.

There are various types of extracellular vesicles that are named for their site of origin in a cell, size, and structural and/or functional properties. In some embodiments of any of the aspects provided herein, the extracellular vesicle is an exosome, ectosome, macrovesicle, microparticle, apoptotic body, vesicular organelle, oncosome, exosphere, exomeres, or cell derived nanovesicle (CDN) ((e.g., by genesis via grating or shearing cells), liposomes or the like known by one of ordinary skill in the art. In various embodiments, the extracellular vesicle comprises a phospholipid bilayer with an exterior phospholipid layer and an interior phospholipid layer, wherein the exterior phospholipid layer has an external surface and an internal surface, wherein the interior phospholipid layer has an internal surface and an external surface, and the internal surface of the exterior phospholipid layer faces the internal surface of the interior phospholipid layer, and the phospholipid bilayer encloses an internal space, wherein the external surface of the interior phospholipid layer faces the internal space and wherein the external surface of the exterior phospholipid layer faces an extracellular environment, and the external surface of the inner phospholipid layer is the internal surface of the extracellular vesicle.

In various embodiments, the extracellular vesicles range in size from 30 nanometers (nm) to 300 nm. In various embodiments, the plurality of EVs range in size from about 30 nm to about 150 nm. In various embodiments, the plurality of EVs or artificial synapses includes one or more artificial synapses that are about 10 nm to about 250 nm in diameter, including those about 10 nm to about 15 nm, about 15 nm to about 20 nm, about 20 nm to about 25 nm, about 25 nm to about 30 nm, about 30 nm to about 35 nm, about 35 nm to about 40 nm, about 40 nm to about 50 nm, about 50 nm to about 60 nm3 about 60 nm to about 70 nm, about 70 nm to about 80 nm, about 80 nm to about 90 nm, about 90 nm to about 95 nm, about 95 nm to about 100 nm, about 100 nm to about 105 nm, about 105 nm to about 110 nm, about 110 nm to about 115 nm, about 115 nm to about 120 nm, about 120 nm to about 125 nm, about 125 nm to about 130 nm, about 130 nm to about 135 nm, about 135 nm to about 140 nm, about 140 nm to about 145 nm, about 145 nm to about 150 nm, about 150 to about 200 nm, about 200 nm to about 250 nm, about 250 nm or more.

In some embodiments of any of the aspects provided herein, the EV is an exosome. Exosomes are membrane-bound EVs that are produced in the endosomal compartment of most eukaryotic cells. As used herein, the term "exosome" refers to a species of extracellular vesicle between about 20 nm to about 400 μm in diameter, e.g, about 30 nm-200 nm in diameter by inward invagination of a portion of a membrane of an endosome (for example an early or late endosome), wherein the endosome is within a cell comprising a plasma membrane, and the exosome is released from the cell upon fusion of another portion of the endosome membrane with the plasma membrane. An exosome may refer to a species of extracellular vesicle between 20 nm-400 μM in diameter, more preferably 30 nm-200 nm in diameter, that originates by budding of a portion of a plasma mem-

brane from a cell wherein the budded portion of the plasma membrane is released to the extracellular environment.

The EVs (e.g., exosomes or cell derived vesicles) provided herein may comprise cargo, for example, peptides, proteins, nucleic acids, lipids, metabolites, carbohydrates, biomolecules, small molecules, large molecules, vesicles, organelles, or fragments thereof. Exosome cargo may be located within the internal space of the exosome. EV cargo may be membrane bound spanning one or both layers of the exosome phospholipid bilayer (for example a transmembrane protein). EV cargo may be in contact with the exterior or interior surface of the exosome, for example through a covalent bond or a non-covalent bond. The phospholipid bilayer of the EV or exosome provided herein may comprise one or more transmembrane proteins, wherein a portion of the one or more transmembrane membrane proteins is located within the internal space of the exosome. The phospholipid bilayer of the EV or exosome provided herein may comprise one or more transmembrane proteins, wherein a portion of the one or more transmembrane membrane proteins traverses the EV phospholipid bilayer. The phospholipid bilayer of the EV may comprise one or more transmembrane proteins, wherein the one or more transmembrane membrane proteins comprises a domain on the exterior of the exosome.

In some embodiments of any of the aspects, the extracellular vesicles or exosomes provided herein endogenously express CD81+, CD82+, CD37+, CD63+, CD9+, CD151+, CD105+, or any combination thereof. In various embodiments, the plurality of artificial synapses includes one or more artificial synapses expressing a biomarker. In certain embodiments, the biomarkers are tetraspanins. In other embodiments, the tetraspanins are one or more selected from the group including CD63, CD81, CD82, CD53, CD151, and CD37. In other embodiments, the artificial synapses express one or more lipid raft associated proteins (e.g., glycosylphosphatidylinositol-anchored proteins and flotillin), cholesterol, sphingolipids such as sphingomyelin, and/or hexosylceramides.

In other embodiments, the biological protein is related to exosome formation and packaging of cytosolic proteins, e.g., Hsp70, Hsp90, 14-3-3 epsilon, PKM2, GW182 and AGO2. In certain embodiments, the artificial synapses express CD63, HSP70, CD105 or combinations thereof. In other embodiments, the artificial synapses do not express CD9 or CD81, or express neither. For example, plurality of artificial synapses can include one or more artificial synapses that are CD63+, HSP+, CD105+, CD9−, and CD81−.

The EVs provided herein are specifically engineered to express fusion polypeptides that elicit biological signaling via a target cell. In some embodiments, the fusion polypeptide is overexpressed to elicit a biological response on a target cell or target polypeptide. The engineered EV comprises at least one fusion polypeptide and can comprise a plurality of the same or different fusion polypeptides provided herein. The fusion polypeptides provided herein comprise a protein of interest domain, also termed the signaling domain.

The fusion polypeptides provided herein can comprise one or more of a protein of interest domain, such that expression of said fusion polypeptide is permitted and that the number of POI domains does not impede protein expression or folding. Furthermore, the EVs provided herein can express more than one fusion protein (e.g., encoded by multiple different nucleic acid constructs). One of skill in the art can appreciate that an engineered EV can include one or more combinations of different signaling domains and/or vesicle targeting domains, or that one can use a plurality of engineered EVs, each including one or more vesicle targeting domains and one or more signaling domains.

In some embodiments, the EVs provided herein comprise one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, or ten or more fusion proteins. The fusion proteins can be encoded by the same vector or separate vectors. In some embodiments of any of the aspects, the engineered extracellular vesicle comprises at least two POI domains and/or at least two vesicle targeting domains.

In some embodiments, the fusion polypeptide comprises one or more, two or more, three or more, four or more, five or more, or six or more POI domains on the same polypeptide or nucleic acid construct encoding said polypeptide. For example, the fusion polypeptides provided herein can express a fusion polypeptide encoding one or more, two or more, three or more, four or more, five or more, or six or more signaling domains. In another example, the fusion polypeptides provided herein can express a fusion polypeptide encoding an immune checkpoint protein or a protein involved in immune or cell synapse or any combination or fragment thereof.

In some embodiments, the EV comprises one or more, two or more, three or more, four or more, five or more, or six or more fusion polypeptides on the same EV. For example, EVs comprising one or more, two or more, three or more, four or more, five or more, or six or more fusion polypeptides wherein the fusion polypeptides encode a signaling domain. In another example, EVs comprising one or more, two or more, three or more, four or more, five or more, or six or more fusion polypeptides wherein the fusion polypeptides encode for one or more immune checkpoint proteins or proteins involved in immune or cell synapse, or any combination or fragment thereof.

In various embodiments, the signaling domain is a protein or peptide of interest, or a fragment thereof. In various embodiments, the protein of interest (signaling domain) is an immune checkpoint protein. The terms "immune checkpoint protein" or "protein involved in immune or cell synapse" can include but are not limited to adenosine A2A receptor (A2AR), Galectin 9, fibrinogen-like protein 1 (FGL-1), platelet endothelial adhesion factor-1 (PECAM-1), tumor necrosis factor gene 6 protein (TSG-6), Stabilin-1 (STAB-1) also known as Clever-1, Neuropilin 1 (NRP1), Neuropilin 2 (NRP2), semaphorin-3A (SEMA3A), semaphorin-3F (SEMA3F), repulsive guidance molecule B (RGMB) also known as DRG11, T-cell immunoglobulin and mucin domain 3 (TIM-3), T cell immunoreceptor with Ig and ITIM domains (TIGIT), human leukocyte antigen (HLA) class I, HLA class II, high mobility group protein B1 (HMGB1), phosphatidylserine, carcinoembryonic antigen-related cell adhesion molecule 1 (CEACAM-1), T-cell receptor (TCR), Src homology 2 domain-containing protein tyrosine phosphatase 1 (SHP-1), SHP-2, F-Box protein 38 (FBXO38), signaling lymphocytic activation molecule (SLAM)-associated protein (SAP) also known as SH2D1A, B7RP1, indoleamine 2,3-dioxygenase (IDO), NADH oxidase 2 (NOX2), tumor necrosis factor receptor (TNFR) superfamily member 18 (TNFRSF18) (also known as activation inducible TNFR family receptor (AITR), glucocorticoid-induced TNFR related (GITR) protein, and CD357), B7-H4 also known as V-set domain containing T-cell activator inhibitor (VTCN1), B7-H5 (also known as V-domain Ig suppressor of T-cell activation (VISTA), platelet receptor Gi24, and stress induced secreted protein 1 (SISP1), B7-H6 (also known as NCR3LG1), B7-H7 (also known as human

endogenous retrovirus-H (HERV-H) long terminal repeat-associating protein 2 (HHLA2), apelin receptor (APLNR), interferon gamma (IFN y) receptor, programmed cell death-1 (PD-1), Protein Wnt-5a (WNT5A), serine/threonine-protein kinase PAK4, interleukin 6 (IL-6), interleukin-10 (IL-10), NKG2 family of C-type lectin receptors (for example NKG2A, B, C, D, E, F and H), ligands of NKG2 family, killer cell immunoglobulin-like receptors, CD-2, cluster of differentiation 4 (CD4), CD8, CD27, CD27 ligand (CD27L, also known as CD70), CD28, CD28H (also known as transmembrane and immunoglobulin domain containing 2 (TMIGD2) and Ig containing and proline-rich receptor-1 (IGPR1)), CD39, CD40, CD44, integrin associated protein (CD47), carcinoembryonic antigen related cell adhesion molecule 1 (CEACAM1 also known as CD66a), CD73, B7-1 (also known as CD80), B7-2 (also known as CD86), CD94, CD96, immunoglobulin superfamily member 2 (IGSF2) also known as CD101, nectin cell adhesion molecule 2 (NECTIN2) (also known as herpesvirus entry mediator B (HVEB), poliovirus receptor related 2 (PRR2, PVRL2 and PVRR2) and CD112), poliovirus receptor related immunoglobulin domain containing protein (PVIRG) also known as CD112R, CD122 (also known as IL5RB and P70-75), OX40 (also known as tumor necrosis factor receptor superfamily member 4 (TNFRSF4) and CD134), OX40 ligand (OX40L), 4-1BB (also known as CD137), CD134 (also known as 4-1BB ligand (4-1BBL) and as tumor necrosis factor ligand superfamily member 9 (TNFSF9) and CD137L), cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) also known as CD152, CD154 (also known as CD40L), poliovirus receptor (PVR) also known as CD155, killer-cell immunoglobulin-like receptors (KIRs) (for example but not limited to CD158 family, CD158a, CD158g, CD158h, KIR2DL1, KIR2DS1, KIRDS3, and KIR2DS5), CD160, signal-regulatory protein alpha (SIRPα) also known as CD172a, OX-2 also known as CD200, CD200R, lymphocyte-activation gene 3 (LAG-3) also known as CD223, CD226, OX40L also known as CD252, herpes virus entry mediator (HVEM) also known as tumor necrosis factor receptor superfamily member 14 (TNFRSF14) and CD270, B- and T-lymphocyte attenuator (BTLA) also known as CD272, programmed cell death ligand-2 (PD-L2) (also known as B7-DC, PDCDILG2, and CD273), programmed cell death-ligand 1 (PD-L1) (also known as B7-H1 and CD274), B7-H2 (also known as inducible T-cell co-stimulator ligand (ICOSLG), B7RP1, and CD275), B7-H3 also known as CD276, inducible T-cell co-stimulator (ICOS) also known as CD278, programed cell death protein 1 (PD-1) also known as CD279, leukocyte-associated Ig-like receptor-1 (LAIR-1) also known as CD305, collagen family of proteins (for example but not limited to collagen I, collagen II, collagen III alpha 1, collagen IV, collagen XXIII alpha 1, collagen XXV alpha 1), sialic acid-binding immunoglobulin-type lectin 7 (SIGLEC7) also known as CD328, sialic acid-binding immunoglobulin-type lectin 7 (SIGLEC9) also known as CD329, natural cytotoxicity triggering receptor 3 (NKp30) also known as CD337, or any isoform, fragment, variation thereof, or a ligand to the aforementioned proteins thereof, or the like known by one of ordinary skill in the art. All variants are encompassed by the present invention.

In some embodiments of any of the aspects provided herein, the protein of interest domain (POI domain) comprises a polypeptide or a fragment thereof or a nucleic acid encoding said polypeptide or fragment thereof selected from the group consisting of: Table 1 (below). Non-limiting examples of nucleic acid sequences that encode the POI domains provided herein are also provided in

TABLE 1

Type I Proteins of Interest Amino Acid Sequence

Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
Human Programmed death-ligand 1 (PD-L1)	>NM_014143.4 *Homo sapiens* CD274 molecule (CD274), transcript variant 1, mRNA AGTTCTGCGCAGCTTCCCGAGGCTCCGCACCAGCCGCGCTTCTGTCCGCCTGCAGGG CATTCCAGAAAGATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTG CTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGC AATATGACAATTGAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTA ATTGTCTATTGGGAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAA GACCTGAAGGTTCAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAG CTCTCCCTGGGAAATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGG GTGTACCGCTGCATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAA GTCAATGCCCCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACC TCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGG ACAAGCAGTGACCATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGA GAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAG ATTTTCTACTGCACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTG GTCATCCCAGAACTACCTCTGGCACATCCTCCAAATGAAAGGACTCACTTGGTAATT CTGGGAGCCATCTTATTATGCCTTGGTGTAGCACTGACATTCATCTTCCGTTTAAGA AAAGGGAGAATGATGGATGTGAAAAAATGTGGCATCCAAGATACAAACTCAAAGAAG CAAAGTGATACACATTTGGAGGAGACGTAATCCAGCATTGGAACTTCTGATCTTCAA GCAGGGATTCTCAACCTGTGGTTTAGGGGTTCATCGGGGCTGAGCGTGACAAGAGGA AGGAATGGGCCCGTGGGATGCAGGCAATGTGGGACTTAAAAGGCCCAAGCACTGAAA ATGGAACCTGGCGAAAGCAGAGGAGGAGAATGAAGAAAGATGGAGTCAAACAGGGAG CCTGGAGGGAGACCTTGATACTTTCAAATGCCTGAGGGGCTCATCGACGCCTGTGAC AGGGAGAAAGGATACTTCTGAACAAGGAGCCTCCAAGCAAATCATCCATTGCTCATC CTAGGAAGACGGGTTGAGAATCCCTAATTTGAGGGTCAGTTCCTGCAGAAGTGCCCT TTGCCTCCACTCAATGCCTCAATTTGTTTTCTGCATGACTGAGAGTCTCAGTGTTGG AACGGGACAGTATTTATGTATGAGTTTTTCCTATTTATTTTGAGTCTGTGAGGTCTT CTTGTCATGTGAGTGTGGTTGTGAATGATTTCTTTTGAAGATATATTGTAGTAGATG TTACAATTTTGTCGCCAAACTAAACTTGCTGCTTAATGATTTGCTCACATCTAGTAA AACATGGAGTATTTGTAAGGTGCTTGGTCTCCTCTATAACTACAAGTATACATTGGA AGCATAAAGATCAAACCGTTGGTTGCATAGGATGTCACCTTTATTTAACCCATTAAT ACTCTGGTTGACCTAATCTTATTCTCAGACCTCAAGTGTCTGTGCAGTATCTGTTCC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ATTTAAATATCAGCTTTACAATTATGTGGTAGCCTACACACATAATCTCATTTCATC GCTGTAACCACCCTGTTGTGATAACCACTATTATTTTACCCATCGTACAGCTGAGGA AGCAAACAGATTAAGTAACTTGCCCAAACCAGTAAATAGCAGACCTCAGACTGCCAC CCACTGTCCTTTTATAATACAATTTACAGCTATATTTTACTTTAAGCAATTCTTTTA TTCAAAAACCATTTATTAAGTGCCCTTGCAATATCAATCGCTGTGCCAGGCATTGAA TCTACAGATGTGAGCAAGACAAAGTACCTGTCCTCAAGGAGCTCATAGTATAATGAG GAGATTAACAAGAAAATGTATTATTACAATTTAGTCCAGTGTCATAGCATAAGGATG ATGCGAGGGGAAAACCCGAGCAGTGTTGCCAAGAGGAGGAAATAGGCCAATGTGGTC TGGGACGGTTGGATATACTTAAACATCTTAATAATCAGAGTAATTTTCATTTACAAA GAGAGGTCGGTACTTAAAATAACCCTGAAAAATAACACTGGAATTCCTTTTCTAGCA TTATATTTATTCCTGATTTGCCTTTGCCATATAATCTAATGCTTGTTTATATAGTGT CTGGTATTGTTTAACAGTTCTGTCTTTTCTATTTAAATGCCACTAAATTTTAAATTC ATACCTTTCCATGATTCAAAATTCAAAAGATCCCATGGGAGATGGTTGGAAAATCTC CACTTCATCCTCCAAGCCATTCAAGTTTCCTTTCCAGAAGCAACTGCTACTGCCTTT CATTCATATGTTCTTCTAAAGATAGTCTACATTTGGAAATGTATGTTAAAAGCACGT ATTTTTAAAATTTTTTTCCTAAATAGTAACACATTGTATGTCTGCTGTGTACTTTGC TATTTTTATTTATTTTAGTGTTTCTTATATAGCAGATGGAATGAATTTGAAGTTCCC AGGGCTGAGGATCCATGCCTTCTTTGTTTCTAAGTTATCTTTCCCATAGCTTTTCAT TATCTTTCATATGATCCAGTATATGTTAAATATGTCCTACATATACATTTAGACAAC CACCATTTGTTAAGTATTTGCTCTAGGACAGAGTTTGGATTTGTTTATGTTTGCTCA AAAGGAGACCCATGGGCTCTCCAGGGTGCACTGAGTCAATCTAGTCCTAAAAAGCAA TCTTATTATTAACTCTGTATGACAGAATCATGTCTGGAACTTTTGTTTTCTGCTTTC TGTCAAGTATAAACTTCACTTTGATGCTGTACTTGCAAAATCACATTTTCTTTCTGG AAATTCCGGCAGTGTACCTTGACTGCTAGCTACCCTGTGCCAGAAAAGCCTCATTCG TTGTGCTTGAACCCTTGAATGCCACCAGCTGTCATCACTACACAGCCCTCCTAAGAG GCTTCCTGGAGGTTTCGAGATTCAGATGCCCTGGGAGATCCCAGAGTTTCCTTTCCC TCTTGGCCATATTCTGGTGTCAATGACAAGGAGTACCTTGGCTTTGCCACATGTCAA GGCTGAAGAAACAGTGTCTCCAACAGAGCTCCTTGTGTTATCTGTTTGTACATGTGC ATTTGTACAGTAATTGGTGTGACAGTGTTCTTTGTGTGAATTACAGGCAAGAATTGT GGCTGAGCAAGGCACATAGTCTACTCAGTCTATTCCTAAGTCCTAACTCCTCCTTGT GGTGTTGGATTTGTAAGGCACTTTATCCCTTTTGTCTCATGTTTCATCGTAAATGGC ATAGGCAGAGATGATACCTAATTCTGCATTTGATTGTCACTTTTTGTACCTGCATTA ATTTAATAAAATATTCTTATTTATTTTGTTACTTGGTACACCAGCATGTCCATTTTC TTGTTTATTTTGTGTTTAATAAAATGTTCAGTTTAACATCCCA (SEQ ID NO: 1) >NP_054862.1 programmed cell death 1 ligand 1 isoform a precursor [*Homo sapiens*] MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE LPLAHPPNERTHLVILGAILLCLGVALTFIFRLRKGRMMDVKKCGIQDTNSKKQSDT HLEET (SEQ ID NO: 2)
Mouse PD-L1	>NM_021893.3 *Mus musculus* CD274 antigen (Cd274), mRNA GAAATCGTGGTCCCCAAGCCTCATGCCAGGCTGCACTTGCACGTCGCGGGCCAGTCT CCTCGCCTGCAGATAGTTCCCAAAACATGAGGATATTTGCTGGCATTATATTCACAG CCTGCTGTCACTTGCTACGGGCGTTTACTATCACGGCTCCAAAGGACTTGTACGTGG TGGAGTATGGCAGCAACGTCACGATGGAGTGCAGATTCCCTGTAGAACGGGAGCTGG ACCTGCTTGCGTTAGTGGTGTACTGGGAAAAGGAAGATGAGCAAGTGATTCAGTTTG TGGCAGGAGAGGAGGACCTTAAGCCTCAGCACAGCAACTTCAGGGGGAGAGCCTCGC TGCCAAAGGACCAGCTTTTGAAGGGAAATGCTGCCCTTCAGATCACAGACGTCAAGC TGCAGGACGCAGGCGTTTACTGCTGCATAATCAGCTACGGTGGTGCGGACTACAAGC GAATCACGCTGAAAGTCAATGCCCCATACCGCAAAATCAACCAGAGAATTTCCGTGG ATCCAGCCACTTCTGAGCATGAACTAATATGTCAGGCCGAGGGTTATCCAGAAGCTG AGGTAATCTGGACAAACAGTGACCACCAACCCGTGAGTGGGAAGAGAAGTGTCACCA CTTCCCGGACAGAGGGGATGCTTCTCAATGTGACCAGCAGTCTGAGGGTCAACGCCA CAGCGAATGATGTTTTCTACTGTACGTTTTGGAGATCACAGCCAGGGCAAAACCACA CAGCGGAGCTGATCATCCCCAGAACTGCCTGCAACACATCCTCCACAGAACAGGACTC ACTGGGTGCTTCTGGGATCCATCCTGTTGTTCCTCATTGTAGTGTCCACGGTCCTCC TCTTCTTGAGAAAACAAGTGAGAATGCTAGATGTGGAGAAATGTGGCGTTGAAGATA CAAGCTCAAAAAACCGAAATGATACACAATTCGAGGAGACGTAAGCAGTGTTGAACC CTCTGATCGTCGATTGGCAGCTTGTGGTCTGTGAAAGAAAGGGCCCATGGGACATGA GTCCAAAGACTCAAGATGGAACCTGAGGGAGAGAACCAAGAAAGTGTTGGGAGAGGA GCCTGGAACAACGGACATTTTTTCCAGGGAGACACTGCTAAGCAAGTTGCCCATCAG TCGTCTTGGGAAATGGATTGAGGGTTCCTGGCTTAGCAGCTGGTCCTTGCACAGTGA CCTTTTCCTCTGCTCAGTGCCGGGATGAGAGATGGAGTCATGAGTGTTGAAGAATAA GTGCCTTCTATTTATTTTGAGTCTGTGTGTTCTCACTTTGGGCATGTAATTATGACT GGTGAATTCTGACGACATGATAGATCTTAAGATGTAGTCACCAAACTCAACTGCTGC TTAGCATCCTCCGTAACTACTGATACAAGCAGGGAACACAGAGGTCACCTGCTTGGT TTGACAGGCTCTTGCTGTCTGACTCAAATAATCTTTATTTTTCAGTCCTCAAGGCTC TTCGATAGCAGTTGTTCTGTATCAGCCTTATAGGTGTCAGGTATAGCACTCAACATC TCATCTCATTACAATAGCAACCCTCATCACCATAGCAACAGCTAACCTCTGTTATCC TCACTTCATAGCCAGGAAGCTGAGCGACTAAGTCACTTGCCCACAGAGTATCAGCTC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TCAGATTTCTGTTCTTCAGCCACTGTCCTTTCAGGATAGAATTTGTCGTTAAGAAAT TAATTTAAAAACTGATTATTGAGTAGCATTGTATATCAATCACAACATGCCTTGTGC ACTGTGCTGGCCTCTGAGCATAAAGATGTACGCCGGAGTACCGGTCGGACATGTTTA TGTGTGTTAAATACTCAGAGAAATGTTCATTAACAAGGAGCTTGCATTTTAGAGACA CTGGAAAGTAACTCCAGTTCATTGTCTAGCATTACATTTACCTCATTTGCTATCCTT GCCATACAGTCTCTTGTTCTCCATGAAGTGTCATGAATCTTGTTGAATAGTTCTTTT ATTTTTTAAATGTTTCTATTTAAATGATATTGACATCTGAGGCGATAGCTCAGTTGG TAAAACCCTTTCCTCACAAGTGTGAAACCCTGAGTCTTATCCCTAGAACCCACATAA AAAACAGTTGCGTATGTTTGTGCATGCTTTTGATCCCAGCACTAGGGAGGCAGAGGC AGGCAGATCCTGAGCTCTCATTGACCACCCAGCCTAGCCTACATGGTTAGCTCCAGG CCTACAGGAGCTGGCAGAGCCTGAAAAACGATGCCTAGACACACACACACACACACA CACACACACACACACACACACACACCATGTACTCATAGACCTAAGTGCACCCTCCTA CACATGCACACACATACAATTCAAACACAAATCAACAGGGAATTGTCTCAGAATGGT CCCCAAGACAAAGAAGAAGAAAAACACCAAACCAGCTCTATTCCCTCAGCCTATCCT CTCTACTCCTTCCTAGAAGCAACTACTATTGTTTTTGTATATAAATTTACCCAACGA CAGTTAATATGTAGAATATATATTAAAGTGTCTGTCAATATATATTATCTCTTTCTT TCTTTCTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT CTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTTCTTTCTTTCTTTCTTTT TTTCTGTCTATCTGTACCTAAATGGTTGCTCACTATGCATTTTCTGTGCTCTTCGCC CTTTTTATTTAATGTATGGATATTTATGCTGCTTCCAGAATGGATCTAAAGCTCTTT GTTTCTAGGTTTTCTCCCCCATCCTTCTAGGCATCTCTCACACTGTCTAGGCCAGAC ACCATGTCTGCTGCCTGAATCTGTAGACACCATTTATAAAGCACGTACTCACCGAGT TTGTATTTGGCTTGTTCTGTGTCTGATTAAAGGGAGACCATGAGTCCCCAGGGTACA CTGAGTTACCCCAGTACCAAGGGGGAGCCTTGTTTGTGTCTCCATGGCAGAAGCAGG CCTGGAGCCATTTTGGTTTCTTCCTTGACTTCTCTCAAACACAGACGCCTCACTTGC TCATTACAGGTTCTCCTTTGGGAATGTCAGCATTGCTCCTTGACTGCTGGCTGCCCT GGAAGGAGCCCATTAGCTCTGTGTGAGCCCTTGACAGCTACTGCCTCTCCTTACCAC AGGGGCCTCTAAGATACTGTTACCTAGAGGTCTTGAGGATCTGTGTTCTCTGGGGGG AGGAAAGGAGGAGGAACCCAGAACTTTCTTACAGTTTTCCTTGTTCTGTCACATGTC AAGACTGAAGGAACAGGCTGGGCTACGTAGTGAGATCCTGTCTCAAAGGAAAGACGA GCATAGCCGAACCCCCGGTGGAACCCCCTCTGTTACCTGTTCACACAAGCTTATTGA TGAGTCTCATGTTAATGTCTTGTTTGTATGAAGTTTAAGAAAATATCGGGTTGGGCA ACACATTCTATTTATTCATTTTATTTGAAATCTTAATGCCATCTCATGGTGTTGGAT TGGTGTGGCACTTTATTCTTTTGTGTTGTGTATAACCATAAATTTTATTTTGCATCA GATTGTCAATGTATTGCATTAATTTAATAAATATTTTTATTTATTAAAAAAAAAAAAA AAAAA (SEQ ID NO: 3)
	>NP_068693.1 programmed cell death 1 ligand 1 precursor [*Mus musculus*] MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYW EKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQITDVKLQDAGVYCC IISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDH QPVSGKRSVTTSRTEGMLLNVTSSLRVNATANDVFYCTFWRSQPGQNHTAELIIPEL PATHPPQNRTHWVLLGSILLFLIVVSTVLLFLRKQVRMLDVEKCGVEDTSSKNRNDT QFEET (SEQ ID NO: 4)
Human PD-L2	>NM_025239.4 *Homo sapiens* programmed cell death 1 ligand 2 (PCD1LG2), mRNA ACTCTCATGTTACGGCAAACCTTAAGCTGAATGAACAACTTTTCTTCTCTTGAATAT ATCTTAACGCCAAATTTTGAGTGCTTTTTTGTTACCCATCCTCATATGTCCCAGCTA GAAAGAATCCTGGGTTGGAGCTACTGCATGTTGATTGTTTTGTTTTTCCTTTTGGCT GTTCATTTTGGTGGCTACTATAAGGAAATCTAACACAAACAGCAACTGTTTTTTGTT GTTTACTTTTGCATCTTTACTTGTGGAGCTGTGGCAAGTCCTCATATCAAATACAGA ACATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGATAGCAG CTTTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGCATGGCAGCAATG TGACCCTGGAATGCAACTTTGACACTGGAAGTCATGTGAACCTTGGAGCAATAACAG CCAGTTTGCAAAAGGTGGAAAATGATACATCCCCACACCGTGAAAGAGCCACTTTGC TGGAGGAGCAGCTGCCCCTAGGGAAGGCCTCGTTCCACATACCTCAAGTCCAAGTGA GGGACGAAGGACAGTACCAATGCATAATCATCTATGGGGTCGCCTGGGACTACAAGT ACCTGACTCTGAAAGTCAAAGCTTCCTACAGGAAAATAAACACTCACATCCTAAAGG TTCCAGAAACAGATGAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAG AAGTATCCTGGCCAAACGTCAGCGTTCCTGCCAACACCAGCCACTCCAGGACCCCTG AAGGCCTCTACCAGGTCACCAGTGTTCTGCGCCTAAAGCCACCCCCTGGCAGAAACT TCAGCTGTGTGTTCTGGAATACTCACGTGAGGGAACTTACTTTGGCCAGCATTGACC TTCAAAGTCAGATGGAACCCAGGACCCATCCAACTTGGCTGCTTCACATTTTCATCC CCTTCTGCATCATTGCTTTCATTTTCATAGCCACAGTGATAGCCCTAAGAAAACAAC TCTGTCAAAAGCTGTATTCTTCAAAAGACACAACAAAAAGACCTGTCACCACAACAA AGAGGGAAGTGAACAGTGCTATCTGAACCTGTGGTCTTGGGAGCCAGGGTGACCTGA TATGACATCTAAAGAAGCTTCTGGACTCTGAACAAGAATTCGGTGGCCTGCAGAGCT TGCCATTTGCACTTTTCAAATGCCTTTGGATGACCCAGCACTTTAATCTGAAACCTG CAACAAGACTAGCCAACACCTGGCCATGAAACTTGCCCCTTCACTGATCTGGACTCA CCTCTGGAGCCTATGGCTTTAAGCAAGCACTACTGCACTTTACAGAATTACCCCACT GGATCCTGGACCCACAGAATTCCTTCAGGATCCTTCTTGCTGCCAGACTGAAAGCAA AAGGAATTATTTCCCCTCAAGTTTTCTAAGTGATTTCCAAAAGCAGAGGTGTGTGGA AATTTCCAGTAACAGAAACAGATGGGTTGCCAATAGAGTTATTTTTTATCTATAGCT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TCCTCTGGGTACTAGAAGAGGCTATTGAGACTATGAGCTCACAGACAGGGCTTCGCA CAAACTCAAATCATAATTGACATGTTTTATGGATTACTGGAATCTTGATAGCATAAT GAAGTTGTTCTAATTAACAGAGAGCATTTAAATATACACTAAGTGCACAAATTGTGG AGTAAAGTCATCAAGCTCTGTTTTTGAGGTCTAAGTCACAAAGCATTTGTTTTAACC TGTAATGGCACCATGTTTAATGGTGGTTTTTTTTTTGAACTACATCTTTCCTTTAAA AATTATTGGTTTCTTTTTATTTGTTTTTACCTTAGAAATCAATTATATACAGTCAAA AATATTTGATATGCTCATACGTTGTATCTGCAGCAATTTCAGATAAGTAGCTAAAAT GGCCAAAGCCCCAAACTAAGCCTCCTTTTCTGGCCCTCAATATGACTTTAAATTTGA CTTTTCAGTGCCTCAGTTTGCACATCTGTAATACAGCAATGCTAAGTAGTCAAGGCC TTTGATAATTGGCACTATGGAAATCCTGCAAGATCCCACTACATATGTGTGGAGCAG AAGGGTAACTCGGCTACAGTAACAGCTTAATTTTGTTAAATTTGTTCTTTATACTGG AGCCATGAAGCTCAGAGCATTAGCTGACCCTTGAACTATTCAAATGGGCACATTAGC TAGTATAACAGACTTACATAGGTGGGCCTAAAGCAAGCTCCTTAACTGAGCAAAATT TGGGGCTTATGAGAATGAAAGGGTGTGAAATTGACTAACAGACAAATCATACATCTC AGTTTCTCAATTCTCATGTAAATCAGAGAATGCCTTTAAAGAATAAAACTCAATTGT TATTCTTCAACGTTCTTTATATATTCTACTTTTGGGTA (SEQ ID NO: 5) >NP_079515.2 programmed cell death 1 ligand 2 precursor [*Homo sapiens*] MIFLLLMLSLELQLHQIAALFTVTVPKELYIIEHGSNVTLECNFDTGSHVNLGAITA SLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQYQCIIIYGVAWDYKY LTLKVKASYRKINTHILKVPETDEVELTCQATGYPLAEVSWPNVSVPANTSHSRTPE GLYQVTSVLRLKPPPGRNFSCVFWNTHVRELTLASIDLQSQMEPRTHPTWLLHIFIP FCIIAFIFIATVIALRKQLCQKLYSSKDTTKRPVTTTKREVNSAI (SEQ ID NO: 6)
Mouse PD-L2	>NM_021396.2 *Mus musculus* programmed cell death 1 ligand 2 (Pdcd1lg2), mRNA GACCACATCATTTTTGTTCCCTTTGTTGGATATATCCTAATGTCAAATGTGGCATAT CTTTGTTGTCTCCTTCTGTCTCCCAACTAGAGAGAACACACTTACGGCTCCTGTCCC GGGCAGGTTTGGTTGTCGGTGTGATTGGCTTCCAGGGAACCTGATACAAGGAGCAAC TGTGTGCTGCCTTTTCTGTGTCTTTGCTTGAGGAGCTGTGCTGGGTGCTGATATTGA CACAGACCATGCTGCTCCTGCTGCCGATACTGAACCTGAGCTTACAACTTCATCCTG TAGCAGCTTTATTCACCGTGACAGCCCCTAAAGAAGTGTACACCGTAGACGTCGGCA GCAGTGTGAGCCTGGAGTGCGATTTTGACCGCAGAGAATGCACTGAACTGGAAGGGA TAAGAGCCAGTTTGCAGAAGGTAGAAAATGATACGTCTCTGCAAAGTGAAAGAGCCA CCCTGCTGGAGGAGCAGCTGCCCCTGGGAAAGGCTTTGTTCCACATCCCTAGTGTCC AAGTGAGAGATTCCGGGCAGTACCGTTGCCTGGTCATCTGCGGGGCCGCCTGGGACT ACAAGTACCTGACGGTGAAAGTCAAAGCTTCTTACATGAGGATAGACACTAGGATCC TGGAGGTTCCAGGTACAGGGGAGGTGCAGCTTACCTGCCAGGCTAGAGGTTATCCCC TAGCAGAAGTGTCCTGGCAAAATGTCAGTGTTCCTGCCAACACCAGCCACATCAGGA CCCCCGAAGGCCTCTACCAGGTCACCAGTGTTCTGCGCCTCAAGCCTCAGCCTAGCA GAAACTTCAGCTGCATGTTCTGGAATGCTCACATGAAGGAGCTGACTTCAGCCATCA TTGACCCTCTGAGTCGGATGGAACCCAAAGTCCCCAGAACGTGGCCACTTCATGTTT TCATCCCGGCCTGCACCATCGCTTTGATCTTCCTGGCCATAGTGATAATCCAGAGAA AGAGGATCTAGGGGAAGCTGTATTACGGAAGAAGATCTGGACCTGCGGTCTTGGGAG TTGGAAGGATCTGATGGGAAACCCTCAAGAGACTTCTGGACTCAAAGTGAGAATCTT GCAGGACCTGCCATTTGCACTTTTGAACCCTTTGGACGGTGACCCAGGGCTCCGAAG AGGAGCTTGTAAGACTGACAATCTTCCCTCTGTCTCAAGACTCTCTGAACAGCAAGA CCCCAATGGCACTTTAGACTTACCCCTGGGATCCTGGACCCCAGTGAGGGCCTAAGG CTCCTAATGACTTTCAGGGTGAGAACAAAAGGAATTGCTCTCCGCCCCACCCCCACC TCCTGCTTTCCGCAGGGAGACATGGAAATTCCCAGTTACTAAAATAGATTGTCAATA GAGTTATTTATAGCCCTCATTTCCTCCGGGGACTTGGAAGCTTCAGACAGGGTTTTT CATAAACAAAGTCATAACTGATGTGTTTTACAGCATCCTAGAATCCTGGCAGCCTCT GAAGTTCTAATTAACTGGAAGCATTTAAGCAACACGTTAAGTACCCCCACTGTGGTA TTTGTTTCTACTTTTCTGTTTTTAAAGTGTGAGTCACAAGGTAATTGTTGTAACCTG TGATATCACTGTTTCTTGTGTCTCTTCTTTCAACTACATCTTTTAAAACAAAACGGT GTGGGGTTTGGTTGTTTTGGTGGTAGTGGTAGTGTTTCTCAGTGGTATCTCCTTAAG AAAAAAAATCATCATGCCAGTGAATTGTTTCTTCAGCCATTTCAGATGGGAAGCTGG AATAGCCTGTCCCCCAAGCTAAGCCTTCTTCCCTAGCTTTCTGCGTGATTTTACATT GAGCATTCCTGTTGCTTTGTTTCTATAACTGTAATGTGGTGATGTCATTGTTAGGGC ACTTGAGGGTGGGCGTTCTGGAAGTCCTTTCAGGTTAGTGTTTGGGGGCAGGGTTGC TCAGAATACATAAAGGTGCTAACTTAAACTGCAGCCATGGAGCTCAGTGAATTCACT AACCTTCGGGCTGTCCAAATGTGCACATTAGCTACTGTGACCCCTGTAGGTTAGGGA GCCTGAAGCCAGCTCTTTACCTGGTGTTTAGACTCAGCAGAATTTGGAGTCAATGGG ACCAAATGGTTGTGAAATTAAGATTTGAAGTGTGCATCTTATTTTATCACCATCTGC CCAACAAAACTTCAGAAAATGCCTTTGAAGCACAAAAATGTAATCGTTTATGTGAAA TCTCTGAGTTGCATTTAGATGCCCATTGCAGCAAGGTGGCTCTCTCACAGATTCCAC ACCTTAGCCTAAGATACCAGACAGCAGGACAGAGAGAAAAGTCCTTCCTGGTGTGCA AACTTCCTTACACTGGACCTCGCCTCTCAGGTGTGTGATTGGTAGGCCAAATCCCGA TAGCCAATCGGTGTTGGGTGCTTTGTCTGCTCTACTGGGAGTCCAGTGGTACAATGG ATTCTGGCAAAATGCTGCCATCTTGGCCCTCGCTGGGCTGCTTTCTAGGATATTCAT AGAGAAAGGGCCGTCCAGATCCAGTATCCTAAAATCCTGAGAGGAGAATATAAGTTA GTGTGTCTCACTATAACTATCTCTATGATCGGTCACATTACTATCTAACAGTTACCA AATACTATATGCCTAATACTGGTAAGCATTTTATACACACCATTGGATTGAATCCTC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TCAAAATCCTCAAAAAGGAAGTTATTAATACCTCCATAGGCAAGGAGCCCAGAACCC AGAGAGGTCAGGCAGTCTAGTTATAGATGCCTGCTTTGTTTAGAAGTGAACAAGAGC ATCAAATTATTAATGTGCCCTGGTTATTAATGCGCCCTGGTTACCTGCTGGATGGAA CATCAAGGTGGACTTTTGGCAGTTGCATACACCCAGAGGTATTTTGGCTATTCACGG ATTAATTTCACACGAAGTGTTTCAGAGACATGTGTAGGGGAAGTCCGGGTTCAGGGG GCCTAAGATTCAAACTCTAGCTTAGCTACGTCTGACCTCCCTAAGCACTAACTTACT ATCAAAAGAATGAGCAGTAAAAGAATGGTGTTTACTGCCTGCCTTTATCAGGCAGTG AACGTGCAGCGGGCAACGAATGCTTGATAAGTGTGTGTCAGTGTGAAGTCCCATGTA CCAGCCGCTGTCCCCACTGCAAAAGCAGCAGAGCGCTCAGACATCATCAGCTGATTT ACCAGCAGCAGATTTCTTCTTCTAGTCCCATCCCTGAAGAAGCTTCCAGCCTAGGTA CATTGCATGGGCTTTGTGCTCCAGGAGTTCCTACACAGCCCTCAACTTCAACACAGG CAAAGTGCTTACTGATCCTCATGTATCTTACAGGGTCCCCTCTACCCACAATACCTC ATTGCTGGAACTTCAAATCTTCCTGAATAAAAGCTTGCCCGTGGTTTAATTA (SEQ ID NO: 7) >NP_067371.1 programmed cell death 1 ligand 2 precursor [*Mus musculus*] MLLLLPILNLSLQLHPVAALFTVTAPKEVYTVDVGSSVSLECDFDRRECTELEGIRA SLQKVENDTSLQSERATLLEEQLPLGKALFHIPSVQVRDSGQYRCLVICGAAWDYKY LTVKVKASYMRIDTRILEVPGTGEVQLTCQARGYPLAEVSWQNVSVPANTSHIRTPE GLYQVTSVLRLKPQPSRNFSCMFWNAHMKELTSAIIDPLSRMEPKVPRTWPLHVFIP ACTIALIFLAIVIIQRKRI (SEQ ID NO: 8)
Human CTLA-4 (CD152)	>NM_005214.5 *Homo sapiens* cytotoxic T-lymphocyte associated protein 4 (CTLA4), transcript variant 1, mRNA GCTTTCTATTCAAGTGCCTTCTGTGTGTGCACATGTGTAATACATATCTGGGATCAA AGCTATCTATATAAAGTCCTTGATTCTGTGTGGGTTCAAACACATTTCAAAGCTTCA GGATCCTGAAAGGTTTTGCTCTACTTCCTGAAGACCTGAACACCGCTCCCATAAAGC CATGGCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTACCAGGAC CTGGCCCTGCACTCTCCTGTTTTTTCTTCTCTTCATCCCTGTCTTCTGCAAAGCAAT GCACGTGGCCCAGCCTGCTGTGGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGT GTGTGAGTATGCATCTCCAGGCAAAGCCACTGAGGTCCGGGTGACAGTGCTTCGGCA GGCTGACAGCCAGGTGACTGAAGTCTGTGCGGCAACCTACATGATGGGGAATGAGTT GACCTTCCTAGATGATTCCATCTGCACGGGCACCTCCAGTGGAAATCAAGTGAACCT CACTATCCAAGGACTGAGGGCCATGGACACGGGACTCTACATCTGCAAGGTGGAGCT CATGTACCCACCGCCATACTACCTGGGCATAGGCAACGGAACCCAGATTTATGTAAT TGATCCAGAACCGTGCCCAGATTCTGACTTCCTCCTCTGGATCCTTGCAGCAGTTAG TTCGGGGTTGTTTTTTTATAGCTTTCTCCTCACAGCTGTTTCTTTGAGCAAAATGCT AAAGAAAAGAAGCCCTCTTACAACAGGGGTCTATGTGAAAATGCCCCCAACAGAGCC AGAATGTGAAAAGCAATTTCAGCCTTATTTTATTCCCATCAATTGAGAAACCATTAT GAAGAAGAGAGTCCATATTTCAATTTCCAAGAGCTGAGGCAATTCTAACTTTTTTGC TATCCAGCTATTTTTATTTGTTTGTGCATTTGGGGGGAATTCATCTCTCTTTAATAT AAAGTTGGATGCGGAACCCAAATTACGTGTACTACAATTTAAAGCAAAGGAGTAGAA AGACAGAGCTGGGATGTTTCTGTCACATCAGCTCCACTTTCAGTGAAAGCATCACTT GGGATTAATATGGGGATGCAGCATTATGATGTGGGTCAAGGAATTAAGTTAGGGAAT GGCACAGCCCAAAGAAGGAAAAGGCAGGGAGCGAGGGAGAAGACTATATTGTACACA CCTTATATTTACGTATGAGACGTTTATAGCCGAAATGATCTTTTCAAGTTAAATTTT ATGCCTTTTATTTCTTAAACAAATGTATGATTACATCAAGGCTTCAAAAATACTCAC ATGGCTATGTTTTAGCCAGTGATGCTAAAGGTTGTATTGCATATATACATATATATA TATATATATATATATATATATATATATATATATATATATATATATTTTAATTTGA TAGTATTGTGCATAGAGCCACGTATGTTTTTGTGTATTTGTTAATGGTTTGAATATA AACACTATATGGCAGTGTCTTTCCACCTTGGGTCCCAGGGAAGTTTTGTGGAGGAGC TCAGGACACTAATACACCAGGTAGAACACAAGGTCATTTGCTAACTAGCTTGGAAAC TGGATGAGGTCATAGCAGTGCTTGATTGCGTGGAATTGTGCTGAGTTGGTGTTGACA TGTGCTTTGGGGCTTTTACACCAGTTCCTTTCAATGGTTTGCAAGGAAGCCACAGCT GGTGGTATCTGAGTTGACTTGACAGAACACTGTCTTGAAGACAATGGCTTACTCCAG GAGACCCACAGGTATGACCTTCTAGGAAGCTCCAGTTCGATGGGCCCAATTCTTACA AACATGTGGTTAATGCCATGGACAGAAGAAGGCAGCAGGTGGCAGAATGGGGTGCAT GAAGGTTTCTGAAAATTAACACTGCTTGTGTTTTTAACTCAATATTTTCCATGAAAA TGCAACAACATGTATAATATTTTTAATTAAATAAAAATCTGTGGTGGTCGTTTTCCG GA (SEQ ID NO: 9) >NP_005205.2 cytotoxic T-lymphocyte protein 4 isoform CTLA4-TM precursor [*Homo sapiens*] MACLGFQRHKAQLNLATRTWPCTLLFFLLFIPVFCKAMHVAQPAVVLASSRGIASFV CEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSSGNQVNL TIQGLRAMDTGLYICKVELMYPPPYYLGIGNGTQIYVIDPEPCPDSDFLLWILAAVS SGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKMPPTEPECEKQFQPYFIPIN (SEQ ID NO: 10)
Mouse CTLA-4 (CD152)	>NM_009843.4 *Mus musculus* cytotoxic T-lymphocyte- associated protein 4 (Ctla4), transcript variant 1, mRNA CTACACATATGTAGCACGTACCTTGGATCAAAGCTGTCTATATAAAGTCCCCGAGTC TGTGTGGGTTCAAACACATCTCAAGGCTTCTGGATCCTGTTGGGTTTTACTCTGCTC CCTGAGGACCTCAGCACATTTGCCCCCCAGCCATGGCTTGTCTTGGACTCCGGAGGT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ACAAAGCTCAACTGCAGCTGCCTTCTAGGACTTGGCCTTTTGTAGCCCTGCTCACTC TTCTTTTCATCCCAGTCTTCTCTGAAGCCATACAGGTGACCCAACCTTCAGTGGTGT TGGCTAGCAGCCATGGTGTCGCCAGCTTTCCATGTGAATATTCACCATCACACAACA CTGATGAGGTCCGGGTGACTGTGCTGCGGCAGACAAATGACCAAATGACTGAGGTCT GTGCCACGACATTCACAGAGAAGAATACAGTGGGCTTCCTAGATTACCCCTTCTGCA GTGGTACCTTTAATGAAAGCAGAGTGAACCTCACCATCCAAGGACTGAGAGCTGTTG ACACGGGACTGTACCTCTGCAAGGTGGAACTCATGTACCCACCGCCATACTTTGTGG GCATGGGCAACGGGACGCAGATTTATGTCATTGATCCAGAACCATGCCCGGATTCTG ACTTCCTCCTTTGGATCCTTGTCGCAGTTAGCTTGGGGTTGTTTTTTTACAGTTTCC TGGTCACTGCTGTTTCTTTGAGCAAGATGCTAAAGAAAAGAAGTCCTCTTACAACAG GGGTCTATGTGAAAATGCCCCCAACAGAGCCAGAATGTGAAAAGCAATTTCAGCCTT ATTTTATTCCCATCAACTGAAAGGCCGTTTATGAAGAAGAAGGAGCATACTTCAGTC TCTAAAAGCTGAGGCAATTTCAACTTTCCTTTTCTCTCCAGCTATTTTTACCTGTTT GTATATTTTAAGGAGAGTATGCCTCTCTTTAATAGAAAGCTGGATGCAAAATTCCAA TTAAGCATACTACAATTTAAAGCTAAGGAGCATGAACAGAGAGCTGGGATATTTCTG TTGTGTCAGAACCATTTTACTAAAAGCATCACTTGGAAGCAGCATAAGGATATAGCA TTATGGTGTGGGGTCAAGGGAACATTAGGGAATGGCACAGCCCAAAGAAAGGAAGGG GGTGAAGGAAGAGATTATATTGTACACATCTTGTATTTACCTGAGAGATGTTTATGA CTTAAATAATTTTTAAATTTTTCATGCTGTTATTTTCTTTAACAATGTATAATTACA CGAAGGTTTAAACATTTATTCACAGAGCTATGTGACATAGCCAGTGGTTCCAAAGGT TGTAGTGTTCCAAGATGTATTTTTAAGTAATATTGTACATGGGTGTTTCATGTGCTG TTGTGTATTTGCTGGTGGTTTGAATATAAACACTATGTATCAGTGTCGTCCCACAGT GGGTCCTGGGGAGGTTTGGCTGGGGAGCTTAGGACACTAATCCATCAGGTTGGACTC GAGGTCCTGCACCAACTGGCTTGGAAACTAGATGAGGCTGTCACAGGGCTCAGTTGC ATAAACCGATGGTGATGGAGTGTAAACTGGGTCTTTACACTCATTTTATTTTTTGTT TCTGCTTTTGTTTTCTTCAATGATTTGCAAGGAAACCAAAAGCTGGCAGTGTTTGTA TGAACCTGACAGAACACTGTCTTCAAGGAAATGCCTCATTCCTGAGACCAGTAGGTT TGTTTTTTTAGGAAGTTCCAATACTAGGACCCCCTACAAGTACTATGGCTCCTCGAA AACACAAAGTTAATGCCACAGGAAGCAGCAGATGGTAGGATGGGATGCACAAGAGTT CCTGAAAACTAACACTGTTAGTGTTTTTTTTTTAACTCAATATTTTCCATGAAAATG CAACCACATGTATAATATTTTTAATTAAATAAAAGTTTCTTGTGATTGTTTT (SEQ ID NO: 11)
	>NP_033973.2 cytotoxic T-lymphocyte protein 4 isoform 1 precursor [*Mus musculus*] MACLGLRRYKAQLQLPSRTWPFVALLTLLFIPVFSEAIQVTQPSVVLASSHGVASFP CEYSPSHNTDEVRVTVLRQTNDQMTEVCATTFTEKNTVGFLDYPFCSGTFNESRVNL TIQGLRAVDTGLYLCKVELMYPPPYFVGMGNGTQIYVIDPEPCPDSDFLLWILVAVS LGLFFYSFLVTAVSLSKMLKKRSPLTTGVYVKMPPTEPECEKQFQPYFIPIN (SEQ ID NO: 12)
Human 4-1BBL (CD137L)	>NM_003811.4 *Homo sapiens* TNF superfamily member 9 (TNFSF9), mRNA AGTCTCTCGTCATGGAATACGCCTCTGACGCTTCACTGGACCCCGAAGCCCCGTGGC CTCCCGCGCCCCGCGCTCGCGCCTGCCGCGTACTGCCTTGGGCCCTGGTCGCGGGGC TGCTGCTGCTGCTGCTGCTCGCTGCCGCCTGCGCCGTCTTCCTCGCCTGCCCCTGGG CCGTGTCCGGGGCTCGCGCCTCGCCCGGCTCCGCGGCCAGCCCGAGACTCCGCGAGG GTCCCGAGCTTTCGCCCGACGATCCCGCCGGCCTCTTGGACCTGCGGCAGGGCATGT TTGCGCAGCTGGTGGCCCAAAATGTTCTGCTGATCGATGGGCCCCTGAGCTGGTACA GTGACCCAGGCCTGGCAGGCGTGTCCCTGACGGGGGGCCTGAGCTACAAAGAGGACA CGAAGGAGCTGGTGGTGGCCAAGGCTGGAGTCTACTATGTCTTCTTTCAACTAGAGC TGCGGCGCGTGGTGGCCGGCGAGGGCTCAGGCTCCGTTTCACTTGCGCTGCACCTGC AGCCACTGCGCTCTGCTGCTGGGGCCGCCGCCCTGGCTTTGACCGTGGACCTGCCAC CCGCCTCCTCCGAGGCTCGGAACTCGGCCTTCGGTTTCCAGGGCCGCTTGCTGCACC TGAGTGCCGGCCAGCGCCTGGGCGTCCATCTTCACACTGAGGCCAGGGCACGCCATG CCTGGCAGCTTACCCAGGGCGCCACAGTCTTGGGACTCTTCCGGGTGACCCCCGAAA TCCCAGCCGGACTCCCTTCACCGAGGTCGGAATAACGTCCAGCCTGGGTGCAGCCCA CCTGGACAGAGTCCGAATCCTACTCCATCCTTCATGGAGACCCCTGGTGCTGGGTCC CTGCTGCTTTCTCTACCTCAAGGGGCTTGGCAGGGGTCCCTGCTGCTGACCTCCCCT TGAGGACCCTCCTCACCCACTCCTTCCCCAAGTTGGACCTTGATATTTATTCTGAGC CTGAGCTCAGATAATATATTATATATATTATATATATATATATATTTCTATTTAAAG AGGATCCTGAGTTTGTGAATGGACTTTTTTAGAGGAGTTGTTTTGGGGGGGGGGGGG TCTTCGACATTGCCGAGGCTGGTCTTGAACTCCTGGACTTAGACGATCCTCCTGCCT CAGCCTCCCAAGCAACTGGGATTCATCCTTTCTATTAATTCATTGTACTTATTTGCT TATTTGTGTGTATTGAGCATCTGTAATGTGCCAGCATTGTGCCCAGGCTAGGGGGCT ATAGAAACATCTAGAAATAGACTGAAAGAAAATCTGAGTTATGGTAATACGTGAGGA ATTTAAAGACTCATCCCCAGCCTCCACCTCCTGTGTGATACTTGGGGGCTAGCTTTT TTCTTTCTTTCTTTTTTTTGAGATGGTCTTGTTCTGTCAACCAGGCTAGAATGCAGC GGTGCAATCATGAGTCAATGCAGCCTCCAGCCTCGACCTCCCGAGGCTCAGGTGATC CTCCCATCTCAGCCTCTCGAGTAGCTGGGACCACAGTTGTGTGCCACCACACTTGGC TAACTTTTTAATTTTTTTGCGGAGACGGTATTGCTATGTTGCCAAGGTTGTTTACAT GCCAGTACAATTTATAATAAACACTCATTTTTCCTCCC (SEQ ID NO: 13)

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	>NP_003802.1 tumor necrosis factor ligand superfamily member 9 [*Homo sapiens*] MEYASDASLDPEAPWPPAPRARACRVLPWALVAGLLLLLLLAAACAVFLACPWAVSG ARASPGSAASPRLREGPELSPDDPAGLLDLRQGMFAQLVAQNVLLIDGPLSWYSDPG LAGVSLTGGLSYKEDTKELVVAKAGVYYVFFQLELRRVVAGEGSGSVSLALHLQPLR SAAGAAALALTVDLPPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQL TQGATVLGLFRVTPEIPAGLPSPRSE (SEQ ID NO: 14)
Mouse 4-1BBL (CD137L)	>NM_009404.3 *Mus musculus* tumor necrosis factor (ligand) superfamily, member 9 (Tnfsf9), mRNA ATAAAGCACGGGCACTGGCGGGAGACGTGCACTGACCGACCGTGGTAATGGACCAGC ACACACTTGATGTGGAGGATACCGCGGATGCCAGACATCCAGCAGGTACTTCGTGCC CCTCGGATGCGGCGCTCCTCAGAGATACCGGGCTCCTCGCGGACGCTGCGCTCCTCT CAGATACTGTGCGCCCCACAAATGCCGCGCTCCCCACGGATGCTGCCTACCCTGCGG TTAATGTTCGGGATCGCGAGGCCGCGTGGCCGCCTGCACTGAACTTCTGTTCCCGCC ACCCAAAGCTCTATGGCCTAGTCGCTTTGGTTTTGCTGCTTCTGATCGCCGCCTGTG TTCCTATCTTCACCCGCACCGAGCCTCGGCCAGCGCTCACAATCACCACCTCGCCCA ACCTGGGTACCCGAGAGAATAATGCAGACCAGGTCACCCCTGTTTCCCACATTGGCT GCCCCAACACTACACAACAGGGCTCTCCTGTGTTCGCCAAGCTACTGGCTAAAAACC AAGCATCGTTGTGCAATACAACTCTGAACTGGCACAGCCAAGATGGAGCTGGGAGCT CATACCTATCTCAAGGTCTGAGGTACGAAGAAGACAAAAAGGAGTTGGTGGTAGACA GTCCCGGGCTCTACTACGTATTTTTGGAACTGAAGCTCAGTCCAACATTCACAAACA CAGGCCACAAGGTGCAGGGCTGGGTCTCTCTTGTTTTGCAAGCAAAGCCTCAGGTAG ATGACTTTGACAACTTGGCCCTGACAGTGGAACTGTTCCCTTGCTCCATGGAGAACA AGTTAGTGGACCGTTCCTGGAGTCAACTGTTGCTCCTGAAGGCTGGCCACCGCCTCA GTGTGGGTCTGAGGGCTTATCTGCATGGAGCCCAGGATGCATACAGAGACTGGGAGC TGTCTTATCCCAACACCACCAGCTTTGGACTCTTTCTTGTGAAACCCGACAACCCAT GGGAATGAGAACTATCCTTCTTGTGACTCCTAGTTGCTAAGTCCTCAAGCTGCTATG TTTTATGGGGTCTGAGCAGGGGTCCCTTCCATGACTTTCTCTTGTCTTTAACTGGAC TTGGTATTTATTCTGAGCATAGCTCAGACAAGACTTTATATAATTCACTAGATAGCA TTAGTAAACTGCTGGGCAGCTGCTAGATAAAAAAAAATTTCTAAATCAAAGTTTATA TTTATATTAATATATAAAAATAAATGTGTTTGT (SEQ ID NO: 15) >NP_033430.1 tumor necrosis factor ligand superfamily member 9 [*Mus musculus*] MDQHTLDVEDTADARHPAGTSCPSDAALLRDTGLLADAALLSDTVRPTNAALPTDAA YPAVNVRDREAAWPPALNFCSRHPKLYGLVALVLLLLIAACVPIFTRTEPRPALTIT TSPNLGTRENNADQVTPVSHIGCPNTTQQGSPVFAKLLAKNQASLCNTTLNWHSQDG AGSSYLSQGLRYEEDKKELVVDSPGLYYVFLELKLSPTFTNTGHKVQGWVSLVLQAK PQVDDFDNLALTVELFPCSMENKLVDRSWSQLLLLKAGHRLSVGLRAYLHGAQDAYR DWELSYPNTTSFGLFLVKPDNPWE (SEQ ID NO: 16)
Human HVEM (CD270)	>NM_003820.4 *Homo sapiens* TNF receptor superfamily member 14 (TNFRSF14), transcript variant 1, DNA ATACCGGCCCTTCCCCTCGGCTTTGCCTGGACAGCTCCTGCCTCCCGCAGGGCCCAC CTGTGTCCCCCAGCGCCGCTCCACCCAGCAGGCCTGAGCCCCTCTCTGCTGCCAGAC ACCCCCTGCTGCCCACTCTCCTGCTGCTCGGGTTCTGAGGCACAGCTTGTCACACCG AGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCCACAGCCGCAGCAATGGCG CTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGA GCCTGAGGCATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGGAGATCCACCCCC AAAACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGAGCCCCCTGCTAC GCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGC CCCAAGTGCAGTCCAGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACA GTGTGTGAACCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAG TGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGCGAGCCGGAACTGC TCCAGGACAGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAG GACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGCCAGAGG GTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGTCAGAACTGCCCCCCGGGG ACCTTCTCTCCCAATGGGACCCTGGAGGAATGTCAGCACCAGACCAAGTGCAGCTGG CTGGTGACGAAGGCCGGAGCTGGGACCAGCAGCTCCCACTGGGTATGGTGGTTTCTC TCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATGTGTG AAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGAAA AGACAGGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCTCCGGAC GTCACCACGGTGGCCGTGGAGGAGACAATACCCTCATTCACGGGGAGGAGCCCAAAC CACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGGCTGCTG AAAGAGGCTGTCCACCTGGCGGAACCACCGGAGCCCGGAGGCTTGGGGGCTCCGCCC TGGGCTGGCTTCCGTCTCCTCCAGTGGAGGGAGAGGTGGGGCCCCTGCTGGGGTAGA GCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCT GCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTCGCTCAC AGACCACACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCACAGC CAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCACATCGGAAGTG ATTTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCTATTTGTCATGAAACAGTGT ATTTGGGGAGATGCTGTGGGAGGATGTAAATATCTTGTTTCTCCTCAAA (SEQ ID NO: 17) >NP_003811.2 tumor necrosis factor receptor superfamily member 14 isoform 1 precursor [*Homo sapiens*] MEPPGDWGPPPWRSTPKTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKC SPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRT ENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS PNGTLEECQHQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRR KPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH (SEQ ID NO: 18)
Mouse HVEM (CD270)	>NM_178931.2 *Mus musculus* tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) (Tnfrsf14), mRNA GCTCTTGGCCTGAAGTTTCTTGATCAAGAAAATGGAACCTCTCCCAGGATGGGGGTC GGCACCCTGGAGCCAGGCCCCTACAGACAACACCTTCAGGCTGGTGCCTTGTGTCTT CCTTTTGAACTTGCTGCAGCGCATCTCTGCCCAGCCCTCATGCAGACAGGAGGAGTT CCTTGTGGGAGACGAGTGCTGCCCCATGTGCAACCCAGGTTACCATGTGAAGCAGGT CTGCAGTGAGCATACAGGCACAGTGTGTGCCCCCTGTCCCCCACAGACATATACCGC CCATGCAAATGGCCTGAGCAAGTGTCTGCCCTGCGGAGTCTGTGATCCAGACATGGG CCTGCTGACCTGGCAGGAGTGCTCCAGCTGGAAGGACACTGTGTGCAGATGCATCCC AGGCTACTTCTGTGAGAACCAGGATGGGAGCCACTGTTCCACATGCTTGCAGCACAC CACCTGCCCTCCAGGGCAGAGGGTAGAGAAGAGAGGGACTCACGACCAGGACACTGT ATGTGCTGACTGCCTAACAGGGACCTTCTCACTTGGAGGGACTCAGGAGGAATGCCT GCCCTGGACCAACTGCAGTGCATTTCAACAGGAAGTAAGACGTGGGACCAACAGCAC AGACACCACCTGCTCCTCCCAGGTCGTCTACTACGTTGTGTCCATCCTTTTGCCACT TGTGATAGTGGGAGCTGGGATAGCTGGATTCCTCATCTGCACGCGAAGACACCTGCA CACCAGCTCAGTGGCCAAGGAGCTGGAGCCTTTCCAGGAACAACAGGAGAACACCAT CAGGTTTCCAGTCACCGAGGTTGGGTTTGCTGAGACCGAGGAGGAGACAGCCTCCAA CTGAACAAATTCTGGGTGACAAGACACCGAGGAGACGT (SEQ ID NO: 19) >NP_849262.1 tumor necrosis factor receptor superfamily member 14 precursor [*Mus musculus*] MEPLPGWGSAPWSQAPTDNTFRLVPCVFLLNLLQRISAQPSCRQEEFLVGDECCPMC NPGYHVKQVCSEHTGTVCAPCPPQTYTAHANGLSKCLPCGVCDPDMGLLTWQECSSW KDTVCRCIPGYFCENQDGSHCSTCLQHTTCPPGQRVEKRGTHDQDTVCADCLTGTFS LGGTQEECLPWTNCSAFQQEVRRGTNSTDTTCSSQVVYYVVSILLPLVIVGAGIAGF LICTRRHLHTSSVAKELEPFQEQQENTIRFPVTEVGFAETEEETASN (SEQ ID NO: 20)
Human FGL1	>NM_004467.4 *Homo sapiens* fibrinogen like 1 (FGL1), transcript variant 1, mRNA AATGCAGTTACAGGATCCTGGGAAGCAGAGTGTCTGGATGGAACCTGAGCTGGGTCT CTGACTCACTTCTGACTTTAGTTTTTTCAAGGGGGAACATGGCAAAGGTGTTCAGTT TCATCCTTGTTACCACCGCTCTGACAATGGGCAGGGAAATTTCGGCGCTCGAGGACT GTGCCCAGGAGCAGATGCGGCTCAGAGCCCAGGTGCGCCTGCTTGAGACCCGGGTCA AACAGCAACAGGTCAAGATCAAGCAGCTTTTGCAGGAGAATGAAGTCCAGTTCCTTG ATAAAGGAGATGAGAATACTGTCATTGATCTTGGAAGCAAGAGGCAGTATGCAGATT GTTCAGAGATTTTCAATGATGGGTATAAGCTCAGTGGATTTTACAAAATCAAACCTC TCCAGAGCCCAGCAGAATTTTCTGTTTATTGTGACATGTCCGATGGAGGAGGATGGA CTGTAATTCAGAGACGATCTGATGGCAGTGAAAACTTTAACAGAGGATGGAAAGACT ATGAAAATGGCTTTGGAAATTTTGTCCAAAAACATGGTGAATATTGGCTGGGCAATA AAAATCTTCACTTCTTGACCACTCAAGAAGACTACACTTTAAAAATCGACCTTGCAG ATTTTGAAAAAAATAGCCGTTATGCACAATATAAGAATTTCAAAGTTGGAGATGAAA AGAATTTCTACGAGTTGAATATTGGGGAATATTCTGGAACAGCTGGAGATTCCCTTG CGGGGAATTTTCATCCTGAGGTGCAGTGGTGGGCTAGTCACCAAAGAATGAAATTCA GCACGTGGGACAGAGATCATGACAACTATGAAGGGAACTGCGCAGAAGAAGATCAGT CTGGCTGGTGGTTTAACAGGTGTCACTCTGCAAACCTGAATGGTGTATACTACAGCG GCCCCTACACGGCTAAAACAGACAATGGGATTGTCTGGTACACCTGGCATGGGTGGT GGTATTCTCTGAAATCTGTGGTTATGAAAATTAGGCCAAATGATTTTATTCCAAATG TAATTTAATTGCTGCTGTTGGGCTTTCGTTTCTGCAATTCAGCTTTGTTTAAAGTGA TTTGAAAAATACTCATTCTGAACATATCCATGCGCAATCATGATAACTGTTGTGAGT AGTGCTTTTCATTCTTCTCACTTGCCTTTGTTACTTAATGTGCTTTCAGTACAGCAG ATATGCAATATTCACCAAATAAATGTAGACTGTGTTAATA (SEQ ID NO: 21) >NP_004458.3 fibrinogen-like protein 1 precursor [*Homo sapiens*] MAKVFSFILVTTALTMGREISALEDCAQEQMRLRAQVRLLETRVKQQQVKIKQLLQE NEVQFLDKGDENTVIDLGSKRQYADCSEIFNDGYKLSGFYKIKPLQSPAEFSVYCDM SDGGGWTVIQRRSDGSENFNRGWKDYENGFGNFVQKHGEYWLGNKNLHFLTTQEDYT LKIDLADPEKNSRYAQYKNFKVGDEKNFYELNIGEYSGTAGDSLAGNFHPEVQWWAS

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	HQRMKFSTWDRDHDNYEGNCAEEDQSGWWFNRCHSANLNGVYYSGPYTAKTDNGIVW YTWHGWWYSLKSVVMKIRPNDFIPNVI (SEQ ID NO: 22)
Mouse FGL1	>NM_145594.2 *Mus musculus* fibrinogen-like protein 1 (Fgl1), mRNA GTTAGAAGTTCCTGGGAGGCTCTGTGTGGATGGACTGAGCCTAGCTAAGTCCTGATT CATTTTGACTTGAGTTCTCTCAGTGGGAAGAATGGGAAAGATTTACAGCTTCGTCCT GGTCGCCATTGCTCTGATGATGGGAAGGGAAGGTTGGGCCCTCGAGAGTGAGAACTG CTTGCGGGAGCAGGTGAGGCTCAGGGCTCAGGTGCACCAGCTTGAGACCCGGGTCAA ACAACAACAGACCATGATTGCACAGCTCTTGCATGAGAAGGAAGTCCAGTTTCTGGA TAAAGGATCGGAGAACAGTTTCATTGACCTTGGAGGCAAGAAGCAGTATGCAGATTG TTCAGAGATTTACAATGACGGATTTAAGCAGAGTGGATTTTACAAAATCAAACCTCT TCAGAGCCTGGCAGAATTCTCTGTTTATTGTGACATGTCTGATGGAGGGGGATGGAC TGTAATTCAGAGACGATCTGATGGCAGTGAGAACTTTAACAGGGGTTGGAATGACTA TGAAAATGGCTTTGGAAACTTTGTCCAAAACAATGGCGAATACTGGCTGGGTAACAA AAACATTAACTTGCTAACTATTCAAGGAGACTACACTTTAAAAATCGACCTGACAGA TTTTGAGAAAAACAGCAGCTTCGCACAATACCAAAGTTTTAAAGTTGGTGATAAAAA GTCTTTTTATGAACTAAATATTGGAGAATATTCTGGCACAGCTGGAGATTCCCTGTC AGGAACTTTTCATCCTGAAGTACAGTGGTGGGCTAGTCACCAAAGGATGAAGTTCAG CACGTGGGACAGAGATAACGACAATTACCAAGGAAACTGTGCTGAGGAAGAGCAGTC TGGCTGGTGGTTTAACAGGTGTCACTCTGCAAACCTGAACGGTGTTTACTACCGTGG TTCCTACAGGGCAGAAACGGATAATGGTGTTGTGTGGTACACCTGGCATGGGTGGTG GTATTCCTTGAAATCTGTGGTTATGAAAATTAGGCCAAGTGATTTTATTCCAAATAT TATTTAGTTGCCCTCATTGGGATCTCCTTTCTGTAATTCATCTTGGTTTACTTGAAA ATAAATATTTGAAAAAGATATAATTCTGAATAACACA (SEQ ID NO: 23) >NP_663569.2 fibrinogen-like protein 1 precursor [*Mus musculus*] MGKIYSFVLVAIALMMGREGWALESENCLREQVRLRAQVHQLETRVKQQQTMIAQLL HEKEVQFLDKGSENSFIDLGGKKQYADCSEIYNDGFKQSGFYKIKPLQSLAEFSVYC DMSDGGGWTVIQRRSDGSENFNRGWNDYENGFGNFVQNNGEYWLGNKNINLLTIQGD YTLKIDLTDFEKNSSFAQYQSFKVGDKKSFYELNIGEYSGTAGDSLSGTFHPEVQWW ASHQRMKFSTWDRDNDNYQGNCAEEEQSGWWFNRCHSANLNGVYYRGSYRAETDNGV VWYTWHGWWYSLKSVVMKIRPSDFIPNII (SEQ ID NO: 24)
Human OX-2 (CD200)	>NM_005944.7 *Homo sapiens* CD200 molecule (CD200), transcript variant 1, mRNA AGAGCTCCAGGCGCACATCCGCAGTCAGCCACCTCGCGCGCGCCTCCAGGAGCAAGG ATGGAGAGGCTGGTGATCAGGATGCCCTTCTCTCATCTGTCTACCTACAGCCTGGTT TGGGTCATGGCAGCAGTGGTGCTGTGCACAGCACAAGTGCAAGTGGTGACCCAGGAT GAAAGAGAGCAGCTGTACACACCTGCTTCCTTAAAATGCTCTCTGCAAAATGCCCAG GAAGCCCTCATTGTGACATGGCAGAAAAAGAAAGCTGTAAGCCCAGAAAACATGGTC ACCTTCAGCGAGAACCATGGGGTGGTGATCCAGCCTGCCTATAAGGACAAGATAAAC ATTACCCAGCTGGGACTCCAAAACTCAACCATCACCTTCTGGAATATCACCCTGGAG GATGAAGGGTGTTACATGTGTCTCTTCAATACCTTTGGTTTTGGGAAGATCTCAGGA ACGGCCTGCCTCACCGTCTATGTACAGCCCATAGTATCCCTTCACTACAAATTCTCT GAAGACCACCTAAATATCACTTGCTCTGCCACTGCCCGCCCAGCCCCCATGGTCTTC TGGAAGGTCCCTCGGTCAGGGATTGAAAATAGTACAGTGACTCTGTCTCACCCAAAT GGGACCACGTCTGTTACCAGCATCCTCCATATCAAAGACCCTAAGAATCAGGTGGGG AAGGAGGTGATCTGCCAGGTGCTGCACCTGGGGACTGTGACCGACTTTAAGCAAACC GTCAACAAAGGCTATTGGTTTTCAGTTCCGCTATTGCTAAGCATTGTTTCCCTGGTA ATTCTTCTCGTCCTAATCTCAATCTTACTGTACTGGAAACGTCACCGGAATCAGGAC CGAGAGCCCTAAATAAGTCACACAGCACCCTGAAAGTGATTCCCTGGTCTACTTGAA TTTGACACAAGAGAAAAGCAGGAGGAAAAGGGGCCATTCTCCAAAGGACCTGAAAGA GCAAAAGAGGTGGGAGCGAAAGCCTTAAGGATCCCACGACTTTTTACTGCCATCTGA GCTACTCAGTGTTTGAATCCCAAGAGGAAGTCAGTTTACCTCTCAGGTCTGTTGTAG GACTTGATTTTGTAAAGCAATGCCATGTTATGTGGTTGAAAGGGCACTGGACTTAGT TAGTATCAGGAGCACTGAGCTCACAGACTGACTTGGGCTCCTACTGGTGGGGACCTC TGTTAGTCACTTTACCTCATCCAAAGTATAAAGGAATTGGACCAAATAATTTACCAC ATAGCTCTAAAACTTAATTTAAAATGTAATTCCAGAAAAAAAAAGGGAATAAGCAAA GGGGGAAGAATTGAAAGAGAGAGAGAAGAAAGAATACAGAGAGCTTACCTTTTGCCT TTCTGTTGATGTTACATCTCTTCTTCCTATGTTCTTAGGTCTATGAGTCTGTTTCCC CATCATTTGGTATCTAGTCCAGTTCCTGCTTACTGCTTTGCTAATAGCTGGCCTTGC TAGAATCCTTGGTTTCACTGCTGTTCTTCATGTGCTTCTATGAGATTTACTCCAACA CAAATAGGACTGAATTTATTGTGAAGTAACATTGGCAATCTTAACTTATTCATTTAA CTTATTTTTATAGCTAGATAAATATTGTTAGTCTTAGACAATAGCTCACATTTTTTG AGAAGCATGCCCTCCCTGTCCATTTGTCTTATAACATGACCCAGCCCTATTTTACGT CATTCTAAATTCAGCCTCATATAATGAAAATACATTATGAAAACAGATGTTTAGGAG ATTTCCTGTATAGCAGTCAGCCAATTCATATGCTTTGTCTCTGCTGGCTTCTTTTTC CATGCGTTAACTTTTCCCAATAGCAGAGGAGGCAAATATGAGCATACAATCCCTTTG TTCTAAAGATATTGTTCCAGCTAGTGGAATGATGTTGAATCTTTAATAACCATAATT AGTTGCTTTTTCAGTATCTTCTGCTTTGTCTGTGTCTATCCAGTGGCCTAGGAATTA AAGTGTAAGTTGTTTTCGCTGTTAAATTGGATATTTATATATATATATAGCAAGATT TTCATGTGTTATTTAATTCTGTATTGTTTCTTATATTTGTAGTAAAATATTGAACAA TTAAAAGTGTTGACTCCAAA (SEQ ID NO: 25)

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	>NP_005935.4 OX-2 membrane glycoprotein isoform a precursor [*Homo sapiens*] MERLVIRMPFSHLSTYSLVWVMAAVVLCTAQVQVVTQDEREQLYTPASLKCSLQNAQ EALIVTWQKKKAVSPENMVTFSENHGVVIQPAYKDKINITQLGLQNSTITFWNITLE DEGCYMCLFNTFGFGKISGTACLTVYVQPIVSLHYKFSEDHLNITCSATARPAPMVF WKVPRSGIENSTVTLSHPNGTTSVTSILHIKDPKNQVGKEVICQVLHLGTVTDFKQT VNKGYWFSVPLLLSIVSLVILLVLISILLYWKRHRNQDREP (SEQ ID NO: 26)
Mouse OX-2 (CD200)	>NM_010818.3 *Mus musculus* CD200 antigen (Cd200), transcript variant 1, mRNA GGGCGTGGTTGGTTGGTCGTCTCTTCCTCCACACTAGAGGAGCTGTAGAGTCTGCCT GTGCAGTGGAGGGGGCTCTCTCTACGGCGAATAGTAGTGTCCCTGCTCACAGGTGTT GCGGAGATATCCTCCATCGTGGAAGAGCTCAGACCCCGAGAAGCTGGTGTCTAGCTG CGGCCCAGAGCAAGGATGGGCAGTCTGGTATTCAGGAGACCTTTCTGCCATCTCTCC ACCTACAGCCTGATTTGGGGCATGGCAGCAGTAGCGCTGAGCACAGCTCAAGTGGAA GTGGTGACCCAGGATGAAAGAAAGGCGCTGCACACAACTGCATCCTTACGATGTTCT CTAAAAACATCCCAGGAACCCTTGATTGTGACATGGCAGAAAAAGAAAGCCGTGAGC CCAGAAAACATGGTCACCTACAGCAAAACCCATGGGGTTGTAATCCAGCCTGCCTAC AAAGACAGGATAAATGTCACAGAGCTGGGACTCTGGAACTCAAGCATCACCTTCTGG AACACAACATTGGAAGATGAGGGCTGCTACATGTGTCTCTTCAACACGTTTGGTTCT CAGAAGGTCTCAGGAACAGCTTGCCTTACCCTCTATGTACAGCCCATAGTACACCTT CACTACAACTATTTTGAAGACCACCTAAACATCACTTGCTCTGCGACTGCCCGTCCA GCCCCTGCCATCTCCTGGAAGGGTACTGGGACAGGAATTGAGAATAGTACCGAGAGT CACTTCCATTCAAATGGGACTACATCTGTCACCAGCATCCTCCGGGTCAAAGACCCC AAAACTCAAGTTGGGAAGGAAGTGATCTGCCAGGTTTTATACCTGGGGAATGTGATT GACTACAAGCAGAGTCTGGACAAAGGATTTTGGTTTTCAGTTCCACTGTTGCTAAGC ATTGTTTCTCTGGTAATTCTTCTGATCTTGATCTCCATCTTACTATACTGGAAACGT CACCGAAATCAGGAGCGGGGTGAATCATCACAGGGGATGCAAAGAATGAAATAAGAG CTCTAAAGAAATTATACAGAACCCTGAACGTGTTTCCCTGGTCTACTTGAATCTGAT GTGAAAGAAAAGCAGGAGGGAAAAGGCCATTCTCCATAGGACCTAAGGAGAGCAAAA GACCAGACACGAGCCTGTGAGGGATTTGACTTTTTGCTGTTGTCCCAGGTCCTCGGT GTTTGCATTCCAAGAGGAAGTCGAGTGCCTCGGGTCTGTTGTAGGACTTGATTTTTT TTTTTTTTGTAGAGCAATGCAGTGCCATGCTGTTAGAAAGGCTCCAGACTTAGAACC ACCAGTGCCAAGCCAGCTCTCAGACCGACTAGGGCTCCCATCGGAGGAACAAATCGT AGTCAACTTACCTCACAGAGCTCTCTGGTCCTTACACAAAGTAGAAAGGAGTGGGAC CAGAAAATTGGCCATGTCTGAAATCTGATGGAATTTTTAGGAAGAAAACTGAAGAAT AAGCAAAAGAAGAAAGAACACAGAAGGGTCCAAAGAGCTTCTGAGAGTACCTTTTGC CTTTCTGTTGGTGTCCCAGCTCTGGTTTTGTTCTTAGGTCCGCCAGTGTGTTTCCCT GTTGTTTGAGTATCTAGTTGACTACCTGCTACTGTTCTGCTGATGGTTGGCCTTGCT AGAATCCCTGACTCCCCTGCCGTTCTCTATGTGCTTCTATGAGGGTTACTATGATGA AAATAGAGCAGAAGATAGTGTGAAGTAACATTGGCAACTGTAATGTGTCCATTTAAC TTATTTTTATAGCACTTAGGCAATATTGTTAGTCTTAGTGAGTAGTTCACATCTTTA CAAAAGCATGCTCTCCCTATCCATTGGGCCCACAATAACACTCTCTTTGAGGCCATT CTGAATCCTGTCTCGTGTAATGATAATATATTATGAAAACAGATACTTTAAGAATTT CCTGTACAGCAGTCAGTTGTTTATTCTCTCTCTCTCTCTCTCTCTCTCTCTCCCTCC CCCACCCCAGCTTCTTTTTCTGTGACTTTGTTTTTCATAAAGAGAAGGCATCTCCTG AATACAATCGCTTTGTTCTGAAGACATCGTGAACTATTAATTCTTAACCCTTTGACA AAACTAGTGAAGTTGTTTTCTGTATCTTTTGCTTCATCTGTCTTTATAGAGTGACCT AGGAATTCAAGTGTAAGTTGTTTCCATTGTTGAACTGGATATTTATATACTTGGTAT GCTTTTCACGTGTTATTTAATTCTGTATAATTTCCTATATTTGTATTAAAATATTGA GCAATTAAAAGTGTCAACTAAATATTTGATGTGGCATTCCCTTGAGAAATATAGAAA TAAAGAATAAAAAAAAAAAAAAAAAA (SEQ ID NO: 27) >NP_034948.3 OX-2 membrane glycoprotein isoform 1 precursor [*Mus musculus*] MGSLVFRRPFCHLSTYSLIWGMAAVALSTAQVEVVTQDERKALHTTASLRCSLKTSQ EPLIVTWQKKKAVSPENMVTYSKTHGVVIQPAYKDRINVTELGLWNSSITFWNTTLE DEGCYMCLENTFGSQKVSGTACLTLYVQPIVHLHYNYFEDHLNITCSATARPAPAIS WKGTGTGIENSTESHFHSNGTTSVTSILRVKDPKTQVGKEVICQVLYLGNVIDYKQS LDKGFWFSVPLLLSIVSLVILLILISILLYWKRHRNQERGESSQGMQRMK (SEQ ID NO: 28)
Human Galectin-9	>NM_009587.3 *Homo sapiens* galectin 9 (LGALS9), transcript variant 1, mRNA CTTTGTTAAGTCGTTCCCTCTACAAAGGACTTCCTAGTGGGTGTGAAAGGCAGCGGT GGCCACAGAGGCGGCGGAGAGATGGCCTTCAGCGGTTCCCAGGCTCCCTACCTGAGT CCAGCTGTCCCCTTTTCTGGGACTATTCAAGGAGGTCTCCAGGACGGACTTCAGATC ACTGTCAATGGGACCGTTCTCAGCTCCAGTGGAACCAGGTTTGCTGTGAACTTTCAG ACTGGCTTCAGTGGAAATGACATTGCCTTCCACTTCAACCCTCGGTTTGAAGATGGA GGGTACGTGGTGTGCAACACGAGGCAGAACGGAAGCTGGGGGCCCGAGGAGAGGAAG ACACACATGCCTTTCCAGAAGGGGATGCCCTTTGACCTCTGCTTCCTGGTGCAGAGC TCAGATTTCAAGGTGATGGTGAACGGGATCCTCTTCGTGCAGTACTTCCACCGCGTG CCCTTCCACCGTGTGGACACCATCTCCGTCAATGGCTCTGTGCAGCTGTCCTACATC AGCTTCCAGAACCCCCGCACAGTCCCTGTTCAGCCTGCCTTCTCCACGGTGCCGTTC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TCCCAGCCTGTCTGTTTCCCACCCAGGCCCAGGGGGCGCAGACAAAAACCTCCCGGC GTGTGGCCTGCCAACCCGGCTCCCATTACCCAGACAGTCATCCACACAGTGCAGAGC GCCCCTGGACAGATGTTCTCTACTCCCGCCATCCCACCTATGATGTACCCCCACCCC GCCTATCCGATGCCTTTCATCACCACCATTCTGGGAGGGCTGTACCCATCCAAGTCC ATCCTCCTGTCAGGCACTGTCCTGCCCAGTGCTCAGAGGTTCCACATCAACCTGTGC TCTGGGAACCACATCGCCTTCCACCTGAACCCCCGTTTTGATGAGAATGCTGTGGTC CGCAACACCCAGATCGACAACTCCTGGGGGTCTGAGGAGCGAAGTCTGCCCCGAAAA ATGCCCTTCGTCCGTGGCCAGAGCTTCTCAGTGTGGATCTTGTGTGAAGCTCACTGC CTCAAGGTGGCCGTGGATGGTCAGCACCTGTTTGAATACTACCATCGCCTGAGGAAC CTGCCCACCATCAACAGACTGGAAGTGGGGGGCGACATCCAGCTGACCCATGTGCAG ACATAGGCGGCTTCCTGGCCCTGGGGCCGGGGGCTGGGGTGTGGGGCAGTCTGGGTC CTCTCATCATCCCCACTTCCCAGGCCCAGCCTTTCCAACCCTGCCTGGGATCTGGGC TTTAATGCAGAGGCCATGTCCTTGTCTGGTCCTGCTTCTGGCTACAGCCACCCTGGA ACGGAGAAGGCAGCTGACGGGGATTGCCTTCCTCAGCCGCAGCAGCACCTGGGGCTC CAGCTGCTGGAATCCTACCATCCCAGGAGGCAGGCACAGCCAGGGAGAGGGGAGGAG TGGGCAGTGAAGATGAAGCCCCATGCTCAGTCCCCTCCCATCCCCCACGCAGCTCCA CCCCAGTCCCAAGCCACCAGCTGTCTGCTCCTGGTGGGAGGTGGCCTCCTCAGCCCC TCCTCTCTGACCTTTAACCTCACTCTCACCTTGCACCGTGCACCAACCCTTCACCCC TCCTGGAAAGCAGGCCTGATGGCTTCCCACTGGCCTCCACCACCTGACCAGAGTGTT CTCTTCAGAGGACTGGCTCCTTTCCCAGTGTCCTTAAAATAAAGAAATGAAAATGCT TGTTGGCACATTCA (SEQ ID NO: 29) >NP_033665.1 galectin-9 isoform long [*Homo sapiens*] MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGND IAFHFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMV NGILFVQYFHRVPFHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFP PRPRGRRQKPPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFI TTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDN SWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRL EVGGDIQLTHVQT (SEQ ID NO: 30)
Mouse Galectin-9	>NM_010708.2 *Mus musculus* lectin, galactose binding, soluble 9 (Lgals9), transcript variant 1, mRNA GCCAAATAGCTGTGGTTTCTGTTTCCTAGCTCAGCCCTGCCCTGCGCAGAGTTCTGT CGTCCACCATCGAGTGAGGAAGAGAGCATTGGTTCCCCTGAGATAGAAGAGATGGCT CTCTTCAGTGCCCAGTCTCCATACATTAACCCGATCATCCCCTTTACTGGACCAATC CAAGGAGGGCTGCAGGAGGGACTTCAGGTGACCCTCCAGGGGACTACCAAGAGTTTT GCACAAAGGTTTGTGGTGAACTTTCAGAACAGCTTCAATGGAAATGACATTGCCTTC CACTTCAACCCCCGGTTTGAGGAAGGAGGGTATGTGGTTTGCAACACGAAGCAGAAC GGACAGTGGGGTCCTGAGGAGAGAAAGATGCAGATGCCCTTCCAGAAGGGGATGCCC TTTGAGCTTTGCTTCCTGGTGCAGAGGTCAGAGTTCAAGGTGATGGTGAACAAGAAA TTCTTTGTGCAGTACCAACACCGCGTACCCTACCACCTCGTGGACACCATCGCTGTC TCCGGCTGCTTGAAGCTGTCCTTTATCACCTTCCAGAACTCTGCAGCCCCTGTCCAG CATGTCTTCTCCACAGTGCAGTTCTCTCAGCCAGTCCAGTTCCCACGGACCCCTAAG GGGCGCAAACAGAAAACTCAGAACTTTCGTCCTGCCCACCAGGCACCCATGGCTCAA ACTACCATCCATATGGTTCACAGCACCCCTGGACAGATGTTCTCTACTCCTGGAATC CCTCCTGTGGTGTACCCCACCCCAGCCTATACCATACCTTTCTACACCCCCATTCCA AATGGGCTTTACCCGTCCAAGTCCATCATGATATCAGGCAATGTCTTGCCAGATGCT ACGAGGTTCCATATCAACCTTCGCTGTGGAGGTGACATTGCTTTCCACCTGAACCCC CGTTTCAATGAGAATGCTGTTGTCCGAAACACTCAGATCAACAACTCCTGGGGGCAG GAAGAGCGAAGTCTGCTTGGGAGGATGCCCTTCAGTCGAGGCCAGAGCTTCTCGGTG TGGATCATATGTGAAGGTCACTGCTTCAAGGTAGCTGTGAATGGTCAACACATGTGT GAATATTACCACCGCCTGAAGAACTTGCAGGATATCAACACTCTAGAAGTGGCGGGT GATATCCAGCTGACCCACGTGCAGACATAGGCAAGGTCTCTGGCCTAGGGATAAGGG CTGGAGCACTCTGCCTGTGTCTTATCTTTCCCCTGTCTCAGCCCTGGCACCATCAGA AGAGATCATCACTTATAGGAATTCCAGGAAGGTGAAATTCCCAATTGACTCCCTCCA CAAAGGGGGTTTTCTAGGCTGTGTGGCACATGGCTGTCAGCCCATAGTCTGAGCCAT TGCCCCCAAGCTAGCTATATACTGAGGGAAGTGACCCTCCTGGGTTTGCTCAGATCT CTGATCGTTCCCCCCTCTGTGGCCCTTTTCTTTCACCCCTCCAGGAGAGCCACCCTG ATATCATCCCACTGGCCTCCAACTGACCCACAATGTCCACAGTAACTTTCCCCCATT CTCACCCAGTATCCATAAAATAAAGAAATAATATTGCTTGTCTACAC (SEQ ID NO: 31) >NP_034838.2 galectin-9 isoform 1 [*Mus musculus*] MALFSAQSPYINPIIPFTGPIQGGLQEGLQVTLQGTTKSFAQRFVVNFQNSFNGNDI AFHFNPRFEEGGYVVCNTKQNGQWGPEERKMQMPFQKGMPFELCFLVQRSEFKVMVN KKFFVQYQHRVPYHLVDTIAVSGCLKLSFITFQNSAAPVQHVFSTVQFSQPVQFPRT PKGRKQKTQNFRPAHQAPMAQTTIHMVHSTPGQMFSTPGIPPVVYPTPAYTIPFYTP IPNGLYPSKSIMISGNVLPDATRFHINLRCGGDIAFHLNPRFNENAVVRNTQINNSW GQEERSLLGRMPFSRGQSFSVWIICEGHCFKVAVNGQHMCEYYHRLKNLQDINTLEV AGDIQLTHVQT (SEQ ID NO: 32)

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
Human PVR (CD155)	>NM_006505.5 *Homo sapiens* PVR cell adhesion molecule (PVR), transcript variant 1, mRNA AGTCACTTGTCTGGAGCTTGAAGAAGTGGGTATTCCCCTTCCCACCCCAGGCACTGG AGGAGCGGCCCCCCGGGGATTCCAGGACCTGAGCTCCGGGAGCTGGACTCGCAGCGA CCGCGGCAGAGCGAGCGGGCGCCGGGAAGCGAGGAGACGCCCGCGGGAGGCCCAGCT GCTCGGAGCAACTGGCATGGCCCGAGCCATGGCCGCCGCGTGGCCGCTGCTGCTGGT GGCGCTACTGGTGCTGTCCTGGCCACCCCCAGGAACCGGGGACGTCGTCGTGCAGGC GCCCACCCAGGTGCCCGGCTTCTTGGGCGACTCCGTGACGCTGCCCTGCTACCTACA GGTGCCCAACATGGAGGTGACGCATGTGTCACAGCTGACTTGGGCGCGGCATGGTGA ATCTGGCAGCATGGCCGTCTTCCACCAAACGCAGGGCCCCAGCTATTCGGAGTCCAA ACGGCTGGAATTCGTGGCAGCCAGACTGGGCGCGGAGCTGCGGAATGCCTCGCTGAG GATGTTCGGGTTGCGCGTAGAGGATGAAGGCAACTACACCTGCCTGTTCGTCACGTT CCCGCAGGGCAGCAGGAGCGTGGATATCTGGCTCCGAGTGCTTGCCAAGCCCCAGAA CACAGCTGAGGTTCAGAAGGTCCAGCTCACTGGAGAGCCAGTGCCCATGGCCCGCTG CGTCTCCACAGGGGGTCGCCCGCCAGCCCAAATCACCTGGCACTCAGACCTGGGCGG GATGCCCAATACGAGCCAGGTGCCAGGGTTCCTGTCTGGCACAGTCACTGTCACCAG CCTCTGGATATTGGTGCCCTCAAGCCAGGTGGACGGCAAGAATGTGACCTGCAAGGT GGAGCACGAGAGCTTTGAGAAGCCTCAGCTGCTGACTGTGAACCTCACCGTGTACTA CCCCCCAGAGGTATCCATCTCTGGCTATGATAACAACTGGTACCTTGGCCAGAATGA GGCCACCCTGACCTGCGATGCTCGCAGCAACCCAGAGCCCACAGGCTATAATTGGAG CACGACCATGGGTCCCCTGCCACCCTTTGCTGTGGCCCAGGGCGCCCAGCTCCTGAT CCGTCCTGTGGACAAACCAATCAACACAACTTTAATCTGCAACGTCACCAATGCCCT AGGAGCTCGCCAGGCAGAACTGACCGTCCAGGTCAAAGAGGGACCTCCCAGTGAGCA CTCAGGCATGTCCCGTAACGCCATCATCTTCCTGGTTCTGGGAATCCTGGTTTTTCT GATCCTGCTGGGGATCGGGATTTATTTCTATTGGTCCAAATGTTCCCGTGAGGTCCT TTGGCACTGTCATCTGTGTCCCTCGAGTACAGAGCATGCCAGCGCCTCAGCTAATGG GCATGTCTCCTATTCAGCTGTGAGCAGAGAGAACAGCTCTTCCCAGGATCCACAGAC AGAGGGCACAAGGTGACAGCGTCGGGACTGAGAGGGGAGAGAGACTGGAGCTGGCAA GGACGTGGGCCTCCAGAGTTGGACCCGACCCCAATGGATGAAGACCCCCTCCAAAGA GACCAGCCTCCCTCCCTGTGCCAGACCTCAAAACGACGGGGGCAGGTGCAAGTTCAT AGGTCTCCAAGACCACCCTCCTTTCATTTGCTAGAAGGACTCACTAGACTCAGGAAA GCTGTTAGGCTCACAGTTACAGTTTATTACAGTAAAAGGACAGAGATTAAGATCAGC AAAGGGAGGAGGTGCACAGCACACGTTCCACGACAGATGAGGCGACGGCTTCCATCT GCCCTCTCCCAGTGGAGCCATATAGGCAGCACCTGATTCTCACAGCAACATGTGACA ACATGCAAGAAGTACTGCCAATACTGCCAACCAGAGCAGCTCACTCGAGATCTTTGT GTCCAGAGTTTTTTGTTTGTCTTGAGACAGGGTCTGGCTCTGTTGGCAGACTAGAGT ACAGTGGTGAGATCACAGTTCATTGCAGCCTTGACTTCTCAACGCCAAGTCATCCTC CCACCTCAGCCTCCTGAGTAGCTATGACTACAGGTATGTGCCACCACGTCTGGCTAA TCTTTTTATTATTTGTAAAGTCGAGGTTTCCCTGTGTTGCCCAGGCTGGTCTTGAAC TCTTGGCTCCAAGTGATACTTCTGCCTTGGCCTCCCAAAGTGCTGAATTAAGCAGCT CACCATCCACACGGCTGACCTCATACATCAAGCCAATACCGTGTGGCCCAAGACCCC CACCATAAATCACATCATTAGCATGAACCACCCAGAGTGGCCCAAGACTCCAAGATC AGCTACCAGGCAGGATATTCCAAGGGCTTAGAGATGAATGCCCAGGAGCTGAGGATA AAGGGCCCGATCTTTCTTTGGGCAAGGTTAAGCCTTTACTGCATAGCAGACCACACA GAAGGGTGTGGGCCACCAGAGAATTTTGGTAAAAATTTGGCCTCTGGCCTTGAGCTT CTAAATCTCTGTATCCGTCAGATCTCTGTGGTTACAAGAAACAGCCACTGACCCTGG TCACCAGAGGCTGCAATTCAGGCCGCAAGCAGCTGCCTGGGGGGTGTCCAAGGAGCA GAGAAAACTACTAGATGTGAACTTGAAGAAGGTTGTCAGCTGCAGCCACTTTCTGCC AGCATCTGCAGCCACTTTCTGCCAGCATCTGCAGCCAGCAAGCTGGGACTGGCAGGA AATAACCCACAAAAGAAGCAAATGCAATTTCCAACACAAGGGGGAAGGGATGCAGGG GGAGGCAGCGCTGCAGTTGCTCAGGACACGCTCCTATAGGACCAAGATGGATGCGAC CCAAGACCCAGGAGGCCCAGCTGCTCAGTGCAACTGACAAGTTAAAAAGGTCTATGA TCTTGAGGGCAGACAGCAGAATTCCTCTTATAAAGAAAACTGTTTGGGAAAATACGT TGAGGGAGAGAAGACCTTGGGCCAAGATGCTAAATGGGAATGCAAAGCTTGAGCTGC TCTGCAAGAGAAAATAAGCAGGACAGAGGATTTGCTCTGGACAGAGATGGAAGAGCC GGGAACAGAGAAGTGTGGGGAAGAGATAGGAACCAGCAGGATGGCAGGGGCAAAGGG CTCAAGGGTGAGGAGGCCAGTGGGACCCCACAGAGTTGGGGAGATAAAGGAACATTG GTTGCTTTGGTGGCACGTAAGCTCCTTGTCTGTCTCCAGCACCCAGAATCTCATTAA AGCTTATTTATTGTACCTCCAGCGGCTGTGTGCAATGGGGTCTTTTGTGGAAATCAA GGAGCAGACAGGTTTCATGTGTACTGTCACCACGTGGGATGGAACCAGAGGCATGGA AGCAAGACGCTAAATGAAGAGGGCCATAAGGGCTGGGATTCCCAGGCACCTTAGGAA CAGCTTGTCTTTTTTTTTTTCCTCTCCAAAAAAAATGTTTAAGGGACGGTGTCTCCT GTCACCCAGGCTGGAGTGCAATGGCACGATCATAGCTCATTGCAGCCTCTAACTCCG GGGCTCAAGCAATCCTCCCACCTCAGCCTACCAAGTAGCTGTGACCACAGCTGCCCC TCACCATGCTAAGCTAATTTTTTTAATTAGATAGTACATAAACGTCCCAAAATTAGA AGATAAAAAGACATGAGGGATCCATTCTAATTTGTGTTTGGAGTGTAATGGTCCAGC TCCATTCTTCTGCACATGGATATCCAGTTTTACACAACACTGTGAATGTAATGAATG CCACTGAATCATACACTCAAAAATAGCTAAAATGGCAAATTGTCTGTTATCTCTTTT TAACCACCATTTTTGAAAATTAATTATACCAAAAAACCATTGAATAGTGCACTTTAT TTATTTATTTATTTGTTTATTTATTTATTTATTTTAGAAATAAGAGTCTCACTTTGT TGCCCAGGCTGGAGTGCAGTGGCGTGATCATGGCTCATTGCAGCCTCGACCTGCTGG GCTCGGGCTATCCTTCCATCTCAGCCTCCCGAGTAGCTGGGACTATAGGTGGGCGCC ACCCCACCTGGCTAAATCTCTTTTTAACTTTTGTAGAGATAGGCATCTCGCTATGTT GCCTAGGCTGGGCTGGAACTCCTGGGCTCAAGTGCTCCTCCTGCCTTGGCCTCCCAA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	AGCGCTAGGATTACAGATGTGAGCCACCGCGCCCACCCTGAACCTTACTTTTTTTGC TCAGTTTCTGGTAATTCAGAGAATGCCTCCTGAGTTGTTCTACACCCACCTCATATT CCATGGGAGGGCTGTACAGGGCTTTTTTAACGAGGCCTCTAAGGACAGGCATTTGTA TCCTTTCCAGCCTTTCACTATTACAATGTTGTAGTGAATAACTTTACACACTGTCAT TTATTTTACTTTTTTTTTTTTTTATTTTAGAGAAAGGAATCTTGCCATCTTGCCCAG GCTGGTCTCAAATTCCTGGGCCCAAACAATCCTCCCGCCTTGGCCTCCTAAAGTACT GGGATTTATAGGCATAAGCCACCGTGCCTGGCCAATGCACACTGTCATTTAGCTCAT GTTAACACCTGAGTGTAGGACACACTCCTGGAGGTGGAATTGCTGGGCCAAAGAGTA TGTTTCTTGTCATTGTGATAGATATTGACAAATGAACCCTCACAGAAGTTGTGCTGA GTTCTGTTCCCACCAGCGACGTAGGCGATGACCTTTTTCTGGAGGGAGGGGGCATCC TTGGAGTCCACAGAGCCAGGAATGGAGAGTGGGCCCAGAATTTTGGTATAGGTGTTG TATAAACTTATAGTAAGGTTAAGAAAACCGCAACTATCCTTATCAGAGACTTGGCGG GGGGCAGGGTATGATGGAGATCATAAGGAGGCTAAAACACTCCACACCCTCCCTCTG CATTGCTCCTGCACGGGAGTCGGGAATCTTTTCAGGTTGATACGATCTCACCTTGAG GAGCTGTGAGGTCCCAGAAGCCTCTGGGTTGCAGATTGCTTGGGGTGAAAATGTCTG TGCTACTGAAATCTAACTTTTTACAAAAAATTACGGGCTGGGCGCAGTGGCTCACGC CTGTAATCCCAGCACTTTGGGAGGCTGCAGCGGGTGGATCACTTGAGGTAAGGAGTT CAAGACCAGACCATAGTGAAACCGTGTCTCTACAAAAAAAATTAGCCAGGTGTGGTG GTGCATGCTTGTAATCCCAGCTACTCAGAAGGCTGAGGTGGGAGAATCCCTTGAACC CGGGAAGTGGAGGCTGGAGTAAACCATGATCGAGTTACTGCACTCCAGCCTGGGTGA CAAGAGTGAGACTCTGTCTCCAAAAAAAAAAAAAAAAAAAAAAAAAACTGGATTGCCT GGCTCTACTCCGGGCACAGCATGCAGGCCCAGTTCTGCTGCTCTGCTGTTTGTTCTG CTTTCCTCCACATATTGGCATCACCCTCTGGTGCCAAGATGGCTGCTGCATTCCAGG CATCACATCCAGACTCAGACCCAGAGAAGCTGCCCATCCCTACCTGGGTGAGCCTTT GTAGGAACGAGAAACCGCATCCAGCAGCAGAAACCTCACCCAGCAGCGTCTTTTCCG GTCTCATTCACCAGCGCCGCCCACCGCTCAACCAATCCCTGGCCAAAAGAATGGGAC CGCCTGGAAGGCTGGACCAAACAGGACCTGCCCTCTGGGGCTGGGGAGAGGCCCAGA TGAAGGCTGCAGGACAGGATGGACTCCTAGACCTCTGTTACCAGCAGTGACTACCTC TGTCTGGGTGGTTGGAACATGTTTGAATTTTATTCTAAGTACTGTCTACAAGTTCTG CAATAAACCTTGACTCTTCTTTTAATAATGCAAAA (SEQ ID NO: 33) >NP_006496.4 poliovirus receptor isoform alpha precursor [*Homo sapiens*] MARAMAAAWPLLLVALLVLSWPPPGTGDVVVQAPTQVPGFLGDSVTLPCYLQVPNME VTHVSQLTWARHGESGSMAVFHQTQGPSYSESKRLEFVAARLGAELRNASLRMFGLR VEDEGNYTCLFVTFPQGSRSVDIWLRVLAKPQNTAEVQKVQLTGEPVPMARCVSTGG RPPAQITWHSDLGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVTCKVEHESF EKPQLLTVNLTVYYPPEVSISGYDNNWYLGQNEATLTCDARSNPEPTGYNWSTTMGP LPPFAVAQGAQLLIRPVDKPINTTLICNVTNALGARQAELTVQVKEGPPSEHSGMSR NAIIFLVLGILVFLILLGIGIYFYWSKCSREVLWHCHLCPSSTEHASASANGHVSYS AVSRENSSSQDPQTEGTR (SEQ ID NO: 34)
Mouse PVR (CD155)	>NM_027514.2 *Mus musculus* poliovirus receptor (Pvr), mRNA AGGCGGCACCCGCTTAGCTGAGATTCCAGCACTTGACTTCAGGGTTTCGGAGAGATA AGGCGCTTGGCCGTTACTAACTGGACTACAAAGAGCTGGATCGGACCGGAACCACAT GGCTCAACTCGCCCGAGCCACCCGCTCCCCGCTGTCATGGCTGCTGCTGCTGTTCTG CTATGCACTCCGGAAAGCGGGTGGGGATATACGTGTGCTGGTGCCCTACAATTCGAC AGGCGTCTTGGGAGGGTCGACCACCTTGCACTGTAGTCTGACTTCTAATGAGAATGT GACTATCACTCAAATAACCTGGATGAAGAAGGATTCAGGTGGATCCCACGCTCTTGT GGCTGTCTTCCACCCCAAGAAGGGGCCCAACATCAAAGAGCCAGAGAGGGTGAAATT CTTGGCTGCCCAACAGGATCTGAGGAACGCATCTCTGGCCATCTCGAACTTAAGTGT AGAAGACGAAGGCATCTATGAATGTCAGATTGCCACATTCCCCAGAGGCAGTAGAAG CACCAATGCCTGGCTGAAGGTGCAAGCCCGACCTAAGAACACTGCAGAGGCCCTGGA GCCCTCTCCCACCTTGATACTGCAGGATGTGGCTAAATGCATCTCTGCCAATGGTCA CCCTCCTGGACGAATCTCTTGGCCCTCGAATGTGAATGGAAGTCACCGTGAAATGAA GGAACCAGGGTCCCAGCCGGGCACCACCACAGTTACCAGCTACCTCTCCATGGTACC TTCTCGCCAGGCAGACGGCAAGAACATCACCTGCACGGTGGAGCATGAAAGCTTACA GGAGCTGGACCAGCTGCTGGTGACCCTTTCCCAACCCTATCCACCTGAAAACGTGTC CATCTCTGGCTATGACGGCAACTGGTATGTTGGCCTCACTAACTTGACCCTGACCTG TGAAGCTCACAGCAAACCAGCGCCTGACATGGCTGGATATAACTGGAGCACGAACAC GGGTGACTTTCCCAACTCTGTTAAGCGCCAGGGCAATATGCTTCTAATCTCCACCGT AGAGGATGGTCTCAATAACACGGTCATTGTGTGCGAAGTCACCAATGCCCTAGGGTC TGGGCAGGGCCAAGTGCACATCATTGTTAAAGAGAAACCTGAGAATATGCAGCAAAA TACAAGATTACACCTAGGCTACATCTTTCTTATCGTCTTTGTCCTCGCTGTAGTCAT CATCATCGCAGCACTATACACTATACGAAGATGCAGGCATGGTCGTGCTCTGCAGTC CAATCCCTCAGAGAGGGAGAACGTCCAGTATTCATCTGTGAACGGCGACTGTAGACT GAACATGGAGCCAAACAGCACAAGGTGACGGTGCTGGGTAGACAGAACTAAGGAACT TGAAGGCATAGCAACTGGAACCCTACTCTCATAAATGAAGAAGCCTCCAGAGAGACT GGCTGCTCAGTGTGATGAGCATAGCAAGTTTGGGGGGTCTCCCAGGATGCTGCCGAA TTCCACGTTGTCAAAAGGACCCATGGAGGCCAGTGTGTTGGCTCACTCTTGACATCT CAGCAAGCTGGGGGGGGGGGGGGAGCATAAAGCAAGGTTGAGTCTAGCTTGGGCTA TAGAGCAAAGCCCTGTCCATACACAAACAAGCTAAGGGGCTTTGAGACGGTCAGAAA CTGAAGTCTTGCTTTGGGTAAGGTAAATCCTCTACCGCATGTATGTGCTAGACTTGA AAGACTTCCACACAGACCTCTTTATAAGTTGACTCCATTGGGGCTATCCCCTCCTCT CTGGACAAGGTCTCTGTATGTAGCCAAGGCTAGGCTCAAACTCACAGAGATATGTCT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GCTTCTACCTCCCCAGTGCTAGAGTTGAAAGTATTTGTGCCACTGCACTTTTCTAGG TCTTCTTTTAATGAAGTAAAGTATATATTTATAAAAAGCTATTTAGTTATATATATA TATATTTTTGAGACTATTTCATAGAGCCCAAGCTAACCTCAAACTTACTATGTAGCC AAGAGTGATGGTAAACTAATTTATTTTAATTTATTTGTCTTCAATTTTAACCATCAC CCAACCCCTGCTCCCTTCCATATCTTCTTTCAATCCATTTCATTGTCTTTTTCTTCC CAGACACTATTCTGACTTACGTCTCCATTACAAACATTTTATTGAACTACATAAAAA TGTGTGAACCACAAAAAAAAAATGTATTTGTCAAAATTGTAGTTGTCTTTCTGAGGC TGACCTGAGTTCTCTGATACCATTCTCTCCAGTTGTATCCAGTTTCCTGTAAACAAT GTGACTTTGTTTTTCTCAGTAGCTAAAACATCCCAATTATGTGAGTGTACACTTTCT TTACTCATTCCTCTGTGGGCCACCAGCTGGGTTGGTTCCATATCTGAGCTATTGTGC ATGGAATTGTCTCTGTGGTGGGTTTAGTAAACTCCCAGGAATGCCTGTACATGTTTG TAGAGGCCAGAAGAAGGCACAAAATCTTGAGCCAGGCTTACATGCACTTGTGAGTAG CCCCACATAGGTGCTAAGAACCCAGTTCAGGTCCTCTGCTGTGGGATGGTGGGCTGT GCACAGAAAGCCTGGTCCCGGTCTAGCAAAGGTCTGGAACTCCGGAGCCGGTGGGCT GTGATTTACACCAGCATGGGATGGAAGGAGTTGGACCTCGCCTCCTGGGCACCTGGC TCCTGTCACATAGCTACAGCCTCCCACAGCCCCCCTATAGGGAGGTATGCAGCATCA ATCACATAGTAGCTGCACTAAGCCCTCCCACATGCAAATAAGGTTTCCCCAAACTCT CAGTCCAAGCCAATGAAAAGTACCTGCTGTCAAACCCTAAATCATCCCCAAAACTCT GTAAGTCCTATCAGGGAATAAAATGTGTGTGAAAACTAAAAAAAAAAAAAAAA (SEQ ID NO: 35)
	>NP_081790.1 poliovirus receptor precursor [*Mus musculus*] MAQLARATRSPLSWLLLLFCYALRKAGGDIRVLVPYNSTGVLGGSTTLHCSLTSNEN VTITQITWMKKDSGGSHALVAVFHPKKGPNIKEPERVKFLAAQQDLRNASLAISNLS VEDEGIYECQIATFPRGSRSTNAWLKVQARPKNTAEALEPSPTLILQDVAKCISANG HPPGRISWPSNVNGSHREMKEPGSQPGTTTVTSYLSMVPSRQADGKNITCTVEHESL QELDQLLVTLSQPYPPENVSISGYDGNWYVGLTNLTLTCEAHSKPAPDMAGYNWSTN TGDFPNSVKRQGNMLLISTVEDGLNNTVIVCEVTNALGSGQGQVHIIVKEKPENMQQ NTRLHLGYIFLIVFVLAVVIIIAALYTIRRCRHGRALQSNPSERENVQYSSVNGDCR LNMEPNSTR (SEQ ID NO: 36)
Human Nectin-2 (CD112) isoform alpha	>NM_002856.3 *Homo sapiens* nectin cell adhesion molecule 2 (NECTIN2), transcript variant alpha, mRNA GTGACGTCAGCGGGTTCGAACCGCCGGAGCTGAGCGAGAGGCCGGGGGTGCCGAGCC GGGCGGGGAGAGCTGGGCCGGGAGAGCAGAACAGGGAGGCTAGAGCGCAGCGGGAAC CGGCCCGGAGCCGGAGCCGGAGCCCCACAGGCACCTACTAAACCGCCCAGCCGATCG GCCCCCACAGAGTGGCCCGCGGGCCTCCGGCCGGGCCCAGTCCCCTCCCGGGCCCTC CATGGCCCGGGCCGCTGCCCTCCTGCCGTCGAGATCGCCGCCGACGCCGCTGCTGTG GCCGCTGCTGCTGCTGCTGCTCCTGGAAACCGGAGCCCAGGATGTGCGAGTTCAAGT GCTACCCGAGGTGCGAGGCCAGCTCGGGGGCACCGTGGAGCTGCCGTGCCACCTGCT GCCACCTGTTCCTGGACTGTACATCTCCCTGGTGACCTGGCAGCGCCCAGATGCACC TGCGAACCACCAGAATGTGGCCGCCTTCCACCCTAAGATGGGTCCCAGCTTCCCCAG CCCGAAGCCTGGCAGCGAGCGGCTGTCCTTCGTCTCTGCCAAGCAGAGCACTGGGCA AGACACAGAGGCAGAGCTCCAGGACGCCACGCTGGCCCTCCACGGGCTCACGGTGGA GGACGAGGGCAACTACACTTGCGAGTTTGCCACCTTCCCCAAGGGGTCCGTCCGAGG GATGACCTGGCTCAGAGTCATAGCCAAGCCCAAGAACCAAGCTGAGGCCCAGAAGGT CACGTTCAGCCAGGACCCTACGACAGTGGCCCTCTGCATCTCCAAAGAGGGCCGCCC ACCTGCCCGGATCTCCTGGCTCTCATCCCTGGACTGGGAAGCCAAAGAGACTCAGGT GTCAGGGACCCTGGCCGGAACTGTCACTGTCACCAGCCGCTTCACCTTGGTGCCCTC GGGCCGAGCAGATGGTGTCACGGTCACCTGCAAAGTGGAGCATGAGAGCTTCGAGGA ACCAGCCCTGATACCTGTGACCCTCTCTGTACGCTACCCTCCTGAAGTGTCCATCTC CGGCTATGATGACAACTGGTACCTCGGCCGTACTGATGCCACCCTGAGCTGTGACGT CCGCAGCAACCCAGAGCCCACGGGCTATGACTGGAGCACGACCTCAGGCACCTTCCC GACCTCCGCAGTGGCCCAGGGCTCCCAGCTGGTCATCCACGCAGTGGACAGTCTGTT CAATACCACCTTCGTCTGCACAGTCACCAATGCCGTGGGCATGGGCCGCGCTGAGCA GGTCATCTTTGTCCGAGAAACCCCCAGGGCCTCGCCCCGAGATGTGGGCCCGCTGGT GTGGGGGGCCGTGGGGGGGACACTGCTGGTGCTGCTGCTTCTGGCTGGGGGGTCCTT GGCCTTCATCCTGCTGAGGGTGAGGAGGAGGAGGAAGAGCCCTGGAGGAGCAGGAGG AGGAGCCAGTGGCGACGGGGGATTCTACGATCCGAAAGCTCAGGTGTTGGGAAATGG GGACCCCGTCTTCTGGACACCAGTAGTCCCTGGTCCCATGGAACCAGATGGCAAGGA TGAGGAGGAGGAGGAGGAGGAAGAGAAGGCAGAGAAAGGCCTCATGTTGCCTCCACC CCCAGCACTCGAGGATGACATGGAGTCCCAGCTGGACGGCTCCCTCATCTCACGGCG GGCAGTTTATGTGTGACCTGGACACAGACAGAGACAGAGCCAGGCCCGGCCCTCCCG CCCCCGACCTGACCACGCCGGCCTAGGGTTCCAGACTGGTTGGACTTGTTCGTCTGG ACGACACTGGAGTGGAACACTGCCTCCCACTTTCTTGGGACTTGGAGGGAGGTGGAA CAGCACACTGGACTTCTCCCGTCTCTAGGGCTGCATGGGGAGCCCGGGGAGCTGAGT AGTGGGGATCCAGAGAGGACCCCCGCCCCCAGAGACTTGGTTTTGGCTCCAGCCTTC CCCTGGCCCCGTGACACTCAGGAGTTAATAAATGCCTTGGAGGAAAACA (SEQ ID NO: 37)
	>NP_002847.1 nectin-2 isoform alpha precursor [*Homo sapiens*] MARAAALLPSRSPPTPLLWPLLLLLLLETGAQDVRVQVLPEVRGQLGGTVELPCHLL PPVPGLYISLVTWQRPDAPANHQNVAAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQ DTEAELQDATLALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQAEAQKV

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TFSQDPTTVALCISKEGRPPARISWLSSLDWEAKETQVSGTLAGTVTVTSRFTLVPS GRADGVTVTCKVEHESFEEPALIPVTLSVRYPPEVSISGYDDNWYLGRTDATLSCDV RSNPEPTGYDWSTTSGTFPTSAVAQGSQLVIHAVDSLFNTTFVCTVTNAVGMGRAEQ VIFVRETPRASPRDVGPLVWGAVGGTLLVLLLLAGGSLAFILLRVRRRRKSPGGAGG GASGDGGFYDPKAQVLGNGDPVFWTPVVPGPMEPDGKDEEEEEEEEKAEKGLMLPPP PALEDDMESQLDGSLISRRAVYV (SEQ ID NO: 38)
Mouse Nectin-2 (CD112) isoform alpha	>NM_001159724.1 *Mus musculus* nectin cell adhesion molecule 2 (Nectin2), transcript variant 2, mRNA GAGCCCTAGGATCGGCTTGGCGAAGAGGGGCGGGGCCTGTGACGTCATGAGTCCGGC CCGCTGGAGCTAAGCGAGGGGCCGGGGGGCGCGGATCCTGAGAGCCAGGCGAGGGAA AGCTGGGCCGAACGAACTGATCCGGGGAGCCGTGAGCGGCGGAAGCCGGCCTGGAGC CGGACACTTCAGACCCCTGACTGCCCTCCCAGCCGATCGGTACACGAAGAGTGGTCC CTAGGCACCCCCTGCCCGGGCCCAGTCCCTCCCCGGGCCCCCCATGGCCCGGGCCGC AGTCCTCCCGCCGTCCAGATTGTCACCGACGCTGCCGTTGTTGCCGCTGCTACTGCT CCTGCTTCAGGAAACAGGAGCCCAAGATGTGCGGGTACGAGTGCTTCCCGAGGTCCG GGGCCGCTTGGGAGGCACCGTGGAGTTACCGTGCCACCTGCTCCCACCCACGACGGA GCGCGTCTCTCAGGTGACCTGGCAGCGCCTGGATGGCACAGTTGTGGCTGCTTTCCA CCCATCCTTCGGAGTGGATTTCCCCAACTCTCAGTTCAGCAAGGACCGTCTGTCCTT TGTCAGAGCGAGACCAGAAACAAACGCAGACCTGCGGGATGCCACACTGGCCTTCCG GGGACTGAGGGTAGAGGACGAGGGCAATTACACCTGCGAGTTTGCCACGTTTCCCAA CGGTACCCGCAGGGGGGTGACCTGGCTCAGAGTCATAGCCCAGCCTGAGAACCACGC TGAAGCCCAGGAGGTCACAATTGGCCCCCAGTCGGTGGCTGTAGCCCGCTGTGTCTC CACTGGGGGCCGCCCCCCTGCCCGAATCACCTGGATCTCATCTCTGGGTGGAGAGGC CAAAGATACTCAGGAGCCAGGGATACAGGCTGGCACCGTCACTATCATCAGCCGATA CTCCTTGGTGCCCGTGGGCCGAGCGGATGGCGTCAAGGTCACGTGTAGAGTGGAACA CGAGAGCTTCGAAGAGCCGATCCTGCTGCCAGTGACCCTCTCTGTGCGCTACCCTCC AGAAGTATCCATCTCCGGCTATGATGACAACTGGTACCTTGGCCGCAGTGAGGCCAT ACTGACCTGTGATGTACGAAGCAACCCAGAGCCCACAGACTATGACTGGAGCACGAC CTCGGGCGTCTTCCCAGCCTCTGCAGTGGCCCAGGGCTCTCAGCTGCTTGTCCACTC TGTGGATCGAATGGTCAACACTACCTTCATCTGTACAGCCACCAACGCTGTGGGGAC AGGCCGTGCTGAGCAGGTCATCCTGGTGCGAGACACCCCCCAGGCCTCCCGAGATGT GGGTCCGCTGGTGTGGGGGGCCGTGGGGGGAACATTGCTGGTGCTACTCCTGGCTGG GGGGTTCCTGGCCTTGATCCTGCTGAGGGGGAGGAGGAGGCGGAAGAGCCCTGGAGG AGGAGGAAATGATGGCGACAGAGGATCCTACGATCCAAAGACTCAGGTGTTTGGGAA CGGGGGTCCTGTCTTCTGGAGGTCAGCATCCCCTGAGCCCATGAGGCCAGATGGCAG GGAGGAAGATGAGGAGGAGGAGGAAGAAATGAAGGCAGAGGAAGGTCTCATGCTACC TCCACACGAGTCACCTAAGGACGACATGGAGTCCCATCTGGATGGCTCCCTCATCTC TCGGCGGGCAGTTTACGTGTGACCCTACGATATAGACACTGGACACATGGAAACACC AAGTTCCACCCTCACTGCCAACCACACCAATGCCAGCCAGCAACGATGGCTAGGGAC CGGTTGGACTGGTTCTTCTGGGGCACACTGGAGTTGGAAGGGCACCGCCCCTGCTTT CAGGATAGAGGACAAGTGGAACCACACAGACTCCTATCTTTAGGGCCTCATGGAGTA GGGGACCCCAGGAGCGCCATGGTGCACACTCAGGACTCCTCAGAGCTTGCTTTCGGC CCCAGCCTAGCCCTGGCCCCGAAACACTCAGGAGCTAATAAATGCCTTGTCGGAAAA AAAAAAAAAAAAAA (SEQ ID NO: 39) >NP_001153196.1 nectin-2 isoform 2 precursor [Mus *musculus*] MARAAVLPPSRLSPTLPLLPLLLLLLQETGAQDVRVRVLPEVRGRLGGTVELPCHLL PPTTERVSQVTWQRLDGTVVAAFHPSFGVDFPNSQFSKDRLSFVRARPETNADLRDA TLAFRGLRVEDEGNYTCEFATFPNGTRRGVTWLRVIAQPENHAEAQEVTIGPQSVAV ARCVSTGGRPPARITWISSLGGEAKDTQEPGIQAGTVTIISRYSLVPVGRADGVKVT CRVEHESFEEPILLPVTLSVRYPPEVSISGYDDNWYLGRSEAILTCDVRSNPEPTDY DWSTTSGVFPASAVAQGSQLLVHSVDRMVNTTFICTATNAVGTGRAEQVILVRDTPQ ASRDVGPLVWGAVGGTLLVLLLAGGFLALILLRGRRRRKSPGGGGNDGDRGSYDPKT QVFGNGGPVFWRSASPEPMRPDGREEDEEEEEEMKAEEGLMLPPHESPKDDMESHLD GSLISRRAVYV (SEQ ID NO: 40)
Human Nectin-2 (CD112) isoform delta	>NM_001042724.2 *Homo sapiens* nectin cell adhesion molecule 2 (NECTIN2), transcript variant delta, mRNA GTGACGTCAGCGGGTTCGAACCGCCGGAGCTGAGCGAGAGGCCGGGGGTGCCGAGCC GGGCGGGGAGAGCTGGGCCGGGAGAGCAGAACAGGGAGGCTAGAGCGCAGCGGGAAC CGGCCCGGAGCCGGAGCCGGAGCCCCACAGGCACCTACTAAACCGCCCAGCCGATCG GCCCCCACAGAGTGGCCCGCGGGCCTCCGGCCGGGCCCAGTCCCCTCCCGGGCCCTC CATGGCCCGGGCCGCTGCCCTCCTGCCGTCGAGATCGCCGCCGACGCCGCTGCTGTG GCCGCTGCTGCTGCTGCTGCTCCTGGAAACCGGAGCCCAGGATGTGCGAGTTCAAGT GCTACCCGAGGTGCGAGGCCAGCTCGGGGGCACCGTGGAGCTGCCGTGCCACCTGCT GCCACCTGTTCCTGGACTGTACATCTCCCTGGTGACCTGGCAGCGCCCAGATGCACC TGCGAACCACCAGAATGTGGCCGCCTTCCACCCTAAGATGGGTCCCAGCTTCCCCAG CCCGAAGCCTGGCAGCGAGCGGCTGTCCTTCGTCTCTGCCAAGCAGAGCACTGGGCA AGACACAGAGGCAGAGCTCCAGGACGCCACGCTGGCCCTCCACGGGCTCACGGTGGA GGACGAGGGCAACTACACTTGCGAGTTTGCCACCTTCCCCAAGGGGTCCGTCCGAGG GATGACCTGGCTCAGAGTCATAGCCAAGCCCAAGAACCAAGCTGAGGCCCAGAAGGT CACGTTCAGCCAGGACCCTACGACAGTGGCCCTCTGCATCTCCAAAGAGGGCCGCCC ACCTGCCCGGATCTCCTGGCTCTCATCCCTGGACTGGGAAGCCAAAGAGACTCAGGT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GTCAGGGACCCTGGCCGGAACTGTCACTGTCACCAGCCGCTTCACCTTGGTGCCCTC GGGCCGAGCAGATGGTGTCACGGTCACCTGCAAAGTGGAGCATGAGAGCTTCGAGGA ACCAGCCCTGATACCTGTGACCCTCTCTGTACGCTACCCTCCTGAAGTGTCCATCTC CGGCTATGATGACAACTGGTACCTCGGCCGTACTGATGCCACCCTGAGCTGTGACGT CCGCAGCAACCCAGAGCCCACGGGCTATGACTGGAGCACGACCTCAGGCACCTTCCC GACCTCCGCAGTGGCCCAGGGCTCCCAGCTGGTCATCCACGCAGTGGACAGTCTGTT CAATACCACCTTCGTCTGCACAGTCACCAATGCCGTGGGCATGGGCCGCGCTGAGCA GGTCATCTTTGTCCGAGAGACCCCCAACACAGCAGGCGCAGGGGCCACAGGCGGCAT CATCGGGGGCATCATCGCCGCCATCATTGCTACTGCTGTGGCTGCCACGGGCATCCT TATCTGCCGGCAGCAGCGGAAGGAGCAGACGCTGCAGGGGGCAGAGGAGGACGAAGA CCTGGAGGGACCTCCCTCCTACAAGCCACCGACCCCAAAAGCGAAGCTGGAGGCACA GGAGATGCCCTCCCAGCTCTTCACTCTGGGGGCCTCGGAGCACAGCCCACTCAAGAC CCCCTACTTTGATGCTGGCGCCTCATGCACTGAGCAGGAAATGCCTCGATACCATGA GCTGCCCACCTTGGAAGAACGGTCAGGACCCTTGCACCCTGGAGCCACAAGCCTGGG GTCCCCCATCCCGGTGCCTCCAGGGCCACCTGCTGTGGAAGACGTTTCCCTGGATCT AGAGGATGAGGAGGGGGAGGAGGAAGAGTATCTGGACAAGATCAACCCCATCTA TGATGCTCTGTCCTATAGCAGCCCCTCTGATTCCTACCAGGGCAAAGGCTTTGTCAT GTCCCGGGCCATGTATGTGTGAGCTGCCATGCGCCTGGCGTCTCACATCTCACCTGT TGATCCCTTAGCTTTCTTGCCAAGGATCTAGTGCCCCCTGACCTCTGGCCAGGCCAC TGTCAGTTAACACATATGCATTCCATTTGTGATGTCTACCTTGGTGGCTCCACTATG ACCCCTAACCCATGAGCCCAGAGAAATTCACCGTGATAATGGAATCCTGGCAACCTT ATCTCATGAGGCAGGAGGTGGGGAAGGTGCTTCTGCACAACCTCTGATCCCAAGGAC TCCTCTCCCAGACTGTGACCTTAGACCATACCTCTCACCCCCCAATGCCTCGACTCC CCCAAAATCACAAAGAAGACCCTAGACCTATAATTTGTCTTCAGGTAGTAAATTCCC AATAGGTCTGCTGGAGTGGGCGCTGAGGGCTCCCTGCTGCTCAGACCTGAGCCCTCC AGGCAGCAGGGTCCCACTTACCCCCTCCCCACCCTGTTCCCCAAAGGTGGGAAAGAG GGGATTCCCCAGCCCAAGGCAGGGTTTTCCCAGCACCCTCCTGTAAGCAGAAGTCTC AGGGTCCAGACCCTTCCCTGAGCCCCCACCCCCACCCCAATTCCTGCCTACCAAGCA AGCAGCCCCAGCCTAGGGTCAGACAGGGTGAGCCTCATACAGACTGTGCCTTGATGG CCCCAGCCTTGGGAGAAGAATTTACTGTTAACCTGGAAGACTACTGAATCATTTTAC CCTTGCCCAGTGGAATAGGACCTAAACATCCCCCTTCCGGGGAAAGTGGGTCATCTG AATTGGGGGTAGCAATTGATACTGTTTTGTAAACTACATTTCCTACAAAATATGAAT TTATACTTTGA (SEQ ID NO: 41) >NP_001036189.1 nectin-2 isoform delta precursor [*Homo sapiens*] MARAAALLPSRSPPTPLLWPLLLLLLLETGAQDVRVQVLPEVRGQLGGTVELPCHLL PPVPGLYISLVTWQRPDAPANHQNVAAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQ DTEAELQDATLALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQAEAQKV TFSQDPTTVALCISKEGRPPARISWLSSLDWEAKETQVSGTLAGTVTVTSRFTLVPS GRADGVTVTCKVEHESFEEPALIPVTLSVRYPPEVSISGYDDNWYLGRTDATLSCDV RSNPEPTGYDWSTTSGTFPTSAVAQGSQLVIHAVDSLFNTTFVCTVTNAVGMGRAEQ VIFVRETPNTAGAGATGGIIGGIIAAIIATAVAATGILICRQQRKEQTLQGAEEDED LEGPPSYKPPTPKAKLEAQEMPSQLFTLGASEHSPLKTPYFDAGASCTEQEMPRYHE LPTLEERSGPLHPGATSLGSPIPVPPGPPAVEDVSLDLEDEEGEEEEEYLDKINPIY DALSYSSPSDSYQGKGFVMSRAMYV (SEQ ID NO: 42)
Mouse Nectin-2 (CD112) isoform beta	>NM_008990.3 *Mus musculus* nectin cell adhesion molecule 2 (Nectin2), transcript variant 1, mRNA GAGCCCTAGGATCGGCTTGGCGAAGAGGGGCGGGGCCTGTGACGTCATGAGTCCGGC CCGCTGGAGCTAAGCGAGGGGCCGGGGGGCGCGGATCCTGAGAGCCAGGCGAGGGAA AGCTGGGCCGAACGAACTGATCCGGGGAGCCGTGAGCGGCGGAAGCCGGCCTGGAGC CGGACACTTCAGACCCCTGACTGCCCTCCCAGCCGATCGGTACACGAAGAGTGGTCC CTAGGCACCCCCTGCCCGGGCCCAGTCCCTCCCCGGGCCCCCCATGGCCCGGGCCGC AGTCCTCCCGCCGTCCAGATTGTCACCGACGCTGCCGTTGTTGCCGCTGCTACTGCT CCTGCTTCAGGAAACAGGAGCCCAAGATGTGCGGGTACGAGTGCTTCCCGAGGTCCG GGGCCGCTTGGGAGGCACCGTGGAGTTACCGTGCCACCTGCTCCCACCCACGACGGA GCGCGTCTCTCAGGTGACCTGGCAGCGCCTGGATGGCACAGTTGTGGCTGCTTTCCA CCCATCCTTCGGAGTGGATTTCCCCAACTCTCAGTTCAGCAAGGACCGTCTGTCCTT TGTCAGAGCGAGACCAGAAACAAACGCAGACCTGCGGGATGCCACACTGGCCTTCCG GGGACTGAGGGTAGAGGACGAGGGCAATTACACCTGCGAGTTTGCCACGTTTCCCAA CGGTACCCGCAGGGGGGTGACCTGGCTCAGAGTCATAGCCCAGCCTGAGAACCACGC TGAAGCCCAGGAGGTCACAATTGGCCCCCAGTCGGTGGCTGTAGCCCGCTGTGTCTC CACTGGGGGCCGCCCCCCTGCCCGAATCACCTGGATCTCATCTCTGGGTGGAGAGGC CAAAGATACTCAGGAGCCAGGGATACAGGCTGGCACCGTCACTATCATCAGCCGATA CTCCTTGGTGCCCGTGGGCCGAGCGGATGGCGTCAAGGTCACGTGTAGAGTGGAACA CGAGAGCTTCGAAGAGCCGATCCTGCTGCCAGTGACCCTCTCTGTGCGCTACCCTCC AGAAGTATCCATCTCCGGCTATGATGACAACTGGTACCTTGGCCGCAGTGAGGCCAT ACTGACCTGTGATGTACGAAGCAACCCAGAGCCCACAGACTATGACTGGAGCACGAC CTCGGGCGTCTTCCCAGCCTCTGCAGTGGCCCAGGGCTCTCAGCTGCTTGTCCACTC TGTGGATCGAATGGTCAACACTACCTTCATCTGTACAGCCACCAACGCTGTGGGGAC AGGCCGTGCTGAGCAGGTCATCCTGGTGCGAGAGTCACCCAGCACAGCAGGAGCAGG GGCCACTGGTGGCATCATTGGAGGTATTATCGCTGCCATCATCGCCACCGCAGTGGC TGGCACAGGCATCCTCATCTGCCGACAACAGCGGAAGGAGCAGAGGCTTCAAGCTGC GGATGAGGAAGAAGAACTGGAAGGACCTCCCTCCTATAAACCACCCACCCCGAAGGC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CAAGCTGGAGGAACCAGAGATGCCCTCTCAACTCTTCACCTTGGGGGCCTCAGAGCA CAGCCCAGTGAAGACGCCATACTTTGATGCTGGTGTCTCTTGTGCTGATCAGGAGAT GCCTCGGTATCACGAGCTGCCCACTCTGGAAGAGCGGTCAGGGCCCCTGCTGTTGGG GGCTACAGGCCTGGGACCTTCTCTTCTGGTGCCTCCAGGACCCAATGTTGTGGAGGG GGTTTCCCTGAGTCTCGAAGATGAGGAGGAAGATGATGAGGAGGAAGACTTCCTGGA TAAAATCAACCCTATTTATGATGCCCTGTCCTACCCCAGCCCCTCTGACTCCTACCA GAGCAAAGACTTTTTTGTGTCACGGGCCATGTATGTGTGAGGGAGGCACAGGGGCTC TGACGTCTCACCTTTCACCCTTGACCCATGAGCTTTCCACCAGTAATCTAGGACACT CTGACTTCCAGGCAGACCAGGGACAACTATCACCCATTGCAATCCACCTGTGACTTC TTAGTGACTCCACCATGACGTCCAATCTATGATGTCTGAGGCAGGCAAACCTGCACA ACTGGAAACCTGGAGATTTTTATCTCCCTTGGCAGGGAGCTCACCATATCCTTCTGC ACCACCTGTGACCCCCCCCCCCCCCCCCCAAGGACTCCTAAGACTACGACCCTTTGACC ATGCCACTCAGTATCTCAAGAACCCTTAAAGTCCCAAAGGAATCGGACCTTGCACTT GTCCTCAGGCAATAGAGTCCAACAGATATGCAAGAACGGGATCAGGGGCTCCCTGTT GCTCAGACCTGAGCCCTCCAGGCAGCAGAAGCTCACCTGATCCCTCCCCACCCTGCT CCCCAAAGGTGAAAAGGAGAGGATTCCCCAATGTAAGGTAGGACCTCCCCATCTCCA CCTACTCCTGCAGGCAGGAATCTCAGGTTTCTCACACCCTCTCCTCAGCACCCAGGT TCCTGTCTCCAGAGCATGAATTCCAGGTCCAATGCTAGAGGGGAGAACCTAATGCAA GTGTGCCTTGCCACCCCAAGTTTGGGAGACTCTGCTCTTATCCTGAGGACTACTGAA TTCTTTTAACCCCTACCCAGTGAGATGAGAACTACATATCCCTCTTTAGGGGATGGT GTGTGTATGTGTGTGTGATGGAGAATCTGGGCATCTGGGTTGGGAATTTTATTTTGT AAGCATTTCCTACATAATATGAGTTTCTACTTTGATAAAGTCTTGTGTTTTCTGTG (SEQ ID NO: 43)
	>NP_033016.3 nectin-2 isoform 1 precursor [*Mus musculus*] MARAAVLPPSRLSPTLPLLPLLLLLLQETGAQDVRVRVLPEVRGRLGGTVELPCHLL PPTTERVSQVTWQRLDGTVVAAFHPSFGVDFPNSQFSKDRLSFVRARPETNADLRDA TLAFRGLRVEDEGNYTCEFATFPNGTRRGVTWLRVIAQPENHAEAQEVTIGPQSVAV ARCVSTGGRPPARITWISSLGGEAKDTQEPGIQAGTVTIISRYSLVPVGRADGVKVT CRVEHESFEEPILLPVTLSVRYPPEVSISGYDDNWYLGRSEAILTCDVRSNPEPTDY DWSTTSGVFPASAVAQGSQLLVHSVDRMVNTTFICTATNAVGTGRAEQVILVRESPS TAGAGATGGIIGGIIAAIIATAVAGTGILICRQQRKEQRLQAADEEEELEGPPSYKP PTPKAKLEEPEMPSQLFTLGASEHSPVKTPYFDAGVSCADQEMPRYHELPTLEERSG PLLLGATGLGPSLLVPPGPNVVEGVSLSLEDEEEDDEEEDFLDKINPIYDALSYPSP SDSYQSKDFFVSRAMYV (SEQ ID NO: 44)
Human IL-10	>NM_000572.3 *Homo sapiens* interleukin 10 (IL10), transcript variant 1, mRNA ACACATCAGGGGCTTGCTCTTGCAAAACCAAACCACAAGACAGACTTGCAAAAGAAG GCATGCACAGCTCAGCACTGCTCTGTTGCCTGGTCCTCCTGACTGGGGTGAGGGCCA GCCCAGGCCAGGGCACCCAGTCTGAGAACAGCTGCACCCACTTCCCAGGCAACCTGC CTAACATGCTTCGAGATCTCCGAGATGCCTTCAGCAGAGTGAAGACTTTCTTTCAAA TGAAGGATCAGCTGGACAACTTGTTGTTAAAGGAGTCCTTGCTGGAGGACTTTAAGG GTTACCTGGGTTGCCAAGCCTTGTCTGAGATGATCCAGTTTTACCTGGAGGAGGTGA TGCCCCAAGCTGAGAACCAAGACCCAGACATCAAGGCGCATGTGAACTCCCTGGGGG AGAACCTGAAGACCCTCAGGCTGAGGCTACGGCGCTGTCATCGATTTCTTCCCTGTG AAAACAAGAGCAAGGCCGTGGAGCAGGTGAAGAATGCCTTTAATAAGCTCCAAGAGA AAGGCATCTACAAAGCCATGAGTGAGTTTGACATCTTCATCAACTACATAGAAGCCT ACATGACAATGAAGATACGAAACTGAGACATCAGGGTGGCGACTCTATAGACTCTAG GACATAAATTAGAGGTCTCCAAAATCGGATCTGGGGCTCTGGGATAGCTGACCCAGC CCCTTGAGAAACCTTATTGTACCTCTCTTATAGAATATTTATTACCTCTGATACCTC AACCCCCATTTCTATTTATTTACTGAGCTTCTCTGTGAACGATTTAGAAAGAAGCCC AATATTATAATTTTTTTCAATATTTATTATTTTCACCTGTTTTTAAGCTGTTTCCAT AGGGTGACACACTATGGTATTTGAGTGTTTTAAGATAAATTATAAGTTACATAAGGG AGGAAAAAAAATGTTCTTTGGGGAGCCAACAGAAGCTTCCATTCCAAGCCTGACCAC GCTTTCTAGCTGTTGAGCTGTTTTCCCTGACCTCCCTCTAATTTATCTTGTCTCTGG GCTTGGGGCTTCCTAACTGCTACAAATACTCTTAGGAAGAGAAACCAGGGAGCCCCT TTGATGATTAATTCACCTTCCAGTGTCTCGGAGGGATTCCCCTAACCTCATTCCCCA ACCACTTCATTCTTGAAAGCTGTGGCCAGCTTGTTATTTATAACAACCTAAATTTGG TTCTAGGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGG CGGGTGGATCACTTGAGGTCAGGAGTTCCTAACCAGCCTGGTCAACATGGTGAAACC CCGTCTCTACTAAAAATACAAAAATTAGCCGGGCATGGTGGCGCGCACCTGTAATCC CAGCTACTTGGGAGGCTGAGGCAAGAGAATTGCTTGAACCCAGGAGATGGAAGTTGC AGTGAGCTGATATCATGCCCCTGTACTCCAGCCTGGGTGACAGAGCAAGACTCTGTC TCAAAAAATAAAAATAAAAATAAATTTGGTTCTAATAGAACTCAGTTTTAACTAGAA TTTATTCAATTCCTCTGGGAATGTTACATTGTTTGTCTGTCTTCATAGCAGATTTTA ATTTTGAATAAATAAATGTATCTTATTCACATCA (SEQ ID NO: 45)
	>NP_000563.1 interleukin-10 isoform 1 precursor [*Homo sapiens*] MHSSALLCCLVLLTGVRASPGQGTQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQM KDQLDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQAENQDPDIKAHVNSLGE NLKTLRLRLRRCHRFLPCENKSKAVEQVKNAFNKLQEKGIYKAMSEFDIFINYIEAY MTMKIRN (SEQ ID NO: 46)

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
Mouse IL-10	>NM_010548.2 *Mus musculus* interleukin 10 (Il10), mRNA ACATTTAGAGACTTGCTCTTGCACTACCAAAGCCACAAGGCAGCCTTGCAGAAAAGA GAGCTCCATCATGCCTGGCTCAGCACTGCTATGCTGCCTGCTCTTACTGACTGGCAT GAGGATCAGCAGGGGCCAGTACAGCCGGGAAGACAATAACTGCACCCACTTCCCAGT CGGCCAGAGCCACATGCTCCTAGAGCTGCGGACTGCCTTCAGCCAGGTGAAGACTTT CTTTCAAACAAAGGACCAGCTGGACAACATACTGCTAACCGACTCCTTAATGCAGGA CTTTAAGGGTTACTTGGGTTGCCAAGCCTTATCGGAAATGATCCAGTTTTACCTGGT AGAAGTGATGCCCCAGGCAGAGAAGCATGGCCCAGAAATCAAGGAGCATTTGAATTC CCTGGGTGAGAAGCTGAAGACCCTCAGGATGCGGCTGAGGCGCTGTCATCGATTTCT CCCCTGTGAAAATAAGAGCAAGGCAGTGGAGCAGGTGAAGAGTGATTTTAATAAGCT CCAAGACCAAGGTGTCTACAAGGCCATGAATGAATTTGACATCTTCATCAACTGCAT AGAAGCATACATGATGATCAAAATGAAAAGCTAAAACACCTGCAGTGTGTATTGAGT CTGCTGGACTCCAGGACCTAGACAGAGCTCTCTAAATCTGATCCAGGGATCTTAGCT AACGGAAACAACTCCTTGGAAAACCTCGTTTGTACCTCTCTCCGAAATATTTATTAC CTCTGATACCTCAGTTCCCATTCTATTTATTCACTGAGCTTCTCTGTGAACTATTTA GAAAGAAGCCCAATATTATAATTTTACAGTATTTATTATTTTTAACCTGTGTTTAAG CTGTTTCCATTGGGGACACTTTATAGTATTTAAAGGGAGATTATATTATATGATGGG AGGGGTTCTTCCTTGGGAAGCAATTGAAGCTTCTATTCTAAGGCTGGCCACACTTGA GAGCTGCAGGGCCCTTTGCTATGGTGTCCTTTCAATTGCTCTCATCCCTGAGTTCAG AGCTCCTAAGAGAGTTGTGAAGAAACTCATGGGTCTTGGGAAGAGAAACCAGGGAGA TCCTTTGATGATCATTCCTGCAGCAGCTCAGAGGGTTCCCCTACTGTCATCCCCCAG CCGCTTCATCCCTGAAAACTGTGGCCAGTTTGTTATTTATAACCACCTAAAATTAGT TCTAATAGAACTCATTTTTAACTAGAAGTAATGCAATTCCTCTGGGAATGGTGTATT GTTTGTCTGCCTTTGTAGCAGACTCTAATTTTGAATAAATGGATCTTATTCG (SEQ ID NO: 47) >NP_034678.1 interleukin-10 precursor [*Mus musculus*] MPGSALLCCLLLLTGMRISRGQYSREDNNCTHFPVGQSHMLLELRTAFSQVKTFFQT KDQLDNILLTDSLMQDFKGYLGCQALSEMIQFYLVEVMPQAEKHGPEIKEHLNSLGE KLKTLRMRLRRCHRFLPCENKSKAVEQVKSDFNKLQDQGVYKAMNEFDIFINCIEAY MMIKMKS (SEQ ID NO: 48)
Human TSG-6	>NM_007115.3 *Homo sapiens* TNF alpha induced protein 6 (TNFAIP6), mRNA AGTCACATTTCAGCCACTGCTCTGAGAATTTGTGAGCAGCCCCTAACAGGCTGTTAC TTCACTACAACTGACGATATGATCATCTTAATTTACTTATTTCTCTTGCTATGGGAA GACACTCAAGGATGGGGATTCAAGGATGGAATTTTTCATAACTCCATATGGCTTGAA CGAGCAGCCGGTGTGTACCACAGAGAAGCACGGTCTGGCAAATACAAGCTCACCTAC GCAGAAGCTAAGGCGGTGTGTGAATTTGAAGGCGGCCATCTCGCAACTTACAAGCAG CTAGAGGCAGCCAGAAAAATTGGATTTCATGTCTGTGCTGCTGGATGGATGGCTAAG GGCAGAGTTGGATACCCCATTGTGAAGCCAGGGCCCAACTGTGGATTTGGAAAAACT GGCATTATTGATTATGGAATCCGTCTCAATAGGAGTGAAAGATGGGATGCCTATTGC TACAACCCACACGCAAAGGAGTGTGGTGGCGTCTTTACAGATCCAAAGCAAATTTTT AAATCTCCAGGCTTCCCAAATGAGTACGAAGATAACCAAATCTGCTACTGGCACATT AGACTCAAGTATGGTCAGCGTATTCACCTGAGTTTTTTAGATTTTGACCTTGAAGAT GACCCAGGTTGCTTGGCTGATTATGTTGAAATATATGACAGTTACGATGATGTCCAT GGCTTTGTGGGAAGATACTGTGGAGATGAGCTTCCAGATGACATCATCAGTACAGGA AATGTCATGACCTTGAAGTTTCTAAGTGATGCTTCAGTGACAGCTGGAGGTTTCCAA ATCAAATATGTTGCAATGGATCCTGTATCCAAATCCAGTCAAGGAAAAAATACAAGT ACTACTTCTACTGGAAATAAAAACTTTTTAGCTGGAAGATTTAGCCACTTATAAAAA AAAAAAAAAGGATGATCAAAACACACAGTGTTTATGTTGGAATCTTTTGGAACTCCT TTGATCTCACTGTTATTATTAACATTTATTTATTATTTTTCTAAATGTGAAAGCAAT ACATAATTTAGGGAAAATTGGAAAATATAGGAAACTTTAAACGAGAAAATGAAACCT CTCATAATCCCACTGCATAGAAATAACAAGCGTTAACATTTTCATATTTTTTTCTTT CAGTCATTTTTCTATTTGTGGTATATGTATATATGTACCTATATGTATTTGCATTTG AAATTTTGGAATCCTGCTCTATGTACAGTTTTGTATTATACTTTTTAAATCTTGAAC TTTATAAACATTTTCTGAAATCATTGATTATTCTACAAAAACATGATTTTAAACAGC TGTAAAATATTCTATGATATGAATGTTTTATGCATTATTTAAGCCTGTCTCTATTGT TGGAATTTCAGGTCATTTTCATAAATATTGTTGCAATAAATATCCTTGAACACACAA AAAAAAAAAAAAAA (SEQ ID NO: 49) >NP_009046.2 tumor necrosis factor-inducible gene 6 protein precursor [*Homo sapiens*] MIILIYLFLLLWEDTQGWGFKDGIFHNSIWLERAAGVYHREARSGKYKLTYAEAKAV CEFEGGHLATYKQLEAARKIGFHVCAAGWMAKGRVGYPIVKPGPNCGFGKTGIIDYG IRLNRSERWDAYCYNPHAKECGGVFTDPKQIFKSPGFPNEYEDNQICYWHIRLKYGQ RIHLSFLDFDLEDDPGCLADYVEIYDSYDDVHGFVGRYCGDELPDDIISTGNVMTLK FLSDASVTAGGFQIKYVAMDPVSKSSQGKNTSTTSTGNKNFLAGRFSHL (SEQ ID NO: 50)
Mouse TSG-6	>NM_009398.2 *Mus musculus* tumor necrosis factor alpha induced protein 6 (Tnfaip6), mRNA CCGCTGCTCTGAGAATTTCGTGTGGGCAGCCCCGACATTGTAACCGGCTCTGCAACC GAAGAGATGGTCGTCCTCCTTTGCTTATGCGTCTTGCTGTGGGAAGAGGCTCACGGA TGGGGATTCAAGAACGGGATCTTTCATAACTCCATATGGCTTGAACAAGCAGCGGGC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GTATACCACAGAGAAGCTCGGGCTGGCAGATACAAGCTCACCTACGCCGAAGCCAAG GCCGTATGTGAATTTGAAGGTGGTCGTCTCGCAACCTACAAGCAGCTAGAGGCAGCC AGAAAAATTGGATTCCATGTCTGTGCTGCTGGATGGATGGCCAAGGGTAGAGTCGGA TACCCCATTGTGAAACCTGGGCCCAACTGTGGATTTGGGAAAACGGGTATCATCGAT TATGGAATCCGGCTCAACAGGAGTGAGCGATGGGATGCCTATTGCTACAACCCACAT GCAAAGGAGTGTGGTGGTGTCTTCACAGATCCGAAGCGAATTTTTAAATCCCCGGGC TTCCCAAATGAGTACGATGACAACCAGGTCTGCTACTGGCACATTCGGCTCAAGTAC GGTCAGCGAATTCACCTGAGCTTTTTGGACTTTGACCTTGAACATGATCCAGGCTGC TTGGCTGACTATGTAGAAATCTATGACAGTTATGATGACGTCCACGGCTTTGTAGGA AGATACTGTGGTGATGAACTTCCAGAAGACATCATTAGCACAGGAAATGTCATGACC TTGAAGTTTCTGAGTGATGCATCCGTCACGGCTGGAGGCTTCCAGATTAAATACGTC ACAGTGGATCCTGCATCTAAATCCAGTCAAGCCAAAAATACAAGTACTACTGGAAAT AAGAAGTTCTTACCTGGAAGGTTTAGCCATCTATAAAAAATTTTTTTTAAAAATGTT CAAAACATCCAGTACAATATTTATATTTGTTTTTGTTGTTGTTGTTGGTTTTTTTTT TTTTATTTTGTTTTGTTTTGTTTTTTTGAGACGGGGTTTCTCTGTATAGCCTTGGCT GTCCTGGAACTCACTTTGAAGACCAGGCTGGCCTCGAACTCAGAAATCCACCTGCCT CCGCCTACCAAGTGCTGGGATTAAAGGCGTCCACCACCACCGCCCGGCTTCAATATT TATATTTGTAGCTCTTGGACCTCGTTTGTTCTCTTTTGTATTTTTATTATTAACATG TATTTATTATTTTTCCAAATGTGAAAGCCATATGTAATTATGTGGAAAATTGACAAA TAAATACAGAGAACTTCAAATGAGTTTTTTTTTTAAATCTCATAATTGTACTACACA GAAATAACTAATGTTAAAGTTTTTAAATGTTTGTCTTTCATTCATTTTTCTACTTGT AGTATATGTACATATGTAACTCTATGATTTGCGTTTGAATTTTGGCATTCTGCCTTT TGTAACCTGATATTTTTAACCTTGACATTGTATAGCTCAAGCACTTCCCAAGATCTC TGAGTTTTCTACAAAATGGGACTTTGTAAATATGATTGTTCCCTGCTTTATTTAAGC TGAATTTATATTAGGATTTAAGGTTGTTTTCATAAATATTGCTGTAATAAATACTTT TGGAT (SEQ ID NO: 51) >NP_033424.1 tumor necrosis factor-inducible gene 6 protein precursor [*Mus musculus*] MVVLLCLCVLLWEEAHGWGFKNGIFHNSIWLEQAAGVYHREARAGRYKLTYAEAKAV CEFEGGRLATYKQLEAARKIGFHVCAAGWMAKGRVGYPIVKPGPNCGFGKTGIIDYG IRLNRSERWDAYCYNPHAKECGGVFTDPKRIFKSPGFPNEYDDNQVCYWHIRLKYGQ RIHLSFLDFDLEHDPGCLADYVEIYDSYDDVHGFVGRYCGDELPEDIISTGNVMTLK FLSDASVTAGGFQIKYVTVDPASKSSQAKNTSTTGNKKFLPGRFSHL (SEQ ID NO: 52)
Human B7-H3 (CD276)	>NM_001024736.2 *Homo sapiens* CD276 molecule (CD276), transcript variant 1, mRNA ATTCGGGCCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGGGCCGCGTCCCTGAG TCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAGCCCAGCTGT CAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGTGCAT GTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAG GTCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCC TTCTCCCCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACA GATACCAAACAGCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTAT GCCAACCGCACGGCCCTCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGG CTGCAGCGCGTGCGTGTGGCGGACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGG GATTTCGGCAGCGCTGCCGTCAGCCTGCAGGTGGCCGCTCCCTACTCGAAGCCCAGC ATGACCCTGGAGCCCAACAAGGACCTGCGGCCAGGGGACACGGTGACCATCACGTGC TCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTCTGGCAGGATGGGCAGGGTGTG CCCCTGACTGGCAACGTGACCACGTCGCAGATGGCCAACGAGCAGGGCTTGTTTGAT GTGCACAGCATCCTGCGGGTGGTGCTGGGTGCAAATGGCACCTACAGCTGCCTGGTG CGCAACCCCGTGCTGCAGCAGGATGCGCACAGCTCTGTCACCATCACACCCCAGAGA AGCCCCACAGGAGCCGTGGAGGTCCAGGTCCCTGAGGACCCGGTGGTGGCCCTAGTG GGCACCGATGCCACCCTGCGCTGCTCCTTCTCCCCCGAGCCTGGCTTCAGCCTGGCA CAGCTCAACCTCATCTGGCAGCTGACAGACACCAAACAGCTGGTGCACAGTTTCACC GAAGGCCGGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCCTCTTCCCGGACCTG CTGGCACAAGGCAATGCATCCCTGAGGCTGCAGCGCGTGCGTGTGGCGGACGAGGGC AGCTTCACCTGCTTCGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTCAGCCTGCAG GTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGG CCAGGGGACACGGTGACCATCACGTGCTCCAGCTACCGGGGCTACCCTGAGGCTGAG GTGTTCTGGCAGGATGGGCAGGGTGTGCCCCTGACTGGCAACGTGACCACGTCGCAG ATGGCCAACGAGCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGCTGGGT GCGAATGGCACCTACAGCTGCCTGGTGCGCAACCCCGTGCTGCAGCAGGATGCGCAC GGCTCTGTCACCATCACAGGGCAGCCTATGACATTCCCCCCAGAGGCCCTGTGGGTG ACCGTGGGGCTGTCTGTCTGTCTCATTGCACTGCTGGTGGCCCTGGCTTTCGTGTGC TGGAGAAAGATCAAACAGAGCTGTGAGGAGGAGAATGCAGGAGCTGAGGACCAGGAT GGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCTCTGAAACACTCTGACAGCAAA GAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGGGAGCTGCTACCCCTCC CTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCCTGCCCCCAACA GATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACACAGACCA CTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTTT TCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCC TGCTGCCTTATTTCACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATC ACCACCCTCTTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ATGCAATATTCAGACTGACTGACCCCCTGCCTTATTTCACCAAAGACACGATGCATA GTCACCCCGGCCTTGTTTCTCCAATGGCCGTGATACACTAGTGATCATGTTCAGCCC TGCTTCCACCTGCATAGAATCTTTTCTTCTCAGACAGGGACAGTGCGGCCTCAACAT CTCCTGGAGTCTAGAAGCTGTTTCCTTTCCCCTCCTTCCTCCTCTTGCTCTAGCCTT AATACTGGCCTTTTCCCTCCCTGCCCCAAGTGAAGACAGGGCACTCTGCGCCCACCA CATGCACAGCTGTGCATGGAGACCTGCAGGTGCACGTGCTGGAACACGTGTGGTTCC CCCCTGGCCCAGCCTCCTCTGCAGTGCCCCTCTCCCCTGCCCATCCTCCCCACGGAA GCATGTGCTGGTCACACTGGTTCTCCAGGGGTCTGTGATGGGGCCCCTGGGGGTCAG CTTCTGTCCCTCTGCCTTCTCACCTCTTTGTTCCTTTCTTTTCATGTATCCATTCAG TTGATGTTTATTGAGCAACTACAGATGTCAGCACTGTGTTAGGTGCTGGGGGCCCTG CGTGGGAAGATAAAGTTCCTCCCTCAAGGACTCCCCATCCAGCTGGGAGACAGACAA CTAACTACACTGCACCCTGCGGTTTGCAGGGGGCTCCTGCCTGGCTCCCTGCTCCAC ACCTCCTCTGTGGCTCAAGGCTTCCTGGATACCTCACCCCCATCCCACCCATAATTC TTACCCAGAGCATGGGGTTGGGGCGGAAACCTGGAGAGAGGGACATAGCCCCTCGCC ACGGCTAGAGAATCTGGTGGTGTCCAAAATGTCTGTCCAGGTGTGGGCAGGTGGGCA GGCACCAAGGCCCTCTGGACCTTTCATAGCAGCAGAAAAGGCAGAGCCTGGGGCAGG GCAGGGCCAGGAATGCTTTGGGGACACCGAGGGGACTGCCCCCCACCCCCACCATGG TGCTATTCTGGGGCTGGGGCAGTCTTTTCCTGGCTTGCCTCTGGCCAGCTCCTGGCC TCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCGGATGTCATCTCTCCCTGC CCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGACTCGGAGGGATTTT GTAAACTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAA (SEQ ID NO: 53)
	>NP_001019907.1 CD276 antigen isoform a precursor [*Homo sapiens*] MLRRRGSPGMGVHVGAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPEPG FSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRV ADEGSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGY PEAEVFWQDGQGVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIW QLTDTKQLVHSFTEGRDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFWQDG QGVPLTGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTIT GQPMTFPPEALWVTVGLSVCLIALLVALAFVCWRKIKQSCEEENAGAEDQDGEGEGS KTALQPLKHSDSKEDDGQEIA (SEQ ID NO: 54)
Mouse B7-H3 (CD276)	>NM_133983.4 *Mus musculus* CD276 antigen (Cd276), mRNA CGGCGCGGCGCGCCAAAGTGACCTGGTACAGCCTGGACCCCAAGCTCATCGGCTTTG TCTGGCTGGCCGCCTGGCCTCTTCCCACTTGGATTTGGATGATCCTGAGGCCTTTGG AGGAACTTCGAGACAAAGGCCCCTCTTCCTCTTCCACGGGCAGGAGCAGCCATTCGC CACGGAGAGCCCAGCTGTCAGCTGTCTCACAGGAAGATGCTTCGAGGATGGGGTGGC CCCAGTGTGGGTGTGTGTGTGCGCACAGCACTGGGGGTGCTGTGCCTCTGCCTCACA GGAGCTGTGGAAGTCCAGGTCTCTGAAGACCCCGTGGTGGCCCTGGTGGACACGGAT GCCACCCTACGCTGCTCCTTTTCCCCAGAGCCTGGCTTCAGTCTGGCACAGCTCAAC CTCATCTGGCAGCTGACAGACACCAAACAGCTGGTGCACAGCTTCACGGAGGGCCGG GACCAAGGCAGTGCCTACTCCAACCGCACAGCGCTCTTCCCTGACCTGTTGGTGCAA GGCAATGCGTCCTTGAGGCTGCAGCGCGTCCGAGTAACCGACGAGGGCAGCTACACC TGCTTTGTGAGCATCCAGGACTTTGACAGCGCTGCTGTTAGCCTGCAGGTGGCCGCC CCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTACGTCCAGGGAAC ATGGTGACCATCACGTGCTCTAGCTACCAGGGCTATCCGGAGGCCGAGGTGTTCTGG AAGGATGGACAGGGAGTGCCCTTGACTGGCAATGTGACCACATCCCAGATGGCCAAC GAGCGGGGCTTGTTCGATGTTCACAGCGTGCTGAGGGTGGTGCTGGGTGCTAACGGC ACCTACAGCTGCCTGGTACGCAACCCGGTGTTGCAGCAAGATGCTCACGGCTCAGTC ACCATCACAGGGCAGCCCCTGACATTCCCCCCTGAGGCTCTGTGGGTAACCGTGGGG CTCTCTGTCTGTCTTGTGGTACTACTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAG ATCAAGCAGAGCTGCGAGGAGGAGAATGCAGGTGCCGAGGACCAGGATGGAGATGGA GAAGGATCCAAGACAGCTCTACGGCCTCTGAAACCCTCTGAAAACAAAGAAGATGAC GGACAAGAAATTGCTTGATTGGGAGCTGCTGCCCTTCCCAGGTGGGGGGCCCACCCT CTGGCAGTGTTGAGCTTCAATGCGAGCCCTTCCCCCAACGAATGGGTTTGTCCCACA GATCTACCCGTTCGTCAAAGGACGTGGTCCATAGACCACCCACAGCCTTACTTTTCC AATGGACTTAATTCCCATCATCCTGCAGCCTCATTTCTCCAGTGACACGATACACGA ACCATCCTGCGGCCTTATTTCCCACGGACACGACACAAAGATGTCCCTCCTCGGTGT TCCTCCAGAGTCGTCTGGTGGCCTTGTGATACGGCGTGAACCTTCTTCCTTCTGCCT TACGTCTAATGGACACACACGCACCACCCCCACACCCTTGCTCCTCCAAAGCCATGC AGACTGTGTAACTGCTATTATTCTCCAAGGGGCATCCTGTGCAGATGAAACCCTGCT TTATTTCCCTGAAGACAGCTGCACAGTGACCTCTTAGTTCTTGCTCCCATGGCCCTG ATGTATCCTAGTTACCAGCCCTCAACCTCAGTTCTGAGGGTGGGATCCCATCGCTCA GCAAGGCTTCATCCTGACCTCCCTGCCCTGATCTGATCTGGCCCTGGCTTTTGTTGT CTCGCTCCCTGACTAAGTGAGATGGGGCACTCTCCCGCCCCCGCCCCCCCCAGGTCA CAGATACCTACCTGCAGCTGTGCGTGCTGGATCACGCACATACTTGCCTTGCATGGT CTCCTGGCTGCCCTGGGCTGTGCCTGTTCTTCCATAGGAAGCAAGTTCTTGTCTCCC TGGTTCTCAGGGCCCCTCAGGGGCTCAGCCTTCAGCCCTGTGCTTCCCCATGTTGGG AATCTTTGTTACCTTTTTCTTCTTTGTAAATTAACATCTGATAACAACCACAGGGTC CAATGGGACTTTCACAGACCTGCCAGCTAGATAAATAATGACAACAGAAGTTTATTA ATATTTTAAGACTTAGGCCTTTTGCTGGGCAGCCTCCCAACTATTCTATCCTGACTA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ATCCTGGCACTATGTCCCACCACATGGCCAGGTCTACCTCTCTGCTCCACTCTCCAT CCACCTCCATGTCTGCCAGCAAATCTCCCGTGATTCAGTTCTTCTCCCAGAGTCCCT ATCTCTGCCCAGAAGTACCATCTTCGACTTCCTGCCCAACTATTGGCCGTCAGCTCT TCATTAAAGCCGATCAGATGTAATTCTAGATTGCCTTAGGCAGGTGAGGAAGAAACA AGTATTTGTAAAATATGAGACCAGCAATGGGCCATAGAAATAACAGCACCAGATCCT GCCAGCATTTAGCCCTCTGTTGGTACAAAATTAACAATTGAATATACAGAGACCTAC TTCCAGAGTGTACCCCAACAACAGGCGTGAGCATGGTGCTGGGTACTAGGGTCCTGC TGGAAAATCAGAGACCTTACCTACAGCTGGGACATGACCTTGCTTCCGACTTACCCA CCACTTCTGGATACCTCACCCTCAGCCCACACTATCCCTGGCCTAGGGCCCAGGGTA GAGCCAGAAACATGGAGAAAGCATGGCCCCTTGCCGTACCTGGAGAACTGGGTATTT TCCAGAGTCTTTATAGATGTGGACTGGAAGGCAGGTGGCCACAGCCGTGCAGACCTG GGTCAGGTCAGAAACCTATGCCATGCTGGGACCTACTCAACAGCAGAAGCATGAAGA GGGCCTGAGGACAAGAAAGGCCTTCTTACCATGGTGCTATTCTGGAGCTGGGATATA TACCTGGCTTGTCTCTGACTGCCCTGGCTTCTGGCAGAACTTCTGATGTCCTCCTGA AGGCCTCTCTCCCACCCCAGTACCTGAGAACCTGAGGATAATTTAAACATGGGACTC TGGCCAGCACCTGGGAGAGACAGGTAGATCTCTGATTTTTGACTCAGCCTGGTCTAT CGAGTGAGTTCCAGGACATCTGGGGCTACACAGAGAAACCATCTTAAAGACTAAAAA TAATAAACATGAGACTGTAAACTGGGTGTATTTTGGGAGAAATAAATGTCTTTTTCT TTCAA (SEQ ID NO: 55) >NP_598744.1 CD276 antigen precursor [*Mus musculus*] MLRGWGGPSVGVCVRTALGVLCLCLTGAVEVQVSEDPVVALVDTDATLRCSFSPEPG FSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYSNRTALFPDLLVQGNASLRLQRVRV TDEGSYTCFVSIQDFDSAAVSLQVAAPYSKPSMTLEPNKDLRPGNMVTITCSSYQGY PEAEVFWKDGQGVPLTGNVTTSQMANERGLFDVHSVLRVVLGANGTYSCLVRNPVLQ QDAHGSVTITGQPLTFPPEALWVTVGLSVCLVVLLVALAFVCWRKIKQSCEEENAGA EDQDGDGEGSKTALRPLKPSENKEDDGQEIA (SEQ ID NO: 56)
Human B7-H4 (VTCN1)	>NM_024626.4 *Homo sapiens* V-set domain containing T cell activation inhibitor 1 (VTCN1), transcript variant 1, mRNA GTGAGTCACCAAGGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGG GAACCTTCCCCAGCCATGGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGC ATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTGGCTTTGGTATTTCAGGG AGACACTCCATCACAGTCACTACTGTCGCCTCAGCTGGGAACATTGGGGAGGATGGA ATCCTGAGCTGCACTTTTGAACCTGACATCAAACTTTCTGATATCGTGATACAATGG CTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATGAGCTG TCGGAGCAGGATGAAATGTTCAGAGGCCGGACAGCAGTGTTTGCTGATCAAGTGATA GTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTAC AAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAAACT GGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGGTCTGGGCATCCCAAGTT GACCAGGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAG AATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATAC TCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAA TCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGT GTCTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATG CTAAAATAATGTGCCTCGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGA TCTACAGAACTATTTCACCACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAAT GAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCAAGAAACAAAAAGAAGCC AAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAAGACATATTAGAA GTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGAGTGATAAGTAAAATG CACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGG GGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTG CTGTAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTT ATATTCCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCAC TTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATG ATGCTTCCAAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAA AAATGATCATAATTTTAGCATAAACAGAGCAGTCGGCGACACCGATTTTATAAATAA ACTGAGCACCTTCTTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCA TCCGTGAATGGTCCAGGGAAGGACCTTTCACCTTGTCTATATGGCATTATGTCATCA CAAGCTCTGAGGCTTCTCCTTTCCATCCTGCGTGGACAGCTAAGACCTCAGTTTTCA ATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTCGCCCCCCATCTCCGGGGG AATGTCTGAAGACAATTTTGGTTACCTCAATGAGGGAGTGGAGGAGGATACAGTGCT ACTACCAACTAGTGGATAGAGGCCAGGGATGCTGCTCAACCTCCTACCATGTACAGG ACGTCTCCCCATTACAACTACCCAATCCGAAGTGTCAACTGTGTCAGGGCTAAGAAA CCCTGGTTTTGAGTAGAAAAGGGCCTGGAAAGAGGGGAGCCAACAAATCTGTCTGCT TCCTCACATTAGTCATTGGCAAATAAGCATTCTGTCTCTTTGGCTGCTGCCTCAGCA CAGAGAGCCAGAACTCTATCGGGCACCAGGATAACATCTCTCAGTGAACAGAGTTGA CAAGGCCTATGGGAAATGCCTGATGGGATTATCTTCAGCTTGTTGAGCTTCTAAGTT TCTTTCCCTTCATTCTACCCTGCAAGCCAAGTTCTGTAAGAGAAATGCCTGAGTTCT AGCTCAGGTTTTCTTACTCTGAATTTAGATCTCCAGACCCTGCCTGGCCACAATTCA AATTAAGGCAACAAACATATACCTTCCATGAAGCACACACAGACTTTTGAAAGCAAG GACAATGACTGCTTGAATTGAGGCCTTGAGGAATGAAGCTTTGAAGGAAAAGAATAC TTTGTTTCCAGCCCCCTTCCCACACTCTTCATGTGTTAACCACTGCCTTCCTGGACC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TTGGAGCCACGGTGACTGTATTACATGTTGTTATAGAAAACTGATTTTAGAGTTCTG ATCGTTCAAGAGAATGATTAAATATACATTTCCTACACCA (SEQ ID NO: 57) >NP_078902.2 V-set domain-containing T-cell activation inhibitor 1 isoform 1 precursor [*Homo sapiens*] MASLGQILFWSIISIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCT FEPDIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNAS LRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAP RWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIE NDIAKATGDIKVTESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK (SEQ ID NO: 58)
Mouse B7-H4 (VTCN1)	>NM_178594.3 *Mus musculus* V-set domain containing T cell activation inhibitor 1 (Vtcn1), mRNA GTGAGTCACAACACCCAGGAGGGCAGCAGCAGGCAGGCAGCTCCACTCACCAAAATC TGGCCCCACACACAGCAGGACTGTGGGAAGGAACTCCCTCTCCATGGCTTCCTTGGG GCAGATCATCTTTTGGAGTATTATTAACATCATCATCATCCTGGCTGGGGCCATCGC ACTCATCATTGGCTTTGGCATTTCAGGCAAGCACTTCATCACGGTCACGACCTTCAC CTCAGCTGGAAACATTGGAGAGGACGGGACCCTGAGCTGCACTTTTGAACCTGACAT CAAACTCAACGGCATCGTCATCCAGTGGCTGAAAGAAGGCATCAAAGGTTTGGTCCA CGAGTTCAAAGAAGGCAAAGACGACCTCTCACAGCAGCATGAGATGTTCAGAGGCCG CACAGCAGTGTTTGCTGATCAGGTGGTAGTTGGCAATGCTTCCCTGAGACTGAAAAA CGTGCAGCTCACGGATGCTGGCACCTACACATGTTACATCCGCACCTCAAAAGGCAA AGGGAATGCAAACCTTGAGTATAAGACCGGAGCCTTCAGTATGCCAGAGATAAATGT GGACTATAATGCCAGTTCAGAGAGTTTACGCTGCGAGGCTCCTCGGTGGTTCCCCCA GCCCACAGTGGCCTGGGCATCTCAAGTCGACCAAGGAGCCAATTTCTCAGAAGTCTC CAACACCAGCTTTGAGTTGAACTCTGAGAATGTGACCATGAAGGTCGTATCTGTGCT CTACAATGTCACAATCAACAACACATACTCCTGTATGATTGAAAACGACATTGCCAA AGCCACCGGGGACATCAAAGTGACAGATTCAGAGGTCAAAAGGCGAAGTCAGCTGCA GTTGCTGAACTCTGGGCCTTCCCCGTGTGTTTTTTCTTCTGCCTTTGTGGCTGGCTG GGCACTCCTATCTCTCTCCTGTTGCCTGATGCTAAGATGAGGGGCCCTGGCTACACA AAAGCATGCAACGTTGCTGGTCCAACAGAATCCCGGAGAACTACAGAAATATTTTCC TCAAGACATGACCTAGTTTTATATTTCTAGAAGAAGATGAAATCATGTCTAGAAGTC TGGAGAGAGCAGACAGGAACAAGATGTGGAAGGAAAACAAAAGTAACCCACAGACAC CCCCGATCGGAACAAGATGGACCTAGAAAATAATTCAACCAAACTAGAGTATACTAA GTGTGCTGTTACAATGTGTGTAGGGTAGGTGTCCTCCCACATCTCAGGGGCCTCCCC TGGTCCACCAGCTCCTGAGTTAGGATGGGCTGTTATGATGTCACTCTGAAGGTTCCT GGATGGTTCCTACTGCCATATACTCATTTTATATTCAGCACATTAAACCATAGTGAA TGCTATGAAAAGCTGCTAATCAGCTGCCACTCCGAGATTCGGAGGTGGCAACGTCTG AGTGACAGGTCCAGTGATTCGCTTCTCCTTAGGATGCTTTTACAAGCTCTTTGGCGT CTCCTCCCACCTGGCAAATGCCAAATGCATAGGGGAGGGTGATCATCATTCTAGGGC AAACAAAATAGTTGAGGGATGCTGATTTCCCAAATCATCCGAATCACTTCTCCCTTG AGCAAACAAGCGCCCTGTTATTTCTCAAATGCTGCTTTGTGAATCAGTCCAGGGCAA GGCGCTCTCCTCATCCCGCTATGTGGCCTTAAGTCATCGTAAGGTTTGAAGTTTCTA CTTTCGATCCTGCATGGAGAGCTATAATCTCAGCTCCCCCGCCCCCCCCACACACAC CTCTGCACACACACCCCCCCCCAACACTGGGAGTAAACCAGGATGATGTCCGTCTTC TCATTCCCCATGTGACCGTTGGCAGTGTAGAGAGACTGATTGTCACAGCTAAAGGAA GAGGGACAACAGGGTCACTGGTGTCTACAGAGATTATATTCTACGTGTCTCACTGAA TTTACACAACTCCAAGTGCCAACCACATCAAGGTCAGGAAATCCTGAACTGGAATAA GAAAGACCCAGAAGATGAATGTGAACAGATCCATTTGCTTCCCGACAGTGGGCACAG ACTTCAGTCTCTGGCTACTGTTCCAAGACCCAGGGCTCTGCAATTGTGTGACATCCT TCAGTGAACCCACATGGGAAATTCTCCATGGAATTATCTTCAGCCCACTGTACTTCT GAATCCCTCTTCCTTCCTTCTGTGCCACACAGCAAGTCTGGCTTAAATGCTGCCTGA TCTCCATTTCAAGTTTTCTGCCTCTGGATTTTTAGATCTCAAGACCATGGACGAAAC ATCAGTTACAGCAACAAAAGTGAATTTTCCGTGCAGAGACTTCTAGGGGTTCTGTTT GTTTTCAGGGTGCTAGAGATCACACTCAGATGCTCATATATGTTAGGTAAATGTTCT CCCACTGAGTTACAGCCCAGCTCACACAGAGACTTCTAAAAGAAAATACGGCCATGC TCTTTGAAATGGAGCATTGAGGGATGAAGTTTGGATGGCGAAGAAAACTTCTCACCA GCTCTCTCCCCACATTCGTGCCAAGCACTGCCTCCCTAGACTTCGGGTCACCATATC TGTACTACGTTTTGATACAGAAGGCTCGAGACCATTCAAGAGAATTATTTAGTACAC (SEQ ID NO: 59) >NP_848709.2 V-set domain containing T-cell activation inhibitor 1 precursor [*Mus musculus*] MASLGQIIFWSIINIIIILAGAIALIIGFGISGKHFITVTTFTSAGNIGEDGTLSCT FEPDIKLNGIVIQWLKEGIKGLVHEFKEGKDDLSQQHEMFRGRTAVFADQVVVGNAS LRLKNVQLTDAGTYTCYIRTSKGKGNANLEYKTGAFSMPEINVDYNASSESLRCEAP RWFPQPTVAWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIE NDIAKATGDIKVTDSEVKRRSQLQLLNSGPSPCVFSSAFVAGWALLSLSCCLMLR (SEQ ID NO: 60)
Human B7-H5 (VISTA)	>NM_022153.2 *Homo sapiens* V-set immunoregulatory receptor (VSIR), mRNA AGTCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCCGGCACCAGAAG TTCCTCTGCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TGGCGCTGGGGATCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTG GCAGCCTTCAAGGTCGCCACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAAC GTCACCCTCACCTGCAGGCTCTTGGGCCCTGTGGACAAAGGGCACGATGTGACCTTC TACAAGACGTGGTACCGCAGCTCGAGGGGCGAGGTGCAGACCTGCTCAGAGCGCCGG CCCATCCGCAACCTCACGTTCCAGGACCTTCACCTGCACCATGGAGGCCACCAGGCT GCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGCTGGAGTCGGCCTCCGACCAC CATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTGGATAGCGGCCTCTAC TGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGTCCATGGTGCC ATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACTGTGTGGTGTACCCA TCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAG GCAGCCTCCAACCGCCGTGCCCAGGAGCTGGTGCGGATGGACAGCAACATTCAAGGG ATTGAAAACCCCGGCTTTGAAGCCTCACCACCTGCCCAGGGGATACCCGAGGCCAAA GTCAGGCACCCCCTGTCCTATGTGGCCCAGCGGCAGCCTTCTGAGTCTGGGCGGCAT CTGCTTTCGGAGCCCAGCACCCCCCTGTCTCCTCCAGGCCCCGGAGACGTCTTCTTC CCATCCCTGGACCCTGTCCCTGACTCTCCAAACTTTGAGGTCATCTAGCCCAGCTGG GGGACAGTGGGCTGTTGTGGCTGGGTCTGGGGCAGGTGCATTTGAGCCAGGGCTGGC TCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTCCCTCCCTCCTGCTCTGGGCTCA GATACTGTGACATCCCAGAAGCCCAGCCCCTCAACCCCTCTGGATGCTACATGGGGA TGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGCTGAGATTCTCCCCTAG AGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAAGTCTCAG AACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCAGC ATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACG GTGGAGAGACTTCTCCCCCGTGGCCGCCTTGGCTCCCCCGTTTTGCCCGAGGCTGCT CTTCTGTCAGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCC ACTGGCCATCGCCACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTG TCAACAGGTTAAGTCAATCTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTT GGTGGTCCCGAAACGGGAAGTACATATTGGGGCATGGTGGCCTCCGTGAGCAAATGG TGTCTTGGGCAATCTGAGGCCAGGACAGATGTTGCCCCACCCACTGGAGATGGTGCT GAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGAGTGGAGAGGGGCACCTGCCCCCCG CCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCCATTGCAAGGGTGCCACACA ATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGATGCTATTAAAAACTA CATGGGGAAACAGGTGCAAACCCTGGAGATGGATTGTAAGAGCCAGTTTAAATCTGC ACTCTGCTGCTCCTCCCCCACCCCCACCTTCCACTCCATACAATCTGGGCCTGGTGG AGTCTTCGCTTCAGAGCCATTCGGCCAGGTGCGGGTGATGTTCCCATCTCCTGCTTG TGGGCATGCCCTGGCTTTGTTTTTATACACATAGGCAAGGTGAGTCCTCTGTGGAAT TGTGATTGAAGGATTTTAAAGCAGGGGAGGAGAGTAGGGGGCATCTCTGTACACTCT GGGGGTAAAACAGGGAAGGCAGTGCCTGAGCATGGGGACAGGTGAGGTGGGGCTGGG CAGACCCCCTGTAGCGTTTAGCAGGATGGGGGCCCCAGGTACTGTGGAGAGCATAGT CCAGCCTGGGCATTTGTCTCCTAGCAGCCTACACTGGCTCTGCTGAGCTGGGCCTGG GTGCTGAAAGCCAGGATTTGGGGCTAGGCGGGAAGATGTTCGCCCAATTGCTTGGGG GGTTGGGGGGATGGAAAAGGGGAGCACCTCTAGGCTGCCTGGCAGCAGTGAGCCCTG GGCCTGTGGCTACAGCCAGGGAACCCCACCTGGACACATGGCCCTGCTTCTAAGCCC CCCAGTTAGGCCCAAAGGAATGGTCCACTGAGGGCCTCCTGCTCTGCCTGGGCTGGG CCAGGGGCTTTGAGGAGAGGGTAAACATAGGCCCGGAGATGGGGCTGACACCTCGAG TGGCCAGAATATGCCCAAACCCCGGCTTCTCCCTTGTCCCTAGGCAGAGGGGGGTCC CTTCTTTTGTTCCCTCTGGTCACCACAATGCTTGATGCCAGCTGCCATAGGAAGAGG GTGCTGGCTGGCCATGGTGGCACACACCTGTCCTCCCAGCACTTTGCAGGGCTGAGG TGGAAGGACCGCTTAAGCCCAGGTGTTCAAGGCTGCTGTGAGCTGTGTTCGAGCCAC TACACTCCAGCCTGGGGACGGAGCAAAACTTTGCCTCAAAACAAATTTTAAAAAGAA AGAAAGAAGGAAAGAGGGTATGTTTTTCACAATTCATGGGGGCCTGCATGGCAGGAG TGGGGACAGGACACCTGCTGTTCCTGGAGTCGAAGGACAAGCCCACAGCCCAGATTC CGGTTCTCCCAACTCAGGAAGAGCATGCCCTGCCCTCTGGGGAGGCTGGCCTGGCCC CAGCCCTCAGCTGCTGACCTTGAGGCAGAGACAACTTCTAAGAATTTGGCTGCCAGA CCCCAGGCCTGGCTGCTGCTGTGTGGAGAGGGAGGCGGCCCGCAGCAGAACAGCCAC CGCACTTCCTCCTCAGCTTCCTCTGGTGCGGCCCTGCCCTCTCTTCTCTGGACCCTT TTACAACTGAACGCATCTGGGCTTCGTGGTTTCCTGTTTTCAGCGAAATTTACTCTG AGCTCCCAGTTCCATCTTCATCCATGGCCACAGGCCCTGCCTACAACGCACTAGGGA CGTCCCTCCCTGCTGCTGCTGGGGAGGGGCAGGCTGCTGGAGCCGCCCTCTGAGTTG CCCGGGATGGTAGTGCCTCTGATGCCAGCCCTGGTGGCTGTGGGCTGGGGTGCATGG GAGAGCTGGGTGCGAGAACATGGCGCCTCCAGGGGGCGGGAGGAGCACTAGGGGCTG GGGCAGGAGGCTCCTGGAGCGCTGGATTCGTGGCACAGTCTGAGGCCCTGAGAGGGA AATCCATGCTTTTAAGAACTAATTCATTGTTAGGAGATCAATCAGGAATTAGGGGCC ATCTTACCTATCTCCTGACATTCACAGTTTAATAGAGACTTCCTGCCTTTATTCCCT CCCAGGGAGAGGCTGAAGGAATGGAATTGAAAGCACCATTTGGAGGGTTTTGCTGAC ACAGCGGGGACTGCTCAGCACTCCCTAAAAACACACCATGGAGGCCACTGGTGACTG CTGGTGGGCAGGCTGGCCCTGCCTGGGGGAGTCCGTGGCGATGGGCGCTGGGGTGGA GGTGCAGGAGCCCCAGGACCTGCTTTTCAAAAGACTTCTGCCTGACCAGAGCTCCCA CTACATGCAGTGGCCCAGGGCAGAGGGGCTGATACATGGCCTTTTTCAGGGGGTGCT CCTCGCGGGGTGGACTTGGGAGTGTGCAGTGGGACAGGGGGCTGCAGGGGTCCTGCC ACCACCGAGCACCAACTTGGCCCCTGGGGTCCTGCCTCATGAATGAGGCCTTCCCCA GGGCTGGCCTGACTGTGCTGGGGGCTGGGTTAACGTTTTCTCAGGGAACCACAATGC ACGAAAGAGGAACTGGGGTTGCTAACCAGGATGCTGGGAACAAAGGCCTCTTGAAGC CCAGCCACAGCCCAGCTGAGCATGAGGCCCAGCCCATAGACGGCACAGGCCACCTGG CCCATTCCCTGGGCATTCCCTGCTTTGCATTGCTGCTTCTCTTCACCCCATGGAGGC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TATGTCACCCTAACTATCCTGGAATGTGTTGAGAGGGATTCTGAATGATCAATATAG CTTGGTGAGACAGTGCCGAGATAGATAGCCATGTCTGCCTTGGGCACGGGAGAGGGA AGTGGCAGCATGCATGCTGTTTCTTGGCCTTTTCTGTTAGAATACTTGGTGCTTTCC AACACACTTTCACATGTGTTGTAACTTGTTTGATCCACCCCCTTCCCTGAAAATCCT GGGAGGTTTTATTGCTGCCATTTAACACAGAGGGCAATAGAGGTTCTGAAAGGTCTG TGTCTTGTCAAAACAAGTAAACGGTGGAACTACGACTAAA (SEQ ID NO: 61)
	>NP_071436.1 V-type immunoglobulin domain-containing suppressor of T-cell activation precursor [*Homo sapiens*] MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLL GPVDKGHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLA QRHGLESASDHHGNFSITMRNLTLLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTG KDAPSNCVVYPSSSQDSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRAQ ELVRMDSNIQGIENPGFEASPPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTP LSPPGPGDVFFPSLDPVPDSPNFEVI (SEQ ID NO: 62)
Mouse B7-H5 (VISTA)	>NM_028732.4 *Mus musculus* V-set immunoregulatory receptor (Vsir), transcript variant 1, mRNA GGGGGCGCTGCTGGGCGGGGAGCTTGCTCGGCCGCCTGCCTCGCCTTGGGCTCAGCA TTCACTCTAGCGAGCGAGCGGCGTGTACAGCCGGCTCCCTGGGCTCCTGGAGTCCCG CTTGCTCCAAGCGCACTCCAGCAGTCTCTTTCTGCTCTTGCCCGGCTCGACGGCGAC ATGGGTGTCCCCGCGGTCCCAGAGGCCAGCAGCCCGCGCTGGGGAACCCTGCTCCTT GCTATTTTCCTGGCTGCATCCAGAGGTCTGGTAGCAGCCTTCAAGGTCACCACTCCA TATTCTCTCTATGTGTGTCCCGAGGGACAGAATGCCACCCTCACCTGCAGGATTCTG GGCCCCGTGTCCAAAGGGCACGATGTGACCATCTACAAGACGTGGTACCTCAGCTCA CGAGGCGAGGTCCAGATGTGCAAAGAACACCGGCCCATACGCAACTTCACATTGCAG CACCTTCAGCACCACGGAAGCCACCTGAAAGCCAACGCCAGCCATGACCAGCCCCAG AAGCATGGGCTAGAGCTAGCTTCTGACCACCACGGTAACTTCTCTATCACCCTGCGC AATGTGACCCCAAGGGACAGCGGCCTCTACTGCTGTCTAGTGATAGAATTAAAAAAC CACCACCCAGAACAACGGTTCTACGGGTCCATGGAGCTACAGGTACAGGCAGGCAAA GGCTCGGGGTCCACATGCATGGCGTCTAATGAGCAGGACAGTGACAGCATCACGGCT GCGGCCCTGGCCACCGGCGCCTGCATCGTGGGAATCCTCTGCCTCCCCCTTATCCTG CTGCTGGTCTATAAGCAGAGACAGGTGGCCTCTCACCGCCGTGCCCAGGAGTTGGTG AGGATGGACAGCAGCAACACCCAAGGAATCGAAAACCCAGGCTTCGAGACCACTCCA CCCTTCCAGGGGATGCCTGAGGCCAAGACCAGGCCGCCACTGTCCTATGTGGCCCAG CGGCAACCTTCGGAGTCAGGACGGTACCTGCTCTCTGACCCCAGCACACCTCTGTCG CCTCCAGGCCCTGGGGACGTCTTTTTCCCATCCCTAGATCCAGTCCCTGACTCCCCT AACTCTGAAGCCATCTAAACCAGCTGGGGAACCATGAACCATGGTACCTGGGTCAGG GATATGTGCACTTGATCTATGGCTGGCCCTTGGACAGTCTTTTAGGCACTGACTCCA GCTTCCTTGCTCCTGCTCTGAGCCTAGACTCTGCTTTTACAAGATGCACAGACCCTC CCCTATCTCTTTCAGACGCTACTTGGGGGGCAGGGAGAAGATGTTGGATTGCTCATT GCTGTTCTCAAGATCTTGGGATGCTGAGTTCTCCCTAGAGACTTGACTTCGACAGCC ACAGATGTCAGATGACCTGCATCCTATGAACGTCCGGCTTGGCAAGAGCCTTTCTTC ATGGAAACCAGTAGCCCGGAGGGGATGAGGTAGGCACCTTGCCACCCTCCCGGGAGA GAGACACAAGATGTGAGAGACTCCTGCTCACTGTGGGGGTGTGGCTGGCCTGCTTGT TTGCCTGAGGATGCTCCTCTGTTGGACTGACTCTATCCCCCTGGATTCTGGAGCTTG GCTGGCCTATGTCCCACCAGAGGAGCATCTCAGCAGCCTTCCACCAGCAACCTGAGG GCCTGCCAGCTTCGTGGCTCTGGGCTCTCATTACCTGTATGGCCGTCCACAGAGCTC AGTGGCCAGAGGCTTTGAAACAGGAAGTACATGTCAGGTTCAGGAACCACTGTGAGC TCATTAGTGTCTTGAGCAATGTGAGGCCTGGACCAGTGGACACGGAGGGAGGGTGGC GAGAGGATGATGGGGATGATGAGGGGAACACGCTCCCTTCCTGTCCTTGTCATCCAC CACTACCACTATTCAGTGTGGAGCAGTGGCAAAGGTGACCGACCTCCACAATGTCCT AGTGATGCTGGACCATTTCTAAGTGTGAAAGAGATGCTATTAAAAACAGTATGTGGC AATGGCTGCCAACAGCTGAGTGGACTGGAGGCACTGGCTTTAAGGCCCTGGAGGTGC AGGGCCCGGTATGGGGATAGGGATGGGAGTTTCAGTGAGGGCCTAGGGATCACTCCG CTTCTGACCACTCTTCTTCTGAGCCTCACCTCAGGGTGACCTTCAGGCACACAGAAG AGCTTGCCCCTGGTCCGATACTACTCTTGGCTCTCATCTCCAGGGTTTGGCATGACC TGGGCACACAGGGGGAGTCTTCAGAAAGGATTTTAAAGCATGAAAAGAAAGGGTAGT TCTTGTGAGGTAGGGATGGGCAGCTGATGTTTGAGAGTGAGGAGGGATACGGCTGGG CAGATCACTCTCCAGTCTCTAGAGGGAAAGTAGCTCTAAGTCTGGGAGAGCAGCAGC CCAGTGGTACCATATGTCTTCTTGCAGCTTCCACTGGCTGGGCTGAACTGGGCATGG GTAGGAAAGCTCCTGTTOTGGGCCTGCAGCCAGGGAGAACCCCATTCATTCCCTGAG GACAGATGGGTGGGGAGAGAAGAGAGAGTTTCAGGCCGGGAAGCAGCAATAAGCTAT CTGCTGGGGACCCAGACAAGTTGTCTGATGAGGTCCAAGATGTGGGATGCCAGTTAT ACCTGGGGCTTGGGGATCCTTAGAGGCTTTGTATCATCATCATAGGAGTGTCGGGGT GGCCAGGGCATCAAAGCCATGACCCCTGTTTTATCCTCAGGGTCCACTCTTCTGCAC CATCCATTGCTCTAGATCTATGCAGTTACTATAGACAGAATGTGTTGTTCTGTTTGG CTTTGGGGATAATGGCCTGGCGAACTGCCAGCTGTTCAGTGGCAGGGCTGTGAGGCC AGTCAAAGACTAGAACCCACAGACCAGCTGAACGATGAGTATAGCCTGTCCCCTGGG GGAGCCTGACCTGTCTCCAGCCCTAAGCTTCAGACCTCACCACTCAGATGACTTCTA AGAATTTGCCTGTGGGGACCCCTGCATGGCTGCAGCTCCGTGGAAAGGAGAGGAGGC CCCCAGCAGAAGAACCACTCGCTTCCTGCCCAGCTTCCTCCTGTAGGGCTCTAAGTC TCTTCTTCTTGGGACCCTGCAAGCAAAGGCATGTCAGCTTGGTGGTTTCCTGTTTTG GGTGAAGTTTTGTGTGGTCCGGGTTCTGTCTACATCCATGAACTTGGGTGCTACCAC CTTGCTGCTGCTGTAGAGACAGCTGCAGGATCTTAGGGTGGAAAATGGAGGTGCCCT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GAGGTGCTAGCCCTTGGGGCAAAAGATGGGGTGGCAATGAGACACAGTGGGGAACTG AGTTCCCCAAGAGGAGGGAGGAGCCCTGTAGCCTCAAGGGCCATATTGGGTTCCTGG TACCAGCAAAAGCCTAGAGAGCGAAGTCTGTATTTTGAGGAGGTAATTGATCCTTAC GGAATCCATCAGAAATTTGGAGCGGGTGCTTTATCTATCTCTGGAGGGTCTCTACCT ATCTCCGATGAAGCTCTCCCTGGGCCTGGGATGGGAGAAACCAGGAGGAAAGGTGTC TGATAAAGCAGGGGCTTCTTGACAAGCCAAAGGGCCACTGGTAGCTGTTGTGGACCG AGCTGACCCTGCTGAAGTATTGTAGTGTGCCTTGGACCAACTTCTCAAAAGAGCAAC CCCGGGGCTACCCTACTTCTGCCAGGAAGAGGCGGAGAAGGGGCTGAGAGGCCTGGA AGGGGCTAGCTCCTTCTTTGAGAACTGCTCCCCGGAGGACTTGGAGGAGGCGGCTAG GCTACGGGCTGCTGAGGGCCCTTTGTCTTTCCTAACCTGGGCACTGTTAGGATGCTC CCTCCTGGAAAAGGCTTTCCTGGGTGTGAGCTAGAGCAGTGTCCATGCCAGCGCTGA ACCTGCCATGGTGGGAGCTGAACTAAAAATTTCTCAGGGAACTAAAATAGGCAAAAG AGGAACTGGGGGAGGAGGGTGCCAGGCAGGATGGGGGGAAGGGAGGGCAGTGCAAAA GTCTCTTGAAACACAGACAGCCCAGCTGAGTGCCAGTCCCAGATCACAGAGAATACG GCTCATCTGGCTCATGTTCTGCATGCTTGCTGCTTTACCCTGGCACTTTCCTTCTCC ACCATGAGTGCGAGTCCTGGGAGTCCTGGGAGGGTGAGGATTAATGCCAGCCTGGGG AGCAGATAGCTGACAGAGTCCTTGGGTAACTGGCTTGAACCAGGACCTCAGGATTCC ACTCTGGGGATCTAGCTTTGTCTGGGCCAGTGAAGATCTCTATAATGGCATTATTGC CAGGGGATAAACATTTCACTGGGTTCTGATCTGTTGGGTGTGGCTTCCTGGAAAATA TGGTGAGAGGAATTCTGCTAAGGATACAGTTGATAAGAAAGTTCTGAGATTGATTAG TAATGCCTGCCTTGGACTCAGGAAGGGAAGTGGCAGTATGAATGCCATGTCTTAATC ATTTTGGTTAAAATATGCTTCCCAAAAGATTTCCACGTGTGTTCTTGTTTATTTGAC ATCTGTCTCCATATCAGTCTTGAAAGCCTTTCTGTGTGTATATATATGATGTTTGCG TGTATATATGTTTTTGTGTGTGCATATGGAAGTCAGAAATCACTGGGTGTCTTCCTC CATTCCTTTGCAATGTATGTTTTTTTTTTTTTACGATTTATTTACTATATGAATGT TTTGCCTGAATACATGCATAGGTGTCACGTACATGCCTGCTGGAACGCTTGGAACTG GAGTTACAGGTGGCTATGAGCTACAGTGTGAGCACTGGGAATCAAACCTGGGTCTTC TGCAAGAGCAACAAATTAAAAGTCAGCTCTTAACTACTTGAGCTATTTTTCCAACTC C (SEQ ID NO: 63) >NP_083008.1 V-type immunoglobulin domain-containing suppressor of T-cell activation isoform 1 precursor [*Mus musculus*] MGVPAVPEASSPRWGTLLLAIFLAASRGLVAAFKVTTPYSLYVCPEGQNATLTCRIL GPVSKGHDVTIYKTWYLSSRGEVQMCKEHRPIRNFTLQHLQHHGSHLKANASHDQPQ KHGLELASDHHGNFSITLRNVTPRDSGLYCCLVIELKNHHPEQRFYGSMELQVQAGK GSGSTCMASNEQDSDSITAAALATGACIVGILCLPLILLLVYKQRQVASHRRAQELV RMDSSNTQGIENPGFETTPPFQGMPEAKTRPPLSYVAQRQPSESGRYLLSDPSTPLS PPGPGDVFFPSLDPVPDSPNSEAI (SEQ ID NO: 64)
Human B7-H7 (HHLA2)	>NM_007072.4 *Homo sapiens* HERV-H LTR-associating 2 (HHLA2), transcript variant 1, mRNA AGTTCTCTTCAAGTCATGTAATCGACTTTTTTGAATTAGTTTTCAGTTTCATTTTGT TTTCCCTAATTCAAGTTGGGAACACTTCATTTTCCCCAATTCAAGTTGGGAACACTT CCTTGGTATTTCCTTGCTACATGGACTTTAGCAAATGCTACTTTACTCTCCTTCCAG CTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTACAGT GAGCCTTTTCCTAGTTTTACTGTTGGAAGCCTAACTCACAGGAGAGATTATGCAATA CAGTCCTGAAGTCAAGGGAGGAGAGCATGTAGGAGAATACTAACCCTGCACAGATTG TGATGGTGATGTGGAATATACTAAAGCCTAGAACGCACCTCCTCTGCATGACTAATA TGTTCTGCACAAGACATGAAGGCACAGACAGCACTGTCTTTCTTCCTCATTCTCATA ACATCTCTGAGTGGATCTCAAGGCATATTCCCTTTGGCTTTCTTCATTTATGTTCCT ATGAATGAACAAATCGTCATTGGAAGACTTGATGAAGATATAATTCTCCCTTCTTCA TTTGAGAGGGGATCCGAAGTCGTAATACACTGGAAGTATCAAGATAGCTATAAGGTT CACAGTTACTACAAAGGCAGTGACCATTTGGAAAGCCAAGATCCCAGATATGCAAAC AGGACATCCCTTTTCTATAATGAGATTCAAAATGGGAATGCGTCGCTATTTTTCAGA AGAGTAAGCCTTCTGGACGAAGGAATTTACACCTGCTATGTAGGAACAGCAATTCAA GTGATTACAAACAAAGTGGTGCTAAAGGTGGGAGTTTTTCTCACACCCGTGATGAAG TATGAAAAGAGGAACACAAACAGCTTCTTAATATGCAGCGTGTTAAGTGTTTATCCT CGTCCAATTATCACGTGGAAAATGGACAACACACCTATCTCTGAAAACAACATGGAA GAAACAGGGTCTTTGGATTCTTTTTCTATTAACAGCCCACTGAATATTACAGGATCA AATTCATCTTATGAATGTACAATTGAAAATTCACTGCTGAAGCAAACATGGACAGGG CGCTGGACGATGAAAGATGGCCTTCATAAAATGCAAAGTGAACACGTTTCACTCTCA TGTCAACCTGTAAATGATTATTTTTCACCAAACCAAGACTTCAAAGTTACTTGGTCC AGAATGAAAAGTGGGACTTTCTCTGTCCTGGCTTACTATCTGAGCTCCTCACAAAAT ACAATTATCAATGAATCCCGATTCTCATGGAACAAAGAGCTGATAAACCAGAGTGAC TTCTCTATGAATTTGATGGATCTTAATCTTTCAGACAGTGGGGAATATTTATGCAAT ATTTCTTCGGATGAATATACTTTACTTACCATCCACACAGTGCATGTAGAACCGAGC CAAGAAACAGCTTCCCATAACAAAGGCTTATGGATTTTGGTGCCCTCTGCGATTTTG GCAGCTTTTCTGCTGATTTGGAGCGTAAAATGTTGCAGAGCCCAGCTAGAAGCCAGG AGGAGCAGACACCCTGCTGATGGAGCCCAACAAGAAAGATGTTGTGTCCCTCCTGGT GAGCGCTGTCCCAGTGCACCCGATAATGGCGAAGAAAATGTGCCTCTTTCAGGAAAA GTATAGGAAATGAGAGAAGACTGTGACAACTCATGACCTGCATCCTTAATATCCAGT GACTTCATCTCCCCTTTCTTCACCACAATTCCAGGCAATGGCCTGTCGGAGCAGACA ATTCTACCACTGCAAAGAGTTGTAACCATTTTCTGGTATCACATTTATTTTTCAAGA CATACTTTTCAAGACATCATTCACTGACCCACTACCTGCATTGAGTATAAATGCCTG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GATGTTAAGGATTCCAATTTAACTTTGAAAAGAACTGTCTCATTCATTTACATTTCT GTTACAGTCAGCCCAGGAGGTTACAGTGAGCTCTCCACTAAGAATCTGGAAGAAATG CATCACTAGGGGTTGATTCCCAATCTGATCAACTGATAATGGGTGAGAGAGCAGGTA AGAGCCAAAGTCACCTTAGTGGAAAGGTTAAAAACCAGAGCCTGGAAACCAAGATGA TTGATTTGACAAGGTATTTTAGTCTAGTTTTATATGAACGGTTGTATCAGGGTAACC AACTCGATTTGGGATGAATCTTAGGGCACCAAAGACTAAGACAGTATCTTTAAGATT GCTAGGGAAAAGGGCCCTATGTGTCAGGCCTCTGAGCCCAAGCCAAGCATCGCATCC CCTGTGATTTGCACGTATACATCCAGATGGCCTAAAGTAACTGAAGATCCACAAAAG AAGTAAAAATAGCCTTAACTGATGACATTCCACCATTGTGATTTGTTCCTGCCCCAC CCTAACTGATCAATGTACTTTGTAATCTCCCCCACCCTTAAGAAGGTACTTTGTAAT CTTCCCCACCCTTAAGAAGGTTCTTTGTAATTCTCCCCACCCTTGAGAATGTACTTT GTGAGATCCACCCTGCCCACAAAACATTGCTCTTAACTTCACCGCCTAACCCAAAAC CTATAAGAACTAATGATAATCCATCACCCTTCGCTGACTCTCTTTTCGGACTCAGCC CACCTGCACCCAGGTGAAATAAACAGCTTTATTGCTCACACAAA (SEQ ID NO: 65)
	>NP_009003.1 HERV-H LTR-associating protein 2 isoform a precursor [*Homo sapiens*] MKAQTALSFFLILITSLSGSQGIFPLAFFIYVPMNEQIVIGRLDEDIILPSSFERGS EVVIHWKYQDSYKVHSYYKGSDHLESQDPRYANRTSLFYNEIQNGNASLFFRRVSLL DEGIYTCYVGTAIQVITNKVVLKVGVFLTPVMKYEKRNTNSFLICSVLSVYPRPIIT WKMDNTPISENNMEETGSLDSFSINSPLNITGSNSSYECTIENSLLKQTWTGRWTMK DGLHKMQSEHVSLSCQPVNDYFSPNQDFKVTWSRMKSGTFSVLAYYLSSSQNTIINE SRFSWNKELINQSDFSMNLMDLNLSDSGEYLCNISSDEYTLLTIHTVHVEPSQETAS HNKGLWILVPSAILAAFLLIWSVKCCRAQLEARRSRHPADGAQQERCCVPPGERCPS APDNGEENVPLSGKV (SEQ ID NO: 66
Mouse BTNL1	>NM_001111094.1 *Mus musculus* butyrophilin-like 1 (Btnl1), mRNA ACCCTTAAATAAGAGCTGAAGATGGCTGCAGCTTTCTCCTAGACTCCTCCAGGAGAA ACTCTAAAGCCAGAGCCTGGGGGCAGCATTGTGTGTCCACCTTGCCACTGAGAACAT CTACGGAAATTGGACACTCTGGCCCCAGCATCCACACGCTTGACTGTTGGCCACAGT AACACAGGTGTGGATGGTCCCCAGAGCCAGGGTCCAGGAGTGCACTGAGGATCCCTG GGGCTTCAAGGAACCCACAGCTCTGTCCAGACGGGAATTTTTTTCCTGAGAACTTTC ACCTGTTGCCCTCCTATGGTGAACCTGGACTTGACCTTCCACTCTGATGATGAAGGG CTCCCCCTCCGTCCCTCCAGCTGGTTGTCTCCTCCCTCTGCTCCTCCTGCTGTTTAC CGGAGTCTCTGGAGAAGTGTCTTGGTTTTCTGTGAAGGGACCAGCTGAGCCCATCAC TGTCCTGCTGGGGACTGAAGCCACCCTGCCCTGCCAGCTGTCTCCTGAACAGAGTGC AGCTCGCATGCACATCCGATGGTACCGTGCCCAGCCCACCCCTGCTGTGCTGGTGTT CCACAACGGACAGGAGCAGGGAGAGGTGCAGATGCCGGAATACAGGGGCAGGACCCA GATGGTGAGACAAGCCATTGACATGGGAAGTGTGGCTCTGCAGATACAGCAGGTCCA GGCCTCTGATGATGGCCTGTACCACTGTCAGTTTACAGATGGCTTCACCTCCCAAGA GGTCTCCATGGAGCTTCGAGTCATAGGTTTAGGCTCTGCCCCTCTTGTTCACATGAC AGGACCTGAGAATGATGGGATCCGAGTGTTGTGCTCCTCAAGTGGCTGGTTCCCAAA ACCCAAAGTGCAATGGAGAGACACCTCCGGGAACATGCTACTGTCCTCCTCTGAGTT GCAGACCCAAGACAGAGAAGGGCTCTTCCAGGTGGAAGTGTCTCTTTTGGTCACAGA TAGAGCTATTGGCAATGTGATCTGCTCCATCCAAAATCCCATGTATGACCAGGAGAA ATCGAAGGCCATCCTCCTCCCAGAGCCCTTCTTCCCCAAGACGTGTCCATGGAAAGT AGCCCTGGTTTGTTCTGTCCTCATACTATTGGTCCTGCTCGGTGGGATCAGCCTTGG AATCTGGAAAGAACATCAAGTCAAAAGGAGAGAAATTAAAAAATGGTCAAAGGAACA TGAAGAAATGCTTCTGTTGAAGAAGGGGACAAAATCTGTACTGAAGATCAGAGATGA CCTCCAGGCCGACCTAGATCGGAGGAAGGCGCTGTACAAAGAAGACTGGAAGAAGGC CTTGCTGTACCCTGACTGGAGGAAGGAGCTGTTCCAGGAGGCTCCTGTGAGGATAAA TTATGAAATGCCTGACCAGGACAAGACAGACTCAAGGACAGAAGAGAACAGAGGTGA GGAGACTGTCAGCAGCTCACAAGTAGACCACAACCTCATCACACTCTCCCAGGAAGG CTTCATGTTGGGAAGATACTACTGGGAGGTGGATGTCAAGGACACAGAGGAGTGGAC ACTAGGAGTTTATGAGCTGTGCACTCAGGATGCATCACTTACAGACCCCTTGAGGAA ATTCAGAGTCCTGGAAAAGAATGGAGATGGATACAGGGCTCTTGACTTCTGTTCCCA AAACATTAATTCGGAAGAACCTCTGCAACTGAAGACACGTCCGCTGAAGATCGCCAT CTTCTTGGATCAGGAAGACAATGACCTCTCTTTCTACAACATGACCGATGAGACACA CATCTTTTCCTTTGCCCAGGTCCCTTTCTTGGGATCACCCTATCCTTACTTCACACG TAATTCCATGGGGCTCTCTGCAACAGCACAGCCCTAAGTGATGTGCACAGGGAATTC AATGGGTGGGTGCTGCAGCGTGCTACCCGTAAGGCCCTCTTAGGCAGGCACAGGGGG CCTCTGACCAAGAGGCCTCTTAACCTGAGACTCCATGAGCCTCGGGGATCAGATCCT GGACAAGATTCTCGGACCATCTGTGTCGTGCATGGTGTTATAGTTATTAATAGCCTT CCTTCTTTTGACAAAAATGTGTTTAATCATTCCTAAGATAAATGAATCCATGGCTTT CTGA (SEQ ID NO: 67)
	>NP_001104564.1 butyrophilin-like protein 1 precursor [*Mus musculus*] MMKGSPSVPPAGCLLPLLLLLFTGVSGEVSWFSVKGPAEPITVLLGTEATLPCQLSP EQSAARMHIRWYRAQPTPAVLVFHNGQEQGEVQMPEYRGRTQMVRQAIDMGSVALQI QQVQASDDGLYHCQFTDGFTSQEVSMELRVIGLGSAPLVHMTGPENDGIRVLCSSSG WFPKPKVQWRDTSGNMLLSSSELQTQDREGLFQVEVSLLVTDRAIGNVICSIQNPMY DQEKSKAILLPEPFFPKTCPWKVALVCSVLILLVLLGGISLGIWKEHQVKRREIKKW

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	SKEHEEMLLLKKGTKSVLKIRDDLQADLDRRKALYKEDWKKALLYPDWRKELFQEAP VRINYEMPDQDKTDSRTEENRGEETVSSSQVDHNLITLSQEGFMLGRYYWEVDVKDT EEWTLGVYELCTQDASLTDPLRKFRVLEKNGDGYRALDFCSQNINSEEPLQLKTRPL KIAIFLDQEDNDLSFYNMTDETHIFSFAQVPFLGSPYPYFTRNSMGLSATAQP (SEQ ID NO: 68)
Human VSIG8	>NM_001013661.1 *Homo sapiens* V-set and immunoglobulin domain containing 8 (VSIG8), mRNA ACTCATTGCACCTTCCTGCCACCCCAGGCAGTGTCTGGGCCCTCAGCTCCCCCTCCC TCCACCTACCCCCTCACACCCACCACTACGACCCCACGGGATACCCAGCCCAGACGG AGGAAACACCGAGCCTAGAGACATGAGAGTTGGAGGAGCATTCCACCTTCTACTCGT GTGCCTGAGCCCAGCACTGCTGTCTGCTGTGCGGATCAACGGGGATGGACAGGAGGT CCTGTACCTGGCAGAAGGTGATAATGTGAGGCTGGGCTGCCCCTACGTCCTGGACCC TGAGGACTATGGTCCCAATGGGCTGGACATCGAGTGGATGCAGGTCAACTCAGACCC CGCCCACCACCGAGAGAACGTGTTCCTTAGTTACCAGGACAAGAGGATCAACCATGG CAGCCTTCCCCATCTGCAGCAGAGGGTCCGCTTTGCAGCCTCAGACCCAAGCCAGTA CGATGCCTCCATCAACCTCATGAACCTGCAGGTATCTGATACAGCCACTTATGAGTG CCGGGTGAAGAAGACCACCATGGCCACCCGGAAGGTCATTGTCACTGTCCAAGCACG ACCTGCAGTGCCCATGTGCTGGACAGAGGGCCACATGACATATGGCAACGATGTGGT GCTGAAGTGCTATGCCAGTGGGGGCTCCCAGCCCCTCTCCTACAAGTGGGCCAAGAT CAGTGGGCACCATTACCCCTATCGAGCTGGGTCTTACACCTCCCAGCACAGCTACCA CTCAGAGCTGTCCTACCAGGAGTCCTTCCACAGCTCCATAAACCAAGGCCTGAACAA TGGGGACCTGGTGTTGAAGGATATCTCCAGAGCAGATGATGGGCTGTATCAGTGCAC AGTGGCCAACAACGTGGGCTACAGTGTTTGTGTGGTGGAGGTGAAGGTCTCAGACTC CCGGCGTATAGGCGTGATCATCGGCATCGTCCTGGGCTCTCTGCTCGCGCTGGGCTG CCTGGCCGTAGGCATCTGGGGGCTCGTCTGCTGCTGCTGCGGGGGCTCCGGGGCTGG CGGCGCCCGCGGTGCCTTCGGCTACGGCAACGGCGGCGGGGTCGGCGGAGGGGCCTG CGGCGACTTGGCTAGTGAGATCAGAGAGGACGCCGTGGCGCCCGGGTGCAAGGCCAG CGGGCGCGGCAGCCGCGTCACCCACCTCCTGGGGTACCCGACGCAGAACGTCAGCCG CTCCCTGCGCCGCAAGTACGCGCCTCCCCCCTGCGGCGGCCCCGAGGACGTGGCCCT GGCGCCCTGCACCGCCGCCGCCGCCTGCGAAGCGGGCCCCTCCCCGGTCTACGTCAA GGTCAAGAGCGCGGAGCCGGCTGACTGCGCCGAGGGGCCGGTGCAGTGCAAGAACGG CCTCTTGGTGTGAGCGCGCGCGCCGGGCCGGGCTGCGCCCCAGCCAGGAGGAGGGCG CGGGGCTCTCTGTCTGCAGCTGGGGACACGTCGGGGCTGGGGACGACCTCGCTCGCC CCAGGCTGCCAGGCGGCTGGGGGTGAAGGCATTTCCCTAAGGAAATGCGTAGGGAGG CAGAGCCTCCTCCCCAAAAGTGGGAAGGGGCGGGCGAGGGCGGAGGAAGGCGATCCT GAGCCTTCTCCGCACCCCCGGGACCGAAGGCTTGGGGGAGAGGGAGGGAGGAGGAGG CTGAGTGTCCTAGAGCGGCTGAGGCCGGAGGCCTGGTGTCCCCAGCCTAAGCAGAGG GCCCCGGGGGCCGGGTGGGTGGGGGTCTGTCTGGACGAATTGTTCTGTGTGTGAGGT CTGAGCTCTGAGGCAGCAGTGTTAGCACAATAAAGAAACATTGAGACGTGA (SEQ ID NO: 69) >NP_001013683.1 V-set and immunoglobulin domain-containing protein 8 precursor [*Homo sapiens*] MRVGGAFHLLLVCLSPALLSAVRINGDGQEVLYLAEGDNVRLGCPYVLDPEDYGPNG LDIEWMQVNSDPAHHRENVFLSYQDKRINHGSLPHLQQRVRFAASDPSQYDASINLM NLQVSDTATYECRVKKTTMATRKVIVTVQARPAVPMCWTEGHMTYGNDVVLKCYASG GSQPLSYKWAKISGHHYPYRAGSYTSQHSYHSELSYQESFHSSINQGLNNGDLVLKD ISRADDGLYQCTVANNVGYSVCVVEVKVSDSRRIGVIIGIVLGSLLALGCLAVGIWG LVCCCCGGSGAGGARGAFGYGNGGGVGGGACGDLASEIREDAVAPGCKASGRGSRVT HLLGYPTQNVSRSLRRKYAPPPCGGPEDVALAPCTAAAACEAGPSPVYVKVKSAEPA DCAEGPVQCKNGLLV (SEQ ID NO: 70)
Mouse VSIG8	>NM_177723.4 *Mus musculus* V-set and immunoglobulin domain containing 8 (Vsig8), transcript variant 1, mRNA ACTCATTGCATCTTCCTGCCACCCCGGGCAGTGTCTGGGCCCTCCGCTCCCCCTCCC TCCACCTGCCCCTTCCACCCACCACCACCAGCCCACTGGAGCCCAGCTCAGGCGGAG GAAAGACCAAGCCTAGAGACATGGGAGTTCGAGGAGCACTCCATCTTCTACTTGTGT GCCTGAGCCCAGCACTGTTGTCTGCTGTAAGGATCAACGGGGATGGCCAGGAGGTCA TGTACCTGGCAGAAGGTGACAATGTGAGGCTAGGCTGTCCCTACCTCCTGGATCCTG AGGATTTGGGTACCAACAGTCTGGACATTGAGTGGATGCAAGTCAACTCAGAGCCCT CACACAGGGAGAATGTTTTTCTTACTTATCAAGACAAGAGGATAGGTCATGGCAACC TCCCCCATCTGCAGCAGAGGGTCCGCTTTGCAGCCTCAGACCCCAGCCAGTACGATG CCTCCATCAACCTCATGAACCTGCAGGTATCTGACACAGCAACCTATGAGTGCCGGG TGAAGAAGACCACCATGGCCACCAGGAAGGTCATTGTCACTGTCCAAGCACGTCCTG CGGTGCCCATGTGTTGGACGGAAGGCCACATGTCAAAGGGCAACGATGTGGTGCTGA AGTGCTTTGCCAACGGAGGCTCTCAGCCCCTCTCCTACAAGTGGGCCAAGATCAGTG GGCACAGTCACCCCTACCGAGCTGGGGCTTACCACTCACAGCACAGCTTCCACTCTG AGCTTTCTTACCAAGAGTCATTCCACAGCACCATCAACCAAGGCCTGGGCAACGGAG ACCTGCTGTTGAAGGGCATCAACGCAGACGACGATGGGCTGTATCAGTGCACAGTGG CCAACCATGTGGGCTACAGCGTCTGTGTGGTAGAGGTGAAAGTCTCAGACTCCCAGC GAGTAGGCATGATCGTTGGAGCAGTGCTGGGCTCTTTGCTCATGCTGGCCTGCCTGG CACTAGGCATCTGGGGGCTCATCTGCTGCTGCTGCGGAGGCGGCGGGGCCGGTGGTG CCCGAGGTGCCTTCGGCTACGGGGTCGGCGGCGGGGTCGGCGGAGGGGCCTGCGGCG ACTTGGCTAGTGAGATCAGAGTGGACGCCGAGGCGCCCGGGTGTAAGGCCAGCGGGC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GCGGCAGCCGCGTCACCCACCTCCTGGGGTACCCGACGCAGAACGTCAGCCGCTCCC TGCGCCGCAAGTACGCGCCTCCGCCCTGCGGCGGCCCCGAGGACGTGGCCCTAGTGC CCCGCACCGCCTCCGCCTCCTGCGAAGCGGGTCCCTCCCCCGTCTACATCAAGGTCA AGAGCGCGGAGCCGGCCGACTGCGCCGACTGTGCCCAGGTCGAGCAGCGCTCGTGCA AGGACGGCCTCTTAGTGTGAGCGCACAGCACCGGGCTGCGCCCCGGCTGGGAGGTGG TTCGGGGGCTCTCTGCCCGCAGCTGGGGACAGGTTCGGGCCAGCAGACCTGGCTCTC TCATTGGCCACCTAGCGGTGGTAAGGAAATTTCCCTCTGAGAAGCCAAGCCGGGCAG ACCCTCCTCCCCTGTAGTGGGAGGAGAGGCGGGGGAGACAGAAAACAGTTCAGAGCT CTCCCTCACCCCTGGTTTCCAGGGAGAGGAAGGGAGAGGAGAGCTGTCGGTATCCCA GAACCGCAGAGGTACAACCCAGATGTCCCCAGCCAAGGCGAGGGCCCCCCAGCCCTG GGTAGGTGGATGTCAGGGCTGAATTGCTCTGTGTGTGAGATCTGAGCTCCAAGGCAA CAGTGTTAGCACAATAAAGAAACTTAAAGACTGAAAAAAAAAAAAAA (SEQ ID NO: 71) >NP_808391.2 V-set and immunoglobulin domain-containing protein 8 precursor [*Mus musculus*] MGVRGALHLLLVCLSPALLSAVRINGDGQEVMYLAEGDNVRLGCPYLLDPEDLGTNS LDIEWMQVNSEPSHRENVFLTYQDKRIGHGNLPHLQQRVRFAASDPSQYDASINLMN LQVSDTATYECRVKKTTMATRKVIVTVQARPAVPMCWTEGHMSKGNDVVLKCFANGG SQPLSYKWAKISGHSHPYRAGAYHSQHSFHSELSYQESFHSTINQGLGNGDLLLKGI NADDDGLYQCTVANHVGYSVCVVEVKVSDSQRVGMIVGAVLGSLLMLACLALGIWGL ICCCCGGGGAGGARGAFGYGVGGGVGGGACGDLASEIRVDAEAPGCKASGRGSRVTH LLGYPTQNVSRSLRRKYAPPPCGGPEDVALVPRTASASCEAGPSPVYIKVKSAEPAD CADCAQVEQRSCKDGLLV (SEQ ID NO: 72)
Human VSIG3 (ISF11)	>NM_001015887.3 *Homo sapiens* immunoglobulin superfamily member 11 (IGSF11), transcript variant 2, mRNA AGTCCTGGGGCAGGGCTGGGTGGCACGGCTGGCGAGCCCGGAACGCCTCTGGTCACA GCTCAGCGTCCGCGGAGCCGGGCGGCGCTGCAGCTGCACTTGGCTCGTCTGTGGGTC TGACAGTCCCAGCTCTGCGCGGGGAACAGCGGCCCGGCGCTGGGTGTGGGAGGACCA GGCTGCCCCAAGAGCGCGGAGACTCACGCCCGCTCCTCTCCTGTTGCGACCGGGAGC CGGGTAGGAGGCAGGCGCGCTCCCTGCGGCCCCGGGATGACTTCTCAGCGTTCCCCT CTGGCGCCTTTGCTGCTCCTCTCTCTGCACGGTGTTGCAGCATCCCTGGAAGTGTCA GAGAGCCCTGGGAGTATCCAGGTGGCCCGGGGTCAGCCAGCAGTCCTGCCCTGCACT TTCACTACCAGCGCTGCCCTCATTAACCTCAATGTCATTTGGATGGTCACTCCTCTC TCCAATGCCAACCAACCTGAACAGGTCATCCTGTATCAGGGTGGACAGATGTTTGAT GGTGCCCCCCGGTTCCACGGTAGGGTAGGATTTACAGGCACCATGCCAGCTACCAAT GTCTCTATCTTCATTAATAACACTCAGTTATCAGACACTGGCACCTACCAGTGCCTG GTCAACAACCTTCCAGACATAGGGGGCAGGAACATTGGGGTCACCGGTCTCACAGTG TTAGTTCCCCCTTCTGCCCCACACTGCCAAATCCAAGGATCCCAGGATATTGGCAGC GATGTCATCCTGCTCTGTAGCTCAGAGGAAGGCATTCCTCGACCAACTTACCTTTGG GAGAAGTTAGACAATACCCTCAAACTACCTCCAACAGCTACTCAGGACCAGGTCCAG GGAACAGTCACCATCCGGAACATCAGTGCCCTGTCTTCAGGTTTGTACCAGTGCGTG GCTTCTAATGCTATTGGAACCAGCACCTGTCTTCTGGATCTCCAGGTTATTTCACCC CAGCCCAGGAACATTGGACTAATAGCTGGAGCCATTGGCACTGGTGCAGTTATTATC ATTTTTTGCATTGCACTAATTTTAGGGGCATTCTTTTACTGGAGAAGCAAAAATAAA GAGGAGGAAGAAGAAGAAATTCCTAATGAAATAAGAGAGGATGATCTTCCACCCAAG TGTTCTTCTGCCAAAGCATTTCACACTGAGATTTCCTCCTCGGACAACAACACACTA ACCTCTTCCAATGCCTACAACAGTCGATACTGGAGCAACAATCCAAAAGTTCATAGA AACACAGAGTCAGTCAGCCACTTCAGTGACTTGGGCCAATCTTTCTCTTTCCACTCA GGCAATGCCAACATACCATCCATTTATGCTAATGGGACCCATCTGGTCCCGGGTCAA CATAAGACTCTGGTAGTGACAGCCAACAGAGGGTCATCACCACAGGTGATGTCCAGG AGCAATGGCTCAGTCAGTAGGAAGCCTCGGCCTCCACACACTCATTCCTACACCATC AGCCACGCAACACTGGAACGAATTGGTGCAGTACCTGTCATGGTACCAGCCCAGAGT CGGGCCGGGTCCTTGGTATAGGACATGAGGAAATGTTGTGTTCAGAAATGAATAAAT GGAATGCCCTCATACAAGGGGGAGGGTGGGGTGGGGAGTGCTGGGAAAGAAACACTT CCTTATAATTATATTAGTAAAATGCACAAAGAAGAAGGCAGTGCTGTTACTTGGCCA CTAAGATGTGTAAAATGGACTGAAATGCTCCATCATGAAGACTTGCTTCCCCACCAA AGATGTCCTGGGATTCTGCTGGATCTCAAAGATGTGCCAAGCCAAGGAAAAAGATAC AAGAGCAGAATAGTACTTAAAATCCAAACTGCCGCCCAGATGGGCTTGTTCTTCATG CCTAACTTAATAATTTTTAAGAGATTAAAGTGCCAGATGGAGTTTAAATATTGAAAT TATTTTAAAAGGTAGGTGTCTTTAAGAAAATAACAAGCAACCCTGTGATATGTTCCG TCTCTCCCAATTCCCTCGTTATATAGAGGGCTTAATGGTATAAATGGTTAATATTGG TCCCAACAGGGCTGACTCTTCTATCATATAATCAAAACTTTTTACATGAGCAAAATT CAGTAAGAAATGGGGGAAGACAAAGGAAACGTCTTTGAGAAGCCCCTTCATATTTAT TTATTTATCTCTTCCTGAACCATGAATTTCATATGTGGAATATTGCTATATTGACAG ATTCTTGCCTGTCTGTGTTATTCTAGGATCTGTTACAGGTCCATGGCAATTACTGTT TATTTTTTCCTGGAAAAATATTTTTTTATAAAAGGCTTTTTTTTTTTTTTAAATACA TGAGAGGCATTGGGCTAAGAAAGAAAAGACTGTTGTATAATACCTTGTTCAATGGTT GTATTTAGTGAGCTCATAGAGGTCCATCATATCATGACCGAGCTAGGTTGTGTGGGC AGGAAGGTAGGGCTAAGGGGTTGTAGCCTTGCTGGGCAGCCTCTCAGAGCAAGGTTG TTCAGATCTCCCTTGCTATTACAGTAGGTTACTATTAATGAGGGCAGCACCTGATGC CTTTTGTACTGAGGTATGTAACTTTCTCCTTATTTGACAAGTAGAAGTTAACTTACT TGTCAGGGAGGGCAGACGTTTTTTTGTTCTGTTTCGTTTTTCAAAATAATGCTTTTT GCAAAAGAGGTAAGACTGAGACTAAAGGTGTTATCTTCTGGTGTGCTCCTGGAAGTG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TCTACCCTACATTTGTGTCAGCTCAGGGTTGCAGTGTTGCCCAGATGCATTTTACAT CACTGTAAAGAGATTACTTTTGTGGTTACTACCTGGCTTGGCTGGCCTTGCGGTTCA CCAGATTAATTTACAAACTCCCCCACTTTATTTTGTGCTATGTAGATCTGGCCATAC TTGCATTAGTGACTGTCTTGCCTTAACCACACTTAAGCAACCCACAAATTTCTTCTC AGATTTGTTTCCTAGATTACTTATGATACTCATCCCATGTCTCAATAAGAGTGTCTT TTCTTTCTGGATGTGTTCTCTTACTCCCTCTTACCACCATACTTTTTGCTCTCTTCT CCTGCAAGCGTAGTCTTCACAGGGAGTGGCTTCCTGACATTTTTTTCAGTTATGTGA ATGAATGGAAACCAACAGCTGCTGCAAACACTGTTTTTCCAAGAAGGCTACACTCAG AACCTAACCATTGCCAACCATTTCAGTATTGATAAAAAGCTGAATTTACTTTAGCAT TACTTATTTTTTTTTCCATTTGATGGTTCTTACTTTGTAAAAATTTAAATAAATGAA TGTCTATACTTTTTATAAAGAAAAGTGAAAATACCATGACACTGAAAAGATGATGCT ATCAGATGCTGTTTAGAAAGCATTTATCTTGCATTTCTTTATTCTTTCTAATTATCT AAAATTCAATAAAATTTTATTCATATAAAATAAGTTGTCATTAATTATCAATACTAA CGAGTATGTCATTTTAAAACTTAGTATTCTCTTTAATGTTACAAGA (SEQ ID NO: 73)
	>NP_001015887.1 immunoglobulin superfamily member 11 isoform b precursor [*Homo sapiens*] MTSQRSPLAPLLLLSLHGVAASLEVSESPGSIQVARGQPAVLPCTFTTSAALINLNV IWMVTPLSNANQPEQVILYQGGQMFDGAPRFHGRVGFTGTMPATNVSIFINNTQLSD TGTYQCLVNNLPDIGGRNIGVTGLTVLVPPSAPHCQIQGSQDIGSDVILLCSSEEGI PRPTYLWEKLDNTLKLPPTATQDQVQGTVTIRNISALSSGLYQCVASNAIGTSTCLL DLQVISPQPRNIGLIAGAIGTGAVIIIFCIALILGAFFYWRSKNKEEEEEEIPNEIR EDDLPPKCSSAKAFHTEISSSDNNTLTSSNAYNSRYWSNNPKVHRNTESVSHFSDLG QSFSFHSGNANIPSIYANGTHLVPGQHKTLVVTANRGSSPQVMSRSNGSVSRKPRPP HTHSYTISHATLERIGAVPVMVPAQSRAGSLV (SEQ ID NO: 74)
Mouse VSIG3 (IGSF11)	>NM_170599.2 *Mus musculus* immunoglobulin superfamily, member 11 (Igsf11), mRNA CGGCTGGTGGTGGCCGCGGCGGCCGGCGAGCCCGGGACGCCCGAGCCTGCCCCGAGC CTCGGCGGAGCGGAGTGGCCTCGGCGCTCCCGTGTCCCGCTTGGTCCCACGCTGCAC CCCGCCGCCCAGGAGCCCGGCGGACGGCGGCTCCCCCGGCGGCTCCGGCATGACTCG GCGGCGCTCCGCTCCGGCGTCCTGGCTGCTCGTGTCGCTGCTCGGTGTCGCAACATC CCTGGAAGTGTCCGAGAGCCCAGGCAGTGTCCAGGTGGCCCGGGGCCAGACAGCAGT CCTGCCCTGCGCCTTCTCCACCAGTGCTGCCCTCCTGAACCTCAATGTCATTTGGAT GGTCATTCCCCTCTCCAATGCAAACCAGCCCGAACAGGTCATTCTTTATCAGGGTGG ACAAATGTTTGACGGCGCCCTCCGGTTCCACGGGAGGGTAGGATTTACCGGCACCAT GCCTGCTACCAATGTCTCGATCTTCATCAATAACACACAGCTGTCAGATACGGGCAC GTACCAGTGCTTGGTGAATAACCTTCCAGACAGAGGGGGCAGAAACATCGGGGTCAC TGGCCTCACAGTGTTAGTCCCCCCTTCTGCTCCACAATGCCAAATCCAAGGATCCCA GGACCTCGGCAGTGACGTCATCCTTCTGTGTAGTTCAGAGGAAGGCATCCCTCGGCC CACGTACCTTTGGGAGAAGTTAGATAATACGCTCAAGCTACCTCCAACAGCCACTCA GGACCAGGTCCAGGGAACAGTCACCATCCGGAATATCAGTGCCCTCTCTTCCGGTCT GTACCAGTGTGTGGCTTCTAATGCCATCGGGACCAGCACCTGTCTGCTGGACCTCCA GGTTATCTCACCCCAGCCCCGGAGCGTTGGAGTAATAGCCGGAGCGGTTGGCACCGG TGCTGTTCTTATCGTCATCTGCCTTGCACTAATTTCAGGGGCGTTCTTTTACTGGAG AAGCAAAAACAAAGAGGAGGAGGAGGAAGAAATTCCTAATGAAATCAGAGAGGATGA TCTTCCCCCTAAATGCTCTTCTGCCAAAGCCTTCCACACGGAGATATCCTCCTCAGA AAATAACACGCTGACCTCTTCCAATACCTACAACAGTCGATACTGGAACAACAATCC AAAACCCCATAGAAACACAGAGTCTTTCAACCACTTCAGTGACTTACGCCAGTCTTT CTCTGGCAATGCAGTTATCCCATCAATCTATGCAAATGGGAACCATCTGGTTTTGGG TCCACATAAGACTCTGGTAGTTACAGCCAACAGAGGGTCATCACCTCAGGTCTTGCC CAGGAACAATGGTTCAGTCAGCAGGAAGCCTTGGCCTCAACACACTCATTCCTACAC AGTAAGCCAAATGACCCTGGAGCGCATCGGTGCAGTGCCTGTCATGGTGCCTGCCCA GAGTCGAGCAGGGTCCCTGGTATAGGATGACTGAGGAAACCATGTTCAGAAGAGAAT AAATGGACCGCCTTCAGGCAAGGGGGGAGCACTGCCTTCAGGCAAGGGGGGAGCACT GCCTTCAGGCAAGAGGGAGAGTGGGATGGGTGAGTGCTGAAAAATAAACTTTTGTTA CGATTCCATTAGCAAAAAGCACAAAGAGGAGGCGTGTGTGAAGTGGCCTGGGGTTGT TCCATAATGAAGACTCAAGAAGACTGTTTCCCCACCACAGATGTCCTGAGATTCAGT TAAAACGAAACATGCTGCATCTCCAGAGATGTGCCAAGCCAAGGAGAATGCTAGAAG CAGAGTAAAGCTTACCCCCCAAACTGTGGTCCAGCTGGACCCCTTCTTTAATTCTTG CCTAACTTAATTATTTTCAGGACCCTTCAAGTGCCAGGTGGAATTTACATAATGAAA TTATTTTTTAAAAATAGGTGTCCTTAGGGAGAGAAAACAGGAGCAAGCTCATGGTCT GGCCTAGTCTCCCTCTCCCACTCCTTCTGATGACACTAGCAATGCATTCCATCTGAC CTGACTTTATCATAGAGGCAAAATTGTTCAGAACACTGGCTGGAGATGGGGAGAAAT AAGGAAACTTCTTGTGAACACCCTACACACACACACACACACACACACACACACACA CACACACACACACACACACACACACACACATTTATTTACCTCCTCCTGAACCATGAA TCGTATTGGTGATTTTGCTATATTGACAGATTCTCATCTGTTACACTCTAGGATCTC TCACAGGTCTGTGGCAATTACTGTTCATGATTTCCTGAAAAAATATTTTTTTAAAAG AAAACTATTTTTTTTAAATACTAGAGAGACAGTGGACTAGGAAAGCGAGAACTTGCC GCCTTGTCTAGTGACTGTATTCAATGACTGAACAGAGGCCCCCCCCACCATACAAGA GTTTTAGGTGATTGAGTGGGTGGAACCAGCTGGAGCCAGGTGGGAGGGGCCTTTACA TTGCCAGCAGGGCCCCAAAGAATTGAGATTGTGTATGGCAACCGTTAATGAGGACAG CGCCTGATGCCTTTTGTACCGAGGAAGATAATTGCCTCTTGTTTGACAAGTAGAGTT TAGTAGGTTATTACAAAAAGGGCAAGAGTTGTTTTGGTTTTGTTTCTTTCAAAATAA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TTTTTTTTCAAAAGAATAACAAGGGTTAGGCAAATGGGGGACCTTCCTGTGTGCTCT TGGGGGTCTGCTCAGCATCTGGAAATTTGGGTGTGCGATTTTCCCTGAACACATTGC ATACCAGTGTAAAAAGACTCTGCCTCCCCCCTTTTTGGCTTTTTTACTGGGCTTGGC TGGCCTTGCAGTTTACCAGATTCATTTACAGACTCTCTGCTCTGTATGGCGCCGCCT GCCATGTCTGTCTTGGTGACTATCCTGCCTTAATCACTTTGCTTTAGGGCAACTCAT GGTGATCTCTTCCAAGATCTGTTTTTAAATTGTTTGGACTACTTGAGCCACAACTCT CAGAGGACATTCCTTTTTTTTTTTTTTTTTTTTTCTCCTTTCTTCCATTGCTTTGTC CCTCTTCCCCTGTGCTTCCTGCCTTCTTTCCCTGTCCCATGGGCACAGTCCTCACAG GGAGTGGCCTCCTCTCTCCAGTGATGTAAGTGAATGGAAGCCATCACTGGCTGCACA TACCTTTTTCAAAAGGGACACTCGGGAAGTCACTGCTGTGACCGTTTCGATGTTGAT AAGAAGGTGAATTTACTGTAGTGTTACCACCTTCTCCCCACTTGATGGTTCTTGACT TTGTAAAAATTTAAATAAATGAATGTCTATACTTTTTAAGGAAAAGAGAAAATACCA TGTCACAGAAAAGGTGAAACTATTAGATGCTGTTTAGAAAGCATTTATCTTGCATTT CTTTATTCTTTCTAATTACCTAAAATTCAATAAAAGTTTATTCATATAAAAAAAAAA AAAAAAAAAA (SEQ ID NO: 75) >NP_733548.2 immunoglobulin superfamily member 11 precursor [*Mus musculus*] MTRRRSAPASWLLVSLLGVATSLEVSESPGSVQVARGQTAVLPCAFSTSAALLNLNV IWMVIPLSNANQPEQVILYQGGQMFDGALRFHGRVGFTGTMPATNVSIFINNTQLSD TGTYQCLVNNLPDRGGRNIGVTGLTVLVPPSAPQCQIQGSQDLGSDVILLCSSEEGI PRPTYLWEKLDNTLKLPPTATQDQVQGTVTIRNISALSSGLYQCVASNAIGTSTCLL DLQVISPQPRSVGVIAGAVGTGAVLIVICLALISGAFFYWRSKNKEEEEEEIPNEIR EDDLPPKCSSAKAFHTEISSSENNTLTSSNTYNSRYWNNNPKPHRNTESFNHFSDLR QSFSGNAVIPSIYANGNHLVLGPHKTLVVTANRGSSPQVLPRNNGSVSRKPWPQHTH SYTVSQMTLERIGAVPVMVPAQSRAGSLV (SEQ ID NO: 76)
Human VSIG4	>NM_007268.3 *Homo sapiens* V-set and immunoglobulin domain containing 4 (VSIG4), transcript variant 1, mRNA ACAGACGCTGGCGGCCACCAGAAGTTTGAGCCTCTTTGGTAGCAGGAGGCTGGAAGA AAGGACAGAAGTAGCTCTGGCTGTGATGGGGATCTTACTGGGCCTGCTACTCCTGGG GCACCTAACAGTGGACACTTATGGCCGTCCCATCCTGGAAGTGCCAGAGAGTGTAAC AGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCACCTATGACCCCCTGCAAGGCTA CACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCTGTCACCATCTT TCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCGCCTGCA TGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCTGGAGATGGA TGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGT CGTGAGAGATAAGATTACTGAGCTCCGTGTCCAGAAACTCTCTGTCTCCAAGCCCAC AGTGACAACTGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCT TCAATGCCAGGCTCGGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGAC TAATAACCAGGAACCCATCAAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGC GGTGATAGCCGACTCAGGCTCCTATTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGA GCAGCACAGCGACATTGTGAAGTTTGTGGTCAAAGACTCCTCAAAGCTACTCAAGAC CAAGACTGAGGCACCTACAACCATGACATACCCCTTGAAAGCAACATCTACAGTGAA GCAGTCCTGGGACTGGACCACTGACATGGATGGCTACCTTGGAGAGACCAGTGCTGG GCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCTCCTTGTGCTGTAT GGTGGTTTTTACCATGGCCTATATCATGCTCTGTCGGAAGACATCCCAACAAGAGCA TGTCTACGAAGCAGCCAGGGCACATGCCAGAGAGGCCAACGACTCTGGAGAAACCAT GAGGGTGGCCATCTTCGCAAGTGGCTGCTCCAGTGATGAGCCAACTTCCCAGAATCT GGGCAACAACTACTCTGATGAGCCCTGCATAGGACAGGAGTACCAGATCATCGCCCA GATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCCTCTGGATTATGAGTTTCT GGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCCATTAGGCCAGGATCTGCTGA CATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCTACCTCTCT TCCTGGATAGCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACTGGC TTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCT GGGCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGG GAAGATGCCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTT GGCATCTTGCCACCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCA GCTATATCCAGGATCATTTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTG TTATTTCACAGGCCAGGGTTCAGTTCTGCTCCTCCACTATAAGTCTAATGTTCTGAC TCTCTCCTGGTGCTCAATAAATATCTAATCATAACAGCAA (SEQ ID NO: 77) >NP_009199.1 V-set and immunoglobulin domain-containing protein 4 isoform 1 precursor [*Homo sapiens*] MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWL VQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCE VTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSP PISYIWYKQQTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKF VVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVF AIILIISLCCMVVFTMAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASG CSSDEPTSQNLGNNYSDEPCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC (SEQ ID NO: 78)

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
Mouse VSIG4	>NM_177789.5 *Mus musculus* V-set and immunoglobulin domain containing 4 (Vsig4), mRNA AGCTACCAGCACTTCCAGGTTCTTCAGCAGCAAGAGGATGGAAGGATGAATAGAAGT AGCTTCAAATAGGATGGAGATCTCATCAGGCTTGCTGTTCCTGGGCCACCTAATAGT GCTCACCTATGGCCACCCCACCCTAAAAACACCTGAGAGTGTGACAGGGACCTGGAA AGGAGATGTGAAGATTCAGTGCATCTATGATCCCCTGAGAGGCTACAGGCAAGTTTT GGTGAAATGGCTGGTAAGACACGGCTCTGACTCCGTCACCATCTTCCTACGTGACTC CACTGGAGACCATATCCAGCAGGCAAAGTACAGAGGCCGCCTGAAAGTGAGCCACAA AGTTCCAGGAGATGTGTCCCTCCAAATAAATACCCTGCAGATGGATGACAGGAATCA CTATACATGTGAGGTCACCTGGCAGACTCCTGATGGAAACCAAGTAATAAGAGATAA GATCATTGAGCTCCGTGTTCGGAAATATAATCCACCTAGAATCAATACTGAAGCACC TACAACCCTGCACTCCTCTTTGGAAGCAACAACTATAATGAGTTCAACCTCTGACTT GACCACTAATGGGACTGGAAAACTTGAGGAGACCATTGCTGGTTCAGGGAGGAACCT GCCAATCTTTGCCATAATCTTCATCATCTCCCTTTGCTGCATAGTAGCTGTCACCAT ACCTTATATCTTGTTCCGCTGCAGGACATTCCAACAAGAGTATGTCTATGGAGTGAG CAGGGTGTTTGCCAGGAAGACAAGCAACTCTGAAGAAACCACAAGGGTGACTACCAT CGCAACTGATGAACCAGATTCCCAGGCTCTGATTAGTGACTACTCTGATGATCCTTG CCTCAGCCAGGAGTACCAAATAACCATCAGATCAACAATGTCTATTCCTGCCTGCTG AACACAGTTTCCAGAAACTAAGAAGTTCTTGCTACTGAAGAAAATAACATCTGCTAA AATGCCCCTACTAAGTCAAGGTCTACTGGCGTAATTACCTGTTACTTATTTACTACT TGCCTTCAACATAGCTTTCTCCCTGGCTTCCTTTCTTCTTAGACAACCTAAAGTATC TATCTAGTCTGCCAATTCTGGGGCCATTGAGAAATCCTGGGTTTGGCTAAGAATATA CTACATGCACCTCAAGAAATCTAGCTTCTGGGCTTCACCCAGAACAATTTTCTTCCT AGGGCCTTCACAACTCTTCTCCAAACAGCAGAGAAATTCCATAGCAGTAGAGGTTCT TTATCATGCCTCCAGACAGCGTGAGTCTCAGTCCTACAAACTCAGACAAGCACATGG GTCTAGGATTACTCCTCTTTCTCTAGGGCCAGATGACTTTTAATTGATATTACTATT GCTACATTATGAATCTAATGCACATGTATTCTTTTGTTGTTAATAAATGTTTAATCA TGACATCAA(SEQ ID NO: 79) >NP_808457.1 V-set and immunoglobulin domain-containing protein 4 precursor [*Mus musculus*] MEISSGLLFLGHLIVLTYGHPTLKTPESVTGTWKGDVKIQCIYDPLRGYRQVLVKWL VRHGSDSVTIFLRDSTGDHIQQAKYRGRLKVSHKVPGDVSLQINTLQMDDRNHYTCE VTWQTPDGNQVIRDKIIELRVRKYNPPRINTEAPTTLHSSLEATTIMSSTSDLTTNG TGKLEETIAGSGRNLPIFAIIFIISLCCIVAVTIPYILFRCRTFQQEYVYGVSRVFA RKTSNSEETTRVTTIATDEPDSQALISDYSDDPCLSQEYQITIRSTMSIPAC (SEQ ID NO: 80)
Human Tim-3 (HAVCR2)	>NM_032782.5 *Homo sapiens* hepatitis A virus cellular receptor 2 (HAVCR2), mRNA ATTTGGAGAGTTAAAACTGTGCCTAACAGAGGTGTCCTCTGACTTTTCTTCTGCAAG CTCCATGTTTTCACATCTTCCCTTTGACTGTGTCCTGCTGCTGCTGCTGCTACTACT TACAAGGTCCTCAGAAGTGGAATACAGAGCGGAGGTCGGTCAGAATGCCTATCTGCC CTGCTTCTACACCCCAGCCGCCCCAGGGAACCTCGTGCCCGTCTGCTGGGGCAAAGG AGCCTGTCCTGTGTTTGAATGTGGCAACGTGGTGCTCAGGACTGATGAAAGGGATGT GAATTATTGGACATCCAGATACTGGCTAAATGGGGATTTCCGCAAAGGAGATGTGTC CCTGACCATAGAGAATGTGACTCTAGCAGACAGTGGGATCTACTGCTGCCGGATCCA AATCCCAGGCATAATGAATGATGAAAAATTTAACCTGAAGTTGGTCATCAAACCAGC CAAGGTCACCCCTGCACCGACTCGGCAGAGAGACTTCACTGCAGCCTTTCCAAGGAT GCTTACCACCAGGGGACATGGCCCAGCAGAGACACAGACACTGGGGAGCCTCCCTGA TATAAATCTAACACAAATATCCACATTGGCCAATGAGTTACGGGACTCTAGATTGGC CAATGACTTACGGGACTCTGGAGCAACCATCAGAATAGGCATCTACATCGGAGCAGG GATCTGTGCTGGGCTGGCTCTGGCTCTTATCTTCGGCGCTTTAATTTTCAAATGGTA TTCTCATAGCAAAGAGAAGATACAGAATTTAAGCCTCATCTCTTTGGCCAACCTCCC TCCCTCAGGATTGGCAAATGCAGTAGCAGAGGGAATTCGCTCAGAAGAAAACATCTA TACCATTGAAGAGAACGTATATGAAGTGGAGGAGCCCAATGAGTATTATTGCTATGT CAGCAGCAGGCAGCAACCCTCACAACCTTTGGGTTGTCGCTTTGCAATGCCATAGAT CCAACCACCTTATTTTTGAGCTTGGTGTTTTGTCTTTTTCAGAAACTATGAGCTGTG TCACCTGACTGGTTTTGGAGGTTCTGTCCACTGCTATGGAGCAGAGTTTTCCCATTT TCAGAAGATAATGACTCACATGGGAATTGAACTGGGACCTGCACTGAACTTAAACAG GCATGTCATTGCCTCTGTATTTAAGCCAACAGAGTTACCCAACCCAGAGACTGTTAA TCATGGATGTTAGAGCTCAAACGGGCTTTTATATACACTAGGAATTCTTGACGTGGG GTCTCTGGAGCTCCAGGAAATTCGGGCACATCATATGTCCATGAAACTTCAGATAAA CTAGGGAAAACTGGGTGCTGAGGTGAAAGCATAACTTTTTTGGCACAGAAAGTCTAA AGGGGCCACTGATTTTCAAAGAGATCTGTGATCCCTTTTTGTTTTTTGTTTTTGAGA TGGAGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAATGGCACAATCTCGGCTCACTGC AAGCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGAGTGGCTGGG ATTACAGGCATGCACCACCATGCCCAGCTAATTTGTTGTATTTTTAGTAGAGACAGG GTTTCACCATGTTGGCCAGTGTGGTCTCAAACTCCTGACCTCATGATTTGCCTGCCT CGGCCTCCCAAAGCACTGGGATTACAGGCGTGAGCCACCACATCCAGCCAGTGATCC TTAAAAGATTAAGAGATGACTGGACCAGGTCTACCTTGATCTTGAAGATTCCCTTGG AATGTTGAGATTTAGGCTTATTTGAGCACTGCCTGCCCAACTGTCAGTGCCAGTGCA TAGCCCTTCTTTTGTCTCCCTTATGAAGACTGCCCTGCAGGGCTGAGATGTGGCAGG AGCTCCCAGGGAAAAACGAAGTGCATTTGATTGGTGTGTATTGGCCAAGTTTTGCTT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GTTGTGTGCTTGAAAGAAAATATCTCTGACCAACTTCTGTATTCGTGGACCAAACTG AAGCTATATTTTTCACAGAAGAAGAAGCAGTGACGGGGACACAAATTCTGTTGCCTG GTGGAAAGAAGGCAAAGGCCTTCAGCAATCTATATTACCAGCGCTGGATCCTTTGAC AGAGAGTGGTCCCTAAACTTAAATTTCAAGACGGTATAGGCTTGATCTGTCTTGCTT ATTGTTGCCCCCTGCGCCTAGCACAATTCTGACACACAATTGGAACTTACTAAAAAT TTTTTTTTACTGTT (SEQ ID NO: 81) >NP_116171.3 hepatitis A virus cellular receptor 2 precursor [*Homo sapiens*] MFSHLPFDCVLLLLLLLLTRSSEVEYRAEVGQNAYLPCFYTPAAPGNLVPVCWGKGA CPVFECGNVVLRTDERDVNYWTSRYWLNGDFRKGDVSLTIENVTLADSGIYCCRIQI PGIMNDEKFNLKLVIKPAKVTPAPTRQRDFTAAFPRMLTTRGHGPAETQTLGSLPDI NLTQISTLANELRDSRLANDLRDSGATIRIGIYIGAGICAGLALALIFGALIFKWYS HSKEKIQNLSLISLANLPPSGLANAVAEGIRSEENIYTIEENVYEVEEPNEYYCYVS SRQQPSQPLGCRFAMP (SEQ ID NO: 82)
Mouse Tim-3 (HAVCR2)	>NM_134250.2 *Mus musculus* hepatitis A virus cellular receptor 2 (Havcr2), mRNA ACCATTTTAACCGAGGAGCTAAAGCTATCCCTACACAGAGCTGTCCTTGGATTTCCC CTGCCAAGTACTCATGTTTTCAGGTCTTACCCTCAACTGTGTCCTGCTGCTGCTGCA ACTACTACTTGCAAGGTCATTGGAAAATGCTTATGTGTTTGAGGTTGGTAAGAATGC CTATCTGCCCTGCAGTTACACTCTATCTACACCTGGGGCACTTGTGCCTATGTGCTG GGGCAAGGGATTCTGTCCTTGGTCACAGTGTACCAACGAGTTGCTCAGAACTGATGA AAGAAATGTGACATATCAGAAATCCAGCAGATACCAGCTAAAGGGCGATCTCAACAA AGGAGACGTGTCTCTGATCATAAAGAATGTGACTCTGGATGACCATGGGACCTACTG CTGCAGGATACAGTTCCCTGGTCTTATGAATGATAAAAAATTAGAACTGAAATTAGA CATCAAAGCAGCCAAGGTCACTCCAGCTCAGACTGCCCATGGGGACTCTACTACAGC TTCTCCAAGAACCCTAACCACGGAGAGAAATGGTTCAGAGACACAGACACTGGTGAC CCTCCATAATAACAATGGAACAAAAATTTCCACATGGGCTGATGAAATTAAGGACTC TGGAGAAACGATCAGAACTGCTATCCACATTGGAGTGGGAGTCTCTGCTGGGTTGAC CCTGGCACTTATCATTGGTGTCTTAATCCTTAAATGGTATTCCTGTAAGAAAAAGAA GTTATCGAGTTTGAGCCTTATTACACTGGCCAACTTGCCTCCAGGAGGGTTGGCAAA TGCAGGAGCAGTCAGGATTCGCTCTGAGGAAAATATCTACACCATCGAGGAGAACGT ATATGAAGTGGAGAATTCAAATGAGTACTACTGCTACGTCAACAGCCAGCAGCCATC CTGACCGCCTCTGGACTGCCACTTTTAAAGGCTCGCCTTCATTTCTGACTTTGGTAT TTCCCTTTTTGAAAACTATGTGATATGTCACTTGGCAACCTCATTGGAGGTTCTGAC CACAGCCACTGAGAAAAGAGTTCCAGTTTTCTGGGGATAATTAACTCACAAGGGGAT TCGACTGTAACTCATGCTACATTGAAATGCTCCATTTTATCCCTGAGTTTCAGGGAT CGGATCTCCCACTCCAGAGACTTCAATCATGCGTGTTGAAGCTCACTCGTGCTTTCA TACATTAGGAATGGTTAGTGTGATGTCTTTGAGACATAGAGGTTTGTGGTATATCTG CAAAGCTCCTGAACAGGTAGGGGGAATAAAGGGCTAAGATAGGAAGGTGAGGTTCTT TGTTGATGTTGAAAATCTAAAGAAGTTGGTAGCTTTTCTAGAGATTTCTGACCTTGA AAGATTAAGAAAAAGCCAGGTGGCATATGCTTAACACTATATAACTTGGGAACCTTA GGCAGGAGGGTGATAAGTTCAAGGTCAGCCAGGGCTATGCTGGTAAGACTGTCTCAA AATCCAAAGACGAAAATAAACATAGAGACAGCAGGAGGCTGGAGATGAGGCTCGGAC AGTGAGGTGCATTTTGTACAAGCACGAGGAATCTATATTTGATCGTAGACCCCACAT GAAAAAGCTAGGCCTGGTAGAGCATGCTTGTAGACTCAAGAGATGGAGAGGTAAAGG CACAACAGATCCCCGGGGCTTGCGTGCAGTCAGCTTAGCCTAGGTGCTGAGTTCCAA GTCCACAAGAGTCCCTGTCTCAAAGTAAGATGGACTGAGTATCTGGCGAATGTCCAT GGGGGTTGTCCTCTGCTCTCAGAAGAGACATGCACATGAACCTGCACACACACACAC ACACACACACACACACACACACACACACACACACACACACACACATGAAATGAAGGTTC TCTCTGTGCCTGCTACCTCTCTATAACATGTATCTCTACAGGACTCTCCTCTGCCTC TGTTAAGACATGAGTGGGAGCATGGCAGAGCAGTCCAGTAATTAATTCCAGCACTCA GAAGGCTGGAGCAGAAGCGTGGAGAGTTCAGGAGCACTGTGCCCAACACTGCCAGAC TCTTCTTACAGAAGAAAAAGGTTACCCGCAAGCAGCCTGCTGTCTGTAAAAGGAAAC CCTGCGAAAGGCAAACTTTGACTGTTGTGTGCTCAAGGGGAACTGACTCAGACAACT TCTCCATTCCTGGAGGAAACTGGAGCTGTTTCTGACAGAAGAACAACCGGTGACTGG GACATACGAAGGCAGAGCTCTTGCAGCAATCTATATAGTCAGCAAAATATTCTTTGG GAGGACAGTCGTCACCAAATTGATTTCCAAGCCGGTGGACCTCAGTTTCATCTGGCT TACAGCTGCCTGCCCAGTGCCCTTGATCTGTGCTGGCTCCCATCTATAACAGAATCA AATTAAATAGACCCCGAGTGAAAATATTAAGTGAGCAGAAAGGTAGCTTTGTTCAAA GATTTTTTTGCATTGGGGAGCAACTGTGTACATCAGAGGACATCTGTTAGTGAGGAC ACCAAAACCTGTGGTACCGTTTTTTCATGTATGAATTTTGTTGTTTAGGTTGCTTCT AGCTAGCTGTGGAGGTCCTGGCTTTCTTAGGTGGGTATGGAAGGGAGACCATCTAAC AAAATCCATTAGAGATAACAGCTCTCATGCAGAAGGGAAAACTAATCTCAAATGTTT TAAAGTAATAAAACTGTACTGGCAAAGTACTTTGAGCATATTTAAA (SEQ ID NO: 83) >NP_599011.2 hepatitis A virus cellular receptor 2 homolog precursor [*Mus musculus*] MFSGLTLNCVLLLLQLLLARSLENAYVFEVGKNAYLPCSYTLSTPGALVPMCWGKGF CPWSQCTNELLRTDERNVTYQKSSRYQLKGDLNKGDVSLIIKNVTLDDHGTYCCRIQ FPGLMNDKKLELKLDIKAAKVTPAQTAHGDSTTASPRTLTTERNGSETQTLVTLHNN

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	NGTKISTWADEIKDSGETIRTAIHIGVGVSAGLTLALIIGVLILKWYSCKKKKLSSL SLITLANLPPGGLANAGAVRIRSEENIYTIEENVYEVENSNEYYCYVNSQQPS (SEQ ID NO: 84)
Human Tim-4 (TIMD4)	>NM_138379.3 *Homo sapiens* T cell immunoglobulin and mucin domain containing 4 (TIMD4), transcript variant 1, mRNA AGACTCCTGGGTCCGGTCAACCGTCAAAATGTCCAAAGAACCTCTCATTCTCTGGCT GATGATTGAGTTTTGGTGGCTTTACCTGACACCAGTCACTTCAGAGACTGTTGTGAC GGAGGTTTTGGGTCACCGGGTGACTTTGCCCTGTCTGTACTCATCCTGGTCTCACAA CAGCAACAGCATGTGCTGGGGGAAAGACCAGTGCCCCTACTCCGGTTGCAAGGAGGC GCTCATCCGCACTGATGGAATGAGGGTGACCTCAAGAAAGTCAGCAAAATATAGACT TCAGGGGACTATCCCGAGAGGTGATGTCTCCTTGACCATCTTAAACCCCAGTGAAAG TGACAGCGGTGTGTACTGCTGCCGCATAGAAGTGCCTGGCTGGTTCAACGATGTAAA GATAAACGTGCGCCTGAATCTACAGAGAGCCTCAACAACCACGCACAGAACAGCAAC CACCACCACACGCAGAACAACAACAACAAGCCCCACCACCACCCGACAAATGACAAC AACCCCAGCTGCACTTCCAACAACAGTCGTGACCACACCCGATCTCACAACCGGAAC ACCACTCCAGATGACAACCATTGCCGTCTTCACAACAGCAAACACGTGCCTTTCACT AACCCCAAGCACCCTTCCGGAGGAAGCCACAGGTCTTCTGACTCCCGAGCCTTCTAA GGAAGGGCCCATCCTCACTGCAGAATCAGAAACTGTCCTCCCCAGTGATTCCTGGAG TAGTGTTGAGTCTACTTCTGCTGACACTGTCCTGCTGACATCCAAAGAGTCCAAAGT TTGGGATCTCCCATCAACATCCCACGTGTCAATGTGGAAAACGAGTGATTCTGTGTC TTCTCCTCAGCCTGGAGCATCTGATACAGCAGTTCCTGAGCAGAACAAAACAACAAA AACAGGACAGATGGATGGAATACCCATGTCAATGAAGAATGAAATGCCCATCTCCCA ACTACTGATGATCATCGCCCCCTCCTTGGGATTTGTGCTCTTCGCATTGTTTGTGGC GTTTCTCCTGAGAGGGAAACTCATGGAAACCTATTGTTCGCAGAAACACACAAGGCT AGACTACATTGGAGATAGTAAAAATGTCCTCAATGACGTGCAGCATGGAAGGGAAGA CGAAGACGGCCTTTTTACCCTCTAACAACGCAGTAGCATGTTAGATTGAGGATGGGG GCATGACACTCCAGTGTCAAAATAAGTCTTAGTAGATTTCCTTGTTTCATAAAAAAG ACTCACTTATTCCATGGATGTCATTGATCCAGGCTTGCTTTAGTTTCATGAATGAAG GGTACTTTAGAGACCACAA (SEQ ID NO: 85) >NP_612388.2 T-cell immunoglobulin and mucin domain-containing protein 4 isoform 1 precursor [*Homo sapiens*] MSKEPLILWLMIEFWWLYLTPVTSETVVTEVLGHRVTLPCLYSSWSHNSNSMCWGKD QCPYSGCKEALIRTDGMRVTSRKSAKYRLQGTIPRGDVSLTILNPSESDSGVYCCRI EVPGWFNDVKINVRLNLQRASTTTHRTATTTTRRTTTTSPTTTRQMTTTPAALPTTV VTTPDLTTGTPLQMTTIAVFTTANTCLSLTPSTLPEEATGLLTPEPSKEGPILTAES ETVLPSDSWSSVESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSSPQPGASDT AVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAPSLGFVLFALFVAFLLRGKLME TYCSQKHTRLDYIGDSKNVLNDVQHGREDEDGLFTL (SEQ ID NO: 86)
Mouse Tim-4 (TIMD4)	>NM_178759.4 *Mus musculus* T cell immunoglobulin and mucin domain containing 4 (Timd4), mRNA AGATCCTATCAAAATGTCCAAGGGGCTTCTCCTCCTCTGGCTGGTGACGGAGCTCTG GTGGCTTTATCTGACACCAGCTGCCTCAGAGGATACAATAATAGGGTTTTTGGGCCA GCCGGTGACTTTGCCTTGTCATTACCTCTCGTGGTCCCAGAGCCGCAACAGTATGTG CTGGGGCAAAGGTTCATGTCCCAATTCCAAGTGCAATGCAGAGCTTCTCCGTACAGA TGGAACAAGAATCATCTCCAGGAAGTCAACAAAATATACACTTTTGGGGAAGGTCCA GTTTGGTGAAGTGTCCTTGACCATCTCAAACACCAATCGAGGTGACAGTGGGGTGTA CTGCTGCCGTATAGAGGTGCCTGGCTGGTTCAATGATGTCAAGAAGAATGTGCGCTT GGAGCTGAGGAGAGCCACAACAACCAAAAAACCAACAACAACCACCCGGCCAACCAC CACCCCTTATGTGACCACCACCACCCCAGAGCTGCTTCCAACAACAGTCATGACCAC ATCTGTTCTCCCAACCACCACACCACCCCAGACACTAGCCACCACTGCCTTCAGTAC AGCAGTGACCACGTGCCCCTCAACAACACCTGGCTCCTTCTCACAAGAAACCACAAA AGGGTCCGCCTTCACTACAGAATCAGAAACTCTGCCTGCATCCAATCACTCTCAAAG AAGCATGATGACCATATCTACAGACATAGCCGTACTCAGGCCCACAGGCTCTAACCC TGGGATTCTCCCATCCACTTCACAGCTGACGACACAGAAAACAACATTAACAACAAG TGAGTCTTTGCAGAAGACAACTAAATCACATCAGATCAACAGCAGACAGACCATCTT GATCATTGCCTGCTGTGTGGGATTTGTGCTAATGGTGTTATTGTTTCTGGCGTTTCT CCTTCGAGGGAAAGTCACAGGAGCCAACTGTTTGCAGAGACACAAGAGGCCAGACAA CACTGAAGATAGTGACAGCGTCCTCAATGACATGTCACACGGGAGGGATGATGAAGA CGGGATCTTCACTCTCTGACTCACCATCTTTATTTAGGATTAAGGATAGGGAATGGC ACTTGAATTGTCAAAATAAGTTTGGGGACATTGTAATTTCCGTTTAAAGTCTCACTC TGTTTACTGATGCTGTGGGTCCTGTCTGGTTGTATCTTCCCACATGAAGGTGCTTTA GAGACACATTTTCCCTGCCTCGTGCCTTAGTCCTCTTTGTTGTTTTGTGGCTAGGTG ACTTTTCACACTGGGCTTGAACACTGTCAGTGATGGTGAAATCCTTGCCACAGCTTT GGGAGTCTCTTGCAGTCTCCCAGCAGTAGAGGGAGTTAGAAATATCCAGAGGGGAAA AAAAAATCTCTCTTTTCAGACAGTATCTGCTTTATTGGTGGTAGCTGAACTTCATTT ATACAGAGCTCCTTTAACCTGTCTGTCTTCTTCTTGGTATCTAAGCTGCCTTTTGTT TTTGTTTTTGTTTTTGTTTTTATGATATTAACTTCTTTTCACATTCAAGTTTCTTTA AAGTTGACTATAGTGCCTTCTGAACTCTTGCAGAGAGTTTGGATTTTGGAAGCTGCC AGGTACCCATCACAGCAGGGGTGCCAGTGACAAGGATGGTGTACAAATGAAACACTG AAGCTATCCAAATAAATTCCTCTAAGTGTAATTCATTTTACTGCAGCACAGGAAGAA CAAATTTGTCTTACAACTTTAATAATTAGTACCATTATGAACCCTAGGAGAGAAATA AGAGCAAATACCTGTTGAATAAATGAATGTAAGAAAATGTGTGTCTGAGCAAGAATA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CTCTGTCTGGCTACTATGGGAAGCTAGCTAGATCTGAAAGACATTCTCAGACTATCC TCATGTTCAAGGCATTAAAGGAATAAGCCTCCAGCCCCTAACCTTAGGAGAATTCTG CAGTCAAGTGAGGAGTTTTTAAAACAGGAATCTCTAGGTTCCAGTCCTCTAGCTATT CTTTTATGCTTAGTCCAGGTAATGAGTTGAACATCCAAGTATTTTTTAAGGACCCAA AGAAATGCAACCAGAGCTATTACCAGAATTTTGGAGTGGTCCTCCTAGAGTTGCCGC ATGTTGCTGGGAAAATTGGGGTCTTAGAGTTCTTAGTCTACTTAATAAAAGAATTTT AAAAAATGG (SEQ ID NO: 87)
	>NP_848874.3 T-cell immunoglobulin and mucin domain-containing protein 4 precursor [*Mus musculus*] MSKGLLLLWLVTELWWLYLTPAASEDTIIGFLGQPVTLPCHYLSWSQSRNSMC WGKGSCPNSKCNAELLRTDGTRIISRKSTKYTLLGKVQFGEVSLTISNTNRGD SGVYCCRIEVPGWFNDVKKNVRLELRRATTTKKPTTTTRPTTTPYVTTTTPEL LPTTVMTTSVLPTTTPPQTLATTAFSTAVTTCPSTTPGSFSQETTKGSAFTTE SETLPASNHSQRSMMTISTDIAVLRPTGSNPGILPSTSQLTTQKTTLTTSESL QKTTKSHQINSRQTILIIACCVGFVLMVLLFLAFLLRGKVTGANCLQRHKRPD NTEDSDSVLNDMSHGRDDEDGIFTL (SEQ ID NO: 88)
Human CEACAM1	>NM_001712.5 *Homo sapiens* CEA cell adhesion molecule 1 (CEACAM1), transcript variant 1, mRNA AGCACAGAGAGTGGAAAACAGCAGAGGTGACAGAGCAGCCGTGCTCGAAGCGT TCCTGGAGCCCAAGCTCTCCTCCACAGGTGAAGACAGGGCCAGCAGGAGACAC CATGGGGCACCTCTCAGCCCCACTTCACAGAGTGCGTGTACCCTGGCAGGGGC TTCTGCTCACAGCCTCACTTCTAACCTTCTGGAACCCGCCCACCACTGCCCAG CTCACTACTGAATCCATGCCATTCAATGTTGCAGAGGGGAAGGAGGTTCTTCT CCTTGTCCACAATCTGCCCCAGCAACTTTTTGGCTACAGCTGGTACAAAGGGG AAAGAGTGGATGGCAACCGTCAAATTGTAGGATATGCAATAGGAACTCAACAA GCTACCCCAGGGCCCGCAAACAGCGGTCGAGAGACAATATACCCCAATGCATC CCTGCTGATCCAGAACGTCACCCAGAATGACACAGGATTCTACACCCTACAAG TCATAAAGTCAGATCTTGTGAATGAAGAAGCAACTGGACAGTTCCATGTATAC CCGGAGCTGCCCAAGCCCTCCATCTCCAGCAACAACTCCAACCCTGTGGAGGA CAAGGATGCTGTGGCCTTCACCTGTGAACCTGAGACTCAGGACACAACCTACC TGTGGTGGATAAACAATCAGAGCCTCCCGGTCAGTCCCAGGCTGCAGCTGTCC AATGGCAACAGGACCCTCACTCTACTCAGTGTCACAAGGAATGACACAGGACC CTATGAGTGTGAAATACAGAACCCAGTGAGTGCGAACCGCAGTGACCCAGTCA CCTTGAATGTCACCTATGGCCCGGACACCCCCACCATTTCCCCTTCAGACACC TATTACCGTCCAGGGGCAAACCTCAGCCTCTCCTGCTATGCAGCCTCTAACCC ACCTGCACAGTACTCCTGGCTTATCAATGGAACATTCCAGCAAAGCACACAAG AGCTCTTTATCCCTAACATCACTGTGAATAATAGTGGATCCTATACCTGCCAC GCCAATAACTCAGTCACTGGCTGCAACAGGACCACAGTCAAGACGATCATAGT CACTGAGCTAAGTCCAGTAGTAGCAAAGCCCCAAATCAAAGCCAGCAAGACCA CAGTCACAGGAGATAAGGACTCTGTGAACCTGACCTGCTCCACAAATGACACT GGAATCTCCATCCGTTGGTTCTTCAAAAACCAGAGTCTCCCGTCCTCGGAGAG GATGAAGCTGTCCCAGGGCAACACCACCCTCAGCATAAACCCTGTCAAGAGGG AGGATGCTGGGACGTATTGGTGTGAGGTCTTCAACCCAATCAGTAAGAACCAA AGCGACCCCATCATGCTGAACGTAAACTATAATGCTCTACCACAAGAAAATGG CCTCTCACCTGGGGCCATTGCTGGCATTGTGATTGGAGTAGTGGCCCTGGTTG CTCTGATAGCAGTAGCCCTGGCATGTTTTCTGCATTTCGGGAAGACCGGCAGG GCAAGCGACCAGCGTGATCTCACAGAGCACAAACCCTCAGTCTCCAACCACAC TCAGGACCACTCCAATGACCCACCTAACAAGATGAATGAAGTTACTTATTCTA CCCTGAACTTTGAAGCCCAGCAACCCACACAACCAACTTCAGCCTCCCCATCC CTAACAGCCACAGAAATAATTTATTCAGAAGTAAAAAAGCAGTAATGAAACCT GTCCTGCTCACTGCAGTGCTGATGTATTTCAAGTCTCTCACCCTCATCACTAG GAGATTCCTTTCCCCTGTAGGGGTAGAGGGGTGGGGACAGAAACAACTTTCTC CTACTCTTCCTTCCTAATAGGCATCTCCAGGCTGCCTGGTCACTGCCCCTCTC TCAGTGTCAATAGATGAAAGTACATTGGGAGTCTGTAGGAAACCCAACCTTCT TGTCATTGAAATTTGGCAAAGCTGACTTTGGGAAAGAGGGACCAGAACTTCCC CTCCCTTCCCCTTTTCCCAACCTGGACTTGTTTTAAACTTGCCTGTTCAGAGC ACTCATTCCTTCCCACCCCCAGTCCTGTCCTATCACTCTAATTCGGATTTGCC ATAGCCTTGAGGTTATGTCCTTTTCCATTAAGTACATGTGCCAGGAAACAAGA GAGAGAGAAAGTAAAGGCAGTAATGCCTTCTCCTATTTCTCCAAAGCCTTGTG TGAACTCACCAAACACAAGAAAATCAAATATATAACCAATAGTGAAATGCCAC ACCTTTGTCCACTGTCAGGGTTGTCTACCTGTAGGATCAGGGTCTAAGCACCT TGGTGCTTAGCTAGAATACCACCTAATCCTTCTGGCAAGCCTGTCTTCAGAGA ACCCACTAGAAGCAACTAGGAAAATCACTTGCCAAAATCCAAGGCAATTCCTG ATGGAAAATGCAAAAGCACATATATGTTTTAATATCTTTATGGGCTCTGTTCA AGGCAGTGCTGAGAGGGAGGGGTTATAGCTTCAGGAGGGAACCAGCTTCTGAT AAACACAATCTGCTAGGAACTTGGGAAAGGAATCAGAGAGCTGCCCTTCAGCG ATTATTTAAATTATTGTTAAAGAATACACAATTTGGGGTATTGGGATTTTTCT CCTTTTCTCTGAGACATTCCACCATTTTAATTTTTGTAACTGCTTATTTATGT GAAAAGGGTTATTTTTACTTAGCTTAGCTATGTCAGCCAATCCGATTGCCTTA GGTGAAAGAAACCACCGAAATCCCTCAGGTCCCTTGGTCAGGAGCCTCTCAAG ATTTTTTTTGTCAGAGGCTCCAAATAGAAAATAAGAAAAGGTTTTCTTCATTC ATGGCTAGAGCTAGATTTAACTCAGTTTCTAGGCACCTCAGACCAATCATCAA CTACCATTCTATTCCATGTTTGCACCTGTGCATTTTCTGTTTGCCCCCATTCA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CTTTGTCAGGAAACCTTGGCCTCTGCTAAGGTGTATTTGGTCCTTGAGAAGTG GGAGCACCCTACAGGGACACTATCACTCATGCTGGTGGCATTGTTTACAGCTA GAAAGCTGCACTGGTGCTAATGCCCCTTGGGGAAATGGGGCTGTGAGGAGGAG GATTATAACTTAGGCCTAGCCTCTTTTAACAGCCTCTGAAATTTATCTTTTCT TCTATGGGGTCTATAAATGTATCTTATAATAAAAAGGAAGGACAGGAGGAAGA CAGGCAAATGTACTTCTCACCCAGTCTTCTACACAGATGGAATCTCTTTGGGG CTAAGAGAAAGGTTTTATTCTATATTGCTTACCTGATCTCATGTTAGGCCTAA GAGGCTTTCTCCAGGAGGATTAGCTTGGAGTTCTCTATACTCAGGTACCTCTT TCAGGGTTTTCTAACCCTGACACGGACTGTGCATACTTTCCCTCATCCATGCT GTGCTGTGTTATTTAATTTTTCCTGGCTAAGATCATGTCTGAATTATGTATGA AAATTATTCTATGTTTTTATAATAAAAATAATATATCAGACATCGA (SEQ ID NO: 89)
	>NP_001703.2 carcinoembryonic antigen-related cell adhesion molecule 1 isoform 1 precursor [*Homo* *sapiens*] MGHLSAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLL LVHNLPQQLFGYSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNAS LLIQNVTQNDTGFYTLQVIKSDLVNEEATGQFHVYPELPKPSISSNNSNPVED KDAVAFTCEPETQDTTYLWWINNQSLPVSPRLQLSNGNRTLTLLSVTRNDTGP YECEIQNPVSANRSDPVTLNVTYGPDTPTISPSDTYYRPGANLSLSCYAASNP PAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNSVTGCNRTTVKTIIV TELSPVVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWFFKNQSLPSSER MKLSQGNTTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLNVNYNALPQENG LSPGAIAGIVIGVVALVALIAVALACFLHFGKTGRASDQRDLTEHKPSVSNHT QDHSNDPPNKMNEVTYSTLNFEAQQPTQPTSASPSLTATEIIYSEVKKQ (SEQ ID NO: 90)
Mouse CEACAM1	>NM_001039185.1 *Mus musculus* carcinoembryonic antigen-related cell adhesion molecule 1 (Ceacam1), transcript variant 1, mRNA AAAGCTCCTTTAAGAAAAGCAGGGCAGATATCAGGGCAGCCTGGCTTAGCAGT AGTGTTGGAGAAGAAGCTAGCAGGCAGGCAGCAGAGACATGGAGCTGGCCTCA GCACATCTCCACAAAGGGCAGGTTCCCTGGGGAGGACTACTGCTCACAGCCTC ACTTTTAGCCTCCTGGAGCCCTGCCACCACTGCTGAAGTCACCATTGAGGCTG TGCCGCCCCAGGTTGCTGAAGACAACAATGTTCTTCTACTTGTTCACAATCTG CCCCTGGCGCTTGGAGCCTTTGCCTGGTACAAGGGAAACACTACGGCTATAGA CAAAGAAATTGCACGATTTGTACCAAATAGTAATATGAATTTCACGGGGCAAG CATACAGCGGCAGAGAGATAATATACAGCAATGGATCCCTGCTCTTCCAAATG ATCACCATGAAGGATATGGGAGTCTACACACTAGATATGACAGATGAAAACTA TCGTCGTACTCAGGCGACTGTGCGATTTCATGTACACCCCATATTATTAAAGC CCAACATCACAAGCAACAACTCCAATCCCGTGGAGGGTGACGACTCCGTATCA TTAACCTGTGACTCTTACACTGACCCTGATAATATAAACTACCTGTGGAGCAG AAATGGTGAAAGCCTTTCAGAAGGTGACAGGCTGAAGCTGTCTGAGGGCAACA GGACTCTCACTTTACTCAATGTCACGAGGAATGACACAGGACCCTATGTGTGT GAAACCCGGAATCCAGTGAGTGTCAACCGAAGTGACCCATTCAGCCTGAACAT TATCTATGGTCCGGACACCCCGATTATATCCCCCTCAGATATTTATTTGCATC CAGGGTCAAACCTCAACCTCTCCTGCCATGCAGCCTCTAACCCACCTGCACAG TACTTTTGGCTTATCAATGAGAAGCCCCATGCATCCTCCCAAGAGCTCTTTAT CCCCAACATCACTACTAATAATAGCGGAACCTATACCTGCTTCGTCAATAACT CTGTCACTGGCCTCAGTAGGACCACAGTCAAGAACATTACAGTCCTTGAGCCA GTGACTCAGCCCTTCCTCCAAGTCACCAACACCACAGTCAAAGAACTAGACTC TGTGACCCTGACCTGCTTGTCGAATGACATTGGAGCCAACATCCAGTGGCTCT TCAATAGCCAGAGTCTTCAGCTCACAGAGAGAATGACACTCTCCCAGAACAAC AGCATCCTCAGAATAGACCCTATTAAGAGGGAAGATGCCGGCGAGTATCAGTG TGAAATCTCGAATCCAGTCAGCGTCAGGAGGAGCAACTCAATCAAGCTGGACA TAATATTTGACCCAACACAAGGAGGCCTCTCAGATGGCGCCATTGCTGGCATC GTGATTGGAGTTGTGGCTGGGGTGGCTCTAATAGCAGGGCTGGCATATTTCCT CTATTCCAGGAAGTCTGGCGGGGGAAGTGACCAGCGAGATCTCACAGAGCACA AACCCTCAGCCTCCAACCACAATCTGGCTCCTTCTGACAACTCTCCTAACAAG GTGGATGACGTCGCATACACTGTCCTGAACTTCAATTCCCAGCAACCCAACCG GCCAACTTCAGCCCCTTCTTCTCCAAGAGCCACAGAAACAGTTTATTCAGAAG TAAAAAAGAAGTGAGCATAATCTGTCCGTCTGTCCTGCTGGCTGCACCAGTGA TGCATTCCCGGATTCTGTTCCTCACTGGAGGGTCTCAGCACACACACACACGT ACACATGCGCGCGCGCACACACACACACACACACACACACACACACTTACACA CACACTCATGCATTCACTCTATTGACTCCTTCAGTGTCTATAGAAGAAAAGGT GGATCCTGGAGCCTACAGAAAACTCAACCCTTCTAGGCTTTCAAATTTGGCTG AGAGTGAGGTATCAAAATTTCTCACCCTTTCACTTTCCTGACCCAGATTGTTG AAAATTGACCTATTCAGAGCACCTTCATTCCCCTCCCAACTCCAAGTCCTGCC CTATCAGAGTCTGACTTGAATTTCCATAAACCTTGGAGGTCACCTAAGTGCTT ACGCCAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAA CAAACCAGAAGCAGGAAATGGCCAGTCCCATATCTTTAAAGGCTGATTGGAAG CCACCATACATGAGAAGATCAAACCTCCATGGGCAATCTACACACCCGACAAC TGTCATGCTTACCCATCTGGGACATTCGAGTCTCTGAACCTTGTGCCCTCACG CCTGAGCCCTTCTCTGAGCCTTTCTCCAGAAAATCCACTCACAGCAACTAGAG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	AGGCTCTTTGTCAGCAACTCCAAGCAAACTGCTAGGCAGGATTCAGAAGAAAA GACAGCATCTCTAACATCCACCAGGAAGGTGCCCAGAAAAGCAGAGCTGGTGA CTTTGGACTGACAGACATCTGGAGTGTGAAAAAGCAGCACAGAGCTAACCTTC GGAGAGTGTTGAAATTATTTGAAAAGAAGCCATATTTGGAGGTATTGGAGTTT TCCTCTTTCTGAGACAATCCACTATTTGAAAATTGTAGCTACTGAATTGCCTC TCAGTATGCGAGCTGATCACTTTGCCTTAGGGCCACTAGATTTCTGTCTCCCT TAGCCCCTCAAGCCCTTTTGATCATGAGTTCCAAACCAAAAATAAATAAATGA ACAGTGAGGCAGTCCCTTGCAGTACCACTGTCATGGGTCAGGCTAAGCCTCCT GCTTTTCTGAATTAGTCAAGAAAAGCCTTGGTTTCCCTTTTTCCATCTCTTTA TCTTGTCTTTCAGATACTGGCCAGAGCCTGGACACTCTTCCTCTGAGATCTCC AGCTTCTCTGCCTTCTTGTGTTTCTTTTAAACTCTAACAAAAACTGTTCTCAC CTTCAAAAAATAAAATAATAACAAGCTTTCCACATCCCCACCAAAGAGGGACC CAGCTAGGTTTCTGGAAACCCAGCACCAGCCTCCAGCTGCCCTTCTGCAGTGT TTCTGCCTCTGTTTCCCTTTCGTTTTGACTTTTTTCCTTCTTTTGAGACAGAG TTCCAGCATGGAGCCTGTGCAGGTTTCAATCCCACAGTAACACCTTCTGCAGC ACCCCACCTGCTCAGACTGCAGCCCTGGCCACCAGGCCTGGCTACCTGGACAT TCTGTCTGCCCTGCACTCTCAGGAAACCTTGGCCTCTGCTACTGTCTGTTTGG CTCATTCAAAGTGTGTCCTTAAAGGAATGCAGTCACCCATGCCAGAGGCAGTG TTTACAGCCTGGAATGCTCTGCACTTCCAGTGGACCAGTGCTCCACCGGAAGT GGGCTGTTAGCAGGGTCCTCTCACCTGGCCCTGGCCTTTCTGTAGCCTTGAAT CCTGCCTTCCCCACCAGGGCACCAGGGATGAGTGCAGCAGCAGGAGGAGAGGC AAACAGTCACCTCAGGAACCTTCTGAGCTAAGGCACACCCTCTGTGCCTGTCA AGCAAAGGTTGTATTGGATATCAAGTGTTTGGTCTCACGCCAAGCCAACAGGC TTTGGAGAGAATTAATTAGTTCTCCTACTCAGGGATTTCTTTCAGTCCTAACA CAGCCTGTGTATATTTTGCTTCACCCACGCAATGCTGGATTATTTAATTTTGC CCGGCTTAAGACAAATCTGAGTTACTTGTAAATTTGCTCTATGTTCATAATAA AAATGTATTATATATCACTGATAGCA (SEQ ID NO: 91) >NP_001034274.1 carcinoembryonic antigen-related cell adhesion molecule 1 isoform 1 precursor [*Mus musculus*] MELASAHLHKGQVPWGGLLLTASLLASWSPATTAEVTIEAVPPQVAEDNNVLL LVHNLPLALGAFAWYKGNTTAIDKEIARFVPNSNMNFTGQAYSGREIIYSNGS LLFQMITMKDMGVYTLDMTDENYRRTQATVRFHVHPILLKPNITSNNSNPVEG DDSVSLTCDSYTDPDNINYLWSRNGESLSEGDRLKLSEGNRTLTLLNVTRNDT GPYVCETRNPVSVNRSDPFSLNIIYGPDTPIISPSDIYLHPGSNLNLSCHAAS NPPAQYFWLINEKPHASSQELFIPNITTNNSGTYTCFVNNSVTGLSRTTVKNI TVLEPVTQPFLQVTNTTVKELDSVTLTCLSNDIGANIQWLENSQSLQLTERMT LSQNNSILRIDPIKREDAGEYQCEISNPVSVRRSNSIKLDIIFDPTQGGLSDG AIAGIVIGVVAGVALIAGLAYFLYSRKSGGGSDQRDLTEHKPSASNHNLAPSD NSPNKVDDVAYTVLNFNSQQPNRPTSAPSSPRATETVYSEVKKK (SEQ ID NO: 92)
Human BTN3A1	>NM_007048.6 *Homo sapiens* butyrophilin subfamily 3 member A1 (BTN3A1), transcript variant 1, mRNA ATTCCTCACGATGACCCGACAGTCTCTGCTTTCTTTTTCCTTTCTTCCAGAAG GAGATTTAACCATAGTAGAAAGAATGGAGAACTATTAACTGCCTTTCTTCTGT GGGCTGTGATTTTCAGAGGGGAATGCTAAGAGGTGATTTTCAATGTTGGGACT CAAAGGTGAAGACACTGAAGGACAGAATTTTTGGCAGAGGAAAGATCTTCTTC GGTCACCATACTTGAGTTAGCTCTAGGGAAGTGGAGGTTTCCATTTGGAATTC TATAGCTTCTTCCAGGTCATAGTGTCTGCCCCCCACCTTCCAGTATCTCCTGA TATGCAGCATGAATGAAAATGGCAAGTTTCCTGGCCTTCCTTCTGCTCAACTT TCGTGTCTGCCTCCTTTTGCTTCAGCTGCTCATGCCTCACTCAGCTCAGTTTT CTGTGCTTGGACCCTCTGGGCCCATCCTGGCCATGGTGGGTGAAGACGCTGAT CTGCCCTGTCACCTGTTCCCGACCATGAGTGCAGAGACCATGGAGCTGAAGTG GGTGAGTTCCAGCCTAAGGCAGGTGGTGAACGTGTATGCAGATGGAAAGGAAG TGGAAGACAGGCAGAGTGCACCGTATCGAGGGAGAACTTCGATTCTGCGGGAT GGCATCACTGCAGGGAAGGCTGCTCTCCGAATACACAACGTCACAGCCTCTGA CAGTGGAAAGTACTTGTGTTATTTCCAAGATGGTGACTTCTATGAAAAAGCCC TGGTGGAGCTGAAGGTTGCAGCACTGGGTTCTGATCTTCACGTTGATGTGAAG GGTTACAAGGATGGAGGGATCCATCTGGAGTGCAGGTCCACTGGCTGGTACCC CCAACCCCAAATACAGTGGAGCAACAACAAGGGAGAGAACATCCCGACTGTGG AAGCACCTGTGGTTGCAGACGGAGTGGGCCTGTATGCAGTAGCAGCATCTGTG ATCATGAGAGGCAGCTCTGGGGAGGGTGTATCCTGTACCATCAGAAGTTCCCT CCTCGGCCTGGAAAAGACAGCCAGCATTTCCATCGCAGACCCCTTCTTCAGGA GCGCCCAGAGGTGGATCGCCGCCCTGGCAGGGACCCTGCCTGTCTTGCTGCTG CTTCTTGGGGGAGCCGGTTACTTCCTGTGGCAACAGCAGGAGGAAAAAAAGAC TCAGTTCAGAAAGAAAAAGAGAGAGCAAGAGTTGAGAGAAATGGCATGGAGCA CAATGAAGCAAGAACAAAGCACAAGAGTGAAGCTCCTGGAGGAACTCAGATGG AGAAGTATCCAGTATGCATCTCGGGGAGAGAGACATTCAGCCTATAATGAATG GAAAAAGGCCCTCTTCAAGCCTGCGGATGTGATTCTGGATCCAAAAACAGCAA ACCCCATCCTCCTTGTTTCTGAGGACCAGAGGAGTGTGCAGCGTGCCAAGGAG CCCCAGGATCTGCCAGACAACCCTGAGAGATTTAATTGGCATTATTGTGTTCT CGGCTGTGAGAGCTTCATATCAGGGAGACATTACTGGGAGGTGGAGGTAGGGG ACAGGAAAGAGTGGCATATAGGGGTGTGCAGTAAGAATGTGCAGAGAAAAGGC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TGGGTCAAAATGACACCTGAGAATGGATTCTGGACTATGGGGCTGACTGATGG GAATAAGTATCGGACTCTAACTGAGCCCAGAACCAACCTGAAACTTCCTAAGC CCCCTAAGAAAGTGGGGGTCTTCCTGGACTATGAGACTGGAGATATCTCATTC TACAATGCTGTGGATGGATCGCATATTCATACTTTCCTGGACGTCTCCTTCTC TGAGGCTCTATATCCTGTTTTCAGAATTTTGACCTTGGAGCCCACGGCCCTGA CTATTTGTCCAGCGTGAAAAGAAGAAGAGAGTTCCTCCAATTCTGACCGAGTG CTGATCATTCCCTAGAGACACCAGTAACCCCGGGCTTAGCTAACGAAAGTGGG GAGCCTCAGGCTGAAGTAACTTTTCTCTGCTTCTCCCTGCCCAGCTCAGAGCT GAGGGCCTCCCCCTCCACAGCAACCAATCACAACCATAAAGCTACAAGCACGC ACTGAAGCACTTTACTGATACTCATTCAATTATTCATATGACAGTTGTTTGAG TTTGGTACCATCTTATTTTCCCCTTATACAGATAAGGAAACTGGGGTGCAGAA AAGTGAATTGACTACAAAGTAGACATGACTAGTTAACAACACAGCTGGGATCT AAACAGCAATAACTAACATTAATGGAGAACTTAAAATGCTCTGAGTGCTGTGT TATGAGCTTTGGTGGATGTCACTCCTTTAATCCTCGCAACACCCTGTCGGGTA GTCTCATTTAGCAAGTATGGAAGTTGAGGCAGGGCAACATTAAGCAACTTACA TAACTCATGCAGTAATTTCTGCAGTTGGGAGATGTTCAGCTTCAGTCCCCGGC CCTATGGCCGTTCTTTTCCACCCTGTTTCTTCCCCCATAGGAAGAACCCACCT GTAGCCCTGAGGTTCTTTTCCCAGGATGGCTCCAGGATAAGGATCACTGTAGG TGGTTGTGGAGTTGACACCCCTGTTGACTCCTTCCCAGCTGATTGTCAGAGCC TTAGACCCAGCACGCCTTGGATTAGCTCTGCAGAGTGTCTTGGTTGAGAGAAT AACCTCACCGTACCCACATGACACGTGATTTGGAAAGAGACTAGAGGCCACAC TTGATAAATCATGGGGAACAGATGTGTTCCACCCAACAAATGTGATAAGTGAT CATGCAGCCAGAGCCAGCCTTCCTTCAATCAAGGTTTCCAGGCAGAGCAAATA CCCTAGAGATTCTCTGTGATATAGGAAATTTGGATGAAGGGAGCTAGAAGAAA TACAGGGATTTTTTTTTTTTTTTAAGATGGAGTCTTACTCTGTTGCTAGGCTG GAGTGCAGTGGTGCGATCTCAGCTCCCTGCAACCTCCACCTCCTGGGTTCAAA CAATTCTCCTGCCTCAGCCTCCCGAGTACTGGGAATATAGGTGCACGCCACCA CACCCAACAAATTTTTGTACTTTTAGTACAGATGAGGGTTCACTATGTTGGCC AGGATGGTCTCGATCTCTTGACCTCATGATCCACCCACCTCGGTCTCCCAAAG TGCTGGGATTACAGGCTTGAGCCACCGGGTGACCGGCTTACAGGGATATTTTT AATCCCGTTATGGACTCTGTCTCCAGGAGAGGGGTCTATCCACCCCTGCTCAT TGGTGGATGTTAAACCAATATTCCTTTCAACTGCTGCCTGCTAGGGAAAAACT ACTCCTCATTATCATCATTATTATTGCTCTCCACTGTATCCCCTCTACCTGGC ATGTGCTTGTCAAGTTCTAGTTGTTCAATAAATTTGTTAATAATGCTGA (SEQ ID NO: 93) >NP_008979.3 butyrophilin subfamily 3 member A1 isoform a precursor [*Homo sapiens*] MKMASFLAFLLLNFRVCLLLLQLLMPHSAQFSVLGPSGPILAMVGEDADLPCH LFPTMSAETMELKWVSSSLRQVVNVYADGKEVEDRQSAPYRGRTSILRDGITA GKAALRIHNVTASDSGKYLCYFQDGDFYEKALVELKVAALGSDLHVDVKGYKD GGIHLECRSTGWYPQPQIQWSNNKGENIPTVEAPVVADGVGLYAVAASVIMRG SSGEGVSCTIRSSLLGLEKTASISIADPFFRSAQRWIAALAGTLPVLLLLLGG AGYFLWQQQEEKKTQFRKKKREQELREMAWSTMKQEQSTRVKLLEELRWRSIQ YASRGERHSAYNEWKKALFKPADVILDPKTANPILLVSEDQRSVQRAKEPQDL PDNPERFNWHYCVLGCESFISGRHYWEVEVGDRKEWHIGVCSKNVQRKGWVKM TPENGFWTMGLTDGNKYRTLTEPRTNLKLPKPPKKVGVFLDYETGDISFYNAV DGSHIHTFLDVSFSEALYPVFRILTLEPTALTICPA (SEQ ID NO: 94)
Human BTN3A2	>NM_007047.5 *Homo sapiens* butyrophilin subfamily 3 member A2 (BTN3A2), transcript variant 1, mRNA GACTCTTACTGTTTCTCATGGTGAGAAGACAATATTTGCTTTCTCTTTTTCCT TTCTTCCGGATGAGAGGCTAAGCCATAATAGAAAGAATGGAGAATTATTGATT GACCGTCTTTATTCTGTGGGCTCTGATTCTCCAATGGGAATACCAAGGGATGG TTTTCCATACTGGAACCCAAAGGTAAAGACACTCAAGGACAGACATTTTTGGC AGAGCATAGATGAAAATGGCAAGTTCCCTGGCTTTCCTTCTGCTCAACTTTCA TGTCTCCCTCCTCTTGGTCCAGCTGCTCACTCCTTGCTCAGCTCAGTTTTCTG TGCTTGGACCCTCTGGGCCCATCCTGGCCATGGTGGGTGAAGACGCTGATCTG CCCTGTCACCTGTTCCCGACCATGAGTGCAGAGACCATGGAGCTGAAGTGGGT AAGTTCCAGCCTAAGGCAGGTGGTGAACGTGTATGCAGATGGAAAGGAAGTGG AAGACAGGCAGAGTGCACCGTATCGAGGGAGAACTTCGATTCTGCGGGATGGC ATCACTGCAGGGAAGGCTGCTCTCCGAATACACAACGTCACAGCCTCTGACAG TGGAAAGTACTTGTGTTATTTCCAAGATGGTGACTTCTATGAAAAAGCCCTGG TGGAGCTGAAGGTTGCAGCACTGGGTTCTAATCTTCACGTCGAAGTGAAGGGT TATGAGGATGGAGGGATCCATCTGGAGTGCAGGTCCACCGGCTGGTACCCCCA ACCCCAAATACAGTGGAGCAACGCCAAGGGAGAGAACATCCCAGCTGTGGAAG CACCTGTGGTTGCAGATGGAGTGGGCCTATATGAAGTAGCAGCATCTGTGATC ATGAGAGGCGGCTCCGGGGAGGGTGTATCCTGCATCATCAGAAATTCCCTCCT CGGCCTGGAAAAGACAGCCAGCATTTCCATCGCAGACCCCTTCTTCAGGAGCG CCCAGCCCTGGATCGCAGCCCTGGCAGGGACCCTGCCTATCTTGCTGCTGCTT CTCGCCGGAGCCAGTTACTTCTTGTGGAGACAACAGAAGGAAATAACTGCTCT GTCCAGTGAGATAGAAAGTGAGCAAGAGATGAAAGAAATGGGATATGCTGCAA CAGAGCGGGAAATAAGCCTAAGAGAGAGCCTCCAGGAGGAACTCAAGAGGAAA AAAATCCAGTACTTGACTCGTGGAGAGGAGTCTTCGTCCGATACCAATAAGTC AGCCTGATGCTCTAATGGAAAAATGGCCCTCTTCAAGCCTGGTGAGGAAATGC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TTCAGATGAGGCTCCACCTTGTTAAATAAATTGGATGTATGGAAAAATAGACT GCAGAAAAGGGGAACTCATTTAGCTCACGAGTGGTCGAGTGAAGATTGAAAAT TAACCTCTGAGGGCCAGCACAGCAGCTCATGCCTGTAATCCTAGCACTTTGGA AGGCTGAGGAGGGCGGATCACAAGGTCAGGAGATCAAGACCATCCTGGCTAAC ACGGTGAAACCCCGTCTCTACTAAAAATACAAAAAATAAAAAATTAGCCGGGC ATGGTGACGGGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAAT GGCATGAACCCGGAAGGCAGAGCTTGCAGTGAGCCGAGATCACGCCACTGCAC TCCAGCCTGGGAGACAGAGCGAGACTCTGTCTCAAGAAAAAAAAAAAAAAAAA AAAAGAAAAGAAAATTAACCTCTGAGTATAAAGCATCAGTGGGCAGAATCAAT GTGGGGAGGGAAACAACAAAAATGTAGAAAGAGGATCCTTGTTGCTTCTTGGG GCCGCATCAGGGTATTGGGTTAGGCAGATACTGACCTTACTTTCATTTCCCCT CTGGTCACTAGACCCCTGGGGCTTTCACCAATGACATTGATGAGAGAATCACA TTCAGGGCAGGCTAGGGACACGGGGTTCTGGAAGGACCTCCTCAGCATGGCCC AAGCCTTGCATGCTGTGGCTCTTAAATCCAGGAAAAATGGCTGACCCCATGGA CACCTCCTCAAACTCTCTGCAGCAGATGTAATTCTGTATCCAGACATGGCAAA TGCCATCCTCCTTGTTTCTGAGGACCAGAGGAGTGTACAGCGTGCTGAGGAGC CCCATGACCTACCAGACAACCCTGAGAGATTTGAATGGCGTTACTGTGTGCTT GGCTGTGAAAGCTTCATGTCAGAGAGACACTACTGGGAGGTGGAAGTGGGGGA CAGAAAAGAGTGGCATATTGGGGTATGTAGTAAGAACGTGGAGAGGAAAAAAG TTTGGGTCAAAATGACACCGGAGAACGGATACTGGACTATGGGCCTGACTGAT GGGAATAAGTATCGGGCTCTCACTGAGCCCAGAACCAACCTGAAACTTCCTGA GCCTCCTAGGAAAGTGGGGGTCATCCTGGACTATGAGACTGGACATATCTCGT TCTACAATGCCACGGATGGATCTCATATCTACACATTTCTGCACGCCTCTTCC TCTGAGCCTCTGTATCCTGTATTCAGAATTTTGACCTTGGAGCCCACTGCCCT GACCGTTTGCCCAATACCAAAAGTAGAGAGTTCCCCCGATCCCGACCTAGTGC CTGATCATTCCCTGGAGATACCACTGACCCCAGGCTTAGCTAATGAAAGTGGG GAGCCTCAGGCTGAAGTAACATCTCTGCTTCTCCCTGCCCAGCCTGGAGCTAA GGGTCTCACCCTCCACAACAGCCAGTCAGAACCATAAAGCTACAGGCACACAC TGAAGCACTTTACTGATATTCATTCAATTATTCCATAGGACAGTTGTTTGAGT TTGGTGCCACCTTATTGGCCCCTTTATACAGATAAGGAAACTGGGGTGTAGAA AAGTGTATTGACTTTACAAAGCAGACAGGAATAGTGAACAACAGAGCTGGGAT CTGAACAACAATGACTAACATTAATGGAGAATTTAAAACGTTCTGAGTGCTGT GTTATGAGCTTTGGTGGGTGTCACTCCTTTAATCCTCACAACACCCTGTCAGG TAGTCTCATTTGGCAAGTATGGAAGCAGAGGCAGGGCAACATTAAGTAGCTTA CATAACTCACACGGTAATTTGTGCAGTTGGGAGATGTTCAGCTTCAGTCCCTG GCCAATTGCCCGTTCTTTTCCAGCCTGATTTTTCCTGCATGGGAAGAGCCCAC ATGTAGCCCTGAGGTTCCCTTCCCAGGACAGCTCCAGGATCGAGATCACTGTG AGTGGTTGTGGAGTTAAGACCCCTATGGACTCCTTCCCAGCTGATTATCAGAG CCTTAGACCCAGCACTCCTTGGATTGGCTCTGCAGAGTGTCTTGGTTGAGAGA ATAACGTTGCAGTTCCCACAGGGCATGTGACTTTGAAAGAGACTAGAGGCCAC ACTCAGTTAATAATGGGGCACAGATGTGTTCCCACCCAACAAATGTGATAAGT GATCGTGCAGCCAGAGCCAGCCTTCCTTCAGTCAAGGTTTCCAGGCAGAGCAA ATACCCTAGAGATTCTCTGTAATATTGGTAATTTGGATGAAGGAAGCTAGAAG AATTACAGGGATGTTTTTAATCCCACTATGGACTCAGTCTCCTGGAAAAGGAT CTGTCCACTCCTGGTCATTGGTGGATGTTAAACCCATATTCCTTTCAACTGCT GCCTGCTAGGGAAAACTGCTCCTCATTATCATCACTATTATTGCTCACCACTG TATCCCCTCTACTGGGCAAGTGCTTGTCAAGTTCTAGTTGTTCAATAAATTTG TTAATAATGCTGA (SEQ ID NO: 95) >NP_008978.2 butyrophilin subfamily 3 member A2 isoform a precursor [*Homo sapiens*] MKMASSLAFLLLNFHVSLLLVQLLTPCSAQFSVLGPSGPILAMVGEDADLPCH LFPTMSAETMELKWVSSSLRQVVNVYADGKEVEDRQSAPYRGRTSILRDGITA GKAALRIHNVTASDSGKYLCYFQDGDFYEKALVELKVAALGSNLHVEVKGYED GGIHLECRSTGWYPQPQIQWSNAKGENIPAVEAPVVADGVGLYEVAASVIMRG GSGEGVSCIIRNSLLGLEKTASISIADPFFRSAQPWIAALAGTLPILLLLLAG ASYFLWRQQKEITALSSEIESEQEMKEMGYAATEREISLRESLQEELKRKKIQ YLTRGEESSSDTNKSA (SEQ ID NO: 96)
Human BTN2A1	>NM_007049.5 *Homo sapiens* butyrophilin subfamily 2 member A1 (BTN2A1), transcript variant 1, mRNA AGATTTCGTTTCCTGCATCTCCAAACATGGCGACCTAGGAGAAGGGGAAGAAC AATTTTTTCTCCTCTTTTGGGAAGGTTTGTGTCTAGTAGTGCCTGTGCCCCTG GGCAGATTGGAGAGAAGAGGGACGACTGGAGAATCGTCGAGAACCAGCGGAGA AAAGAAAAAGCAACGTTTAATTCTAGAAGGCCTCCTGTCCCTGCCTGCTCTGG GTGCTCATGGAATCAGCTGCTGCCCTGCACTTCTCCCGGCCAGCCTCCCTCCT CCTCCTCCTCCTCAGCCTGTGTGCACTGGTCTCAGCCCAGTTTATTGTCGTGG GGCCCACTGATCCCATCTTGGCCACGGTTGGAGAAAACACTACGTTACGCTGC CATCTGTCACCCGAGAAAAATGCTGAGGACATGGAGGTGCGGTGGTTCCGGTC TCAGTTCTCCCCCGCAGTGTTTGTGTATAAAGGTGGCAGAGAGAGAACAGAGG AGCAGATGGAGGAGTACCGAGGAAGAACCACCTTTGTGAGCAAAGACATCAGC AGGGGCAGCGTGGCCCTGGTCATACACAACATCACAGCCCAGGAAAACGGCAC CTACCGCTGTTACTTCCAAGAAGGCAGGTCCTACGATGAGGCCATCCTGCACC TCGTAGTGGCAGGACTAGGCTCTAAGCCCCTCATTTCAATGAGGGGCCATGAA GACGGGGGCATCCGGCTGGAGTGCATATCTAGAGGGTGGTACCCAAAGCCCCT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CACAGTGTGGAGGGACCCCTACGGTGGGGTTGCGCCTGCCCTGAAAGAGGTCT CCATGCCTGATGCAGACGGCCTCTTCATGGTCACCACGGCTGTGATCATCAGA GACAAGTCTGTGAGGAACATGTCCTGCTCTATCAACAACACCCTGCTCGGCCA GAAGAAAGAAAGTGTCATTTTTATTCCAGAATCCTTTATGCCCAGTGTGTCTC CCTGTGCAGTGGCCCTGCCTATCATTGTGGTTATTCTGATGATACCCATTGCC GTATGCATCTATTGGATCAACAAACTCCAAAAGGAAAAAAAGATTCTGTCAGG GGAAAAGGAGTTTGAACGGGAAACAAGAGAAATTGCTCTAAAGGAACTGGAGA AAGAACGTGTGCAAAAAGAGGAAGAACTTCAAGTAAAAGAGAAACTTCAAGAA GAATTGCGATGGAGAAGAACATTCTTACATGCTGTTGATGTGGTCCTGGATCC AGACACCGCTCATCCCGATCTCTTCCTGTCAGAGGACCGGAGAAGTGTGAGAA GGTGCCCCTTCAGGCACCTAGGGGAGAGCGTGCCTGACAACCCAGAGAGATTC GACAGTCAGCCTTGTGTCCTAGGCCGGGAGAGCTTCGCTTCAGGGAAACATTA CTGGGAGGTGGAGGTGGAAAACGTGATTGAGTGGACTGTGGGGGTCTGTAGAG ACAGTGTTGAGAGGAAAGGGGAGGTCCTGCTGATTCCTCAGAATGGCTTCTGG ACCTTGGAGATGCATAAAGGGCAATACCGGGCCGTGTCCTCCCCTGATAGGAT TCTCCCTTTGAAGGAGTCCCTTTGCCGGGTGGGCGTCTTCCTGGACTATGAAG CTGGAGATGTCTCCTTCTACAACATGAGGGACAGATCGCACATCTACACATGT CCCCGTTCAGCCTTTTCCGTGCCTGTGAGGCCCTTCTTCAGGTTGGGGTGTGA GGACAGCCCCATCTTCATCTGCCCTGCACTCACAGGAGCCAATGGGGTCACGG TGCCTGAAGAGGGCCTGACACTTCACAGAGTGGGGACCCACCAGAGCCTATAG AATCAATTCCTTGGTCTCACAGCCATGTAGACAAGCCCTGGTCATCTCAGCAG CCACCGCACAACACCCCTGGTGGAAGACACGCCCTCCTCCCCTCTGGTCACAC AAGAGAACATCTTCCAGCTGCCTCTTTCACACCCACTACAGACCTCAGCCCCA GTTTTCTCCTCCTCACTAGGCTGTGTTTTTAGTAGTTCCTTTGCTTGTAACTA TGGGATGGGATCCAGGCATAGGGAACTAGTTGTTACACAGCTCCCAGCCAAGA AGAAAGTGTGAGAAGTTGATGGGCAGCAAACCTGCTGTTTAACATCAGGGTGA CCACATTAAGCCCAGTATTCCAGTTGGCACCAGAAGATATGGACTTGGAATGA GGCCTACAGGGTTCACCAGGATGTAAGAGGAGAGAGGAATCCACAGGACCACC AGAGAGGAGAGGGAACCAGATATGCAGATCAGAGATAGAGGAAGTGGAACCAG AGAGCTGGGAGGGACCAAGGTTGTAAGGGTGGCTAAGTCCCACCATAACAGCT AAGGGGACCTGGGAGATGATGGCTCATTTCCACCCAGCCCCAGGATTTCCAGA GCGCACATCCACAGGCCTGGACCTGGGATGAAGATGAATGAAGAACATGGATG CACGTGGATGTAGTTTGGCTCAGGTGTCCCTGCAGTTGGCAAGGAGTCAGTAC TCAGTCCCTGAGTGTGGCTGAAATTTGAGGTCCTGGCTGAGCCAAGGAGTAAT GGACCAGATCTACCTCAGTATTCAAGTTCAGTGGGGACACCAGTGGCTTCAAA CTTCCTGGTTTCATGATATCTTGAGACGCCTTACAAATGATGGAGGATTCCAA AGAGTTTTTGTTTATTTGGGTTAATATTTGTTGGTATTTATGGCATTTGAGAT TGAAACTAAGAAATGTTTTAATTTATTACCTTTACAACATTTATTTACATTAC ATACATACATTTACAACATTTATTAATTTATATTAAAATAGCATGAATAAGCC AATTATAGGTTAATATAAGTAGAATGTTTGTGAAAAATAAGTATGGTATCCAA AGCAAAATAAATTTTATTGTGAAGTGTG (SEQ ID NO: 97)
	>NP_008980.1 butyrophilin subfamily 2 member A1 isoform 1 precursor [*Homo sapiens*] MESAAALHFSRPASLLLLLLSLCALVSAQFIVVGPTDPILATVGENTTLRCHL SPEKNAEDMEVRWFRSQFSPAVFVYKGGRERTEEQMEEYRGRTTFVSKDISRG SVALVIHNITAQENGTYRCYFQEGRSYDEAILHLVVAGLGSKPLISMRGHEDG GIRLECISRGWYPKPLTVWRDPYGGVAPALKEVSMPDADGLFMVTTAVIIRDK SVRNMSCSINNTLLGQKKESVIFIPESFMPSVSPCAVALPIIVVILMIPIAVC IYWINKLQKEKKILSGEKEFERETREIALKELEKERVQKEEELQVKEKLQEEL RWRRTFLHAVDVVLDPDTAHPDLFLSEDRRSVRRCPFRHLGESVPDNPERFDS QPCVLGRESFASGKHYWEVEVENVIEWTVGVCRDSVERKGEVLLIPQNGFWTL EMHKGQYRAVSSPDRILPLKESLCRVGVFLDYEAGDVSFYNMRDRSHIYTCPR SAFSVPVRPFFRLGCEDSPIFICPALTGANGVTVPEEGLTLHRVGTHQSL (SEQ ID NO: 98)
Human BTNL8	>NM_001040462.3 *Homo sapiens* butyrophilin like 8 (BTNL8), transcript variant 2, mRNA AGAACAGCGCAGTTTGCCCTCCGCTCACGCAGAGCCTCTCCGTGGCTTCCGCA CCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCATCCGTCACCTCTC CTGTCATCCGTTTCCATGCCGTGAGGTCCATTCACAGAACACATCCATGGCTC TCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAG GTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATT CTCCTGTTTCCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCT TCAGGGGCCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAG CCATTTATGCAGATGCCACAGTATCAAGGCAGGACAAAACTGGTGAAGGATTC TATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTACTGTGTTGGATG CTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCATC TGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCTCATTTCCATCACGGG ATATGTTGATAGAGACATCCAGCTACTCTGTCAGTCCTCGGGCTGGTTCCCCC GGCCCACAGCGAAGTGGAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCC AGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGT CCAAGAGAACGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCC GAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGAGCCTATATCG TGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTGG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGG AACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAA CACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGT TTCTGATCTGAAAACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACT CTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCA GGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCGTGGG AGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG ATCATGGGTACTGGGTCCTCAGACTGAATGGAGAACATTTGTATTTCACATTA AATCCCCGTTTTATCAGCGTCTTCCCCAGGACCCCACCTACAAAAATAGGGGT CTTCCTGGACTATGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGT CCCTTATTTATACCCTGACATGTCGGTTTGAAGGCTTATTGAGGCCCTACATT GAGTATCCGTCCTATAATGAGCAAAATGGAACTCCCATAGTCATCTGCCCAGT CACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCCAG AGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCCTCCCCAGG GGTGAAATGTAGGATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGT CTCTCTCCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATG AAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCT GGGAGGGAAGAAGGCTGACATTACATTTAGTTTGCTCTCACTCCATCTGGCTA AGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCGTCAGGAATTCCCATCT CACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAGATC TTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAG TAA (SEQ ID NO: 99) >NP_001035552.1 butyrophilin-like protein 8 isoform 2 precursor [*Homo sapiens*] MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEV RFFRGQFSSVVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITV LDAGLYGCRISSQSYYQKAIWELQVSALGSVPLISITGYVDRDIQLLCQSSGW FPRPTAKWKGPQGQDLSTDSRTNRDMHGLFDVEISLTVQENAGSISCSMRHAH LSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSKFQWKI QAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPQEV PHSEKRFTRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTL SPDHGYWVLRLNGEHLYFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNIN DQSLIYTLTCRFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASA IPETSNSESSSQATTPFLPRGEM (SEQ ID NO: 100)
Human BTN2A2	>NM_006995.5 *Homo sapiens* butyrophilin subfamily 2 member A2 (BTN2A2), transcript variant 1, mRNA GGGACTTTTTGGACACCCAGAGAACAGGTCCCAGATACCGAGTCCGCAACTCC AAACATCGCGATTAATAGGAGGCCTCTGGTCTCTGCCTGCCCTGGGTGCTCAT GGAACCAGCTGCTGCTCTGCACTTCTCCCTGCCAGCCTCCCTCCTCCTCCTCC TGCTCCTCCTCCTTCTCAGCCTGTGTGCACTGGTCTCAGCCCAGTTTACTGTC GTGGGGCCAGCTAATCCCATCCTGGCCATGGTGGGAGAAAACACTACATTACG CTGCCATCTGTCACCCGAGAAAAATGCTGAGGACATGGAGGTGCGGTGGTTCC GGTCTCAGTTCTCCCCCGCAGTGTTTGTGTATAAGGGTGGGAGAGAGAGAACA GAGGAGCAGATGGAGGAGTACCGGGGAAGAATCACCTTTGTGAGCAAAGACAT CAACAGGGGCAGCGTGGCCCTGGTCATACATAACGTCACAGCCCAGGAGAATG GGATCTACCGCTGTTACTTCCAAGAAGGCAGGTCCTACGATGAGGCCATCCTA CGCCTCGTGGTGGCAGGCCTTGGGTCTAAGCCCCTCATTGAAATCAAGGCCCA AGAGGATGGGAGCATCTGGCTGGAGTGCATATCTGGAGGGTGGTACCCAGAGC CCCTCACAGTGTGGAGGGACCCCTACGGTGAGGTTGTGCCCGCCCTGAAGGAG GTTTCCATCGCTGATGCTGACGGCCTCTTCATGGTCACCACAGCTGTGATCAT CAGAGACAAGTATGTGAGGAATGTGTCCTGCTCTGTCAACAACACCCTGCTCG GCCAGGAGAAGGAAACTGTCATTTTTATTCCAGAATCCTTTATGCCCAGCGCA TCTCCCTGGATGGTGGCCCTAGCTGTCATCCTGACCGCATCTCCCTGGATGGT GTCCATGACTGTCATCCTGGCTGTTTTCATCATCTTCATGGCTGTCAGCATCT GTTGCATCAAGAAACTTCAAAGGGAAAAAAAGATTCTGTCAGGGGAAAAGAAA GTTGAACAAGAGGAAAAAGAAATTGCACAGCAACTTCAAGAAGAATTGCGATG GAGAAGAACATTCTTACATGCTGCTGATGTGGTCCTGGATCCAGACACCGCTC ATCCCGAGCTCTTCCTGTCAGAGGACCGGAGAAGTGTGAGGCGGGGCCCCTAC AGGCAGAGAGTGCCTGACAACCCAGAGAGATTCGACAGTCAGCCTTGTGTCCT GGGATGGGAGAGCTTCGCCTCAGGGAAACATTACTGGGAGGTGGAGGTGGAAA ACGTGATGGTGTGGACTGTGGGGGTCTGCAGACACAGTGTTGAGAGGAAAGGG GAGGTCCTGCTGATTCCTCAGAATGGCTTCTGGACCCTGGAGATGTTTGGAAA CCAATACCGGGCCCTGTCCTCCCCTGAGAGGATTCTCCCTTTGAAGGAGTCCC TTTGCCGGGTGGGCGTCTTCCTGGACTATGAAGCTGGAGATGTCTCCTTCTAC AACATGAGGGACAGATCGCACATCTACACATGTCCCCGTTCAGCCTTTACTGT GCCTGTGAGGCCCTTCTTCAGGTTAGGGTCTGATGACAGCCCCATCTTCATCT GCCCTGCACTCACAGGAGCCAGTGGGGTCATGGTGCCTGAAGAGGGCCTGAAA CTTCACAGAGTGGGGACCCACCAGAGCCTATAGAATCAATTCCTTGGACTCAC AGCCATGCAGATAAGCCCTGGCCATCTCAGCAGCCACCGCACAACCCCCCTAA TGAAAGACACGCCCTCCTCCCCTCTGGTCACGTAAGAGAACATCTTCCAGCTG CCTTTTTCACACCCACTCCAGCCCTCTGCCCCAGTTTTCTCCTCCTCACTAGT CTGTGGCTTTAGTAGTTCCTTTGCTTGTAATTATGGGATGGGATCCAGGCATA GGGAACTAGTTGTTTCATAGCTCCCAGTCAAAAAGAAAGTGAGAGAAGCTGTT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GGGCAGCGAACCTACTGTTTAAAATCAGGATAACCACATTAAGCCCAATATGC CAGTTGGCACCAGATGCTGTGGACTTGGAATGAGGCCAACAGGGTTCACCAGG ATGAGAGAGGAGAGAGGAATCCACAGGACCACCAGAAGGGAGAGGGAACCAGA TATGCAGATCAGAGATAGAGGAAGTGGAACCAGAGAGCTGGGAGGGACCAAGG TTGTAAGGATGGCTAAGTCCCACCATAAGAGCTAAAGGGTCCTGGGAGATGAT GGCTCATTTCCACCCAACCCCAGGATTTCCACAGCACACACCCACAGGCCTGG ACCTGGGATGAAGATGAATGAAGAACATGGACTCATGTGGATGTGGTTTGGCT CAGATGTCCCTGCAATAAACAAGGGGTCAGTACTTAGTCCCTGAGTGTGGTTG AGGTTTGAGGTCCTGGTCGAGCAGGGCAGTACTGGACCAGGTCTACGTCAGCA TTCAGGTTCAATGGGGACACCAGTGGCTTCAAACTTCCTGATCTAATTATGTT TTTAGACACTTAGAAGTTATTGAGGACTTTAAAGAGCTTTTGTTTATTTGGGT TAATATTTATGACATTTGACATTGAAACAAAAATTTAAAATGTTATCTTTTAA TTTATGTTAAAATAGCATTAATAAATCAGTTATAGGTTAATGTAGATAGGATG TTTTGTGAAAAAGCAATCTATTGTGTCCAAATAAAAAAACAAAAAGTGTGACA CTGGTTAACTTTTTCCAGATCTCATGTCTGGCTTAATAAGAGATATTTGTATT ATCATATCTGCCTTTGTATTAAACCTATTGGTATATCATAGGTCATGTTAGCT CAAAAAAACTTTACTGCACACTACTGAGAGAATGAGATGAAAAACGATTAATG TTTCATTATTATTATTGTGAAAATATTATTAACACTGGGGACTCCTTAAGAGT ACATCAGAGTTCTCTCTAGGAATCCCAAAACCACATTTTGAAACTAGAATAGT GGATCCTGGAAGTTAATCCATGTGCTGGTTAATTTTAGATGTCAACCTGACTG GATTAAGGAATACCTAGACAGCTGGTACAACATTATTTCTGGGTGTGTCTGTG AGTGTGTTTCCAGAAGAGATTGGCAAGTGAGTCAGTGGGAAATTCTCTCCTTC TGTTGGCTGGGTGCCCAATACAACAAAAAGGCAGAGGAAAGGCAAATTCTTCT CTCCTCTGGAGCTGAGACACTCTTCTTCTTCTGCCCTTGGACATCAGAACTCC TGGCTCTCCGGCCTTTGAACTTCAGGACTTGTACCAGGAGGCCCTGGGTTCTC AGGCCTTTGGCTTTGGACTGAGAGTTACACAATCAGCTTCCCTGGTTCTGAGG CTTTCAGACTTAAACTGAGCCATGCTACCAGCATCCCAGGGTCTCCAGCCTAC AGATGAGCTGTTGTGCGATTTCTTAGCCTCCATAATCACATGAGCCAATCTCC TTAATAAATGCCTGCTCATAGATCTGTATCTACATCTATATCTGTATGTGCAT CTATATCTATGCCTATATCTATATCTATATCATATTGATTTTGTCTCTCTGGA GAACCCTGACTAATAAAATGAGGCATCTAAAA (SEQ ID NO: 101) >NP_008926.2 butyrophilin subfamily 2 member A2 isoform a precursor [*Homo sapiens*] MEPAAALHFSLPASLLLLLLLLLSLCALVSAQFTVVGPANPILAMVGENTTL RCHLSPEKNAEDMEVRWFRSQFSPAVFVYKGGRERTEEQMEEYRGRITFVSKD INRGSVALVIHNVTAQENGIYRCYFQEGRSYDEAILRLVVAGLGSKPLIEIKA QEDGSIWLECISGGWYPEPLTVWRDPYGEVVPALKEVSIADADGLFMVTTAVI IRDKYVRNVSCSVNNTLLGQEKETVIFIPESFMPSASPWMVALAVILTASPWM VSMTVILAVFIIFMAVSICCIKKLQREKKILSGEKKVEQEEKEIAQQLQEELR WRRTFLHAADVVLDPDTAHPELFLSEDRRSVRRGPYRQRVPDNPERFDSQPCV LGWESFASGKHYWEVEVENVMVWTVGVCRHSVERKGEVLLIPQNGFWTLEMFG NQYRALSSPERILPLKESLCRVGVFLDYEAGDVSFYNMRDRSHIYTCPRSAFT VPVRPFFRLGSDDSPIFICPALTGASGVMVPEEGLKLHRVGTHQSL (SEQ ID NO: 102)
Mouse BTN2A2	>NM_175938.3 *Mus musculus* butyrophilin, subfamily 2, member A2 (Btn2a2), transcript variant 1, mRNA GAAATTGTGAGACTTGCACGCGGAATGGGTCCTCCGAGGTCTGCTGTCGCGAG TCCCAGCACTTTGCAAGTAATGGAGAACAGAAAATTCTTTCCTCTCTACTGTA GCAGTTTGTTCTCTGGTGGCGACTGTGCTCAGCGACAAGTTGGAGAGTAGAGA AAAGGCAAGATAATCAGCATTTGAGGGTCAGAGAAGAAAAGAAAACGCAGTTA ATTCTAGAAGGTTTTCTGTCCACACGTGACCTAGGTGACTCTGTCCTGAAGAC CTATGGAGCCTACAACTTCCCTGCGTTCTTGCCCGATAGCCTCCCTTCTCTTC TTCTTGGTCCTCAGCCTGTTTGTGCTGGTCTCAGCCCAGTTTACTGTCATAGG ACCAGCTGAGCCCATCCTGGCCATGGTAGGAGAGAATACCACACTACACTGCC ACCTGTCACCAGAGAGAAATGCCGAAGAGATGGAGGTGCGGTGGTTCCGGTGG CGTTTCTTCCCTGCAGTGCTGGTGTACAGAGGCCATCAAGAGAGACCAGAGGA GCAGATGGTGGCATACCGAGGAAGAACCACCTTCATGCGCACAGACATCAGCA AGGGAAGAGTTGCGCTCATTATCCACAATGTCACAGCCTATGACAATGGCATC TACTGCTGTTACTTCCAGGAAGGCAGGTCCTATGACCAGGCAACCATGAAGCT TATGGTGGCAAGCCTTGGCTCTGAGCCACTTATTAAAATGAAGACACTTGAGG ATGGGAGCATCTTGCTAGAGTGCACATCTGAAGGGTGGTACCCAGAGCCCCGA GCTGTGTGGAGAGACCCCTATGATGAAGTTGTACCTGCCCTGGAGGAGGAGTA TACAGCTGACAGAGAAGGCCTCTTCACAGTCACCATGACTATAATCATCAGGG ACTGCTCTGTGAGGAACATGACCTGCTCTGTCAATAACACTCTGCTCAGCCAG GAGGTGGAAAGTGTGATTCTCATTCCAGAATCCTTCGTGCCCAGCCTTCCTCT GTGGATGGTGGCTGTGGCTGTCACTCTGCCTGTAGTAATGCTGATTCTCCTCA CATCTGGAAGCATCTGCCTTGTCAAGAAACACCGCAGGAAGAAATCTATTCTG TCAGCTGAAAAAGAAGCCGAATATGAAGAGAAGGAAGCTGCACGGCAACTTCA AGAGGAACTGCGATGGAGACGAACCCTCTTACATGCTGCTGACGTGGTCCTGG ACCCAGATACAGCTCATCCTGAGCTCTTCCTGTCAGATGACCAGAGAAGTGTA ATACGAGGCTCTTCGAGGCAGAGTGTGCCTGACAACCCTGAGAGATTTGACTG CCGTCCATGTGTCCTGGGCAGGGAAAGCTTCTCCTCAGGGAAGCATTACTGGG AGGTGGAGGTGGAAAATGTAATGGTGTGGGCCATTGGTGTTTGTAGAGACAGC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GTGGAAAGGAAAGGGGAGGCCCTGTTGGTTCCTCAGAATGGCTTCTGGACCCT GGAGATGTTTGGAAGCCAGTATCGAGCCCTGTCCTCCCCAGAAAAGATCATAC CTCTGAAAGAGCGTCTTCACCGTATAGCTGTCTTCCTGGACTGTGAGGGTGGA GATATTTCTTTCTACAACATGAGAGACAGATCACACATTTACACATGTCCTCC TGTGACTTTCACTGGGCCCCTGAGACCCTTCTTTAGGCTTGGTTCTGATGACA GTCCCCTGTTCATCTGTCCAGCATTCACAGGGGCACAGGGAGTTACAATACCT GAGGGTGGCTTATTCCTATATAAGACAAGACCAATTTCTCAGAGCCTTGTAAG GAAGCCATAGCTCTCTACACAGTACCATCTGTTGGAGACTAGACCCCATGTCC TTCAGATCACATGGAGCATCTTCCAGCTGCCACCTTCACACATACTTCAGGCC CAGTCCTCAGATTACTACATCATTTCTTCTAACTATGGGCCTAGGTAGAGCCA GTCTTAGGGGACTATTGCTGTAATACAGCTCTCTCCTGAGAAGAAAGTGTGAG AAGGGCAGAAAACTTGGAGTTTCAACATGCTGCTCTGGTCACAGTGGATATCA GGCAAGAGCAACAGGGTGGATCAGGATGTAAGAAGTGAGAACTACAGAGGAAG GAGACAGATAAAGATGAATTGAGGCCGAAGATGGAGGAAATGGACTGAAGAGC TCTGGGGTAAGCCCTATGTGACAGCTGTGGATAGGTAGGAGCTAATGGTCCAT TGATATCCAAAGCCAAAGATTTAAATATCACATAGTGTGTCTGGAGTGTATAT CTGTAGACCTACACATGAGAGGAAACAATCATAGTGATGAACTGGATGTAAGC TGGCTCAGACGTCCCTACAATAAACACTTCTGAGTTCCATGTCTGTGCTCAGT AAGAATGGCTTGAGGCTTGCGGTCCATGCTGAGCAGCCAGGTCCACATGAATC GGATTTACTAGAGTAGGTAGCAGTTCAAGTTCCTTAGGCTCAGGATGTCTTCC TTTCCCCCAAGCCCTTCCCCCTTCAAGATAGGTCTCACTATGTAGACCAGGCC AGCCTCCACCTCCAGAGTTCTGGGATTAAAGACAAGCACAACCATGTCCAGTT TATGAGCTTGTGATATATACAGAAGATTAAGTTCTGTGTTCTTGGGTTAGTAA CTGTTGAGATTTGTTTTGAGTCATGCTCTCACTGGCTAGCACTGCTCTTGACT TTCTCTCCCCATCTTTTTGTTATTGCTTTTCAAGACATGGTTTCACTGTGTAT TTCTGGCTGATAAGCTGATTTTGAATTCACAGAGATCTGCCTCTGCCTCCTGA GTGCTGGGATTAAAGGTGTGTTACACTACGCCTGGCTTCACTCTATCTCTTCA GTGTGGGGATTATAGGTTTATACTATCATGCCTAACTAATGTCTGTTGCTGCA TATGACATTTGAACTTTAGAACAGAAAAACAACTATACATATTAATATATATT AAACTAATAATAAGC (SEQ ID NO: 103) >NP_787952.2 butyrophilin subfamily 2 member A2 isoform 1 precursor [*Mus musculus*] MEPTTSLRSCPIASLLFFLVLSLFVLVSAQFTVIGPAEPILAMVGENTTLHCH LSPERNAEEMEVRWFRWRFFPAVLVYRGHQERPEEQMVAYRGRTTFMRTDISK GRVALIIHNVTAYDNGIYCCYFQEGRSYDQATMKLMVASLGSEPLIKMKTLED GSILLECTSEGWYPEPRAVWRDPYDEVVPALEEEYTADREGLFTVTMTIIIRD CSVRNMTCSVNNTLLSQEVESVILIPESFVPSLPLWMVAVAVTLPVVMLILLT SGSICLVKKHRRKKSILSAEKEAEYEEKEAARQLQEELRWRRTLLHAADVVLD PDTAHPELFLSDDQRSVIRGSSRQSVPDNPERFDCRPCVLGRESFSSGKHYWE VEVENVMVWAIGVCRDSVERKGEALLVPQNGFWTLEMFGSQYRALSSPEKIIP LKERLHRIAVFLDCEGGDISFYNMRDRSHIYTCPPVTFTGPLRPFFRLGSDDS PLFICPAFTGAQGVTIPEGGLFLYKTRPISQSLVRKP(SEQ ID NO: 104)
Human BTN1A1	>NM_001732.3 *Homo sapiens* butyrophilin subfamily 1 member A1 (BTN1A1), mRNA AGCTTTCTCACTTGGTAGCAGTGGCCTCTTGTGCCTTTTTCTCCAAGATCACC CAGGCTGAAGCTCCTGAGGGGACTCACATCAGTTATCTTGCTGCTCCAGAAGG GTGGGAGATGGCAGTTTTCCCAAGCTCCGGTCTCCCCAGATGTCTGCTCACCC TCATTCTCCTCCAGCTGCCCAAACTGGATTCAGCTCCCTTTGACGTGATTGGA CCCCCGGAGCCCATCCTGGCCGTTGTGGGTGAGGACGCCGAGCTGCCCTGTCG CCTGTCTCCGAACGCGAGCGCCGAGCACTTGGAGCTACGCTGGTTCCGAAAGA AGGTTTCGCCGGCCGTGCTGGTGCATAGGGACGGGCGCGAGCAGGAAGCCGAG CAGATGCCCGAGTACCGCGGGCGGGCGACGCTGGTCCAGGACGGCATCGCCAA GGGGCGCGTGGCCTTGAGGATCCGTGGCGTCAGAGTCTCTGACGACGGGGAGT ACACGTGCTTTTTCAGGGAGGATGGAAGCTACGAAGAAGCCCTGGTGCATCTG AAGGTGGCTGCTCTGGGCTCTGACCCTCACATCAGTATGCAAGTTCAAGAGAA TGGAGAAATCTGTCTGGAGTGCACCTCAGTGGGATGGTACCCAGAGCCCCAGG TGCAGTGGAGAACTTCCAAGGGAGAGAAGTTTCCATCTACATCAGAGTCCAGG AATCCTGATGAAGAAGGTTTGTTCACTGTGGCTGCTTCAGTGATCATCAGAGA CACTTCTGCGAAAAATGTGTCCTGCTACATCCAGAATCTCCTTCTTGGCCAGG AGAAGAAAGTAGAAATATCCATACCAGCTTCCTCCCTCCCAAGGCTGACTCCC TGGATAGTGGCTGTGGCTGTCATCCTGATGGTTCTAGGACTTCTCACCATTGG GTCCATATTTTTCACTTGGAGACTATACAACGAAAGACCCAGAGAGAGGAGGA ATGAATTCAGCTCTAAAGAGAGACTCCTGGAAGAACTCAAATGGAAAAAGGCT ACCTTGCATGCAGTTGATGTGACTCTGGACCCAGACACAGCTCATCCCCACCT CTTTCTTTATGAGGATTCAAAATCTGTTCGACTGGAAGATTCACGTCAGAAAC TGCCTGAGAAAACAGAGAGATTTGACTCCTGGCCCTGTGTGTTGGGCCGTGAG ACCTTCACCTCAGGAAGGCATTACTGGGAGGTGGAGGTGGGAGACAGGACTGA CTGGGCAATCGGCGTGTGTAGGGAGAATGTGATGAAGAAAGGATTTGACCCCA TGACTCCTGAGAATGGGTTCTGGGCTGTAGAGTTGTATGGAAATGGGTACTGG GCCCTCACTCCTCTCCGGACCCCTCTCCCATTGGCAGGGCCCCCACGCCGGGT TGGGATTTTCCTAGACTATGAATCAGGAGACATCTCCTTCTACAACATGAATG ATGGATCTGATATCTATACTTTCTCCAATGTCACTTTCTCTGGCCCCCTCCGG CCCTTCTTTTGCCTATGGTCTAGCGGTAAAAAGCCCCTGACCATCTGCCCAAT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TGCTGATGGGCCTGAGAGGGTCACAGTCATTGCTAATGCCCAGGACCTTTCTA AGGAGATCCCATTGTCCCCCATGGGGGAGGACTCTGCCCCTAGGGATGCAGAC ACTCTCCATTCTAAGCTAATCCCTACCCAACCCAGCCAAGGGGCACCTTAAGG AATATCTCAGCTCATCTGTTTTCCTTTCCTCTAACCCCTCTCCTCCATAGCCT TCTGAGGCTTCACCTGCTAGCTTTACCCAGTCTGTTTCTTCCTGTTGGGTGGC AATTAATTAATCCTGTGAAGGTTACATTGCTGCTGCTAGAGAGGGTGGGGATT GCACCTTCCAAATCTGTTTCTGTACCAATATTTGGGGGATGGAGGGGTGACTC AAACTGCTTCTAGTGTTCTCCTAATCCCTTAAGACTAGAACCTATAGGAAACT ACTTGGAGCAAACTCAAAGGACAGATTAGGGATCGAGATTGGGTCAGGTTAGC ATGGGGTTGTGGTTGAAATATCTTGGTATCCAGGATAAGGGTATGTGGAAAAA CAGGCTTTAGGCAAGTGGAAAATTCAAAATGTGCTGTGAAAGGACAATCTCAG GCTGAAATCCCATAAAGGAACTTGGAGGGAATATTATGATGGAGGGAAGTGAG GTGAATCCAGGCACATGATGAACACCTGGCTCATCCATAGAGTTTTCACAGCC TATATCGCAAATTTTCTAAGCCACGTCCTATAGGACAGAGGAGACTGGCCCCA CTTCTATGGGTCTGAGCTGTGGAAAAGGGAGAGCAGAGAGGAACTGAGATGAG CAGGGATGAAGGGTCAGGCAGAAAGCGTGATAGAGGAGAGAATTTTTGACAAA ACTCAAAAGTTGTTTGCACAGCTGTTCTTTGTACCCTGTTCCTTTCTCTGCGC CCTCCTGTTTCTCCCTTGCCTGGAAGTCATTCCACCCTCAATTTGTTGATCCA CAAGTTTCCAGTTGTCCTCTTCTTTTTGTTATAGCATCTCTCTATTTCAAAGA CATTCCTAGAAGTCATCCTTCAGTGATATCACCACTTGCTCAGTCACCATCTC AACCTTATGTCACCTCAGCCCTCATCTCAATGCCCAAACCCCTTACACACACC TTCAGTTAGCTTCAACTGCCTCCGTTTCCACACTGTGCACCTTTCACTTTCCC TACCCAGCTTTCCTACATGCTGCCTCTCCTCAGGGTCCCCTGAATGCTGCATC ATTGTGTTCAGTGCAGCTGGACTGATTGCACCTGTGTATTTGCCCCTGAGCAC TTTCCTTTACACATGTGGCTTGTCTTGCCAATAGACTCCAGGCTTATACCTTC CATTTCCATCGTATTCTCCAGTTTCCAGGATAGACGTTGCTCATCGTCTTTAC CTAATAAATAAGTTTGTCTGATTGCTGAAA (SEQ ID NO: 105) >NP_001723.2 butyrophilin subfamily 1 member A1 precursor [*Homo sapiens*] MAVFPSSGLPRCLLTLILLQLPKLDSAPFDVIGPPEPILAVVGEDAELPCRLS PNASAEHLELRWFRKKVSPAVLVHRDGREQEAEQMPEYRGRATLVQDGIAKGR VALRIRGVRVSDDGEYTCFFREDGSYEEALVHLKVAALGSDPHISMQVQENGE ICLECTSVGWYPEPQVQWRTSKGEKFPSTSESRNPDEEGLFTVAASVIIRDTS AKNVSCYIQNLLLGQEKKVEISIPASSLPRLTPWIVAVAVILMVLGLLTIGSI FFTWRLYNERPRERRNEFSSKERLLEELKWKKATLHAVDVTLDPDTAHPHLFL YEDSKSVRLEDSRQKLPEKTERFDSWPCVLGRETFTSGRHYWEVEVGDRTDWA IGVCRENVMKKGFDPMTPENGFWAVELYGNGYWALTPLRTPLPLAGPPRRVGI FLDYESGDISFYNMNDGSDIYTFSNVTFSGPLRPFFCLWSSGKKPLTICPIAD GPERVTVIANAQDLSKEIPLSPMGEDSAPRDADTLHSKLIPTQPSQGAP (SEQ ID NO: 106)
Mouse BTN1A1	>NM_013483.3 *Mus musculus* butyrophilin, subfamily 1, member A1 (Btn1a1), mRNA AACAGCACACAGCCTTCTTCCTTCTGAAGAGCTCTCTCTTTGGCCCCGGGGTG ACAAGCAGCCCTTTTCACTTGATCACTGTGGCTCTGGCTCCCTTTTCCTCTGG GTCTGTCGAAATCGCCTGAAGCTCTTGGCGGGCTTCATTGCCCCAGTTAGCTC AGAGATGGCAGTTCCCACCAACTCCTGCCTCCTGGTCTGTCTGCTCACCCTCA CTGTCCTACAGCTGCCCACGCTGGATTCGGCAGCTCCCTTCGATGTGACCGCA CCTCAGGAGCCAGTGTTGGCCCTAGTGGGCTCAGATGCCGAGCTGACCTGTGG CTTTTCCCCAAACGCGAGCTCAGAATACATGGAGCTGCTGTGGTTTCGACAGA CGAGGTCGACAGCGGTACTTCTATACCGGGATGGCCAGGAGCAGGAGGGCCAG CAGATGACGGAGTACCGCGGGAGGGCGACGCTGGCGACAGCCGGGCTTCTAGA CGGCCGCGCTACTCTGCTGATCCGAGATGTCAGGGTCTCAGACCAGGGGGAGT ACCGGTGCCTTTTCAAAGACAACGACGACTTCGAGGAGGCCGCCGTATACCTC AAAGTGGCTGCTGTGGGTTCAGATCCTCAAATCAGTATGACGGTTCAAGAGAA TGGAGAAATGGAGCTGGAGTGCACCTCCTCTGGATGGTACCCAGAGCCTCAGG TGCAGTGGAGAACAGGCAACAGAGAGATGCTACCATCCACGTCAGAGTCCAAG AAGCATAATGAGGAAGGCCTGTTCACTGTGGCAGTTTCAATGATGATCAGAGA CAGCTCCATAAAGAACATGTCCTGCTGCATCCAGAATATCCTCCTTGGCCAGG GGAAGGAAGTAGAGATCTCCTTACCAGCTCCCTTCGTGCCAAGGCTGACTCCC TGGATAGTAGCTGTGGCTATCATCTTACTGGCCTTAGGATTTCTCACCATTGG GTCCATATTTTTCACTTGGAAACTATACAAGGAAAGATCCAGTCTGCGGAAGA AGGAATTTGGCTCTAAAGAGAGACTTCTGGAAGAACTCAGATGCAAAAAGACT GTACTGCATGAAGTTGACGTGACTCTGGATCCAGACACAGCCCACCCCCACCT CTTCCTGTATGAAGATTCAAAGTCAGTTCGATTGGAAGATTCACGTCAGATCC TGCCTGATAGACCAGAGAGATTTGACTCCTGGCCCTGTGTGTTGGGCCGTGAG ACCTTTACTTCAGGGAGACATTACTGGGAGGTGGAGGTGGGAGATAGAACTGA CTGGGCCATTGGTGTGTGTAGGGAGAATGTGGTGAAGAAAGGGTTTGACCCCA TGACTCCTGATAATGGGTTCTGGGCTGTGGAGTTGTATGGAAATGGGTACTGG GCCCTCACCCCACTCAGGACCTCTCTCCGATTAGCAGGGCCCCCTCGCAGAGT TGGGGTTTTTCTGGACTATGACGCAGGAGACATTTCCTTCTACAACATGAGTA ACGGATCTCTTATCTATACTTTCCCTAGCATCTCTTTCTCTGGCCCCCTCCGT CCCTTCTTTTGTCTGTGGTCCTGTGGTAAAAAGCCCCTGACCATCTGTTCAAC TGCCAATGGGCCTGAGAAAGTCACAGTCATTGCTAATGTCCAGGACGACATTC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CCTTGTCCCCGCTGGGGGAAGGCTGTACTTCTGGAGACAAAGACACTCTCCAT TCTAAACTGATCCCGTTCTCACCTAGCCAAGCGGCACCATAACAAATATTCCA GCTTCACGACTTTGCCTTCCTTTGACTAATCCCTCATGCCCCGAAGCTTCAGC TGTTGGCTTCTTGCAGCCCTGCTTCTTCCTGGTGGATGGAGATTAATTCACAT TGGGAAGGTTAGGTATGTTGCTGCCAGACAAGGCAGGAAGAAAGGCCATCCTA GTTTGTTTCTGTACTAACAGTGGGGAGGAAGAGAGCTGAATCCTAAACTATTT CCAGTGCTCATATTCCTTCAGGCCAGAGCCTATAGAGAAGGATTTGGTACAAT CACTCGAGGGATCAAGAGGCAATTAGGTTGGCATGGAATTATGGCAGAAACAT CTGGAATAGGGGTATGTGGAATGACAGGTTTTAGGTAAGGGAGAACAAAACCA AACCATAGGATGCTGAGAAAGAAAGATCTTGGACTAAACTCCTAAAAAAGCAC TTAGAGAAGATATGACAGGCAAATGAAGTGAATTTGGTCTAATTTGATACACT TGCCCTGTCCCTAGGGTTTTTCAGTTATATCTCAATTTTTTTGTTGTTAATTA CATTTTTGACAGCTTCATACATGTATATAATGCATTCTAATTACTCTCACTCT CCTCTATTCTGTCTTATTTCCCTCCCCTCCCCTCATACCTTCCTTCTTGCTTC AAACCTGGCACACTGAGTTTAATGGGCTATCATGGGAACATGGATTTAGAGCT TTCCTCTGAGCTCAAGAGAGCAGGTGTGACTGAATACAGTGATTTCCCCTCTC CTACAATCAATCAGCAGTCAATAGCTCAGCTGGGAGGGGTAGGGCCTCATGAG ACTTCCCCTATCAAGGCTAAATGTTGAAAGGGCCAGTTTTTAGCACCTGTGAG ATCATGATTGCAAGAGCCCAGAAGACAGCATTGCTCGGTCATTCTCCCTACCC TTTGGCTTTTCTGGTOTTTTGTCCTCTCTTTCAGGATGTGTCTGAACTCTGTA TCTTAAGTTTTCTATGTCATGTTCTATAAGATAGAGGAGACTGGCCCTGCTTG TTTGAGAGCAATGTGAGCAAGCTAGCAAGAGACAGAAAGGAGCGGAGATGAAT AGGGGTAGAGAAAATTTTTAAACAAACCCTCCAGGTGTGTGTGTGTGTGTGTG TGTCTTCCTCTTTTTTGACCTCCCTAAAGGTCAATCCAACCTCACATTATTGA CTCCACTAGGTGGGGGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG TGTGTTTTAAGATAGAGGTTTACTATGTAGCTTAGGCTGGCTTTGAATTCCTG ATCCTCCTGCCTCTACCTTCCAAGTGCTGGAAACATAGCCACATCCACCACCC CTATCCAGTCCACCTGGTTTGATTCAGCAACGCTCAGGTAGCATCGCTGTTTG ATCTGGAGCTGCCAGCTCCCTCGGCCCCCACTGCAATGCTTAACCCCCTCACA GGCACCTTCCCTTGCCTAACACTGCCATCCTTTTCCACACTGAGCCATTTGCT CAATGTAGCCTACCCAGGTATCCTGCTTTCTGGTCCCCAAAGTTACACCATGA TGCTCAGCACAGCTGGACAGTTTGTCCCAATTTGTGTGTGTCCTCCTGTTTGT ATGGGACTTCTTTTTGTCAATGGCCTGTGTGTGTATCCAAGCTCTTCCACTTC TATTGTATTTTTCCGGCTTCTAAAACAGATGTTACCAAATAAAGAAAGAGAAA GAAAAAAAA (SEQ ID NO: 107) >NP_038511.1 butyrophilin subfamily 1 member A1 precursor [*Mus musculus*] MAVPTNSCLLVCLLTLTVLQLPTLDSAAPFDVTAPQEPVLALVGSDAELTCGF SPNASSEYMELLWFRQTRSTAVLLYRDGQEQEGQQMTEYRGRATLATAGLLDG RATLLIRDVRVSDQGEYRCLFKDNDDFEEAAVYLKVAAVGSDPQISMTVQENG EMELECTSSGWYPEPQVQWRTGNREMLPSTSESKKHNEEGLFTVAVSMMIRDS SIKNMSCCIQNILLGQGKEVEISLPAPFVPRLTPWIVAVAIILLALGFLTIGS IFFTWKLYKERSSLRKKEFGSKERLLEELRCKKTVLHEVDVTLDPDTAHPHLF LYEDSKSVRLEDSRQILPDRPERFDSWPCVLGRETFTSGRHYWEVEVGDRTDW AIGVCRENVVKKGFDPMTPDNGFWAVELYGNGYWALTPLRTSLRLAGPPRRVG VFLDYDAGDISFYNMSNGSLIYTFPSISFSGPLRPFFCLWSCGKKPLTICSTA NGPEKVTVIANVQDDIPLSPLGEGCTSGDKDTLHSKLIPFSPSQAAP (SEQ ID NO: 108)
Human TIGIT	>NM_173799.4 *Homo sapiens* T cell immunoreceptor with Ig and ITIM domains (TIGIT), mRNA ACATCTGCTTCCTGTAGGCCCTCTGGGCAGAAGCATGCGCTGGTGTCTCCTCC TGATCTGGGCCCAGGGGCTGAGGCAGGCTCCCCTCGCCTCAGGAATGATGACA GGCACAATAGAAACAACGGGGAACATTTCTGCAGAGAAAGGTGGCTCTATCAT CTTACAATGTCACCTCTCCTCCACCACGGCACAAGTGACCCAGGTCAACTGGG AGCAGCAGGACCAGCTTCTGGCCATTTGTAATGCTGACTTGGGGTGGCACATC TCCCCATCCTTCAAGGATCGAGTGGCCCCAGGTCCCGGCCTGGGCCTCACCCT CCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTATCACACCT ACCCTGATGGGACGTACACTGGGAGAATCTTCCTGGAGGTCCTAGAAAGCTCA GTGGCTGAGCACGGTGCCAGGTTCCAGATTCCATTGCTTGGAGCCATGGCCGC GACGCTGGTGGTCATCTGCACAGCAGTCATCGTGGTGGTCGCGTTGACTAGAA AGAAGAAAGCCCTCAGAATCCATTCTGTGGAAGGTGACCTCAGGAGAAAATCA GCTGGACAGGAGGAATGGAGCCCCAGTGCTCCCTCACCCCCAGGAAGCTGTGT CCAGGCAGAAGCTGCACCTGCTGGGCTCTGTGGAGAGCAGCGGGGAGAGGACT GTGCCGAGCTGCATGACTACTTCAATGTCCTGAGTTACAGAAGCCTGGGTAAC TGCAGCTTCTTCACAGAGACTGGTTAGCAACCAGAGGCATCTTCTGGAAGATA CACTTTTGTCTTTGCTATTATAGATGAATATATAAGCAGCTGTACTCTCCATC AGTGCTGCGTGTGTGTGTGTGTGTGTATGTGTGTGTGTGTTCAGTTGAGTGAA TAAATGTCATCCTCTTCTCCATCTTCATTTCCTTGGCCTTTTCGTTCTATTCC ATTTTGCATTATGGCAGGCCTAGGGTGAGTAACGTGGATCTTGATCATAAATG CAAAATTAAAAAATATCTTGACCTGGTTTTAAATCTGGCAGTTTGAGCAGATC CTATGTCTCTGAGAGACACATTCCTCATAATGGCCAGCATTTTGGGCTACAAG GTTTTGTGGTTGATGATGAGGATGGCATGACTGCAGAGCCATCCTCATCTCAT TTTTTCACGTCATTTTCAGTAACTTTCACTCATTCAAAGGCAGGTTATAAGTA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	AGTCCTGGTAGCAGCCTCTATGGGGAGATTTGAGAGTGACTAAATCTTGGTAT CTGCCCTCAAGAACTTACAGTTAAATGGGGAGACAATGTTGTCATGAAAAGGT ATTATAGTAAGGAGAGAAGGAGACATACACAGGCCTTCAGGAAGAGACGACAG TTTGGGGTGAGGTAGTTGGCATAGGCTTATCTGTGATGAAGTGGCCTGGGAGC ACCAAGGGGATGTTGAGGCTAGTCTGGGAGGAGCAGGAGTTTTGTCTAGGGAA CTTGTAGGAAATTCTTGGAGCTGAAAGTCCCACAAAGAAGGCCCTGGCACCAA GGGAGTCAGCAAACTTCAGATTTTATTCTCTGGGCAGGCATTTCAAGTTTCCT TTTGCTGTGACATACTCATCCATTAGACAGCCTGATACAGGCCTGTAGCCTCT TCCGGCCGTGTGTGCTGGGGAAGCCCCAGGAAACGCACATGCCCACACAGGGA GCCAAGTCGTAGCATTTGGGCCTTGATCTACCTTTTCTGCATCAATACACTCT TGAGCCTTTGAAAAAAGAACGTTTCCCACTAAAAAGAAAATGTGGATTTTTAA AATAGGGACTCTTCCTAGGGGAAAAAGGGGGGCTGGGAGTGATAGAGGGTTTA AAAAATAAACACCTTCAAACTAACTTCTTCGAACCCTTTTATTCACTCCCTGA CGACTTTGTGCTGGGGTTGGGGTAACTGAACCGCTTATTTCTGTTTAATTGCA TTCAGGCTGGATCTTAGAAGACTTTTATCCTTCCACCATCTCTCTCAGAGGAA TGAGCGGGGAGGTTGGATTTACTGGTGACTGATTTTCTTTCATGGGCCAAGGA ACTGAAAGAGAATGTGAAGCAAGGTTGTGTCTTGCGCATGGTTAAAAATAAAG CATTGTCCTGCTTCCTAAGACTTAGACTGGGGTTGACAATTGTTTTAGCAACA AGACAATTCAACTATTTCTCCTAGGATTTTTATTATTATTATTTTTTCACTTT TCTACCAAATGGGTTACATAGGAAGAATGAACTGAAATCTGTCCAGAGCTCCA AGTCCTTTGGAAGAAAGATTAGATGAACGTAAAAATGTTGTTGTTTGCTGTGG CAGTTTACAGCATTTTTCTTGCAAAATTAGTGCAAATCTGTTGGAAATAGAAC ACAATTCACAAATTGGAAGTGAACTAAAATGTAATGACGAAAAGGGAGTAGTG TTTTGATTTGGAGGAGGTGTATATTCGGCAGAGGTTGGACTGAGAGTTGGGTG TTATTTAACATAATTATGGTAATTGGGAAACATTTATAAACACTATTGGGATG GTGATAAAATACAAAAGGGCCTATAGATGTTAGAAATGGGTCAGGTTACTGAA ATGGGATTCAATTTGAAAAAAATTTTTTTAAATAGAACTCACTGAACTAGATT CTCCTCTGAGAACCAGAGAAGACCATTTCATAGTTGGATTCCTGGAGACATGC GCTATCCACCACGTAGCCACTTTCCACATGTGGCCATCAACCACTTAAGATGG GGTTAGTTTAAATCAAGATGTGCTGTTATAATTGGTATAAGCATAAAATCACA CTAGATTCTGGAGATTTAATATGAATAATAAGAATACTATTTCAGTAGTTTTG GTATATTGTGTGTCAAAAATGATAATATTTTGGATGTATTGGGTGAAATAAAA TATTAACATTA (SEQ ID NO: 109) >NP_776160.2 T-cell immunoreceptor with Ig and ITIM domains precursor [*Homo sapiens*] MRWCLLLIWAQGLRQAPLASGMMTGTIETTGNISAEKGGSIILQCHLSSTTAQ VTQVNWEQQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTLQSLTVNDTGEY FCIYHTYPDGTYTGRIFLEVLESSVAEHGARFQIPLLGAMAATLVVICTAVIV VVALTRKKKALRIHSVEGDLRRKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCG EQRGEDCAELHDYFNVLSYRSLGNCSFFTETG (SEQ ID NO: 110)
Mouse TIGIT	>NM_001146325.1:98-823 *Mus musculus* T cell immunoreceptor with Ig and ITIM domains (Tigit), mRNA ATGCATGGCTGGCTGCTCCTGGTCTGGGTCCAGGGGCTGATACAGGCTGCCTT CCTCGCTACAGGAGCCACAGCAGGCACGATAGATACAAAGAGGAACATCTCTG CAGAGGAAGGTGGCTCTGTCATCTTACAGTGTCACTTCTCCTCTGACACAGCT GAAGTGACCCAAGTCGACTGGAAGCAGCAGGACCAGCTTCTGGCCATTTATAG TGTTGACCTGGGGTGGCATGTCGCTTCAGTCTTCAGTGATCGGGTGGTCCCAG GCCCCAGCCTAGGCCTCACCTTCCAGTCTCTGACAATGAATGACACGGGAGAG TACTTCTGTACCTATCATACGTATCCTGGTGGGATTTACAAGGGGAGAATATT CCTGAAGGTCCAAGAAAGCTCAGTGGCTCAGTTCCAGACTGCCCCGCTTGGAG GAACCATGGCTGCTGTGCTGGGACTCATTTGCTTAATGGTCACAGGAGTGACT GTACTGGCTAGAAAGAAGTCTATTAGAATGCATTCTATAGAAAGTGGCCTTGG GAGAACAGAAGCGGAGCCACAGGAATGGAACCTGAGGAGTCTCTCATCCCCTG GAAGCCCTGTCCAGACACAAACTGCCCCTGCTGGTCCCTGTGGAGAGCAGGCA GAAGATGACTATGCTGACCCACAGGAATACTTTAATGTCCTGAGCTACAGAAG CCTAGAGAGCTTCATTGCTGTATCGAAGACTGGCTAA (SEQ ID NO: 111) >NP_001139797.1 T-cell immunoreceptor with Ig and ITIM domains precursor [*Mus musculus*] MHGWLLLVWVQGLIQAAFLATGATAGTIDTKRNISAEEGGSVILQCHFSSDTA EVTQVDWKQQDQLLAIYSVDLGWHVASVFSDRVVPGPSLGLTFQSLTMNDTGE YFCTYHTYPGGIYKGRIFLKVQESSVAQFQTAPLGGTMAAVLGLICLMVTGVT VLARKKSIRMHSIESGLGRTEAEPQEWNLRSLSSPGSPVQTQTAPAGPCGEQA EDDYADPQEYFNVLSYRSLESFIAVSKTG (SEQ ID NO: 112)
Human CD27L (CD70)	>NM_001252.5 *Homo sapiens* CD70 molecule (CD70), transcript variant 1, mRNA AGAGAGGGGCAGGCTGGTCCCCTGACAGGTTGAAGCAAGTAGACGCCCAGGAG CCCCGGGAGGGGGCTGCAGTTTCCTTCCTTCCTTCTCGGCAGCGCTCCGCGCC CCCATCGCCCCTCCTGCGCTAGCGGAGGTGATCGCCGCGGCGATGCCGGAGGA GGGTTCGGGCTGCTCGGTGCGGCGCAGGCCCTATGGGTGCGTCCTGCGGGCTG CTTTGGTCCCATTGGTCGCGGGCTTGGTGATCTGCCTCGTGGTGTGCATCCAG CGCTTCGCACAGGCTCAGCAGCAGCTGCCGCTCGAGTCACTTGGGTGGGACGT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	AGCTGAGCTGCAGCTGAATCACACAGGACCTCAGCAGGACCCCAGGCTATACT GGCAGGGGGGCCCAGCACTGGGCCGCTCCTTCCTGCATGGACCAGAGCTGGAC AAGGGGCAGCTACGTATCCATCGTGATGGCATCTACATGGTACACATCCAGGT GACGCTGGCCATCTGCTCCTCCACGACGGCCTCCAGGCACCACCCCACCACCC TGGCCGTGGGAATCTGCTCTCCCGCCTCCCGTAGCATCAGCCTGCTGCGTCTC AGCTTCCACCAAGGTTGTACCATTGCCTCCCAGCGCCTGACGCCCCTGGCCCG AGGGGACACACTCTGCACCAACCTCACTGGGACACTTTTGCCTTCCCGAAACA CTGATGAGACCTTCTTTGGAGTGCAGTGGGTGCGCCCCTGACCACTGCTGCTG ATTAGGGTTTTTTAAATTTTATTTTATTTTATTTAAGTTCAAGAGAAAAAGTG TACACACAGGGGCCACCCGGGGTTGGGGTGGGAGTGTGGTGGGGGGTAGTGGT GGCAGGACAAGAGAAGGCATTGAGCTTTTTCTTTCATTTTCCTATTAAAAAAT ACAAAAATCA (SEQ ID NO: 113)
	>NP_001243.1 CD70 antigen isoform 1 [*Homo sapiens*] MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFAQAQQQLPLESL GWDVAELQLNHTGPQQDPRLYWQGGPALGRSFLHGPELDKGQLRIHRDGIYMV HIQVTLAICSSTTASRHHPTTLAVGICSPASRSISLLRLSFHQGCTIASQRLT PLARGDTLCTNLTGTLLPSRNTDETFFGVQWVRP (SEQ ID NO: 114)
Mouse CD27L (CD70)	>NM_011617.2 *Mus musculus* CD70 antigen (Cd70), mRNA GAAGGTGCCAAAAGCTCCAGGGGATTTCCCTGCCCTCCGAGAAGAGGCCCAGT TCTTCCCCTGCATCGGACATCCCCGAGGTTCTAAGGGCAGGTCAAGGCAGGCA GAAGCTTCAAAAGCTCGGCTGAGGAGGCTACAGCTTCCCGCTGCCTTCAGGCC GCTGCTTCCGTGCAGGGATGCCGGAGGAAGGTCGCCCTTGCCCCTGGGTTCGC TGGAGCGGGACCGCGTTCCAGCGCCAATGGCCATGGCTGCTGCTGGTGGTGTT TATTACTGTGTTTTGCTGTTGGTTTCATTGTAGCGGACTACTCAGTAAGCAGC AACAGAGGCTGCTGGAGCACCCTGAGCCGCACACAGCTGAGTTACAGCTGAAT CTCACAGTTCCTCGGAAGGACCCCACACTGCGCTGGGGAGCAGGCCCAGCCTT GGGAAGGTCCTTCACACACGGACCAGAGCTGGAGGAGGGCCATCTGCGTATCC ATCAAGATGGCCTCTACAGGCTGCATATCCAGGTGACACTGGCCAACTGCTCT TCCCCAGGCAGCACCCTGCAGCACAGGGCCACCCTGGCTGTGGGCATCTGCTC CCCCGCTGCGCACGGCATCAGCTTGCTGCGTGGGCGCTTTGGACAGGACTGTA CAGTGGCATTACAGCGCCTGACATACCTGGTCCACGGAGATGTCCTCTGTACC AACCTCACCCTGCCTCTGCTGCCGTCCCGCAACGCTGATGAGACCTTCTTTGG AGTTCAGTGGATATGCCCTTGACCACAACTCCAGGATGACTTGTGAATATTTT TTTTCTTTTCAAGTTCTACGTATTTATAAATGTATATAGTACACATA (SEQ ID NO: 115)
	>NP_035747.1 0D70 antigen [*Mus musculus*] MPEEGRPCPWVRWSGTAFQRQWPWLLLVVFITVFCCWFHCSGLLSKQQQRLLE HPEPHTAELQLNLTVPRKDPTLRWGAGPALGRSFTHGPELEEGHLRIHQDGLY RLHIQVTLANCSSPGSTLQHRATLAVGICSPAAHGISLLRGRFGQDCTVALQR LTYLVHGDVLCTNLTLPLLPSRNADETFFGVQWICP (SEQ ID NO: 116)
Human CD30L (CD153)	>NM_001244.4 *Homo sapiens* TNF superfamily member 8 (TNFSF8), transcript variant 1, mRNA GTCATTTTCCTACGCGCCCTCTGACATCAGCCACCTTCTCTGTAGCTAGTTTC TCTGCACACAACTTAATCCCTGGCAATGAAAAATGAACCTCTCCCCCACCCTT GCTGCCGCCTCTCGCCTCACGCCCCCAGAGAAGAGTTTCTCCACCAGGCAGCA GGTGAAGGTTTTTTTCCAAGTCACATGATTCAGGATTCAGGGGGAGAATCCTT CTTGGAACAGAGATGGGCCCAGAACTGATCAGATGAAGAGAGATAAGGTGTG ATGTGGGGAAGACTATATAAAGAATGGACCCAGGGCTGCAGCAAGCACTCAAC GGAATGGCCCCTCCTGGAGACACAGCCATGCATGTGCCGGCGGGCTCCGTGGC CAGCCACCTGGGGACCACGAGCCGCAGCTATTTCTATTTGACCACAGCCACTC TGGCTCTGTGCCTTGTCTTCACGGTGGCCACTATTATGGTGTTGGTCGTTCAG AGGACGGACTCCATTCCCAACTCACCTGACAACGTCCCCCTCAAAGGAGGAAA TTGCTCAGAAGACCTCTTATGTATCCTGAAAAGGGCTCCATTCAAGAAGTCAT GGGCCTACCTCCAAGTGGCAAAGCATCTAAACAAAACCAAGTTGTCTTGGAAC AAAGATGGCATTCTCCATGGAGTCAGATATCAGGATGGGAATCTGGTGATCCA ATTCCCTGGTTTGTACTTCATCATTTGCCAACTGCAGTTTCTTGTACAATGCC CAAATAATTCTGTCGATCTGAAGTTGGAGCTTCTCATCAACAAGCATATCAAA AAACAGGCCCTGGTGACAGTGTGTGAGTCTGGAATGCAAACGAAACACGTATA CCAGAATCTCTCTCAATTCTTGCTGGATTACCTGCAGGTCAACACCACCATAT CAGTCAATGTGGATACATTCCAGTACATAGATACAAGCACCTTTCCTCTTGAG AATGTGTTGTCCATCTTCTTATACAGTAATTCAGACTGAACAGTTTCTCTTGG CCTTCAGGAAGAAAGCGCCTCTCTACCATACAGTATTTCATCCCTCCAAACAC TTGGGCAAAAAGAAAACTTTAGACCAAGACAAACTACACAGGGTATTAAATAG TATACTTCTCCTTCTGTCTCTTGGAAAGATACAGCTCCAGGGTTAAAAAGAGA GTTTTTAGTGAAGTATCTTTCAGATAGCAGGCAGGGAAGCAATGTAGTGTGGT GGGCAGAGCCCCACACAGAATCAGAAGGGATGAATGGATGTCCCAGCCCAACC TCTAATTCACTGTATGGTCTTGATCTATTTCTTCTGTTTTGAGAGCCTCCAGT TAAAATGGGGCTCCAGTACCAGAGCAGCTAGCAACTCTGCCCTAATGGGAAAT GAAGGGGAGCTGGGTGTGAGTGTTTACACTGTGCCCTTCACGGGATACTTCTT TTATCTGCAGATGGCCTAATACTTAGTTGTCCAAGTCGCGATCAAGGACTCTC TCACACAGGAAACTTCCCTATACTGGCAGATACACTTGTGACTGAACCATGCC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CAGTTTATGCCTGTCTGACTGTCACTCTGGCACTAGGAGGCTGATCTTGTACT CCATATGACCCCACCCCTAGGAACCCCCAGGGAAAACCAGGCTGGGACAGCCC CCTGTTCCTGAGATGGAAAGCACAAATTTAATACACCACCACAATGGAAAACA AGTTCAAAGACTTTTACTTACAGATCCTGGACAGAAAGGGCATAATGAGTCTG AAGGGCAGTCCTCCTTCTCTAGGTTACATGAGGCAGGAATAAGAAGTCAGACA GAGACAGCAAGACAGTTAACAATGTAGGTAAAGAAATAGGGTGTGGTCACTCT CAATTCACTGGCAAATGCCTGAATGGTCTGTCTGAAGGAAGCAACAGAGAAGT GGGGAATCCAGTCTGCTAGGCAGGAAAGATGCCTCTAAGTTCTTGTCTCTGGC CAGAGGTGTGGTATAGAACCAGAAACCCATATCAAGGGTGACTAAGCCCGGCT TCTGGTATGAGAAATTAAACTTGTATACAAAATGGTTGCCAAGGCAACATAAA ATTATAAGAATTCACTATACCTTCCCCTCCCTGGAACTCAGGATCCAAGTCTA GAAAATGAAAGGACTGGGTTTGAATTGCTTCAAAACCTCTTCCATCTCAGAAG ACCAGACCCTGGGAACTGAGATTCCAGACACAATTTTGGAAGCTCTCCAACCA AAATAAGGCCCCCCTACCCCAGTATATAATTGAAGACACTAGTAACACCTGAC TGCATCTCATCTCAGCAGAGCCAGAATATGGGGACAAGGTTCAGGGTGCCCTG CTGAATGGTGTGAACAGCAGGATCTCAAGGATGTAATGGAAAGAACTACCACA CTGACCATCCAGAATCTAAGAGACCATCTGGGTGTTTGGGAAACCATCTGACG AGGCCTGACTCTATTCCAGTTAGATTGACAATAATTGAGCAGCAGGCATTTTT CATTTCTGGTCAGGAAAGCATTGTGCCTTTAGCAAACAATCAGTGTGCAACAG TGATGTGGTCATCTAGCCAGGGAATGGCTGCTCCATCCCCTGCATAATATATT CCTGCTTCAAACACCTCTCAGAAAACCAGTTCCGCGAGGGTTTTTATATCCCC ACAAAGTTGTTGAGAGACAATGATGACCCTGGAAGTGGGGAGGAGGACTTCTG AGAAACAGCAACCTCTCTCCTGATTGGGGTAGCCATGAGATTTCTCTAGCTAT ATCCAACTTGGCATCTGTACATCATCTTTGGAGGAACATCTTATTTGTGGAAG GACCTTGACAAGCCGTTTGAGATGGAATGTAGGCCCTGATGTTATGCTTCAGT AAAAAAAGATGGAAGCTTCCCTGCTATACCAAAACATGGAGCAAAATTTGCAT TTTTCTCAAGAAGGAGAGAAAAGGAGTAGGACTCCAGCAAAGTTTGTCAGAAG GAAAGCTAGAAAAGATTTAAAAGAAAAAAAGAAAGAACAAATCAGCAGTGGTG GTATGGATGAAAGGGACTTGAGAGAACAAAAATGGCTAAGGGAAAATTTTAAG TCATCTGCTGAGCAGTGTGCTGTGTCAACCTCCTCCTAGGTCTCCTCTATGAA ATATTTAGTAAAGTCTACATTTCTCTTTAACTCTTTCTGTGAGTAGATTCTTT GGGAGAAGCAGGCATTGGAAGAGGTGTTGAATTCAGCAAGCCAAATGGTCTGT GGTAAAAAACAAAACAGACTTTGAGACTCAAGGCTAAAAAAACAGGGAAATGG CTGGCATTTGAGTCACACACTAACTGCATAGGACAAATGAATCTTGCTTAAAC CAACTCATGCATTCTTGAAAAGGTATATGCAACCCAACTGTGTGTTAACTAAG CAATTTTTTTGCCATCTCACATTCTAACTCGAGAAAGATTCCATTTTCATTTT TCACCAACTGTTCTCTGAGCAGAGGTACCTGACTTTTGCACTGTGAGTGGTTT CTAATCTCAGTCTCTGTCAAGCAATGCTAAGAAAGCCAACACCTAAAGACACA AGGGGTACATCATTTAAATGAATAATGTAACCAAACAAACAAAAAAAGAGAAT AATCATTAATAACTCAACTGATAGATATGTAGGGAGTAGGCAACCCAGGAAGT TTAAAACTAAATTCTGTTACTCTTGAGGGTTAACCAGCCCCTGGGAATGTTAT GAGCAAATGATACTCCATGAGTAAAATGATATCTATGCAAGTAAAATAAATAA TTTATCTAACTGGGAA (SEQ ID NO: 117) >NP_001235.1 tumor necrosis factor ligand superfamily member 8 isoform 1 [*Homo sapiens*] MDPGLQQALNGMAPPGDTAMHVPAGSVASHLGTTSRSYFYLTTATLALCLVFT VATIMVLVVQRTDSIPNSPDNVPLKGGNCSEDLLCILKRAPFKKSWAYLQVAK HLNKTKLSWNKDGILHGVRYQDGNLVIQFPGLYFIICQLQFLVQCPNNSVDLK LELLINKHIKKQALVTVCESGMQTKHVYQNLSQFLLDYLQVNTTISVNVDTFQ YIDTSTFPLENVLSIFLYSNSD (SEQ ID NO: 118)
Mouse CD30L (CD153)	>NM_009403.3 *Mus musculus* tumor necrosis factor (ligand) superfamily, member 8 (Tnfsf8), mRNA AGATTAATCCCAGGCGATGAAAAATGAACCTCTCCCCCACCCTTGCAGCCACC CTTCGCCTCACGCCCCCAGAGAAGAGTTTCTCCATCCGGCAACTGGTGAAGGC TTTTTTCCAAGTCACATGATCCAGGATGCAGGGGAAAATCCTTCTTGGAACAG AGCTGGGTACAGAACCGAATCAGATGAGGAGAGATAAGGTGTGATGTGGGACA GACTATATAAAGCATGGAGCCAGGGCTGCAACAAGCAGGCAGCTGTGGGGCTC CTTCCCCTGACCCAGCCATGCAGGTGCAGCCCGGCTCGGTAGCCAGCCCCTGG AGAAGCACGAGGCCCTGGAGAAGCACAAGTCGCAGCTACTTCTACCTCAGCAC CACCGCACTGGTGTGCCTTGTTGTGGCAGTGGCGATCATTCTGGTACTGGTAG TCCAGAAAAAGGACTCCACTCCAAATACAACTGAGAAGGCCCCCCTTAAAGGA GGAAATTGCTCAGAGGATCTCTTCTGTACCCTGAAAAGTACTCCATCCAAGAA GTCATGGGCCTACCTCCAAGTGTCAAAGCATCTCAACAATACCAAACTGTCAT GGAACGAAGATGGCACCATCCACGGACTCATATACCAGGACGGGAACCTGATA GTCCAATTCCCTGGCTTGTACTTCATCGTTTGCCAACTGCAGTTCCTCGTGCA GTGCTCAAATCATTCTGTGGACCTGACATTGCAGCTCCTCATCAATTCCAAGA TCAAAAAGCAGACGTTGGTAACAGTGTGTGAGTCTGGAGTTCAGAGTAAGAAC ATCTACCAGAATCTCTCTCAGTTTTTGCTGCATTACTTACAGGTCAACTCTAC CATATCAGTCAGGGTGGATAATTTCCAGTATGTGGATACAAACACTTTCCCTC TTGATAATGTGCTATCCGTCTTCTTATATAGTAGCTCAGACTGAATAGTTGTT CTTAACCTTTATGAAAATGCTGTCTACCATACAGTACTTCATCTGTCCAAACA TGGGCCAAAGAAAATATTAGGACAACTCAAACTAAGCATGTGAGTTAGTGCAC TTCTCTTTCTGTCCTTTGGAAAAATACAAACCCAGGATTTAGAAAGTGGAGTC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TCCTTCAGATGCACAAACAGGAAAGAATGTGATATGTGCACAGAGACCTACTT GGGCACTAGAAGGGGTTGAGTTGTCCCAGTATAACCACTAATTCACTGACCTT GAGCCATTTTTCCTTCCCCTGGAACTTGGGGTCTGAATCTGGAAAAGTAGGAG ATGAGATTTACATTTCCCCAATATTTTCTTCAACTCAGAAGACGAGACTGTGG AGCTGAGCTCCCTACACAGATGAAGGCCTCCCATGGCATGAGGAAAATGATGG TACCAGTAATGTCTGTCTGACTGTCATCTCAGCAAGTCCTAAGGACTTCCATG CTGCCTTGTTGAAAGATACTCTAACCTCTTGTAATGGGCAAAGTGATCCTGTC TCTCACTGAGGGGAGTAGCTGCTGCCATCTCCTGAGACATACATGGAGACATT TTCTGCCCAAATTCCATTCTGTGTGCAGTTTTTAAGTATTCCCCCAAAAGTTC TTGACAATGAGAACTTTGAATGTGGGAAGAGCTTCTGGACAGCAAACATTAAC AGCTTCTCCTGACCAGAGAGACCATGCAAGCTTGGTCTTAGACCCATCAAGCT TGAGGTTTCTACATTGTGGGAGACAGACTTTTGACAAACCATTTGAGTTGATG TCTGGGCCCCTGGGAGTTCTCCTTCAGTAAGGAGAGCAAGCCGTTCTAGTGCT GTGTCAGAGGATGGAGTAAAATAGACACTTTTCTGAAGGAAAGGAGAACAAAG TTCCAGAAAAAGGCTAGAAAATGTTTAAAAGGAAAAGAAAAAACTCAGCTTTT CTCATATGAGAGGAACCCAGAAAAACAACACTGAAAAAGAAGAGTGGCTCTGT CAACCTCCTCTTAGGTCTCCTCCTCTCTAGTTATTGGGAAAGGAGTTGCATGG TACAGGACAAGTTCTGGTGTGTGGTCAAATAGAATCAGATGTGGAGAACACCA TGCAGAGAATAAGGAGACCTGTCATATTTGTGTTGTACTCAAATGAGGGGCAA ATGAATCTTAGGCTAAATCAAATAACAGTCTCTGTCAAGCTGTGCTCAGAAAG TCAACCACTGAAGATGGAGGGTGAGGCACGTCATTTAAAAAAAGTGAAATGTA GC (SEQ ID NO: 119) >NP_033429.1 tumor necrosis factor ligand superfamily member 8 [*Mus musculus*] MEPGLQQAGSCGAPSPDPAMQVQPGSVASPWRSTRPWRSTSRSYFYLSTTALV CLVVAVAIILVLVVQKKDSTPNTTEKAPLKGGNCSEDLFCTLKSTPSKKSWAY LQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNH SVDLTLQLLINSKIKKQTLVTVCESGVQSKNIYQNLSQFLLHYLQVNSTISVR VDNFQYVDTNTFPLDNVLSVFLYSSSD (SEQ ID NO: 120)
Human GITRL	>NM_005092.4 *Homo sapiens* TNF superfamily member 18 (TNFSF18), mRNA ATCACTTGTGAATTTTTGTTTTCCACAGCTCTCATTTCTCCAAAAATGTGTTT GAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAGA GATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTT TGCTCCTTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGA GCCCTGTATGGCTAAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTT CTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTGGAGATACTTCAG AATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTACAATGA TGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTC TAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTT GGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAA TACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCCTAGAGAC TTGATTTGATCTCCTCATTCCCTTCAGCACATGTAGAGGTGCCAGTGGGTGGA TTGGAGGGAGAAGATATTCAATTTCTAGAGTTTGTCTGTCTACAAAAATCAAC ACAAACAGAACTCCTCTGCACGTGAATTTTCATCTATCATGCCTATCTGAAAG AGACTCAGGGGAAGAGCCAAAGACTTTTGGTTGGATCTGCAGAGATACTTCAT TAATCCATGATAAAACAAATATGGATGACAGAGGACATGTGCTTTTCAAAGAA TCTTTATCTAATTCTTGAATTCATGAGTGGAAAAATGGAGTTCTATTCCCATG GAAGATTTACCTGGTATGCAAAAAGGATCTGGGGCAGTAGCCTGGCTTTGTTC TCATATTCTTGGGCTGCTGTAATTCATTCTTCTCATACTCCCATCTTCTGAGA CCCTCCCAATAAAAAGTAGACTGATAGGATGGCCACAGATATGCCTACCATAC CCTACTTTAGATATGGTGGTGTTAGAAGATAAAGAACAATCTGAGAACTATTG GAATAGAGGTACAAGTGGCATAAAATGGAATGTACGCTATCTGGAAATTTCTC TTGGTTTTATCTTCCTCAGGATGCAGGGTGCTTTAAAAAGCCTTATCAAAGGA GTCATTCCGAACCCTCACGTAGAGCTTTGTGAGACCTTACTGTTGGTGTGTGT GTCTAAACATTGCTAATTGTAAAGAAAGAGTAACCATTAGTAATCATTAGGTT TAACCCCAGAATGGTATTATCATTACTGGATTATGTCATGTAATGATTTAGTA TTTTTAGCTAGCTTTCCACAGTTTGCAAAGTGCTTTCGTAAAACAGTTAGCAA TTCTATGAAGTTAATTGGGCAGGCATTTGGGGGAAAATTTTAGTGATGAGAAT GTGATAGCATAGCATAGCCAACTTTCCTCAACTCATAGGACAAGTGACTACAA GAGGCAATGGGTAGTCCCCTGCATTGCACTGTCTCAGCTTTAGAATTGTTATT TCTGCTATCGTGTTATAAGACTCTAAAACTTAGCGAATTCACTTTTCAGGAAG CATATTCCCCTTTAGCCCAAGGTGAGCAGAGTGAAGCTACAACAGATCTTTCC TTTACCAGCACACTTTTTTTTTTTTTCCTGCCTGAATCAGGGAGATCCAGGAT GCTGTTCAGGCCTTATCCCAACCAAATTCCCCTCTTCACTTTGCAGGGCCCAT CTTAGTCAAATGTGCTAACTTCTAAAATAATAAATAGCACTAATTCAAAATTT TTGGACTCTTAAATTAGCTACTTGCAGGTTCTTGTTGAAAGGTATATAATATT ACATTGTAAACAAATTTAAAATATTTATGGATATTTGTGAAAAGCTGCATTAT GTTAAATAATATTACATGTAAAGCTATTTAAAAGAGGTTTTTTTTGTATTTTG TTTAACAAAAATTGCTCAGGAGCATGCTAAGCCTGAGGCCAAGTTGTTTCTTA GTATGACTTTTTAAAAAAACATCTGCTGAGTAGCTACAGGGCCAAAGACTTGG AGAGCTTGTTTCTGTTGCATTTGCATATCTTCTCAGGAAATTAAAGTGTGTCA TACATATGTGTGTGTGTGTGTGTGTGTGTGTGTATATGTGTGTGTGTATATAT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ATGTATACTTATAAAATCTTGGTGTTCTTGATCTTTGTTGTGTTATAAGCAAT GTGTGCTGGAGTGGGCTGGTGCTAGCTTATAAGCACATATTATTAAATTTTCA GGAATGTTGCACTTTAGTTATTAACTATAGGCATTCTTGAAATTGGCTATGGT GGGAGTATTTATACCATGTAAATTGGCAAACACTACACATTTTCCTTTTGGAC AGCTAGTTCACCAGCACACCACTGTGAAACTCTCCTTAATGACTCCTCTCTGC CCCCGCTTCATTCCTGGGATAATCATAGCAGACTAAGGGAGAAAATGAAATTG TAAAAATTTGGCATACTGGTGATTTCTCAGGGCAAGCAGAGGTTACTACAGCT GCAGCTAGAGGGATGACTACCAACAGGTGACCTTTACATTTTCCTGATGTTAT AATTTTAGCTTTTGTTTTCAATGTATACTGTTTTCCTGTTTCTCCACATAGTA GTCTGCATTTTAAATCTATAATAAAACATGCTGATAACTGG (SEQ ID NO: 121)
	>NP_005083.3 tumor necrosis factor ligand superfamily member 18 [*Homo sapiens*] MCLSHLENMPLSHSRTQGAQRSSWKLWLFCSIVMLLFLCSFSWLIFIFLQLET AKEPCMAKFGPLPSKWQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNAN YNDVAPFEVRLYKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIFNSEHQVL KNNTYWGIILLANPQFIS (SEQ ID NO: 122)
Mouse GITRL	>NM_183391.3 *Mus musculus* tumor necrosis factor (ligand) superfamily, member 18 (Tnfsf18), mRNA TTGTGGGTATCTGCTTTCCCCAGTTCTCATTCCATCAGAGAACGAGTTCTAGC CTCATGGAGGAAATGCCTTTGAGAGAATCAAGTCCTCAAAGGGCAGAGAGGTG CAAGAAGTCATGGCTCTTGTGCATAGTGGCTCTGTTACTGATGTTGCTCTGTT CTTTGGGTACACTGATCTATACTTCACTCAAGCCAACTGCCATCGAGTCCTGC ATGGTTAAGTTTGAACTATCATCCTCAAAATGGCACATGACATCTCCCAAACC TCACTGTGTGAATACGACATCTGATGGGAAGCTGAAGATACTGCAGAGTGGCA CATATTTAATCTACGGCCAAGTGATTCCTGTGGATAAGAAATACATAAAAGAC AATGCCCCCTTCGTAGTACAGATATATAAAAAGAATGATGTCCTACAAACTCT AATGAATGATTTTCAAATCTTGCCTATAGGAGGGGTTTATGAACTGCATGCTG GAGATAACATATATCTGAAGTTCAACTCTAAAGACCATATTCAGAAAACTAAC ACATACTGGGGGATCATCTTAATGCCTGATCTACCATTCATCTCTTAGAGATT GGGTTTGGTCTCCTCATCTTCTTCTTTGTATCCCGAGATGCTGGTGGGTGGGT TGGAGGGGGATGATTGATGGCAATGCACACAGTTTGTGAGGGCTTACAAATTG ACACAATCAGAGCCTCTTGGCATATAAAATTTTAGCCCTCATATCTGTCTGAA GAGGACTCAGCAAATGGGCCAATCCCTAATGTTGGGTCTGCAAATGGACTTGT ACAATCCATGATAAAAAGGAGTATGGGCCACAGAAGACAGAAACTCTTCCAAA GAATGTCTTTCTAACCTTGATCCCTGGGTAGAATGAGATCCTGTTTCCATGGG AGTCTTACTTGGCTTGCAAAAAAGGGTGTAGGGCAGTAGCTTGGCCTTTTTTC CATCATAATTTCCTTGAGCTGTTTTACCTTAATCCCTCCAAACTCTCACCTTC TGAGAGCCTCCTAATGAAACATTGTTAGACTGGTGGGGTGGCCAAGACATGCC AACAACACCCTTCTTTAGAGGTGGTGTTTTTAGAGGACAGAGAACATTATGAA GCCTAGAGCAGCAGAGGTCAAGATGCCACGAAATGGAATTGATCTGGGAATTT TTTTTTTTTTTCATTCTCAGGATGCAGGTTCATTCTGAACTTTCCCCTAGGCC TTCATTGCTTTTGTGTGTATGTGTGCATAAATTCTGCAAATAGAAAAATGAGA GTTTGCACCAGTACTCACTAGATTTAACACCAGAAAGTGGTACTTTTCTGGCT GTATTATGCCATGATAGCACATTTTCTGTTGGTGTTCCCTAACTGACAAGTAT AACAGTTTTCCTAAACCACACAACAATGCTATGATGTTAATGGGGTAGATATT TTTGGAAAAAAATTGCACAGTGAGAACATGGGTAGATGAACCCTAAGACTCTT ACCTCAATTCAGAACTCGCAAGGAGTTAAGTGAGTGGGGTCTTCATTAGACCA TTCACATGGTCTCTGCTTTGAAACTGGCGTTGCTACTGTCTCATTATACATCA CTAAAATGGAATTAACTCAACTTTGAAATGGATGCATCGACTTTACCCCAAGG TGTCCAGAATGAAGCTACAAGACTTTTACCAGCAGTCATTTTCCTTTTGCCTG GAGCAAGAAGATCCAGGATACTGTTGGAAGAGTTCATCTCACTCAACCATGCT GACTTTCCAAAGTAATAATGAACATTTGTGTTCAAATTTTGGATTCTGTTAAA TTTAGCCAGCTTGTGAGTTCTTGTCGAAAAGTATTTTAAACCAATTTACACTA TTTATGGGTATTTGTGAAAAGCTATATAGTGATATTTTATATATAACTAATTT AAAATATTTTTATTTTATGTAACAAAAATACTATAGGCTAAGCTATTTCTTCT TATTTTTTTATGAATACTTGCTGAATTGCCATAGGGCACAAAGACTCTTCTGT TTGCATATCTTCTCAGGAAATTAAAATTGTATCACATGTATTTATAAGAA (SEQ ID NO: 123)
	>NP_899247.3 tumor necrosis factor ligand superfamily member 18 [*Mus musculus*] MEEMPLRESSPQRAERCKKSWLLCIVALLLMLLCSLGTLIYTSLKPTAIESCM VKFELSSSKWHMTSPKPHCVNTTSDGKLKILQSGTYLIYGQVIPVDKKYIKDN APFVVQIYKKNDVLQTLMNDFQILPIGGVYELHAGDNIYLKFNSKDHIQKTNT YWGIILMPDLPFIS (SEQ ID NO: 124)
Human CD40L (CD154)	>NM_000074.3 *Homo sapiens* CD40 ligand (CD40LG), mRNA AATCCTGAGTAAGGTGGCCACTTTGACAGTCTTCTCATGCTGCCTCTGCCACC TTCTCTGCCAGAAGATACCATTTCAACTTTAACACAGCATGATCGAAACATAC AACCAAACTTCTCCCCGATCTGCGGCCACTGGACTGCCCATCAGCATGAAAAT TTTTATGTATTTACTTACTGTTTTTCTTATCACCCAGATGATTGGGTCAGCAC TTTTTGCTGTGTATCTTCATAGAAGGTTGGACAAGATAGAAGATGAAAGGAAT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CTTCATGAAGATTTTGTATTCATGAAAACGATACAGAGATGCAACACAGGAGA AAGATCCTTATCCTTACTGAACTGTGAGGAGATTAAAAGCCAGTTTGAAGGCT TTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAAGAAAGAAAACAGCTTT GAAATGCAAAAAGGTGATCAGAATCCTCAAATTGCGGCACATGTCATAAGTGA GGCCAGCAGTAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTACA CCATGAGCAACAACTTGGTAACCCTGGAAAATGGGAAACAGCTGACCGTTAAA AGACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGA AGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTA GATTCGAGAGAATCTTACTCAGAGCTGCAAATACCCACAGTTCCGCCAAACCT TGCGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCAGGTGC TTCGGTGTTTGTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCACTGGCT TCACGTCCTTTGGCTTACTCAAACTCTGAACAGTGTCACCTTGCAGGCTGTGG TGGAGCTGACGCTGGGAGTCTTCATAATACAGCACAGCGGTTAAGCCCACCCC CTGTTAACTGCCTATTTATAACCCTAGGATCCTCCTTATGGAGAACTATTTAT TATACACTCCAAGGCATGTAGAACTGTAATAAGTGAATTACAGGTCACATGAA ACCAAAACGGGCCCTGCTCCATAAGAGCTTATATATCTGAAGCAGCAACCCCA CTGATGCAGACATCCAGAGAGTCCTATGAAAAGACAAGGCCATTATGCACAGG TTGAATTCTGAGTAAACAGCAGATAACTTGCCAAGTTCAGTTTTGTTTCTTTG CGTGCAGTGTCTTTCCATGGATAATGCATTTGATTTATCAGTGAAGATGCAGA AGGGAAATGGGGAGCCTCAGCTCACATTCAGTTATGGTTGACTCTGGGTTCCT ATGGCCTTGTTGGAGGGGGCCAGGCTCTAGAACGTCTAACACAGTGGAGAACC GAAACCCCCCCCCCCCCCCCCGCCACCCTCTCGGACAGTTATTCATTCTCTTTC AATCTCTCTCTCTCCATCTCTCTCTTTCAGTCTCTCTCTCTCAACCTCTTTCT TCCAATCTCTCTTTCTCAATCTCTCTGTTTCCCTTTGTCAGTCTCTTCCCTCC CCCAGTCTCTCTTCTCAATCCCCCTTTCTAACACACACACACACACACACACA CACACACACACACACACACACACACACACACAGAGTCAGGCCGTTGCTAGTCAGT TCTCTTCTTTCCACCCTGTCCCTATCTCTACCACTATAGATGAGGGTGAGGAG TAGGGAGTGCAGCCCTGAGCCTGCCCACTCCTCATTACGAAATGACTGTATTT AAAGGAAATCTATTGTATCTACCTGCAGTCTCCATTGTTTCCAGAGTGAACTT GTAATTATCTTGTTATTTATTTTTTGAATAATAAAGACCTCTTAACATTA (SEQ ID NO: 125) >NP_000065.1 CD40 ligand [*Homo sapiens*] MIETYNQTSPRSAATGLPISMKIFMYLLTVFLITQMIGSALFAVYLHRRLDKI EDERNLHEDFVFMKTIQRCNTGERSLSLLNCEEIKSQFEGFVKDIMLNKEETK KENSFEMQKGDQNPQIAAHVISEASSKTTSVLQWAEKGYYTMSNNLVTLENGK QLTVKRQGLYYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTH SSAKPCGQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL (SEQ ID NO: 126)
Mouse CD40L	>NM_011616.2 *Mus musculus* CD40 ligand (Cd40lg), mRNA CTTTCAGTCAGCATGATAGAAACATACAGCCAACCTTCCCCCAGATCCGTGGC AACTGGACTTCCAGCGAGCATGAAGATTTTTATGTATTTACTTACTGTTTTCC TTATCACCCAAATGATTGGATCTGTGCTTTTTGCTGTGTATCTTCATAGAAGA TTGGATAAGGTCGAAGAGGAAGTAAACCTTCATGAAGATTTTGTATTCATAAA AAAGCTAAAGAGATGCAACAAAGGAGAAGGATCTTTATCCTTGCTGAACTGTG AGGAGATGAGAAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTAAACAAA GAAGAGAAAAAAGAAAACAGCTTTGAAATGCAAAGAGGTGATGAGGATCCTCA AATTGCAGCACACGTTGTAAGCGAAGCCAACAGTAATGCAGCATCCGTTCTAC AGTGGGCCAAGAAAGGATATTATACCATGAAAAGCAACTTGGTAATGCTTGAA AATGGGAAACAGCTGACGGTTAAAAGAGAAGGACTCTATTATGTCTACACTCA AGTCACCTTCTGCTCTAATCGGGAGCCTTCGAGTCAACGCCCATTCATCGTCG GCCTCTGGCTGAAGCCCAGCAGTGGATCTGAGAGAATCTTACTCAAGGCGGCA AATACCCACAGTTCCTCCCAGCTTTGCGAGCAGCAGTCTGTTCACTTGGGCGG AGTGTTTGAATTACAAGCTGGTGCTTCTGTGTTTGTCAACGTGACTGAAGCAA GCCAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTCTGA ACAGTGCGCTGTCCTAGGCTGCAGCAGGGCTGATGCTGGCAGTCTTCCCTATA CAGCAAGTCAGTTAGGACCTGCCCTGTGTTGAACTGCCTATTTATAACCCTAG GATCCTCCTCATGGAGAACTATTTATTATGTACCCCCAAGGCACATAGAGCTG GAATAAGAGAATTACAGGGCAGGCAAAAATCCCAAGGGACCCTGCTCCCTAAG AACTTACAATCTGAAACAGCAACCCCACTGATTCAGACAACCAGAAAAGACAA AGCCATAATACACAGATGACAGAGCTCTGATGAAACAACAGATAACTAATGAG CACAGTTTTGTTGTTTTATGGGTGTGTCGTTCAATGGACAGTGTACTTGACTT ACCAGGGAAGATGCAGAAGGGCAACTGTGAGCCTCAGCTCACAATCTGTTATG GTTGACCTGGGCTCCCTGCGGCCCTAGTAGG (SEQ ID NO: 127) >NP_035746.2 CD40 ligand [*Mus musculus*] MIETYSQPSPRSVATGLPASMKIFMYLLTVFLITQMIGSVLFAVYLHRRLDKV EEEVNLHEDFVFIKKLKRCNKGEGSLSLLNCEEMRRQFEDLVKDITLNKEEKK ENSFEMQRGDEDPQIAAHVVSEANSNAASVLQWAKKGYYTMKSNLVMLENGKQ LTVKREGLYYVYTQVTFCSNREPSSQRPFIVGLWLKPSSGSERILLKAANTHS SSQLCEQQSVHLGGVFELQAGASVFVNVTEASQVIHRVGFSSFGLLKL (SEQ ID NO: 128)

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
Human LIGHT (CD258)	>NM_003807.5 *Homo sapiens* TNF superfamily member 14 (TNFSF14), transcript variant 1, mRNA CGAGACTCCATCTCAAAAACAAAACAAATAAACGAACAAAAAAACCCACAACG TATTATTTTCTTGTTTACGAGGTTTCTTGTCTCTCTGGCTCCACCAGAAGAGG AGCAGGGACCCTTCTTGCTGTTGTTCATTGCTGCATCCCCCACACCGAGAGCA GAGCCTGGCATGGGCAGAAAGTCCTCAGTCGATATTTGGTGGCCCCAAGCGAA TGAAGCATCCAAGAAGGGAAAGCTGGGGGCTCCCCACTGCACTTGCCACCTGA GTCACATTTTCAGAAGCCTCTGGAAAGTCGTGCACAGCCCAGGAGTGTTGAGC AATTTCGGTTTCCTCTGAGGTTGAAGGACCCAGGCGTGTCAGCCCTGCTCCAG ACACCTTGGGCATGGAGGAGAGTGTCGTACGGCCCTCAGTGTTTGTGGTGGAT GGACAGACCGACATCCCATTCACGAGGCTGGGACGAAGCCACCGGAGACAGTC GTGCAGTGTGGCCCGGGTGGGTCTGGGTCTCTTGCTGTTGCTGATGGGGGCCG GGCTGGCCGTCCAAGGCTGGTTCCTCCTGCAGCTGCACTGGCGTCTAGGAGAG ATGGTCACCCGCCTGCCTGACGGACCTGCAGGCTCCTGGGAGCAGCTGATACA AGAGCGAAGGTCTCACGAGGTCAACCCAGCAGCGCATCTCACAGGGGCCAACT CCAGCTTGACCGGCAGCGGGGGGCCGCTGTTATGGGAGACTCAGCTGGGCCTG GCCTTCCTGAGGGGCCTCAGCTACCACGATGGGGCCCTTGTGGTCACCAAAGC TGGCTACTACTACATCTACTCCAAGGTGCAGCTGGGCGGTGTGGGCTGCCCGC TGGGCCTGGCCAGCACCATCACCCACGGCCTCTACAAGCGCACACCCCGCTAC CCCGAGGAGCTGGAGCTGTTGGTCAGCCAGCAGTCACCCTGCGGACGGGCCAC CAGCAGCTCCCGGGTCTGGTGGGACAGCAGCTTCCTGGGTGGTGTGGTACACC TGGAGGCTGGGGAGAAGGTGGTCGTCCGTGTGCTGGATGAACGCCTGGTTCGA CTGCGTGATGGTACCCGGTCTTACTTCGGGGCTTTCATGGTGTGAAGGAAGGA GCGTGGTGCATTGGACATGGGTCTGACACGTGGAGAACTCAGAGGGTGCCTCA GGGGAAAGAAAACTCACGAAGCAGAGGCTGGGCGTGGTGGCTCTCGCCTGTAA TCCCAGCACTTTGGGAGGCCAAGGCAGGCGGATCACCTGAGGTCAGGAGTTCG AGACCAGCCTGGCTAACATGGCAAAACCCCATCTCTACTAAAAATACAAAAAT TAGCCGGACGTGGTGGTGCCTGCCTGTAATCCAGCTACTCAGGAGGCTGAGGC AGGATAATTTTGCTTAAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAC ACCACTGCACTCCAACCTGGGAAACGCAGTGAGACTGTGCCTCAAAAAAAAGA AAGGAAGAAAAAAGAAAACTCAGGAAACAGATCTTGGGGGACACTCCAGGGAA CCCAAAACTCAAAGGCGGAGAGCTCAGTGGGCACCACCAAGGCGAGATGAAGC CCCAGCAGGCACCTTCAGAAGACCCACGTAGACTGCAGACCCTGCCACGGACA ATACTAAGGACAAAAACCCAGAGACTTGGGGTCTGTGGGCCCCCAAACATGGG GTAAAGTTGATTTGCCTGATATTCAGGAAGAAGGGGTGAGGGGTGGGTATTTA TGCTTTTGATTCAGAAGAAAGTGGGGCTTGGGATTCCAGGGACTTGGCTGGGG GTGGGAAACTTCATCCACTTCCCTACTCTCATCATGAGTACGGACAGGGTGGG CGGGAGACTGATCATCGGGACTCATCATGAAGAGCCCAGCCCCACCCCACATA CTCAGATCCCACCCACAGACTGGTGGCCACACCTCAGCCTGGTCACAAAGAGT TACACTCAGATACATGAGCACGGCAGCGTGCTCATAACTGTTTAACAACCAGC TGTCCTGGGAGGGGGACAGCTTTGTAATGTTTGCCAATTTCCATGGTGTAAAT GCTACCACCATGGCTGATTTCATCACTGCCAAGCATAGACATCCCTAATAGGA CACCACGGATCTGTCCCCGGCATCCGGCCCAGGGCCTGGCACAAAGCATGCTC TAGGGAAATGCTTGCTGATTGAAAGGAAGGAAGAATGACTCTACAGTCACACC TATGGCATCCCACAAAATCTGTCACATGGCTGCATAATCTCAGCCACTCTTTC ACAACTATAGACTCATACACGCGAAGTGCCAGATTCATGCACAACCACACAAT CACATGGAAGTCACAGACGGCATCACAGACAGTCACAGCACTGTGTGTATGTT ATAACACAAGCACACAAAACTCAGACAGCATCCCAGCTACACAGCCACTCCCA GAGGTGTCACCGTCACACTTGGTAATTAATACTCATTACATTAGACACAGACA GACCAAGTTATAGTCAGACCTGGTTACACACATACACACACACAATATCACCA TGACAAATACACATTACACACACACAACATCACAATGACAAACACACATTACA CACACAACATCACGATGACAAACACACATTACACACACAACATCACGATGACA AACACACATTACACACACATCACAATGACAAACACAACATTACACACACACAA CATCACAATGACACACACATCACACACACATCACAATGACAAACACACAACAT TACACACATATACACACAGCCTGAGGGCCCTCCCCAGCCCAGACTAACACATC TCGGGGTGAGGACCAGACCTTGTTCATAACCCTGGGCCTCTTAACCACTGATC TTTGAAATAAATGGCAAATAGTTGTACCTGGATCTGTCTAGTTCTTAGGGGAA CAAACTGAAGAAGGGTGGAGAGGAATTGTCAGGCCTAAAGAGCCCCACAGGGA AAGGGAGGAGTCGGATGGGGGGCAACCATCAGCAACAAGTGGTGGCTCCTAGA GGCAGAGGGATGGAGGTAATGACCCATGGAGGTCATTCTACAGATGAGGAACC TGGACCCAGTTGGCTCAAGTCCATGCAGGAAATGTGGGGGAAACCAGAGACCT CACGTCTGGATCTGGCTTCCTCTCCAATCCACAATTCCTGAGGAAGTAGAGGC TACATCCCGCAAGACGCCCTTATTAGACACATCCAGGACAGAATGACAATCCG CCAAGCCAGCTGGAAGCATAAAACACAGGGAGCTGGTGGGTTGGGTGGGGGCA GATAATGATATGCATACAAATTAGAGGGTCTATGCAAATGAGCATTGCTGCAG TGTGGCTGGAGGGAATCCTTAGTTCCTAGGATTCTAGGATATGGGTTTCGACC CCAGAGGTGAATGTATTGTTATTATTGTTTTGTTGTTGTTGTGAATGACAAGT CAAAATTTGTGGGTTATTGTTGTTATCGCCAATAGTATTCTTGTCATTGTTGC ACAGTACAGAGATGAAGGAAACAGATTTTGCAATCAGATGATCCTGGGTTCTG AGTCCACTCTGCCACTCACCAGCTATATGACCTCCAGCAATTTCCATCACCTC TCAATGCTTCAGTTTCCCCATCGGCAAGATGGTTGTGGGGGGAGAGGAACAAC AGTACAGATTCACCATCCCAAATTCAAAATGCTCCAAAATCTAGGCCGGGCGT GGTGGCTCATACCTGTAATCCCAGCACTTTGGGAGGTCAAAGTGGACGGATAA CCTGAGGTCAGGAGCTCCAGACCAGCCTGGCCAACATGGCGAAACCCCATCTC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TACTAAAAATACAAAAAATTACCTGGGTGTGGTGGGGGGCACCTGTAACCCCA GCTACTCGGGAGGCTGAGGCAGGAACCCTGGAGGTTGAGGTTGCAGTGAGCTG AGATCACACCACTGCACTCCAGCCTGGGTGACAGAGCAAGGCTCCCATCTCAA AAAACAAAAAAACATGCTCCAAAATCTGAAACTCTTTGAGCCCCAGTGTGATG CCACAAGTGGGAAATTCCACAACTCATCACATGTGATAGATTGCAGTGGAAAT GCAGGCACACACCACGAAGTTTACTCAGCATCCTCAAAGGAAATCCCCGTCAG TAGCTATATATCATTTTCTCACATGCCAGATAGGTATCTCTCATCTTTTACTG TTAGGTACTTCTGTGTTGAATAGGTGGAGGAAAATGATTGCTGGTTAGTAGTA TATAAATTCAGAGTCAGGAAGGATGGTGATGTCGGCTGGGTGCAGTGGCTCAT GCCTGTAATTCCAATGTGATACCCTACCTTGTGTTTAACGTGATTGACTCTCC CTTAGCTGAGAGGGCCAGGCAGACTCTATTTTGGCTTCTTCGCTTGCAGTCTC TCACCCACCCCCCTTCCTCAAGGACTTAAGCTGACTCCCAGCACATCCAAGAA TGCGATTACTGATAAGATACTGTGACAAGCTATATCCACAATTCCCAGGAATT CGTCCGGTTGATAGCACCCAAAGCCCCCGCGTCTATCACCTTGTGATAGATTT AAAGCCCCTGCACCTGGAACTGTTTGTTTTTCTGTTACCATTTATCTTTTTCA CTTTCTTGCCTGTTTTGCTTCTGTAAAATTGCTTCAGCTCGGCTCCCTCTTCC CCTTCTAAACCAAGGTATAAAAAGAAACCTAGCCCCTTCTTTGGGGTGGAGAG AATTTTGAGCGCTAGCCGTCTCTCAGTCGCCGGCTAATAAAGGACTCCTGAAT TAGTCTAA (SEQ ID NO: 129) >NP_003798.2 tumor necrosis factor ligand superfamily member 14 isoform 1 [*Homo sapiens*] MEESVVRPSVFVVDGQTDIPFTRLGRSHRRQSCSVARVGLGLLLLLMGAGLAV QGWFLLQLHWRLGEMVTRLPDGPAGSWEQLIQERRSHEVNPAAHLTGANSSLT GSGGPLLWETQLGLAFLRGLSYHDGALVVTKAGYYYIYSKVQLGGVGCPLGLA STITHGLYKRTPRYPEELELLVSQQSPCGRATSSSRVWWDSSFLGGVVHLEAG EKVVVRVLDERLVRLRDGTRSYFGAFMV (SEQ ID NO: 130)
Mouse LIGHT	>NM_019418.3 *Mus musculus* tumor necrosis factor (ligand) superfamily, member 14 (Tnfsf14), mRNA TTTTGCAGTTTGCACAGCCCGAGCGTGTTGGGCAATTGTGGTTTCCTCCGGAG AGGAGGAACTCAGGCTTGCCAACCCTTTCCCTGGGCTTCGGAGCCTCAGCTGC TCTGGCATGGAGAGTGTGGTACAGCCTTCAGTGTTTGTGGTGGATGGACAGAC GGACATCCCATTCAGGCGGCTGGAACAGAACCACCGGAGACGGCGCTGTGGCA CTGTCCAGGTCAGCCTGGCCCTGGTGCTGCTGCTAGGTGCTGGGCTGGCCACT CAGGGCTGGTTTCTCCTGAGACTGCATCAACGTCTTGGAGACATAGTAGCTCA TCTGCCAGATGGAGGCAAAGGCTCCTGGGAGAAGCTGATACAAGATCAACGAT CTCACCAGGCCAACCCAGCAGCACATCTTACAGGAGCCAACGCCAGCTTGATA GGTATTGGTGGACCTCTGTTATGGGAGACACGACTTGGCCTGGCCTTCTTGAG GGGCTTGACGTATCATGATGGGGCCCTGGTGACCATGGAGCCCGGTTACTACT ATGTGTACTCCAAAGTGCAGCTGAGCGGCGTGGGCTGCCCCCAGGGGCTGGCC AATGGCCTCCCCATCACCCATGGACTATACAAGCGCACATCCCGCTACCCGAA GGAGTTAGAACTGCTGGTCAGTCGGCGGTCACCCTGTGGCCGGGCCAACAGCT CCCGAGTCTGGTGGGACAGCAGCTTCCTGGGCGGCGTGGTACATCTGGAGGCT GGGGAAGAGGTGGTGGTCCGCGTGCCTGGAAACCGCCTGGTCAGACCACGTGA CGGCACCAGGTCCTATTTCGGAGCTTTCATGGTCTGAAGGCTGCGGTGACAAT GTATTTTGTGGAGGGACCTCTCCAGGACTCACCTCAAACCCAGCAATAGGGTT TGAAGTCCTCCCTTTAAGGAGCCCTGAACTCTGCAGTGCTCGGGGCGGTGTAG ACTGOTGACCTGCTTTGGGCAATCTTCAAATCAGAGACCTGGAGACTTGGGGC GTGGAGCCCAGGAGCGAGGGGTCAGCTCATTTGCCTGATATTCAGGAAGAAAG AATCAAGCTGGGGTATTTATGCTTCTGATGCAAACACTGAGATTTCGGCTTTC TGGGTTTTGAGCTGGAGGCAAGAAACCTTCCCAGAGTGTCATCAGGACCATGT TGGCAGGACTTGGGGCTCCAGACTTGCCACCACACTCTGGCCTCTCCCATCCA TCCGCTGCATTGGTTTCCAGCCACCAAAACAGCACTGGCCCCCTGGCTGCAAC TGGCCAGGTACGAGCTTCTGAGCACCTACATTCCTCAGGGACATCTTGATGAG ATCTCAGTACTCAGTCCAATGCGCAGCAGCGACAGACATGCCAGGAATGGTTG GTCAGAAGGGAAGGGAGGAAAGGGAGGAAAGAAGGGAATGCAGAAGAGAAGGG GGGAAAACAAGACCAAAACAAAACAGCAACAACAAAGCGGCAGGGAGGAGGTG ACACCCTTGGGGATACTTTAGTCAACACACTTAGAACAGATTGTGCCAGGCCT GTTGGATTCCTGGAGTTGATGGGATCGTGGGAAGGCACAATGGGGAGCAAGTG GGCTTGGGTTATGGCTCAGTGGGTAAAGTGCAATTATGGGGATCTGAGTTTGA ATCCCTGGTACCCATATAAAGACACAGATGCGGTGATGGGCACTTGTGACAAT GAGATCATCAATAGGGAATGGAGACAGGAGGGACCTCTGGGGTTCACTGGCCA GGCAGTCTAGCTGAATCAAAGAGCTCCAAGTTCAGTCGATAGCTCCTGAAGAT GACAACTGAGGCTATTCTCCAAACCCCACACGCAGGACACATGCGTAATAAAT AAAATTTTAAAAAT (SEQ ID NO: 131) >NP_062291.1 tumor necrosis factor ligand superfamily member 14 [*Mus musculus*] MESVVQPSVFVVDGQTDIPFRRLEQNHRRRRCGTVQVSLALVLLLGAGLATQG WFLLRLHQRLGDIVAHLPDGGKGSWEKLIQDQRSHQANPAAHLTGANASLIGI GGPLLWETRLGLAFLRGLTYHDGALVTMEPGYYYVYSKVQLSGVGCPQGLANG LPITHGLYKRTSRYPKELELLVSRRSPCGRANSSRVWWDSSFLGGVVHLEAGE EVVVRVPGNRLVRPRDGTRSYFGAFMV (SEQ ID NO: 132)

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
Human TL1	>NM_005118.4 *Homo sapiens* TNF superfamily member 15 (TNFSF15), transcript variant 1, mRNA AGAGGTGCCTCCAGGAGCAGCAGGAGCATGGCCGAGGATCTGGGACTGAGCTT TGGGGAAACAGCCAGTGTGGAAATGCTGCCAGAGCACGGCAGCTGCAGGCCCA AGGCCAGGAGCAGCAGCGCACGCTGGGCTCTCACCTGCTGCCTGGTGTTGCTC CCCTTCCTTGCAGGACTCACCACATACCTGCTTGTCAGCCAGCTCCGGGCCCA GGGAGAGGCCTGTGTGCAGTTCCAGGCTCTAAAAGGACAGGAGTTTGCACCTT CACATCAGCAAGTTTATGCACCTCTTAGAGCAGACGGAGATAAGCCAAGGGCA CACCTGACAGTTGTGAGACAAACTCCCACACAGCACTTTAAAAATCAGTTCCC AGCTCTGCACTGGGAACATGAACTAGGCCTGGCCTTCACCAAGAACCGAATGA ACTATACCAACAAATTCCTGCTGATCCCAGAGTCGGGAGACTACTTCATTTAC TCCCAGGTCACATTCCGTGGGATGACCTCTGAGTGCAGTGAAATCAGACAAGC AGGCCGACCAAACAAGCCAGACTCCATCACTGTGGTCATCACCAAGGTAACAG ACAGCTACCCTGAGCCAACCCAGCTCCTCATGGGGACCAAGTCTGTATGCGAA GTAGGTAGCAACTGGTTCCAGCCCATCTACCTCGGAGCCATGTTCTCCTTGCA AGAAGGGGACAAGCTAATGGTGAACGTCAGTGACATCTCTTTGGTGGATTACA CAAAAGAAGATAAAACCTTCTTTGGAGCCTTCTTACTATAGGAGGAGAGCAAA TATCATTATATGAAAGTCCTCTGCCACCGAGTTCCTAATTTTCTTTGTTCAAA TGTAATTATAACCAGGGGTTTTCTTGGGGCCGGGAGTAGGGGGCATTCCACAG GGACAACGGTTTAGCTATGAAATTTGGGGCCCAAAATTTCACACTTCATGTGC CTTACTGATGAGAGTACTAACTGGAAAAAGGCTGAAGAGAGCAAATATATTAT TAAGATGGGTTGGAGGATTGGCGAGTTTCTAAATATTAAGACACTGATCACTA AATGAATGGATGATCTACTCGGGTCAGGATTGAAAGAGAAATATTTCAACACC TTCCTGCTATACAATGGTCACCAGTGGTCCAGTTATTGTTCAATTTGATCATA AATTTGCTTCAATTCAGGAGCTTTGAAGGAAGTCCAAGGAAAGCTCTAGAAAA CAGTATAAACTTTCAGAGGCAAAATCCTTCACCAATTTTTCCACATACTTTCA TGCCTTGCCTAAAAAAAATGAAAAGAGAGTTGGTATGTCTCATGAATGTTCAC ACAGAAGGAGTTGGTTTTCATGTCATCTACAGCATATGAGAAAAGCTACCTTT CTTTTGATTATGTACACAGATATCTAAATAAGGAAGTATGAGTTTCACATGTA TATCAAAAATACAACAGTTGCTTGTATTCAGTAGAGTTTTCTTGCCCACCTAT TTTGTGCTGGGTTCTACCTTAACCCAGAAGACACTATGAAAAACAAGACAGAC TCCACTCAAAATTTATATGAACACCACTAGATACTTCCTGATCAAACATCAGT CAACATACTCTAAAGAATAACTCCAAGTCTTGGCCAGGCGCAGTGGCTCACAC CTGTAATCCCAACACTTTGGGAGGCCAAGGTGGGTGGATCATCTAAGGCCGGG AGTTCAAGACCAGCCTGACCAACGTGGAGAAACCCCATCTCTACTAAAAATAC AAAATTAGCCGGGCGTGGTAGCGCATGGCTGTAATCCTGGCTACTCAGGAGGC CGAGGCAGAAGAATTGCTTGAACTGGGGAGGCAGAGGTTGCGGTGAGCCCAGA TCGCGCCATTGCACTCCAGCCTGGGTAACAAGAGCAAAACTCTGTCCAAAAAA AAAAAAATAAAATAATAACTCCAAGCCTTTAAAAAATATCATCTGAAACTGTT ACATCAGATTTCTGGCACTCTACTGACTGTGGAAGATAGCCAGCTGACTGGAA GATAGCCAGCTGATTAGTTCCCTGAAGAAACCTGAAGACAGATACCTGGTTAA CTAGATCAACTACACTGCCAACTTGTTTGATGCTGAGAGACAATGGACTTATT CCATGGGGGAAGGGAAAAAAGAAGTCAATCACCAAATCTGAAGAAGTTAACCT AGATCTTTGAGGTTTGATTTGCAACTTTATATGCAGAGTATTATGTGGGTATT TTCCCTTAAAATATTCAAAGGGATTTACATATGGGATTAGCTAATGAGCCTAG CCAAGACCTTCCCTGGAGGACAGGCTGGTCATTGCGGAGGTCCCTTCTGTGCT TCAGTGGGTTCATATCCTCTAGTCCGTATGATTTTCCTACGCTAATATGTCAA GGGCAGGAGAGGCAGCTCTGTTCTCCTAGCCTTTGTTGACTTGTCTGCAAAGC AGGAATCTGCCCATTTGTTTCCAAGGAGCAAATGAGCTCATGAGAATGAAAGA TGTTAACTTCATGCATTCTGTGCCATCTGAGCATTTCGGTATTATATGACTGG TGACCCTTGGCCCGTATTATAAATGCTTCCTATCCTGGGAGACCTCATGGATG AGTCTGAGAGGAAATTTGGCACCAAAATCACTCTCACTCTGGTTTCCAGTAGA CTATAGAGGCAGAGAGGCATTTGAGAGGCTCCTGAGCAAAGTGTCCAGTGTAG CAGGAGCACTTCATTAATATTTATTGAGTTATAATTAAATAAAAATTAATTTC TGATTTCTCAGTTTGGAGGTTAAGGCTCTAAATATATTTTCTAACCTCTGCTA GGCTAACTTAAGCCAGGCCTTTTTCTTGCCTTCCCTTTCTCAAAACAGTCAGC ACAGACTCAGTGGGAGCACAGAGGAGTGTGGTCACCTCCACCTGGCTCACCAG AGTCTTCATAGAGGAAGTGAAGCCTGGAAGAAACTGGGCGGGCCCCAGATGAC CACAGGGAAAGGGCATCTCAGATGGAGGAATTACCCTTGACTTAAAGCAGAAA AGAAAGATTTCTCAGTAACTCCAAAACTTGCTTGATAGGAGAATATTCCCTCA ACCAATTCCTAGGACAATATTTATTGGTAGATCAAGAATGTTTCCTCAATAAC TCTAGTCTAGCTCCATGATCAGAACTAACACCCATTAAAAACATAAAATGTTC TTTCTGAACCGGTCTTCATGGTGCGTGAGAGCACCAAGCAGCTTTGGTATGCA GGAGGAGTTTTGCACAGAAGAGTGGCCTGCTCAAACCTGCCCACTGTTCTGTA GGTGATCTGGTGGATCTGGAAATTTATCCCAAGACAGGAATTTCCTAATATTC GAAGACATTTGAGGCTTTGGGAAATTCTCTGCTGTGCATTTATTTGGCTCCTG TCATAAGCTTGTTTTTTAAAGAATGTATCATAGCTCAAGTTTTTACTGCTGAT TTTGTTAAATTCTGTATAGTATATTTTTTACGGAAAGGCACAGTCAGACATTC CTAATAGGGCTCATGTCAGAACTTCTGTTCCCAAGGCATTATCTCCATAGCAA AAATTAGTGCACTGTTTTCAAAAGTGAGGTGGGAAAATGCTTTTAAGATCATG TGATGTTCCCCTAAAAGGGGTTAATGGGGTGTATTCAGGGTTTGGGAGGGAGG AAGAAGCATGCTTTAGAAAACAGTAAATTTAGGGAGAAAATGCTTTGTTGGTT AAATGTCACTCAAAAGGCTGAATTCAAATCAATTCCACAAACATTTACTGAGT ACCTACTGCCCCTGGGGACACAGAGATAAATTATTTAGTCTCAGACACACTCA TTCTAACTTCCCAGCACCTCTACTGTCTGCAGATTCTTTAATTTATTTTGGTT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GTATTAGCTAATTAATTCGTAAACTTTAGGCACATGGATCTATTCTCATTATG AAAATGGATGCCATTTGATTAAGGCTGATGACTAACAAAATGATTTGTGTTTA CTCGAAGTGTTTTTTTAAAAATAGCTACTCAAGGATAGTTTTCCATAAATCAA GAAGGTAAAAAAGTTCCCATTTTTTATTGTAGAATCCATTATTTAAACTACAT GTAGAGACAGGTTATTATTTGCTATATTCAAGTTTGGTCATCAATACCCTTAA AAATATTAGAATTTTATGGATGACCCAGAAATGCTTTGAAAATCTGTGTTCCT CAGCAAATACAGAGACCATGATCAAAATGCACAGAATCACTAACATTTTGATG CTAGCATGGTTTCAGTCTATTTGGCAGAACAGAATTGATTATGCTACTAAAAT TTCTTTTTCTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTTGCTTTGTCAC CCAGGCTGAAGTGCAGTGGCAGGATCTCAGTTCACTGCAACCTCTGCCTCCCA GGTTCACGCCATTCTCCTGCTTCAGCCTCCCGAGTAGCTGGGACTACAGGCTC CCACCACCATGCCCGGCTAATTTTTTGCATTTTTAGTAGAGACGGGGTTTCAC CGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCGCCTCAG CCTTCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCCCGGACTCTGATT TTTTTTTTACTAAGGTACAGTAAGAAAAGGGAAAAGTGTACGTTTTCACTTCC TGAAATATGTCAGGTTGAATCAATAATAGAGCACACCAGAACTCTTGGCTCCA TTTCAACCTAAACTATTCAGTTCTCATCACCCCAGAGGAAATTCCGCCTCTGT GCTGGTCAGTAATCCCCCTGGATTATAAAAGTTTAACTAACTCACTGTGCACA AGGCACGGCCATTGCCAACATTCTCTTGCAAGGTATTTTCCCAAGCCCTTACC CAATTCTGTTTCCATGATTGTGACATTGGGGATTAATTCTGCAAGACAGAACT GTTTATATTCTGTACCTTAAAAACACATGCAAACATCTCTTGCCTTAAGATTT CTGGCTTTCCTATGGCCCAGAGTCCTAGAAGTGTTTTGATATTTGTAGCAGAA TTTTCAAGTGTACATCCTTATCCTGGATATTAACATTTTTGCATCATATTGGC AGCTGGACCTACAGAGAATTTAGTAGACTGTTAACCTAATAAGCCTTGAATCC TTTTGCACCAGTGGTGAGAGAATGTGGATCAGAGCCATCACCTCCATGCCCCG TCACCCTCTAACAACCACATTTACAACTTCCCCAGCTCTGAGACACACTTGCC TCCACCCCTTCCATCACCCCATTTTAAGATGAAAATACCACACCAGCCTGGAA GGAAGAAGTTACTTGCCCAGGGCCACATAGTGAGTTAAGGGCTGATCTAGAGC TAGGAAGCTGTCTTCCTGAACCATAATCCTGGACTCTTCTAACCTCTCTACTC ATCGCAAATAGAGTTCATTTTAGTGATTTGAAGGAAGATGGGACAAGTATTTT CAAACACCTGTAGGACAACATGGAAGTGGGAGGAGACTTCTACTGTAGCTCCC CAGAGAAGAGAGCTAGGGCTACAGAGTTGCAGTTACAAGGTTGCCCTCTCTGG CTTGATCCCCAAAGGAATTTTCTACTCCAAAATAGAATTTTTCTAGGATGCTA TTTCTCAGTCCCTGGAGATACTCAAACAAAGGGCTTGTCACAAGGGTTTTTGT AGAAGCTATTCTTCACAGAGGTTGGGGGAGAGATTAAGCCAAAGGATCTCTGA GGTCTTTTTCAAATCTATAATTATGTGGCCTTTTGTTCATTGACTTCCATGTG TTCTAGTTGATCATTACAAACCTGGCAGGCCTTCTCAAGGGTTCAGTAATTAG CTGTCATTTCCCATTTGTCCAGAGAGTGTCCAACACAAAATACCCCTAAGATC TTGGCCAATAGAGAAATGTCATGGAATTTTAGAAATGACAGTATCTGCGGAGT TTATTCCAAGTTATATCATTTCAAAGATGAAGAAACCCAGGCTCAGAGGGAGC CATCACATCCACACCCTGTCACCCTTCGTGGCCAGTGCCAGACAGTAGCTAGT TGGATGCTAAAAGTAGAATTTAGATATCTTAACAATAAGCCCAGCAGTCTTTC AACTTCATTCGTAAATCATTTTTGTTTTGAGCATCTGTCACGTGGCAGCACTT GCCTGGATACTGGAGAGCTGAGAAGGAATGCGACAGGCAAGTCCTACTCTCAC AGTGTATACATTCAGGAGGAACAAGACACACAGTGCCAAGTAAATAAAGTAGC TGAACTTCATCAAATGATTTTATTCTTAAAGTCATTAAAGCATGTAATGTTCC CCTTTTTTTGTTTCAGGGGTGTACAGATTGAAGAAGTGTAGGTGTTTATGTGG TTTTAGTGACAAACCCCATGTGCTTTCATTGATTTTATGTTTTATGTTAAAAC ATCAACCGCAAGGTAAAATGCATATTGTATGTTGTTGGATACGTACTTAACTG GTATGCATCCCATGTCTTTGGGTACTAGTGTATGAATTCTAATCTCTGTAAAT GAAATGTTGTATGTGTTAATATATTTAATAGATGTAACTTAATAAACTGGCAT TGAAGACTGAA (SEQ ID NO: 133) >NP_005109.2 tumor necrosis factor ligand superfamily member 15 isoform VEGI-251 precursor [*Homo sapiens*] MAEDLGLSFGETASVEMLPEHGSCRPKARSSSARWALTCCLVLLPFLAGLTTY LLVSQLRAQGEACVQFQALKGQEFAPSHQQVYAPLRADGDKPRAHLTVVRQTP TQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMT SECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTKSVCEVGSNWFQPI YLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL (SEQ ID NO: 134)
Mouse TL1	>NM_177371.4 *Mus musculus* tumor necrosis factor (ligand) superfamily, member 15 (Tnfsf15), mRNA ATCAGAAGTCTCTCCAAGACAGCAGAAGGATGGCAGAGGAGCTGGGGTTGGGC TTCGGAGAAGGAGTCCCAGTGGAAGTGCTGCCGGAAGGCTGTAGACACAGGCC AGAGGCCAGGGCCGGGCTAGCTGCCAGGAGCAAAGCCTGCCTGGCTCTCACCT GCTGCCTGTTGTCATTTCCCATCCTCGCAGGACTTAGCACCCTCCTAATGGCT GGCCAGCTCCGGGTCCCCGGAAAAGACTGTATGCTTCGGGCCATAACAGAAGA GAGATCTGAGCCTTCACCACAGCAAGTTTACTCACCTCCCAGAGGCAAGCCGA GAGCACACCTGACAATTAAGAAACAAACCCCAGCACCACATCTGAAAAATCAG CTCTCTGCTCTACACTGGGAACATGACCTAGGGATGGCCTTCACCAAGAACGG GATGAAGTACATCAACAAATCCCTGGTGATCCCAGAGTCAGGAGACTATTTCA TCTACTCCCAGATCACATTCCGAGGGACCACATCTGTGTGTGGTGACATCAGT CGGGGGAGACGACCAAACAAGCCAGACTCCATCACCATGGTTATCACCAAGGT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	AGCAGACAGCTACCCTGAGCCTGCCCGCCTACTAACAGGGTCCAAGTCTGTGT GTGAAATAAGCAACAACTGGTTCCAGTCCCTCTACCTTGGGGCCACGTTCTCC TTGGAAGAAGGAGACAGACTAATGGTAAACGTCAGTGACATCTCCTTGGTGGA TTACACAAAAGAAGATAAAACTTTCTTTGGAGCTTTCTTGCTATAAGGAGGAG AAAACCATCATTCCAAGGGGCTCCCCTGCCTCCTACTTTCCAATTTCCTTTTC TCATATGGATCTATAAACAGGGGCTTTAGAGGGATCAGGGAAGGGGACAGTGG TTTAGCTATATAATTTAGGAACCCAATATTGATCCGTATATGCCTTATGGACT AAAATAGTAAATGGAAAACCCAGTACAGCTCATGTTTGATAGAGACCTGCTGG GTTTTAAAAATTGAAACACGCCTCATCCAATGGCACAATCTACTGATTTCAGG ACAGAACCTTTCCACAGTGCCCTCTGTCCAAGTCCTTTCTGAATTCAGCAGTT CAGTTAGAGCTGAATTCGACAATGAACTTACTCCAGATCAAGAGCTAAAGACA GAATCCAAAGAAAGACTGAGAAAATGATGTTATTTCTCCAAGAGGCAATGCAT TTCCACATTCTTTTGTGCCTAACCTAAAAAATAAGAAAGAAGAAAGGAAGGAA GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG GAAGGAAGGGACAAGAAAAGACAAGACAAGACAAGAAAAAAGAAAAAATGGTA TTTCTCGTGAATATTCCCTAAAAGGAATTGGTTTTCTGCTGTGAAGGAGAAAC CTCACCTTTCTTCTGATTGCATCCTTTAGTATCCAAACATACAAGTGGGAATT CCAAATGCACATGGAACATAGAACACTTTTATTATTGTGAGAACATGTTTATT GAGTACCTACTATGCTCTGGGCACTCAGCCCACAGGACCATGAAGAGAAAGTC AAATTTTCTTAAAAACTAAATGAATCCTCAATACATACTTCCTGATCAACTAC CACTCAAAATGTATAACTTCCAAAGTATAACTTCAAGTCAGCCATCTAGGTGG TTTCTTGGGTAAAGGTGCTTGTCATTAAGCCTGACACCTGGGTTTGACCTCCC AGAACCCAAAAGCTGGAAGGAGAGAATTGGTTCCCACAAATTATCCTCAAACC CCCATACAAATGATGTGGCATGCACACATGTAACTAAATAAATAAGTGTAAAA CAAAAACAAAAACAAAATTTTAAAGAAAAATTTCAAGTCCTGAAAGACAGCAT TCCTGAGAATGTTGTCTCCATCGTTGTCCAGTATAGGCTAACCAGCTGATAGA GACACTGAAGGAATTTAAAGACAGACATCAAGTGAAATGGAGCACTGTAGAAA CACTTGATTCATGCCAGGAGTCAATGTACTATGAAGACCAACAACAAAGTGTC AGTCATCAAATCCAGAGGTGTTTATCTAGATCTGCTTTCAAGTTTGGTTTGCA GCCTTTATATAGTCTCTATTACAAATGCTCGTGTCATGGTAGATGCCACAAGG AGTCAGAGGGTAAACTTAGCCCCAAACCACTGCTGAGCCATCTTCTAGGAAAC CTTCGAAGCAGAGCTGGGCAGCGTGACTCCCACACAATGACTGGGAAAGTAGT AGCTGATCAAAATTTGTTGAGTAATAATTTGTTAGAAAATTCATCTCCACTGC CTACTAAACCTAAGTTGTATACTATCTAGCTTCTGCTAAGCCAACTTACATTG GCCACTTTTTCTGTCTTCAACTTCTTGAAGTATCACAGGTCTCAGTGAGAACA CAGGGAAAGGTGAGGTCGCCTTCCCCTGGTTCTTCATAGGGGAAACCACACCT GAAAGAAGATGAGCAGCCTGAGGTGACCTGGAGGAAGGGCTGTCTCAGAAGAA GGACTTATTTTTTGGCTTAGGTCTAAAACCTTGAGAGTAATGCTCACTGGTCA ATTGAGGATGCTTTATCAATGACTCCAGTCTGACTCCAAGGTCAGAAAGGAGA GTGAGATGCTCTCTCTGCCTGCATATATCTTCATGGAACATGAGAATATTGAG CAACATAGACTTATAGGAAAACACTTGCCCAAAAGTAGCCAGAGTGACCTGGT CATCCCCTCTACTAAACCCAAGCTTTGTGTCAAGGGCCTTCAAAGCTGCCCAG AAGTGATCTGGATGGCTTGGGAATTTATCCAAGACAGGAATTTCCTGACAGCC AAAGATGCTTGAGTCCTTGTGCCTGACATGCATTTATTTTGCCCCTGTTTATT GAAGACTGTAACTGTTGATTTGTGGGTATACATACATACATACATACATACAT ACATACATACATACATATGCTGTCATGAAGGCAGCATCAAACATTACTAATTG GACTCAAACCAGCATTTCTGTTTCCAAGATACTAAGTATTCCCATGCAAACAG GAGCATGCTATTTTTCTAAAGCAAAATGAAAAAAATAGTTTTGAAAGTATATA TATGATGGAGTCAAGTGTAATGGCATACATCTGTAAACCCAGCACATGGGATG CTGAGCCAGGAGGATTGCCGTGAGTTTGAGGAGAACAGGGGCTAAATAGTAAT TTTCAGGAAAGCCTTGCCTATATAACAAGACCTTGTCTCAAATGAAAAAAAAA AAAAAAATAGACCCCAGGCTGGTCCTTGGAGATAAGGTAATATATTCATTGGG TGAGGGGGTGTGTGTTTTGGAAAATAGTTAATTTAGTGAGAAATGCTTTTCGG TCAAATGCATCTCAAAGGCTGCTGAATTCAAATCGGGTCTGTAAATGCTTACC TAGTGCTTGCTTGCCCTGGGGACAGAGACATAAATTACTTTAGTCTCAGATCC ACTCGTTCTAACAGATTGGCATCTCCATCGTCTGTGGAGCTTTTAATCACTCT GTTTGTATTAGCTAATTAATTAGCTAACTTGAGACACACTGATATTTTCTTAT TATAAACATGGGTGCCATTTGATAAAAGACAATCATTAACAAAATGGTTCGAA TTTCCGCTTAAGTGATCTTCTTTTTTCCTTTTCATTTTTTTTAACTAGCTAAT CAAAGGTAGTTTCCCAAAAATAAATGCAAAGGGAGTATAAAGAAAAAATTCCC TGTGGTGGGAGCTAGTATTGAAACAACAGTATCAAAGAGGCTGTTACCTACTG GCCTCAAATTTTGGCAGGAACGCCTTTGAAAATGTTAGAACTTTACGGACAGC CTAGAGGTGCTTTGAAAAGTCTCTGTTGCCAACAAAAGCCATTAATCAGCATG CGGCACAGGTTACTCAAATTTTGACCTTGACTGTTTTTTAGATCTGTTACACA GAACACAACTTCTGGGCTGTAATCTCTGATGTGGATTTGGTGATTTACTAAGG TACCGTGGGAAACAAGGAAAGTGTACTTGTACCACATCGTTTCTCAGTGCATG TCAGAGTCTACTCAACAGCAGGGCATGCCAGAGCCTTGGATACATTCCGGGAC AAACTATGTCACTCCTAAGGAAATTCCAAGTGTGTGCCTGTCAAGCACTCTGG ATCATAGAAGCCCACGAGTTCACTGTGCACAAGGCACAGCCATGGCCAGCACT CTCTTGCATGGTATTTCTCTTAAGCTCTTACTCAATCACGGTCCCATGATTGT GACATTGGGGATTAATTGCTTGAGCAGGTTTATTTACAGTCTGTTCCTTGCAA AATACATGCAGATATGTCTGGCCTCAAAATCCCCTGATTGTTTTAGGGCTTAG AGAATACTGGGGATGTTTTTGCTGTTTTCAGATGTACTTTATTTAAGCTTGCA GAATTACCCTGAATATTAACAGTGTTCTAAGATATTGCCTGCTAGCTTCTGGC TAATTTACTAGTGGTGACAGTATCAGATCAGAGTATCTATATTTATGTCTTGC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TATTATAGTTAAAACTTCCTGATCTCTGTAACACACTCACCCCTACCTCATCT ATCTACCCATCTTGTGGATGTAGCTGTGAGAAGACTCACAAGCCCGAGTTGCA GTTACTTTTCTGAAGCAACATAGTATGTTAATGGAATGGCCAGAACTCTACTC TTGGCACATGGCACTGAATTTGATGCCACTAAAAGAAAAATTGAAGGCAGAAA TATTTTTTACTATGCATGGGACAACGTAGAAGAGCAAGGAGACTGCTTACACA TGGTGGTCACATCTCTGGCTTCATCCCTAAACCAATTTTCTGACCCCAAGTCG ATTTTTTTTCATGTAGTTATTGTTCATTTTCTGGAAAGAGTCAAGCAAAAAGA GAGTTTTATAGAAACCATTGCATCATGGAGGTCAGGGGAGGGATTAAGCCAAA GAATTCCTTCTCCAAATCTATAGCCATATGGCCACCCTTTGGTGTACTTCTAT TTGATCATGACAAACCTGAGAGCCCTGCCCAGAGTTCAGTGGATCCTAATGAA CTCCAAGAGTAATTCATTCCCTCACCAACTCTAGGGGCTTGGCCAGTGCAGAA AATGTCATGGGATTTTAAAGTTAACATGAGCTGCTATCCAAACTTATGTCTCT TTAAGAATGGAGAGACACAGGCCAGGAGAGGTAACATATGAAGCCTGGTATTG GGCAGTAGCTTGATGGAGTATTGAGGCTAAAAGTAGACTTCCTGCCCCTGACC ATACACAACACCCTTTCAGTTTGATCCATGGTGGTCTTATTCTACTTTATTTT GAGCACCTGTCACACCTAGTTACTGTCATGCCAAGAAGGTCCATAACAGGCAA ATCCTACTCTGCTGTGTGCACACAAGAGGAAGGAGGCTCACAGTAGCAAGTAA ACAGATAAGCAAACGTACACGATTTTCGTCTTAAAGTCATTAAGACACACGCG TACCCCTCTTTTGTTTCAGAGGGTATACAGGCTGAACAGATGTCAGTGTTCAC CTATTCTTATTGATAAGCCCCATGTGCTTTCATTGGTTGAATGTTTTATGTTA AAACGTCATATTGCCATCGTAAAATGCATATTGTATGTTGTTGGGTATATAAT TAACTAATATGCATCGCATGTATGAATTCTAATCTCTGTAAATGAAAACTTAT ATATGTTAACATATGTAATAGTTATAATTTAATAAACTGACACTGGAGACTAC (SEQ ID NO: 135) >NP_796345.4 tumor necrosis factor ligand superfamily member 15 [*Mus musculus*] MAEELGLGFGEGVPVEVLPEGCRHRPEARAGLAARSKACLALTCCLLSFPILA GLSTLLMAGQLRVPGKDCMLRAITEERSEPSPQQVYSPPRGKPRAHLTIKKQT PAPHLKNQLSALHWEHDLGMAFTKNGMKYINKSLVIPESGDYFIYSQITFRGT TSVCGDISRGRRPNKPDSITMVITKVADSYPEPARLLTGSKSVCEISNNWFQS LYLGATFSLEEGDRLMVNVSDISLVDYTKEDKTFFGAFLL (SEQ ID NO: 136)
Human CD80	>NM_005191.4 *Homo sapiens* CD80 molecule (CD80), mRNA AAACCCTCTGTAAAGTAACAGAAGTTAGAAGGGGAAATGTCGCCTCTCTGAAG ATTACCCAAAGAAAAAGTGATTTGTCATTGCTTTATAGACTGTAAGAAGAGAA CATCTCAGAAGTGGAGTCTTACCCTGAAATCAAAGGATTTAAAGAAAAAGTGG AATTTTTCTTCAGCAAGCTGTGAAACTAAATCCACAACCTTTGGAGACCCAGG AACACCCTCCAATCTCTGTGTGTTTTGTAAACATCACTGGAGGGTCTTCTACG TGAGCAATTGGATTGTCATCAGCCCTGCCTGTTTTGCACCTGGGAAGTGCCCT GGTCTTACTTGGGTCCAAATTGTTGGCTTTCACTTTTGACCCTAAGCATCTGA AGCCATGGGCCACACACGGAGGCAGGGAACATCACCATCCAAGTGTCCATACC TCAATTTCTTTCAGCTCTTGGTGCTGGCTGGTCTTTCTCACTTCTGTTCAGGT GTTATCCACGTGACCAAGGAAGTGAAAGAAGTGGCAACGCTGTCCTGTGGTCA CAATGTTTCTGTTGAAGAGCTGGCACAAACTCGCATCTACTGGCAAAAGGAGA AGAAAATGGTGCTGACTATGATGTCTGGGGACATGAATATATGGCCCGAGTAC AAGAACCGGACCATCTTTGATATCACTAATAACCTCTCCATTGTGATCCTGGC TCTGCGCCCATCTGACGAGGGCACATACGAGTGTGTTGTTCTGAAGTATGAAA AAGACGCTTTCAAGCGGGAACACCTGGCTGAAGTGACGTTATCAGTCAAAGCT GACTTCCCTACACCTAGTATATCTGACTTTGAAATTCCAACTTCTAATATTAG AAGGATAATTTGCTCAACCTCTGGAGGTTTTCCAGAGCCTCACCTCTCCTGGT TGGAAAATGGAGAAGAATTAAATGCCATCAACACAACAGTTTCCCAAGATCCT GAAACTGAGCTCTATGCTGTTAGCAGCAAACTGGATTTCAATATGACAACCAA CCACAGCTTCATGTGTCTCATCAAGTATGGACATTTAAGAGTGAATCAGACCT TCAACTGGAATACAACCAAGCAAGAGCATTTTCCTGATAACCTGCTCCCATCC TGGGCCATTACCTTAATCTCAGTAAATGGAATTTTTGTGATATGCTGCCTGAC CTACTGCTTTGCCCCAAGATGCAGAGAGAGAAGGAGGAATGAGAGATTGAGAA GGGAAAGTGTACGCCCTGTATAACAGTGTCCGCAGAAGCAAGGGGCTGAAAAG ATCTGAAGGTCCCACCTCCATTTGCAATTGACCTCTTCTGGGAACTTCCTCAG ATGGACAAGATTACCCCACCTTGCCCTTTACGTATCTGCTCTTAGGTGCTTCT TCACTTCAGTTGCTTTGCAGGAAGTGTCTAGAGGAATATGGTGGGCACAGAAG TAGCTCTGGTGACCTTGATCAAGGTGTTTTGAAATGCAGAATTCTTGAGTTCT GGAAGGGACTTTAGAGAATACCAGTGTTATTAATGACAAAGGCACTGAGGCCC AGGGAGGTGACCCGAATTATAAAGGCCAGCGCCAGAACCCAGATTTCCTAACT CTGGTGCTCTTTCCCTTTATCAGTTTGACTGTGGCCTGTTAACTGGTATATAC ATATATATGTCAGGCAAAGTGCTGCTGGAAGTAGAATTTGTCCAATAACAGGT CAACTTCAGAGACTATCTGATTTCCTAATGTCAGAGTAGAAGATTTTATGCTG CTGTTTACAAAAGCCCAATGTAATGCATAGGAAGTATGGCATGAACATCTTTA GGAGACTAATGGAAATATTATTGGTGTTTACCCAGTATTCCATTTTTTTCATT GTGTTCTCTATTGCTGCTCTCTCACTCCCCCATGAGGTACAGCAGAAAGGAGA ACTATCCAAAACTAATTTCCTCTGACATGTAAGACGAATGATTTAGGTACGTC AAAGCAGTAGTCAAGGAGGAAAGGGATAGTCCAAAGACTTAACTGGTTCATAT TGGACTGATAATCTCTTTAAATGGCTTTATGCTAGTTTGACCTCATTTGTAAA ATATTTATGAGAAAGTTCTCATTTAAAATGAGATCGTTGTTTACAGTGTATGT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ACTAAGCAGTAAGCTATCTTCAAATGTCTAAGGTAGTAACTTTCCATAGGGCC TCCTTAGATCCCTAAGATGGCTTTTTCTCCTTGGTATTTCTGGGTCTTTCTGA CATCAGCAGAGAACTGGAAAGACATAGCCAACTGCTGTTCATGTTACTCATGA CTCCTTTCTCTAAAACTGCCTTCCACAATTCACTAGACCAGAAGTGGACGCAA CTTAAGCTGGGATAATCACATTATCATCTGAAAATCTGGAGTTGAACAGCAAA AGAAGACAACATTTCTCAAATGCACATCTCATGGCAGCTAAGCCACATGGCTG GGATTTAAAGCCTTTAGAGCCAGCCCATGGCTTTAGCTACCTCACTATGCTGC TTCACAAACCTTGCTCCTGTGTAAAACTATATTCTCAGTGTAGGGCAGAGAGG TCTAACACCAACATAAGGTACTAGCAGTGTTTCCCGTATTGACAGGAATACTT AACTCAATAATTCTTTTCTTTTCCATTTAGTAACAGTTGTGATGACTATGTTT CTATTCTAAGTAATTCCTGTATTCTACAGCAGATACTTTGTCAGCAATACTAA GGGAAGAAACAAAGTTGAACCGTTTCTTTAATAA (SEQ ID NO: 137)
	>NP__005182.1 T-lymphocyte activation antigen CD80 precursor [*Homo sapiens*] MGHTRRQGTSPSKCPYLNFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHN VSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITNNLSIVILAL RPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNIRR IICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNH SFMCLIKYGHLRVNQTFNWNTTKQEHFPDNLLPSWAITLISVNGIFVICCLTY CFAPRCRERRRNERLRRESVRPV (SEQ ID NO: 138)
Mouse CD80	>NM_009855.2 *Mus musculus* CD80 antigen (Cd80), transcript variant 2, mRNA GAGTTTTATACCTCAATAGACTCTTACTAGTTTCTCTTTTTCAGGTTGTGAAA CTCAACCTTCAAAGACACTCTGTTCCATTTCTGTGGACTAATAGGATCATCTT TAGCATCTGCCGGGTGGATGCCATCCAGGCTTCTTTTTCTACATCTCTGTTTC TCGATTTTTGTGAGCCTAGGAGGTGCCTAAGCTCCATTGGCTCTAGATTCCTG GCTTTCCCCATCATGTTCTCCAAAGCATCTGAAGCTATGGCTTGCAATTGTCA GTTGATGCAGGATACACCACTCCTCAAGTTTCCATGTCCAAGGCTCATTCTTC TCTTTGTGCTGCTGATTCGTCTTTCACAAGTGTCTTCAGATGTTGATGAACAA CTGTCCAAGTCAGTGAAAGATAAGGTATTGCTGCCTTGCCGTTACAACTCTCC TCATGAAGATGAGTCTGAAGACCGAATCTACTGGCAAAAACATGACAAAGTGG TGCTGTCTGTCATTGCTGGGAAACTAAAAGTGTGGCCCGAGTATAAGAACCGG ACTTTATATGACAACACTACCTACTCTCTTATCATCCTGGGCCTGGTCCTTTC AGACCGGGGCACATACAGCTGTGTCGTTCAAAAGAAGGAAAGAGGAACGTATG AAGTTAAACACTTGGCTTTAGTAAAGTTGTCCATCAAAGCTGACTTCTCTACC CCCAACATAACTGAGTCTGGAAACCCATCTGCAGACACTAAAAGGATTACCTG CTTTGCTTCCGGGGGTTTCCCAAAGCCTCGCTTCTCTTGGTTGGAAAATGGAA GAGAATTACCTGGCATCAATACGACAATTTCCCAGGATCCTGAATCTGAATTG TACACCATTAGTAGCCAACTAGATTTCAATACGACTCGCAACCACACCATTAA GTGTCTCATTAAATATGGAGATGCTCACGTGTCAGAGGACTTCACCTGGGAAA AACCCCCAGAAGACCCTCCTGATAGCAAGAACACACTTGTGCTCTTTGGGGCA GGATTCGGCGCAGTAATAACAGTCGTCGTCATCGTTGTCATCATCAAATGCTT CTGTAAGCACAGAAGCTGTTTCAGAAGAAATGAGGCAAGCAGAGAAACAAACA ACAGCCTTACCTTCGGGCCTGAAGAAGCATTAGCTGAACAGACCGTCTTCCTT TAGTTCTTCTCTGTCCATGTGGGATACATGGTATTATGTGGCTCATGAGGTAC AATCTTTCTTTCAGCACCGTGCTAGCTGATCTTTCGGACAACTTGACACAAGA TAGAGTTAACTGGGAAGAGAAAGCCTTGAATGAGGATTTCTTTCCATCAGGAA GCCTACGGGCAAGTTTGCTGGGCCTTTGATTGCTTGATGACTGAAGTGGAAAG GCTGAGCCCACTGTGGGTGGTGCTAGCCCTGGGCAGGGGCAGGTGACCCTGGG TGGTATAAGAAAAAGAGCTGTCACTAAAAGGAGAGGTGCCTAGTCTTACTGCA ACTTGATATGTCATGTTTGGTTGGTGTCTGTGGGAGGCCTGCCCTTTTCTGAA GAGAAGTGGTGGGAGAGTGGATGGGGTGGGGGCAGAGGAAAAGTGGGGGAGAG GGCCTGGGAGGAGAGGAGGGAGGGGGACGGGGTGGGGGTGGGGAAAACTATGG TTGGGATGTAAAAACGATAATAATATAAATATTAAATAAAAAGAGAGTATTGA GCAAA (SEQ ID NO: 139)
	>NP_033985.3 T-lymphocyte activation antigen CD80 precursor [*Mus musculus*] MACNCQLMQDTPLLKFPCPRLILLFVLLIRLSQVSSDVDEQLSKSVKDKVLLP CRYNSPHEDESEDRIYWQKHDKVVLSVIAGKLKVWPEYKNRTLYDNTTYSLII LGLVLSDRGTYSCVVQKKERGTYEVKHLALVKLSIKADFSTPNITESGNPSAD TKRITCFASGGFPKPRFSWLENGRELPGINTTISQDPESELYTISSQLDFNTT RNHTIKCLIKYGDAHVSEDFTWEKPPEDPPDSKNTLVLFGAGFGAVITVVVIV VIIKCFCKHRSCFRRNEASRETNNSLTFGPEEALAEQTVFL (SEQ ID NO: 140)
Human CD86	>NM_175862.5 *Homo sapiens* CD86 molecule (CD86), transcript variant 1, mRNA AGTCATTGCCGAGGAAGGCTTGCACAGGGTGAAAGCTTTGCTTCTCTGCTGCT GTAACAGGGACTAGCACAGACACACGGATGAGTGGGGTCATTTCCAGATATTA GGTCACAGCAGAAGCAGCCAAAATGGATCCCCAGTGCACTATGGGACTGAGTA ACATTCTCTTTGTGATGGCCTTOCTGOTCTCTGGTGCTGCTCCTCTGAAGATT CAAGCTTATTTCAATGAGACTGCAGACCTGCCATGCCAATTTGCAAACTCTCA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	AAACCAAAGCCTGAGTGAGCTAGTAGTATTTTGGCAGGACCAGGAAAACTTGG TTCTGAATGAGGTATACTTAGGCAAAGAGAAATTTGACAGTGTTCATTCCAAG TATATGGGCCGCACAAGTTTTGATTCGGACAGTTGGACCCTGAGACTTCACAA TCTTCAGATCAAGGACAAGGGCTTGTATCAATGTATCATCCATCACAAAAAGC CCACAGGAATGATTCGCATCCACCAGATGAATTCTGAACTGTCAGTGCTTGCT AACTTCAGTCAACCTGAAATAGTACCAATTTCTAATATAACAGAAAATGTGTA CATAAATTTGACCTGCTCATCTATACACGGTTACCCAGAACCTAAGAAGATGA GTGTTTTGCTAAGAACCAAGAATTCAACTATCGAGTATGATGGTGTTATGCAG AAATCTCAAGATAATGTCACAGAACTGTACGACGTTTCCATCAGCTTGTCTGT TTCATTCCCTGATGTTACGAGCAATATGACCATCTTCTGTATTCTGGAAACTG ACAAGACGCGGCTTTTATCTTCACCTTTCTCTATAGAGCTTGAGGACCCTCAG CCTCCCCCAGACCACATTCCTTGGATTACAGCTGTACTTCCAACAGTTATTAT ATGTGTGATGGTTTTCTGTCTAATTCTATGGAAATGGAAGAAGAAGAAGCGGC CTCGCAACTCTTATAAATGTGGAACCAACACAATGGAGAGGGAAGAGAGTGAA CAGACCAAGAAAAGAGAAAAAATCCATATACCTGAAAGATCTGATGAAGCCCA GCGTGTTTTTAAAAGTTCGAAGACATCTTCATGCGACAAAAGTGATACATGTT TTTAATTAAAGAGTAAAGCCCATACAAGTATTCATTTTTTCTACCCTTTCCTT TGTAAGTTCCTGGGCAACCTTTTTGATTTCTTCCAGAAGGCAAAAAGACATTA CCATGAGTAATAAGGGGGCTCCAGGACTCCCTCTAAGTGGAATAGCCTCCCTG TAACTCCAGCTCTGCTCCGTATGCCAAGAGGAGACTTTAATTCTCTTACTGCT TCTTTTCACTTCAGAGCACACTTATGGGCCAAGCCCAGCTTAATGGCTCATGA CCTGGAAATAAAATTTAGGACCAATACCTCCTCCAGATCAGATTCTTCTCTTA ATTTCATAGATTGTGTTTTTTTTTTAAATAGACCTCTCAATTTCTGGAAAACT GCCTTTTATCTGCCCAGAATTCTAAGCTGGTGCCCCACTGAATTTTGTGTGTA CCTGTGACTAAACAACTACCTCCTCAGTCTGGGTGGGACTTATGTATTTATGA CCTTATAGTGTTAATATCTTGAAACATAGAGATCTATGTACTGTAATAGTGTG ATTACTATGCTCTAGAGAAAAGTCTACCCCTGCTAAGGAGTTCTCATCCCTCT GTCAGGGTCAGTAAGGAAAACGGTGGCCTAGGGTACAGGCAACAATGAGCAGA CCAACCTAAATTTGGGGAAATTAGGAGAGGCAGAGATAGAACCTGGAGCCACT TCTATCTGGGCTGTTGCTAATATTGAGGAGGCTTGCCCCACCCAACAAGCCAT AGTGGAGAGAACTGAATAAACAGGAAAATGCCAGAGCTTGTGAACCCTGTTTC TCTTGAAGAACTGACTAGTGAGATGGCCTGGGGAAGCTGTGAAAGAACCAAAA GAGATCACAATACTCAAAAGAGAGAGAGAGAGAGAAAAAAGAGAGATCTTGATCC ACAGAAATACATGAAATGTCTGGTCTGTCCACCCCATCAACAAGTCTTGAAAC AAGCAACAGATGGATAGTCTGTCCAAATGGACATAAGACAGACAGCAGTTTCC CTGGTGGTCAGGGAGGGGTTTTGGTGATACCCAAGTTATTGGGATGTCATCTT CCTGGAAGCAGAGCTGGGGAGGGAGAGCCATCACCTTGATAATGGGATGAATG GAAGGAGGCTTAGGACTTTCCACTCCTGGCTGAGAGAGGAAGAGCTGCAACGG AATTAGGAAGACCAAGACACAGATCACCCGGGGCTTACTTAGCCTACAGATGT CCTACGGGAACGTGGGCTGGCCCAGCATAGGGCTAGCAAATTTGAGTTGGATG ATTGTTTTTGCTCAAGGCAACCAGAGGAAACTTGCATACAGAGACAGATATAC TGGGAGAAATGACTTTGAAAACCTGGCTCTAAGGTGGGATCACTAAGGGATGG GGCAGTCTCTGCCCAAACATAAAGAGAACTCTGGGGAGCCTGAGCCACAAAAA TGTTCCTTTATTTTATGTAAACCCTCAAGGGTTATAGACTGCCATGCTAGACA AGCTTGTCCATGTAATATTCCCATGTTTTTACCCTGCCCCTGCCTTGATTAGA CTCCTAGCACCTGGCTAGTTTCTAACATGTTTTGTGCAGCACAGTTTTTAATA AATGCTTGTTACATTCA (SEQ ID NO: 141) >NP_787058.5 T-lymphocyte activation antigen CD86 isoform 1 precursor [*Homo sapiens*] MDPQCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNQSLSEL VVFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFDSDSWTLRLHNLQIKDKG LYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEIVPISNITENVYINLTCSS IHGYPEPKKMSVLLRTKNSTIEYDGVMQKSQDNVTELYDVSISLSVSFPDVTS NMTIFCILETDKTRLLSSPFSIELEDPQPPPDHIPWITAVLPTVIICVMVFCL ILWKWKKKKRPRNSYKCGTNTMEREESEQTKKREKIHIPERSDEAQRVFKSSK TSSCDKSDTCF (SEQ ID NO: 142)
Mouse CD86	>NM_019388.3 *Mus musculus* CD86 antigen (Cd86), mRNA ATTGCTGAGGAAGAAAGAGGAGCAAGCAGACGCGTAAGAGTGGCTCCTGTAGG CAGCACGGACTTGAACAACCAGACTCCTGTAGACGTGTTCCAGAACTTACGGA AGCACCCACGATGGACCCCAGATGCACCATGGGCTTGGCAATCCTTATCTTTG TGACAGTCTTGCTGATCTCAGATGCTGTTTCCGTGGAGACGCAAGCTTATTTC AATGGGACTGCATATCTGCCGTGCCCATTTACAAAGGCTCAAAACATAAGCCT GAGTGAGCTGGTAGTATTTTGGCAGGACCAGCAAAAGTTGGTTCTGTACGAGC ACTATTTGGGCACAGAGAAACTTGATAGTGTGAATGCCAAGTACCTGGGCCGC ACGAGCTTTGACAGGAACAACTGGACTCTACGACTTCACAATGTTCAGATCAA GGACATGGGCTCGTATGATTGTTTTATACAAAAAAAGCCACCCACAGGATCAA TTATCCTCCAACAGACATTAACAGAACTGTCAGTGATCGCCAACTTCAGTGAA CCTGAAATAAAACTGGCTCAGAATGTAACAGGAAATTCTGGCATAAATTTGAC CTGCACGTCTAAGCAAGGTCACCCGAAACCTAAGAAGATGTATTTTCTGATAA CTAATTCAACTAATGAGTATGGTGATAACATGCAGATATCACAAGATAATGTC ACAGAACTGTTCAGTATCTCCAACAGCCTCTCTCTTTCATTCCCGGATGGTGT GTGGCATATGACCGTTGTGTGTGTTCTGGAAACGGAGTCAATGAAGATTTCCT CCAAACCTCTCAATTTCACTCAAGAGTTTCCATCTCCTCAAACGTATTGGAAG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GAGATTACAGCTTCAGTTACTGTGGCCCTCCTCCTTGTGATGCTGCTCATCAT TGTATGTCACAAGAAGCCGAATCAGCCTAGCAGGCCCAGCAACACAGCCTCTA AGTTAGAGCGGGATAGTAACGCTGACAGAGAGACTATCAACCTGAAGGAACTT GAACCCCAAATTGCTTCAGCAAAACCAAATGCAGAGTGAAGGCAGTGAGAGCC TGAGGAAAGAGTTAAAAATTGCTTTGCCTGAAATAAGAAGTGCAGAGTTTCTC AGAATTCAAAAATGTTCTCAGCTGATTGGAATTCTACAGTTGAATAATTAAAG AACAAAATACACAACAGTGTCCATATTTTATCCTGTTTCCTTTCCAAGTTTTT GGGCAATGTCAATTGTGTCCCCTATGCCAGGAGCAGACATCTATTTTGTCTTG CTTTGTTTAACTCAGTGCACACTCATAGGCCAAGAGCACTGAAATGGCTTCTT TCCCAGGAATAACATTTTGGATCAATCTCTCCTACTTGAGATCAGATTCTTCT TCTAATTTTGCATAGTGTGTTTTTATATGGAACTCCTTGTTGTAGGAATACTG GCTTTTATCTGTCTTGCACACTTGCATACTTATATACTTATACCTGGACAGCT ACCTCTTCAGTCAGGATGGGAGTGGTATATTTGGTGATGTTATTTGATGTGTT CGTGTTGCTATCTTAAAACAGCAAAGAGCATATACTATAGTAGCTCAACTACA ATGATCTAGAGAAAGACCCAGCACTTATAAGAAACACTGTCCCTCCATCAGGG TCAATAATGAATACAATGACCTAAGTAATATACAGGTGACAGCAACAGCACAG AGTTCTCAGTGCTGGCAAATCAAGAAACACAAATATGGAACCATCTCTAGATC CAAGAGCCACTCCTACCTGGGCTGCCACAGATACTGGAAGAATCCACCTGCCT GGCCAGCAAGTCACAACTTAGCAGGCAGCACTGAAGAAAGCAAGATGTACTGT ATGCCCTTTTAAGAAAATGCCTGGAAAGGTCTGGAGAATGCTGTGCAAGGATA AGACAGCCAAGCACTCAAAACCAGGAGACATCACTAGAATCCAACCAACAAAT GTTTATGGAAGGACTGATCTGCCCAGTCCATTGAAAAGTCAAGAGGTCAGAGA TAGACCAGTGTGTGTCTCAATGGATGTAGATATCAGCCACCTCGGTGCTCAAC AGGTATTTTATGATCTCCTTGTTTCAAATTCATCTAGATGTAGAACTAGGGAG AGAGCAGTCACATTGATGAAAGGCTAGGACTCTTTCAGCTCATGGCTTGTGTG GAAGGAGGGAAAGCAGAAATCACAACACTCTGAGACTACTGTAGTCTGCAGAT ACCTGAGTGGGTGTGGCTTGGCCTTTCAAAGGACAAAGAGCAACTAATGCTGA AAGCACATAGTGTATCTATACGGCATGGAATAGTCATCACCCAGACTTAAAGA GAACTTTGGCAGGTCTGAGCAGCAAAATATTGTTGTTTCCATTTTACATAAAG GGCCCTGGAGGGCTATAGACTATTCCGCTGGCAGGGCTCATGCTTGTAATGTG TCCATCTTGATTCACCCTGTGCAGACTCTTAAGATCTGGCCAGTTACCAACAT GTTCTGTACAGAGTGGATTTCAATAAAGTTTTCTTGAATTTTTTCAAG (SEQ ID NO: 143) >NP_062261.3 T-lymphocyte activation antigen 0D86 precursor [*Mus musculus*] MDPRCTMGLAILIFVTVLLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSEL VVFWQDQQKLVLYEHYLGTEKLDSVNAKYLGRTSFDRNNWTLRLHNVQIKDMG SYDCFIQKKPPTGSIILQQTLTELSVIANFSEPEIKLAQNVTGNSGINLTCTS KQGHPKPKKMYFLITNSTNEYGDNMQISQDNVTELFSISNSLSLSFPDGVWHM TVVCVLETESMKISSKPLNFTQEFPSPQTYWKEITASVTVALLLVMLLIIVCH KKPNQPSRPSNTASKLERDSNADRETINLKELEPQIASAKPNAE (SEQ ID NO: 144)
Human LFA-3 (CD58)	>NM_001779.3 *Homo sapiens* CD58 molecule (CD58), transcript variant 1, mRNA GAACTTAGGGCTGCTTGTGGCTGGGCACTCGCGCAGAGGCCGGCCCGACGAGC CATGGTTGCTGGGAGCGACGCGGGGCGGGCCCTGGGGGTCCTCAGCGTGGTCT GCCTGCTGCACTGCTTTGGTTTCATCAGCTGTTTTTCCCAACAAATATATGGT GTTGTGTATGGGAATGTAACTTTCCATGTACCAAGCAATGTGCCTTTAAAAGA GGTCCTATGGAAAAAACAAAAGGATAAAGTTGCAGAACTGGAAAATTCTGAAT TCAGAGCTTTCTCATCTTTTAAAAATAGGGTTTATTTAGACACTGTGTCAGGT AGCCTCACTATCTACAACTTAACATCATCAGATGAAGATGAGTATGAAATGGA ATCGCCAAATATTACTGATACCATGAAGTTCTTTCTTTATGTGCTTGAGTCTC TTCCATCTCCCACACTAACTTGTGCATTGACTAATGGAAGCATTGAAGTCCAA TGCATGATACCAGAGCATTACAACAGCCATCGAGGACTTATAATGTACTCATG GGATTGTCCTATGGAGCAATGTAAACGTAACTCAACCAGTATATATTTTAAGA TGGAAAATGATCTTCCACAAAAAATACAGTGTACTCTTAGCAATCCATTATTT AATACAACATCATCAATCATTTTGACAACCTGTATCCCAAGCAGCGGTCATTC AAGACACAGATATGCACTTATACCCATACCATTAGCAGTAATTACAACATGTA TTGTGCTGTATATGAATGGTATTCTGAAATGTGACAGAAAACCAGACAGAACC AACTCCAATTGATTGGTAACAGAAGATGAAGACAACAGCATAACTAAATTATT TTAAAAACTAAAAAGCCATCTGATTTCTCATTTGAGTATTACAATTTTTGAAC AACTGTTGGAAATGTAACTTGAAGCAGCTGCTTTAAGAAGAAATACCCACTAA CAAAGAACAAGCATTAGTTTTGGCTGTCATCAACTTATTATATGACTAGGTGC TTGCTTTTTTTGTCAGTAAATTGTTTTTACTGATGATGTAGATACTTTTGTAA ATAAATGTAAATATGTACACAAGTGA (SEQ ID NO: 145)

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	>NP_001770.1 lymphocyte function-associated antigen 3 isoform 1 [*Homo sapiens*] MVAGSDAGRALGVLSVVCLLHCFGFISCFSQQIYGVVYGNVTFHVPSNVPLKE VLWKKQKDKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEME SPNITDTMKFFLYVLESLPSPTLTCALTNGSIEVQCMIPEHYNSHRGLIMYSW DCPMEQCKRNSTSIYFKMENDLPQKIQCTLSNPLFNTTSSIILTTCIPSSGHS RHRYALIPIPLAVITTCIVLYMNGILKCDRKPDRTNSN (SEQ ID NO: 146)
Human SLAM (CD150)	>NM_003037.5 *Homo sapiens* signaling lymphocytic activation molecule family member 1 (SLAMF1), transcript variant 1, mRNA AGACAGCCTCTGCTGCATGACACGAAGCTTGCTTCTGCCTGGCATCTGTGAGC AGCTGCCAGGCTCCGGCCAGGATCCCTTCCTTCTCCTCATTGGCTGATGGATC CCAAGGGGCTCCTCTCCTTGACCTTCGTGCTGTTTCTCTCCCTGGCTTTTGGG GCAAGCTACGGAACAGGTGGGCGCATGATGAACTGCCCAAAGATTCTCCGGCA GTTGGGAAGCAAAGTGCTGCTGCCCCTGACATATGAAAGGATAAATAAGAGCA TGAACAAAAGCATCCACATTGTCGTCACAATGGCAAAATCACTGGAGAACAGT GTCGAGAACAAAATAGTGTCTCTTGATCCATCCGAAGCAGGCCCTCCACGTTA TCTAGGAGATCGCTACAAGTTTTATCTGGAGAATCTCACCCTGGGGATACGGG AAAGCAGGAAGGAGGATGAGGGATGGTACCTTATGACCCTGGAGAAAAATGTT TCAGTTCAGCGCTTTTGCCTGCAGTTGAGGCTTTATGAGCAGGTCTCCACTCC AGAAATTAAAGTTTTAAACAAGACCCAGGAGAACGGGACCTGCACCTTGATAC TGGGCTGCACAGTGGAGAAGGGGGACCATGTGGCTTACAGCTGGAGTGAAAAG GCGGGCACCCACCCACTGAACCCAGCCAACAGCTCCCACCTCCTGTCCCTCAC CCTCGGCCCCCAGCATGCTGACAATATCTACATCTGCACCGTGAGCAACCCTA TCAGCAACAATTCCCAGACCTTCAGCCCGTGGCCCGGATGCAGGACAGACCCC TCAGAAACAAAACCATGGGCAGTGTATGCTGGGCTGTTAGGGGGTGTCATCAT GATTCTCATCATGGTGGTAATACTACAGTTGAGAAGAAGAGGTAAAACGAACC ATTACCAGACAACAGTGGAAAAAAAAAGCCTTACGATCTATGCCCAAGTCCAG AAACCAGGTCCTCTTCAGAAGAAACTTGACTCCTTCCCAGCTCAGGACCCTTG CACCACCATATATGTTGCTGCCACAGAGCCTGTCCCAGAGTCTGTCCAGGAAA CAAATTCCATCACAGTCTATGCTAGTGTGACACTTCCAGAGAGCTGACACCAG AGACCAACAAAGGGACTTTCTGAAGGAAAATGGAAAAACCAAAATGAACACTG AACTTGGCCACAGGCCCCAAGTTTCCTCTGGCAGACATGCTGCACGTCTGTAC CCTTCTCAGATCAACTCCCTGGTGATGTTTCTTCCACATACATCTGTGAAATG AACAAGGAAGTGAGGCTTCCCAAGAATTTAGCTTGCTGTGCAGTGGCTGCAGG CGCAGAACAGAGCGTTACTTGATAACAGCGTTCCATCTTTGTGTTGTAGCAGA TGAAATGGACAGTAATGTGAGTTCAGACTTTGGGCATCTTGCTCTTGGCTGGA ACTGGATAATAAAAATCAGACTGAAAGCCAGGACATCTGAGTACCTATCTCAC ACACTGGACCACCAGTCACAAAGTCTGGAAAAGTTTACATTTTGGCTATCTTT ACTTTGTTCTGGGAGCTGATCATGATAACCTGCAGACCTGATCAAGCCTCTGT GCCTCAGTTTCTCTCTCAGGATAAAGAGTGAATAGAGGCTGAAGGGTGAATTT CTTATTATACATAAAACACTCTGATATTATTGTATAAAGGAAGCTAAGAATAT TATTTTATTTGCAAAACCCAGAAGCTAAAAAGTCAATAAACAGAAAGAATGAT TTTGAGATCTCTGAGTTTTGAACAGTGGACTGGAAACCATGTAAGAGCCTTAA AAGTACAGTTCTGTGCAAATGGCATTCAGTTTTAAAGAAAAACGTAGCAAATG TTTGATGGTGCTGTTACAAAGGAGCTTGGAATACTCAGAGGAACTTGTCCCAT GGTGATTTTTCACTTCTCAAAATGATGTTTAAATCCCAGTTCTCTGTTGATTC CCTTGAACAACAAACCTGGAACCTCAGCTAAGACTCTCTGTGACCAGATTCTG AACCTCTTATATCCAGGGCTTCAAGGGGTATTGCAGGTCAAGGTOTTTCCTAG GCACTTTCTACTCCCTGCATACCTCTCCTCACACTAAATTTATCCTCTAGTAG AAAATTAAGTTATTTTGGTCTAACAGCTTCAAATCTTTGAATGCTCAATAACT TATTTTGCAAGCTGCAGGCAGAAAGAGACTTTTTAAGTAAAGTCCTTTGTTTT TTCCTATTCTCTGCTTTTAGACAGGCTGTCCTCAATTTAAGCCCTGCTTTTTC TTATTGTTTCTTATATAAACTTGGTAAGTACTGTAAGAAACAGCCACTATCAT ACCATTGCATAATAAGGAGCACCAACTTCCCAGCTCAAAACTCAGGTCCTTAT TGCCTTGTATCTTACCTCCTCTATGAGGTCAATTCACATTGTAAGCCTGTTGC TTAGTGCATCTCGTTTCCTGGTACCAGCTTCTTTAATAGAGTTCTTAGTTGCA ATCAACAGAAGCTGGCTTTGGCTTTTTTATGTAGAAAAGGAACCTATTGAAAA GATACTGATTGGTTCCAATAACTGCTAGAAGTTTCTGCAAAACCATGCTTTGA AAGTGAGCAGGAAAAGAAGAGACTAGGCTGTGGCTGGGAGCACAGCCAAAATT ACAAAACCAGCCCAGGGATGATGATCCTGTTCATGCACAGCCACTGTCCCCAG CACTAGGCACAGACTCTACCACTGCCTCACTGTCTCTGOTGGACTTGGAAACT TGATATTACTGTTACTGCTGCACTGTCTGCCATGAAAATGAATTCTCCAGGGT CCCTTCTTCATCCTTTCATCTCTAGCTTATAATTCAAAGTCTGGGATTGAGTG GCCAATCCTAGGTCACATGTCCATGTCCTATCTCCAAGGGGGGCTGGGAATTG AATATCTGGCATTTTCCACTTTCACTTCTTATGAATTAAGGAATTCTACAAAT AATAGAAGTGGGATTCAGGTGGTAGGCAGACAAAAAAGCCTCACAATTATCCA CTACGCCACCCTTGTATAACCTTACCCTCATTCACTGTCTACTCTCAAAACTG TGGAGCTACTAATGAAGATTTGTAAACCCGGGCTTATGAGCACCCATTCCTTT ACTACAACTCAGATTGCTCTAGAAGCTCAGTTCCCAGCACTTGGATTTTTCCA GTAGCTGAATTCTACCTGAAGGAAGGGCAGAAACAAAGGGTGAAGAAGAGGCT ATCACTTCCAAGTATCCTGCACCCCTGGGCTCAAGACCTCACTGGGGAGGGAG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TCTTTTGGGCCACCCACCAAACAGCACTGGCATTATGCCTCTCACCCTAGACC ATGGTTACACGTGGTAAAACAACCCCTTCTGGTGATACATTCACAACTCTCTA GTTTCCCCCAAATGGCACTATGGGGAGCGGGAGCTTGCCTTTTCCTCAGACTT AAAACAATAAGTTTTCCCCGTGTTTCCCCTCTAATGCTGTTTTCTTTTGACCA AGCATGTCTGAATTCTAGAGAAGTCAGGAGGAACACACCCATTCTCGGTTTGA AGGGACTGATGTTCTGAAGTACAACTGGGCACAGTCCCAGGCTCTTCAGGACG CTTCCTCCATTCACACAGCGGGGATGTGATTGTTACAGCGGGTGGTGTGTGCT GGCTGAGAAGCCACTGTGAATTGATTCTTCTTCTGAAGTTTATGTTTCTACTT TTTGGAAATGAATAAATTACAGCCAGTCCATCAAGGAAA (SEQ ID NO: 147)
	>NP_003028.1 signaling lymphocytic activation molecule isoform b precursor [*Homo sapiens*] MDPKGLLSLTFVLFLSLAFGASYGTGGRMMNCPKILRQLGSKVLLPLTYERIN KSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAGPPRYLGDRYKFYLENLTLG IRESRKEDEGWYLMTLEKNVSVQRFCLQLRLYEQVSTPEIKVLNKTQENGTCT LILGCTVEKGDHVAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADNIYICTVS NPISNNSQTFSPWPGCRTDPSETKPWAVYAGLLGGVIMILIMVVILQLRRRGK TNHYQTTVEKKSLTIYAQVQKPGPLQKKLDSFPAQDPCTTIYVAATEPVPESV QETNSITVYASVTLPES (SEQ ID NO: 148)
Mouse SLAM (CD150)	>NM_013730.4 *Mus musculus* signaling lymphocytic activation molecule family member 1 (Slamf1), transcript variant 1, mRNA GAGCTTCTTCCTTGGGGGTAACAGTAAGCAGCTGTCCTGCCGAGCTGAGCTGA GCTGAGCTCACAGCTGGGGACCCTGTCTGCGATTGCTGGCTAATGGATCCCAA AGGATCCCTTTCCTGGAGAATACTTCTGTTTCTCTCCCTGGCTTTTGAGTTGA GCTACGGAACAGGTGGAGGTGTGATGGATTGCCCAGTGATTCTCCAGAAGCTG GGACAGGACACGTGGCTGCCCCTGACGAATGAACATCAGATAAATAAGAGCGT GAACAAAAGTGTCCGCATCCTCGTCACCATGGCGACGTCCCCAGGAAGCAAAT CCAACAAGAAAATTGTGTCTTTTGATCTCTCTAAAGGGAGCTATCCAGATCAC CTGGAGGATGGCTACCACTTTCAATCAAAAAACCTGAGCCTGAAGATCCTCGG GAACAGGCGGGAGAGTGAAGGATGGTACTTGGTGAGCGTGGAGGAGAACGTTT CTGTTCAGCAATTCTGCAAGCAGCTGAAGCTTTATGAACAGGTCTCCCCTCCA GAGATTAAAGTGCTAAACAAAACCCAGGAGAACGAGAATGGGACCTGCAGCTT GCTGTTGGCCTGCACAGTGAAGAAAGGGGACCATGTGACTTACAGCTGGAGTG ATGAGGCAGGCACCCACCTGCTGAGCCGAGCCAACCGCTCCCACCTCCTGCAC ATCACTCTTAGCAACCAGCATCAAGACAGCATCTACAACTGCACCGCAAGCAA CCCTGTCAGCAGTATCTCTAGGACCTTCAACCTATCATCGCAAGCATGCAAGC AGGAATCCTCCTCAGAATCGAGTCCATGGATGCAATATACTCTTGTACCACTG GGGGTCGTTATAATCTTCATCCTGGTTTTCACGGCAATAATAATGATGAAAAG ACAAGGTAAATCAAATCACTGCCAGCCACCAGTGGAAGAAAAAAGCCTTACTA TTTATGCCCAAGTACAGAAATCAGGGCCTCAAGAGAAGAAACTTCATGATGCC CTAACAGATCAGGACCCCTGCACAACCATTTATGTGGCTGCCACAGAGCCTGC CCCAGAGTCTGTCCAGGAACCAAACCCCACCACAGTTTATGCCAGTGTGACAC TGCCAGAGAGCTGACCCATATACCCAGTGAAAGGACTTTTTGAAGGAGGATAG AAGAACCAAAATCCACACTGAACTGGACCCCGGGTCCCAAGTTCTCTGTGACA GAAACTGCACATCTGTAACCTTCTCCAATCAGTTCCCTGGTGACGGATCTGCA CAGGCGTGCTTATGAAGTAGATGAGAAGTGAGGCTTCCTGGGCATGCAACCTG CTCTGCTGCTGACACAGATATGAAGCAGAGATCCCGTGGTACAGTGTACCATC TTTGCTGTAGCAGATAATGTGGGTTTAGGCATCTCACTCTTTGCTGGACTGGA TAACAGAACTCAAAAAAAAACCAACAAGCCAAAGACATAGACTCCATCTCAGA TGGCTGAGCACAAAGTATAAAAGCCATTTTGGCTCTCTGGACTTTATTCTGGA AGCTGATCCTGATCACCTCAAGGCCAAGGGCTCCATGCCTCAGTTTCTCTCTC ACCCTCTAGATGAAGAGGGAACAAAGCATAAAGAGTGAAATCCTTGTTGTCTG AGATCATTCTATAAACGAACTGACATTTTATTTGCAAAACTCAAGCTAGTAAT TCAGTAGACTTGAAGATGATTTTAGAGCCTCTTATGCTTCAAACAACAGAATG AAATCCATCCAATGTTCTTCAAAGTGTGGTTCTCTGATTAAGTCAAAGCAACA CTGTTTGGCAATGCTGCTGTAAAGTTGCCTGGAATACTCAGAGGAACTTGTCC CAGGGAGGTTTTTTTCACTTCTTCAAAGAACTTTTGAATTTAAGTTCTCTGTT TATTCCCTTGAGCAAAACTCTGGAACCTCAAGAGTCTCTCTCCGTTGGTTCTG AGGCCATTTTATAGCCTAGGCCTCCTGTGGATCTACATGTGTATCACCCACTT CCTATCTCACTGCATACCTCTGTGTAGTAGTAAATTTAACCTCAAGTAGAAAA TTAAATTATTTTGGATGATCAGTTCCAAATGATTAGATGTTTAGTCTCTTATA ATAGGATGTAGGTAGAGTCTATATAAAGTCCTATATTCTTCACGTTGTCTGTC CTCAGAGAGACCATCTTTCAACCTATCTTCCTTCTTGCACAACTTTGGCAAAT ACTTTAAAAATAACCATTGTGGAGATGGGGAGAGGTCTAAATGGATAATAGTA CTTGCTTTGCAAACATGAAGATCTGGGTTCAAACTCCCAGTGTCCATGTAAAA AGATAAGTGTGGTTGAGTGTGCCAGTAACATAGACACAGATAGGTCCTGAGAC TTTGCTCCCTAGCCTTCCCAGCCAGGCATAAATGTCAAGTCCCCTGAGAGTGA CAGAGGAAGATACTCCCCCCACACACACACACATACACGCACAGTGATACACA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TATACATGCATACAAAAAAAAAACTTATTGTAACAAAGAACACCAACTGCCTG GCTCAAAACTCTCATGTCCCATTACTCTGTACCTTTCTGTATTTAGATAATTT ACAGTGTGAGTTCTGOTGTTCCATGTATCCTATTTGTGTTACTAACTTATGTC AAAGTATTTCTAATTATAATCAACAAAAGCTAACTTTG (SEQ ID NO: 149) >NP_038758.2 signaling lymphocytic activation molecule isoform 1 precursor [*Mus musculus*] MDPKGSLSWRILLFLSLAFELSYGTGGGVMDCPVILQKLGQDTWLPLTNEHQI NKSVNKSVRILVTMATSPGSKSNKKIVSFDLSKGSYPDHLEDGYHFQSKNLSL KILGNRRESEGWYLVSVEENVSVQQFCKQLKLYEQVSPPEIKVLNKTQENENG TCSLLLACTVKKGDHVTYSWSDEAGTHLLSRANRSHLLHITLSNQHQDSIYNC TASNPVSSISRTFNLSSQACKQESSSESSPWMQYTLVPLGVVIIFILVFTAII MMKRQGKSNHCQPPVEEKSLTIYAQVQKSGPQEKKLHDALTDQDPCTTIYVAA TEPAPESVQEPNPTTVYASVTLPES (SEQ ID NO: 150)
Human CD40	>NM_001250.6 *Homo sapiens* CD40 molecule (CD40), transcript variant 1, mRNA AGTGGTCCTGCCGCCTGGTCTCACCTCGCTATGGTTCGTCTGCCTCTGCAGTG CGTCCTCTGGGGCTGCTTGCTGACCGCTGTCCATCCAGAACCACCCACTGCAT GCAGAGAAAAACAGTACCTAATAAACAGTCAGTGOTGTTCTTTGTGCCAGCCA GGACAGAAACTGGTGAGTGACTGCACAGAGTTCACTGAAACGGAATGCCTTCC TTGCGGTGAAAGCGAATTCCTAGACACCTGGAACAGAGAGACACACTGCCACC AGCACAAATACTGCGACCCCAACCTAGGGCTTCGGGTCCAGCAGAAGGGCACC TCAGAAACAGACACCATCTGCACCTGTGAAGAAGGCTGGCACTGTACGAGTGA GGCCTGTGAGAGCTGTGTCCTGCACCGCTCATGCTCGCCCGGCTTTGGGGTCA AGCAGATTGCTACAGGGGTTTCTGATACCATCTGCGAGCCCTGCCCAGTCGGC TTCTTCTCCAATGTGTCATCTGCTTTCGAAAAATGTCACCCTTGGACAAGCTG TGAGACCAAAGACCTGGTTGTGCAACAGGCAGGCACAAACAAGACTGATGTTG TCTGTGGTCCCCAGGATCGGCTGAGAGCCCTGGTGGTGATCCCCATCATCTTC GGGATCCTGTTTGCCATCCTCTTGGTGCTGGTCTTTATCAAAAAGGTGGCCAA GAAGCCAACCAATAAGGCCCCCCACCCCAAGCAGGAACCCCAGGAGATCAATT TTCCCGACGATCTTCCTGGCTCCAACACTGCTGCTCCAGTGCAGGAGACTTTA CATGGATGCCAACCGGTCACCCAGGAGGATGGCAAAGAGAGTCGCATCTCAGT GCAGGAGAGACAGTGAGGCTGCACCCACCCAGGAGTGTGGCCACGTGGGCAAA CAGGCAGTTGGCCAGAGAGCCTGGTGCTGCTGCTGCTGTGGCGTGAGGGTGAG GGGCTGGCACTGACTGGGCATAGCTCCCCGCTTCTGCCTGCACCCCTGCAGTT TGAGACAGGAGACCTGGCACTGGATGCAGAAACAGTTCACCTTGAAGAACCTC TCACTTCACCCTGGAGCCCATCCAGTCTCCCAACTTGTATTAAAGACAGAGGC AGAAGTTTGGTGGTGGTGGTGTTGGGGTATGGTTTAGTAATATCCACCAGACC TTCCGATCCAGCAGTTTGGTGCCCAGAGAGGCATCATGGTGGCTTCCCTGCGC CCAGGAAGCCATATACACAGATGCCCATTGCAGCATTGTTTGTGATAGTGAAC AACTGGAAGCTGCTTAACTGTCCATCAGCAGGAGACTGGCTAAATAAAATTAG AATATATTTATACAACAGAATCTCAAAAACACTGTTGAGTAAGGAAAAAAAGG CATGCTGCTGAATGATGGGTATGGAACTTTTTAAAAAAGTACATGCTTTTATG TATGTATATTGCCTATGGATATATGTATAAATACAATATGCATCATATATTGA TATAACAAGGGTTCTGGAAGGGTACACAGAAAACCCACAGCTCGAAGAGTGGT GACGTCTGGGGTGGGGAAGAAGGGTCTGGGGGAGGGTTGGTTAAAGGGAGATT TGGCTTTCCCATAATGCTTCATCATTTTTCCCAAAAGGAGAGTGAATTCACAT AATGCTTATGTAATTAAAAAATCATCAAACATGTAAAAA (SEQ ID NO: 151) >NP_001241.1 tumor necrosis factor receptor superfamily member 5 isoform 1 precursor [*Homo* *sapiens*] MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTE FTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCE EGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFE KCHPWTSCETKDLVVQQAGTNKTDVVCGPQDRLRALVVIPIIFGILFAILLVL VFIKKVAKKPTNKAPHPKQEPQEINFPDDLPGSNTAAPVQETLHGCQPVTQED GKESRISVQERQ (SEQ ID NO: 152)
Mouse CD40	>NM_170703.2 *Mus musculus* CD40 antigen (Cd40), transcript variant 2, mRNA AGCAGGGACTTTGGAGTGACTTGTGGCTTCAGCAGGAGCCCTGTGATTTGGCT CTTCTGATCTCGCCCTGCGATGGTGTCTTTGCCTCGGCTGTGCGCGCTATGGG GCTGCTTGTTGACAGCGGTCCATCTAGGGCAGTGTGTTACGTGCAGTGACAAA CAGTACCTCCACGATGGCCAGTGCTGTGATTTGTGCCAGCCAGGAAGCCGACT GACAAGCCACTGCACAGCTCTTGAGAAGACCCAATGCCACCCATGTGACTCAG GCGAATTCTCAGCCCAGTGGAACAGGGAGATTCGCTGTCACCAGCACAGACAC TGTGAACCCAATCAAGGGCTTCGGGTTAAGAAGGAGGGCACCGCAGAATCAGA CACTGTCTGTACCTGTAAGGAAGGACAACACTGCACCAGCAAGGATTGCGAGG CATGTGCTCAGCACACGCCCTGTATCCCTGGCTTTGGAGTTATGGAGATGGCC ACTGAGACCACTGATACCGTCTGTCATCCCTGCCCAGTCGGCTTCTTCTCCAA TCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAGTCCCGG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ATGCGAGCCCTGCTGGTCATTCCTGTCGTGATGGGCATCCTCATCACCATTTT CGGGGTGTTTCTCTATATCAAAAAGGTGGTCAAGAAACCAAAGGATAATGAGA TCTTACCCCCTGCGGCTCGACGGCAAGATCCCCAGGAGATGGAAGATTATCCC GGTCATAACACCGCTGCTCCAGTGCAGGAGACGCTGCACGGGTGTCAGCCTGT CACACAGGAGGATGGTAAAGAGAGTCGCATCTCAGTGCAGGAGCGGCAGGTGA CAGACAGCATAGCCTTGAGGCCCCTGGTCTGAACCCTGGAACTGCTTTGGAGG CGATGGCTCGGCTCGGGAGCAGGGGCCTGGCTCTGAGGACTGCTTGCTGACCT TTGAAGTTTGAGATGAGCCAAGACAGAGCCCAGTGCAGCTAACTCTCATGCCT GCCCCCTATCATTTCTCAACTTGCTTTTTAAGGATGGAGGGAGAGCTCGGGCA TCGGGGGTCCACAGTGATACCTACCAAGTGCAGCAGTGCAGGACCCAGAGTCG TCTTGCTGCGGCGTTCACTGTAAGGAGTCATGGACACAGGAGTCCGTGGCCCA CAGCTTGTGCTGCTAGAGGGCACCTGGTTGCCCATCAGCAGGGTACTGGCTAA ATAAATCTGTAATTATTTATACAATGACATCTCAGAAACTCTAGCAGGTGGGG CAGAAAACAGGTAGTAGAATGATGGGTAGAGAAATAGCTTTTAAAACACATTC CAAGGCAGGTAAGATGGCTTTTGTGAGTAAAGGAGCTTGCTGCCCAAACCCGG TTACCTGATTTTGATCCCTGGGACTTCATGGTAAAAGGGAGAGAACCAAATCC AGAGGGTTGTCATTTGACCTCCATGTGTGCTCTGTGGTAATGTACCCCGTGTG TGCACATGTGCACATATCCTAAAATGGATGTGGTGGTGTATTGTAGAAATTAT TTAATCCCGCCCTGGGGTTTCTACCTGTGTGTTACCATTTAGTTCTTGAATAA AAGACACACTCAACCTTTATATTTACAATAA (SEQ ID NO: 153) >NP_733804.1 tumor necrosis factor receptor superfamily member 5 isoform 2 precursor [*Mus musculus*] MVSLPRLCALWGCLLTAVHLGQCVTCSDKQYLHDGQCCDLCQPGSRLTSHCTA LEKTQCHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGTAESDTVCTCK EGQHCTSKDCEACAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFE KCYPWTRFKVPDASPAGHSCRDGHPHHHFRGVSLYQKGGQETKG (SEQ ID NO: 154)
Human CD28	>NM_006139.4 *Homo sapiens* CD28 molecule (CD28), transcript variant 1, mRNA ACACTTCGGGTTCCTCGGGGAGGAGGGGCTGGAACCCTAGCCCATCGTCAGGA CAAAGATGCTCAGGCTGCTCTTGGCTCTCAACTTATTCCCTTCAATTCAAGTA ACAGGAAACAAGATTTTGGTGAAGCAGTCGCCCATGCTTGTAGCGTACGACAA TGCGGTCAACCTTAGCTGCAAGTATTCCTACAATCTCTTCTCAAGGGAGTTCC GGGCATCCCTTCACAAAGGACTGGATAGTGCTGTGGAAGTCTGTGTTGTATAT GGGAATTACTCCCAGCAGCTTCAGGTTTACTCAAAAACGGGGTTCAACTGTGA TGGGAAATTGGGCAATGAATCAGTGACATTCTACCTCCAGAATTTGTATGTTA ACCAAACAGATATTTACTTCTGCAAAATTGAAGTTATGTATCCTCCTCCTTAC CTAGACAATGAGAAGAGCAATGGAACCATTATCCATGTGAAAGGGAAACACCT TTGTCCAAGTCCCCTATTTCCCGGACCTTCTAAGCCCTTTTGGGTGCTGGTGG TGGTTGGTGGAGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTTATT ATTTTCTGGGTGAGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAA CATGACTCCCCGCCGCCCCGGGCCCACCCGCAAGCATTACCAGCCCTATGCCC CACCACGCGACTTCGCAGCCTATCGCTCCTGACACGGACGCCTATCCAGAAGC CAGCCGGCTGGCAGCCCCCATCTGCTCAATATCACTGCTCTGGATAGGAAATG ACCGCCATCTCCAGCCGGCCACCTCAGGCCCCTGTTGGGCCACCAATGCCAAT TTTTCTCGAGTGACTAGACCAAATATCAAGATCATTTTGAGACTCTGAAATGA AGTAAAAGAGATTTCCTGTGACAGGCCAAGTCTTACAGTGCCATGGCCCACAT TCCAACTTACCATGTACTTAGTGACTTGACTGAGAAGTTAGGGTAGAAAACAA AAAGGGAGTGGATTCTGGGAGCCTCTTCCCTTTCTCACTCACCTGCACATCTC AGTCAAGCAAAGTGTGGTATCCACAGACATTTTAGTTGCAGAAGAAAGGCTAG GAAATCATTCCTTTTGGTTAAATGGGTGTTTAATCTTTTGGTTAGTGGGTTAA ACGGGGTAAGTTAGAGTAGGGGGAGGGATAGGAAGACATATTTAAAAACCATT AAAACACTGTCTCCCACTCATGAAATGAGCCACGTAGTTCCTATTTAATGCTG TTTTCCTTTAGTTTAGAAATACATAGACATTGTCTTTTATGAATTCTGATCAT ATTTAGTCATTTTGACCAAATGAGGGATTTGGTCAAATGAGGGATTCCCTCAA AGCAATATCAGGTAAACCAAGTTGCTTTCCTCACTCCCTGTCATGAGACTTCA GTGTTAATGTTCACAATATACTTTCGAAAGAATAAAATAGTTCTCCTACATGA AGAAAGAATATGTCAGGAAATAAGGTCACTTTATGTCAAAATTATTTGAGTAC TATGGGACCTGGCGCAGTGGCTCATGCTTGTAATCCCAGCACTTTGGGAGGCC GAGGTGGGCAGATCACTTGAGATCAGGACCAGCCTGGTCAAGATGGTGAAACT CCGTCTGTACTAAAAATACAAAATTTAGCTTGGCCTGGTGGCAGGCACCTGTA ATCCCAGCTGCCCAAGAGGCTGAGGCATGAGAATCGCTTGAACCTGGCAGGCG GAGGTTGCAGTGAGCCGAGATAGTGCCACAGCTCTCCAGCCTGGGCGACAGAG TGAGACTCCATCTCAAACAACAACAACAACAACAACAACAACAACAAACCACA AAATTATTTGAGTACTGTGAAGGATTATTTGTCTAACAGTTCATTCCAATCAG ACCAGGTAGGAGCTTTCCTGTTTCATATGTTTCAGGGTTGCACAGTTGGTCTC TTTAATGTCGGTGTGGAGATCCAAAGTGGGTTGTGGAAAGAGCGTCCATAGGA GAAGTGAGAATACTGTGAAAAAGGGATGTTAGCATTCATTAGAGTATGAGGAT GAGTCCCAAGAAGGTTCTTTGGAAGGAGGACGAATAGAATGGAGTAATGAAAT TCTTGCCATGTGCTGAGGAGATAGCCAGCATTAGGTGACAATCTTCCAGAAGT GGTCAGGCAGAAGGTGCCCTGGTGAGAGCTCCTTTACAGGGACTTTATGTGGT TTAGGGCTCAGAGCTCCAAAACTCTGGGCTCAGCTGCTCCTGTACCTTGGAGG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TCCATTCACATGGGAAAGTATTTTGGAATGTGTCTTTTGAAGAGAGCATCAGA GTTCTTAAGGGACTGGGTAAGGCCTGACCCTGAAATGACCATGGATATTTTTC TACCTACAGTTTGAGTCAACTAGAATATGCCTGGGGACCTTGAAGAATGGCCC TTCAGTGGCCCTCACCATTTGTTCATGCTTCAGTTAATTCAGGTGTTGAAGGA GCTTAGGTTTTAGAGGCACGTAGACTTGGTTCAAGTCTCGTTAGTAGTTGAAT AGCCTCAGGCAAGTCACTGCCCACCTAAGATGATGGTTCTTCAACTATAAAAT GGAGATAATGGTTACAAATGTCTCTTCCTATAGTATAATCTCCATAAGGGCAT GGCCCAAGTCTGTCTTTGACTCTGCCTATCCCTGACATTTAGTAGCATGCCCG ACATACAATGTTAGCTATTGGTATTATTGCCATATAGATAAATTATGTATAAA AATTAAACTGGGCAATAGCCTAAGAAGGGGGGAATATTGTAACACAAATTTAA ACCCACTACGCAGGGATGAGGTGCTATAATATGAGGACCTTTTAACTTCCATC ATTTTCCTGTTTCTTGAAATAGTTTATCTTGTAATGAAATATAAGGCACCTCC CACTTTTATGTATAGAAAGAGGTCTTTTAATTTTTTTTTAATGTGAGAAGGAA GGGAGGAGTAGGAATCTTGAGATTCCAGATCGAAAATACTGTACTTTGGTTGA TTTTTAAGTGGGCTTCCATTCCATGGATTTAATCAGTCCCAAGAAGATCAAAC TCAGCAGTACTTGGGTGCTGAAGAACTGTTGGATTTACCCTGGCACGTGTGCC ACTTGCCAGCTTCTTGGGCACACAGAGTTCTTCAATCCAAGTTATCAGATTGT ATTTGAAAATGACAGAGCTGGAGAGTTTTTTGAAATGGCAGTGGCAAATAAAT AAATACTTTTTTTTAAATGGAAAGACTTGATCTATGGTAATAAATGATTTTGT TTTCTGACTGGAAAAATAGGCCTACTAAAGATGAATCACACTTGAGATGTTTC TTACTCACTCTGCACAGAAACAAAGAAGAAATGTTATACAGGGAAGTCCGTTT TCACTATTAGTATGAACCAAGAAATGGTTCAAAAACAGTGGTAGGAGCAATGC TTTCATAGTTTCAGATATGGTAGTTATGAAGAAAACAATGTCATTTGCTGCTA TTATTGTAAGAGTCTTATAATTAATGGTACTCCTATAATTTTTGATTGTGAGC TCACCTATTTGGGTTAAGCATGCCAATTTAAAGAGACCAAGTGTATGTACATT ATGTTCTACATATTCAGTGATAAAATTACTAAACTACTATATGTCTGCTTTAA ATTTGTACTTTAATATTGTCTTTTGGTATTAAGAAAGATATGCTTTCAGAATA GATATGCTTCGCTTTGGCAAGGAATTTGGATAGAACTTGCTATTTAAAAGAGG TGTGGGGTAAATCCTTGTATAAATCTCCAGTTTAGCCTTTTTTGAAAAAGCTA GACTTTCAAATACTAATTTCACTTCAAGCAGGGTACGTTTCTGGTTTGTTTGC TTGACTTCAGTCACAATTTCTTATCAGACCAATGGCTGACCTCTTTGAGATGT CAGGCTAGGCTTACCTATGTGTTCTGTGTCATGTGAATGCTGAGAAGTTTGAC AGAGATCCAACTTCAGCCTTGACCCCATCAGTCCCTCGGGTTAACTAACTGAG CCACCGGTCCTCATGGCTATTTTAATGAGGGTATTGATGGTTAAATGCATGTC TGATCCCTTATCCCAGCCATTTGCACTGCCAGCTGGGAACTATACCAGACCTG GATACTGATCCCAAAGTGTTAAATTCAACTACATGCTGGAGATTAGAGATGGT GCCAATAAAGGACCCAGAACCAGGATCTTGATTGCTATAGACTTATTAATAAT CCAGGTCAAAGAGAGTGACACACACTCTCTCAAGACCTGGGGTGAGGGAGTCT GTGTTATCTGCAAGGCCATTTGAGGCTCAGAAAGTCTCTCTTTCCTATAGATA TATGCATACTTTCTGACATATAGGAATGTATCAGGAATACTCAACCATCACAG GCATGTTCCTACCTCAGGGCCTTTACATGTCCTGTTTACTCTGTCTAGAATGT CCTTCTGTAGATGACCTGGCTTGCCTCGTCACCCTTCAGGTCCTTGCTCAAGT GTCATCTTCTCCCCTAGTTAAACTACCCCACACCCTGTCTGCTTTCCTTGCTT ATTTTTCTCCATAGCATTTTACCATCTCTTACATTAGACATTTTTCTTATTTA TTTGTAGTTTATAAGCTTCATGAGGCAAGTAACTTTGCTTTGTTTCTTGCTGT ATCTCCAGTGCCCAGAGCAGTGCCTGGTATATAATAAATATTTATTGACTGAG TGAA (SEQ ID NO: 155) >NP_006130.1 T-cell-specific surface glycoprotein CD28 isoform 1 precursor [*Homo sapiens*] MLRLLLALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRA SLHKGLDSAVEVCVVYGNYSQQLQVYSKTGFNCDGKLGNESVTFYLQNLYVNQ TDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVV GGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPP RDFAAYRS (SEQ ID NO: 156)
Mouse CD28	>NM_007642.4 *Mus musculus* CD28 antigen (Cd28), mRNA AGACCTTGGCAGATGTGACTTCAGTTCACACCACACTCTGCCTTGCTCACAGA GGAGGGGCTGCAGCCCTGGCCCTCATCAGAACAATGACACTCAGGCTGCTGTT CTTGGCTCTCAACTTCTTCTCAGTTCAAGTAACAGAAAACAAGATTTTGGTAA AGCAGTCGCCCCTGCTTGTGGTAGATAGCAACGAGGTCAGCCTCAGCTGCAGG TATTCCTACAACCTTCTCGCAAAGGAATTCCGGGCATCCCTGTACAAGGGCGT GAACAGCGACGTGGAAGTCTGTGTCGGGAATGGGAATTTTACCTATCAGCCCC AGTTTCGCTCGAATGCCGAGTTCAACTGCGACGGGGATTTCGACAACGAAACA GTGACGTTCCGTCTCTGGAATCTGCACGTCAATCACACAGATATTTACTTCTG CAAAATTGAGTTCATGTACCCTCCGCCTTACCTAGACAACGAGAGGAGCAATG GAACTATTATTCACATAAAAGAGAAACATCTTTGTCATACTCAGTCATCTCCT AAGCTGTTTTGGGCACTGGTCGTGGTTGCTGGAGTCCTGTTTTGTTATGGCTT GCTAGTGACAGTGGCTCTTTGTGTTATCTGGACAAATAGTAGAAGGAACAGAC TCCTTCAAAGTGACTACATGAACATGACTCCCCGGAGGCCTGGGCTCACTCGA AAGCCTTACCAGCCCTACGCCCCTGCCAGAGACTTTGCAGCGTACCGCCCCTG ACAGGGACCCCTATCCAGAAGCCCGCCGGCTGGTACCCGTCTACCTGCTCATC ATCACTGCTCTGGATAGGAAAGGACAGCCTCATCTTCAGCCGGCCACTTTGGA CCTCTACTGGGCCACCAATGCCAACTATTTTAGAGTGTCTAGATCTAACATCA TGATCATCTTGAGACTCTGGAATGAATGACAGAAGCTTCTATGGCAGGATAAA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)

GTCTGTGTGGCTTGACCCAAACTCAAGCTTAATACATTTATTGACTTGATTGG
GGAAGTTAGAGTAGAGCAATCAAAAAGATCATTCATTCAGCCTTGGGAAGTCA
ATTTGCAGGCTCCTGGATGAGCCCTGCCCCGTTTTCACTTGCCAGCACATTTC
AGTCATGTGGTGTGATAGCCAAAGATGTTTTGGACAGAGAAGAAAGGATAGAA
AAACCTTCTCTTTGGCTAAGTTGGTGTTTGGGGTGGGGATAGGTTAGAGTATA
GTACTTAACTATTTGAAAAATAATGAAAACACTTTTTTCACTCATGAAATGAG
CCACTTAGCTCCTAAATAGTGTTTTCCTGTTAGTTTAGAAAGTTGTGGACATA
TTTTTTTAATGATTTCTGACCATTTTTAATCACATTGACTCATGGAATGGCCT
CAAAGCACCCCCCAGTGCTTCTTTCCTCATTCCCGGTCATGGGAACTCAGTAT
TATTAATAGTCACAACATGATTTCAGAACTAGATAGCCCTCCCACACCAAGAA
GAATGTGAGAGGAAGTAAGGTCACTTTATGTAAAAAAAAAAAAAAAACAAACGC
GTACACATATGTATGTATACATACATACCTATGTGCACACACACACACATATA
CATACACACAAAATGCTATGAAGAGTTATCTGTTTAGTAGCCTGTTATAGTCA
AATCATTTTAAGTTTCAACTTCTTACAGTTGGGCCACTTGTTGTCCTTTGTGG
ATGGATATCTGAAATTGTGTCTATATATTGCTAGTCATGATACTGTGAACAAA
AAGGGTAGTGTTAGTATTTGTCAGGGTGGTAAGGATGCATTCCAGGAAGCTTC
CTCTGAGGAAGGGAATGAGGTCATTCTTGCCATGTATGAAAGACATAGATGTT
TTCCAGAAGGCACCATTGGGAGCCCCAGTATAAGTTCCTTTAGACTCTACAGT
TTAGAGGGATTTTATATGTCCTAGGACTCAGGACTCCAGAACTTTGTGGGCTC
AGCTGCTTCATACCATGGGGATACATTGACATGAACAATTATTTTGGAATGTG
TCTTTAGGGACGACATCAAAGTTCTCAAGTACCTACAAGACCTGATACTGGAA
TGAAGGTGGACTTTCTTTTTTGCTTCCAGTTCGGATCAACTGGAATGTATCTG
GGGACCTTGAAGAACGGCTGTCCAGCTGTCTTCACCATTTGTATAGTGCTTTG
AATTATTCAGAGGTTTTAAAGTCAGGAAGACCTGGTTTAAAAAACATTTCATT
ATGAGTTAAATGGCCTCAGGCAAGTCACTGTTCATCCAAGTCTATGACTCCTC
AACTGTAAGATGGCCACACTGAAACTTGCTAAGATCCTCTGGCCTCTGCCTCC
CAAGAGTTGGGATTTCAGGAGTGCACAATCATGACCCAAACTCGTGATAATCT
CTCAGCTTCAATAACTTTCCAGCTAATTGGAATATCCTGTAATCAAACATGAG
GCATTTCCCCTCCCCCCACTGTTTTTGTGTATAAAGAGATCTTTAAACTTTTT
TTTTAATATGAGGGGTAAGAAAAGATAGGAATCTTTTAATTCTAGACAGAAGA
TATTGTGCTTTGGTTTTTTTTTTTTTTAATGGCTTCTATTCTGTGCTTTTAAT
TAAACCAGAGAAGGCCAAGATTAGCCCTACTTGTGTGATAAAAGAATGCTGGC
CCTTGTGATTGCAGTCAGCCTCTTGACACATAGAGTTCTTGAATCTAAGTTAT
AAAATTATATTTGAAAATGACAGAGCTGGAGAATTTATAGAAAGGGTCATAGC
AAATAACAAACCATTTTTTTTTAAACGGAAAGATTTGGTCTTTGGCAATCAAT
AACTTTGTTTTCTAACTGGAAAAGGAGGTTTACTGGAGATGAATCACACCTGA
AAGTTTTCATACCTCCTCTGAACACAACCGAAACATAGGTGTCCAAAGCCTTT
CGCTCTCGGTATGAACCAACAGGCGGGTTAAAAACACTGGGTCAGAGTAAAGC
TTTTGCAGTTTCAGATGTAGTGTGTATGAAGAAAACTATGTCACTTGCTGCTA
TTATTGTAAGAGTCTAAGAACTAAAGGTGTGCCTGTAATTTCTAATTATGAGC
TCACCTATTTGGTACCGAGCATGCCAATTTTAAAGAGACCCGGTGTACCTTAT
AGCTACATCCAATGATAAAATTACCACACTAGCACATGCCTGTGTTTAAACTC
GTGCTTTAATGTTTTTCTTAGGGCAGGTATGCACCCCCTTTGCAGTGAGTTGG
GAGAGATTTTGAAAAAGTGTATGACAAACATTTTTAACACCTTTGGTTTCCTC
TCTCTGTGTCTCTTTGTCTCTGTCTCTCTCTTTCTCTCCTGTGCATATGTCTC
CCCTCCCTCACTTCTCTGTCTCTTCCTCTCTCCCTCTCTCTGTCTTTCTCTGT
GTGTCTCTCTGTCTCTGTGTATCTCTCTGTCTGTCTCTTTCTCTGCAGATTTT
CAAAACGTTGTTTTTCTATGGAAGAAATACAAGCTGTGGTTGGTTTGCTACGA
GTCAGTAGCAGTTTATCAGTAGGCCAATGTTTTATCTCTTGGAGATTTCAGTC
TGGGTTTACCCAATGTATTCTCTGTAATGTGACTGCTGGGGACAGATATAACT
TGATTGAGCCTTCAAATCATTTAGGTCTTCAATCATTTAGTCAACGGAGTGAG
CCACTAATCTGCAATGGCTATTTTAATATGCATACTGATGGTCAAATGGATGT
CTGATCTCTCATCCCAGCTTTCTGTACTACCATATGGGAACTATATGTAACTT
GTATACTTACCTGAATATGTTAAATTCAACTACATGGTAAGATGGACCAGAAA
TTGCAATGTTCATGTCCATATAGCCACCATTAACCCAAGTTAAGCACAGTAGT
GTGGGTTCTCTCAGGACTTGTGAATGAGTTTATGCTCTCTACAAAGACAGGTG
AAGCTTAAATCTCTCTTGCACTGCTATGTTTATGCAAATATCAAGATTGTTTC
TGTACCAGGGACTTAACACATTCTATTCATACTATTTTCCCTGTCTACAATGT
TATTTCATAGATATCTACTTGGTTTGCTCTTACTTCCTTGACATATTTGCCCA
AATGCCACCTTCAACTGTAGTTAATTACCTGTACAACCTGTCTCCATGCCTTG
TTTTATTTTCTCTATAACTCTACTAATAGGTATTTTTCTTATTTATTGGTTTA
TTGCCTGTTTTTTTTCCTAAATCTACACCGGATCTCCAAAGGGAAAGAACTCC
ATTTGCTTTGATTTTATTGCTGTATCCCCAGTGCCTAGAATAATGCTTAGCCT
GCAATAAATATTTATTCATTGACT (SEQ ID NO: 157)

>NP_031668.3 T-cell-specific surface glycoprotein
CD28 precursor [*Mus musculus*]
MTLRLLFLALNFFSVQVTENKILVKQSPLLVVDSNEVSLSCRYSYNLLAKEFR
ASLYKGVNSDVEVCVGNGNFTYQPQFRSNAEFNCDGDFDNETVTFRLWNLHVN
HTDIYFCKIEFMYPPPYLDNERSNGTIIHIKEKHLCHTQSSPKLFWALVVVAG
VLFCYGLLVTVALCVIWTNSRRNRLLQSDYMNMTPRRPGLTRKPYQPYAPARD
FAAYRP (SEQ ID NO: 158)

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
Human CD28H	>NM_144615.2 *Homo sapiens* transmembrane and immunoglobulin domain containing 2 (TMIGD2), transcript variant 1, mRNA GGAAGTCTGTCAACTGGGAGGGGGAGAGGGGGGTGATGGGCCAGGAATGGGGT CCCCGGGCATGGTGCTGGGCCTCCTGGTGCAGATCTGGGCCCTGCAAGAAGCC TCAAGCCTGAGCGTGCAGCAGGGGCCCAACTTGCTGCAGGTGAGGCAGGGCAG TCAGGCGACCCTGGTCTGCCAGGTGGACCAGGCCACAGCCTGGGAACGGCTCC GTGTTAAGTGGACAAAGGATGGGGCCATCCTGTGTCAACCGTACATCACCAAC GGCAGCCTCAGCCTGGGGGTCTGCGGGCCCCAGGGACGGCTCTCCTGGCAGGC ACCCAGCCATCTCACCCTGCAGCTGGACCCTGTGAGCCTCAACCACAGCGGGG CGTACGTGTGCTGGGCGGCCGTAGAGATTCCTGAGTTGGAGGAGGCTGAGGGC AACATAACAAGGCTCTTTGTGGACCCAGATGACCCCACACAGAACAGAAACCG GATCGCAAGCTTCCCAGGATTCCTCTTCGTGCTGCTGGGGGTGGGAAGCATGG GTGTGGCTGCGATCGTGTGGGGTGCCTGGTTCTGGGGCCGCCGCAGCTGCCAG CAAAGGGACTCAGGTAACAGCCCAGGAAATGCATTCTACAGCAACGTCCTATA CCGGCCCCGGGGGGCCCCAAAGAAGAGTGAGGACTGCTCTGGAGAGGGGAAGG ACCAGAGGGGCCAGAGCATTTATTCAACCTCCTTCCCGCAACCGGCCCCCCGC CAGCCGCACCTGGCGTCAAGACCCTGCCCCAGCCCGAGACCCTGCCCCAGCCC CAGGCCCGGCCACCCCGTCTCTATGGTCAGGGTCTCTCCTAGACCAAGCCCCA CCCAGCAGCCGAGGCCAAAAGGGTTCCCCAAAGTGGGAGAGGAGTGAGAGATC CCAGGAGACCTCAACAGGACCCCACCCATAGGTACACACAAAAAAGGGGGGAT CGAGGCCAGACACGGTGGCTCACGCCTGTAATCCCAGCAGTTTGGGAAGCCGA GGCGGGTGGAACACTTGAGGTCAGGGGTTTGAGACCAGCCTGGCTTGAACCTG GGAGGCGGAGGTTGCAGTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGC GACAGAGTGAGACTCCGTCTCAAAAAAAACAAAAAGCAGGAGGATTGGGAGCC TGTCAGCCCCATCCTGAGACCCCGTCCTCATTTCTGTAATGATGGATCTCGCT CCCACTTTCCCCCAAGAACCTAATAAAGGCTTGTGAAGAAAAAGCAAAAAAAA AAAAAAAAAA (SEQ ID NO: 159) >NP_653216.2 transmembrane and immunoglobulin domain-containing protein 2 isoform 1 precursor [*Homo sapiens*] MGSPGMVLGLLVQIWALQEASSLSVQQGPNLLQVRQGSQATLVCQVDQATAWE RLRVKWTKDGAILCQPYITNGSLSLGVCGPQGRLSWQAPSHLTLQLDPVSLNH SGAYVCWAAVEIPELEEAEGNITRLFVDPDDPTQNRNRIASFPGFLFVLLGVG SMGVAAIVWGAWFWGRRSCQQRDSGNSPGNAFYSNVLYRPRGAPKKSEDCSGE GKDQRGQSIYSTSFPQPAPRQPHLASRPCPSPRPCPSPRPGHPVSMVRVSPRP SPTQQPRPKGFPKVGEE (SEQ ID NO: 160)
Human CD2	>NM_001328609.2 *Homo sapiens* CD2 molecule (CD2), transcript variant 1, mRNA AGTCTCACTTCAGTTCCTTTTGCATGAAGAGCTCAGAATCAAAAGAGGAAACC AACCCCTAAGATGAGCTTTCCATGTAAATTTGTAGCCAGCTTCCTTCTGATTT TCAATGTTTCTTCCAAAGGTGCAGTCTCCAAAGAGATTACGAATGCCTTGGAA ACCTGGGGTGCCTTGGGTCAGGACATCAACTTGGACATTCCTAGTTTTCAAAT GAGTGATGATATTGACGATATAAAATGGGAAAAAACTTCAGACAAGAAAAAGA TTGCACAATTCAGAAAAGAGAAAGAGACTTTCAAGGAAAAAGATACATATAAG CTATTTAAAAATGGAACTCTGAAAATTAAGCATCTGAAGACCGATGATCAGGA TATCTACAAGGTATCAATATATGATACAAAAGGAAAAAATGTGTTGGAAAAAA TATTTGATTTGAAGATTCAAGAGAGGGTCTCAAAACCAAAGATCTCCTGGACT TGTATCAACACAACCCTGACCTGTGAGGTAATGAATGGAACTGACCCCGAATT AAACCTGTATCAAGATGGGAAACATCTAAAACTTTCTCAGAGGGTCATCACAC ACAAGTGGACCACCAGCCTGAGTGCAAAATTCAAGTGCACAGCAGGGAACAAA GTCAGCAAGGAATCCAGTGTCGAGCCTGTCAGCTGTCCAGGAGGCAGCATCCT TGGCCAGAGTAATGGGCTCTCTGCCTGGACCCCTCCCAGCCATCCCACTTCTC TTCCTTTTGCAGAGAAAGGTCTGGACATCTATCTCATCATTGGCATATGTGGA GGAGGCAGCCTCTTGATGGTCTTTGTGGCACTGCTCGTTTTCTATATCACCAA AAGGAAAAAACAGAGGAGTCGGAGAAATGATGAGGAGCTGGAGACAAGAGCCC ACAGAGTAGCTACTGAAGAAAGGGGCCGGAAGCCCCACCAAATTCCAGCTTCA ACCCCTCAGAATCCAGCAACTTCCCAACATCCTCCTCCACCACCTGGTCATCG TTCCCAGGCACCTAGTCATCGTCCCCCGCCTCCTGGACACCGTGTTCAGCACC AGCCTCAGAAGAGGCCTCCTGCTCCGTCGGGCACACAAGTTCACCAGCAGAAA GGCCCGCCCCTCCCCAGACCTCGAGTTCAGCCAAAACCTCCCCATGGGGCAGC AGAAAACTCATTGTCCCCTTCCTCTAATTAAAAAAGATAGAAACTGTCTTTTT CAATAAAAAGCACTGTGGATTTCTGCCCTCCTGATGTGCATATCCGTACTTCC ATGAGGTGTTTTCTGTGTGCAGAACATTGTCACCTCCTGAGGCTGTGGGCCAC AGCCACCTCTGCATCTTCGAACTCAGCCATGTGGTCAACATCTGGAGTTTTTG GTCTCCTCAGAGAGCTCCATCACACCAGTAAGGAGAAGCAATATAAGTGTGAT TGCAAGAATGGTAGAGGACCGAGCACAGAAATCTTAGAGATTTCTTGTCCCCT CTCAGGTCATGTGTAGATGCGATAAATCAAGTGATTGGTGTGCCTGGGTCTCA CTACAAGCAGCCTATCTGCTTAAGAGACTCTGGAGTTTCTTATGTGCCCTGGT GGACACTTGCCCACCATCCTGTGAGTAAAAGTGAAATAAAAGCTTTGACTAGA (SEQ ID NO: 161)

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	>NP_001315538.1 T-cell surface antigen CD2 isoform 1 precursor [*Homo sapiens*] MSFPCKFVASFLLIFNVSSKGAVSKEITNALETWGALGQDINLDIPSFQMSDD IDDIKWEKTSDKKKIAQFRKEKETFKEKDTYKLFKNGTLKIKHLKTDDQDIYK VSIYDTKGKNVLEKIFDLKIQERVSKPKISWTCINTTLTCEVMNGTDPELNLY QDGKHLKLSQRVITHKWTTSLSAKFKCTAGNKVSKESSVEPVSCPGGSILGQS NGLSAWTPPSHPTSLPFAEKGLDIYLIIGICGGGSLLMVFVALLVFYITKRKK QRSRRNDEELETRAHRVATEERGRKPHQIPASTPQNPATSQHPPPPPGHRSQA PSHRPPPPGHRVQHQPQKRPPAPSGTQVHQQKGPPLPRPRVQPKPPHGAAENS LSPSSN (SEQ ID NO: 162)
Mouse CD2	>NM_013486.2 *Mus musculus* CD2 antigen (Cd2), mRNA GCCTCACCACAGTCCTGACAGAAAGAACTCAGAGTCACCCCTGGGAAAAGAAC TCTAAAGATGAAATGTAAATTCCTGGGTAGCTTCTTTCTGCTCTTCAGCCTTT CCGGCAAAGGGGCGGACTGCAGAGACAATGAGACCATCTGGGGTGTCTTGGGT CATGGCATCACCCTGAACATCCCCAACTTTCAAATGACTGATGATATTGATGA GGTGCGATGGGTAAGGAGGGGCACCCTGGTCGCAGAGTTTAAAAGGAAGAAGC CACCTTTTTTGATATCAGAAACGTATGAGGTCTTAGCAAACGGATCCCTGAAG ATAAAGAAGCCGATGATGAGAAACGACAGTGGCACCTATAATGTAATGGTGTA TGGCACAAATGGGATGACTAGGCTGGAGAAGGACCTGGACGTGAGGATTCTGG AGAGGGTCTCAAAGCCCATGATCCACTGGGAATGCCCCAACACAACCCTGACC TGTGCGGTCTTGCAAGGGACAGATTTTGAACTGAAGCTGTATCAAGGGGAAAC ACTACTCAATAGTCTCCCCCAGAAGAACATGAGTTACCAGTGGACCAACCTGA ACGCACCATTCAAGTGTGAGGCGATAAACCCGGTCAGCAAGGAGTCTAAGATG GAAGTTGTTAACTGTCCAGAGAAAGGTCTGTCCTTCTATGTCACAGTGGGGGT CGGTGCAGGAGGACTCCTCTTGGTGCTCTTGGTGGCGCTTTTTATTTTCTGTA TCTGCAAGAGGAGAAAACGGAACAGGAGGAGAAAAGATGAAGAGCTGGAAATA AAAGCTTCCAGAACAAGCACTGTGGAAAGGGGCCCCAAGCCGCACTCAACCCC AGCCGCAGCAGCGCAGAATTCAGTGGCGCTCCAAGCTCCTCCTCCACCTGGCC ATCACCTCCAGACACCTGGCCATCGTCCCTTGCCTCCAGGCCACCGTACCCGT GAGCACCAGCAGAAGAAGAGACCTCCTCCATCAGGCACACAGATTCACCAGCA GAAAGGCCCTCCTTTACCCAGACCCCGAGTTCAGCCAAAACCTCCCTGTGGGA GTGGAGATGGTGTTTCACTGCCGCCCCCTAATTAAGAAGGCAGAGTTCGTCAT TTCCAATAAAAAGCTGTGTGGATTTATCTTC (SEQ ID NO: 163) >NP_038514.1 T-cell surface antigen CD2 precursor [*Mus musculus*] MKCKFLGSFFLLFSLSGKGADCRDNETIWGVLGHGITLNIPNFQMTDDIDEVR WVRRGTLVAEFKRKKPPFLISETYEVLANGSLKIKKPMMRNDSGTYNVMVYGT NGMTRLEKDLDVRILERVSKPMIHWECPNTTLTCAVLQGTDFELKLYQGETLL NSLPQKNMSYQWTNLNAPFKCEAINPVSKESKMEVVNCPEKGLSFYVTVGVGA GGLLLVLLVALFIFCICKRRKRNRRRKDEELEIKASRTSTVERGPKPHSTPAA AAQNSVALQAPPPPGHHLQTPGHRPLPPGHRTREHQQKKRPPPSGTQIHQQKG PPLPRPRVQPKPPCGSGDGVSLPPPN (SEQ ID NO: 164)
Human LFA-3 (CD58)	>NM_001779.3 *Homo sapiens* CD58 molecule (CD58), transcript variant 1, mRNA GAACTTAGGGCTGCTTGTGGCTGGGCACTCGCGCAGAGGCCGGCCCGACGAGC CATGGTTGCTGGGAGCGACGCGGGGCGGGCCCTGGGGGTCCTCAGCGTGGTCT GCCTGCTGCACTGCTTTGGTTTCATCAGCTGTTTTTCCCAACAAATATATGGT GTTGTGTATGGGAATGTAACTTTCCATGTACCAAGCAATGTGCCTTTAAAAGA GGTCCTATGGAAAAAACAAAAGGATAAAGTTGCAGAACTGGAAAATTCTGAAT TCAGAGCTTTCTCATCTTTTAAAAATAGGGTTTATTTAGACACTGTGTCAGGT AGCCTCACTATCTACAACTTAACATCATCAGATGAAGATGAGTATGAAATGGA ATCGCCAAATATTACTGATACCATGAAGTTCTTTCTTTATGTGCTTGAGTCTC TTCCATCTCCCACACTAACTTGTGCATTGACTAATGGAAGCATTGAAGTCCAA TGCATGATACCAGAGCATTACAACAGCCATCGAGGACTTATAATGTACTCATG GGATTGTCCTATGGAGCAATGTAAACGTAACTCAACCAGTATATATTTTAAGA TGGAAAATGATCTTCCACAAAAAATACAGTGTACTCTTAGCAATCCATTATTT AATACAACATCATCAATCATTTTGACAACCTGTATCCCAAGCAGCGGTCATTC AAGACACAGATATGCACTTATACCCATACCATTAGCAGTAATTACAACATGTA TTGTGCTGTATATGAATGGTATTCTGAAATGTGACAGAAAACCAGACAGAACC AACTCCAATTGATTGGTAACAGAAGATGAAGACAACAGCATAACTAAATTATT TTAAAAACTAAAAAGCCATCTGATTTCTCATTTGAGTATTACAATTTTTGAAC AACTGTTGGAAATGTAACTTGAAGCAGCTGCTTTAAGAAGAAATACCCACTAA CAAAGAACAAGCATTAGTTTTGGCTGTCATCAACTTATTATATGACTAGGTGC TTGCTTTTTTTGTCAGTAAATTGTTTTTACTGATGATGTAGATACTTTTGTAA ATAAATGTAAATATGTACACAAGTGA (SEQ ID NO: 165) >NP_001770.1 lymphocyte function-associated antigen 3 isoform 1 [*Homo sapiens*] MVAGSDAGRALGVLSVVCLLHCFGFISCFSQQIYGVVYGNVTFHVPSNVPLKE VLWKKQKDKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEME

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	SPNITDTMKFFLYVLESLPSPTLTCALTNGSIEVQCMIPEHYNSHRGLIMYSW DCPMEQCKRNSTSIYFKMENDLPQKIQCTLSNPLFNTTSSIILTTCIPSSGHS RHRYALIPIPLAVITTCIVLYMNGILKCDRKPDRTNSN (SEQ ID NO: 166)
Human CD48	>NM_001778.4 *Homo sapiens* CD48 molecule (CD48), transcript variant 1, mRNA CTTTTTCTAGCCAGGCTCTCAACTGTCTCCTGCGTTGCTGGGAAGTTCTGGAA GGAAGCATGTGCTCCAGAGGTTGGGATTCGTGTCTGGCTCTGGAATTGCTACT GCTGCCTCTGTCACTCCTGGTGACCAGCATTCAAGGTCACTTGGTACATATGA CCGTGGTCTCCGGCAGCAACGTGACTCTGAACATCTCTGAGAGCCTGCCTGAG AACTACAAACAACTAACCTGGTTTTATACTTTCGACCAGAAGATTGTAGAATG GGATTCCAGAAAATCTAAGTACTTTGAATCCAAATTTAAAGGCAGGGTCAGAC TTGATCCTCAGAGTGGCGCACTGTACATCTCTAAGGTCCAGAAAGAGGACAAC AGCACCTACATCATGAGGGTGTTGAAAAAGACTGGGAATGAGCAAGAATGGAA GATCAAGCTGCAAGTGCTTGACCCTGTACCCAAGCCTGTCATCAAAATTGAGA AGATAGAAGACATGGATGACAACTGTTATCTGAAACTGTCATGTGTGATACCT GGCGAGTCTGTAAACTACACCTGGTATGGGGACAAAAGGCCCTTCCCAAAGGA GCTCCAGAACAGTGTGCTTGAAACCACCCTTATGCCACATAATTACTCCAGGT GTTATACTTGCCAAGTCAGCAATTCTGTGAGCAGCAAGAATGGCACGGTCTGC CTCAGTCCACCCTGTACCCTGGCCCGGTCCTTTGGAGTAGAATGGATTGCAAG TTGGCTAGTGGTCACGGTGCCCACCATTCTTGGCCTGTTACTTACCTGAGATG AGCTCTTTTAACTCAAGCGAAACTTCAAGGCCAGAAGATCTTGCCTGTTGGTG ATCATGCTCCTCACCAGGACAGAGACTGTATAGGCTGACCAGAAGCATGCTGC TGAATTATCAACGAGGATTTTCAAGTTAACTTTTAAATACTGGTTATTATTTA ATTTTATATCCCTTTGTTGTTTTCTAGTACACAGAGATATAGAGATACACATG CTTTTTTCCCACCCAAAATTGTGACAACATTATGTGAATGTTTTATTATTTTT TAAAATAAACATTTGATATAATTGTCAATTAACTGAA (SEQ ID NO: 167) >NP_001769.2 CD48 antigen isoform 1 precursor [*Homo sapiens*] MCSRGWDSCLALELLLLPLSLLVTSIQGHLVHMTVVSGSNVTLNISESLPENY KQLTWFYTFDQKIVEWDSRKSKYFESKFKGRVRLDPQSGALYISKVQKEDNST YIMRVLKKTGNEQEWKIKLQVLDPVPKPVIKIEKIEDMDDNCYLKLSCVIPGE SVNYTWYGDKRPFPKELQNSVLETTLMPHNYSRCYTCQVSNSVSSKNGTVCLS PPCTLARSFGVEWIASWLVVTVPTILGLLLT (SEQ ID NO: 168)
Mouse CD48	>NM_007649.5 *Mus musculus* CD48 antigen (Cd48), transcript variant 1, mRNA ATACGACTTCCGGTTTTGGGTTTTGCTTCCTGATTGAAGGGCAGGCGCCCTGA CTTCTCTTACAGTTGTCTCCAGTGTTCTGGGGAAGCTTCTCTAAGTATTATGT GCTTCATAAAACAGGGATGGTGTCTGGTCCTGGAACTGCTACTGCTGCCCTTG GGAACTGGATTTCAAGGTCATTCAATACCAGATATAAATGCCACCACCGGCAG CAATGTAACCCTGAAAATCCATAAGGACCCACTTGGACCATATAAACGTATCA CCTGGCTTCATACTAAAAATCAGAAGATTTTAGAGTACAACTATAATAGTACA AAGACAATCTTCGAGTCTGAATTTAAAGGCAGGGTTTATCTTGAAGAAAACAA TGGTGCACTTCATATCTCTAATGTCCGGAAAGAGGACAAAGGTACCTACTACA TGAGAGTGCTGCGTGAAACTGAGAACGAGTTGAAGATAACCCTGGAAGTATTT GATCCTGTGCCCAAGCCTTCCATAGAAATCAATAAGACTGAAGCGTCGACTGA TTCCTGTCACCTGAGGCTATCGTGTGAGGTAAAGGACCAGCATGTTGACTATA CTTGGTATGAGAGCTCGGGACCTTTCCCCAAAAAGAGTCCAGGATATGTGCTC GATCTCATCGTCACACCACAGAACAAGTCTACATTTTACACCTGCCAAGTCAG CAATCCTGTAAGCAGCAAGAACGACACAGTGTACTTCACTCTACCTTGTGATC TAGCCAGATCTTCTGGAGTATGTTGGACTGCAACTTGGCTAGTGGTCACAACA CTCATCATTCACAGGATCCTGTTAACCTGACAAGAACTCTTCTCACCCAAGAA GGCAACTTGGAAGCACAGAGTCTTGCCTTCATCCCTAGCAGTGTTCCTAGCCA GCGAAGCAACTCTGGCTCTATTGGACAAAGGAAAATGTGTTACTGAACGTCTG CGAGAGTTTGCATGCATGCTCTATGAAACAAGCACAGGACCTTGTACAGTGCT CCACCACTGACCTGTGTGCCCAGTCCTTTACAAAGATTTCAAATCAACCTTTT AAAAACTGTGCATAATATCTAATTTTATATACCCTAGTTGTTTCCCAACATAT ATTAAAGATAAATGCATTCTTTTTACCAAAATGTGACTATATTATTTTCATGT TTTCATATCTCTTTTTAAAATAAATTCTTTTAAAAAACT (SEQ ID NO: 169) >NP_031675.1 0048 antigen isoform 1 precursor [*Mus musculus*] MCFIKQGWCLVLELLLLPLGTGFQGHSIPDINATTGSNVTLKIHKDPLGPYKR ITWLHTKNQKILEYNYNSTKTIFESEFKGRVYLEENNGALHISNVRKEDKGTY YMRVLRETENELKITLEVFDPVPKPSIEINKTEASTDSCHLRLSCEVKDQHVD YTWYESSGPFPKKSPGYVLDLIVTPQNKSTFYTCQVSNPVSSKNDTVYFTLPC DLARSSGVCWTATWLVVTTLIIHRILLT (SEQ ID NO: 170)

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
Human CD226	>NM_006566.4 *Homo sapiens* CD226 molecule (CD226), transcript variant 1, mRNA GCAGATGGGAAGAAGCGTTAGAGCGAGCAGCACTCACATCTCAAGAACCAGCC TTTCAAACAGTTTCCAGAGATGGATTATCCTACTTTACTTTTGGCTCTTCTTC ATGTATACAGAGCTCTATGTGAAGAGGTGCTTTGGCATACATCAGTTCCCTTT GCCGAGAACATGTCTCTAGAATGTGTGTATCCATCAATGGGCATCTTAACACA GGTGGAGTGGTTCAAGATCGGGACCCAGCAGGATTCCATAGCCATTTTCAGCC CTACTCATGGCATGGTCATAAGGAAGCCCTATGCTGAGAGGGTTTACTTTTTG AATTCAACGATGGCTTCCAATAACATGACTCTTTTCTTTCGGAATGCCTCTGA AGATGATGTTGGCTACTATTCCTGCTCTCTTTACACTTACCCACAGGGAACTT GGCAGAAGGTGATACAGGTGGTTCAGTCAGATAGTTTTGAGGCAGCTGTGCCA TCAAATAGCCACATTGTTTCGGAACCTGGAAAGAATGTCACACTCACTTGTCA GCCTCAGATGACGTGGCCTGTGCAGGCAGTGAGGTGGGAAAAGATCCAGCCCC GTCAGATCGACCTCTTAACTTACTGCAACTTGGTCCATGGCAGAAATTTCACC TCCAAGTTCCCAAGACAAATAGTGAGCAACTGCAGCCACGGAAGGTGGAGCGT CATCGTCATCCCCGATGTCACAGTCTCAGACTCGGGGCTTTACCGCTGCTACT TGCAGGCCAGCGCAGGAGAAAACGAAACCTTCGTGATGAGATTGACTGTAGCC GAGGGTAAAACCGATAACCAATATACCCTCTTTGTGGCTGGAGGGACAGTTTT ATTGTTGTTGTTTGTTATCTCAATTACCACCATCATTGTCATTTTCCTTAACA GAAGGAGAAGGAGAGAGAGAAGAGATCTATTTACAGAGTCCTGGGATACACAG AAGGCACCCAATAACTATAGAAGTCCCATCTCTACCAGTCAACCTACCAATCA ATCCATGGATGATACAAGAGAGGATATTTATGTCAACTATCCAACCTTCTCTC GCAGACCAAAGACTAGAGTTTAAGCTTATTCTTGACATGAGTGCATTAGTAAT GACTCTTATGTACTCATGCATGGATCTTTATGCAATTTTTTTCCACTACCCAA GGTCTACCTTAGATACTAGTTGTCTGAATTGAGTTACTTTGATAGGAAAAATA CTTCATTACCTAAAATCATTTTTCATAGAACTGTTTCAGAAAACCTGACTCTA ACTGGTTTATATACAAAAGAAAACTTACTGTATCATATAACAGAATGATCCAG GGGAGATTAAGCTTTGGGCAAGGGCTATTTACCAGGGCTTAAATGTTGTGTCT AGAATTAAGTATGGGCATAAACTGGCTTCTGAATCCCTTTCCAGAGTGTTGGA TCCATTTCCCTGGTCTTGGCCTCACTCTCATGCAGGCTTTCCTCTTGTGTTGG CAAGATGGCTGCCAACTCTTGGCAATTCATACATCCTTGTTTCTGTCTGGTAG AGAGTTTGCTTCTCAAATGGAGCAAACAAATTTGATTATTTTTTCATTGTTAA ATAGGCAACATGACCAGAAAGGATGGAATGGCTTAAGTAAACTAAGGGTTCAC TTCTAGAGCTGAGAAGCAGGGTCAAAGCACAATACTGGGCAATTCAGAGCATG GTTAGAAGAGGAAAGGGGAGTCTCAAAGCTGGAGAGTTTACCAACAAATATTG ACTGCAGTGATTAACCAAGACATTTTTGTTAACTAAAAAGTGAAATATGGGAT GGATTCTAGAAATGGGGTATCTCTGTCCATACTTCTAGAATCCACTCTATCAG CATAGTCCAGAAGAATACCTGGCAGTAGAAGAAATGAATATTCAAGAGGAAGA TAAATGCGAGAGGGCAATCCTTTACTATTCTCATATTTATTTATCTCTCATTC TGTATAGAATTCTTGCCGCCATCCCAGGTCTAGCCTTAGGAGCAAATGTAGTA GATAGTCGAATAATAAATAACTTAATGTTTTGGACATATTTTGTCTACTTTTG AGAATTATTTTTAATATGTAAATTCTCTCAAAAGGGTCAGGCACCTAGTTATT ATTTTTTAATGATTATGTGAAAGTTGAATATAATATACCACTAAAAGTGACAG TTGAAAGTGGTGGCATAGGACGGTAGGGTAGAAATTTGGGAGGGAAAAAAGAA ATTGGGAGGGTACAGGCAACAGGAGAAAGGAATCAAACCACAGAAAAATACAA AGGGAAACTTCTGCTTCACTATTCAGACAAAGACAGCCCTAATGACATCACCA ACAGTCAAAGCAATTAGAGACCATACCTAATATTGTTTAAATTCTAGATGTAG GCTAACAATGAAAAGTATTTGCCAAACTGAATAAAACTGTCATGGTTACCTTG AAAGGACAATGGTTATTGTTAAATATAGTGATCATTCATGTCTAAAAGATTCA TTATTTATCTCTAAAGATTTCTAAAGACCACCATCTAGAAAAGATTCATTATG AAGGCTGTATTTAAATATCAAAGTTGTGGACTTCATGATAATCTTAAATAAAG CAAATCCAAATTCTCCTGTTGCCTAGACAGATTCTAAGATGTAATTTACACTT TTAAGCTAATTAGTGAGTATTTTATGATTTTAGCCTTAAACACCATGTATGCC AAATAATGCACTTGTTTTGTGAATTACAGAAATGGTAAGTGCCCACATTTCTG TGAATTATAAAATTTGTGAGTTTCTTTTAACCCTTTTCAGGAGTGAAAAAATA AAAACGACCATTTCCTGGTTGTGCTTAAGTATATGCAAGAAGGGTAAACTCTC ATTTTTATTATGTTTGCTTAAAGATCTTTTTATACCTGGATTCATGAAATGTT TCCACAAATATATTAGTGTAACAAACTTGAAAGGCAGTTTACAAGAAAGCACT CTACTATCAGATCAATCAAAGATTCTGTGAGTGAATTTATTGGTTTGCATGGT GAAGCAAGCTTAGCATCAATTAAAAGGTAAATAATTTCTTTTCTGAATGGTAA AGACAATCAAAATATTACTTTCTGGAAAACTCCAATAACCAAATTCTCAATGA TTAGTGTATGTGAGCAGGAAAACATTTTTACAGTTGTAGTATGGGGAAATATA AATCCAATTTTAAGAGAGAAAATTATGACTGGGTGTGGAAGGGACAGTATAGT CAGATACCATTGTCATGGTGGTTTTTACTGGGAACTTCATGAAAGACTTTTGT AGCAAACCACTGCAGTATTGCAAAGCCTCCAGAACATTTGGAACTTGTCTCTT TTTCCTTGTGTGTGTTTGTGTTTTTGGTCTCTCATTCAAAATATTGATGAGAA CTATTTACTCTGTCCTTTCTTCTCTATATATTCTTCCTCTACAGAGTGTAGGG TTTTTTCAGGAATTTGGAGCCATCTGAAGTCCTCCCAAAAATTCTCTGACGTC TTCTGATGCTCCTGTTATACCCTCAGGGGTAATGCTTGTGAAATTCCATTCAT TCATTTTCTTTCTCTGGACATCTTTACTTACCAAAGCACTTTCATTGTCATCT TTTTAACATCATTCTTAATTCGTGATAGTTTTGGGACTCTCCCTAGTGTATGT TTCTCCCCCTCTACTCTTTTGCACCTATGATTCTGATTGTTACTAAGAAAGCA GATGAAAAACAGATCCACAGAATAAACGATCAGAATTCCAGTAAATTCTATTT TAAATACAGATACTTTTTACAAGTTGCTGCTTTGGAAGCAAAATGCTTCTTAA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GTTTTACATATATATATATATATATACATATATATATACACATATAATTTATA TCGATGGATAATACATTAAGAATCTATGCTTCCTTTGAATGCCATTAATATTT ATGTTAAAGTAACCAATGAAAGGAAATTACTTTGTTATAATAAGATAGGAAGA CTTGTTAATGGAGTACACAGTTTTGTCAGGGAAAGAACACATCTTATTGAACT ATGATGACTATGCATTGACTATATTATTATAAGAGATACCTTCAAACTTTATT TAAAGAACTTTAGGTATAATATGTTGAGAAAATAAAATAGAAATTTCATTTAC TTGTAATCATGCTTAAAATGGGAGGCAGGTAGGTGAAGATATAATTTTTAGTA AAAACTCCAATTTATGTTTTAAGTAATTCAGTGTATTACTAAAATACTATATA TATAAACTTAAAATACATGGGTTATCAATTTAAAAGACAAAGTAAGTAAAAAT ACTTTTAGTAGGCATTCGTGGATTGTGAACATCCAAGTTATATTGGTTTGTAT AGAATGGCATTAAGTAAAAATTACAGCTGTATAACAGTAGTTTTCTAAATTGA GAGAGTCCACATTGTAATTAGAGATCACTGTGACCAAAATGCTTCTCCTTGAT TTATAATGATGTACTGTATTTTGTACTGCTTATATGAAATTTCAGCAAGATTG ACGATATTATAAAGATGCTTATAAAGTGTAAGTGGAGACGCTAAATTGTGAGT ACAAAGTTTCTTTTTCACAACAGTGATAAGAAAATATCTTTAAAAAATATAAG ACAATATAAACATGTCATCATTAGTTTAGCTACTATTAAAATGTAACATCTAG AAAGTACTGATCTCCACCTTCAGACTTCTGTATAAGTATATTTTTTCACTGAT CTGTTCATTAGAGTTCTTCCAGCCAAGACTCTGGGCTCTTAAAACATGTATCT GAAAACTAAAAACAAGTTAATTTTTTTAAAAGCTTCTCTATTTCTAGTGATTC AATAGGTAGAAAAATAGCTTCTAGAATTAACTGCAATGCTTTCTAAGGAAATT TTATAAATCCTCAAGGTCGGTTTACACATATTTTTCCAGATTCAGAGCACTAA CTATCTTGTAAGATGTAAGAAAAGGTCCATTTGGAAGTATGAGTAATAAATGT CTGGGATAATTCTGGTTTATTTCGTATTATCCTTGTTAGAATAAGTTATATGG TCAACCTGTTCAGAACACTTTTTCTAGTGTTAGTGTGTACTTTTGGATTTTTG GTTCTTGTAGGGTATAGAAATATTTTCCTTTGTCTTGTATTCTGTTGTTTTGA ATGAATAAAACACAATGTTTCACGATCACTACTTTCATTTGCCATGGAGAAAT AGCAGGGAAAAATTTCTACAGAATAAAATTAACTGATGAATTACATGCAGAAA AAATTCAAATCAATGATACATTGTAATTTTTATCTCAATGCAATGTTCTTTGT ATTTTATTTTATTATTATTTTTTTGAGACGGAGTTTCACTTTTGTTGCCCGGG CTGGAGTGCAATGGCACAATCTCGGCTCACCACAACCTCTGCCTCCCGGATTC AAGTGATTCTCCTGCCTCAGCCTCCTGAATAGCTGGGATTACAGGCATATGCC AACATGCCTGGCTAATTTTGTATTTTTAGTGGAGACGGGGTTTCTCCACGTTG GTCAGACTTGTCTTGAACTCTGGACCTCAGGTGATCCACCTGCCTCAGCCTCC TAAATTGCTGGGATTACAGGCATGAGCGACCACTCCTGGCCTTGTTCTTTGTA TTTTATAAGTGCATGTAGTGCAAAGGGTCAAAGGGCTTTACAGGTTTTTTGTT TGTTTGTTTTTGTTTTTCCCGAAACATAGTAGTCCCTTGCCCTTCCTCATTTT TGTTACCTTGAGACAACAAATTTTACTACTTCTAACTCATTATTTTATTTATG TTCACTTTTCTGAATAGCATGCTTATGACACTAATACTTTTTTTTTCAATTTT AGACATTCATTATTCATTTAGATGTCTTTCTCTCCCCAAACTCACCACATAAA ATACTCTTCTCATGTCTCTTTCAGAAATATTTGTATTAAAATATGATTATATC AATATTTGGCATTTATTTCTTATGACCTTGCCAGTACTCTTAGTTAAACTACA TGGTAAAAATGATTTTGCTTTCCCTCCTACATAACTTTTTTTCCACCTAGAGC TAATAATTGTCATTCTGGGGACTGACTTTTTCTGTATTTACCATAAATTGACC TGAAACTCCCCTGTGATGCAGCAGGAATTCTACCAACGTCAACTTCCTTAGAA AGACTCCATTAGAAGCTTGACTTGGGGCTAGAAGGAGAGGCACACAACTGCCA TCCTGGTGTCTCCCTTCATCCAGAAAAAGGGGGAGGAATACATGAAACCTAGA ATCCACTCTAAAACATTTTCCAGAACAAAAGGACATGTGTTTCCGTGTTGTAA ATGTTTAACGAGTGCCCATAACAAGGAATAATAAGTCTATTATGTTTGCTTTT GTGTCTGTAAAAGTTGGGGGTATTGGTTGTAAGCACGAAAACAGATACTGACT GTTGAAGAAAAAAAAAAATACGAGGTCAGGAGTTTGAGACCAACTTGGCCAAT ATGGTGAAACCCTGTCTTAGTAAAAATAGAAAAATTAGCCAGGCCTGGTGGCA CGCACCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGAAGAATCGCTTGAAC CCGGGAGGCAGAGGTTGCAGTGAGCCAAGATCGCACCACTGCACTCCACCCTG GGCAACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA GTTAAGTATTTGAACATAGGGGTGGCTCATAGAATTCCCAGGACACCCGATGG AGTAGGCTTGCAAAACACAACATGTGGCAACTCCAGTGGGAAACGAGGCAGGA AACACTCGTTTCCTGCAGAAAGCAACAATTTGGGCTTCGATACCCTCCCTAGA ACACAGGGCAGTGAATCTGAGCAGCATCAGTACCCCACGTTCGGATGAGTCCT GAGCCCCTATTTTTATTCACTGACTTATTCCAAAATCAGTGTCTCTTAAATAT ATCTGGAAGGCAGCAGCTTGTATCTCCCCCTTCAGCTTCCATAGTGGCAGTCA GGGTACAACTTACTTTCCAAACAGAACACACTGCGACATTCCCTCCAGGCTCG TTGAAGAACTTCAACTGACAAATGTCCCTCCTCGACCAGATGATAGTTTTCTT AAAGGCAGGGTTTAATATACCCTTTTATAAATGTTTCAAGGCCCTGTGTAATA CCTGAGTTTATTCCAGATGTAACTAAATATATCCAAGATTGTTTTAAAATAAA TTGCTGAAAAAACAAATAAATACAGTTAGTATCTATATCAATATTCTCAGTTG GCAGTTTTGCAATAATGGCCGATAGTTCATTTTTAGTAACACTATTGACATTG CATTTGGATATTAGGGTTTACTAATCATCCGCATGTATACATTGCATATTTTT CTAGACTTTAACTTTATTCAAATCTATTGATTTTTAAACCTGCAACTTATGTC TAGACACAGGTATACCTTTACAAGAACTACCATTTTTTTTGGTAACATACTAC CTCCAAAATTTCAAGTAAGAAGTTGATTTTTGTCCATTTTTAAATGGAAAACT TGTAATCAAAATGCCACAAAATTATACTGTGTATCATTTGACCTATAGAAACC AATATTATTACAGGAAGAAAGCAGAGCCAATCTTCTACCTGTGGTCAAATAAG TGGAGGCCCTTTCTAGACTAAGTTCTCATGAGTTTAAAATACCAAGCATAAGT TCTCCAAATTCCTGAAAAGGAAGCCTTGTGTTGTATTGCCCAGCCATATTTGT AAGACATAAAAATAAAACTTGAGAAGAAGCTATGATAACTTACTTTCTTCATT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CTTCAAAATTTACATAATCTCAACTGATTTTATGTTTTTATGAAAATGCATTC TTAAGATATATCCTTATTCAATCATGTATTCATTACATCCTTTATGCCAGGTA TCCAAAAGTACTTACAGTGACTAAGACCATTATTCTTTGATCAGCTGCCTGAG TAAGACTTTGAGCTCTCCAATATACTCTCAGTGATACTAAGTTTTCTGAGTAA CAGCTTTGGATGTGGCTTCAGTTGAGCTGATTTATCCCACACTTTATTTTTAT CGTATAATGGTCCTCAGAAGCAAATTTTGATTTTAGCTCACATAAAAAATGTA CAAAGAAATGTAATGGCTCAGTAGCTTCTAGAGATAGAGATTACTCTTCTAAC CTTTCTGTAATTTTGTATGTCTATTTTATAATTCTTTCAATGTCTAATGAATA GCTATCTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGT GGTGCGACCTCGGCTCACCGCAAGCTGCGTCTTCCAGGTTCACGCCATTCTCC TGCCTCAGCCTCCCGAGTAGCTGGGACTTCAGGCGCCCACCACCATGCCCAGC TAATTTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCGTGTTAGCCAGGGTG GTCTCGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAACGTGCTGG GATTACAGGAGTGAGCCACCGCGCCCGGCCTCCTTAGTTTCTTAAGGTGGAAG CCTAGATTATTGATTTTATATGTTGTTTTCTTTTCCAATAGTGGCACTTAATG CTATAAATTTCACTTTGTTCCACAAGTTTTGGTAAGCTCTATTTTTATTTTCA TTTAGTCCAAAATATTTTAAAATTTCTTTTGATATTTCTTCTTTGAGCCATGA ATTATTTACAATGTGTTGTTTAATCTCTATATATTTTGGGATTTTTCTACTTT ATATCTCTTACAGATTTCTAACTTAATTTCATCATGTTTTAAAAACATTCTTT GTATAATTTCTATTCTTTTAAATTTTTCAGGTGTATTTTATGGCCCAGAATAT GGTCTATCTTGTAGAATGTTTCATGTGATCTTAAGAAGAATGTTCATTCTGCT GTTGAGTGTAATATTCTACAAATGTCCATTAGATTAAACTGATTGATACCACC GTTCAGATTATCTATATCCTTTCTGATTTTCCCTCTTCTTGATCTATCACATA CTGACAGATCAAGTGATCAAGTCTCGTTAAAGACTGCAAGTAAAATAGTGGAT TTTTCTATTTCTCCTTGCAGTTTTGTTAGTTTTTGTCTCATGTATCTTGATAC TCTTGTTAGTACATATACTTTCAGAATCGTTAGGTTTTCTTGGAGAATTGACC CCTTTACCACATGTAATGTCCCTTTTATTCTTGATAATCTTTCTTGTTCTGTC TGCTTTTTCTGATATTAACATAACTTTCAGTTTTTTAAAAAATTAACATTAGC ATCTCACATCTTTATCCTTTTAATTTTAAATTATCTAAATATTTATATTTAAT GTGCCTTTCTTATAGACAATGTATAGTTGCGTCTATTTGTAATTTCCCCACTT TTCTTACTTAAAAATGTTGTAGATATATAGGAGTTGTATATATTTGGGGGGTA CATGTGATGTTTTGATACCTGTATACAATATGTAATGATCATATTGGGTAATC GTGATATCTGTCACCTCTAACATTCATCTTTTTTGTGTGTTTAAACCCACCAC TTCTAATTGGTACATTTAGATTATTCAAATTTAAGTGATTATTGATATAGTTG GATTAATATCTACTATGTTTGTAACTTTTCTATCCTTGCACTCGTTCTTTCTT TTTTATCCTCCTTTTTCTGTGTTCTCTGATTTTAACTGGGGTTTTTACATGAT TTAATTTTCTCTCGTGGCATATCTTTCATTGATCAACCTAGGTTTTTCTCCTT TTCCCCTCTTTTTTTTGGTATTTATTCTATTTAGTGTTATCTGAGCTACCTGA GTTGGTGTCTATCACTAATTTTGGCAAGTTCCCAGACGTTATTACTTCTAACA TTCTTTTGCTCCATTCTTTCTTCTTCTTCAATTATTCCATAGTCTTGAATATT CTGGGTTTTTCCCACTCTTTGAATTTTAGTTTGAAAAGTTTCTATTGGCCTAG CTTCAAAGTCATTCATTCTTCCTTCGGGGTTCCAAGTCAACTGATAATTGCAT CAAAGATATCCTTCCTTTCTATTACTATGTTTTTTATTGCTACCATTTCTTTT TTATTCCTTCTTAGTGTTTCCATCTTTCTTCTTACATTATCCATCTGTTGTCT ATTTTTTTCATGAGAGCTCTTAACATATTAATGATAAGTTCCATGTCTGATAA TTCTGACACGTGTCATGTCTCTATCTGGTTCCAATGATTGCTTTATCTCTTCA GACCATGACTTTTCTTGCCTTTTGACGTTCTTTGACATTTTTTTTGAATTTTT TGTTGCAAGCCAGATCTGGTGTGTTATGTAATAGGAACAGGTAAATAAGTCTT TAGCTTGCAGACTTATCTTAATCTGACTAACTATTAGACTGTGTTTAAAGTCT GTTATAACCATAGGTGCTAAATTTCTTCAAATTCCTCTAGTGTCTTTGTTTTG TTTGTTCATGTGTTTTTCCCCTTCTTGAGTTCAGGCTTCCCTAAGTGCTCCTC TTCAGAGAGACTTTCTGTCTTTCAGCTCTTTCCTCTGCAATTCACTGTTACTA TACTGGAGCCCTGTTGGTGTAGTACTAAGCTGTGGGAAAGGAGAGTGCTCTGT AATCTTACAGTGAAATCTCAGTOTTTTAGTGGGTCTGTGTCTGGGACATTCAC AGAGCTTCTCCAGTGGTATTGCTTCCTCATCCTCAACTCTCTTTCCTGGCTGC AGCATTCCCAATGTATTTCTTTGAAGGCCTGCCCCCTGTTGACTGTTATTTTC CCTCTTTCCTTAAGTGGGACAGGGAGACTTCAGGGGCTGGGATGAGGTTTGGG AATTGTGCTTGGCAGAGTCCTTTCCATCTTTGTTACCAAGAAGGTTCATGGCT TATTTCTCAATGGATGTCCCTCTCTATCTGTTGCCAGAGCCACGAGGAAATTT TTCTTGGATCCTCATAATGAGAACCTTGGAGTTTCCTACTGGAAAAGCCCTTG AATGTGTGGAGTGCCTCAAGAGCACAGCCCCCATGGGTTTCTTGCTCACACCA GTCCACAAACAGATGCCAGCAATTCACCCAACTTACCATATAAAGGCTCATAC TAGTTTATGGCTCCAGTGCTTTGACTCCAGATAAATGGCTATTGGTTGCGTAT CTCTCTGGATGTATCTGTATCTCCAGATTTTGGGGTGGCAGTTTGCTCAGGAC CTTGGTTCTCTAATAGGTCTAATAAGAAAAGTCATTGATTTTCAGCTTTCCAA CTTTCCAGCTTTGTCTTGTTATAAGCATGGCAGCAACATCTTCCATGCCTTAA CATGATGACACTAAAGGCAGAAGTCGATCTCCATGTATAAACATTTTAACACA TATGTTTTTTGTTATCGTGGTTTCTGACCTGTCTCTTTGCCCTGACTTTCTGA TACTGCACTAGGGTTCCTGTTGCTGGACTCCATTCCATATGACTTGCTCTCGT CTAGGCTGCTCTTTGGCTCATCTTTATAAATCATGATCCAAAATGAAGCACAT ATTTATTTTTTAAATAAATATGAAATGAAGTATAGACATCAAACTGAAGATGA GTAGATCATACTGAGTTTCACTGTCTGTGCTTGGATCAACATCAGGCCTTATA CAAATATTCAAGTCCAGAGGCAAAAGGTAATAAGGAAAATTTGTAGCACAAGC CACAAGGAGATAACATGTCAAGTCTATGCGATTGGAAATAAACTAAAGATGAA CTGCTGGGGATGCTCACTCATCACAGAGCTCAGTCTAAAGCACCAGATTTCAC

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	AAGCATTTTTTGGGGGAAATTCTGTTAAAATGAAATATGAGTCACATGGTGGT GTTTCACTCATCATATGTGTTCAATATTAATTCATTTTAAGGTTTAGTTGCAC AAAAGGTAAATGAGAATTAGAAGACTCCATGGGTAAGAGGAGCCACAGAAGTA AAGCATTGTCAAGGGTTCTATGTCTATATATTTAGATATTAGGCTTCTGAGAA AAAAACACAATAGGAAGGAAGATGAACACAACAGAGGGCAGAAGGTCTATACG TCCTGAGGCCTTTTATGCAACGTTTGTTTGTGGAATGTTTTTTAAGAATGTGT GAGAGTCATTTTAATGTGAAATAAAGACCTACGTCTACA (SEQ ID NO: 171)
	>NP_006557.2 CO226 antigen isoform a precursor [*Homo sapiens*] MDYPTLLLALLHVYRALCEEVLWHTSVPFAENMSLECVYPSMGILTQVEWFKI GTQQDSIAIFSPTHGMVIRKPYAERVYFLNSTMASNNMTLFFRNASEDDVGYY SCSLYTYPQGTWQKVIQVVQSDSFEAAVPSNSHIVSEPGKNVTLTCQPQMTWP VQAVRWEKIQPRQIDLLTYCNLVHGRNFTSKFPRQIVSNCSHGRWSVIVIPDV TVSDSGLYRCYLQASAGENETFVMRLTVAEGKTDNQYTLFVAGGTVLLLLFVI SITTIIVIFLNRRRRRERRDLFTESWDTQKAPNNYRSPISTSQPTNQSMDDTR EDIYVNYPTFSRRPKTRV (SEQ ID NO: 172)
Mouse CD226	>NM_178687.2 *Mus musculus* CD226 antigen (Cd226), transcript variant 1, mRNA ACACAGAAGACTTCTTGACTTCAGGAGACACTGCTGTATGAAACAGTGCTTGC TATCAGTGGCTGCTGGAAGAGGCTGTGGTGGAAAGAAAACCTCAACTGCAGGC CAGAGTTGGTTCCCCAAAAGAGGCAAACTCCCAGTGCTAGCCAGAGGCTAGGA AGCTCTAAGCAACCCACTTATCTGCAAGGAGAGTTACGCCCAAAGAGCATCAA GTCCAACCTCCTGAACTGTTTCCAGAGATGGCTTATGTTACTTGGCTTTTGGC TATTCTTCATGTGCACAAAGCACTGTGTGAAGAGACATTGTGGGACACAACAG TTCGGCTTTCTGAGACTATGACTCTGGAATGTGTATATCCATTGACGCATAAC TTAACCCAGGTGGAGTGGACCAAGAACACTGGCACAAAGACAGTGAGCATAGC AGTTTACAACCCTAACCATAATATGCATATAGAATCTAACTACCTCCATAGAG TACACTTCCTAAACTCAACAGTGGGGTTCCGCAACATGAGCCTTTCCTTTTAC AATGCCTCAGAAGCAGACATTGGCATCTACTCCTGCTTGTTTCATGCTTTCCC AAATGGACCTTGGGAAAAGAAGATAAAAGTAGTCTGGTCAGATAGTTTTGAGA TAGCAGCACCCTCGGATAGCTACCTGTCTGCAGAACCTGGACAAGATGTCACA CTCACTTGCCAGCTTCCAAGGACTTGGCCAGTGCAACAAGTCATATGGGAAAA AGTCCAGCCCCATCAGGTAGACATCTTAGCTTCCTGTAACCTATCTCAAGAGA CAAGATACACTTCAAAGTACCTAAGACAAACAAGGAGCAACTGTAGCCAGGGG AGCATGAAGAGCATCCTCATCATTCCAAATGCCATGGCCGCTGACTCAGGACT TTACAGATGTCGCTCAGAGGCCATTACAGGAAAAAACAAGTCCTTTGTCATAA GGCTGATCATAACTGATGGTGGAACCAATAAACATTTTATCCTTCCCATCGTT GGAGGGTTAGTTTCACTGTTACTTGTCATCCTAATTATCATCATTTTCATTTT ATATAACAGGAAGAGACGGAGACAGGTGAGAATTCCACTTAAAGAGCCCAGGG ATAAACAGAGTAAGGTAGCCACCAACTGCAGAAGTCCTACTTCTCCCATCCAG TCTACAGATGATGAAAAAGAGGACATTTATGTAAACTATCCAACTTTCTCTCG AAGACCAAAACCAAGACTCTAAGCTGCTCTTTTGGCCTGAACACATTAGTGAT GACTTCTATGGCATGGAATTTTACCCATGATTTCCTTACCACTAGGATCTACA TTGATAAAAAAAATTGATTAAATTTATTTCATCTCATATATAGAAGTACTTTA TTACCTGGAAACATTCTTAATAGAGATTCATTAGAAAACCCAAATCTAATGTT CATGTGTTCAAGGAACCTTCTTCCATTATGTAACAGAACAGTCTAGAGAAGAT TAAGGACCACATGGCTTTCTTGCTCTACTTGAAATTAATTGTGAGCATAAGCT TGTTTCTGGAGTCTTCTTACATTGTTGGTTCTACTTACATACTACTGGTCCAA CTCTCATGCTGTTTCTCTCAGATGTTCCCATGATGGTTGCCAAGGACACTTGA TAGAAAGACTACTGGTTAAACACAATAAACAAAGTTCATTATTCACTTATTAG CAAGAAGGTAGCATTATCATAAAGGATTAGATGACTTAAGTTAGCTATAGGTT CAAGACCTGGACTAAAGTATTACTTGGAAATTCTGAGTATTGCTAAAAAGGAG GATGAAAGGGACCTAGAAGTTGAGTTATTACTAAAAACTTTGAGTGCGAAGAT ATTACTCATTAACCAGATAACAAGTGAATATGCTGTAGCATCAACATAATTCA AAAGAGTAAAGAAATGGCTAGGAATGAGGTAGTTGTGTAATTATTTCTTCTCT TACTAGTTTCAAATAAATTCATCTCTAATTCTATAGAGAATTCTTGCCTCCCA TTCAGGACTGGCCTTCTATACAGTGAGATGGTCCAGTAAGAAATAATTTTTAT TAGTGTTTTTTCTATTTTGAGAATTATTTTAATATATATTTTAATATATAAAC TTGTGAGTTAAATTTTTTTTTTGCAAAATTAGCACATGAAAAGAGATTGATGG TTTTAAGTAGTAGAACACAGTAGTGTAGGAATCTGAGAGCAGAGAGTTTGGGA GGGGGTGAAGAGAAAACAACATCACCAAATAGTGATATATAAGAGAAAATCTG TGCTTCAGAGTTTGATCAGGGCCATCTCTCCCAACTCTGCTGGAACTGAGAGA ATGCACCTGATGTTGTCTCCATTTTAGATAGAGAAAAAAAAAACCCGAATATT TATAAAACTAAATAAAACTATAGTTACCTCAAAACTATGGGGATCACTATAAC ATAGAATAGAATAGAATAGAATAGAATAGAATAGAATAGAATAGAATAG (SEQ ID NO: 173)
	>NP_848802.2 CD226 antigen isoform a precursor [*Mus musculus*] MAYVTWLLAILHVHKALCEETLWDTTVRLSETMTLECVYPLTHNLTQVEWTKN TGTKTVSIAVYNPNHNMHIESNYLHRVHFLNSTVGFRNMSLSFYNASEADIGI YSCLFHAFPNGPWEKKIKVVWSDSFEIAAPSDSYLSAEPGQDVTLTCQLPRTW

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	PVQQVIWEKVQPHQVDILASCNLSQETRYTSKYLRQTRSNCSQGSMKSILIIP NAMAADSGLYRCRSEAITGKNKSFVIRLIITDGGTNKHFILPIVGGLVSLLLV ILIIIIFILYNRKRRRQVRIPLKEPRDKQSKVATNCRSPTSPIQSTDDEKEDI YVNYPTFSRRPKPRL (SEQ ID NO: 174)
Human DR3	>NM_003790.3 *Homo sapiens* TNF receptor superfamily member 25 (TNFRSF25), transcript variant 2, mRNA GAAGGCGGAACCACGACGGGCAGAGAGCACGGAGCCGGGAAGCCCCTGGGCGC CCGTCGGAGGGCTATGGAGCAGCGGCCGCGGGGCTGCGCGGCGGTGGCGGCGG CGCTCCTCCTGGTGCTGCTGGGGGCCCGGGCCCAGGGCGGCACTCGTAGCCCC AGGTGTGACTGTGCCGGTGACTTCCACAAGAAGATTGGTCTGTTTTGTTGCAG AGGCTGCCCAGCGGGGCACTACCTGAAGGCCCCTTGCACGGAGCCCTGCGGCA ACTCCACCTGCCTTGTGTGTCCCCAAGACACCTTCTTGGCCTGGGAGAACCAC CATAATTCTGAATGTGCCCGCTGCCAGGCCTGTGATGAGCAGGCCTCCCAGGT GGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAG GCTGGTTTGTGGAGTGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCTTCTAC TGCCAACCATGCCTAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTCTG TTCCCGCAGAGATACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATG GCGATGGCTGCGTGTCCTGCCCCACGAGCACCCTGGGGAGCTGTCCAGAGCGC TGTGCCGCTGTCTGTGGCTGGAGGCAGATGTTCTGGGTCCAGGTGCTCCTGGC TGGCCTTGTGGTCCCCCTCCTGCTTGGGGCCACCCTGACCTACACATACCGCC ACTGCTGGCCTCACAAGCCCCTGGTTACTGCAGATGAAGCTGGGATGGAGGCT CTGACCCCACCACCGGCCACCCATCTGTCACCCTTGGACAGCGCCCACACCCT TCTAGCACCTCCTGACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGGTA ACAGCTGGACCCCTGGCTACCCCGAGACCCAGGAGGCGCTCTGCCCGCAGGTG ACATGGTCCTGGGACCAGTTGCCCAGCAGAGCTCTTGGCCCCGCTGCTGCGCC CACACTCTCGCCAGAGTCCCCAGCCGGCTCGCCAGCCATGATGCTGCAGCCGG GCCCGCAGCTCTACGACGTGATGGACGCGGTCCCAGCGCGGCGCTGGAAGGAG TTCGTGCGCACGCTGGGGCTGCGCGAGGCAGAGATCGAAGCCGTGGAGGTGGA GATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCAGC AGCAGCCCGCGGGCCTCGGAGCCGTTTACGCGGCCCTGGAGCGCATGGGGCTG GACGGCTGCGTGGAAGACTTGCGCAGCCGCCTGCAGCGCGGCCCGTGACACGG CGCCCACTTGCCACCTAGGCGCTCTGGTGGCCCTTGCAGAAGCCCTAAGTACG GTTACTTATGCGTGTAGACATTTTATGTCACTTATTAAGCCGCTGGCACGGCC CTGCGTAGCAGCACCAGCCGGCCCCACCCCTGCTCGCCCCTATCGCTCCAGCC AAGGCGAAGAAGCACGAACGAATGTCGAGAGGGGGTGAAGACATTTCTCAACT TCTCGGCCGGAGTTTGGCTGAGATCGCGGTATTAAATCTGTGAAAGAAAACAA AACAAAACAAAAACGGCTTCTTGGCGTTTCTGCGGGGCTGGGGTGTTAAGTGG ACTGGACTTTTCTCGAGGGATTCGAAGGGGACGGGAATCTTGTCACCCCGGGA TCTGGCACCCATGGTGGAGTCCAGTGTGGCCTTAGCTCCCAAGCCTGCCCCTC CCGAGTCCACTCTGGCTCAATTACCCCGAGAAGGAGAGAGCAAGTCGCGGCCA CAGCGAGTGAGTGAACCGGAGCCCAGATGAGAGCGCTTTAATGGGGCTGCGAG GTGGCGGAGACAGGGTCGGGATGGGGTGCAGCAGTTGGAGACACAGGGTCAGG GCCCCTCATCCTCTATTCACTCCACCGGGGCAGTGAAAGGGTCCCGGCAGCGA GTGGGTC (SEQ ID NO: 175) >NP_003781.1 tumor necrosis factor receptor superfamily member 25 isoform 2 precursor [*Homo sapiens*] MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPA GHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALEN CSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRD TDCGTCLPGFYEHGDGCVSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLVV PLLLGATLTYTYRHCWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTLLAPP DSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSWDQLPSRALGPAAAPTLSP ESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRF RDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP (SEQ ID NO: 176)
Mouse DR3	>NM_033042.4 *Mus musculus* tumor necrosis factor receptor superfamily, member 25 (Tnfrsf25), transcript variant 2, mRNA CTGCGTGGAGGGGAAATGGGCCAGAGGCTGCTGGCAGGGGGCCTCCTCTGCTG TACACAAGCTGGTTTTGTAGACAGTGAGAGGGAAGCTGATCCCAGTCCCCTAA CCCTGTTCTGCCCAGGAGCCTGAGAACTGAGCTTACTCGGGCAAATGCTAGGG CTTCAGAAATGGAGGAGCTGCCTAGGAGGGAGAGGTCACCTCCTGGGGCAGCC ACACCAGGGTCAACTGCACGTGTTCTCCAGCCTCTGTTCCTACCACTGCTGCT GCTGCTGCTGCTGCTGCTTGGTGGCCAGGGCCAGGGCGGCATGTCTGGCAGGT GTGACTGTGCCAGTGAGTCCCAGAAGAGGTATGGCCCGTTTTGTTGCAGGGGC TGCCCAAAGGGACACTACATGAAGGCCCCCTGCGCAGAACCCTGTGGCAACTC CACCTGCCTTCCCTGTCCCTCGGACACCTTCTTGACCAGAGACAACCACTTTA AGACTGACTGTACCCGCTGCCAAGTCTGTGATGAAGAGGCCCTTCAAGTGACC CTTGAGAACTGCTCGGCAAAGTCGGACACCCACTGTGGCTGCCAGTCAGGCTG GTGTGTTGACTGCTCCACCGAGCCATGTGGGAAAAGCTCACCTTTCTCTTGTG TCCCATGCGGGGCTACAACACCAGTCCATGAGGCTCCAACCCCCCTGTTTTGG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GTCCAGGTGCTTCTAGGAGTCGCGTTCCTTTTTGGGGCTATCCTGATCTGTGC ATATTGTCGATGGCAGCCTTGTAAGGCCGTGGTCACTGCAGACACAGCTGGGA CGGAGACCCTGGCCTCACCACAGACTGCCCATCTCTCAGCCTCAGACAGCGCC CACACCCTCCTGGCACCTCCAAGCAGTACTGGGAAAATCTGTACCACTGTOCA GTTGGTAGGCAACAACTGGACCCCTGGCTTATCCCAGACTCAGGAGGTGGTCT GCGGACAGGCCTCACAACCCTGGGATCAGCTGCCAAACAGAACTCTTGGAACT CCTCTGGCATCTCCGCTCTCGCCAGCGCCCCCTGCGGGCTCTCCGGCTGCTGT GCTCCAGCCTGGCCCGCAGCTCTACGATGTGATGGATGCGGTCCCAGCACGAA GGTGGAAGGAGTTCGTGCGCACGCTGGGGCTGCGGGAAGCGGAAATTGAAGCC GTGGAGGTGGAAATCTGCCGCTTCCGAGACCAGCAGTATGAGATGCTCAAGCG CTGGCGTCAGCAGCAGCCTGCAGGCCTCGGTGCCATCTATGCGGCTCTGGAGC GCATGGGTCTGGAAGGCTGTGCCGAGGACCTGCGCAGCCGCCTGCAGCGTGGC CCGTGATGGAAGGTCCATCAGCCACTTTGACACCCTAGTGACCCTTGAAGGAG CCTTAAGTATTGTTACTTATGCGTGTAGACATTTTATGTCAATTACTAACCCC CTGCCGTGGTCCTGCGTAGCAGGGCTGGCTGCCTCACTTTTGCTTATCTGCAG CACGGAGCTCCTGCTAAGGGAAGCGTCATGGAGAAATACCAGAAGGGGCCAAG TGATTGGTTGCTCAGCTGTTAATTAGCCCGAGTTTGGACTTGGTATTAAATTT CGTAAGAAAAGCAGCTGCTTG (SEQ ID NO: 177) >NP_149031.2 tumor necrosis factor receptor superfamily member 25 isoform 2 precursor [*Mus musculus*] MEELPRRERSPPGAATPGSTARVLQPLFLPLLLLLLLLLGGQGQGGMSGRCDC ASESQKRYGPFCCRGCPKGHYMKAPCAEPCGNSTCLPCPSDTFLTRDNHFKTD CTRCQVCDEEALQVTLENCSAKSDTHCGCQSGWCVDCSTEPCGKSSPFSCVPC GATTPVHEAPTPLFWVQVLLGVAFLFGAILICAYCRWQPCKAVVTADTAGTET LASPQTAHLSASDSAHTLLAPPSSTGKICTTVQLVGNNWTPGLSQTQEVVCGQ ASQPWDQLPNRTLGTPLASPLSPAPPAGSPAAVLQPGPQLYDVMDAVPARRWK EFVRTLGLREAEIEAVEVEICRFRDQQYEMLKRWRQQQPAGLGAIYAALERMG LEGCAEDLRSRLQRGP (SEQ ID NO: 178)
Human DcR3	>NM_003823.4 *Homo sapiens* TNF receptor superfamily member 6b (TNFRSF6B), mRNA GGACTTGGGCGGCCCCTCCGCAGGCGGACCGGGGGCAAAGGAGGTGGCATGTC GGTCAGGCACAGCAGGGTCCTGTGTCCGCGCTGAGCCGCGCTCTCCCTGCTCC AGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTGTGCCTGG TGTTGGCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAA ACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGC CCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCA CGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTA GAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGCACG GGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCG CGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTG ATTGCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGG CACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACT GCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACC CTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGA GGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCA AGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCG ACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCAC GGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGC TGCGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTC CCTGTGCACTGATCCTGGCCCCCTCTTATTTATTCTACATCCTTGGCACCCCA CTTGCACTGAAAGAGGCTTTTTTTTAAATAGAAGAAATGAGGTTTCTTAAAGC TTATTTTTATAAAGCTTTTTCATAAAA (SEQ ID NO: 179) >NP_003814.1 tumor necrosis factor receptor superfamily member 6B precursor [*Homo sapiens*] MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCP PGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACH ATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFS ASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECE RAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELL GAQDGALLVRLLQALRVARMPGLERSVRERFLPVH (SEQ ID NO: 180)
Human FasL	>NM_000639.3 *Homo sapiens* Fas ligand (FASLG), transcript variant 1, mRNA AGCAGTCAGCAACAGGGTCCCGTCCTTGACACCTCAGCCTCTACAGGACTGAG AAGAAGTAAAACCGTTTGCTGGGGCTGGCCTGACTCACCAGCTGCCATGCAGC AGCCCTTCAATTACCCATATCCCCAGATCTACTGGGTGGACAGCAGTGCCAGC TCTCCCTGGGCCCCTCCAGGCACAGTTCTTCCCTGTCCAACCTCTGTGCCCAG AAGGCCTGGTCAAAGGAGGCCACCACCACCACCGCCACCGCCACCACTACCAC CTCCGCCGCCGCCGCCACCACTGCCTCCACTACCGCTGCCACCCCTGAAGAAG AGAGGGAACCACAGCACAGGCCTGTGTCTCCTTGTGATGTTTTTCATGGTTCT GGTTGCCTTGGTAGGATTGGGCCTGGGGATGTTTCAGCTCTTCCACCTACAGA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	AGGAGCTGGCAGAACTCCGAGAGTCTACCAGCCAGATGCACACAGCATCATCT TTGGAGAAGCAAATAGGCCACCCCAGTCCACCCCCTGAAAAAAAGGAGCTGAG GAAAGTGGCCCATTTAACAGGCAAGTCCAACTCAAGGTCCATGCCTCTGGAAT GGGAAGACACCTATGGAATTGTCCTGCTTTCTGGAGTGAAGTATAAGAAGGGT GGCCTTGTGATCAATGAAACTGGGCTGTACTTTGTATATTCCAAAGTATACTT CCGGGGTCAATCTTGCAACAACCTGCCCCTGAGCCACAAGGTCTACATGAGGA ACTCTAAGTATCCCCAGGATCTGGTGATGATGGAGGGGAAGATGATGAGCTAC TGCACTACTGGGCAGATGTGGGCCCGCAGCAGCTACCTGGGGGCAGTGTTCAA TCTTACCAGTGCTGATCATTTATATGTCAACGTATCTGAGCTCTCTCTGGTCA ATTTTGAGGAATCTCAGACGTTTTTCGGCTTATATAAGCTCTAAGAGAAGCAC TTTGGGATTCTTTCCATTATGATTCTTTGTTACAGGCACCGAGAATGTTGTAT TCAGTGAGGGTCTTCTTACATGCATTTGAGGTCAAGTAAGAAGACATGAACCA AGTGGACCTTGAGACCACAGGGTTCAAAATGTCTGTAGCTCCTCAACTCACCT AATGTTTATGAGCCAGACAAATGGAGGAATATGACGGAAGAACATAGAACTCT GGGCTGCCATGTGAAGAGGGAGAAGCATGAAAAAGCAGCTACCAGGTGTTCTA CACTCATCTTAGTGCCTGAGAGTATTTAGGCAGATTGAAAAGGACACCTTTTA ACTCACCTCTCAAGGTGGGCCTTGCTACCTCAAGGGGGACTGTCTTTCAGATA CATGGTTGTGACCTGAGGATTTAAGGGATGGAAAAGGAAGACTAGAGGCTTGC ATAATAAGCTAAAGAGGCTGAAAGAGGCCAATGCCCCACTGGCAGCATCTTCA CTTCTAAATGCATATCCTGAGCCATCGGTGAAACTAACAGATAAGCAAGAGAG ATGTTTTGGGGACTCATTTCATTCCTAACACAGCATGTGTATTTCCAGTGCAA TTGTAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATGACTAAAGAGA GAATGTAGATATTGTGAAGTACATATTAGGAAAATATGGGTTGCATTTGGTCA AGATTTTGAATGCTTCCTGACAATCAACTCTAATAGTGCTTAAAAATCATTGA TTGTCAGCTACTAATGATGTTTTCCTATAATATAATAAATATTTATGTAGATG TGCATTTTTGTGAAATGAAAACATGTAATAAAAAGTATATGTTAGGATACAAA TAA (SEQ ID NO: 181) >NP_000630.1 tumor necrosis factor ligand superfamily member 6 isoform 1 [*Homo sapiens*] MQQPFNYPYPQIYWVDSSASSPWAPPGTVLPCPTSVPRRPGQRRPPPPPPPPP LPPPPPPPPLPPLPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFH LQKELAELRESTSQMHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMP LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNNLPLSHKVY MRNSKYPQDLVMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELS LVNFEESQTFFGLYKL (SEQ ID NO: 182)
Mouse FasL	>NM_010177.4 *Mus musculus* Fas ligand (TNF superfamily, member 6) (Fasl), transcript variant 1, mRNA TGAGGCTTCTCAGCTTCAGATGCAAGTGAGTGGGTGTCTCACAGAGAAGCAAA GAGAAGAGAACAGGAGAAAGGTGTTTCCCTTGACTGCGGAAACTTTATAAAGA AAACTTAGCTTCTCTGGAGCAGTCAGCGTCAGAGTTCTGTCCTTGACACCTGA GTCTCCTCCACAAGGCTGTGAGAAGGAAACCCTTTCCTGGGGCTGGGTGCCAT GCAGCAGCCCATGAATTACCCATGTCCCCAGATCTTCTGGGTAGACAGCAGTG CCACTTCATCTTGGGCTCCTCCAGGGTCAGTTTTTCCCTGTCCATCTTGTGGG CCTAGAGGGCCGGACCAAAGGAGACCGCCACCTCCACCACCACCTGTGTCACC ACTACCACCGCCATCACAACCACTCCCACTGCCGCCACTGACCCCTCTAAAGA AGAAGGACCACAACACAAATCTGTGGCTACCGGTGGTATTTTTCATGGTTCTG GTGGCTCTGGTTGGAATGGGATTAGGAATGTATCAGCTCTTCCACCTGCAGAA GGAACTGGCAGAACTCCGTGAGTTCACCAACCAAAGCCTTAAAGTATCATCTT TTGAAAAGCAAATAGCCAACCCCAGTACACCCTCTGAAAAAAAAGAGCCGAGG AGTGTGGCCCATTTAACAGGGAACCCCCACTCAAGGTCCATCCCTCTGGAATG GGAAGACACATATGGAACCGCTCTGATCTCTGGAGTGAAGTATAAGAAAGGTG GCCTTGTGATCAACGAAACTGGGTTGTACTTCGTGTATTCCAAAGTATACTTC CGGGGTCAGTCTTGCAACAACCAGCCCCTAAACCACAAGGTCTATATGAGGAA CTCTAAGTATCCTGAGGATCTGGTGCTAATGGAGGAGAAGAGGTTGAACTACT GCACTACTGGACAGATATGGGCCCACAGCAGCTACCTGGGGGCAGTATTCAAT CTTACCAGTGCTGACCATTTATATGTCAACATATCTCAACTCTCTCTGATCAA TTTTGAGGAATCTAAGACCTTTTTCGGCTTGTATAAGCTTTAAAAGAAAAAGC ATTTTAAAATGATCTACTATTCTTTATCATGGGCACCAGGAATATTGTCTTGA ATGAGAGTCTTCTTAAGACCTATTGAGATTAATTAAGACTACATGAGCCACAA AGACCTCATGACCGCAAGGTCCAACAGGTCAGCTATCCTTCATTTTCTCGAGG TCCATGGAGTGGTCCTTAATGCCTGCATCATGAGCCAGATGGAAGGAGGTCTG TGACTGAGGGACATAAAGCTTTGGGCTGCTGTGTGACAATGCAGAGGCACAGA GAAAGAACTGTCTGATGTTAAATGGCCAAGAGAATTTTAACCATTGAAGAAGA CACCTTTACACTCACTTCCAGGGTGGGTCTACTTACTACCTCACAGAGGCCGT TTTTGAGACATAGTTGTGGTATGAATATACAAGGGTGAGAAAGGAGGCTCATT TGACTGATAAGCTAGAGACTGAAAAAAAGACAGTGTCTCATTGGCACCATCTT TACTGTTACCTAATGTTTTCTGAGCCGACCTTTGATCCTAACGGAGAAGTAAG AGGGATGTTTGAGGCACAAATCATTCTCTACATAGCATGCATACCTCCAGTGC AATGATGTCTGTGTGTTTGTATGTATGAGAGCAAACAGATTCTAAGGAGTCAT ATAAATAAAATATGTACATTATGGAGTACATATTAGAAACCTGTTACATTTGA TGCTAGATATCTGAATGTTTCTTGGCAATAAACTCTAATAGTCTTCAAAATCT TTTATTATCAGCTACTGATGCTGTTTTTCTTTAATACAACTAGTATTTATGCT

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CTGAACATCCTAATGAGGAAAAGACAAATAAAATTATGTTATAGAATACAGAA ATGCCTTAAGGACATAGACTTTGGAAA (SEQ ID NO: 183) >NP_034307.1 tumor necrosis factor ligand superfamily member 6 isoform 1 [*Mus musculus*] MQQPMNYPCPQIFWVDSSATSSWAPPGSVFPCPSCGPRGPDQRRPPPPPPPVS PLPPPSQPLPLPPLTPLKKKDHNTNLWLPVVFFMVLVALVGMGLGMYQLFHLQ KELAELREFTNQSLKVSSFEKQIANPSTPSEKKEPRSVAHLTGNPHSRSIPLE WEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCNNQPLNHKVYMR NSKYPEDLVLMEEKRLNYCTTGQIWAHSSYLGAVFNLTSADHLYVNISQLSLI NFEESKTFFGLYKL (SEQ ID NO: 184)
Human TIM-1 (CD365)	>NM_012206.3 *Homo sapiens* hepatitis A virus cellular receptor 1 (HAVCR1), transcript variant 1, mRNA GACCAGGAGTCAGTTTGGCGGTTATGTGTGGGGAAGAAGCTGGGAAGTCAGGG GCTGTTTCTGTGGACAGCTTTCCCTGTCCTTTGGAAGGCACAGAGCTCTCAGC TGCAGGGAACTAACAGAGCTCTGAAGCCGTTATATGTGGTCTTCTCTCATTTC CAGCAGAGCAGGCTCATATGAATCAACCAACTGGGTGAAAAGATAAGTTGCAA TCTGAGATTTAAGACTTGATCAGATACCATCTGGTGGAGGGTACCAACCAGCC TGTCTGCTCATTTTCCTTCAGGCTGATCCCATAATGCATCCTCAAGTGGTCAT CTTAAGCCTCATCCTACATCTGGCAGATTCTGTAGCTGGTTCTGTAAAGGTTG GTGGAGAGGCAGGTCCATCTGTCACACTACCCTGCCACTACAGTGGAGCTGTC ACATCCATGTGCTGGAATAGAGGCTCATGTTCTCTATTCACATGCCAAAATGG CATTGTCTGGACCAATGGAACCCACGTCACCTATCGGAAGGACACACGCTATA AGCTATTGGGGGACCTTTCAAGAAGGGATGTCTCTTTGACCATAGAAAATACA GCTGTGTCTGACAGTGGCGTATATTGTTGCCGTGTTGAGCACCGTGGGTGGTT CAATGACATGAAAATCACCGTATCATTGGAGATTGTGCCACCCAAGGTCACGA CTACTCCAATTGTCACAACTGTTCCAACCGTCACGACTGTTCGAACGAGCACC ACTGTTCCAACGACAACGACTGTTCCAATGACGACTGTTCCAACGACAACTGT TCCAACAACAATGAGCATTCCAACGACAACGACTGTTCTGACGACAATGACTG TTTCAACGACAACGAGCGTTCCAACGACAACGAGCATTCCAACAACAACAAGT GTTCCAGTGACAACAACTGTCTCTACCTTTGTTCCTCCAATGCCTTTGCCCAG GCAGAACCATGAACCAGTAGCCACTTCACCATCTTCACCTCAGCCAGCAGAAA CCCACCCTACGACACTGCAGGGAGCAATAAGGAGAGAACCCACCAGCTCACCA TTGTACTCTTACACAACAGATGGGAATGACACCGTGACAGAGTCTTCAGATGG CCTTTGGAATAACAATCAAACTCAACTGTTCCTAGAACATAGTCTACTGACGG CCAATACCACTAAAGGAATCTATGCTGGAGTCTGTATTTCTGTCTTGGTGCTT CTTGCTCTTTTGGGTGTCATCATTGCCAAAAAGTATTTCTTCAAAAAGGAGGT TCAACAACTAAGTGTTTCATTTAGCAGCCTTCAAATTAAAGCTTTGCAAAATG CAGTTGAAAAGGAAGTCCAAGCAGAAGACAATATCTACATTGAGAATAGTCTT TATGCCACGGACTAAGACCCAGTGGTGCTCTTTGAGAGTTTACGCCCATGAGT GCAGAAGACTGAACAGACATCAGCACATCAGACGTCTTTTAGACCCCAAGACA ATTTTTCTGTTTCAGTTTCATCTGGCATTCCAACATGTCAGTGATACTGGGTA GAGTAACTCTCTCACTCCAAACTGTGTATAGTCAACCTCATCATTAATGTAGT CCTAATTTTTTATGCTAAAACTGGCTCAATCCTTCTGATCATTGCAGTTTTCT CTCAAATATGAACACTTTATAATTGTATGTTCTTTTTAGACCCCATAAATCCT GTATACATCAAAGAGAA (SEQ ID NO: 185) >NP_036338.2 hepatitis A virus cellular receptor 1 isoform a precursor [*Homo sapiens*] MHPQVVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCS LFTCQNGIVWTNGTHVTYRKDTRYKLLGDLSRRDVSLTIENTAVSDSGVYCCR VEHRGWFNDMKITVSLEIVPPKVTTTPIVTTVPTVTTVRTSTTVPTTTTVPMT TVPTTTVPTTMSIPTTTTVLTTMTVSTTTSVPTTTSIPTTTSVPVTTTVSTFV PPMPLPRQNHEPVATSPSSPQPAETHPTTLQGAIRREPTSSPLYSYTTDGNDT VTESSDGLWNNNQTQLFLEHSLLTANTTKGIYAGVCISVLVLLALLGVIIAKK YFFKKEVQQLSVSFSSLQIKALQNAVEKEVQAEDNIYIENSLYATD (SEQ ID NO: 186)
Mouse TIM-1	>NM_134248.2 *Mus musculus* hepatitis A virus cellular receptor 1 (Havcr1), transcript variant 1, mRNA GTCAGTACCATGAATCAGATTCAAGTCTTCATTTCAGGCCTCATACTGCTTCT CCCAGGCGCTGTGGATTCTTATGTGGAAGTAAAGGGGGTGGTGGGTCACCCTG TCACACTTCCATGTACTTACTCAACATATCGTGGAATCACAACGACATGTTGG GGCCGAGGGCAATGCCCATCTTCTGCTTGTCAAAATACACTTATTTGGACCAA TGGACATCGTGTCACCTATCAGAAGAGCAGTCGGTACAACTTAAAGGGGCATA TTTCAGAAGGAGATGTGTCCTTGACGATAGAGAACTCTGTTGAGAGTGACAGT GOTCTGTATTGTTGTCGAGTGGAGATTOCTGOATGGTTTAATGATCAGAAAGT GACCTTTTCATTGCAAGTTAAACCAGAGATTCCCACACGTCCTCCAAGAAGAC CCACAACTACAAGGCCCACAGCTACAGGAAGACCCACGACTATTTCAACAAGA TCCACACATGTACCAACATCAACCAGAGTCTCTACCTCCACTCCTCCAACATC TACACACACATGGACTCACAAACCAGAACCCACTACATTTTGTCCCCATGAGA CAACAGCTGAGGTGACAGGAATCCCATCCCATACTCCTACAGACTGGAATGGC ACTGTGACATCCTCAGGAGATACCTGGAGTAATCACACTGAAGCAATCCCTCC AGGGAAGCCGCAGAAAAACCCTACTAAGGGCTTCTATGTTGGCATCTGCATCG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CAGCCCTGCTGCTACTGCTCCTTGTGAGCACCGTGGCTATCACCAGGTACATA CTTATGAAAAGGAAGTCAGCATCTCTAAGCGTGGTTGCCTTCCGTGTCTCTAA GATTGAAGCTTTGCAGAACGCAGCGGTTGTGCATTCCCGAGCTGAAGACAACA TCTACATTGTTGAAGATAGACCTTGAGGGGCAGAATGAGTACCAGTGGCCCTC TGAGGGACCTTCTGCCTGAGATTTATAGAGACTGTCACTGATGTCATAGAGTC ACACCCATTACAGCGCCAAGGCGATTTTCTGTGTTGGTTCTTCCAGCTGCAGC AGAGAGGGTAACCCTCTACTGTGTATACTCAAAACTCAGATTAACATCATCCT AATTTTGGTATCTGCACCACCTCCGTGTCTCTGCTCACTACAGAGATTCTCTC AAACATGAACGTTTTAGAAGTTTGTGTTTCCCTTAGTCAATGTAATCATTGGT AATACTATTCTATTCTTGGTTACTAAAACCATTACTAAGAGAGGGATAGGAAT TAAAAGTTGGTGTGAGGGGCCTCCTGAATTTAGAAGCACTTGATTCTGTTTTA TCTACTTTCTTGAAATGTTACTTCTACCCTTCCCAATGGGTAAAATCATGGGA GCATGGTGCCCTCATAGATAAATAGAAGAGAGTCTATTGCTGCCAATATAGAT GGTTATGCTTTCTCATAGCTCTGAAAATATGACACATTTATTATGAGGTTGAT CTTAGGATAAGGATAGGTGTTTTATGTCAGGAGAGGTTATCATGGTGAATATG GACCAGCAGACAGCAGTGGAGGAAAATAATGAACCAAGGGATTGAGTTCATTA GTGCTAATTCTACTCCACTCCTGTCTTTATGCTCCTAAACTTACTGACTGAGC TCTGAATTAGGTGCTAGGAGGAGACAATGCAGACATGAAAGGGGAAGGAGCGC CTTCAGGACACAGGCTCTCTGCTGAGAGAAGTCCTATTTGCAGGTGTGATAGA GGTTGGGACAATCTCTGAGTTGTAAATTTCTAATTGTCTTCAGGCCATATTTA TAGTTAAATTCATTTCCGAAAGACATAGCATCTTCCCCAATGGGTCAGTTTGT CAAAATCAATAAAATATTTTGTTTTGCTAAGAATTAAAAAAAAAAAAAAAAAA A (SEQ ID NO: 187)
	>NP_599009.2 hepatitis A virus cellular receptor 1 homolog isoform a precursor [*Mus musculus*] MNQIQVFISGLILLLPGAVDSYVEVKGVVGHPVTLPCTYSTYRGITTTCWGRG QCPSSACQNTLIWTNGHRVTYQKSSRYNLKGHISEGDVSLTIENSVESDSGLY CCRVEIPGWFNDQKVTFSLQVKPEIPTRPPRRPTTTRPTATGRPTTISTRSTH VPTSTRVSTSTPPTSTHTWTHKPEPTTFCPHETTAEVTGIPSHTPTDWNGTVT SSGDTWSNHTEAIPPGKPQKNPTKGFYVGICIAALLLLLLVSTVAITRYILMK RKSASLSVVAFRVSKIEALQNAAVVHSRAEDNIYIVEDRP (SEQ ID NO: 188)
Human PD-1	>NM_005018.3 *Homo sapiens* programmed cell death 1 (PDCD1), mRNA GCTCACCTCCGCCTGAGCAGTGGAGAAGGCGGCACTCTGGTGGGGCTGCTCCA GGCATGCAGATCCCACAGGCGCCCTGGCCAGTCGTCTGGGCGGTGCTACAACT GGGCTGGCGGCCAGGATGGTTCTTAGACTCCCCAGACAGGCCCTGGAACCCCC CCACCTTCTCCCCAGCCCTGCTCGTGGTGACCGAAGGGGACAACGCCACCTTC ACCTGCAGCTTCTCCAACACATCGGAGAGCTTCGTGCTAAACTGGTACCGCAT GAGCCCCAGCAACCAGACGGACAAGCTGGCCGCCTTCCCCGAGGACCGCAGCC AGCCCGGCCAGGACTGCCGCTTCCGTGTCACACAACTGCCCAACGGGCGTGAC TTCCACATGAGCGTGGTCAGGGCCCGGCGCAATGACAGCGGCACCTACCTCTG TGGGGCCATCTCCCTGGCCCCCAAGGCGCAGATCAAAGAGAGCCTGCGGGCAG AGCTCAGGGTGACAGAGAGAAGGGCAGAAGTGCCCACAGCCCACCCCAGCCCC TCACCCAGGCCAGCCGGCCAGTTCCAAACCCTGGTGGTTGGTGTCGTGGGCGG CCTGCTGGGCAGCCTGGTGCTGCTAGTCTGGGTCCTGGCCGTCATCTGCTCCC GGGCCGCACGAGGGACAATAGGAGCCAGGCGCACCGGCCAGCCCCTGAAGGAG GACCCCTCAGCCGTGCCTGTGTTCTCTGTGGACTATGGGGAGCTGGATTTCCA GTGGCGAGAGAAGACCCCGGAGCCCCCCGTGCCCTGTGTCCCTGAGCAGACGG AGTATGCCACCATTGTCTTTCCTAGCGGAATGGGCACCTCATCCCCCGCCCGC AGGGGCTCAGCTGACGGCCCTCGGAGTGCCCAGCCACTGAGGCCTGAGGATGG ACACTGCTCTTGGCCCCTCTGACCGGCTTCCTTGGCCACCAGTGTTCTGCAGA CCCTCCACCATGAGCCCGGGTCAGCGCATTTCCTCAGGAGAAGCAGGCAGGGT GCAGGCCATTGCAGGCCGTCCAGGGGCTGAGCTGCCTGGGGGCGACCGGGGCT CCAGCCTGCACCTGCACCAGGCACAGCCCCACCACAGGACTCATGTCTCAATG CCCACAGTGAGCCCAGGCAGCAGGTGTCACCGTCCCCTACAGGGAGGGCCAGA TGCAGTCACTGCTTCAGGTCCTGCCAGCACAGAGCTGCCTGCGTCCAGCTCCC TGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCCTGCGGCCCGGGGCT GAAGGCGCCGTGGCCCTGCCTGACGCCCCGGAGCCTCCTGCCTGAACTTGGGG GCTGGTTGGAGATGGCCTTGGAGCAGCCAAGGTGCCCCTGGCAGTGGCATCCC GAAACGCCCTGGACGCAGGGCCCAAGACTGGGCACAGGAGTGGGAGGTACATG GGGCTGGGGACTCCCCAGGAGTTATCTGCTCCCTGCAGGCCTAGAGAAGTTTC AGGGAAGGTCAGAAGAGCTCCTGGCTGTGGTGGGCAGGGCAGGAAACCCCTCC ACCTTTACACATGCCCAGGCAGCACCTCAGGCCCTTTGTGGGGCAGGGAAGCT GAGGCAGTAAGCGGGCAGGCAGAGCTGGAGGCCTTTCAGGCCCAGCCAGCACT CTGGCCTCCTGCCGCCGCATTCCACCCCAGCCCCTCACACCACTCGGGAGAGG GACATCCTACGGTCCCAAGGTCAGGAGGGCAGGGCTGGGGTTGACTCAGGCCC CTCCCAGCTGTGGCCACCTGGGTGTTGGGAGGGCAGAAGTGCAGGCACCTAGG GCCCCCCATGTGCCCACCCTGGGAGCTCTCCTTGGAACCCATTCCTGAAATTA TTTAAAGGGGTTGGCCGGGCTCCCACCAGGGCCTGGGTGGGAAGGTACAGGCG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TTCCCCCGGGGCCTAGTACCCCCGCCGTGGCCTATCCACTCCTCACATCCACA CACTGCACCCCCACTCCTGGGGCAGGGCCACCAGCATCCAGGCGGCCAGCAGG CACCTGAGTGGCTGGGACAAGGGATCCCCCTTCCCTGTGGTTCTATTATATTA TAATTATAATTAAATATGAGAGCATGCTAA (SEQ ID NO: 189) >NP_005009.2 programmed cell death protein 1 precursor [*Homo sapiens*] MQIPQAPWPVVWAVLQLGWRPGWFLDSPDRPWNPPTFSPALLVVTEGDNATFT CSFSNTSESFVLNWYRMSPSNQTDKLAAFPEDRSQPGQDCRFRVTQLPNGRDF HMSVVRARRNDSGTYLCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSPS PRPAGQFQTLVVGVVGGLLGSLVLLVWVLAVICSRAARGTIGARRTGQPLKED PSAVPVFSVDYGELDFQWREKTPEPPVPCVPEQTEYATIVFPSGMGTSSPARR GSADGPRSAQPLRPEDGHCSWPL (SEQ ID NO: 190)
Mouse PD-1	>NM_008798.3 *Mus musculus* programmed cell death 1 (Pdcd1), mRNA TGAGCAGCGGGGAGGAGGAAGAGGAGACTGCTACTGAAGGCGACACTGCCAGG GGCTCTGGGCATGTGGGTCCGGCAGGTACCCTGGTCATTCACTTGGGCTGTGC TGCAGTTGAGCTGGCAATCAGGGTGGCTTCTAGAGGTCCCCAATGGGCCCTGG AGGTCCCTCACCTTCTACCCAGCCTGGCTCACAGTGTCAGAGGGAGCAAATGC CACCTTCACCTGCAGCTTGTCCAACTGGTCGGAGGATCTTATGCTGAACTGGA ACCGCCTGAGTCCCAGCAACCAGACTGAAAAACAGGCCGCCTTCTGTAATGGT TTGAGCCAACCCGTCCAGGATGCCCGCTTCCAGATCATACAGCTGCCCAACAG GCATGACTTCCACATGAACATCCTTGACACACGGCGCAATGACAGTGGCATCT ACCTCTGTGGGGCCATCTCCCTGCACCCCAAGGCAAAAATCGAGGAGAGCCCT GGAGCAGAGCTCGTGGTAACAGAGAGAATCCTGGAGACCTCAACAAGATATCC CAGCCCCTCGCCCAAACCAGAAGGCCGGTTTCAAGGCATGGTCATTGGTATCA TGAGTGCCCTAGTGGGTATCCCTGTATTGCTGCTGCTGGCCTGGGCCCTAGCT GTCTTCTGCTCAACAAGTATGTCAGAGGCCAGAGGAGCTGGAAGCAAGGACGA CACTCTGAAGGAGGAGCCTTCAGCAGCACCTGTCCCTAGTGTGGCCTATGAGG AGCTGGACTTCCAGGGACGAGAGAAGACACCAGAGCTCCCTACCGCCTGTGTG CACACAGAATATGCCACCATTGTCTTCACTGAAGGGCTGGGTGCCTCGGCCAT GGGACGTAGGGGCTCAGCTGATGGCCTGCAGGGTCCTCGGCCTCCAAGACATG AGGATGGACATTGTTCTTGGCCTCTTTGACCAGATTCTTCAGCCATTAGCATG CTGCAGACCCTCCACAGAGAGCACCGGTCCGTCCCTCAGTCAAGAGGAGCATG CAGGCTACAGTTCAGCCAAGGCTCCCAGGGTCTGAGCTAGCTGGAGTGACAGC CCAGCGCCTGCACCAATTCCAGCACATGCACTGTTGAGTGAGAGCTCACTTCA GGTTTACCACAAGCTGGGAGCAGCAGGCTTCCCGGTTTCCTATTGTCACAAGG TGCAGAGCTGGGGCCTAAGCCTATGTCTCCTGAATCCTACTGTTGGGCACTTC TAGGGACTTGAGACACTATAGCCAATGGCCTCTGTGGGTTCTGTGCCTGGAAA TGGAGAGATCTGAGTACAGCCTGCTTTGAATGGCCCTGTGAGGCAACCCCAAA GCAAGGGGGTCCAGGTATACTATGGGCCCAGCACCTAAAGCCACCCTTGGGAG ATGATACTCAGGTGGGAAATTCGTAGACTGGGGGACTGAACCAATCCCAAGAT CTGGAAAAGTTTTGATGAAGACTTGAAAAGCTCCTAGCTTCGGGGGTCTGGGA AGCATGAGCACTTACCAGGCAAAAGCTCCGTGAGCGTATCTGCTGTCCTTCTG CATGCCCAGGTACCTCAGTTTTTTTCAACAGCAAGGAAACTAGGGCAATAAAG GGAACCAGCAGAGCTAGAGCCACCCACACATCCAGGGGGGCACTTGACTCTCC CTACTCCTCCTAGGAACCAAAAGGACAAAGTCCATGTTGACAGCAGGGAAGGA AAGGGGGATATAACCTTGACGCAAACCAACACTGGGGTGTTAGAATCTCCTCA TTCACTCTGTCCTGGAGTTGGGTTCTGGCTCTCCTTCACACCTAGGACTCTGA AATGAGCAAGCACTTCAGACAGTCAGGGTAGCAAGAGTCTAGCTGTCTGGTGG GCACCCAAAATGACCAGGGCTTAAGTCCCTTTCCTTTGGTTTAAGCCCGTTAT AATTAAATGGTACCAAAAGCTTTAA (SEQ ID NO: 191) >NP_032824.1 programmed cell death protein 1 precursor [*Mus musculus*] MWVRQVPWSFTWAVLQLSWQSGWLLEVPNGPWRSLTFYPAWLTVSEGANATFT CSLSNWSEDLMLNWNRLSPSNQTEKQAAFCNGLSQPVQDARFQIIQLPNRHDF HMNILDTRRNDSGIYLCGAISLHPKAKIEESPGAELVVTERILETSTRYPSPS PKPEGRFQGMVIGIMSALVGIPVLLLLAWALAVFCSTSMSEARGAGSKDDTLK EEPSAAPVPSVAYEELDFQGREKTPELPTACVHTEYATIVFTEGLGASAMGRR GSADGLQGPRPPRHEDGHCSWPL (SEQ ID NO: 317)
mScarlet	>KY021423.1 Synthetic construct mScarlet gene, partial cds, mRNA ATGGTGAGCAAGGGCGAGGCAGTGATCAAGGAGTTCATGCGGTTCAAGGTGCA CATGGAGGGCTCCATGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGG GCCGCCCCTACGAGGGCACCCAGACCGCCAAGCTGAAGGTGACCAAGGGTGGC CCCCTGCCCTTCTCCTGGGACATCCTGTCCCCTCAGTTCATGTACGGCTCCAG GGCCTTCACCAAGCACCCCGCCGACATCCCCGACTACTATAAGCAGTCCTTCC CCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGCCGTG ACCGTGACCCAGGACACCTCCCTGGAGGACGGCACCCTGATCTACAAGGTGAA GCTCCGCGGCACCAACTTCCCTCCTGACGGCCCCGTAATGCAGAAGAAGACAA TGGGCTGGGAAGCGTCCACCGAGCGGTTGTACCCCGAGGACGGCGTGCTGAAG GGCGACATTAAGATGGCCCTGCGCCTGAAGGACGGCGGCCGCTACCTGGCGGA

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CTTCAAGACCACCTACAAGGCCAAGAAGCCCGTGCAGATGCCCGGCGCCTACA ACGTCGACCGCAAGTTGGACATCACCTCCCACAACGAGGACTACACCGTGGTG GAACAGTACGAACGCTCCGAGGGCCGCCACTCCACCGGCGGCATGGACGAGCT GTACAAG (SEQ ID NO: 192) >APD76535.1 mScarlet, partial [synthetic construct] MVSKGEAVIKEFMRFKVHMEGSMNGHEFEIEGEGEGRPYEGTQTAKLKVTKGG PLPFSWDILSPQFMYGSRAFTKHPADIPDYYKQSFPEGFKWERVMNFEDGGAV TVTQDTSLEDGTLIYKVKLRGTNFPPDGPVMQKKTMGWEASTERLYPEDGVLK GDIKMALRLKDGGRYLADFKTTYKAKKPVQMPGAYNVDRKLDITSHNEDYTVV EQYERSEGRHSTGGMDELYK (SEQ ID NO: 193)
Nanoluciferase	>JQ513379. 1 NanoLuc reporter vector pNL1.1.CMV[Nluc/CMV], complete sequence, mRNA GGCCTAACTGGCCTCAATATTGGCCATTAGCCATATTATTCATTGGTTATATA GCATAAATCAATATTGGCTATTGGCCATTGCATACGTTGTATCTATATCATAA TATGTACATTTATATTGGCTCATGTCCAATATGACCGCCATGTTGGCATTGAT TATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCA TATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAA CGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACT GCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGA CGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTAC GGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATG GTGATGCGGTTTTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGACTCACG GGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACC AAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCCGCCCCGTTGACGCAA ATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGT GAACCGTCAGATCACTAGAAGCTTTATTGCGGTAGTTTATCACAGTTAAATTG CTAACGCAGTCAGTGGGCCTCGGCGGCCAAGCTTGGCAATCCGGTACTGTTGG TAAAGCCACC**ATGGTCTTCACACTCGAAGATTTCGTTGGGGACTGGCGACAGA** **CAGCCGGCTACAACCTGGACCAAGTCCTTGAACAGGGAGGTGTGTCCAGTTTG** **TTTCAGAATCTCGGGGTGTCCGTAACTCCGATCCAAAGGATTGTCCTGAGCGG** **TGAAAATGGGCTGAAGATCGACATCCATGTCATCATCCCGTATGAAGGTCTGA** **GCGGCGACCAAATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTG** **GATGATCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGG** **GGTTACGCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCG** **TGTTCGACGGCAAAAAGATCACTGTAACAGGGACCCTGTGGAACGGCAACAAA** **ATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCTGTTCCGAGTAAC** **CATCAACGGAGTGACCGGCTGGCGGCTGTGCGAACGCATTCTGGCGTAA**TTCT AGAGTCGGGGCGGCCGGCCGCTTCGAGCAGACATGATAAGATACATTGATGAG TTTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAAT TTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTA ACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAG GTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTAAAATCGATAAGGATCC GTCGACCGATGCCCTTGAGAGCCTTCAACCCAGTCAGCTCCTTCCGGTGGGCG CGGGGCATGACTATCGTCGCCGCACTTATGACTGTCTTCTTTATCATGCAACT CGTAGGACAGGTGCCGGCAGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTG CGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAT ACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAG GCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCAT AGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTG GCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCC TCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTT CTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAG TTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTC AGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCT ACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGG TGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAG AAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCA CGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCT TTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTT GGTCTGACAGCGGCCGCAAATGCTAAACCACTGCAGTGGTTACCAGTGCTTGA TCAGTGAGGCACCGATCTCAGCGATCTGCCTATTTCGTTCGTCCATAGTGGCC TGACTCCCCGTCGTGTAGATCACTACGATTCGTGAGGGCTTACCATCAGGCCC CAGCGCAGCAATGATGCCGCGAGAGCCGCGTTCACCGGCCCCCGATTTGTCAG CAATGAACCAGCCAGCAGGGAGGGCCGAGCGAAGAAGTGGTCCTGCTACTTTG TCCGCCTCCATCCAGTCTATGAGCTGCTGTCGTGATGCTAGAGTAAGAAGTTC GCCAGTGAGTAGTTTCCGAAGAGTTGTGGCCATTGCTACTGGCATCGTGGTAT CACGCTCGTCGTTCGGTATGGCTTCGTTCAACTCTGGTTCCCAGCGGTCAAGC CGGGTCACATGATCACCCATATTATGAAGAAATGCAGTCAGCTCCTTAGGGCC TCCGATCGTTGTCAGAAGTAAGTTGGCCGCGGTGTTGTCGCTCATGGTAATGG

TABLE 1-continued

Type I Proteins of Interest Amino Acid Sequence	
Protein of Interest	Transcript Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CAGCACTACACAATTCTCTTACCGTCATGCCATCCGTAAGATGCTTTTCCGTG ACCGGCGAGTACTCAACCAAGTCGTTTTGTGAGTAGTGTATACGGCGACCAAG CTGCTCTTGCCCGGCGTCTATACGGGACAACACCGCGCCACATAGCAGTACTT TGAAAGTGCTCATCATCGGGAATCGTTCTTCGGGGCGGAAAGACTCAAGGATC TTGCCGCTATTGAGATCCAGTTCGATATAGCCCACTCTTGCACCCAGTTGATC TTCAGCATCTTTTACTTTCACCAGCGTTTCGGGGTGTGCAAAAACAGGCAAGC AAAATGCCGCAAAGAAGGGAATGAGTGCGACACGAAAATGTTGGATGCTCATA CTCGTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTACTAGTACGTCTC TCAAGGATAAGTAAGTAATATTAAGGTACGGGAGGTATTGGACAGGCCGCAAT AAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGAT AGTACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAA AATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCT (SEQ ID NO: 194) >AFJ15599.1 NanoLuc luciferase [NanoLuc reporter vector pNL1.1.CMV[Nluc/CMV]] MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENG LKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTP NMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTING VTGWRLCERILA (SEQ ID NO: 195)

The polypeptides provided in Table 1 above are involved in a range of biological processes, including but not limited to, suppressing the adaptive arm of the immune system (e.g., PD-L1); cellular adhesion (e.g., nectin), immune activation (e.g., HVEM), and the like. The POI domains can also be used to track, purify, or identify the engineered EVs from native EVs (e.g., mScarlet and nanoluciferase). The genes, transcripts, polypeptides, variants, and fragments thereof can be used in any combination from Table 1 to be expressed by an engineered EV provided herein. In some embodiments, the POI domain is the human polypeptide. In some embodiments, the POI domain is a homologue of the human polypeptide (e.g., mouse).

In some embodiments of any of the aspects, the engineered cell or EV provided herein comprises an exogenous nucleic acid encoding one or more exogenous polypeptide(s) selected from the group consisting of: the polypeptides listed in Table 1.

In some embodiments of any of the aspects, the POI domain is PD-L1 or a fragment thereof. In some embodiments of any of the aspects, the POI domain is PD-L2 or a fragment thereof. In some embodiments of any of the aspects, the POI domain is FGL1 or a fragment thereof. In some embodiments of any of the aspects, the POI domain is 4-1BBL or a fragment thereof. In some embodiments of any of the aspects, the POI domain is CTLA or a fragment thereof.

In some embodiments of any of the aspects, the POI domain substantially binds to one or more of a target polypeptide. In some embodiments of any of the aspects, the target polypeptide is a cellular receptor. In some embodiments of any of the aspects, the target polypeptide is an immunosuppressive polypeptide. In some embodiments of any of the aspects, the target polypeptide is an immunostimulatory polypeptide. The engineered exosomes provided herein can be designed to activate, block, or modulate a given target polypeptide with the appropriate POI domain that binds to or modulates the function or expression of the target polypeptide. Non-limiting examples of target polypeptides include those listed in Table 2 (below).

TABLE 2

Exemplary Target Polypeptides			
PD-1	VISTA	LAG-3	CD44
CD80	BTLA	CD112	IL10RA
CD86	CD160	CD200R	IL10RB
CD28	HVEM	CD200	Tim-3
ICOS	CD2	Galectin 9	TNFRSF25
CD28H	SLAM CD150	TIM-3	TNFRSF6B
PD-Ll	CD58	CD226	CD113
CTLA-4	TIM-1	CD155	CD27
4-1BB (CD137)	TIM-4	CD112	CD30
GITR	CD40	DR3	LFA-3 (CD58)
CD27L	CD30L	GITRL	CD40L
CD48	CD244	DcR3	CD28H
LFA-3 (CD58)	CD98	TNF Receptor Superfamily members	TNF receptor associated factor (TRAF) family members
Butyrophilin family members	PD-L2	Nectin	TIM family members
B7/CD28 family members	SLAM family members	Nectin-like binding receptors	Collagen family proteins
LAIR-1 (CD305)			

The EVs provided herein further comprise at least one fusion protein comprising a vesicle targeting domain. In various embodiments, the vesicle targeting domain provided herein is capable of binding or anchoring the fusion polypeptide provided herein to an extracellular vesicle, e.g., via targeting of the phospholipid bilayer membrane. In various embodiments, the vesicle targeting domain is a GPI domain (i.e., GPI linker, GPI anchor), fatty acylation site, or prenylation site. One of skill in the art can appreciate that the aforementioned refer to peptide or protein sites, wherein covalent lipid attachment supports embedding of the lipid in a cell membrane (i.e., phospholipid bilayer).

Biochemical forces that anchor EV targeting domains to the EV phospholipid bilayer may include, but are not limited to, electrostatic forces, affinity for EVs through protein-protein interactions with natively resident proteins (e.g., CD81, CD63, CD9, ALIX, TSG101. CD98, CD298, MARCKS, PTGFRN, Lactadherin (MFGe8)), association or affinity for negatively or positively curved phospholipids, association or affinity for negatively or positively charged domains of resident membrane associated proteins, etc., or the like.

Additional non-limiting examples of membrane targeting domains that can be used and their properties are further described in detail, e.g., Alberts B, Johnson A, Lewis J, et al., Molecular Biology of the Cell, 4th edition, New York: Garland Science, 2002. Membrane Proteins; Marilyn D.Resh, Fatty acylation of proteins: new insights into membrane targeting of myristoylated and palmitoylated proteins. Biochimica et Biophysica Acta (BBA)-Molecular Cell Research. Volume 1451, Issue 1, 12 Aug. 1999, Pages 1-16, doi: 10.1016/S0167-4889 (99) 00075-0; Ann Apolloni, et al., H-ras but Not K-ras Traffics to the Plasma Membrane through the Exocytic Pathway, Molecular and Cellular Biology April 2000, 20 (7) 2475-2487, doi: 10.1128/MCB.20.7.2475-2487.2000; Rosie Dawaliby et. al., Phosphatidylethanolamine Is a Key Regulator of Membrane Fluidity in Eukaryotic Cells, Membrane Biology, VOLUME 291, ISSUE 7, doi: 10.1074/jbc.M115.706523; R. J. Deschenes, Protein Palmitoylation, Encyclopedia of Biological Chemistry (Second Edition), Academic Press, 2013, Pages 645-647, ISBN 9780123786319, doi: 10.1016/B978-O-12-378630-2.00022-0; Charuta C. Palsuledesai and Mark D. Distefano, Protein Prenylation: Enzymes, Therapeutics, and Biotechnology Applications, ACS Chemical Biology 2015 10 (1), 51-62, doi: 10.1021/cb500791f; Hung M E, Leonard J N. Stabilization of exosome-targeting peptides via engineered glycosylation, J Biol Chem, 2015 Mar. 27; 290 (13): 8166-72, doi: 10.1074/jbc.M114.621383; Udenwobele Daniel Ikenna, et. al., Myristoylation: An Important Protein Modification in the Immune Response, Frontiers in Immunology, Vol: 8, 2017, doi: 10.3389/fimmu.2017.00751; Kinoshita Taroh 2020Biosynthesis and biology of mammalian GPI-anchored proteins Open Biol. 10190290, doi: 10.1098/rsob.190290, the contents of which are incorporated herein by reference in their entireties.

In some embodiments, the fusion polypeptide comprises one or more, two or more, three or more, four or more, five or more, or six or more vesicle targeting domains on the same polypeptide or nucleic acid construct encoding said polypeptide. For example, the fusion polypeptides provided herein can comprise PD-L1 and Glycosylphosphatidylinositol (GPI).

In some embodiments, the vesicle targeting domain is a prenylated protein. Prenylated proteins are proteins that have at least one prenylation site. Prenylation occurs when a 15-carbon or 20-carbon, farnesyl or geranylgeranyl isoprenoid, respectively, is covalently bound via a thioether bond to a cysteine at or near the carboxy terminus of a protein. In general, a prenylation site comprises an amino acid sequence CAAX, wherein C represents cysteine, A represents an aliphatic amino acid (glycine, alanine, valine, leucine, or isoleucine), and X represents alanine, methionine, serine, leucine, or glutamine.

In some embodiments, the vesicle targeting domain is a fatty acylated protein. Fatty acylated proteins are proteins that have been modified post-translationally by covalent attachment of one or more fatty acids, generally with a saturated fatty acid that comprises 14-carbon (e.g., myristic acid) via myristoylation or 16-carbons (e.g., palmitic acid) via palmitoylation. For example, proteins destined to become myristoylated begin with the amino acids Met-Gly-X-X-X followed by a serine or threonine at position 6 and lysine or arginine at position 7 and/or 8 wherein X can be any amino acid. The methionine is removed and a myristate is linked to the glycine via an amide bond. Palmitoylation herein means a posttranslational covalent attachment of fatty acids (e.g., palmitic acid) to cysteine (S-palmitoylation), serine and/or threonine (O-palmitoylation), and to the amino group of lysine (N-palmitoylation) of proteins.

Palmitoylated proteins may be acylated by attachment of a thioester linkage to a sulfhydryl group of cysteine, or via a palmitate linked to the amino group of an N-terminal cysteine. Palmitoylation sites may be present near the N- or C-terminus of a protein.

In some embodiments, the vesicle targeting domain is a glycosylphosphatidylinositol (GPI) anchor. A glycosylphosphatidylinositol (GPI) anchor ("GPI anchor") or "GPI sticky binder" are used interchangeably and refer to a means of stably anchoring a protein to an outer leaflet (e.g., exterior layer of a phospholipid bilayer) of a cell membrane. A GPI anchor comprises a glycan, a phosphoethanolamine linker, a phospholipid tail, and may be modified by various glycan sidechains. The glycan core comprises phosphoinositol, glucosamine, and mannose residues wherein said mannose residues may be modified for example with phosphoethanolamine or carbohydrates. The phosphoethanolamine is amide-bonded to the carboxyl terminus of a protein during the process of GPI attachment. In some embodiments, the vesicle targeting domain may have affinity to EV resident proteins, e.g., CD81, CD63, CD9, ALIX, TSG101, CD98, CD298, MARCKS, PTGFRN, Lactadherin (MFGe8).

Sticky binders can include a sequence for one or more myristoylation and/or palmitoylation (Myr/Palm) sites fused to a transmembrane domain from 4F2 (CD98). For example, the myristoylation sequence from the MARCKS protein may be modified to encode for one or more myristoylation and palmitoylation sites, wherein the modified MARCKS protein sequence is fused to a protein sequence of the transmembrane domain from 4F2 via a covalent peptide bond. A Myr/Palm followed by the 4F2 transmembrane domain can improve loading of the fusion proteins provided herein when compared with 4F2 transmembrane domain alone or Myr/Palm alone.

Non-limiting examples of vesicle targeting domains that enhance fusion polypeptide structure and function on the extracellular vesicles are provided in Table 3 (below).

TABLE 3

Exosome Targeting Domain	
Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
Human CD55 (DAF) Glycosylphosphatidylinositol (GPI)	>NM_000574.5 *Homo sapiens* CD55 molecule (Cromer blood group) (CD55), transcript variant 1, mRNA CTGCTTACTGCAACTCGCTCCGGCCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCG GCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCGTGCC CGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTG CCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCC AGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGA

TABLE 3-continued

Exosome Targeting Domain

Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	AGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAG TCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCT AAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTAC TGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAA ACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAA ATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTC GACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCC AGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCA AGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGG ATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGA GTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTC TCAGAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACC TGTTTCCAGGACAACCAAGCATTTTCATGAAACAACC**CCAAATAAAGGAAGTGGAAC** **CACTTCAGGTACTACCCGTCTTCTATCTGGGCAGACGTGTTTCACGTTGACAGGTTT** **GCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG**CCAAAGAAGAGTTAAGAAGA AAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGA TAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTG TTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTAGC ACACCTACACCTCTTGAAAATAGAACAACTTGCAGAATTGAGAGTGATTCCTTTCCT AAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGGGATCACGAGGAAAA GAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCACTTATAAAGG AAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAG TCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATCTTTGG CTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAACAT GCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTGA ATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTT GACTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATT ATATATTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTG TAATATTTATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACA AGAAAAGTTGAAGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAAT GATCCCATTTTTTGGTATCATGTAGTATGTGAAATTTATTCTTAAACGTGACTACTT TATTTCTAAATAAGAAATTCCCTACCTGCTTCCTACAAGCAGTTCAGAATGCCATGC CTTGGTTGTCCTAGTGTGAATAATTTTCAGCTACTTTAAAATTATATTGTACTTTCT CAAGCATGTCATATCCTTTCCTATTAGAGTATCTATATTACTTGTTACTGATTTACC TGAAGGCAATCTGATTAATTTCTAGGTTTTTACCATATTCTTGTCATCTTGCCAATT ACATTTTAAGTGTTAGACTAGACTAAGATGTACTAGTTGTATAGAATATAACTAGA TTTATTATGGCAATGTTTATTTTGTCATTTTGCTTCATCTGTTTTGTTGTTGAAGTA CTTTAAATTTCATACGTTCATGGCATTTCACTGTAAAGACTTTAATGTGTATTTCTT AAAATAAAACTTTTTTTCCTCCTTAA (SEQ ID NO: 196) >NP_000565.1 complement decay-accelerating factor isoform 1 preproprotein [*Homo sapiens*] MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPE DTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPTRLNSASLKQPYI TQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRN GQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCPAP PQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRG KSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVSRTTKHFHE TT**PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT** (SEQ ID NO: 197)
Human CD59 Glycosylphosphatidylinositol (GPI)	>NM_203330.2 *Homo sapiens* CD59 molecule (CD59 blood group) (CD59), transcript variant 1, mRNA GGGGCCGGGGGGCGGAGCCTTGCGGGCTGGAGCGAAAGAATGCGGGGGCTGA GCGCAGAAGCGGCTCGAGGCTGGAAGAGGATCTTGGGCGCCGCCAGTCTCTC TCTGTTGCCCAAGCTGGAGTGCAGTGGCACAGTCTTGGCTCACTGCAACCTC CACCTCCTGGGTGCAAGCGATTCTCGTGTCTCAGCCTCTCAAGTAGCTGGGA TTACAGTCTTTAGCACCAGTTGGTGTAGGAGTTGAGACCTACTTCACAGTAG TTCTGTGGACAATCACAATGGGAATCCAAGGAGGGTCTGTCCTGTTCGGGCT GCTGCTCGTCCTGGCTGTCTTCTGCCATTCAGGTCATAGCCTGCAGTGCTAC AACTGTCCTAACCCAACTGCTGACTGCAAAACAGCCGTCAATTGTTCATCTG ATTTTGATGCGTGTCTCATTACCAAAGCTGGGTTACAAGTGTATAACAAGTG TTGGAAGTTTGAGCATTGCAATTTCAACGACGTCACAACCCGCTTGAGGGAA AATGAGCTAACGTACTACTGCTGCAAGAAG**GACCTGTGTAACTTTAACGAAC** **AGCTTGAAAATGGTGGGACATCCTTATCAGAGAAAACAGTTCTTCTGCTGGT** **GACTCCATTTCTGGCAGCAGCCTGGAGCCTTCATCCCTAA**GTCAACACCAGG AGAGCTTCTCCCAAACTCCCCGTTCCTGCGTAGTCCGCTTTCTCTTGCTGCC ACATTCTAAAGGCTTGATATTTTCCAAATGGATCCTGTTGGGAAAGAATAAA ATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGA CCAGTCCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAA GTAGGTGTGACTTGAACTAGATTGCATGCTTCCTCCTTTGCTCTTGGGAAGA CCAGCTTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTT TTCCTCTGGCTCCTTGGATGTAGTCAGTTAGCATCATTAGTACATCTTTGGA GGGTGGGGCAGGAGTATATGAGCATCCTCTCTCACATGGAACGCTTTCATAA

TABLE 3-continued

Exosome Targeting Domain	
Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ACTTCAGGGATCCCGTGTTGCCATGGAGGCATGCCAAATGTTCCATATGTGG GTGTCAGTCAGGGACAACAAGATCCTTAATGCAGAGCTAGAGGACTTCTGGC AGGGAAGTGGGGAAGTGTTCCAGATAGCAGGGCATGAAAACTTAGAGAGGTA CAAGTGGCTGAAAATCGAGTTTTTCCTCTGTCTTTAAATTTTATATGGGCTT TGTTATCTTCCACTGGAAAAGTGTAATAGCATACATCAATGGTGTGTTAAAG CTATTTCCTTGCCTTTTTTTTATTGGAATGGTAGGATATCTTGGCTTTGCCA CACACAGTTACAGAGTGAACACTCTACTACATGTGACTGGCAGTATTAAGTG TGCTTATTTTAAATGTTACTGGTAGAAAGGCAGTTCAGGTATGTGTGTATAT AGTATGAATGCAGTGGGGACACCCTTTGTGGTTACAGTTTGAGACTTCCAAA GGTCATCCTTAATAACAACAGATCTGCAGGGGTATGTTTTACCATCTGCATC CAGCCTCCTGCTAACTCCTAGCTGACTCAGCATAGATTGTATAAAATACCTT TGTAACGGCTCTTAGCACACTCACAGATGTTTGAGGCTTTCAGAAGCTCTTC TAAAAAATGATACACACCTTTCACAAGGGCAAACTTTTTCCTTTTCCCTGTG TATTCTAGTGAATGAATCTCAAGATTCAGTAGACCTAATGACATTTGTATTT TATGATCTTGGCTGTATTTAATGGCATAGGCTGACTTTTGCAGATGGAGGAA TTTCTTGATTAATGTTGAAAAAAAACCCTTGATTATACTCTGTTGGACAAAC CGAGTGCAATGAATGATGCTTTTCTGAAAATGAAATATAACAAGTGGGTGAA TGTGGTTATGGCCGAAAAGGATATGCAGTATGCTTAATGGTAGCAACTGAAA GAAGACATCCTGAGCAGTGCCAGCTTTCTTCTGTTGATGCCGTTCCCTGAAC ATAGGAAAATAGAAACTTGCTTATCAAAACTTAGCATTACCTTGGTGCTCTG TGTTCTCTGTTAGCTCAGTGTCTTTCCTTACATCAATAGGTTTTTTTTTTTT TTTTTGGCCTGAGGAAGTACTGACCATGCCCACAGCCACCGGCTGAGCAAAG AAGCTCATTTCATGTGAGTTCTAAGGAATGAGAAACAATTTTGATGAATTTA AGCAGAAAATGAATTTCTGGGAACTTTTTTGGGGGCGGGGGGGTGGGGAATT CAGCCACACTCCAGAAAGCCAGGAGTCGACAGTTTTGGAAGCCTCTCTCAGG ATTGAGATTCTAGGATGAGATTGGCTTACTGCTATCTTGTGTCATGTACCCA CTTTTTGGCCAGACTACACTGGGAAGAAGGTAGTCCTCTAAAGCAAAATCTG AGTGCCACTAAATGGGGAGATGGGGCTGTTAAGCTGTCCAAATCAACAAGGG TCATATAAATGGCCTTAAACTTTGGGGTTGCTTTCTGCAAAAAGTTGCTGTG ACTCATGCCATAGACAAGGTTGAGTGCCTGGACCCAAAGGCAATACTGTAAT GTAAAGACATTTATAGTACTAGGCAAACAGCACCCCAGGTACTCCAGGCCCT CCTGGCTGGAGAGGGCTGTGGCAATAGAAAATTAGTGCCAACTGCAGTGAGT CAGCCTAGGTTAAATAGAGAGTGTAAGAGTGCTGGACAGGAACCTCCACCCT CATGTCACATTTCTTCAATGTGACCCTTCTGGCCCCTCTCCTCCTGACAGCG GAACAATGACTGCCCCGATAGGTGAGGCTGGAGGAAGAATCAGTCCTGTCCT TGGCAAGCTCTTCACTATGACAGTAAAGGCTCTCTGCCTGCTGCCAAGGCCT GTGACTTTCTAACCTGGCCTCACGCTGGGTAAGCTTAAGGTAGAGGTGCAGG ATTAGCAAGCCCACCTGGCTACCAGGCCGACAGCTACATCCTCCAACTGACC CTGATCAACGAAGAGGGATTCATGTGTCTGTCTCAGTTGGTTCCAAATGAAA CCAGGGAGCAGGGGAGTTAGGAATCGAACACCAGTCATGCCTACTGGCTCTC TGCTCGAGAGCCAATACCCTGTGCCCTCCACTCATCTGGATTTACAGGAACT GTCATAGTGTTCAGTATTGGGTGGTGATAAGCCCATTGGATTGTCCCCTTGG GGGGATGAGCTAGGGGTGCAAGGAACACCTGATGAGTAGATAAGTGGAGCTC ATGGTATTTCCTGAAAGATGCTAATCTATTTGCCAAACTTGGTCTTGAATGT ACTGGGGGCTTCAAGGTATGGGTATATTTTTCTTGTGTCCTTGCAGTTAGCC CCCATGTCTTATGTGTGTCCTGAAAAAATAAGAGCCTGCCCAAGACTTTGGG CCTCTTGACAGAATTAACCACTTTTATACATCTGAGTTCTCTTGGTAAGTTC TTTAGCAGTGTTCAAAGTCTACTAGCTCGCATTAGTTTCTGTTGCTGCCAAC AGATCTGAACTAATGCTAACAGATCCCCCTGAGGGATTCTTGATGGGCTGAG CAGCTGGCTGGAGCTAGTACTGACTGACATTCATTGTGATGAGGGCAGCTTT CTGGTACAGGATTCTAAGCTCTATGTTTTATATACATTTTCATCTGTACTTG CACCTCACTTTACACAAGAGGAAACTATGCAAAGTTAGCTGGATCGCTCAAG GTCACTTAGGTAAGTTGGCAAGTCCATGCTTCCCACTCAGCTCCTCAGGTCA GCAAGTCTACTTCTCTGCCTATTTTGTATACTCTCTTTAATATGTGCCTAGC TTTGGAAAGTCTAGAATGGGTCCCTGGTGCCTTTTTACTTTGAAGAAATCAG TTTCTGCCTCTTTTTGGAAAAGAAAACAAAGTGCAATTGTTTTTTACTGGAA AGTTACCCAATAGCATGAGGTGAACAGGACGTAGTTAGGCCTTCCTGTAAAC AGAAAATCATATCAAAACACTATCTTCCCATCTGTTTCTCAATGCCTGCTAC TTCTTGTAGATATTTCATTTCAGGAGAGCAGCAGTTAAACCCGTGGATTTTG TAGTTAGGAACCTGGGTTCAAACCCTCTTCCACTAATTGGCTATGTCTCTGG ACAAGTTTTTTTTTTTTTTTTTTTTTTTTAAACCCTTTCTGAACTTTCACTTTCT ATGTCTACCTCAAAGAATTGTTGTGAGGCTTGAGATAATGCATTTGTAAAGG GTCTGCCAGATAGGAAGATGCTAGTTATGGATTTACAAGGTTGTTAAGGCTG TAAGAGTCTAAAACCTACAGTGAATCACAATGCATTTACCCCCACTGACTTG GACATAAGTGAAAACTAGCCAGAAGTCTCTTTTTCAAATTACTTACAGGTTA TTCAATATAAAATTTTTGTAATGGATAATCTTATTTATCTAAACTAAAGCTT CCTGTTTATACACACTCCTGTTATTCTGGGATAAGATAAATGACCACAGTAC CTTAATTTCTAGGTGGGTGCCTGTGATGGTTCATTGTAGGTAAGGACATTTT CTCTTTTTCAGCAGCTGTGTAGGTCCAGAGCCTCTGGGAGAGGAGGGGGGTA GCATGCACCCAGCAGGGGACTGAACTGGGAAACTCAAGGTTCTTTTTACTGT GGGGTAGTGAGCTGCCTTTCTGTGATCGGTTTCCCTAGGGATGTTGCTGTTC CCCTCCTTGCTATTCGCAGCTACATACAACGTGGCCAACCCCAGTAGGCTGA TCCTATATATGATCAGTGCTGGTGCTGACTCTCAATAGCCCCACCCAAGCTG GCTATAGGTTTACAGATACATTAATTAGGCAACCTAAAATATTGATGCTGGT

TABLE 3-continued

Exosome Targeting Domain	
Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GTTGGTGTGACATAATGCTATGGCCAGAACTGAAACTTAGAGTTATAATTCA TGTATTAGGGTTCTCCAGAGGGACAGAATTAGTAGGATATATGTATATATGA AAGGGAGGTTATTAGGGAGAACTGGCTCCCACAGTTAGAAGGCGAAGTCGCA CAATAGGCCGTCTGCAAGCTGGGTTAGAGAGAAGCCAGTAGTGGCTCAGCCT GAGTTCAAAAACCTCAAAACTGGGGAAGCTGACAGTGCAGCCAGCCTTCAGT CTGTGGCCAAAGGCCCAAGAGCCCCTGGCAACCAACCCACTGGTGCAAGTCC TAGATTCCAAAGGCTGAAGAACCTGGAGTCTGATGTCCAAGAGCAGGAAGAG TGGAAGAAAGCCAGAAGACTCAGCAAACAAGGTAGACAGTGTCTACCACCAT AGTGGCCATACCAAAGAGGCTACCGATTCCTTCCTGCTACCTGGATCCCTGA AGTTGCCCTGGTCTCTGCACCTTCTAAACCTAGTTCTTAAGAGCTTTCCATT ACATGAGCTGTCTCAAAGCCCTCCAATAAATTCTCAGTGTAAGCTTCTGTTG CTTGTGGACAGAAAATTCTGACAGACCTACCCTATAAGTGTTACTGTCAGGA TAACATGAGAACGCACAACAGTAAGTGGTCACTAAGTGTTAGCTACGGTTAT TTTGCCCAAGGTAGCATGGCTAGTTGATGCCGGTTGATGGGGCTTAAACCCA GCTCCCTCATCTTCCAGGCCTCTGTACTCCCTATTCCACTAAACTACCTCTC AGGTTTATTTTTTTAAATTCTTACTCTGCAAGTACATAGGACCACATTTACC TGGGAAAACAAGAATAAAGGCTGCTCTGCATTTTTTAGAAACTTTTTTGAAA GGGAGATGGGAATGCCTGCACCCCCAAGTCCAGACCAACACAATGGTTAATT GAGATGAATAATAAAGGAAAGACTGTTCTGGGCTTCCCAGAATAGCTTGGTC CTTAAATTGTGGCACAAACAACCTCCTGTCAGAGCCAGCCTCCTGCCAGGAA GAGGGGTAGGAGACTAGAGGCCGTGTGTGCAGCCTTGCCCTGAAGGCTAGGG TGACAATTTGGAGGCTGTCCAAACACCCTGGCCTCTAGAGCTGGCCTGTCTA TTTGAAATGCCGGCTCTGATGCTAATCGGCGACCCTCAGGCAAGTTACTTAA CCTTACATGCCTCAGTTTTCTCATCTGGAAAATGAGAACCCTAGGTTTAGGG TTGTTAGAAAAGTTAAATGAGTTAAGACAAGTGCCTGGGACACAGTAGCCTC TTGTGTGTGTTTATCATTATGTCCTCAGCAGGTCGTAGAAGCAGCTTCTCAG GTGTGAGGCTGGCGCGATTATCTGGAGTGGGTTGGGTTTTCTAGGATGGACC CCCTGCTGCATTTTCCTCATTCATCCACCAGGGCTTAATGGGGAATCAAGGA ATCCATGTGTAACTGTATAATAACTGTAGCCACACTCCAATGACCACCTACT AGTTGTCCCTGGCACTGCTTATACATATGTCCATCAAATCAATCCTATGAAG TAGATACTGTCTTCATTTTATAGATCAGAGACAATTGGGGTTCAGAGAGCTG ATGTGATTTTCCCAGGGTCACAGAGAGTCCCAGATTCAGGCACAACTCTTGT ATTCCAAGACACAACCACTACATGTCCAAAGGCTGCCCAGAGCCACCGGGCA CGGCAAATTGTGACATATCCCTAAAGAGGCTGAGCACCTGGTCAGGATCTGA TGGCTGACAGTGTGTCCAGATGCAGAGCTGGAGTGGGGGAGGGGAAGGGGGG CTCCTTGGGACAGAGAAGGCTTTCTGTGCTTTCTCTGAAGGGAGCAGTCTGA GGACCAAGGGAACCCGGCAAACAGCACCTCAGGTACTCCAGGCCCTCCTGGC TGGAGAGGGCTGTGGCAATGGAAAATTAGTGCCAACTGCAATGAGTCAGCCT CGGTTAAATAGAGAGTGAAGAATGCTGGACAGGAACCTCCACCCTCATGTCA CATTTCTTCAGTGTGACCCTTCTGGCCCCTCTCCTCCTGACAGCGGAACAAT GACTGCCCCGATAGGTGAGGCTGGAGGAAGAATCAGTCCTGTCCTTGGCAAG CTCTTCACTATGACAGTAAAGGCTCTCTGCCTGCTGCCAAGGCCTGTGACTT TCTAACCTGGCCTCACGCTGGGTAAGCTTAAGGTAGAGGTGCAGGATTAGCA AGCCCACCTGGCTACCAGGCCGACAGCTACATCTTTCAACTGACCCTGATCA ACGAAGAGGGACTTGTGTCTCTCAGTTGGTTCCAAATGAAACCAGGGAGCAG GGGCGTTAGGAAGCTCCAACAGGATGGTACTTAATGGGGCATTTGAGTGGAG AGGTAGGTGACATAGTGCTTTGGAGCCCAGGGAGGGAAAGGTTCTGCTGAAG TTGAATTCAAGACTGTTCTTTCATCACAAACTTGAGTTTCCTGGACATTTGT TTGCAGAAACAACCGTAGGGTTTTGCCTTAACCTCGTGGGTTTATTATTACC TCATAGGGACTTTGCCTCCTGACAGCAGTTTATGGGTGTTCATTGTGGCACT TGAGTTTTCTTGCATACTTGTTAGAGAAACCAAGTTTGTCATCAACTTCTTA TTTAACCCCCTGGCTATAACTTCATGGATTATGTTATAATTAAGCCATCCAG AGTAAAATCTGTTTAGATTATCTTGGAGTAAGGGGGAAAAAATCTGTAATTT TTTCTCCTCAACTAGATATATACATAAAAAATGATTGTATTGCTTCATTTAA AAAATATAACGCAAAATCTCTTTTCCTTCTAAAAAAAAAAAAAAAAAAA (SEQ ID NO: 321) >NP_976075.1 CD59 glycoprotein preproprotein [*Homo sapiens*] MGIQGGSVLFGLLLVLAVFCHSGHSLQCYNCPNPTADCKTAVNCSSDFDACL ITKAGLQVYNKCWKFEHCNFNDVTTRLRENELTYYCCKK**DLCNFNEQLENGG** **TSLSEKTVLLLVTPFLAAAWSLHP** (SEQ ID NO: 198)
Human C1C2 from MFGE8	NM_005928.4 *Homo sapiens* milk fat globule-EGF factor 8 protein (MFGE8), transcript variant 1, mRNA AGAACCCCGCGGGGTCTGAGCAGCCCAGCGTGCCCATTCCAGCGCCCGCGTCCCCGC AGCATGCCGCGCCCCCGCCTGCTGGCCGCGCTGTGCGGCGCGCTGCTCTGCGCCCCC AGCCTCCTCGTCGCCCTGGATATCTGTTCCAAAAACCCCTGCCACAACGGTGGTTTA TGCGAGGAGATTTCCCAAGAAGTGCGAGGAGATGTCTTCCCCTCGTACACCTGCACG TGCCTTAAGGGCTACGCGGGCAACCACTGTGAGACGAAATGT**GTCGAGCCACTGGGC** **CTGGAGAATGGGAACATTGCCAACTCACAGATCGCCGCCTCGTCTGTGCGTGTGACC** **TTCTTGGGTTTGCAGCATTGGGTCCCGGAGCTGGCCCGCCTGAACCGCGCAGGCATG** **GTCAATGCCTGGACACCCAGCAGCAATGACGATAACCCCTGGATCCAGGTGAACCTG** **CTGCGGAGGATGTGGGTAACAGGTGTGGTGACGCAGGGTGCCAGCCGCTTGGCCAGT** **CATGAGTACCTGAAGGCCTTCAAGGTGGCCTACAGCCTTAATGGACACGAATTCGAT**

TABLE 3-continued

Exosome Targeting Domain

Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TTCATCCATGATGTTAATAAAAAACACAAGGAGTTTGTGGGTAACTGGAACAAAAAC **GCGGTGCATGTCAACCTGTTTGAGACCCCTGTGGAGGCTCAGTACGTGAGATTGTAC** **CCCACGAGCTGCCACACGGCCTGCACTCTGCGCTTTGAGCTACTGGGCTGTGAGCTG** **AACGGATGCGCCAATCCCCTGGGCCTGAAGAATAACAGCATCCCTGACAAGCAGATC** **ACGGCCTCCAGCAGCTACAAGACCTGGGGCTTGCATCTCTTCAGCTGGAACCCCTCC** **TATGCACGGCTGGACAAGCAGGGCAACTTCAACGCCTGGGTTGCGGGGAGCTACGGT** **AACGATCAGTGGCTGCAGGTGGACCTGGGCTCCTCGAAGGAGGTGACAGGCATCATC** **ACCCAGGGGGCCCGTAACTTTGGCTCTGTCCAGTTTGTGGCATCCTACAAGGTTGCC** **TACAGTAATGACAGTGCGAACTGGACTGAGTACCAGGACCCCAGGACTGGCAGCAGT** **AAGATCTTCCCTGGCAACTGGGACAACCACTCCCACAAGAAGAACTTGTTTGAGACG** **CCCATCCTGGCTCGCTATGTGCGCATCCTGCCTGTAGCCTGGCACAACCGCATCGCC** **CTGCGCCTGGAGCTGCTGGGCTGTTAG**TGGCCACCTGCCACCCCCAGGTCTTCCTGC TTTCCATGGGCCCGCTGCCTCTTGGCTTCTCAGCCCCTTTAAATCACCATAGGGCTG GGGACTGGGGAAGGGGAGGGTGTTCAGAGGCAGCACCACCACACAGTCACCCCTCCC TCCCTCTTTCCCACCCTCCACCTCTCACGGGCCCTGCCCCAGCCCCTAAGCCCCGTC CCCTAACCCCCAGTCCTCACTGTCCTGTTTTCTTAGGCACTGAGGGATCTGAGTAGG TCTGGGATGGACAGGAAAGGGCAAAGTAGGGCGTGTGGTTTCCCTGCCCCTGTCCGG ACCGCCGATCCCAGGTGCGTGTGTCTCTGTCTCTCCTAGCCCCTCTCTCACACATCA CATTCCCATGGTGGCCTCAAGAAAGGCCCGGAAGCGCCAGGCTGGAGATAACAGCCT CTTGCCCGTCGGCCCTGCGTCGGCCCTGGGGTACCATGTGGCCACAACTGCTGTGGC CCCCTGTCCCCAAGACACTTCCCCTTGTCTCCCTGGTTGCCTCTCTTGCCCCTTGTC CTGAAGCCCAGCGACACAGAAGGGGGTGGGGCGGGTCTATGGGGAGAAAGGGAGCGA GGTCAGAGGAGGGCATGGGTTGGCAGGGTGGGCGTTTGGGGCCCTCTATGCTGGCTT TTCACCCCAGAGGACACAGGCAGCTTCCAAAATATATTTATCTTCTTCACGGGAA (SEQ ID NO: 199) >NP_005919.2 lactadherin isoform a preproprotein [*Homo sapiens*] MPRPRLLAALCGALLCAPSLLVALDICSKNPCHNGGLCEEISQEVRGDVFPSYTCTC LKGYAGNHCETKC**VEPLGLENGNIANSQIAASSVRVTFLGLQHWVPELARLNRAGMV** **NAWTPSSNDDNPWIQVNLLRRMWVTGVVTQGASRLASHEYLKAFKVAYSLNGHEFDF** **IHDVNKKHKEFVGNWNKNAVHVNLFETPVEAQYVRLYPTSCHTACTLRFELLGCELN** **GCANPLGLKNNSIPDKQITASSSYKTWGLHLFSWNPSYARLDKQGNFNAWVAGSYGN** **DQWLQVDLGSSKEVTGIITQGARNFGSVQFVASYKVAYSNDSANWTEYQDPRTGSSK** **IFPGNWDNHSHKKNLFETPILARYVRILPVAWHNRIALRLELLGC** (SEQ ID NO: 200)
Human 4F2 (CD98)	>NM_002394.6 *Homo sapiens* solute carrier family 3 member 2 (SLC3A2), transcript variant 3, mRNA GCATTGCGGCTTGGTTTTCTCACCCAGTGCATGTGGCAGGAGCGGTGAGATC ACTGCCTCACGGCGATCCTGGACTGACGGTCACGACTGCCTACCCTCTAACC CTGTTCTGAGCTGCCCCTTGCCCACACACCCCAAACCTGTGTGCAGGATCCG CCTCCATGGAGCTACAGCCTCCTGAAGCCTCGATCGCCGTCGTGTCGATTCC GCGCCAGTTGCCTGGCTCACATTCGGAGGCTGGTGTCCAGGGTCTCAGCGCG GGGGACGACTCAGAGTTGGGGTCTCACTGTGTTGCCCAGACTGGTCTCGAAC TCTTGGCCTCAGGTGATCCTCTTCCCTCAGCTTCCCAGAATGCCGAGATGAT AGAGACGGGGTCTGACTGTGTTACCCAGGCTGGTCTTCAACTCTTGGCCTCA AGTGATCCTCCTGCCTTAGCTTCCAAGAATGCTGAGGTTACAGGCACC**ATGA** **GCCAGGACACCGAGGTGGATATGAAGGAGGTGGAGCTGAATGAGTTAGAGCC** **CGAGAAGCAGCCGATGAACGCGGCGTCTGGGGCGGCCATGTCCCTGGCGGGA** **GCCGAGAAGAATGGTCTGGTGAAGATCAAGGTGGCGGAAGACGAGGCGGAGG** **CGGCAGCCGCGGCTAAGTTCACGGGCCTGTCCAAGGAGGAGCTGCTGAAGGT** **GGCAGGCAGCCCCGGCTGGGTACGCACCCGCTGGGCACTGCTG**CTGCTCTTC TGGCTCGGCTGGCTCGGCATGCTTGCTGGTGCCGTGGTCATAATCGTGCGAG CGCCGCGTTGTCGCGAGCTACCGGCGCAGAAGTGGTGGCACACGGGCGCCCT CTACCGCATCGGCGACCTTCAGGCCTTCCAGGGCCACGGCGCGGGCAACCTG GCGGGTCTGAAGGGGCGTCTCGATTACCTGAGCTCTCTGAAGGTGAAGGGCC TTGTGCTGGGTCCAATTCACAAGAACCAGAAGGATGATGTCGCTCAGACTGA CTTGCTGCAGATCGACCCCAATTTTGGCTCCAAGGAAGATTTTGACAGTCTC TTGCAATCGGCTAAAAAAAAAGAGCATCCGTGTCATTCTGGACCTTACTCCCA ACTACCGGGGTGAGAACTCGTGGTTCTCCACTCAGGTTGACACTGTGGCCAC CAAGGTGAAGGATGCTCTGGAGTTTTGGCTGCAAGCTGGCGTGGATGGGTTC CAGGTTCGGGACATAGAGAATCTGAAGGATGCATCCTCATTCTTGGCTGAGT GGCAAAATATCACCAAGGGCTTCAGTGAAGACAGGCTCTTGATTGCGGGGAC TAACTCCTCCGACCTTCAGCAGATCCTGAGCCTACTCGAATCCAACAAAGAC TTGCTGTTGACTAGCTCATACCTGTCTGATTCTGGTTCTACTGGGGAGCATA CAAAATCCCTAGTCACACAGTATTTGAATGCCACTGGCAATCGCTGGTGCAG CTGGAGTTTGTCTCAGGCAAGGCTCCTGACTTCCTTCTTGCCGGCTCAACTT CTCCGACTCTACCAGCTGATGCTCTTCACCCTGCCAGGGACCCCTGTTTTCA GCTACGGGGATGAGATTGGCCTGGATGCAGCTGCCCTTCCTGGACAGCCTAT GGAGGCTCCAGTCATGCTGTGGGATGAGTCCAGCTTCCCTGACATCCCAGGG GCTGTAAGTGCCAACATGACTGTGAAGGGCCAGAGTGAAGACCCTGGCTCCC TCCTTTCCTTGTTCCGGCGGCTGAGTGACCAGCGGAGTAAGGAGCGCTCCCT ACTGCATGGGGACTTCCACGCGTTCTCCGCTGGGCCTGGACTCTTCTCCTAT ATCCGCCACTGGGACCAGAATGAGCGTTTTCTGGTAGTGCTTAACTTTGGGG

TABLE 3-continued

Exosome Targeting Domain

Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ATGTGGGCCTCTCGGCTGGACTGCAGGCCTCCGACCTGCCTGCCAGCGCCAG CCTGCCAGCCAAGGCTGACCTCCTGCTCAGCACCCAGCCAGGCCGTGAGGAG GGCTCCCCTCTTGAGCTGGAACGCCTGAAACTGGAGCCTCACGAAGGGCTGC TGCTCCGCTTCCCCTACGCGGCCTGACTTCAGCCTGACATGGACCCACTACC CTTCTCCTTTCCTTCCCAGGCCCTTTGGCTTCTGATTTTTCTCTTTTTTAAA AACAAACAAACAAACTGTTGCAGATTATGAGTGAACCCCCAAATAGGGTGTT TTCTGCCTTCAAATAAAAGTCACCCCTGCATGGTGAA (SEQ ID NO: 201) >NP_002385.3 4F2 cell-surface antigen heavy chain isoform c [*Homo sapiens*] **MELQPPEASIAVVSIPRQLPGSHSEAGVQGLSAGDDSELGSHCVAQTGLELL** **ASGDPLPSASQNAEMIETGSDCVTQAGLQLLASSDPPALASKNAEVTGTMSQ** **DTEVDMKEVELNELEPEKQPMNAASGAAMSLAGAEKNGLVKIKVAEDEAEAA** **AAAKFTGLSKEELLKVAGSPGWVRTRWALLLLFWLGWLGMLAGAVVIIV**RAP RCRELPAQKWWHTGALYRIGDLQAFQGHGAGNLAGLKGRLDYLSSLKVKGLV LGPIHKNQKDDVAQTDLLQIDPNFGSKEDFDSLLQSAKKKSIRVILDLTPNY RGENSWFSTQVDTVATKVKDALEFWLQAGVDGFQVRDIENLKDASSFLAEWQ NITKGFSEDRLLIAGTNSSDLQQILSLLESNKDLLLTSSYLSDSGSTGEHTK SLVTQYLNATGNRWCSWSLSQARLLTSFLPAQLLRLYQLMLFTLPGTPVFSY GDEIGLDAAALPGQPMEAPVMLWDESSFPDIPGAVSANMTVKGQSEDPGSLL SLFRRLSDQRSKERSLLHGDFHAFSAGPGLFSYIRHWDQNERFLVVLNFGDV GLSAGLQASDLPASASLPAKADLLLSTQPGREEGSPLELERLKLEPHEGLLL RFPYAA (SEQ ID NO: 202)
Human TFR2	>NM_003227.4 *Homo sapiens* transferrin receptor 2 (TFR2), transcript variant 1, mRNA ATCGCTGGGGGACAGCCTGCAGGCTTCAGGAGGGGACACAAGC**ATGGAGCGG** **CTTTGGGGTCTATTCCAGAGAGCGCAACAACTGTCCCCAAGATCCTCTCAGA** **CCGTCTACCAGCGTGTGGAAGGCCCCCGGAAAGGGCACCTGGAGGAGGAAGA** **GGAAGACGGGGAGGAGGGGGCGGAGACATTGGCCCACTTCTGCCCCATGGAG** **CTGAGGGGCCCTGAGCCCCTGGGCTCTAGACCCAGGCAGCCAAACCTCATTC** **CCTGGGCGGCAGCAGGACGGAGGGCTGCCCCCTACCTG**GTCCTGACGGCCCT GCTGATCTTCACTGGGGCCTTCCTACTGGGCTACGTCGCCTTCCGAGGGTCC TGCCAGGCGTGCGGAGACTCTGTGTTGGTGGTCAGTGAGGATGTCAACTATG AGCCTGACCTGGATTTCCACCAGGGCAGACTCTACTGGAGCGACCTCCAGGC CATGTTCCTGCAGTTCCTGGGGGAGGGGCGCCTGGAGGACACCATCAGGCAA ACCAGCCTTCGGGAACGGGTGGCAGGCTCGGCCGGGATGGCCGCTCTGACTC AGGACATTCGCGCGGCGCTCTCCCGCCAGAAGCTGGACCACGTGTGGACCGA CACGCACTACGTGGGGCTGCAATTCCCGGATCCGGCTCACCCCAACACCCTG CACTGGGTCGATGAGGCCGGGAAGGTCGGAGAGCAGCTGCCGCTGGAGGACC CTGACGTCTACTGCCCCTACAGCGCCATCGGCAACGTCACGGGAGAGCTGGT GTACGCCCACTACGGGCGGCCCGAAGACCTGCAGGACCTGCGGGCCAGGGGC GTGGATCCAGTGGGCCGCCTGCTGCTGGTGCGCGTGGGGGTGATCAGCTTCG CCCAGAAGGTGACCAATGCTCAGGACTTCGGGGCTCAAGGAGTGCTCATATA CCCAGAGCCAGCGGACTTCTCCCAGGACCCACCCAAGCCAAGCCTGTCCAGC CAGCAGGCAGTGTATGGACATGTGCACCTGGGAACTGGAGACCCCTACACAC CTGGCTTCCCTTCCTTCAATCAAACCCAGTTCCCTCCAGTTGCATCATCAGG CCTTCCCAGCATCCCAGCCCAGCCCATCAGTGCAGACATTGCCTCCCGCCTG CTGAGGAAGCTCAAAGGCCCTGTGGCCCCCCAAGAATGGCAGGGGAGCCTCC TAGGCTCCCCTTATCACCTGGGCCCCGGGCCACGACTGCGGCTAGTGGTCAA CAATCACAGGACCTCCACCCCCATCAACAACATCTTCGGCTGCATCGAAGGC CGCTCAGAGCCAGATCACTACGTTGTCATCGGGGCCCAGAGGGATGCATGGG GCCCAGGAGCAGCTAAATCCGCTGTGGGGACGGCTATACTCCTGGAGCTGGT GCGGACCTTTTCCTCCATGGTGAGCAACGGCTTCCGGCCCCGCAGAAGTCTC CTCTTCATCAGCTGGGACGGTGGTGACTTTGGAAGCGTGGGCTCCACGGAGT GGCTAGAGGGCTACCTCAGCGTGCTGCACCTCAAAGCCGTAGTGTACGTGAG CCTGGACAACGCAGTGCTGGGGGATGACAAGTTTCATGCCAAGACCAGCCCC CTTCTGACAAGTCTCATTGAGAGTGTCCTGAAGCAGGTGGATTCTCCCAACC ACAGTGGGCAGACTCTCTATGAACAGGTGGTGTTCACCAATCCCAGCTGGGA TGCTGAGGTGATCCGGCCCCTACCCATGGACAGCAGTGCCTATTCCTTCACG GCCTTTGTGGGAGTCCCTGCCGTCGAGTTCTCCTTTATGGAGGACGACCAGG CCTACCCATTCCTGCACACAAAGGAGGACACTTATGAGAACCTGCATAAGGT GCTGCAAGGCCGCCTGCCCGCCGTGGCCCAGGCCGTGGCCCAGCTCGCAGGG CAGCTCCTCATCCGGCTCAGCCACGATCGCCTGCTGCCCCTCGACTTCGGCC GCTACGGGGACGTCGTCCTCAGGCACATCGGGAACCTCAACGAGTTCTCTGG GGACCTCAAGGCCCGCGGGCTGACCCTGCAGTGGGTGTACTCGGCGCGGGGG GACTACATCCGGGCGGCGGAAAAGCTGCGGCAGGAGATCTACAGCTCGGAGG AGAGAGACGAGCGACTGACACGCATGTACAACGTGCGCATAATGCGGGTGGA GTTCTACTTCCTTTCCCAGTACGTGTCGCCAGCCGACTCCCCGTTCCGCCAC ATCTTCATGGGCCGTGGAGACCACACGCTGGGCGCCCTGCTGGACCACCTGC GGCTGCTGCGCTCCAACAGCTCCGGGACCCCCGGGGCCACCTCCTCCACTGG CTTCCAGGAGAGCCGTTTCCGGCGTCAGCTAGCCCTGCTCACCTGGACGCTG CAAGGGGCAGCCAATGCGCTTAGCGGGGATGTCTGGAACATTGATAACAACT TCTGAGGCCCTGGGGATCCTCACATCCCCGTCCCCCAGTCAAGAGCTCCTCT GCTCCTCGCTTGAATGATTCAGGGTCAGGGAGGTGGCTCAGAGTCCACCTCT

TABLE 3-continued

Exosome Targeting Domain	
Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CATTGCTGATCAATTTCTCATTACCCCTACACATCTCTCCACGGAGCCCAGA CCCCAGCACAGATATCCACACACCCCAGCCCTGCAGTGTAGCTGACCCTAAT GTGACGGTCATACTGTCGGTTAATCAGAGAGTAGCATCCCTTCAATCACAGC CCCTTCCCCTTTCTGGGGTCCTCCATACCTAGAGACCACTCTGGGAGGTTTG CTAGGCCCTGGGACCTGGCCAGCTCTGTTAGTGGGAGAGATCGCTGGCACCA TAGCCTTATGGCCAACAGGTGGTCTGTGGTGAAAGGGGCGTGGAGTTTCAAT ATCAATAAACCACCTGATATCAATAA (SEQ ID NO: 203) >NP_003218.2 transferrin receptor protein 2 isoform 1 [*Homo sapiens*] **MERLWGLFQRAQQLSPRSSQTVYQRVEGPRKGHLEEEEEDGEEGAETLAHFC** **PMELRGPEPLGSRPRQPNLIPWAAAGRRAAPYLVLTALLIFTGAFLLGYVAF** **RGS**CQACGDSVLVVSEDVNYEPDLDFHQGRLYWSDLQAMFLQFLGEGRLEDT IRQTSLRERVAGSAGMAALTQDIRAALSRQKLDHVWTDTHYVGLQFPDPAHP NTLHWVDEAGKVGEQLPLEDPDVYCPYSAIGNVTGELVYAHYGRPEDLQDLR ARGVDPVGRLLLVRVGVISFAQKVTNAQDFGAQGVLIYPEPADFSQDPPKPS LSSQQAVYGHVHLGTGDPYTPGFPSFNQTQFPPVASSGLPSIPAQPISADIA SRLLRKLKGPVAPQEWQGSLLGSPYHLGPGPRLRLVVNNHRTSTPINNIFGC IEGRSEPDHYVVIGAQRDAWGPGAAKSAVGTAILLELVRTFSSMVSNGFRPR RSLLFISWDGGDFGSVGSTEWLEGYLSVLHLKAVVYVSLDNAVLGDDKFHAK TSPLLTSLIESVLKQVDSPNHSGQTLYEQVVFTNPSWDAEVIRPLPMDSSAY SFTAFVGVPAVEFSFMEDDQAYPFLHTKEDTYENLHKVLQGRLPAVAQAVAQ LAGQLLIRLSHDRLLPLDFGRYGDVVLRHIGNLNEFSGDLKARGLTLQWVYS ARGDYIRAAEKLRQEIYSSEERDERLTRMYNVRIMRVEFYFLSQYVSPADSP FRHIFMGRGDHTLGALLDHLRLLRSNSSGTPGATSSTGFQESRFRRQLALLT WTLQGAANALSGDVWNIDNNF (SEQ ID NO: 204)
Human ADAM10	>NM_001110.4 *Homo sapiens* ADAM metallopeptidase domain 10 (ADAM10), transcript variant 1, mRNA GTTGCCGGCCCCTGAAGTGGAGCGAGAGGGAGGTGCTTCGCCGTTTCTCCTG CCAGGGGAGGTCCCGGCTTCCCGTGGAGGCTCCGGACCAAGCCCCTTCAGCT TCTCCCTCCGGATCGATGTGCTGCTGTTAACCCGTGAGGAGGCGGCGGCGGC GGCAGCGGCAGCGGAAGATGGTGTTGCTGAGAGTGTTAATTCTGCTCCTCTC CTGGGCGGCGGGGATGGGAGGTCAGTATGGGAATCCTTTAAATAAATATATC AGACATTATGAAGGATTATCTTACAATGTGGATTCATTACACCAAAAACACC AGCGTGCCAAAAGAGCAGTCTCACATGAAGACCAATTTTTACGTCTAGATTT CCATGCCCATGGAAGACATTTCAACCTACGAATGAAGAGGGACACTTCCCTT TTCAGTGATGAATTTAAAGTAGAAACATCAAATAAAGTACTTGATTATGATA CCTCTCATATTTACACTGGACATATTTATGGTGAAGAAGGAAGTTTTAGCCA TGGGTCTGTTATTGATGGAAGATTTGAAGGATTCATCCAGACTCGTGGTGGC ACATTTTATGTTGAGCCAGCAGAGAGATATATTAAAGACCGAACTCTGCCAT TTCACTCTGTCATTTATCATGAAGATGATATTAACTATCCCCATAAATACGG TCCTCAGGGGGGCTGTGCAGATCATTCAGTATTTGAAAGAATGAGGAAATAC CAGATGACTGGTGTAGAGGAAGTAACACAGATACCTCAAGAAGAACATGCTG CTAATGGTCCAGAACTTCTGAGGAAAAAACGTACAACTTCAGCTGAAAAAAA TACTTGTCAGCTTTATATTCAGACTGATCATTTGTTCTTTAAATATTACGGA ACACGAGAAGCTGTGATTGCCCAGATATCCAGTCATGTTAAAGCGATTGATA CAATTTACCAGACCACAGACTTCTCCGGAATCCGTAACATCAGTTTCATGGT GAAACGCATAAGAATCAATACAACTGCTGATGAGAAGGACCCTACAAATCCT TTCCGTTTCCCAAATATTGGTGTGGAGAAGTTTCTGGAATTGAATTCTGAGC AGAATCATGATGACTACTGTTTGGCCTATGTCTTCACAGACCGAGATTTTGA TGATGGCGTACTTGGTCTGGCTTGGGTTGGAGCACCTTCAGGAAGCTCTGGA GGAATATGTGAAAAAAGTAAACTCTATTCAGATGGTAAGAAGAAGTCCTTAA ACACTGGAATTATTACTGTTCAGAACTATGGGTCTCATGTACCTCCCAAAGT CTCTCACATTACTTTTGCTCACGAAGTTGGACATAACTTTGGATCCCCACAT GATTCTGGAACAGAGTGCACACCAGGAGAATCTAAGAATTTGGGTCAAAAAG AAAATGGCAATTACATCATGTATGCAAGAGCAACATCTGGGGACAAACTTAA CAACAATAAATTCTCACTCTGTAGTATTAGAAATATAAGCCAAGTTCTTGAG AAGAAGAGAAACAACTGTTTTGTTGAATCTGGCCAACCTATT**TGTGGAAATG** **GAATGGTAGAACAAGGTGAAGAATGTGATTGTGGCTATAGTGACCAGTGTAA** **AGATGAATGCTGCTTCGATGCAAATCAACCAGAGGGAAGAAAATGCAAACTG** **AAACCTGGGAAACAGTGCAGTCCAAGTCAAGGTCCTTGTTGTACAGCACAGT** **GTGCATTCAAGTCAAAGTCTGAGAAGTGTCGGGATGATTCAGACTGTGCAAG** **GGAAGGAATATGTAATGGCTTCACAGCTCTCTGCCCAGCATCTGACCCTAAA** **CCAAACTTCACAGACTGTAATAGGCATACACAAGTGTGCATTAATGGGCAAT** **GTGCAGGTTCTATCTGTGAGAAATATGGCTTAGAGGAGTGTACGTGTGCCAG** **TTCTGATGGCAAAGATGATAAAGAATTATGCCATGTATGCTGTATGAAGAAA** **ATGGACCCATCAACTTGTGCCAGTACAGGGTCTGTGCAGTGGAGTAGGCACT** **TCAGTGGTCGAACCATCACCCTGCAACCTGGATCCCCTTGCAACGATTTTAG** **AGGTTACTGTGATGTTTTCATGCGGTGCAGATTAGTAGATGCTGATGGTCCT** **CTAGCTAGGCTTAAAAAAGCAATTTTTAGTCCAGAGCTCTATGAAAACATTG** **CTGAATGGATTGTGGCTCATTGGTGGGCAGTATTACTTATGGGAATTGCTCT** **GATCATGCTAATGGCTGGATTTATTAAGATATGCAGTGTTCATACTCCAAGT** **AGTAATCCAAAGTTGCCTCCTCCTAAACCACTTCCAGGCACTTTAAAGAGGA**

TABLE 3-continued

Exosome Targeting Domain	
Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GGAGACCTCCACAGCCCATTCAGCAACCCCAGCGTCAGCGGCCCCGAGAGAG **TTATCAAATGGGACACATGAGACGCT**AACTGCAGCTTTTGCCTTGGTTCTTC CTAGTGCCTACAATGGGAAAACTTCACTCCAAAGAGAAACCTATTAAGTCAT CATCTCCAAACTAAACCCTCACAAGTAACAGTTGAAGAAAAAATGGCAAGAG ATCATATCCTCAGACCAGGTGGAATTACTTAAATTTTAAAGCCTGAAAATTC CAATTTGGGGGTGGGAGGTGGAAAAGGAACCCAATTTTCTTATGAACAGATA TTTTTAACTTAATGGCACAAAGTCTTAGAATATTATTATGTGCCCCGTGTTC CCTGTTCTTCGTTGCTGCATTTTCTTCACTTGCAGGCAAACTTGGCTCTCAA TAAACTTTTACCACAAATTGAAATAAATATATTTTTTTCAACTGCCAATCAA GGCTAGGAGGCTCGACCACCTCAACATTGGAGACATCACTTGCCAATGTACA TACCTTGTTATATGCAGACATGTATTTCTTACGTACACTGTACTTCTGTGTG CAATTGTAAACAGAAATTGCAATATGGATGTTTCTTTGTATTATAAAATTTT TCCGCTCTTAATTAAAAATTACTGTTTAATTGACATACTCAGGATAACAGAG AATGGTGGTATTCAGTGGTCCAGGATTCTGTAATGCTTTACACAGGCAGTTT TGAAATGAAAATCAATTTACCTTTCTGTTACGATGGAGTTGGTTTTGATACT CATTTTTTCTTTATCACATGGCTGCTACGGGCACAAGTGACTATACTGAAGA ACACAGTTAAGTGTTGTGCAAACTGGACATAGCAGCACATACTACTTCAGAG TTCATGATGTAGATGTCTGGTTTCTGCTTACGTCTTTTAAACTTTCTAATTC AATTCCATTTTTCAATTAATAGGTGAAATTTTATTCATGCTTTGATAGAAAT TATGTCAATGAAATGATTCTTTTTATTTGTAGCCTACTTATTTGTGTTTTTC ATATATCTGAAATATGCTAATTATGTTTTCTGTCTGATATGGAAAAGAAAAG CTGTGTCTTTATCAAAATATTTAAACGGTTTTTTCAGCATATCATCACTGAT CATTGGTAACCACTAAAGATGAGTAATTTGCTTAAGTAGTAGTTAAAATTGT AGATAGGCCTTCTGACATTTTTTTTCCTAAAATTTTTAACAGCATTGAAGGT GAAACAGCACAATGTCCCATTCCAAATTTATTTTTGAAACAGATGTAAATAA TTGGCATTTTAAAGAGAAAGCAAAAACATTTAATGTATTAACAGGCTTATTG CTATGCAGGAAATAGAAGGGGCATTACAAAAATTGAAGCTTGTGACATATTT ATTGCTTCTGTTTTCCAACTACATCACTTCAACTAGAAGTAAAGCTATGATT TTCCTGACTTCACATAGGAGGCAAATTTAGAGAAAGTTGTAAAGATTTCTAT GTTTTGGGTTTTTTTTTTCCTTTTTTTTTTAAGAGTATAAGGTTTACACA ATCATTCTCATAATGTGACGCAAGCCAGCAAGGCCAAAAATGCTAGAGAAAA TAACGGGATCTCTTCCTTGTAAACTTGTACAGTATGTGGTGACTTTTTCAAA ATACAGCTTTTTGTACATGATTTAGAGACAAATTTTGTACATGAAACCCCAG ATAGACTATAAATAATTCTAAACAAACAAGTAGGTAGATATGTATGTAATTG CTTTTAAATCATTTAAATGCCTTTGTTTTTGGACTGTGCAAAGGTTGGAAGT GGGTTTGCATTTCTAAAATGGTGACTTTTATTCTGCAAGAGTTCTTAGTAAC TTCTTGAGTGTGGTAGACTTTGGAACATGTAAATTTTTTGCTTGTAATGTTA TCCTGTGGTAGGATTTTGGCAGGTACACACACTGCCCTATTTTATTTTGAGT CTAAGTTAAATGTTTTCTGAAAAGAGATACATGCACTGAACTCTTTCCACTG CGAATCAAGATGTGGTAATATAAAAGGATCAAGACAAATGAGATCTAATACT ACTGTCAGTTTTAATGTCCACTGTGTTTTATACAGTATCTTTTTTTGTTCAC TTTGGAAATTTTTACTAAAAATTGCAAAAAATAAAGTATTGTGCAAAGATGT AAGGTTTTTTGAAACTTGAAATGCATTAATAAATAGACGATTAAATCAACTT GAAGGTTCTATACTCTTTGAACTCTGAGAACTATCACAAGAAGCTTCCCACA AGGCAGTGTTTTCTTACAGTTGTCTCTTCCTACAAAAGTATAGATTATCTTT ATTCTTAATACTTTGGAATCCATGTAGAAAATTTCCAGTTAGATACTCTGCG TACACACAATAAACCTTTTTAAAACACCCAACTAATCTCAACTGCATTACAT TGTTTCTAATCAATATTCAGTGCTTGTCTTGGTGGAAGAGGTGAGTCATTTT GAAAACTTATGGTCTTGTTTTTATGTGTTTTTCAAAGTTTTGAATGCTAAGT ACCTCATTTATTTTAAAAAGCCTAGTTTAATGATAAGTTTGTTTAAAATTTT GAGCCATCATTTTTCTCTTCATAGCAAATAAGGAGAGAATTGACATTTCAGT GTTACCTAGAAAAGGAATTGTAAGCCCAGAATAATTCCCTGCATGAGGTAAT CTGCTTCAAATTCTTTTTTTAGTCAAGGTTAGCTATAAGTAATACTTGTTAA ATGAGTAAATATGTAATACTTTGTGAATTACTTTGTTAATTTAGGAGCATCA AATGTATATTATGTTTAGTTATTTATGAAACTCTCAATATTGATTGATTTGG GTAATTATAAATTAGTTATTTTTACTTGTAATTGAATGCTTAAATTCTGTTT ACAGTCCGTCCTCTCTCCCTCCATCCCTCCCTCCCCAGTTTTATAAATTCAG GTACCAATTCACAAACAAAATCAGAAATAAAATAAATTTATTGACTGCTTCT GGATTTAGCATTCCCTGTAGTGTCAAGCAATGTCATGCAGTTTGGGGAAGCA TTTATTTAAGGAAATGACAACTTTCTCTGATCAGTCTTGTTTTGTGAGGTGT CTTCAACACTTTATGCTTTGGGTACTTCGTGTTTGTCACAGTCTTAGGATAG TGAAATCTGATTTGTCCAAGCGGAGCAAACTACTCGACCCTCAGTCCTTGTA TTTGTCCCTGTAGTAAGACCTAATTATTATTATTTCTTAAAGATGGGATTGG TGTCCTTGGCAACTATGAAATTTCGGGGCTTGTGCATGAGAAGGCATTTCTT ATTAAGTATTTCTAATTGAAGGTATCAGAGTGTCAAGCATTACAAACCTGGA CAGTTCACCTGGAGGAGTACAAGAAGAGATATTCATTATCCATATTTAAAGG GTCAAGGTTTCCCAAAACCAGGGTGCAAGCCAGATGTAGTTTTAAAGCAGCT GCCAGGGACAGTTCATCTTTAGAGAAGTCACTAAAGTTGTAAGAAATTTTAG TTTCCCCAAAACCACTTTCAACTTCTTAGAAACTAGAAAGACAATTGGTTTG CCCCACAGAGGACAACTTCAGTTTCAGCATCTCTCATGTTGTGTTCTTGATT AAAAACAACTTCCATTTGATATACTTTTCCGTTTATTACCAGTTTAGTTTTT TCACTATTGTTTCTGTATTCAACTCTTTATATGATTAGGATAGAAATTTAGC CCTTCTGTTTTATATTACTATATTGTTTGTGTGTCTTAGATATATACATGTA TGTACTATTTTCAGTAGAAATTCATGTATTTTATAATTGGTAAGTTCTTCAG

TABLE 3-continued

Exosome Targeting Domain	
Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	AGCATCTCTTCTATAAAAAGCAACAGGATGCTAGGTAAAACGGAGCATTGAG CAAAATACTGATTAGTTTTTGCTTTTTCCTGAAATCTACACTAAAGTGATAG GGTGTGGGGTAATCCAACAAGGACAAGGTGAATTGAACAAGAACGAAATCTG GAAGCAGATGAAGGAGTACTATTGATTGGGCAGACCCAGGGAAGTCAAATCC TAAACCAGCAGTGGGAACACAACAGAATGGTGTAGTTTGCACTGGTAAGATT TGGGTACCTGGCAGGGCTGGGTGCGGTGGCTCACACCTGTAATCCCAGCACT TTGGGAGGCCAAGGCGGGTGGATCACTTGAGGTCAGGAGTTCGAGACCACCC TGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAGCTGGGCGTGGTG GCACATGCTTGTAATCCCAGCTACTCGGGAGGCAGAGGCAGGAGATTTGCTT GAACCCGGGAGGCAGAGGCAGGAGATTTGCTTGAACCCAGGAGGCAGAGGCT GCAGTGAGCCGCGATTGCGCCATTGCACTCCAGCCTGGGTGACAGAGCGAGA CTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAATTTGAGTACCTGGCCTTTGTTACTTTTTTTCTATGTGTGTGACAAAA ACATAATATGCACACTTTTGTAACCCACCTTTCTCATTTAATGGTACATTGA TAATGTATATCACATTAACTACTCTAAATATTTCTGTGGATGTATGTTTTTT TTTTTCTTAACCAATTTCCCATTGTTTGGACATGTAGGTTCCACATTGTTTA TTATTTTAAACAATTCTAAAGAATTTTAAACAATTCTTAGGAAAATCCTCAG CCTAATAATGAAATTAATTCCTAAAAGTGGAATTGTTGGGGTAAAGGTTTTT TGAGGGACATTGATAAAAATTATGGTACTGTCTCCCAGATAGATGTACCAAG TTATACTACCACGATTTAATATATATATATATATATATTAAATCAGAGTCCC ATCCTTAGAAATCCACATATATGCAGCCACATGAATGTATTAGAAACAATAA TAGAAGACTCATGCTTAATTCAGTTGATTAGCTTTAGACATAATTCAAATGC AAGTCAAATTGAGTGCCCTAATTGTGGTCTCTTAAGTACCATTTTTCTTCAA GGGAACCAGACTCCTTTGGATAAATCACTAATTCCACCTGTAAGAAAGAAAT GTACAAGAAGAACCTAGGAAACATTGTTTTGTACCAGATCAGAAAGATTCAG GAGGCACCTTAGAAGTTACCACTGGCCAAGGCTGAGATAACTTTAGCATCAG CAAGGATAATATCTGCAAGAGATTGAAACTCATAGTATTGTATTTAACTCTG TGAGTTAATGATGGTAGTGGACAGAATTATAGTTACCTTTGGGATACGCTTT TAAAGAAATTCCAGGTAATAAGAGAAATGATAGAATTAGGATATCACCATTT TACCCCCCCAACAATTTATGGATCTAGACAATAATCGCCAGTGACTGCTAAC CTCACAAAGTGAGAGCAATCAGATTTTGTGCCTCCTAATGGAAGTACATATA CCACCTATGAAGCAGTTCTGCCAAAAGTCACATCTCATCATGATGAAGCCTC CTGATCTAACTACCCCTTCATTAGAAATACAGGGGACAGAGGGACAAATAAT ATACAAGGGACTCAATCAGCAAAATCCAGACTCTGGAAAACTACAAGACATA TGGTCCTGCTTCAACAACAGAAATGCAAAGAGAAAAGACAACGATGGGTTAA AGGAGACTTAAGAGCTACATCTATCAAGACAATTTATGGACTTATTTGGATA CTGATTTGAACAAACTGTTGAGACCATTGGAAAAATGTGAAAAGTGGATATT TGATATTAAGGTTTTTAATTATTTTTAGGTGTGATAATGGTATTGTTACATT TTTTAAAGGACCCCTTTTAGAGATGCAAATTGAAACACTTAAAAAATGAAAT GATACGATGTATAAGTTTTTGCTTAAAAATAAGGATTGAAGTTGGCTGGTGT GTGTGGATATAGTTGAAACAAGATTGGCTGTGAGTTGATAATTATTGAAGCT GGGTGATGGGCACTTGGGGATTTATTATACTATTTTCTCTACCTGTGTTTAT ATTTGAAATTTTTCATAGAAGTTTTAAAATGTGGCCAGTTGTGATGGCTCAT ACCTGTAATCCCAACACTTTGGGAGGCCAAGGTGGGAGGATCACTTGAGCTC AGGAGTTAGAGACCAGCCTGGGCAAAATAGTGAGACTCCATCTCAAAGAAAA AAAAAAAGTGTTTTAAATGTGAATCAAATTCCTATAGAAGCTGATTCATTAC TGTTTTTATTTTAGCAGTAATTCATGATAATGACCTGTATTCATAATGATTT TCATAATGATTGTTTTAGTGGAATTAAACTTGAACCAGTCAAGCTAACATAA TTATATTCTGCTCCAGTTACAATGAATAATTAATTGATTTCAACTGCTAGGG TGAACTCTTGAAGCTATCAGTCATCCAGCAATCTTAGCAAGCAGGCCATTGG GTCCCTGTTTGCTCTGTCTCTCTCTCTCTCTCTCACTGTTGAAGGGCTTAGC TAACTACTTAAGTAAAATATTTGTTCTCTGTTAAACATGTCAAGGAGTATGG TCAGCTTATCCACATTAAGCCTGTGTGTCCCACGTTGGAGTAAATGTTAAGT AGCTCACTACAATAAACTAGATTCTTCTGCCCTCTCTTGTTTAAATGATCAT GTTCCCTGGAGGTGGAAATAGATCTTTAAAAAGATATTCTGTAGTTGTTTGT TCTCAGTGTAAAAAAATGAGAATAATTTGATAAGAGTGTAGGTTGTCTTATA TAAAAAGTGGTTCCATTTGCATGAATTTTAGAAAAATCATTTTGGAAAAATG AAGGCTATGTGGTTATACTGAACACATTAAGCAATTTTATTCTTTATTTTAA ATGAATATTTTATTATCGTTTTCTTCCCTTGCCCTTTGGGTATGGGAGTTAG CCTTTGTGTTTCTAAATACAACAGGCCGGTTTTTATAAATTAAGGTGTCAAT ATATTCTTCATTATTTAGTTTTGTGATTGTGGTTAGTTTTCATTTTTCTTAA GTATCTGCTAGTAGCATCTGTAATTAAGTGAAGTGACCTGTTAACCATTTTC CTCTTTCTCCTCCTTTCCTCCTCCTTGAAACATATCAGAGCATGTTTGAAAT TCTTTGGCTTTTATGGTATGCATTTGCTGATATGCATTGACCAGTTACCTTA CTCACAGATACTTCTTAGGCACTTGATTGTGCCAGGGCCTTGGCTAGATGAT AAGAATACAGTAGTGAACTTAACAGTTTCCCTGCCCTGGTGAAGCGTATGGT CTTGTAGGTGAGATAGATATCAGATAATCATGTGAATAAATGTACAATTCCA GCTGTGATACATGCTGAGGAGGAGGTTTTTGGTGATCCAAGAGCTGATCATG CAGAGATAGGACTGAGAAAGGAGGGTGGGACGTTGTCACAGCTGATAATGCA GAGATAGGACTGAGAAAGGAGGGTGGGACATCAGGAAGGTCAGAGAATTCCT TATGAAAGTGATGCTTGAGTCAAAATATGATGGATGAAGAGAGTTTAAATAG ATTACATAGAATTTTTAATAATGTCGATTGGTTATATACTGGGCACTGATAG CTGATTTTTCTTTGGGGAAAGGTATGTCAGCCTAGTCATTCAGATTCCTTTA TTTTTTTAAATGTTTTTTCATTTTTTGCTTTGCATTGCATTCATTTGCTGAA

TABLE 3-continued

Exosome Targeting Domain	
Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GAGCTGGCTTGTACTTTGGCAGGTGTCATACTTGGTTATTCTCCTTAGGATA TTGGCCCAACAATCTGGGAGTTGTGAAAGGCGCTTCGCTTTTCAGACCTGGG CGTCTGTATCATGACTATCATAAATTTAGGATTAAGACACCTAGCCTCCTAC CAGGATGAATGAGGTGTCCATGTGACCTGCTGTGCCCTGGAATTTTATACAT CTTTCTCTCATAGCACACACCATATTACAATATAATCCTGCCTCATCTAAGC CAAACTTTCGAGAGAATCATTTACACTCAGTGGCTACTTCAGCTCCCATTCA CTTATCAACCTGCTGCAATTTTTCACAGCCCCCAAAGGACTGCAGTCTGTGC CTTCAGGGAGCTGAGGGTCTAGCGGAAGGAAAGAAACCAGCAGTTACAGTAC AGAGGGGTTTGTGTTGGAAACTCTACAAACACAGGATGCCCTGGTAGCTCAG AGGAAGTGCATATCGAGCATGGTAGGTAGGTAGTGGGAAGAGCCAAGATGAC TTCCCAGAGGAGAAAAGCTGGACCTGAGTTTTGGAGTTTCGGTAAAAGTTTG CTCTAACTAGTCCAAGCTGCTGTCACAAGCTTTTAGAAATGATGTAACCATG GGGCAGTTGACTGTCGTCATGTTCTTTGCTATTTTCATGACTCTGGATGTGC TTTTCCTATTCCCTGGATTGCCCTTTCCCTCGATTCCTCTGCAGGACTGGGC TTTATTAATCTCCATTTCCTTGAGCTTGGCTATAGTAGGTGTTCAATAAACA TTTGTTTTGTTGTGTGCTTTGTAAATAGGCAATGAAGCTGATTTCACAAGAT AGGCACAAAAGTTAGTTTCATTACAACACATTACCAACAGCTGTATTTTTAA CTTTTAACATATCTCATTCTAAATCCTGTGGCAGCACAACCTCCTTCCGTCA TACCTGGAGATAAATTTTCTTTCAAAATCTAATATGCACTGTATTTATAGAA TATGAAACATACCGACCATGTTTTGCAAAAATGGGAAAGGCATAACTTAGCT TTGGGGCATGTAAGTAACAACTCCTGATAGGAGAAGAAATGTATTCAGAAAG CTCAAATTAGAAATAAAATGGGAGACTCTA (SEQ ID NO: 205) >NP_001101.1 disintegrin and metalloproteinase domain-containing protein 10 isoform 1 preproprotein [*Homo sapiens*] MVLLRVLILLLSWAAGMGGQYGNPLNKYIRHYEGLSYNVDSLHQKHQRAKRA VSHEDQFLRLDFHAHGRHFNLRMKRDTSLFSDEFKVETSNKVLDYDTSHIYT GHIYGEEGSFSHGSVIDGRFEGFIQTRGGTFYVEPAERYIKDRTLPFHSVIY HEDDINYPHKYGPQGGCADHSVFERMRKYQMTGVEEVTQIPQEEHAANGPEL LRKKRTTSAEKNTCQLYIQTDHLFFKYYGTREAVIAQISSHVKAIDTIYQTT DFSGIRNISFMVKRIRINTTADEKDPTNPFRFPNIGVEKFLELNSEQNHDDY CLAYVFTDRDFDDGVLGLAWVGAPSGSSGGICEKSKLYSDGKKKSLNTGIIT VQNYGSHVPPKVSHITFAHEVGHNFGSPHDSGTECTPGESKNLGQKENGNYI MYARATSGDKLNNNKFSLCSIRNISQVLEKKRNNCFVESGQPI**CGNGMVEQG** **EECDCGYSDQCKDECCFDANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSK** **SEKCRDDSDCAREGICNGFTALCPASDPKPNFTDCNRHTQVCINGQCAGSIC** **EKYGLEECTCASSDGKDDKELCHVCCMKKMDPSTCASTGSVQWSRHFSGRTI** **TLQPGSPCNDFRGYCDVFMRCRLVDADGPLARLKKAIFSPELYENIAEWIVA** **HWWAVLLMGIALIMLMAGFIKICSVHTPSSNPKLPPPKPLPGTLKRRRPPQP** **IQQPQRQRPRESYQMGHMRR** (SEQ ID NO: 206)
Transmembrane domain 2 or transmembrane domain 3 from Human CD9	>NM_001769.4 *Homo sapiens* CD9 molecule (CD9), transcript variant 1, mRNA AGCCGCCTGCATCTGTATCCAGCGCCAGGTCCCGCCAGTCCCAGCTGCGCGC GCCCCCCAGTCCCGCACCCGTTCGGCCCAGGCTAAGTTAGCCCTCACCATGC CGGTCAAAGGAGGCACCAAGTGCATCAAATACCTGCTGTTCGGATTTAACTT CATCTTCTGGCTTGCCGGGATTGCTGTCCTTGCCATTGGACTATGGCTCCGA TTCGACTCTCAGACCAAGAGCATCTTCGAGCAAGAAACTAATAATAATAATT CCAGC**TTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATGAT** **GCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGC**ATG CTGGGACTGTTCTTCGGCTTCCTCTTGGTGATATTCGCCATTGAAATAGCTG CGGCCATCTGGGGATATTCCCACAAGGATGAGGTGATTAAGGAAGTCCAGGA GTTTTACAAGGACACCTACAACAAGCTGAAAACCAAGGATGAGCCCCAGCGG GAAACGCTGAAAGCCATCCACTATGCGTTGAACTGCTGTGGTTTGGCTGGGG GCGTGGAACAGTTTATCTCAGACATCTGCCCCAAGAAGGACGTACTCGAAAC CTTCACCGTGAAGTCCTGTCCTGATGCCATCAAAGAGGTCTTCGACAATAAA TTCCACATCATCGGCGCAGTGGGCATCGGCATTGCCGTGGTCATGATATTTG GCATGATCTTCAGTATGATCTTGTGCTGTGCTATCCGCAGGAACCGCGAGAT GGTCTAGAGTCAGCTTACATCCCTGAGCAGGAAAGTTTACCCATGAAGATTG GTGGGATTTTTTGTTTGTTTGTTTTGTTTTGTTTGTTGTTTGTTGTTTGTTT TTTTGCCACTAATTTTAGTATTCATTCTGCATTGCTAGATAAAAGCTGAAGT TACTTTATGTTTGTCTTTTAATGCTTCATTCAATATTGACATTTGTAGTTGA GCGGGGGGTTTGGTTTGCTTTGGTTTATATTTTTTCAGTTGTTTGTTTTTGC TTGTTATATTAAGCAGAAATCCTGCAATGAAAGGTACTATATTTGCTAGACT CTAGACAAGATATTGTACATAAAAGAATTTTTTTGTCTTTAAATAGATACAA ATGTCTATCAACTTTAATCAAGTTGTAACTTATATTGAAGACAATTTGATAC ATAATAAAAAATTATGACAATGTCCTGGA (SEQ ID NO: 207) >NP_001760.1 CD9 antigen isoform 1 [*Homo sapiens*] MPVKGGTKCIKYLLFGFNFIFWLAGIAVLAIGLWLRFDSQTKSIFEQETNNN NSS**FYTGVYILIGAGALMMLVGFLGCCGAVQESQC**MLGLFFGFLLVIFAIEI AAAIWGYSHKDEVIKEVQEFYKDTYNKLKTKDEPQRETLKAIHYALNCCGLA GGVEQFISDICPKKDVLETFTVKSCPDAIKEVFDNKFHIIGAVGIGIAVVMI FGMIFSMILCCAIRRNREMV (SEQ ID NO: 208)

TABLE 3-continued

Exosome Targeting Domain

Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
Human CD298	>NM_001679.4 *Homo sapiens* ATPase Na+/K+ transporting subunit beta 3 (ATP1B3), mRNA AGTCGGCTCGAGTACTCCCCGTAACGAGGAGGTGTTCTCGGCCGTCCCACCC TTCACTGCCGTCTCCGGGCTGCGCCGCCGGAGCCGGGACGCGCCTCCGCAGC CCTCGCCGCCTCCATCCCCGCGGCCGCAGCTCCTCTCGCCGTCCGCGCGCAC ACCATGACGAAGAACGAGAAGAAGTCCCTCAACCAGAGCCTGGCCGAGTGGA AGCTCTTCATCTACAACCCGACCACCGGAGAATTCCTGGGGCGCACCGCCAA GAGCTGGGGTTTGATCTTGCTCTTCTACCTAGTTTTTTATGGGTTCCTGGCT GCACTCTTCTCATTCACGATGTGGGTTATGCTTCAGACTCTCAACGATGAGG TTCCAAAATACCGTGACCAGATTCCTAGCCCAGGACTCATGGTTTTTCCAAA ACCAGTGACCGCATTGGAATATACATTCAGTAGGTCTGATCCAACTTCGTAT GCAGGGTACATTGAAGACCTTAAGAAGTTTCTAAAACCATATACTTTAGAAG AACAGAAGAACCTCACAGTCTGTCCTGATGGAGCACTTTTTGAACAGAAGGG TCCAGTTTATGTTGCATGTCAGTTTCCTATTTCATTACTTCAAGCATGCAGT GGTATGAATGATCCTGATTTTGGCTATTCTCAAGGAAACCCTTGTATTCTTG TGAAAATGAACAGAATAATTGGATTAAAGCCTGAAGGAGTGCCAAGGATAGA TTGTGTTTCAAAGAATGAAGATATACCAAATGTAGCAGTTTATCCTCATAAT GGAATGATAGACTTAAAATATTTCCCATATTATGGGAAAAAACTGCATGTTG GGTATCTACAGCCATTGGTTGCTGTTCAGGTCAGCTTTGCTCCTAACAACAC TGGGAAAGAAGTAACAGTTGAGTGCAAGATTGATGGATCAGCCAACCTAAAA AGTCAGGATGATCGTGACAAGTTTTTGGGACGAGTTATGTTCAAAATCACAG CACGTGCATAGTATGAGTAGGATATCTCCACAGAGTAAATGTTGTGTTGTCT GTCTTCATTTTGTAACAGCTGGACCTTCCATTCTAGAATTATGAGACCACCT TGGAGAAAGGTGTGTGGTACATGACATTGGGTTACATCATAACGTGCTTCCA GATCATAGTGTTCAGTGTCCTCTGAAGTAACTGCCTGTTGCCTCTGCTGCCC TTTGAACCAGTGTACAGTCGCCAGATAGGGACCGGTGAACACCTGATTCCAA ACATGTAGGATGGGGGTCTTGTCCTCTTTTTATGTGGTTTAATTGCCAAGTG TCTAAAGCTTAATATGCCGTGCTATGTAAATATTTTATGGATATAACAACTG TCATATTTTGATGTCAACAGAGTTTTAGGGATAAAATGGTACCCGGCCAACA TCAAGTGACTTTATAGCTGCAAGAAATGTGGTATGTGGAGAAGTTCTGTATG TGAGGAAGGAAAAAAAGAAAATAAAAGTGTGTTTGAAAAATATTATCTTGGG TTCTTTGTAAAATTTATTTTTTACATGCTGAATTAGCCTCGATCTTTTTGAT TAAGAGCACAAACTTTTTTTTGTAAAACATGTAAAAAAAAAAACTGGGATTA ATTTTTAGTGTTGGAACTGCCTCTTATTTTAGGCTGTAGATAAAATAGCATT TTTAGGTTAGCCAGTGTGACTATGCACCTAATTTTTTATGAGATTAAATTCA TAAGACTTAATTTGTACAATAGTTTGTGAAATATCTTGTTACTGCTTTTATT TAGCAGACTGTGGACTGTAATAAAGTATATAAATTGTGAAATATAAAAACTT GGAACTTATTCAAAGCTTCAAAGCAAA (SEQ ID NO: 209) >NP_001670.1 sodium/potassium-transporting ATPase subunit beta-3 [*Homo sapiens*] MTKNEKKSLNQSLAEWKLFIYNPTTGEFLGRTAKSWGLILLFYLVFYGFLAA LFSFTMWVMLQTLNDEVPKYRDQIPSPGLMVFPKPVTALEYTFSRSDPTSYA GYIEDLKKFLKPYTLEEQKNLTVCPDGALFEQKGPVYVACQFPISLLQACSG MNDPDFGYSQGNPCILVKMNRIIGLKPEGVPRIDCVSKNEDIPNVAVYPHNG MIDLKYFPYYGKKLHVGYLQPLVAVQVSFAPNNTGKEVTVECKIDGSANLKS QDDRDKFLGRVMFKITARA (SEQ ID NO: 210)
Lipid affinity tag modified from Human KRAS	>NM_004985.5 *Homo sapiens* KRAS proto-oncogene, GTPase (KRAS), transcript variant b, mRNA CTAGGCGGCGGCCGCGGCGGCGGAGGCAGCAGCGGCGGCGGCAGTGGCGGCG GCGAAGGTGGCGGCGGCTCGGCCAGTACTCCCGGCCCCCGCCATTTCGGACT GGGAGCGAGCGCGGCGCAGGCACTGAAGGCGGCGGCGGGGCCAGAGGCTCAG CGGCTCCCAGGTGCGGGAGAGAGGCCTGCTGAAAATGACTGAATATAAACTT GTGGTAGTTGGAGCTGGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAA TTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGATTCCTACAG GAAGCAAGTAGTAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGACACA GCAGGTCAAGAGGAGTACAGTGCAATGAGGGACCAGTACATGAGGACTGGGG AGGGCTTTCTTTGTGTATTTGCCATAAATAATACTAAATCATTTGAAGATAT TCACCATTATAGAGAACAAATTAAAAGAGTTAAGGACTCTGAAGATGTACCT ATGGTCCTAGTAGGAAATAAATGTGATTTGCCTTCTAGAACAGTAGACACAA AACAGGCTCAGGACTTAGCAAGAAGTTATGGAATTCCTTTTATTGAAACATC AGCAAAGACAAGACAGGGTGTTGATGATGCCTTCTATACATTAGTTCGAGAA ATTCGAAAACATAAAGAAAAGATGAGCAAAGATGGT**AAAAAGAAGAAAAAGA** **AGTCAAAGACAAAGTGTGTAATTATG**TAAATACAATTTGTACTTTTTTCTTA AGGCATACTAGTACAAGTGGTAATTTTTGTACATTACACTAAATTATTAGCA TTTGTTTTAGCATTACCTAATTTTTTTCCTGCTCCATGCAGACTGTTAGCTT TTACCTTAAATGCTTATTTTAAAATGACAGTGGAAGTTTTTTTTTCCTCTAA GTGCCAGTATTCCCAGAGTTTTGGTTTTTGAACTAGCAATGCCTGTGAAAAA GAAACTGAATACCTAAGATTTCTGTCTTGGGGCTTTTGGTGCATGCAGTTGA TTACTTCTTATTTTTCTTACCAATTGTGAATGTTGGTGTGAAACAAATTAAT GAAGCTTTTGAATCATCCCTATTCTGTGTTTTATCTAGTCACATAAATGGAT TAATTACTAATTTCAGTTGAGACCTTCTAATTGGTTTTTACTGAAACATTGA GGGAACACAAATTTATGGGCTTCCTGATGATGATTCTTCTAGGCATCATGTC CTATAGTTTGTCATCCCTGATGAATGTAAAGTTACACTGTTCACAAAGGTTT

TABLE 3-continued

Exosome Targeting Domain	
Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TGTCTCCTTTCCACTGCTATTAGTCATGGTCACTCTCCCCAAAATATTATAT TTTTTCTATAAAAAGAAAAAAATGGAAAAAAATTACAAGGCAATGGAAACTA TTATAAGGCCATTTCCTTTTCACATTAGATAAATTACTATAAAGACTCCTAA TAGCTTTTCCTGTTAAGGCAGACCCAGTATGAAATGGGGATTATTATAGCAA CCATTTTGGGGCTATATTTACATGCTACTAAATTTTTATAATAATTGAAAAG ATTTTAACAAGTATAAAAAATTCTCATAGGAATTAAATGTAGTCTCCCTGTG TCAGACTGCTCTTTCATAGTATAACTTTAAATCTTTTCTTCAACTTGAGTCT TTGAAGATAGTTTTAATTCTGCTTGTGACATTAAAAGATTATTTGGGCCAGT TATAGCTTATTAGGTGTTGAAGAGACCAAGGTTGCAAGGCCAGGCCCTGTGT GAACCTTTGAGCTTTCATAGAGAGTTTCACAGCATGGACTGTGTCCCCACGG TCATCCAGTGTTGTCATGCATTGGTTAGTCAAAATGGGGAGGGACTAGGGCA GTTTGGATAGCTCAACAAGATACAATCTCACTCTGTGGTGGTCCTGCTGACA AATCAAGAGCATTGCTTTTGTTTCTTAAGAAAACAAACTCTTTTTTAAAAAT TACTTTTAAATATTAACTCAAAAGTTGAGATTTTGGGGTGGTGGTGTGCCAA GACATTAATTTTTTTTTTAAACAATGAAGTGAAAAAGTTTTACAATCTCTAG GTTTGGCTAGTTCTCTTAACACTGGTTAAATTAACATTGCATAAACACTTTT CAAGTCTGATCCATATTTAATAATGCTTTAAAATAAAAATAAAAACAATCCT TTTGATAAATTTAAAATGTTACTTATTTTAAAATAAATGAAGTGAGATGGCA TGGTGAGGTGAAAGTATCACTGGACTAGGAAGAAGGTGACTTAGGTTCTAGA TAGGTGTCTTTTAGGACTCTGATTTTGAGGACATCACTTACTATCCATTTCT TCATGTTAAAAGAAGTCATCTCAAACTCTTAGTTTTTTTTTTTTACAACTAT GTAATTTATATTCCATTTACATAAGGATACACTTATTTGTCAAGCTCAGCAC AATCTGTAAATTTTTAACCTATGTTACACCATCTTCAGTGCCAGTCTTGGGC AAAATTGTGCAAGAGGTGAAGTTTATATTTGAATATCCATTCTCGTTTTAGG ACTCTTCTTCCATATTAGTGTCATCTTGCCTCCCTACCTTCCACATGCCCCA TGACTTGATGCAGTTTTAATACTTGTAATTCCCCTAACCATAAGATTTACTG CTGCTGTGGATATCTCCATGAAGTTTTCCCACTGAGTCACATCAGAAATGCC CTACATCTTATTTCCTCAGGGCTCAAGAGAATCTGACAGATACCATAAAGGG ATTTGACCTAATCACTAATTTTCAGGTGGTGGCTGATGCTTTGAACATCTCT TTGCTGCCCAATCCATTAGCGACAGTAGGATTTTTCAAACCTGGTATGAATA GACAGAACCCTATCCAGTGGAAGGAGAATTTAATAAAGATAGTGCTGAAAGA ATTCCTTAGGTAATCTATAACTAGGACTACTCCTGGTAACAGTAATACATTC CATTGTTTTAGTAACCAGAAATCTTCATGCAATGAAAAATACTTTAATTCAT GAAGCTTACTTTTTTTTTTTGGTGTCAGAGTCTCGCTCTTGTCACCCAGGCT GGAATGCAGTGGCGCCATCTCAGCTCACTGCAACCTCCATCTCCCAGGTTCA AGCGATTCTCGTGCCTCGGCCTCCTGAGTAGCTGGGATTACAGGCGTGTGCC ACTACACTCAACTAATTTTTGTATTTTTAGGAGAGACGGGGTTTCACCCTGT TGGCCAGGCTGGTCTCGAACTCCTGACCTCAAGTGATTCACCCACCTTGGCC TCATAAACCTGTTTTGCAGAACTCATTTATTCAGCAAATATTTATTGAGTGC CTACCAGATGCCAGTCACCACACAAGGCACTGGGTATATGGTATCCCCAAAC AAGAGACATAATCCCGGTCCTTAGGTAGTGCTAGTGTGGTCTGTAATATCTT ACTAAGGCCTTTGGTATACGACCCAGAGATAACACGATGCGTATTTTAGTTT TGCAAAGAAGGGGTTTGGTCTCTGTGCCAGCTCTATAATTGTTTTGCTACGA TTCCACTGAAACTCTTCGATCAAGCTACTTTATGTAAATCACTTCATTGTTT TAAAGGAATAAACTTGATTATATTGTTTTTTTATTTGGCATAACTGTGATTC TTTTAGGACAATTACTGTACACATTAAGGTGTATGTCAGATATTCATATTGA CCCAAATGTGTAATATTCCAGTTTTCTCTGCATAAGTAATTAAAATATACTT AAAAATTAATAGTTTTATCTGGGTACAAATAAACAGGTGCCTGAACTAGTTC ACAGACAAGGAAACTTCTATGTAAAAATCACTATGATTTCTGAATTGCTATG TGAAACTACAGATCTTTGGAACACTGTTTAGGTAGGGTGTTAAGACTTACAC AGTACCTCGTTTCTACACAGAGAAAGAAATGGCCATACTTCAGGAACTGCAG TGCTTATGAGGGGATATTTAGGCCTCTTGAATTTTTGATGTAGATGGGCATT TTTTTAAGGTAGTGGTTAATTACCTTTATGTGAACTTTGAATGGTTTAACAA AAGATTTGTTTTTGTAGAGATTTTAAAGGGGGAGAATTCTAGAAATAAATGT TACCTAATTATTACAGCCTTAAAGACAAAAATCCTTGTTGAAGTTTTTTTAA AAAAAGCTAAATTACATAGACTTAGGCATTAACATGTTTGTGGAAGAATATA GCAGACGTATATTGTATCATTTGAGTGAATGTTCCCAAGTAGGCATTCTAGG CTCTATTTAACTGAGTCACACTGCATAGGAATTTAGAACCTAACTTTTATAG GTTATCAAAACTGTTGTCACCATTGCACAATTTTGTCCTAATATATACATAG AAACTTTGTGGGGCATGTTAAGTTACAGTTTGCACAAGTTCATCTCATTTGT ATTCCATTGATTTTTTTTTTCTTCTAAACATTTTTTCTTCAAACAGTATATA ACTTTTTTTAGGGGATTTTTTTTTAGACAGCAAAAACTATCTGAAGATTTCC ATTTGTCAAAAAGTAATGATTTCTTGATAATTGTGTAGTAATGTTTTTTAGA ACCCAGCAGTTACCTTAAAGCTGAATTTATATTTAGTAACTTCTGTGTTAAT ACTGGATAGCATGAATTCTGCATTGAGAAACTGAATAGCTGTCATAAAATGA AACTTTCTTTCTAAAGAAAGATACTCACATGAGTTCTTGAAGAATAGTCATA ACTAGATTAAGATCTGTGTTTTAGTTTAATAGTTTGAAGTGCCTGTTTGGGA TAATGATAGGTAATTTAGATGAATTTAGGGGAAAAAAAAGTTATCTGCAGAT ATGTTGAGGGCCCATCTCTCCCCCCACACCCCCACAGAGCTAACTGGGTTAC AGTGTTTTATCCGAAAGTTTCCAATTCCACTGTCTTGTGTTTTCATGTTGAA AATACTTTTGCATTTTTCCTTTGAGTGCCAATTTCTTACTAGTACTATTTCT TAATGTAACATGTTTACCTGGAATGTATTTTAACTATTTTTGTATAGTGTAA ACTGAAACATGCACATTTTGTACATTGTGCTTTCTTTTGTGGGACATATGCA GTGTGATCCAGTTGTTTTCCATCATTTGGTTGCGCTGACCTAGGAATGTTGG

TABLE 3-continued

Exosome Targeting Domain

Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TCATATCAAACATTAAAAATGACCACTCTTTTAATTGAAATTAACTTTTAAA TGTTTATAGGAGTATGTGCTGTGAAGTGATCTAAAATTTGTAATATTTTTGT CATGAACTGTACTACTCCTAATTATTGTAATGTAATAAAAATAGTTACAGTG AC (SEQ ID NO: 211) >NP_004976.2 GTPase KRas isoform b [*Homo sapiens*] MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCL LDILDTAGQEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVK DSEDVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSAKTRQGVDDAF YTLVREIRKHKEKMSKDG**KKKKKKSKTKCVIM** (SEQ ID NO: 212) >Lipid affinity tag nucleotide sequence AAAAAGAAGAAAAAGAAGAAGAAGACAAAGTGTGTAATTATG (SEQ ID NO: 213) >Lipid affinity tag peptide sequence KKKKKKKKTKCVIM (SEQ ID NO: 214)
Myr/Palm tag modified from Human MARCKS	>NM_002356.7 *Homo sapiens* myristoylated alanine rich protein kinase C substrate (MARCKS), mRNA GCACTTGGGCGTTGGACCCCGCATCTTATTAGCAACCAGGGAGATTTCTCCA TTTTCCTCTTGTCTACAGTGCGGCTACAAATCTGGGATTTTTTTATTACTTC TTTTTTTTTCGAACTACACTTGGGCTCCTTTTTTTGTGCTCGACTTTTCCAC CCTTTTTCCCTCCCTCCTGTGCTGCTGCTTTTTGATCTCTTCGACTAAAATT TTTTTATCCGGAGTGTATTTAATCGGTTCTGTTCTGTCCTCTCCACCACCCC CACCCCCCTCCCTCCGGTGTGTGTGCCGCTGCCGCTGTTGCCGCCGCCGCTG CTGCTGCTGCTCGCCCCGTCGTTACACCAACCCGAGGCTCTTTGTTTCCCCT CTTGGATCTGTTGAGTTTCTTTGTTGAAGAAGCCAGC**ATGGGTGCCCAGTTC** **TCCAAGACC**GCAGCGAAGGGAGAAGCCGCCGCGGAGAGGCCTGGGGAGGCGG CTGTGGCCTCGTCGCCTTCCAAAGCGAACGGACAGGAGAATGGCCACGTGAA GGTAAACGGCGACGCTTCGCCCGCGGCCGCCGAGTCGGGCGCCAAGGAGGAG CTGCAGGCCAACGGCAGCGCCCCGGCCGCCGACAAGGAGGAGCCCGCGGCCG CCGGGAGCGGGGCGGCGTCGCCCTCCGCGGCCGAGAAAGGTGAGCCGGCCGC CGCCGCTGCCCCCGAGGCCGGGGCCAGCCCGGTAGAGAAGGAGGCCCCCGCG GAAGGCGAGGCTGCCGAGCCCGGCTCGCCCACGGCCGCGGAGGGAGAGGCCG CGTCGGCCGCCTCCTCGACTTCTTCGCCCAAGGCCGAGGACGGGGCCACGCC CTCGCCCAGCAACGAGACCCCGAAAAAAAAAAAAGAAGCGCTTTTCCTTCAAG AAGTCTTTCAAGCTGAGCGGCTTCTCCTTCAAGAAGAACAAGAAGGAGGCTG GAGAAGGCGGTGAGGCTGAGGCGCCCGCTGCCGAAGGCGGCAAGGACGAGGC CGCCGGGGGCGCAGCTGCGGCCGCCGCCGAGGCGGGCGCGGCCTCCGGGGAG CAGGCAGCGGCGCCGGGCGAGGAGGCGGCAGCGGGCGAGGAGGGGGCGGCGG GTGGCGACCCGCAGGAGGCCAAGCCCCAGGAGGCCGCTGTCGCGCCAGAGAA GCCGCCCGCCAGCGACGAGACCAAGGCCGCCGAGGAGCCCAGCAAGGTGGAG GAGAAAAAGGCCGAGGAGGCCGGGGCCAGCGCCGCCGCCTGCGAGGCCCCCT CCGCCGCCGGGCCCGGCGCGCCCCCGGAGCAGGAGGCAGCCCCCGCGGAGGA GCCCGCGGCCGCCGCAGCCTCGTCAGCCTGCGCAGCCCCCTCACAGGAGGCC CAGCCCGAGTGCAGTCCAGAAGCCCCCCCAGCGGAGGCGGCAGAGTAAAAGA GCAAGCTTTTGTGAGATAATCGAAGAACTTTTCTCCCCCGTTTGTTTGTTGG AGTGGTGCCAGGTACTGGTTTTGGAGAACTTGTCTACAACCAGGGATTGATT TTAAAGATGTCTTTTTTTATTTTACTTTTTTTTAAGCACCAAATTTTGTTGT TTTTTTTTTTTCTCCCCTCCCCACAGATCCCATCTCAAATCATTCTGTTAAC CACCATTCCAACAGGTCGAGGAGAGCTTAAACACCTTCTTCCTCTGCCTTGT TTCTCTTTTATTTTTTATTTTTTCGCATCAGTATTAATGTTTTTGCATACTT TGCATCTTTATTCAAAAGTGTAAACTTTCTTTGTCAATCTATGGACATGCCC ATATATGAAGGAGATGGGTGGGTCAAAAAGGGATATCAAATGAAGTGATGGG GTCACAATGGGGAAATTGAAGTGGTGCATAACATTGCCAAAATAGTGTGCCA CTAGAAATGGTGTAAAGGCTGTCTTTTTTTTTTTTTTAAAAGAAAAGTTATT ACCATGTATTTTGTGAGGCAGGTTTACAACACTACAAGTCTTGAGTTAAGAA GGAAAGAGGAAAAAAGAAAAAACACCAATACCCAGATTTAAAAAAAAAAAAA CGATCATAGTCTTAGGAGTTCATTTAAACCATAGGAACTTTTCACTTATCTC ATGTTAGCTGTACCAGTCAGTGATTAAGTAGAACTACAAGTTGTATAGGCTT TATTGTTTATTGCTGGTTTATGACCTTAATAAAGTGTAATTATGTATTACCA GCAGGGTGTTTTTAACTGTGACTATTGTATAAAAACAAATCTTGATATCCAG AAGCACATGAAGTTTGCAACTTTCCACCCTGCCCATTTTTGTAAAACTGCAG TCATCTTGGACCTTTTAAAACACAAATTTTAAACTCAACCAAGCTGTGATAA GTGGAATGGTTACTGTTTATACTGTGGTATGTTTTTGATTACAGCAGATAAT GCTTTCTTTTCCAGTCGTCTTTGAGAATAAAGGAAAAAAAATCTTCAGATGC AATGGTTTTGTGTAGCATCTTGTCTATCATGTTTTGTAAATACTGGAGAAGC TTTGACCAATTTGACTTAGAGATGGAATGTAACTTTGCTTACAAAAATTGCT ATTAAACTCCTGCTTAAGGTGTTCTAATTTTCTGTGAGCACACTAAAAGCGA AAAATAAATGTGAATAAAATGTACAAATTTGTTGTGTTTTTTTATGTTCTAA TAATACTGAGACTTCTAGGTCTTAGGTTAATTTTTAGGAAGATCTTGCATGC CATCAGGAGTAAATTTTATTGTGGTTCTTAATCTGAAGTTTTCAAGCTCTGA AATTCATAATCCGCAGTGTCAGATTACGTAGAGGAAGATCTTACAACATTTC CATGTCAAATCTGTTACCATTTATTGGCATTTAGTTTTCATTTAAGAATTGA ACATAATTATTTTTATTGTAGCTATATAGCATGTCAGATTAAATCATTTACA ACAAAAGGGGTGTGAACCTAAGACTATTTAAATGTCTTATGAGAAAATTTCA

TABLE 3-continued

Exosome Targeting Domain	
Exosome Targeting Domain/Sticky Binder	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TAAAGCCATTCTCTTGTCATTCAGGTCCAGAAACAAATTTTAAACTGAGTGA GAGTCTATAGAATCCATACTGCAGATGGGTCATGAAATGTGACCAAATGTGT TTCAAAAATTGATGGTGTATTACCTGCTATTGTAATTGCTTAGTGCTTGGCT AATTTCCAAATTATTGCATAATATGTTCTACCTTAAGAAAACAGGTTTATGT AACAAAGTAATGGTGTTGAATGGATGATGTCAGTTCATGGGCCTTTAGCATA GTTTTAAGCATCCTTTTTTTTTTTTTTTTTTGAAAGTGTGTTAGCATCTTGT TACTCAAAGGATAAGACAGACAATAATACTTCACTGAATCTTAATAATCTTT ACTAGTTTACCTCCTCTGCTCTTTGCCACCCGATAACTGGATATCTTTTCCT TCAAAGGACCCTAAACTGATTGAAATTTAAGATATGTATCAAAAACATTATT TCATTTAATGCACATCTGTTTTGCTGTTTTTGAGCAGTGTGCAGTTTAGGGT TCATGATAAATCATTGAACCACATGTGTAACAACTGAATGCCAAATCTTAAA CTCATTAGAAAAATAACAAATTAGGTTTTGACACGCATTCTTAATTGGAATA ATGGATCAAAAATAGTGGTTCATGACCTTACCAAACACCCTTGCTACTAATA AAATCAAATAACACTTAGAAGGGTATGTATTTTTAGTTAGGGTTTCTTGATC TTGGAGGATGTTTGAAAGTTAAAAATTGAATTTGGTAACCAAAGGACTGATT TATGGGTCTTTCCTATCTTAACCAACGTTTTCTTAGTTACCTAGATGGCCAA GTACAGTGCCTGGTATGTAGTAAGACTCAGTAAAAAAGTGGATTTTTAAAAA TAACTCCCAAAGTGAATAGTCAAAAATCCTGTTAGCAAACTGTTATATATTG CTAAGTTTGTTCTTTTAACAGCTGGAATTTATTAAGATGCATTATTTTGATT TTATTCACTGCCTAAAACACTTTGGGTGGTATTGATGGAGTTGGTGGATTTT CCTCCAAGTGATTAAATGAAATTTGACGTATCTTTTCATCCAAAGTTTTGTA CATCATGTTTTCTAACGGAAAAAAATGTTAATATGGCTTTTTTGTATTACTA AAAATAGCTTTGAGATTAAGGAAAAATAAATAACTCTTGTACAGTTCAGTAT TGTCTATTAAATCTGTATTGGCAGTATGTATAATGGCATTTGCTGTGGTTAC AAAATACTTCCTCTGGGTTATAATAATCATTTGATCCAATTCCTATTGCTTG TAAAATAAAGTTTTACCAGTTGATATAATCAA (SEQ ID NO: 215) >NP_002347.5 myristoylated alanine-rich C-kinase substrate [*Homo sapiens*] **MGAQFSKT**AAKGEAAAERPGEAAVASSPSKANGQENGHVKVNGDASPAAAES GAKEELQANGSAPAADKEEPAAAGSGAASPSAAEKGEPAAAAAPEAGASPVE KEAPAEGEAAEPGSPTAAEGEAASAASSTSSPKAEDGATPSPSNETPKKKKK RFSFKKSFKLSGFSFKKNKKEAGEGGEAEAPAAEGGKDEAAGGAAAAAAEAG AASGEQAAAPGEEAAAGEEGAAGGDPQEAKPQEAAVAPEKPPASDETKAAEE PSKVEEKKAEEAGASAAACEAPSAAGPGAPPEQEAAPAEEPAAAAASSACAA PSQEAQPECSPEAPPAEAAE (SEQ ID NO: 216) >Myr/Palm tag modified from Human MARCKS, nucleotide sequence ATGGGTTGCTGTTTCTCCAAGACC (SEQ ID NO: 217) >Myr/Palm tag modified from Human MARCKS, peptide sequence MGCCFSKT (SEQ ID NO: 218)

In some embodiments of any of the aspects provided herein, the fusion polypeptide further comprises a peptide linker. The linker may be flexible, rigid, or cleavable. Further, the linker can be linked directly or via another linker (e.g., a peptide of one, two, three, four, five, six, seven, eight, nine, ten or more amino acids) to the fusion polypeptides described herein. Linkers can be configured according to a specific need, e.g., based on at least one of the following characteristics. In some embodiments of any of the aspects, linkers can be configured to have a sufficient length and flexibility such that it can allow for a cleavage at a target site. In some embodiments of any of the aspects, linkers can be configured to allow multimerization of the fusion polypeptides provided herein. In some embodiments of any of the aspects, linkers can be configured to facilitate expression and purification of the fusion proteins or engineered extracellular vesicles provided herein.

In some embodiments of any of the aspects, a linker can be configured to have any length in a form of a peptide, peptidomimetic, an aptamer, a protein, a nucleic acid (e.g., DNA or RNA), or any combinations thereof. For example, in one embodiment, the linker may be a polypeptide linker such as Gly-Ser-Ser-Gly (SEQ ID NO: 319) or a variation thereof as known by one of ordinary skill in the art. In another embodiment the linker may be a protein sequence for a self-cleavable peptide. For example, 2A sequences such as P2A, E2A, F2A, and T2A code for self-cleavable peptides by inducing ribosomal slippage on the mRNA at the 2A site which prevents peptide bond formation. The slippage will result in two separate peptides after translation. This allows the expression of two separate proteins from one promoter region. Any combination of the proteins described herein may be expressed with a self-cleavable peptide as known by one of ordinary skill in the art.

In some embodiments of any of the aspects, the polypeptide linker is a non-cleavable linker. In some embodiments of any of the aspects, a linker can be a chemical linker of any length.

In some embodiments of any of the aspects, the linker is an Fc linker. An exemplary nucleic acid sequence encoding an Fc polypeptide is:

>KY053479.1 Synthetic construct Fc-adiponectin gene, complete cds (SEQ ID NO: 219)

ATGTACAGGATGCAACTCCTGTCTTGCATTGCACTAAGTCTTGCACTTGTC

ACGAACTCGATATCGGCCATGGTTAGATCTGACAAAACTCACACATGCCCA

-continued

CCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCC

CCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC

GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG

TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGAC

TGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA

GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA

CAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC

AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG

TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG

CTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG

AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCT

CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGCC

AGCGGAAGTGGCGGAGGAGGCGGTCCTGGAGAAGGTGCCTATGTATACCGC

TCAGCATTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCC

ATTCGCTTTACCAAGATCTTCTACAATCAGCAAAACCACTATGATGGCTCC

ACTGGTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCAC

ATCACAGTCTATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAG

GCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTGGACCAGGCC

TCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG

GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGAC

TCCACCTTCACAGGCTTTCTTCTCTACCATGACACCAACTCTAGAAAGCTT

CCTGGAGAAGGTGCCTATGTATACCGCTCAGCATTCAGTGTGGGATTGGAG

ACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAGATCTTCTAC

AATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCACTGCAACATT

CCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATATGAAGGATGTG

AAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAG

TACCAGGAAAATAATGTGGACCAGGCCTCCGGCTCTGTGCTCCTGCATCTG

GAGGTGGGCGACCAAGTCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAAT

GGACTCTATGCTGATAATGACAATGACTCCACCTTCACAGGCTTTCTTCTC

TACCATGACACCAACACTAGTCCTGGAGAAGGTGCCTATGTATACCGCTCA

GCATTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATT

CGCTTTACCAAGATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACT

GGTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACATC

ACAGTCTATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCT

ATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTGGACCAGGCCTCC

GGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAGGTG

TATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCC

ACCTTCACAGGCTTTCTTCTCTACCATGACACCAACTAA.

The amino acid sequence of the Fc linker is:

>Fc Translation (SEQ ID NO: 220)

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP

EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK

VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY

PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS

CSVMHEALHNHYTQKSLSLSPGK.

In some embodiments of any of the aspects, the linker is a P2A peptide linker. P2A is a self-cleaving peptide sequence allowing for expression of two proteins from one promoter. In some embodiments, the P2A linker is encoded by the nucleic acid sequence: GCTACTAACTTCAGCCTGCTGAAGCAG (SEQ ID NO: 221). The amino acid sequence of P2A is ATNFSLKQAGDVENPGP (SEQ ID NO: 222).

In some embodiments of any of the aspects, the linker provides a multimerization (e.g., dimerization) domain wherein one fusion polypeptide may connect with another fusion polypeptide at each fusion polypeptide's respective multimerization domain. Multimerization of multiple fusion polypeptides will provide multiple fusion polypeptides within close proximity to one another to one or more a target receptor on the target cell, wherein the multiple fusion peptides will enhance receptor clustering on the target cell. Clustering receptors on a target cell will result in enhanced signal transduction. Without receptor clustering a signal may be weaker or not occur all together. For example, Fc domain sequences presented herein dimerize resulting in two fusion polypeptides connected by a covalent bond via the two Fc domains on their respective fusion polypeptide. One preferred embodiment of an Fc domain is from IgG4, herein labeled 4Fc. In other embodiments Fc may be from IgG1, herein labeled Fc. In certain embodiments Fc from other immunoglobulin, (e.g., IgG2, IgG3, etc.) may be used.

Additional non-limiting examples of linkers that can be used and their properties are further described in detail, e.g., in Chen X, Zaro J L, Shen W C. Fusion protein linkers: property, design and functionality. *Adv Drug Deliv Rev.* 2013; 65 (10): 1357-1369. doi: 10.1016/j.addr.2012.09.039; O'Shea E K, Lumb K J, Kim P S. Peptide 'Velcro': design of a heterodimeric coiled coil. Curr Biol. 1993 Oct. 1; 3 (10): 658-67. doi: 10.1016/0960-9822 (93) 90063-t. PMID: 15335856; and Müller K M, Arndt K M, Alber T. Protein fusions to coiled-coil domains. Methods Enzymol. 2000; 328:261-82. doi: 10.1016/s0076-6879 (00) 28402-4. PMID: 11075350, the contents of which are incorporated herein by reference in their entireties.

The engineered extracellular vesicle compositions provided herein can comprise variations in the configuration of the POI domain, linkers, and/or vesicle targeting domain. The specific combination and localization of these domains can enhance fusion polypeptide anchoring, function, or therapeutic effect, e.g., modulating inflammation.

Thus, in one aspect, provided herein is an engineered extracellular vesicle comprising: at least one fusion polypeptide comprising: (i) at least one protein of interest (POI) domain or a fragment thereof; and (ii) at least one vesicle targeting domain, wherein the POI domain is in an extracellular position relative to a lipid membrane of the extracellular vesicle.

In some embodiments, the POI domain or a fragment thereof is a N-terminal domain of the fusion polypeptide. In some embodiments, the vesicle targeting domain or a fragment thereof is a C-terminal domain of the fusion polypeptide.

In another aspect, provided herein is an engineered extracellular vesicle comprising: at least one fusion polypeptide comprising: (i) at least one protein of interest (POI) domain or a fragment thereof; and (ii) at least one vesicle targeting domain, wherein the POI domain is in an extracellular position relative to a lipid membrane of the extracellular vesicle, and wherein the vesicle targeting domain is a transmembrane domain relative to a lipid membrane of the extracellular vesicle.

In some embodiments, the POI domain or a fragment thereof is a C-terminal domain of the fusion polypeptide. In some embodiments, the vesicle targeting domain or a fragment thereof is a N-terminal domain of the fusion polypeptide. In some embodiments, the vesicle targeting domain is in a luminal position relative to the lipid membrane of the extracellular vesicle.

In some embodiments, the linker is in an exterior position relative to the lipid membrane of the extracellular vesicle. In some embodiments, the linker is a transmembrane linker. In some embodiments, the linker is in a luminal position relative to the lipid membrane of the extracellular vesicle.

The engineered extracellular vesicle compositions provided herein can comprise one or more of the following fusion polypeptide sequences in Table 4.

TABLE 4

Full Length Constructs	
Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
hCTLA4-Fc-GPI	>Artificial sequence; **hCTLA4**-Fc-*GPI*, DNA **ATGGCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTACCAGGACC** **TGGCCCTGCACTCTCCTGTTTTTTCTTCTCTTCATCCCTGTCTTCTGCAAAGCAATG** **CACGTGGCCCAGCCTGCTGTGGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTG** **TGTGAGTATGCATCTCCAGGCAAAGCCACTGAGGTCCGGGTGACAGTGCTTCGGCAG** **GCTGACAGCCAGGTGACTGAAGTCTGTGCGGCAACCTACATGATGGGGAATGAGTTG** **ACCTTCCTAGATGATTCCATCTGCACGGGCACCTCCAGTGGAAATCAAGTGAACCTC** **ACTATCCAAGGACTGAGGGCCATGGACACGGGACTCTACATCTGCAAGGTGGAGCTC** **ATGTACCCACCGCCATACTACCTGGGCATAGGCAACGGAACCCAGATTTATGTAATT** **GATCCAGAACCGTGCCCAGATTCTGAC**ATCGATGACAAAACTCACACATGCCCACCG TGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCC AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTC TCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAG CCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAAC CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGTGGAACC* *ACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTG* *CTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 223) > Artificial sequence; **hCTLA4**-Fc-*GPI*, Amino Acid **MACLGFQRHKAQLNLATRTWPCTLLFFLLFIPVFCKAMHVAQPAVVLASSRGIASFV** **CEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSSGNQVNL** **TIQGLRAMDTGLYICKVELMYPPPYYLGIGNGTQIYVIDPEPCPDSD**IDDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*PNKGSGT* *TSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 224)
hPDL1-GPI	> Artificial sequence; **hPDL1**-*GPI*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAA** **CTACCTCTGGCACATCCTCCAAATGAAAGG***CCAAATAAAGGAAGTGGAACCACTTCA* *GGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGG* *ACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 225) >Amino Acid Sequence; **hPDL1**-GPI, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC**

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE** **LPLAHPPNER***PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 226)
hPDL1-C1C2	>Artificial Sequence; **hPDL1**-*C1C2*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAA** **CTACCTCTGGCACATCCTCCAAATGAAAGG**ATCGAT*GTCGAGCCACTGGGCATGGAG* *AATGGGAACATTGCCAACTCACAGATCGCCGCCTCATCTGTGCGTGTGACCTTCTTG* *GGTTTGCAGCATTGGGTCCCGGAGCTGGCCCGCCTGAACCGCGCAGGCATGGTCAAT* *GCCTGGACACCCAGCAGCAATGACGATAACCCCTGGATCCAGGTGAACCTGCTGCGG* *AGGATGTGGGTAACAGGTGTGGTGACGCAGGGTGCCAGCCGCTTGGCCAGTCATGAG* *TACCTGAAGGCCTTCAAGGTGGCCTACAGCCTTAATGGACACGAATTCGATTTCATC* *CATGATGTTAATAAAAAACACAAGGAGTTTGTGGGTAACTGGAACAAAAACGCGGTG* *CATGTCAACCTGTTTGAGACCCCTGTGGAGGCTCAGTACGTGAGATTGTACCCCACG* *AGCTGCCACACGGCCTGCACTCTGCGCTTTGAGCTACTGGGCTGTGAGCTGAACGGA* *TGCGCCAATCCCCTGGGCCTGAAGAATAACAGCATCCCTGACAAGCAGATCACGGCC* *TCCAGCAGCTACAAGACCTGGGGCTTGCATCTCTTCAGCTGGAACCCCTCCTATGCA* *CGGCTGGACAAGCAGGGCAACTTCAACGCCTGGGTTGCGGGGAGCTACGGTAACGAT* *CAGTGGCTGCAGATCTTCCCTGGCAACTGGGACAACCACTCCCACAAGAAGAACTTG* *TTTGAGACGCCCATCCTGGCTCGCTATGTGCGCATCCTGCCTGTAGCCTGGCACAAC* *CGCATCGCCCTGCGCCTGGAGCTGCTGGGCTGTTAG* (SEQ ID NO: 227) >Artificial Sequence, **hPDL1**-*C1C2*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE** **LPLAHPPNER**ID*VEPLGMENGNIANSQIAASSVRVTFLGLQHWVPELARLNRAGMVN* *AWTPSSNDDNPWIQVNLLRRMWVTGVVTQGASRLASHEYLKAFKVAYSLNGHEFDFI* *HDVNKKHKEFVGNWNKNAVHVNLFETPVEAQYVRLYPTSCHTACTLRFELLGCELNG* *CANPLGLKNNSIPDKQITASSSYKTWGLHLFSWNPSYARLDKQGNFNAWVAGSYGND* *QWLQIFPGNWDNHSHKKNLFETPILARYVRILPVAWHNRIALRLELLGC* (SEQ ID NO: 228)
hPDL1-Fc-GPI	>Artificial Sequence; **hPDL1**-Fc-GPI, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAA** **CTACCTCTGGCACATCCTCCAAATGAAAGG**ATCGATGACAAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGTGGA* *ACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGT* *TTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 229)

TABLE 4-continued

Full Length Constructs	
	Nucleic Acid Sequence (SEQ ID NO:)
Fusion Polypeptide	Amino Acid Sequence (SEQ ID NO:)
	> Artificial Sequence; **hPDL1**-Fc-*GPI*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE** **LPLAHPPNER**IDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGKID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 230)
hPDL2-C1C2	>Artificial Sequence; **hPDL2**-*C1C2*, DNA **ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGATAGCAGCT** **TTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGCATGGCAGCAATGTG** **ACCCTGGAATGCAACTTTGACACTGGAAGTCATGTGAACCTTGGAGCAATAACAGCC** **AGTTTGCAAAAGGTGGAAAATGATACATCCCCACACCGTGAAAGAGCCACTTTGCTG** **GAGGAGCAGCTGCCCCTAGGGAAGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGG** **GACGAAGGACAGTACCAATGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTAC** **CTGACTCTGAAAGTCAAAGCTTCCTACAGGAAAATAAACACTCACATCCTAAAGGTT** **CCAGAAACAGATGAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAA** **GTATCCTGGCCAAACGTCAGCGTTCCTGCCAACACCAGCCACTCCAGGACCCCTGAA** **GGCCTCTACCAGGTCACCAGTGTTCTGCGCCTAAAGCCACCCCCTGGCAGAAACTTC** **AGCTGTGTGTTCTGGAATACTCACGTGAGGGAACTTACTTTGGCCAGCATTGACCTT** **CAAAGTCAGATGGAACCCAGGACCCATCCAACT**ATCGAT*GTCGAGCCACTGGGCATG* *GAGAATGGGAACATTGCCAACTCACAGATCGCCGCCTCATCTGTGCGTGTGACCTTC* *TTGGGTTTGCAGCATTGGGTCCCGGAGCTGGCCCGCCTGAACCGCGCAGGCATGGTC* *AATGCCTGGACACCCAGCAGCAATGACGATAACCCCTGGATCCAGGTGAACCTGCTG* *CGGAGGATGTGGGTAACAGGTGTGGTGACGCAGGGTGCCAGCCGCTTGGCCAGTCAT* *GAGTACCTGAAGGCCTTCAAGGTGGCCTACAGCCTTAATGGACACGAATTCGATTTC* *ATCCATGATGTTAATAAAAAACACAAGGAGTTTGTGGGTAACTGGAACAAAAACGCG* *GTGCATGTCAACCTGTTTGAGACCCCTGTGGAGGCTCAGTACGTGAGATTGTACCCC* *ACGAGCTGCCACACGGCCTGCACTCTGCGCTTTGAGCTACTGGGCTGTGAGCTGAAC* *GGATGCGCCAATCCCCTGGGCCTGAAGAATAACAGCATCCCTGACAAGCAGATCACG* *GCCTCCAGCAGCTACAAGACCTGGGGCTTGCATCTCTTCAGCTGGAACCCCTCCTAT* *GCACGGCTGGACAAGCAGGGCAACTTCAACGCCTGGGTTGCGGGGAGCTACGGTAAC* *GATCAGTGGCTGCAGATCTTCCCTGGCAACTGGGACAACCACTCCCACAAGAAGAAC* *TTGTTTGAGACGCCCATCCTGGCTCGCTATGTGCGCATCCTGCCTGTAGCCTGGCAC* *AACCGCATCGCCCTGCGCCTGGAGCTGCTGGGCTGTTAG* (SEQ ID NO: 231) >Artificial Sequence; **hPDL2**-*C1C2*, Amino Acid **MIFLLLMLSLELQLHQIAALFTVTVPKELYIIEHGSNVTLECNFDTGSHVNLGAITA** **SLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQYQCIIIYGVAWDYKY** **LTLKVKASYRKINTHILKVPETDEVELTCQATGYPLAEVSWPNVSVPANTSHSRTPE** **GLYQVTSVLRLKPPPGRNFSCVFWNTHVRELTLASIDLQSQMEPRTHPT**ID*VEPLGM* *ENGNIANSQIAASSVRVTFLGLQHWVPELARLNRAGMVNAWTPSSNDDNPWIQVNLL* *RRMWVTGVVTQGASRLASHEYLKAFKVAYSLNGHEFDFIHDVNKKHKEFVGNWNKNA* *VHVNLFETPVEAQYVRLYPTSCHTACTLRFELLGCELNGCANPLGLKNNSIPDKQIT* *ASSSYKTWGLHLFSWNPSYARLDKQGNFNAWVAGSYGNDQWLQIFPGNWDNHSHKKN* *LFETPILARYVRILPVAWHNRIALRLELLGC* (SEQ ID NO: 232)
hPDL2-Fc-GPI	>Artificial Sequence; **hPDL2**-Fc-*GPI*, DNA **ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGATAGCAGCT** **TTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGCATGGCAGCAATGTG** **ACCCTGGAATGCAACTTTGACACTGGAAGTCATGTGAACCTTGGAGCAATAACAGCC** **AGTTTGCAAAAGGTGGAAAATGATACATCCCCACACCGTGAAAGAGCCACTTTGCTG** **GAGGAGCAGCTGCCCCTAGGGAAGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGG** **GACGAAGGACAGTACCAATGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTAC** **CTGACTCTGAAAGTCAAAGCTTCCTACAGGAAAATAAACACTCACATCCTAAAGGTT** **CCAGAAACAGATGAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAA** **GTATCCTGGCCAAACGTCAGCGTTCCTGCCAACACCAGCCACTCCAGGACCCCTGAA** **GGCCTCTACCAGGTCACCAGTGTTCTGCGCCTAAAGCCACCCCCTGGCAGAAACTTC** **AGCTGTGTGTTCTGGAATACTCACGTGAGGGAACTTACTTTGGCCAGCATTGACCTT** **CAAAGTCAGATGGAACCCAGGACCCATCCAACT**ATCGATGACAAAACTCACACATGC CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCA AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTG GACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTG GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC AAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG CTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG

TABLE 4-continued

Full Length Constructs	
Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCAC TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGT* *GGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACA* *GGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 233) >Artificial Sequence; **hPDL2**-Fc-*GPI*, Amino Acid **MIFLLLMLSLELQLHQIAALFTVTVPKELYIIEHGSNVTLECNFDTGSHVNLGAITA** **SLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQYQCIIIYGVAWDYKY** **LTLKVKASYRKINTHILKVPETDEVELTCQATGYPLAEVSWPNVSVPANTSHSRTPE** **GLYQVTSVLRLKPPPGRNFSCVFWNTHVRELTLASIDLQSQMEPRTHPT**IDDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*PNKGS* *GTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 234)
4F2-h41BBL	>Artificial Sequence; *4F2*-**41BBL**, DNA *ATGAGCCAGGACACCGAGGTGGATATGAAGGAGGTGGAGCTGAATGAGTTAGAGCCC* *GAGAAGCAGCCGATGAACGCGGCGTCTGGGGCGGCCATGTCCCTGGCGGGAGCCGAG* *AAGAATGGTCTGGTGAAGATCAAGGTGGCGGAAGACGAGGCGGAGGCGGCAGCCGCG* *GCTAAGTTCACGGGCCTGTCCAAGGAGGAGCTGCTGAAGGTGGCAGGCAGCCCCGGC* *TGGGTACGCACCCGCTGGGCACTGCTGCTGCTCTTCTGGCTCGGCTGGCTCGGCATG* *CTTGCTGGTGCCGTGGTCATAATCGTG***GCCTGCCCCTGGGCCGTGTCCGGGGCTCGC** **GCCTCGCCCGGCTCCGCGGCCAGCCCGAGACTCCGCGAGGGTCCCGAGCTTTCGCCC** **GACGATCCCGCCGGCCTCTTGGACCTGCGGCAGGGCATGTTTGCGCAGCTGGTGGCC** **CAAAATGTTCTGCTGATCGATGGGCCCCTGAGCTGGTACAGTGACCCAGGCCTGGCA** **GGCGTGTCCCTGACGGGGGGCCTGAGCTACAAAGAGGACACGAAGGAGCTGGTGGTG** **GCCAAGGCTGGAGTCTACTATGTCTTCTTTCAACTAGAGCTGCGGCGCGTGGTGGCC** **GGCGAGGGCTCAGGCTCCGTTTCACTTGCGCTGCACCTGCAGCCACTGCGCTCTGCT** **GCTGGGGCCGCCGCCCTGGCTTTGACCGTGGACCTGCCACCCGCCTCCTCCGAGGCT** **CGGAACTCGGCCTTCGGTTTCCAGGGCCGCTTGCTGCACCTGAGTGCCGGCCAGCGC** **CTGGGCGTCCATCTTCACACTGAGGCCAGGGCACGCCATGCCTGGCAGCTTACCCAG** **GGCGCCACAGTCTTGGGACTCTTCCGGGTGACCCCCGAAATCCCAGCCGGACTCCCT** **TCACCGAGGTCGGAATAA** (SEQ ID NO: 235) >Artificial Sequence; *4F2*-**h41BBL**, Amino Acid *MSQDTEVDMKEVELNELEPEKQPMNAASGAAMSLAGAEKNGLVKIKVAEDEAEAAAA* *AKFTGLSKEELLKVAGSPGWVRTRWALLLLFWLGWLGMLAGAVVIIV***ACPWAVSGAR** **ASPGSAASPRLREGPELSPDDPAGLLDLRQGMFAQLVAQNVLLIDGPLSWYSDPGLA** **GVSLTGGLSYKEDTKELVVAKAGVYYVFFQLELRRVVAGEGSGSVSLALHLQPLRSA** **AGAAALALTVDLPPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQ** **GATVLGLFRVTPEIPAGLPSPRSE** (SEQ ID NO: 236)
hPDL1-4Fc-GPI	>Artificial Sequence; **hPDL1**-4Fc-*GPI*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAA** **CTACCTCTGGCACATCCTCCAAATGAAAGG**GAGTCCAAATATGGTCCCCCATGCCCA TCATGCCCAGCACCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAA CCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGAC GTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTG CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTC AGGGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGTAAGGAGTACAAGTGCAAG GTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGGAGGACAACTACAAGACCACGCCTCCCGTGCTG

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGG CAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC ACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA*CCAAATAAAGGAAGTGGAACCACT* *TCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTT* *GGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 237) >Artificial Sequence; **hPDL1**-4Fc-*GPI*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE** **LPLAHPPNER**ESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVRVLTVLHQDWLNGKEYKCK VSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPEDNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHY TQKSLSLSPGK*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 238)
hPDL1-GPI-P2A- hFGL1-GPI	>Artificial Sequence; **hPDL1**-*GPI*-P2A-**hFGL1**-*GPI*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAA** **CTACCTCTGGCACATCCTCCAAATGAAAGG***CCAAATAAAGGAAGTGGAACCACTTCA* *GGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGG* *ACGCTAGTAACCATGGGCTTGCTGACT*GGAAGCGGAGCTACTAACTTCAGCCTGCTG AAGCAGGCTGGCGACGTGGAGGAGAACCCTGGACCT**ATGGCAAAGGTGTTCAGTTTC** **ATCCTTGTTACCACCGCTCTGACAATGGGCAGGGAAATTTCGGCGCTCGAGGACTGT** **GCCCAGGAGCAGATGCGGCTCAGAGCCCAGGTGCGCCTGCTTGAGACCCGGGTCAAA** **CAGCAACAGGTCAAGATCAAGCAGCTTTTGCAGGAGAATGAAGTCCAGTTCCTTGAT** **AAAGGAGATGAGAATACTGTCATTGATCTTGGAAGCAAGAGGCAGTATGCAGATTGT** **TCAGAGATTTTCAATGATGGGTATAAGCTCAGTGGATTTTACAAAATCAAACCTCTC** **CAGAGCCCAGCAGAATTTTCTGTTTATTGTGACATGTCCGATGGAGGAGGATGGACT** **GTAATTCAGAGACGATCTGATGGCAGTGAAAACTTTAACAGAGGATGGAAAGACTAT** **GAAAATGGCTTTGGAAATTTTGTCCAAAAACATGGTGAATATTGGCTGGGCAATAAA** **AATCTTCACTTCTTGACCACTCAAGAAGACTACACTTTAAAAATCGACCTTGCAGAT** **TTTGAAAAAAATAGCCGTTATGCACAATATAAGAATTTCAAAGTTGGAGATGAAAAG** **AATTTCTACGAGTTGAATATTGGGGAATATTCTGGAACAGCTGGAGATTCCCTTGCG** **GGGAATTTTCATCCTGAGGTGCAGTGGTGGGCTAGTCACCAAAGAATGAAATTCAGC** **ACGTGGGACAGAGATCATGACAACTATGAAGGGAACTGCGCAGAAGAAGATCAGTCT** **GGCTGGTGGTTTAACAGGTGTCACTCTGCAAACCTGAATGGTGTATACTACAGCGGC** **CCCTACACGGCTAAAACAGACAATGGGATTGTCTGGTACACCTGGCATGGGTGGTGG** **TATTCTCTGAAATCTGTGGTTATGAAAATTAGGCCAAATGATTTTATTCCAAATGTA** **ATT***CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCAC* *ACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACT* *TAG* (SEQ ID NO: 239) >Artificial Sequence; **hPDL1**-*GPI*-P2A-**hFGL1**-*GPI*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE** **LPLAHPPNER***PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT*GSGATNFSLL KQAGDVEENPGP**MAKVFSFILVTTALTMGREISALEDCAQEQMRLRAQVRLLETRVK** **QQQVKIKQLLQENEVQFLDKGDENTVIDLGSKRQYADCSEIFNDGYKLSGFYKIKPL** **QSPAEFSVYCDMSDGGGWTVIQRRSDGSENFNRGWKDYENGFGNFVQKHGEYWLGNK** **NLHFLTTQEDYTLKIDLADFEKNSRYAQYKNFKVGDEKNFYELNIGEYSGTAGDSLA** **GNFHPEVQWWASHQRMKFSTWDRDHDNYEGNCAEEDQSGWWFNRCHSANLNGVYYSG** **PYTAKTDNGIVWYTWHGWWYSLKSVVMKIRPNDFIPNVI***PNKGSGTTSGTTRLLSGH* *TCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 240)
Myr-mScarlet	>Artificial Sequence; Myr-**mScarlet**, DNA *ATGGGTTGCTGTTTCTCCAAGACCG*GCTCGAGCGGC**GTGAGCAAGGGCGAGGCAGTG** **ATCAAGGAGTTCATGCGGTTCAAGGTGCACATGGAGGGCTCCATGAACGGCCACGAG** **TTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCACCCAGACCGCCAAG** **CTGAAGGTGACCAAGGGTGGCCCCCTGCCCTTCTCCTGGGACATCCTGTCCCCTCAG**

TABLE 4-continued

Full Length Constructs	
Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TTCATGTACGGCTCCAGGGCCTTCACCAAGCACCCCGCCGACATCCCCGACTACTAT **AAGCAGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGC** **GGCGCCGTGACCGTGACCCAGGACACCTCCCTGGAGGACGGCACCCTGATCTACAAG** **GTGAAGCTCCGCGGCACCAACTTCCCTCCTGACGGCCCCGTAATGCAGAAGAAGACA** **ATGGGCTGGGAAGCGTCCACCGAGCGGTTGTACCCCGAGGACGGCGTGCTGAAGGGC** **GACATTAAGATGGCCCTGCGCCTGAAGGACGGCGGCCGCTACCTGGCGGACTTCAAG** **ACCACCTACAAGGCCAAGAAGCCCGTGCAGATGCCCGGCGCCTACAACGTCGACCGC** **AAGTTGGACATCACCTCCCACAACGAGGACTACACCGTGGTGGAACAGTACGAACGC** **TCCGAGGGCCGCCACTCCACCGGCGGCATGGACGAGCTGTACAAG** (SEQ ID NO: 241) >Artificial Sequence; *Myr*-**mScarlet**, Amino Acid *MGCCFSKT*GSSG**VSKGEAVIKEFMRFKVHMEGSMNGHEFEIEGEGEGRPYEGTQTAK** **LKVTKGGPLPFSWDILSPQFMYGSRAFTKHPADIPDYYKQSFPEGFKWERVMNFEDG** **GAVTVTQDTSLEDGTLIYKVKLRGTNFPPDGPVMQKKTMGWEASTERLYPEDGVLKG** **DIKMALRLKDGGRYLADFKTTYKAKKPVQMPGAYNVDRKLDITSHNEDYTVVEQYER** **SEGRHSTGGMDELYK** (SEQ ID NO: 242)
Myr-NanoLuc Luciferase	> Artificial Sequence; *Myr*-**NanoLuc**, DNA *ATGGGTTGCTGTTTCTCCAAGACCGGCTCGAGCGGC***GTCTTCACACTCGAAGATTTC** **GTTGGGGACTGGCGACAGACAGCCGGCTACAACCTGGACCAAGTCCTTGAACAGGGA** **GGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACTCCGATCCAAAGGATT** **GTCCTGAGCGGTGAAAATGGGCTGAAGATCGACATCCATGTCATCATCCCGTATGAA** **GGTCTGAGCGGCGACCAAATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCT** **GTGGATGATCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGG** **GTTACGCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTC** **GACGGCAAAAAGATCACTGTAACAGGGACCCTGTGGAACGGCAACAAAATTATCGAC** **GAGCGCCTGATCAACCCCGACGGCTCCCTGCTGTTCCGAGTAACCATCAACGGAGTG** **ACCGGCTGGCGGCTGTGCGAACGCATTCTGGCGTAA** (SEQ ID NO: 243) >Artificial Sequence; *Myr*-**NanoLuc**, Amino Acid *MGCCFSKT*GSSGVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRI VLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDG VTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGV TGWRLCERILA (SEQ ID NO: 244)
hSecPDL1-GPI	>Artificial Sequence; **hSecPDL1**-*GPI*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGGT** **AATATTCTGAATGTGTCCATTAAAATATGTCTAACACTGTCCCCTAGCACC***CCAAAT* *AAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTC* *ACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 245) >Artificial Sequence; **hSecPDL1**-*GPI*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPG** **NILNVSIKICLTLSPST***PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 246)
Tfr2-h41BBL	>Artificial Sequence; *Tfr2*-**h41BBL**, DNA *ATGGAGCGGCTTTGGGGTCTATTCCAGAGAGCGCAACAACTGTCCCCAAGATCCTCT* *CAGACCGTCTACCAGCGTGTGGAAGGCCCCCGGAAAGGGCACCTGGAGGAGGAAGAG* *GAAGACGGGGAGGAGGGGGCGGAGACATTGGCCCACTTCTGCCCCATGGAGCTGAGG* *GGCCCTGAGCCCCTGGGCTCTAGACCCAGGCAGCCAAACCTCATTCCCTGGGCGGCA* *GCAGGACGGAGGGCTGCCCCCTACCTGGTCCTGACGGCCCTGCTGATCTTCACTGGG* *GCCTTCCTACTGGGCTACGTCGCCTTCCGAGGGTCC**GCCTGCCCCTGGGCCGTGTCC*** ***GGGGCTCGCGCCTCGCCCGGCTCCGCGGCCAGCCCGAGACTCCGCGAGGGTCCCGAG*** ***CTTTCGCCCGACGATCCCGCCGGCCTCTTGGACCTGCGGCAGGGCATGTTTGCGCAG*** ***CTGGTGGCCCAAAATGTTCTGCTGATCGATGGGCCCCTGAGCTGGTACAGTGACCCA*** ***GGCCTGGCAGGCGTGTCCCTGACGGGGGGCCTGAGCTACAAAGAGGACACGAAGGAG*** ***CTGGTGGTGGCCAAGGCTGGAGTCTACTATGTCTTCTTTCAACTAGAGCTGCGGCGC*** ***GTGGTGGCCGGCGAGGGCTCAGGCTCCGTTTCACTTGCGCTGCACCTGCAGCCACTG***

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CGCTCTGCTGCTGGGGCCGCCGCCCTGGCTTTGACCGTGGACCTGCCACCCGCCTCC *TCCGAGGCTCGGAACTCGGCCTCGGTTTCCAGGGCCGCTTGCTGCACCTGAGTGCCG* *GCCAGCGCCTGGGCGTCCATCTTCACACTGAGGCCAGGGCACGCCATGCCTGGCAGC* *TTACCCAGGGCGCCACAGTCTTGGGACTCTTCCGGGTGACCCCCGAAATCCCAGCCG* *GACTCCCTTCACCGAGGTCGGAATAA* (SEQ ID NO: 247) >Artificial Sequence; *Tfr2*-**h41BBL**, Amino Acid *MERLWGLFQRAQQLSPRSSQTVYQRVEGPRKGHLEEEEEDGEEGAETLAHFCPMELR* *GPEPLGSRPRQPNLIPWAAAGRRAAPYLVLTALLIFTGAFLLGYVAFRGS***ACPWAVS** **GARASPGSAASPRLRGPELSPDDPAGLLDLRQGMFAQLVAQNVLLIDGPLSWYSDPG** **LAGVSLTGGLSYKEDTKELVVAKAGVYYVFFQLELRRVVAGEGSGSVSLALHLQPLR** **SAAGAAALALTVDLPPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQL** **TQGATVLGLFRVTPEIPAGLPSPRSE** (SEQ ID NO: 248)
CD9tm3-h41BBL	>Artificial Sequence; *CD9tm3*-**h41BBL**, DNA *ATGGGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGCATGCTGGGACTGTTCTTCGGC* *TTCCTCTTGGTGATATTCGCCATTGAAATAGCTGCGGCCATCTGGGGATATTCCCAC* *AAGGATGAG***GCCTGCCCCTGGGCCGTGTCCGGGGCTCGCGCCTCGCCCGGCTCCGCG** **GCCAGCCCGAGACTCCGCGAGGGTCCCGAGCTTTCGCCCGACGATCCCGCCGGCCTC** **TTGGACCTGCGGCAGGGCATGTTTGCGCAGCTGGTGGCCCAAAATGTTCTGCTGATC** **GATGGGCCCCTGAGCTGGTACAGTGACCCAGGCCTGGCAGGCGTGTCCCTGACGGGG** **GGCCTGAGCTACAAAGAGGACACGAAGGAGCTGGTGGTGGCCAAGGCTGGAGTCTAC** **TATGTCTTCTTTCAACTAGAGCTGCGGCGCGTGGTGGCCGGCGAGGGCTCAGGCTCC** **GTTTCACTTGCGCTGCACCTGCAGCCACTGCGCTCTGCTGCTGGGGCCGCCGCCCTG** **GCTTTGACCGTGGACCTGCCACCCGCCTCCTCCGAGGCTCGGAACTCGGCCTTCGGT** **TTCCAGGGCCGCTTGCTGCACCTGAGTGCCGGCCAGCGCCTGGGCGTCCATCTTCAC** **ACTGAGGCCAGGGCACGCCATGCCTGGCAGCTTACCCAGGGCGCCACAGTCTTGGGA** **CTCTTCCGGGTGACCCCCGAAATCCCAGCCGGACTCCCTTCACCGAGGTCGGAATAA** (SEQ ID NO: 249) >Artificial Sequence; *CD9tm3*-**h41BBL**, Amino Acid *MGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDE***ACPWAVSGARASPGSA** **ASPRLREGPELSPDDPAGLLDLRQGMFAQLVAQNVLLIDGPLSWYSDPGLAGVSLTG** **GLSYKEDTKELVVAKAGVYYVFFQLELRRVVAGEGSGSVSLALHLQPLRSAAGAAAL** **ALTVDLPPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLG** **LFRVTPEIPAGLPSPRSE** (SEQ ID NO: 250)
Myr/Palm-4F2-h41BBL	>Artificial Sequence; *Myr/Palm-4F2*-**h41BBL**, DNA *ATGGGTTGCTGTTTCTCCAAGACCGGCTCGAGOGGCAGCCAGGACACCGAGGTGGAT* *ATGAAGGAGGTGGAGCTGAATGAGTTAGAGCCCGAGAAGCAGCCGATGAACGCGGCG* *TCTGGGGCGGCCATGTCCCTGGCGGGAGCCGAGAAGAATGGTCTGGTGAAGATCAAG* *GTGGCGGAAGACGAGGCGGAGGCGGCAGCCGCGGCTAAGTTCACGGGCCTGTCCAAG* *GAGGAGCTGCTGAAGGTGGCAGGCAGCCCCGGCTGGGTACGCACCCGCTGGGCACTG* *CTGCTGCTCTTCTGGCTCGGCTGGCTCGGCATGCTTGCTGGTGCCGTGGTCATAATC* *GTG***GCCTGCCCCTGGGCCGTGTCCGGGGCTCGCGCCTCGCCCGGCTCCGCGGCCAGC** **CCGAGACTCCGCGAGGGTCCCGAGCTTTCGCCCGACGATCCCGCCGGCCTCTTGGAC** **CTGCGGCAGGGCATGTTTGCGCAGCTGGTGGCCCAAAATGTTCTGCTGATCGATGGG** **CCCCTGAGCTGGTACAGTGACCCAGGCCTGGCAGGCGTGTCCCTGACGGGGGGCCTG** **AGCTACAAAGAGGACACGAAGGAGCTGGTGGTGGCCAAGGCTGGAGTCTACTATGTC** **TTCTTTCAACTAGAGCTGCGGCGCGTGGTGGCCGGCGAGGGCTCAGGCTCCGTTTCA** **CTTGCGCTGCACCTGCAGCCACTGCGCTCTGCTGCTGGGGCCGCCGCCCTGGCTTTG** **ACCGTGGACCTGCCACCCGCCTCCTCCGAGGCTCGGAACTCGGCCTTCGGTTTCCAG** **GGCCGCTTGCTGCACCTGAGTGCCGGCCAGCGCCTGGGCGTCCATCTTCACACTGAG** **GCCAGGGCACGCCATGCCTGGCAGCTTACCCAGGGCGCCACAGTCTTGGGACTCTTC** **CGGGTGACCCCCGAAATCCCAGCCGGACTCCCTTCACCGAGGTCGGAATAA** (SEQ ID NO: 251) >Artificial Sequence; *Myr/Palm-4F2*-**h41BBL**, Amino Acid *MGCCFSKTGSSGSQDTEVDMKEVELNELEPEKQPMNAASGAAMSLAGAEKNGLVKIK* *VAEDEAEAAAAAKFTGLSKEELLKVAGSPGWVRTRWALLLLFWLGWLGMLAGAVVII* *V***ACPWAVSGARASPGSAASPRLREGPELSPDDPAGLLDLRQGMFAQLVAQNVLLIDG** **PLSWYSDPGLAGVSLTGGLSYKEDTKELVVAKAGVYYVFFQLELRRVVAGEGSGSVS** **LALHLQPLRSAAGAAALALTVDLPPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTE** **ARARHAWQLTQGATVLGLFRVTPEIPAGLPSPRSE** (SEQ ID NO: 252)
Myr/Palm-Link-41BBL (41BBL transmembrane domain included)	>Artificial Sequence; Myr/Palm-Link-**41BBL**, DNA *ATGGGTTGCTGTTTCTCCAAGACCGGCTCGAGCGGC***TGGGCCCTGGTCGCGGGGCTG** **CTGCTGCTGCTGCTGCTCGCTGCCGCCTGCGCCGTCTTCCTCGCCTGCCCCTGGGCC** **GTGTCCGGGGCTCGCGCCTCGCCCGGCTCCGCGGCCAGCCCGAGACTCCGCGAGGGT** **CCCGAGCTTTCGCCCGACGATCCCGCCGGCCTCTTGGACCTGCGGCAGGGCATGTTT** **GCGCAGCTGGTGGCCCAAAATGTTCTGCTGATCGATGGGCCCCTGAGCTGGTACAGT** **GACCCAGGCCTGGCAGGCGTGTCCCTGACGGGGGGCCTGAGCTACAAAGAGGACACG** **AAGGAGCTGGTGGTGGCCAAGGCTGGAGTCTACTATGTCTTCTTTCAACTAGAGCTG** **CGGCGCGTGGTGGCCGGCGAGGGCTCAGGCTCCGTTTCACTTGCGCTGCACCTGCAG**

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CCACTGCGCTCTGCTGCTGGGGCCGCCGCCCTGGCTTTGACCGTGGACCTGCCACCC **GCCTCCTCCGAGGCTCGGAACTCGGCCTTCGGTTTCCAGGGCCGCTTGCTGCACCTG** **AGTGCCGGCCAGCGCCTGGGCGTCCATCTTCACACTGAGGCCAGGGCACGCCATGCC** **TGGCAGCTTACCCAGGGCGCCACAGTCTTGGGACTCTTCCGGGTGACCCCCGAAATC** **CCAGCCGGACTCCCTTCACCGAGGTCGGAATAA** (SEQ ID NO: 253) >Artificial Sequence; *Myr/Palm*-Link-**41BBL**, Amino Acid *MGCCFSKT*GSSG**WALVAGLLLLLLLAAACAVFLACPWAVSGARASPGSAASPRLREG** **PELSPDDPAGLLDLRQGMFAQLVAQNVLLIDGPLSWYSDPGLAGVSLTGGLSYKEDT** **KELVVAKAGVYYVFFQLELRRVVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPP** **ASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTPEI** **PAGLPSPRSE** (SEQ ID NO: 254)
hPDL1-Link-GPI	>Artificial Sequence; **hPDL1**-Link-*GPI*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAANGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTG**GGCTCGAGCGGC *CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACG* *TGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 255) >Artificial Sequence; **hPDL1**-Link-*GPI*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAEL**GSSG *PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 256)
hSecPDL1-CD9tm2	>Artificial Sequence; **hSecPDL1**-*CD9tm2*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGGT** **AATATTCTGAATGTGTCCATTAAAATATGTCTAACACTGTCCCCTAGCACC***TTCTAC* *ACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTG* *GGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGCTAG* (SEQ ID NO: 257) >Artificial Sequence; **hSecPDL1**-*CD9tm2*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPG** **NILNVSIKICLTLSPST***FYTGVYILIGAGALMMLVGFLGCCGAVQESQC* (SEQ ID NO: 258)
hSecPDL1-CD9tm2-modified KRAS	>Artificial Sequence; hSecPDL1-*CD9tm2*-*KRAS*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC**

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGGT **AATATTCTGAATGTGTCCATTAAAATATGTCTAACACTGTCCCCTAGCACC***TTCTAC* *ACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTG* *GGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGC*<u>*AAAAAGAAGAAAAAGAAGTCAAAG*</u> <u>*ACAAAGTGTGTAATTATGTAA*</u> (SEQ ID NO: 259) >Artificial Sequence; **hSecPDL1**-*CD9tm2-*<u>*KRAS*</u>, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPG** **NILNVSIKICLTLSPST***FYTGVYILIGAGALMMLVGFLGCCGAVQESQC*<u>*KKKKKKKSK*</u> <u>*TKCVIM*</u> (SEQ ID NO: 260)
hSecPDL1- CD9tm4	>Artificial Sequence; **hSecPDL1**-*CD9tm4*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGGT** **AATATTCTGAATGTGTCCATTAAAATATGTCTAACACTGTCCCCTAGCACC***ATCGGC* *GCAGTGGGCATCGGCATTGCCGTGGTCATGATATTTGGCATGATCTTCAGTATGATC* *TTGTGCTGTGCTATCCGCAGGAACCGCGAGATGGTCTAG* (SEQ ID NO: 261) >Artificial Sequence; **hSecPDL1**-*CD9tm4*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTIAINTTTNEIFYCTFRRLDPEENHTAELVIPG** **NILNVSIKICLTLSPST***IGAVGIGIAVVMIFGMIFSMILCCAIRRNREMV* (SEQ ID NO: 262)
hSecPDL1-CD81	>Artificial Sequence; **hSecPDL1**-*CD81*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGGT** **AATATTCTGAATGTGTCCATTAAAATATGTCTAACACTGTCCCCTAGCACC***CTGTAC* *CTCATCGGCATTGCTGCCATCGTGGTCGCTGTGATCATGATCTTCGAGATGATCCTG* *AGCATGGTGCTGTGCTGTGGCATCCGGAACAGCTCCGTGTACTGA* (SEQ ID NO: 263) >Artificial Sequence; **hSecPDL1**-*CD81*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPG** **NILNVSIKICLTLSPST***LYLIGIAAIVVAVIMIFEMILSMVLCCGIRNSSVY* (SEQ ID NO: 264)
hCD200-Fc-GPI	>Artificial Sequence; **hCD200**-<u>Fc</u>-*GPI*, DNA **ATGGAGAGGCTGGTGATCAGGATGCCCTTCTCTCATCTGTCTACCTACAGCCTGGTT** **TGGGTCATGGCAGCAGTGGTGCTGTGCACAGCACAAGTGCAAGTGGTGACCCAGGAT** **GAAAGAGAGCAGCTGTACACACCTGCTTCCTTAAAATGCTCTCTGCAAAATGCCCAG** **GAAGCCCTCATTGTGACATGGCAGAAAAAGAAAGCTGTAAGCCCAGAAAACATGGTC** **ACCTTCAGCGAGAACCATGGGGTGGTGATCCAGCCTGCCTATAAGGACAAGATAAAC** **ATTACCCAGCTGGGACTCCAAAACTCAACCATCACCTTCTGGAATATCACCCTGGAG** **GATGAAGGGTGTTACATGTGTCTCTTCAATACCTTTGGTTTTGGGAAGATCTCAGGA** **ACGGCCTGCCTCACCGTCTATGTACAGCCCATAGTATCCCTTCACTACAAATTCTCT** **GAAGACCACCTAAATATCACTTGCTCTGCCACTGCCCGCCCAGCCCCCATGGTCTTC**

TABLE 4-continued

Full Length Constructs	
Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TGGAAGGTCCCTCGGTCAGGGATTGAAAATAGTACAGTGACTCTGTCTCACCCAAAT **GGGACCACGTCTGTTACCAGCATCCTCCATATCAAAGACCCTAAGAATCAGGTGGGG** **AAGGAGGTGATCTGCCAGGTGCTGCACCTGGGGACTGTGACCGACTTTAAGCAAACC** **GTCAACAAAGGC**ATCGATGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG GTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACC TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCC CTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACC* *CGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTA* *ACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 265) >Artificial Sequence; **hCD200**-Fc-*GPI*, Amino Acid **MERLVIRMPFSHLSTYSLVWVMAAVVLCTAQVQVVTQDEREQLYTPASLKCSLQNAQ** **EALIVTWQKKKAVSPENMVTFSENHGVVIQPAYKDKINITQLGLQNSTITFWNITLE** **DEGCYMCLFNTFGFGKISGTACLTVYVQPIVSLHYKFSEDHLNITCSATARPAPMVF** **WKVPRSGIENSTVTLSHPNGTTSVTSILHIKDPKNQVGKEVICQVLHLGTVTDFKQT** **VNKG**IDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGKID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 266)
hFGL1-GPI	>Artificial Sequence; **hFGL1**-*GPI*, DNA **ATGGCAAAGGTGTTCAGTTTCATCCTTGTTACCACCGCTCTGACAATGGGCAGGGAA** **ATTTCGGCGCTCGAGGACTGTGCCCAGGAGCAGATGCGGCTCAGAGCCCAGGTGCGC** **CTGCTTGAGACCCGGGTCAAACAGCAACAGGTCAAGATCAAGCAGCTTTTGCAGGAG** **AATGAAGTCCAGTTCCTTGATAAAGGAGATGAGAATACTGTCATTGATCTTGGAAGC** **AAGAGGCAGTATGCAGATTGTTCAGAGATTTTCAATGATGGGTATAAGCTCAGTGGA** **TTTTACAAAATCAAACCTCTCCAGAGCCCAGCAGAATTTTCTGTTTATTGTGACATG** **TCCGATGGAGGAGGATGGACTGTAATTCAGAGACGATCTGATGGCAGTGAAAACTTT** **AACAGAGGATGGAAAGACTATGAAAATGGCTTTGGAAATTTTGTCCAAAAACATGGT** **GAATATTGGCTGGGCAATAAAAATCTTCACTTCTTGACCACTCAAGAAGACTACACT** **TTAAAAATCGACCTTGCAGATTTTGAAAAAAATAGCCGTTATGCACAATATAAGAAT** **TTCAAAGTTGGAGATGAAAAGAATTTCTACGAGTTGAATATTGGGGAATATTCTGGA** **ACAGCTGGAGATTCCCTTGCGGGGAATTTTCATCCTGAGGTGCAGTGGTGGGCTAGT** **CACCAAAGAATGAAATTCAGCACGTGGGACAGAGATCATGACAACTATGAAGGGAAC** **TGCGCAGAAGAAGATCAGTCTGGCTGGTGGTTTAACAGGTGTCACTCTGCAAACCTG** **AATGGTGTATACTACAGCGGCCCCTACACGGCTAAAACAGACAATGGGATTGTCTGG** **TACACCTGGCATGGGTGGTGGTATTCTCTGAAATCTGTGGTTATGAAAATTAGGCCA** **AATGATTTTATTCCAAATGTAATT***CCAAATAAAGGAAGTGGAACCACTTCAGGTACT* *ACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTA* *GTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 267) >Artificial Sequence; **hFGL1**-*GPI*, Amino Acid **MAKVFSFILVTTALTMGREISALEDCAQEQMRLRAQVRLLETRVKQQQVKIKQLLQE** **NEVQFLDKGDENTVIDLGSKRQYADCSEIFNDGYKLSGFYKIKPLQSPAEFSVYCDM** **SDGGGWTVIQRRSDGSENFNRGWKDYENGFGNFVQKHGEYWLGNKNLHFLTTQEDYT** **LKIDLADFEKNSRYAQYKNFKVGDEKNFYELNIGEYSGTAGDSLAGNFHPEVQWWAS** **HQRMKFSTWDRDHDNYEGNCAEEDQSGWWFNRCHSANLNGVYYSGPYTAKTDNGIVW** **YTWHGWWYSLKSVVMKIRPNDFIPNVI***PNKGSGTTSGTTRLLSGHTCFTLTGLLGTL* *VTMGLLT* (SEQ ID NO: 268)
hGa19-Fc-GPI	>Artificial Sequence; **hGa19**-Fc-*GPI*, DNA **ATGGCCTTCAGCGGTTCCCAGGCTCCCTACCTGAGTCCAGCTGTCCCCTTTTCTGGG** **ACTATTCAAGGAGGTCTCCAGGACGGACTTCAGATCACTGTCAATGGGACCGTTCTC** **AGCTCCAGTGGAACCAGGTTTGCTGTGAACTTTCAGACTGGCTTCAGTGGAAATGAC** **ATTGCCTTCCACTTCAACCCTCGGTTTGAAGATGGAGGGTACGTGGTGTGCAACACG** **AGGCAGAACGGAAGCTGGGGGCCCGAGGAGAGGAAGACACACATGCCTTTCCAGAAG** **GGGATGCCCTTTGACCTCTGCTTCCTGGTGCAGAGCTCAGATTTCAAGGTGATGGTG** **AACGGGATCCTCTTCGTGCAGTACTTCCACCGCGTGCCCTTCCACCGTGTGGACACC** **ATCTCCGTCAATGGCTCTGTGCAGCTGTCCTACATCAGCTTCCAGAACCCCCGCACA** **GTCCCTGTTCAGCCTGCCTTCTCCACGGTGCCGTTCTCCCAGCCTGTCTGTTTCCCA** **CCCAGGCCCAGGGGGCGCAGACAAAAACCTCCCGGCGTGTGGCCTGCCAACCCGGCT** **CCCATTACCCAGACAGTCATCCACACAGTGCAGAGCGCCCCTGGACAGATGTTCTCT** **ACTCCCGCCATCCCACCTATGATGTACCCCCACCCCGCCTATCCGATGCCTTTCATC**

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ACCACCATTCTGGGAGGGCTGTACCCATCCAAGTCCATCCTCCTGTCAGGCACTGTC **CTGCCCAGTGCTCAGAGGTTCCACATCAACCTGTGCTCTGGGAACCACATCGCCTTC** **CACCTGAACCCCCGTTTTGATGAGAATGCTGTGGTCCGCAACACCCAGATCGACAAC** **TCCTGGGGGTCTGAGGAGCGAAGTCTGCCCCGAAAAATGCCCTTCGTCCGTGGCCAG** **AGCTTCTCAGTGTGGATCTTGTGTGAAGCTCACTGCCTCAAGGTGGCCGTGGATGGT** **CAGCACCTGTTTGAATACTACCATCGCCTGAGGAACCTGCCCACCATCAACAGACTG** **GAAGTGGGGGGCGACATCCAGCTGACCCATGTGCAGACA**ATCGATGACAAAACTCAC ACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC CCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAG ATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCAC AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGATCCAAATAAA *GGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACG* *TTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 269) >Artificial Sequence; **hGal9**-Fc-*GPI*, Amino Acid **MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGND** **IAFHFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMV** **NGILFVQYFHRVPFHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFP** **PRPRGRRQKPPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFI** **TTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDN** **SWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRL** **EVGGDIQLTHVQT**IDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGKID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 270)
hCD200-GPI	>Artificial Sequence; **hCD200**-*GPI*, DNA **ATGGAGAGGCTGGTGATCAGGATGCCCTTCTCTCATCTGTCTACCTACAGCCTGGTT** **TGGGTCATGGCAGCAGTGGTGCTGTGCACAGCACAAGTGCAAGTGGTGACCCAGGAT** **GAAAGAGAGCAGCTGTACACACCTGCTTCCTTAAAATGCTCTCTGCAAAATGCCCAG** **GAAGCCCTCATTGTGACATGGCAGAAAAAGAAAGCTGTAAGCCCAGAAAACATGGTC** **ACCTTCAGCGAGAACCATGGGGTGGTGATCCAGCCTGCCTATAAGGACAAGATAAAC** **ATTACCCAGCTGGGACTCCAAAACTCAACCATCACCTTCTGGAATATCACCCTGGAG** **GATGAAGGGTGTTACATGTGTCTCTTCAATACCTTTGGTTTTGGGAAGATCTCAGGA** **ACGGCCTGCCTCACCGTCTATGTACAGCCCATAGTATCCCTTCACTACAAATTCTCT** **GAAGACCACCTAAATATCACTTGCTCTGCCACTGCCCGCCCAGCCCCCATGGTCTTC** **TGGAAGGTCCCTCGGTCAGGGATTGAAAATAGTACAGTGACTCTGTCTCACCCAAAT** **GGGACCACGTCTGTTACCAGCATCCTCCATATCAAAGACCCTAAGAATCAGGTGGGG** **AAGGAGGTGATCTGCCAGGTGCTGCACCTGGGGACTGTGACCGACTTTAAGCAAACC** **GTCAACAAAGGC***CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTA* *TCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGC* *TTGCTGACTTAG* (SEQ ID NO: 271) >Artificial Sequence; **hCD200**-*GPI*, Amino Acid **MERLVIRMPFSHLSTYSLVWVMAAVVLCTAQVQVVTQDEREQLYTPASLKCSLQNAQ** **EALIVTWQKKKAVSPENMVTFSENHGVVIQPAYKDKINITQLGLQNSTITFWNITLE** **DEGCYMCLFNTFGFGKISGTACLTVYVQPIVSLHYKFSEDHLNITCSATARPAPMVF** **WKVPRSGIENSTVTLSHPNGTTSVTSILHIKDPKNQVGKEVICQVLHLGTVTDFKQT** **VNKG***PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 272)
hGal9-GPI	>Artificial Sequence; **hGal9**-*GPI*, DNA **ATGGCCTTCAGCGGTTCCCAGGCTCCCTACCTGAGTCCAGCTGTCCCCTTTTCTGGG** **ACTATTCAAGGAGGTCTCCAGGACGGACTTCAGATCACTGTCAATGGGACCGTTCTC** **AGCTCCAGTGGAACCAGGTTTGCTGTGAACTTTCAGACTGGCTTCAGTGGAAATGAC** **ATTGCCTTCCACTTCAACCCTCGGTTTGAAGATGGAGGGTACGTGGTGTGCAACACG** **AGGCAGAACGGAAGCTGGGGGCCCGAGGAGAGGAAGACACACATGCCTTTCCAGAAG** **GGGATGCCCTTTGACCTCTGCTTCCTGGTGCAGAGCTCAGATTTCAAGGTGATGGTG** **AACGGGATCCTCTTCGTGCAGTACTTCCACCGCGTGCCCTTCCACCGTGTGGACACC** **ATCTCCGTCAATGGCTCTGTGCAGCTGTCCTACATCAGCTTCCAGAACCCCCGCACA** **GTCCCTGTTCAGCCTGCCTTCTCCACGGTGCCGTTCTCCCAGCCTGTCTGTTTCCCA** **CCCAGGCCCAGGGGGCGCAGACAAAAACCTCCCGGCGTGTGGCCTGCCAACCCGGCT** **CCCATTACCCAGACAGTCATCCACACAGTGCAGAGCGCCCCTGGACAGATGTTCTCT** **ACTCCCGCCATCCCACCTATGATGTACCCCCACCCCGCCTATCCGATGCCTTTCATC** **ACCACCATTCTGGGAGGGCTGTACCCATCCAAGTCCATCCTCCTGTCAGGCACTGTC**

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CTGCCCAGTGCTCAGAGGTTCCACATCAACCTGTGCTCTGGGAACCACATCGCCTTC **CACCTGAACCCCCGTTTTGATGAGAATGCTGTGGTCCGCAACACCCAGATCGACAAC** **TCCTGGGGGTCTGAGGAGCGAAGTCTGCCCCGAAAAATGCCCTTCGTCCGTGGCCAG** **AGCTTCTCAGTGTGGATCTTGTGTGAAGCTCACTGCCTCAAGGTGGCCGTGGATGGT** **CAGCACCTGTTTGAATACTACCATCGCCTGAGGAACCTGCCCACCATCAACAGACTG** **GAAGTGGGGGGCGACATCCAGCTGACCCATGTGCAGACA***CCAAATAAAGGAAGTGGA* *ACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGT* *TTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 273) >Artificial Sequence; **hGal9**-*GPI*, Amino Acid **MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGND** **IAFHFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMV** **NGILFVQYFHRVPFHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFP** **PRPRGRRQKPPGVWPANPAPITQTVIHTVQSAPGQMPSTPAIPPMMYPHPAYPMPFI** **TTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDN** **SWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRL** **EVGGDIQLTHVQT***PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 274)
hHVEM-GPI	>Artificial Sequence; **hHVEM**-*GPI*, DNA ***ATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGGAGATCCACCCCCAAAACCGAC*** ***GTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGAGCCCCCTGCTACGCCCCAGCT*** ***CTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGC*** ***AGTCCAGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAA*** ***CCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAGTGTCTGCAG*** ***TGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGCGAGCCGGAACTGCTCCAGGACA*** ***GAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGAC*** ***CACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAG*** ***GGAGGCACCGAGAGTCAGGACACCCTGTGTCAGAACTGCCCCCCGGGGACCTTCTCT*** ***CCCAATGGGACCCTGGAGGAATGTCAGCACCAGACCAAGTGCAGCTGGCTGGTGACG*** ***AAGGCCGGAGCTGGGACCAGCAGCTCCCACTGGGTA****CCAAATAAAGGAAGTGGAACC* *ACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTG* *CTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 275) >Artificial Sequence; **hHVEM**-*GPI*, Amino Acid **MEPPGDWGPPPWRSTPKTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKC** **SPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRT** **ENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS** **PNGTLEECQHQTKCSWLVTKAGAGTSSSHWV***PNKGSGTTSGTTRLLSGHTCFTLTGL* *LGTLVTMGLLT* (SEQ ID NO: 276)
hPDL2-GPI	>Artificial Sequence; **hPDL2**-*GPI*, DNA **ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGATAGCAGCT** **TTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGCATGGCAGCAATGTG** **ACCCTGGAATGCAACTTTGACACTGGAAGTCATGTGAACCTTGGAGCAATAACAGCC** **AGTTTGCAAAAGGTGGAAAATGATACATCCCCACACCGTGAAAGAGCCACTTTGCTG** **GAGGAGCAGCTGCCCCTAGGGAAGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGG** **GACGAAGGACAGTACCAATGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTAC** **CTGACTCTGAAAGTCAAAGCTTCCTACAGGAAAATAAACACTCACATCCTAAAGGTT** **CCAGAAACAGATGAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAA** **GTATCCTGGCCAAACGTCAGCGTTCCTGCCAACACCAGCCACTCCAGGACCCCTGAA** **GGCCTCTACCAGGTCACCAGTGTTCTGCGCCTAAAGCCACCCCCTGGCAGAAACTTC** **AGCTGTGTGTTCTGGAATACTCACGTGAGGGAACTTACTTTGGCCAGCATTGACCTT** **CAAAGTCAGATGGAACCCAGGACCCATCCAACT***CCAAATAAAGGAAGTGGAACCACT* *TCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTT* *GGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 277) >Artificial Sequence; **hPDL2**-*GPI*, Amino Acid **MIFLLLMLSLELQLHQIAALFTVTVPKELYIIEHGSNVTLECNFDTGSHVNLGAITA** **SLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQYQCIIIYGVAWDYKY** **LTLKVKASYRKINTHILKVPETDEVELTCQATGYPLAEVSWPNVSVPANTSHSRTPE** **GLYQVTSVLRLKPPPGRNFSCVFWNTHVRELTLASIDLQSQMEPRTHPT***PNKGSGTT* *SGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 278)
hTSG6-GPI	>Artificial Sequence; **hTSG6**-*GPI*, DNA **ATGATCATCTTAATTTACTTATTTCTCTTGCTATGGGAAGACACTCAAGGATGGGGA** **TTCAAGGATGGAATTTTTCATAACTCCATATGGCTTGAACGAGCAGCCGGTGTGTAC** **CACAGAGAAGCACGGTCTGGCAAATACAAGCTCACCTACGCAGAAGCTAAGGCGGTG** **TGTGAATTTGAAGGCGGCCATCTCGCAACTTACAAGCAGCTAGAGGCAGCCAGAAAA** **ATTGGATTTCATGTCTGTGCTGCTGGATGGATGGCTAAGGGCAGAGTTGGATACCCC** **ATTGTGAAGCCAGGGCCCAACTGTGGATTTGGAAAAACTGGCATTATTGATTATGGA** **ATCCGTCTCAATAGGAGTGAAAGATGGGATGCCTATTGCTACAACCCACACGCAAAG** **GAGTGTGGTGGCGTCTTTACAGATCCAAAGCAAATTTTTAAATCTCCAGGCTTCCCA**

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	AATGAGTACGAAGATAACCAAATCTGCTACTGGCACATTAGACTCAAGTATGGTCAG **CGTATTCACCTGAGTTTTTTAGATTTTGACCTTGAAGATGACCCAGGTTGCTTGGCT** **GATTATGTTGAAATATATGACAGTTACGATGATGTCCATGGCTTTGTGGGAAGATAC** **TGTGGAGATGAGCTTCCAGATGACATCATCAGTACAGGAAATGTCATGACCTTGAAG** **TTTCTAAGTGATGCTTCAGTGACAGCTGGAGGTTTCCAAATCAAATATGTTGCAATG** **GATCCTGTATCCAAATCCAGTCAAGGAAAAAATACAAGTACTACTTCTACTGGAAAT** **AAAAACTTTTTAGCTGGAAGATTTAGCCACTTA**ATCGAT*CCAAATAAAGGAAGTGGA* *ACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGT* *TTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 279) >Artificial Sequence; **hTSG6**-*GPI*, Amino Acid **MIILIYLFLLLWEDTQGWGFKDGIFHNSIWLERAAGVYHREARSGKYKLTYAEAKAV** **CEFEGGHLATYKQLEAARKIGFHVCAAGWMAKGRVGYPIVKPGPNCGFGKTGIIDYG** **IRLNRSERWDAYCYNPHAKECGGVFTDPKQIFKSPGFPNEYEDNQICYWHIRLKYGQ** **RIHLSFLDFDLEDDPGCLADYVEIYDSYDDVHGFVGRYCGDELPDDIISTGNVMTLK** **FLSDASVTAGGFQIKYVAMDPVSKSSQGKNTSTTSTGNKNFLAGRFSHL**ID*PNKGSG* **TTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT** (SEQ ID NO: 280)
hHVEM-Fc-GPI	>Artificial Sequence; **hHVEM**-Fc-*GPI*, DNA **ATGGAGCCTCCTGGAGACTGGGGGCCTCCT**CCCTGGAGATCCACCCCCAAAACCGAC **GTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGAGCCCCCTGCTACGCCCCAGCT** **CTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGC** **AGTCCAGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAA** **CCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAGTGTCTGCAG** **TGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGCGAGCCGGAACTGCTCCAGGACA** **GAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGAC** **CACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAG** **GGAGGCACCGAGAGTCAGGACACCCTGTGTCAGAACTGCCCCCCGGGGACCTTCTCT** **CCCAATGGGACCCTGGAGGAATGTCAGCACCAGACCAAGTGCAGCTGGCTGGTGACG** **AAGGCCGGAGCTGGGACCAGCAGCTCCCACTGGGTAA**TCGATGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCC CCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTG GTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT GTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAAC CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGA* *AGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTG* *ACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 281) >Artificial Sequence; **hHVEM**-Fc-*GPI*, Amino Acid **MEPPGDWGPPPWRSTPKTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKC** **SPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRT** **ENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS** **PNGTLEECQHQTKCSWLVTKAGAGTSSSHWV**IDDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*PNKGSGTTSGTTRLLSGHTCFTL* *TGLLGTLVTMGLLT* (SEQ ID NO: 282)
hPDL1-GPI-P2A- hHVEM-GPI	>Artificial Sequence; **hPDL1**-*GPI*-P2A-**hHVEM**-*GPI*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAA** **CTACCTCTGGCACATCCTCCAAATGAAAGG***CCAAATAAAGGAAGTGGAACCACTTCA* *GGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGG* *ACGCTAGTAACCATGGGCTTGCTGACT*GGAAGCGGAGCTACTAACTTCAGCCTGCTG AAGCAGGCTGGCGACGTGGAGGAGAACCCTGGACCT**ATGGAGCCTCCTGGAGACTGG**

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GGGCCTCCTCCCTGGAGATCCACCCCCAAAACCGACGTCTTGAGGCTGGTGCTGTAT **CTCACCTTCCTGGGAGCCCCCTGCTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGAC** **GAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTTATCGTGTGAAG** **GAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCCTGCCCTCCAGGCACCTAC** **ATTGCCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGCCAAATGTGTGACCCAGCC** **ATGGGCCTGCGCGCGAGCCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGCTGC** **AGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCT** **TACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGAC** **ACCCTGTGTCAGAACTGCCCCCCGGGGACCTTCTCTCCCAATGGGACCCTGGAGGAA** **TGTCAGCACCAGACCAAGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC** **AGCTCCCACTGGGTA***CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTT* *CTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATG* *GGCTTGCTGACTTAG* (SEQ ID NO: 283) >Artificial Sequence; **hPDL1**-*GPI*-P2A-**hHVEM**-*GPI*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE** **LPLAHPPNER***PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLTGS*GATNFSLL KQAGDVEENPGP**MEPPGDWGPPPWRSTPKTDVLRLVLYLTFLGAPCYAPALPSCKED** **EYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPA** **MGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQD** **TLCQNCPPGTFSPNGTLEECQHQTKCSWINTKAGAGTSSSHWV***PNKGSGTTSGTTRL* *LSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 284)
mCTLA4-Fc-GPI	>Artificial Sequence; **mCTLA4**-Fc-*GPI*, DNA **ATGGCTTGTCTTGGACTCCGGAGGTACAAAGCTCAACTGCAGCTGCCTTCTAGGACT** **TGGCCTTTTGTAGCCCTGCTCACTCTTCTTTTCATCCCAGTCTTCTCTGAAGCCATA** **CAGGTGACCCAACCTTCAGTGGTGTTGGCTAGCAGCCATGGTGTCGCCAGCTTTCCA** **TGTGAATATTCACCATCACACAACACTGATGAGGTCCGGGTGACTGTGCTGCGGCAG** **ACAAATGACCAAATGACTGAGGTCTGTGCCACGACATTCACAGAGAAGAATACAGTG** **GGCTTCCTAGATTACCCCTTCTGCAGTGGTACCTTTAATGAAAGCAGAGTGAACCTC** **ACCATCCAAGGACTGAGAGCTGTTGACACGGGACTGTACCTCTGCAAGGTGGAACTC** **ATGTACCCACCGCCATACTTTGTGGGCATGGGCAACGGGACGCAGATTTATGTCATT** **GATCCAGAACCATGCCCGGATTCTGA**ATCGATGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCA AGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATA ATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGC CCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACC AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGT GGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACT CCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGC AGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGTGGAACCA* *CTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGC* *TTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 285) >Artificial Sequence; **mCTLA4**-Fc-*GPI*, Amino Acid **MACLGLRRYKAQLQLPSRTWPFVALLTLLFIPVFSEAIQVTQPSVVLASSHGVASFP** **CEYSPSHNTDEVRVTVLRQTNDQMTEVCATTFTEKNTVGFLDYPFCSGTFNESRVNL** **TIQGLRAVDTGLYLCKVELMYPPPYFVGMGNGTQIYVIDPEPCPDSD** IDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG KID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 286)
mPDL1-C1C2	>Artificial Sequence; **mPDL1**-*C1C2*, DNA **ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTT** **ACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGCAACGTCACGATG** **GAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGG** **GAAAAGGAAGATGAGCAAGTGATTCAGTTTGTGGCAGGAGAGGAGGACCTTAAGCCT** **CAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGA** **AATGCTGCCCTTCAGATCACAGACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGC** **ATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCA** **TACCGCAAAATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTA** **ATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGACCAC** **CAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGACAGAGGGGATGCTTCTC** **AATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGATGTTTTCTACTGTACG**

TABLE 4-continued

Full Length Constructs	
Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	TTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTG **CCTGCAACACATCCTCCACAGAACAGGACT**ATCGAT*GTCGAGCCACTGGGCATGGAG* *AATGGGAACATTGCCAACTCACAGATCGCCGCCTCATCTGTGCGTGTGACCTTCTTG* *GGTTTGCAGCATTGGGTCCCGGAGCTGGCCCGCCTGAACCGCGCAGGCATGGTCAAT* *GCCTGGACACCCAGCAGCAATGACGATAACCCCTGGATCCAGGTGAACCTGCTGCGG* *AGGATGTGGGTAACAGGTGTGGTGACGCAGGGTGCCAGCCGCTTGGCCAGTCATGAG* *TACCTGAAGGCCTTCAAGGTGGCCTACAGCCTTAATGGACACGAATTCGATTTCATC* *CATGATGTTAATAAAAAACACAAGGAGTTTGTGGGTAACTGGAACAAAAACGCGGTG* *CATGTCAACCTGTTTGAGACCCCTGTGGAGGCTCAGTACGTGAGATTGTACCCCACG* *AGCTGCCACACGGCCTGCACTCTGCGCTTTGAGCTACTGGGCTGTGAGCTGAACGGA* *TGCGCCAATCCCCTGGGCCTGAAGAATAACAGCATCCCTGACAAGCAGATCACGGCC* *TCCAGCAGCTACAAGACCTGGGGCTTGCATCTCTTCAGCTGGAACCCCTCCTATGCA* *CGGCTGGACAAGCAGGGCAACTTCAACGCCTGGGTTGCGGGGAGCTACGGTAACGAT* *CAGTGGCTGCAGATCTTCCCTGGCAACTGGGACAACCACTCCCACAAGAAGAACTTG* *TTTGAGACGCCCATCCTGGCTCGCTATGTGCGCATCCTGCCTGTAGCCTGGCACAAC* *CGCATCGCCCTGCGCCTGGAGCTGCTGGGCTGTTAG* (SEQ ID NO: 287) >Artificial Sequence; **mPDL1**-*C1C2*, Amino Acid **MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYW** **EKEDEQVIQFVAGEEDLKPQHSNFSGRASLPKDQLLKGNAALQITDVKLQDAGVYCC** **IISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDH** **QPVSGKRSVTTSRTEGMLLNVTSSLRVNATANDVFYCTFWRSQPGQNHTAELIIPEL** **PATHPPQNRT**ID*VEPLGMENGNIANSQIAASSVRVTFLGLQHWVPELARLNRAGMVN* *AWTPSSNDDNPWIQVNLLRRMWVTGVVTQGASRLASHEYLKAFKVAYSLNGHEFDFI* *HDVNKKHKEFVGNWNKNAVHVNLFETPVEAQYVRLYPTSCHTACTLRFELLGCELNG* *CANPLGLKNNSIPDKQITASSSYKTWGLHLFSWNPSYARLDKQGNFNAWVAGSYGND* *QWLQIFPGNWDNHSHKKNLFETPILARYVRILPVAWHNRIALRLELLGC* (SEQ ID NO: 288)
mPDL1-Fc-GPI	>Artificial Sequence; **mPDL1**-Fc-*GPI*, DNA **ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTT** **ACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGCAACGTCACGATG** **GAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGG** **GAAAAGGAAGATGAGCAAGTGATTCAGTTTGTGGCAGGAGAGGAGGACCTTAAGCCT** **CAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGA** **AATGCTGCCCTTCAGATCACAGACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGC** **ATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCA** **TACCGCAAAATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTA** **ATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGACCAC** **CAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGACAGAGGGGATGCTTCTC** **AATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGATGTTTTCTACTGTACG** **TTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTG** **CCTGCAACACATCCTCCACAGAACAGGACT**ATCGATGACAAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGTGGA* *ACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGT* *TTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 289) >Artificial Sequence; **mPDL1**-Fc-*GPI*, Amino Acid **MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYW** **EKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQITDVKLQDAGVYCC** **IISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDH** **QPVSGKRSVTTSRTEGMLLNVTSSLRVNATANDVPYCTFWRSQPGQNHTAELIIPEL** **PATHPPQNRT**IDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGKID*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 290)
mPDL1-GPI	>Artificial Sequence; **mPDL1**-*GPI*, DNA **ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTT** **ACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGCAACGTCACGATG** **GAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGG** **GAAAAGGAAGATGAGCAAGTGATTCAGTTTGTGGCAGGAGAGGAGGACCTTAAGCCT**

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGA **AATGCTGCCCTTCAGATCACAGACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGC** **ATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCA** **TACCGCAAAATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTA** **ATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGACCAC** **CAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGAZAGAGGGGATGCTTCTC** **AATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGATGTTTTCTACTGTACG** **TTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTG** **CCTGCAACACATCCTCCACAGAACAGGACT***CCAAATAAAGGAAGTGGAACCACTTCA* *GGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGG* *ACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 291) >Artificial Sequence; **mPDL1**-*GPI*, Amino Acid **MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYW** **EKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQITDVKLQDAGVYCC** **IISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDH** **QPVSGKRSVTTSRTEGMLLNVTSSLRVNATANDVFYCTFWRSQPGQNHTAELIIPEL** **PATHPPQNRT***PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 292)
mPDL2-C1C2	>Artificial Sequence; **mPDL2**-*C1C2*, DNA **ATGCTGCTCCTGCTGCCGATACTGAACCTGAGCTTACAACTTCATCCTGTAGCAGCT** **TTATTCACCGTGACAGCCCCTAAAGAAGTGTACACCGTAGACGTCGGCAGCAGTGTG** **AGCCTGGAGTGCGATTTTGACCGCAGAGAATGCACTGAACTGGAAGGGATAAGAGCC** **AGTTTGCAGAAGGTAGAAAATGATACGTCTCTGCAAAGTGAAAGAGCCACCCTGCTG** **GAGGAGCAGCTGCCCCTGGGAAAGGCTTTGTTCCACATCCCTAGTGTCCAAGTGAGA** **GATTCCGGGCAGTACCGTTGCCTGGTCATCTGCGGGGCCGCCTGGGACTACAAGTAC** **CTGACGGTGAAAGTCAAAGCTTCTTACATGAGGATAGACACTAGGATCCTGGAGGTT** **CCAGGTACAGGGGAGGTGCAGCTTACCTGCCAGGCTAGAGGTTATCCCCTAGCAGAA** **GTGTCCTGGCAAAATGTCAGTGTTCCTGCCAACACCAGCCACATCAGGACCCCCGAA** **GGCCTCTACCAGGTCACCAGTGTTCTGCGCCTCAAGCCTCAGCCTAGCAGAAACTTC** **AGCTGCATGTTCTGGAATGCTCACATGAAGGAGCTGACTTCAGCCATCATTGACCCT** **CTGAGTCGGATGGAACCCAAAGTCCCCAGAACG**ATCGAT*GTCGAGCCACTGGGCATG* *GAGAATGGGAACATTGCCAACTCACAGATCGCCGCCTCATCTGTGCGTGTGACCTTC* *TTGGGTTTGCAGCATTGGGTCCCGGAGCTGGCCCGCCTGAACCGCGCAGGCATGGTC* *AATGCCTGGACACCCAGCAGCAATGACGATAACCCCTGGATCCAGGTGAACCTGCTG* *CGGAGGATGTGGGTAACAGGTGTGGTGACGCAGGGTGCCAGCCGCTTGGCCAGTCAT* *GAGTACCTGAAGGCCTTCAAGGTGGCCTACAGCCTTAATGGACACGAATTCGATTTC* *ATCCATGATGTTAATAAAAAACACAAGGAGTTTGTGGGTAACTGGAACAAAAACGCG* *GTGCATGTCAACCTGTTTGAGACCCCTGTGGAGGCTCAGTACGTGAGATTGTACCCC* *ACGAGCTGCCACACGGCCTGCACTCTGCGCTTTGAGCTACTGGGCTGTGAGCTGAAC* *GGATGCGCCAATCCCCTGGGCCTGAAGAATAACAGCATCCCTGACAAGCAGATCACG* *GCCTCCAGCAGCTACAAGACCTGGGGCTTGCATCTCTTCAGCTGGAACCCCTCCTAT* *GCACGGCTGGACAAGCAGGGCAACTTCAACGCCTGGGTTGCGGGGAGCTACGGTAAC* *GATCAGTGGCTGCAGATCTTCCCTGGCAACTGGGACAACCACTCCCACAAGAAGAAC* *TTGTTTGAGACGCCCATCCTGGCTCGCTATGTGCGCATCCTGCCTGTAGCCTGGCAC* *AACCGCATCGCCCTGCGCCTGGAGCTGCTGGGCTGTTAG* (SEQ ID NO: 293) >Artificial Sequence; **mPDL2**-*C1C2*, Amino Acid **MLLLLPILNLSLQLHPVAALFTVTAPKEVYTVDVGSSVSLECDFDRRECTELEGIRA** **SLQKVENDTSLQSERATLLEEQLPLGKALFHIPSVQVRDSGQYRCLVICGAAWDYKY** **LTVKVKASYMRIDTRILEVPGTGEVQLTCQARGYPLAEVSWQNVSVPANTSHIRTPE** **GLYQVTSVLRLKPQPSRNFSCMFWNAHMKELTSAIIDPLSRMEPKVPRT**ID*VEPLGM* *ENGNIANSQIAASSVRVTFLGLQHWVPELARLNRAGMVNAWTPSSNDDNPWIQVNLL* *RRMWVTGVVTQGASRLASHEYLKAFKVAYSLNGHEFDFIHDVNKKHKEFVGNWNKNA* *VHVNLFETPVEAQYVRLYPTSCHTACTLRFELLGCELNGCANPLGLKNNSIPDKQIT* *ASSSYKTWGLHLFSWNPSYARLDKQGNFNAWVAGSYGNDQWLQIFPGNWDNHSHKKN* *LFETPILARYVRILPVAWHNRIALRLELLGC* (SEQ ID NO: 294)
mPDL2-Fc-GPI	>Artificial Sequence; **mPDL2**-Fc-*GPI*, DNA **ATGCTGCTCCTGCTGCCGATACTGAACCTGAGCTTACAACTTCATCCTGTAGCAGCT** **TTATTCACCGTGACAGCCCCTAAAGAAGTGTACACCGTAGACGTCGGCAGCAGTGTG** **AGCCTGGAGTGCGATTTTGACCGCAGAGAATGCACTGAACTGGAAGGGATAAGAGCC** **AGTTTGCAGAAGGTAGAAAATGATACGTCTCTGCAAAGTGAAAGAGCCACCCTGCTG** **GAGGAGCAGCTGCCCCTGGGAAAGGCTTTGTTCCACATCCCTAGTGTCCAAGTGAGA** **GATTCCGGGCAGTACCGTTGCCTGGTCATCTGCGGGGCCGCCTGGGACTACAAGTAC** **CTGACGGTGAAAGTCAAAGCTTCTTACATGAGGATAGACACTAGGATCCTGGAGGTT** **CCAGGTACAGGGGAGGTGCAGCTTACCTGCCAGGCTAGAGGTTATCCCCTAGCAGAA** **GTGTCCTGGCAAAATGTCAGTGTTCCTGCCAACACCAGCCACATCAGGACCCCCGAA** **GGCCTCTACCAGGTCACCAGTGTTCTGCGCCTCAAGCCTCAGCCTAGCAGAAACTTC** **AGCTGCATGTTCTGGAATGCTCACATGAAGGAGCTGACTTCAGCCATCATTGACCCT** **CTGAGTCGGATGGAACCCAAAGTCCCCAGAACG**ATCGAT<u>GACAAAACTCACACATGC</u> <u>CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCA</u> <u>AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTG</u>

TABLE 4-continued

Full Length Constructs	
Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTG GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC AAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG CTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCAC TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*CCAAATAAAGGAAGT* *GGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACA* *GGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 295) >Artificial Sequence; **mPDL2**-Fc-*GPI*, Amino Acid **MLLLLPILNLSLQLHPVAALFTVTAPKEVYTVDVGSSVSLECDFDRRECTELEGIRA** **SLQKVENDTSLQSERATLLEEQLPLGKALFHIPSVQVRDSGQYRCLVICGAAWDYKY** **LTVKVKASYMRIDTRILEVPGTGEVQLTCQARGYPLAEVSWQNVSVPANTSHIRTPE** **GLYQVTSVLRLKPQPSRNFSCMFWNAHNKELTSAIIDPLSRMEPKVPRT**IDDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKID*PNKGS* *GTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 296)
mPDL1-mFc-GPI	>Artificial Sequence; **mPDL1**-mFc-*GPI*, DNA **ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTT** **ACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGCAACGTCACGATG** **GAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGG** **GAAAAGGAAGATGAGCAAGTGATTCAGTTTGTGGCAGGAGAGGAGGACCTTAAGCCT** **CAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGA** **AATGCTGCCCTTCAGATCACAGACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGC** **ATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCA** **TACCGCAAAATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTA** **ATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGACCAC** **CAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGACAGAGGGGATGCTTCTC** **AATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGATGTTTTCTACTGTACG** **TTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTG** **CCTGCAACACATCCTCCACAGAACAGGACT**GGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATT ACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAG GTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCC CGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCAC CAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGCAGCTTTCCCT GCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCGAAGGCTCCACAGGTG TACACCATTCCACCTCCCAAGGAGCAGATGGCCAAGGATAAAGTCAGTCTGACCTGC ATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGAATGGGCAG CCAGCGGAGAACTACAAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTTC GTCTACAGCAAGCTCAATGTGCAGAAGAGCAACTGGGAGGCAGGAAATACTTTCACC TGCTCTGTGTTACATGAGGGCCTGCACAACCACCATACTGAGAAGAGCCTCTCCCAC TCTCCTGGTAAA*CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTA* *TCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGC* *TTGCTGACTTAG* (SEQ ID NO: 297) >Artificial Sequence; **mPDL1**-mFc-*GPI*, Amino Acid **MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYW** **EKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQITDVKLQDAGVYCC** **IISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDH** **QPVSGKRSVTTSRTEGMLLNVTSSLRVNATANDVFYCTFWRSQPGQNHTAELIIPEL** **PATHPPQNRT**GCKPCICTVPEVSSVFIFPPPKPKDVLTITLTPKVTCVVVDISKDDPE VQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFP APIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQ PAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSH SPGK*PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 298)
mPDL2-GPI	>Artificial Sequence; **mPDL2**-*GPI*, DNA **ATGCTGCTCCTGCTGCCGATACTGAACCTGAGCTTACAACTTCATCCTGTAGCAGCT** **TTATTCACCGTGACAGCCCCTAAAGAAGTGTACACCGTAGACGTCGGCAGCAGTGTG** **AGCCTGGAGTGCGATTTTGACCGCAGAGAATGCACTGAACTGGAAGGGATAAGAGCC** **AGTTTGCAGAAGGTAGAAAATGATACGTCTCTGCAAAGTGAAAGAGCCACCCTGCTG** **GAGGAGCAGCTGCCCCTGGGAAAGGCTTTGTTCCACATCCCTAGTGTCCAAGTGAGA** **GATTCCGGGCAGTACCGTTGCCTGGTCATCTGCGGGGCCGCCTGGGACTACAAGTAC** **CTGACGGTGAAAGTCAAAGCTTCTTACATGAGGATAGACACTAGGATCCTGGAGGTT** **CCAGGTACAGGGGAGGTGCAGCTTACCTGCCAGGCTAGAGGTTATCCCCTAGCAGAA**

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	GTGTCCTGGCAAAATGTCAGTGTTCCTGCCAACACCAGCCACATCAGGACCCCCGAA **GGCCTCTACCAGGTCACCAGTGTTCTGCGCCTCAAGCCTCAGCCTAGCAGAAACTTC** **AGCTGCATGTTCTGGAATGCTCACATGAAGGAGCTGACTTCAGCCATCATTGACCCT** **CTGAGTCGGATGGAACCCAAAGTCCCCAGAACG***CCAAATAAAGGAAGTGGAACCACT* *TCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTT* *GGGACGCTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 299) >Artificial Sequence; **mPDL2**-*GPI*, Amino Acid **MLLLLPILNLSLQLHPVAALFTVTAPKEVYTVDVGSSVSLECDFDRRECTELEGIRA** **SLQKVENDTSLQSERATLLEEQLPLGKALFHIPSVQVRDSGQYRCLVICGAAWDYKY** **LTVKVKASYMRIDTRILEVPGTGEVQLTCQARGYPLAEVSWQNVSVPANTSHIRTPE** **GLYQVTSVLRLKPQPSRNFSCMFWNAHMKELTSAIIDPLSRMEPKVPRT***PNKGSGTT* *SGTTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 300)
mPDL1-GPI-P2A-mHVEM-GPI	>Artificial Sequence; **mPDL**1-*GPI*-P2A-**mHVEM**-*GPI*, DNA **ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTT** **ACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGCAACGTCACGATG** **GAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGG** **GAAAAGGAAGATGAGCAAGTGATTCAGTTTGTGGCAGGAGAGGAGGACCTTAAGCCT** **CAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGA** **AATGCTGCCCTTCAGATCACAGACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGC** **ATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCA** **TACCGCAAAATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTA** **ATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGACCAC** **CAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGACAGAGGGGATGCTTCTC** **AATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGATGTTTTCTACTGTACG** **TTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTG** **CCTGCAACACATCCTCCACAGAACAGGACT***CCAAATAAAGGAAGTGGAACCACTTCA* *GGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGG* *ACGCTAGTAACCATGGGCTTGCTGACT*GGAAGCGGAGCTACTAACTTCAGCCTGCTG AAGCAGGCTGGCGACGTGGAGGAGAACCCTGGACCT**ATGGAACCTCTCCCAGGATGG** **GGGTCGGCACCCTGGAGCCAGGCCCCTACAGACAACACCTTCAGGCTGGTGCCTTGT** **GTCTTCCTTTTGAACTTGCTGCAGCGCATCTCTGCCCAGCCCTCATGCAGACAGGAG** **GAGTTCCTTGTGGGAGACGAGTGCTGCCCCATGTGCAACCCAGGTTACCATGTGAAG** **CAGGTCTGCAGTGAGCATACAGGCACAGTGTGTGCCCCCTGTCCCCCACAGACATAT** **ACCGCCCATGCAAATGGCCTGAGCAAGTGTCTGCCCTGCGGAGTCTGTGATCCAGAC** **ATGGGCCTGCTGACCTGGCAGGAGTGCTCCAGCTGGAAGGACACTGTGTGCAGATGC** **ATCCCAGGCTACTTCTGTGAGAACCAGGATGGGAGCCACTGTTCCACATGCTTGCAG** **CACACCACCTGCCCTCCAGGGCAGAGGGTAGAGAAGAGAGGGACTCACGACCAGGAC** **ACTGTATGTGCTGACTGCCTAACAGGGACCTTCTCACTTGGAGGGACTCAGGAGGAA** **TGCCTGCCCTGGACCAACTGCAGTGCATTTCAACAGGAAGTAAGACGTGGGACCAAC** **AGCACAGACACCACCTGCTCCTCCCAG***CCAAATAAAGGAAGTGGAACCACTTCAGGT* *ACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACG* *CTAGTAACCATGGGCTTGCTGACTTAG* (SEQ ID NO: 301) >Artificial Sequence; **mPDL1**-*GPI*-P2A-**mHVEM**-*GPI*, Amino Acid **MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYW** **EKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQITDVKLQDAGVYCC** **IISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDH** **QPVSGKRSVTTSRTEGMLLNVTSSLRVNATANDVFYCTFWRSQPGQNHTAELIIPEL** **PATHPPQNRT***PNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLTGSGATNFSLL* KQAGDVEENPGP**MEPLPGWGSAPWSQAPTDNTFRLVPCVFLLNLLQRISAQPSCRQE** **EFLVGDECCPMCNPGYHVKQVCSEHTGTVCAPCPPQTYTAHANGLSKCLPCGVCDPD** **MGLLTWQECSSWKDTVCRCIPGYFCENQDGSHCSTCLQHTTCPPGQRVEKRGTHDQD** **TVCADCLTGTFSLGGTQEECLPWTNCSAFQQEVRRGTNSTDTTCSSQ***PNKGSGTTSG* *TTRLLSGHTCFTLTGLLGTLVTMGLLT* (SEQ ID NO: 302)
hPDL1-ADAM10	>Artificial Sequence; **hPDL1**-*ADAM10*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAA** **CTACCTCTGGCACATCCTCCAAATGAAAGG***TGTGGAAATGGAATGGTAGAACAAGGT* *GAAGAATGTGATTGTGGCTATAGTGACCAGTGTAAAGATGAATGCTGCTTCGATGCA* *AATCAACCAGAGGGAAGAAAATGCAAACTGAAACCTGGGAAACAGTGCAGTCCAAGT*

TABLE 4-continued

Full Length Constructs

Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	CAAGGTCCTTGTTGTACAGCACAGTGTGCATTCAAGTCAAAGTCTGAGAAGTGTCGG *GATGATTCAGACTGTGCAAGGGAAGGAATATGTAATGGCTTCACAGCTCTCTGCCCA* *GCATCTGACCCTAAACCAAACTTCACAGACTGTAATAGGCATACACAAGTGTGCATT* *AATGGGCAATGTGCAGGTTCTATCTGTGAGAAATATGGCTTAGAGGAGTGTACGTGT* *GCCAGTTCTGATGGCAAAGATGATAAAGAATTATGCCATGTATGCTGTATGAAGAAA* *ATGGACCCATCAACTTGTGCCAGTACAGGGTCTGTGCAGTGGAGTAGGCACTTCAGT* *GGTCGAACCATCACCCTGCAACCTGGATCCCCTTGCAACGATTTTAGAGGTTACTGT* *GATGTTTTCATGCGGTGCAGATTAGTAGATGCTGATGGTCCTCTAGCTAGGCTTAAA* *AAAGCAATTTTTAGTCCAGAGCTCTATGAAAACATTGCTGAATGGATTGTGGCTCAT* *TGGTGGGCAGTATTACTTATGGGAATTGCTCTGATCATGCTAATGGCTGGATTTATT* *AAGATATGCAGTGTTaATACTCCAAGTAGTAATCCAAAGTTGCCTCCTCCTAAACCA* *CTTCCAGGCACTTTAAAGAGGAGGAGACCTCCACAGCCCATTCAGCAACCCCAGCGT* *CAGCGGCCCCGAGAGAGTTATCAAATGGGACACATGAGACGCTAA* (SEQ ID NO: 303) >Artificial Sequence; **hPDL1**-ADAM10, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKEPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE** **LPLAHPPNER***CGNGMVEQGEECDCGYSDQCKDECCFDANQPEGRKCKLKPGKQCSPS* *QGPCCTAQCAFKSKSEKCRDDSDCAREGICNGFTALCPASDPKPNFTDCNRHTQVCI* *NGQCAGSICEKYGLEECTCASSDGKDDEELCHVCCMKKMDPSTCASTGSVQWSRHFS* *GRTITLQPGSPCNDFRGYCDVFMRCRLVDADGPLARLKKAIFSPELYENIAEWIVAH* *WWAVLLMGIALIMLMAGFIKICSVHTPSSNPKLPPPKPLPGTLKRRRPPQPIQQPQR* *QRPRESYQMGHMRR* (SEQ ID NO: 304)
hPDL1-4Fc-CD9tm2	>Artificial Sequence; **hPDL1**-4Fc-*CD9tm2*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAA** **CTACCTCTGGCACATCCTCCAAATGAAAGG**GAGTCCAAATATGGTCCCCCATGCCCA TCATGCCCAGCACCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAA CCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGAC GTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTG CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTC AGGGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGTAAGGAGTACAAGTGCAAG GTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGGAGGACAACTACAAGACCACGCCTCCCGTGCTG GACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGG CAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC ACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA*TTCTACACAGGAGTCTATATTCTG* *ATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTG* *CAGGAGTCCCAGTGC* (SEQ ID NO: 305) >Artificial Sequence; **hPDL1**-4Fc-*CD9tm2*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE** **LPLAHPPNER**ESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVRVLTVLHQDWLNGKEYKCK VSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPEDNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHY TQKSLSLSPGK*FYTGVYILIGAGALMMLVGFLGCCGAVQESQCVIM* (SEQ ID NO: 306)
hPDL1-4Fc-CD9tm2-modified KRas	>Artificial Sequence; **hPDL1**-4Fc-*CD9tm2-KRAS*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC**

TABLE 4-continued

Full Length Constructs	
Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAA** **CTACCTCTGGCACATCCTCCAAATGAAAGG**GAGTCCAAATATGGTCCCCCATGCCCA TCATGCCCAGCACCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAA CCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGAC GTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTG CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTC AGGGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGTAAGGAGTACAAGTGCAAG GTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGGAGGACAACTACAAGACCACGCCTCCCGTGCTG GACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGG CAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC ACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA*TTCTACACAGGAGTCTATATTCTG* *ATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTG* *CAGGAGTCCCAGTGCAAAAAGAAGAAAAAGAAGAAGAAGACAAAGTGTGTAATTATG* *TAA* (SEQ ID NO: 307) >Artificial Sequence; **hPDL1**-4Fc-*CD9tm2*-*KRAS*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE** **LPLAHPPNER**ESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVRVLTVLHQDWLNGKEYKCK VSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPEDNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHY TQKSLSLSPGK*FYTGVYILIGAGALMMLVGFLGCCGAVQESQCKKKKKKKKTKCVIM* (SEQ ID NO: 308)
hPDL1-Fc-CD9tm2	>Artificial Sequence; **hPDL1**-Fc-*CD9tm2*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAA** **CTACCTCTGGCACATCCTCCAAATGAAAGG**ATCGATGACAAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*TTCTACACAGGAGTCTAT* *ATTCTGATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGG* *GCTGTGCAGGAGTCCCAGTGCGTAATTATGTAA* (SEQ ID NO: 309) >Artificial Sequence; **hPDL1**-Fc-*CD9tm2*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE** **LPLAHPPNER**IDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGKID*FYTGVYILIGAGALMMLVGFLGCCGAVQESQCVIM* (SEQ ID NO: 310)

TABLE 4-continued

Full Length Constructs	
Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
hPDL1-Fc-CD9tm2-modified KRAS	>Artificial Sequence; **hPDL1**-Fc-*CD9tm2*-*KRAS*, DNA **ATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCATTTGCTGAACGCATTT** **ACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATT** **GAATGCAAATTCCCAGTAGAAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGG** **GAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTT** **CAGCATAGTAGCTACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGA** **AATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGC** **ATGATCAGCTATGGTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCA** **TACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAA** **CTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTCTGGAAGCAGTGAC** **CATCAAGTCCTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTT** **TTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGC** **ACTTTTAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAA** **CTACCTCTGGCACATCCTCCAAATGAAAGG**ATCGATGACAAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCQCCCCAAAA CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATCGAT*TTCTACACAGGAGTCTAT* *ATTCTGATCGGAGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGG* *GCTGTGCAGGAGTCCCAGTGCAAAAAGAAGAAAAAGAAGAAGAAGACAAAGTGTGTA* *ATTATGTAA* (SEQ ID NO: 311) >Artificial Sequence; **hPDL1**-Fc-*CD9tm2*-*KRAS*, Amino Acid **MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYW** **EMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRC** **MISYGGADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEGYPKAEVIWTSSD** **HQVLSGKTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPE** **LPLAHPPNER**IDDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGKID*FYTGVYILIGAGALMMLVGFLGCCGAVQESQCKKKKKKKKTKCV* *IM* (SEQ ID NO: 312)
mPDL1-mFc-CD9tm2	>Artificial Sequence; **mPDL1**-mFc-*CD9tm2*, DNA **ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTT** **ACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGCAACGTCACGATG** **GAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGG** **GAAAAGGAAGATGAGCAAGTGATTCAGTTTGTGGCAGGAGAGGAGGACCTTAAGCCT** **CAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGA** **AATGCTGCCCTTCAGATCACAGACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGC** **ATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCA** **TACCGCAAAATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTA** **ATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGACCAC** **CAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGACAGAGGGGATGCTTCTC** **AATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGATGTTTTCTACTGTACG** **TTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTG** **CCTGCAACACATCCTCCACAGAACAGGACT**GGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATT ACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAG GTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCC CGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCAC CAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGCAGCTTTCCCT GCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCGAAGGCTCCACAGGTG TACACCATTCCACCTCCCAAGGAGCAGATGGCCAAGGATAAAGTCAGTCTGACCTGC ATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGAATGGGCAG CCAGCGGAGAACTACAAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTTC GTCTACAGCAAGCTCAATGTGCAGAAGAGCAACTGGGAGGCAGGAAATACTTTCACC TGCTCTGTGTTACATGAGGGCCTGCACAACCACCATACTGAGAAGAGCCTCTCCCAC TCTCCTGGTAAA*TTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATG* *ATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGCGTAATT* *ATGTAA* (SEQ ID NO: 313) >Artificial Sequence; **mPDL1**-mFc-*CD9tm2*, Amino Acid **MRIFAGIIFTACCHLLRAFTITAPKDLYVVEYGSNVTMECRFPVERELDLLALVVYW** **EKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQITDVKLQDAGVYCC**

TABLE 4-continued

Full Length Constructs	
Fusion Polypeptide	Nucleic Acid Sequence (SEQ ID NO:) Amino Acid Sequence (SEQ ID NO:)
	IISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDH **QPVSGKRSVTTSRTEGMLLNVTSSLRVNATANDVFYCTFWRSQPGQNHTAELIIPEL** **PATHPPQNRT**GCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPE VQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFP APIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQ PAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSH SPGKP*FYTGVYILIGAGALMMLVGFLGCCGAVQESQCVIM* (SEQ ID NO: 314)
mPDL1-mFc-CD9tm2-modified KRAS	>Artificial Sequence; **mPDL1**-mFc-*CD9tm2-KRAS*, DNA **ATGAGGATATTTGCTGGCATTATATTCACAGCCTGCTGTCACTTGCTACGGGCGTTT** **ACTATCACGGCTCCAAAGGACTTGTACGTGGTGGAGTATGGCAGCAACGTCACGATG** **GAGTGCAGATTCCCTGTAGAACGGGAGCTGGACCTGCTTGCGTTAGTGGTGTACTGG** **GAAAAGGAAGATGAGCAAGTGATTCAGTTTGTGGCAGGAGAGGAGGACCTTAAGCCT** **CAGCACAGCAACTTCAGGGGGAGAGCCTCGCTGCCAAAGGACCAGCTTTTGAAGGGA** **AATGCTGCCCTTCAGATCACAGACGTCAAGCTGCAGGACGCAGGCGTTTACTGCTGC** **ATAATCAGCTACGGTGGTGCGGACTACAAGCGAATCACGCTGAAAGTCAATGCCCCA** **TACCGCAAAATCAACCAGAGAATTTCCGTGGATCCAGCCACTTCTGAGCATGAACTA** **ATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGACCAC** **CAACCCGTGAGTGGGAAGAGAAGTGTCACCACTTCCCGGACAGAGGGGATGCTTCTC** **AATGTGACCAGCAGTCTGAGGGTCAACGCCACAGCGAATGATGTTTTCTACTGTACG** **TTTTGGAGATCACAGCCAGGGCAAAACCACACAGCGGAGCTGATCATCCCAGAACTG** **CCTGCAACACATCCTCCACAGAACAGGACT**GGTTGTAAGCCTTGCATATGTACAGTC CCAGAAGTATCATCTGTCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATT ACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAG GTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCC CGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCAC CAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGCAGCTTTCCCT GCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCGAAGGCTCCACAGGTG TACACCATTCCACCTCCCAAGGAGCAGATGGCCAAGGATAAAGTCAGTCTGACCTGC ATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGAATGGGCAG CCAGCGGAGAACTACAAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTTC GTCTACAGCAAGCTCAATGTGCAGAAGAGCAACTGGGAGGCAGGAAATACTTTCACC TGCTCTGTGTTACATGAGGGCCTGCACAACCACCATACTGAGAAGAGCCTCTCCCAC TCTCCTGGTAAA*TTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATG* *ATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGC*AAAAAG *AAGAAAAAGAAGAAGAAGACAAAGTGTGTAATTATGTAA* (SEQ ID NO: 315) >Artificial Sequence; **mPDL1**-mFc-*CD9tm2-KRAS*, Amino Acid **MRIFAGIIFTACCHLLRAFTITAPEDLYVVEYGSNVTMECRFPVERELDLLALVVYW** **EKEDEQVIQFVAGEEDLKPQHSNFRGRASLPKDQLLKGNAALQITDVKLQDAGVYCC** **IISYGGADYKRITLKVNAPYRKINQRISVDPATSEHELICQAEGYPEAEVIWTNSDH** **QPVSGKRSVTTSRTEGMLLNVTSSLRVNATANDVFYCTFWRSQPGQNHTAELIIPEL** **PATHPPQNRT**GCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPE VQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFP APIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQ PAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSH SPGK*FYTGVYILIGAGALMMLVGFLGCCGAVQESQCKKKKKKKKTKCVIM* (SEQ ID NO: 316)

In some embodiments of any of the aspects, the fusion polypeptides provided herein comprise two or more POI domains. The specific combinations of POI domains can be used to regulate inflammatory immune responses. Non-limiting examples of additive and synergistic combinations of POIs that can modulate inflammatory signaling pathways are provided in Table 5 (below).

TABLE 5

Exemplary POI combinations and combined targets for modulating inflammation.		
POIs (LIGANDS)	COMBINED TARGETS	PUTATIVE ADDITIVE or SYNERGISTIC MOA
PD-L1 or PD-L2 HVEM	PD-1 BTLA	Differential use of Shp phosphatases. BTLA inhibits both TCR and CD28 phosphorylation (via Shpl) while PD-1 inhibits CD28 phosphorylation (via Shp2).
PD-L1 or PD-L2 FGL1	PD-1 LAG-3	LAG-3 exerts differential inhibitory impacts on various types of lymphocytes and shows synergy with PD-1 to inhibit immune responses.
PD-L1 or PD-L2 CEACAM-1 or GAL9	PD-1 TIM-3	PD-1 and Tim-3 have non-redundant downstream signaling mechanisms.
PD-L1 or PD-L2 CD155	PD-1 TIGIT	Differential use of Shp phosphatases. Non-redundantly regulate T cell responses.

TABLE 5-continued

Exemplary POI combinations and combined targets for modulating inflammation.

POIs (LIGANDS)	COMBINED TARGETS	PUTATIVE ADDITIVE or SYNERGISTIC MOA
PD-L1 or PD-L2 VSIG3	PD-1 VISTA	PD-1 and VISTA non-redundantly regulate T cell responses. VISTA contains cytosolic SH3 binding domains for adapter proteins.
CEACAM-1 or GAL9 CD155	TIM-3 TIGIT	TIGIT and TIM-3 have non-redundant downstream signaling mechanisms.
PD-L1 or PD-L2 FGL1 CEACAM-1 or GAL9	PD-1 LAG-3 TIM-3	PD-1, LAG-3 and TIM-3 have non-redundant downstream signaling mechanisms.

Methods of Preparing Extracellular Vesicle Compositions

In another aspect, provided herein is a method of preparing an engineered extracellular vesicle provided herein. Generally, the method comprises providing a population of cells expressing a vector construct encoding one or more sticky binder (vesicle targeting domain) and one or more signaling domains (POI domain).

The EVs provided herein can be isolated and purified form any biological source, e.g., cells. The cells that produce the engineered EVs provided herein can be from any viable non-human source or organism. Usually the organism is an animal, vertebrate, or mammal. In some embodiments, the cell described herein is from a human. The cells described herein can be from any tissue isolated from an organism by methods known in the art. The scientific literature provides guidance for one of ordinary skill in the art to isolate, prepare, and culture cells as necessary for use in the compositions and methods described herein. One of skill in the art can appreciate that the cell source of the EVs may alter the cellular protein expression and the native or endogenous cargo within the EV. It is contemplated herein that this can be leveraged for therapeutic effect depending on the disease or disorder being treated.

In some embodiments, the population of cells has been altered by exposure to environmental conditions (e.g., hypoxia), small molecule addition, presence/absence of exogenous factors (e.g., growth factors, cytokines) at the time, or substantially contemporaneous with, isolating the plurality of artificial synapses in a manner altering the regulatory state of the cell. In various embodiments, the cells are HEK 293 cells, MSCs, PER.C, fibrosarcoma HT-1080 or HuH7 cell lines.

The method comprises providing a population of cells and culturing the cells in serum-free or un-concentrated conditioned medium. This includes, for example, artificial synapses secreted into media as conditioned by a population of cells in culture, further including cell lines capable of serial passaging. In certain embodiments, the cells in culture are grown to 10, 20, 30, 40, 50, 60, 70, 80, 90, or 90% or more confluency when artificial synapses (engineered EVs) are isolated.

The methods provided herein further comprise contacting the cells provided herein with a nucleic acid vector encoding the at least one fusion polypeptide provided herein. The vector can be added to the cell culture medium of the cells by methods known in the art and discussed further below.

A vector is a nucleic acid construct designed for delivery to a host cell or for transfer of genetic material between different host cells. As used herein, a vector can be viral or non-viral. The term "vector" encompasses any genetic element that is capable of replication when associated with the proper control elements and that can transfer genetic material to cells. A vector can include, but is not limited to, a cloning vector, an expression vector, a plasmid, phage, transposon, cosmid, artificial chromosome, virus, virion, etc. In some embodiments of any of the aspects, the vector is selected from the group consisting of: a plasmid, a cosmid and a viral vector.

"Expression" refers to the cellular processes involved in producing RNA and proteins and as appropriate, secreting proteins, including where applicable, but not limited to, for example, transcription, transcript processing, translation and protein folding, modification and processing. "Expression products" include RNA transcribed from a gene, and polypeptides obtained by translation of mRNA transcribed from a gene.

In some embodiments, a vector is capable of driving expression of one or more sequences in a mammalian cell; i.e., the vector is a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987. Nature 329:840) and pMT2PC (Kaufman, et al., 1987. *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are typically provided by one or more regulatory elements. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, simian virus 40, and others disclosed herein and known in the art. For other suitable expression systems for both prokaryotic and eukaryotic cells see, e.g., Chapters 16 and 17 of Sambrook, et al., MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In some embodiments, the recombinant expression vector is capable of directing expression of the exogenous fusion polypeptide nucleic acid sequence preferentially in a particular cell type (e.g., via tissue-specific regulatory elements).

Tissue-specific and inducible regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, et al., 1987. *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. hnmunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO J.* 8:729-733) and immunoglobulins (Baneiji, et al., 1983. *Cell* 33:729-740; Queen and Baltimore, 1983. *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund, et al., 1985. *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264, 166). Developmentally-regulated promoters are also encompassed, e.g., the murine hox promoters (Kessel and Gruss, 1990. *Science* 249:374-379) and the α-fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3:537-546).

In some embodiments, the at least one nucleic acid sequence described herein is delivered to the cell described herein via an integrating vector. Integrating vectors have their delivered genetic material (or a copy of it) permanently incorporated into a host cell chromosome. Non-integrating vectors remain episomal which means the nucleic acid contained therein is never integrated into a host cell chromosome. Examples of integrating vectors include retroviral vectors, lentiviral vectors, hybrid adenoviral vectors, and herpes simplex viral vectors.

In some embodiments, the at least one nucleic acid sequence described herein is delivered to the cell described herein via a non-integrative vector. Non-integrative vectors include non-integrative viral vectors. Non-integrative viral vectors eliminate one of the primary risks posed by integrative retroviruses, as they do not incorporate their genome into the host DNA. One example is the Epstein Barr oriP/Nuclear Antigen-1 ("EBNA1") vector, which is capable of limited self-replication and known to function in mammalian cells. Containing two elements from Epstein-Barr virus, oriP and EBNA1, binding of the EBNA1 protein to the virus replicon region oriP maintains a relatively long-term episomal presence of plasmids in mammalian cells. This particular feature of the oriP/EBNA1 vector makes it ideal for generation of integration-free host cells. Other non-integrative viral vectors include adenoviral vectors and the adeno-associated viral (AAV) vectors.

Another non-integrative viral vector is RNA Sendai viral vector, which can produce protein without entering the nucleus of an infected cell. The F-deficient Sendai virus vector remains in the cytoplasm of infected cells for a few passages, but is diluted out quickly and completely lost after several passages (e.g., 10 passages). This permits a self-limiting transient expression of a chosen heterologous gene or genes in a target cell. This aspect can be helpful, e.g., for the transient introduction of reprogramming factors, among other uses. As noted above, in some embodiments, the nucleic acid sequence described herein is expressed in the cells from a viral vector.

A "viral vector" includes a nucleic acid vector construct that includes at least one element of viral origin and has the capacity to be packaged into a viral vector particle. The viral vector can contain a nucleic acid encoding a polypeptide described herein in place of non-essential viral genes. The vector and/or particle can be utilized for the purpose of transferring nucleic acids into cells either in vitro or in vivo.

The nucleic acids described herein can be delivered using any transfection reagent or other physical means that facilitates entry of nucleic acids into a cell. Methods of non-viral delivery of nucleic acids include lipofection, nucleofection, microinjection, electroporation, biolistics, virosomes, liposomes, immunoliposomes, polycation or lipid: nucleic acid conjugates, naked DNA, artificial virions, and agent-enhanced uptake of DNA. Lipofection is described in e.g., U.S. Pat. Nos. 5,049,386, 4,946,787; and 4,897,355) and lipofection reagents are sold commercially (e.g., Transfectam™ and Lipofectin™). Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those of Felgner, WO 91/17424; WO 91/16024. Delivery can be to cells (e.g., in vitro or ex vivo administration) or target tissues (e.g., in vivo administration).

The preparation of lipid: nucleic acid complexes, including targeted liposomes such as immunolipid complexes, is well known to one of skill in the art (see, e.g., Crystal, Science 270:404-410 (1995); Blaese et al., Cancer Gene Ther. 2:291-297 (1995); Behr et al., Bioconjugate Chem. 5:382-389 (1994); Remy et al., Bioconjugate Chem. 5:647-654 (1994); Gao et al., Gene Therapy 2:710-722 (1995); Ahmad et al., Cancer Res. 52:4817-4820 (1992); U.S. Pat. Nos. 4,186,183, 4,217,344, 4,235,871, 4,261,975, 4,485,054, 4,501,728, 4,774,085, 4,837,028, and 4,946,787).

An "agent that increases cellular uptake" is a molecule that facilitates transport of a molecule, e.g., nucleic acid, or peptide or polypeptide, or other molecule that does not otherwise efficiently transit the cell membrane across a lipid membrane. For example, a nucleic acid can be conjugated to a lipophilic compound (e.g., cholesterol, tocopherol, etc.), a cell penetrating peptide (CPP) (e.g., penetratin, TAT, Syn1B, etc.), or a polyamine (e.g., spermine). Further examples of agents that increase cellular uptake are disclosed, for example, in Winkler (2013). *Oligonucleotide conjugates for therapeutic applications. Ther. Deliv.* 4 (7); 791-809. The one or more nucleic acid sequences encoding the fusion polypeptides provided herein can be delivered to the cell by any method discussed above or known in the art.

In some embodiments of any of the aspects, the vectors provided herein comprise a nucleic acid modification by methods known in the art. In some embodiments, the cell can be genetically manipulated to express one or more vectors, each encoding one or more vesicle targeting domains and/or one or more signaling domains. In certain embodiments, the population of cells has been genetically manipulated. This includes, for example, knockout (KO) or transgenic (TG) cell lines, wherein an endogenous gene has been removed and/or an exogenous introduced in a stable, persistent manner. In certain embodiments, this further includes transient knockdown of one or more genes and associated coding and non-coding transcripts within the population of cells, via any number of methods known in the art, such as introduction of dsRNA, siRNA, microRNA, etc. This further includes transient expression of one or more genes and associated coding and non-coding transcripts within the population of cells, via any number of methods known in the art, such as introduction of a vector, plasmid, artificial plasmid, replicative and/or non-replicative virus, etc.

In certain embodiments the cell population has been manipulated to knockout the expression of one or more endogenous gene sequences that encode for metalloendopeptidases. In certain embodiments the cell population has been manipulated to knockout the expression of one or more endogenous gene sequences that code for metalloproteinases. In certain embodiments the cell population has been manipulated to knockout the expression of one or more endogenous gene sequences that encode for a disintegrin and metalloproteinase (ADAM). For example, the cell population can be manipulated to knock of the expression of one or more gene sequences that encode for ADAM1, ADAM2, ADAM7, ADAM8, ADAM9, ADAM10, ADAM11, ADAM12, ADAM15, ADAM17, ADAM18, ADAM19, ADAM20, ADAM21, ADAM22, ADAM23, ADAM28, ADAM29, ADAM30, ADAM33, etc.

In certain embodiments the cell population has been manipulated to knockout the expression of one or more endogenous genes that encode for enzymes that hydrolyze the inositol phosphate linkage in proteins anchored by phosphatidylinositol glycans, thereby preventing the release of proteins attached to the plasma membrane via GPI anchors. For example, the cell population can be manipulated to knock of the expression of phosphatidylinositol-glycan-specific phospholipase D (GPLD1).

In certain embodiments, the population of cells has been genetically manipulated. This includes, for example, knock-in of an exogenous genetic sequence, wherein the exogenous genetic sequence is expressed in a stable, persistent manner. In certain embodiments, the cell population has been manipulated to knock-in recombinase recognition sequences (e.g., FRT), transgenic reporters such as antibiotic resistance genes, fluorescent or enzymatic reporter genes, etc. or the like.

In some embodiments, the method comprises a step of isolating the engineered extracellular vesicles provided herein. Particulates within the medium are removed by a

series of specific centrifugation steps and the media is filtered. The general method of isolating extracellular vesicles as provided herein is depicted in FIG. **21** of the working examples. Methods of isolating and purifying the extracellular vesicles and exosomes are known in the art and further described, e.g., in Whitford W, Guterstam P. Exosome manufacturing status. Future Med Chem. 2019 May; 11(10):1225-1236. doi: 10.4155/fmc-2018-0417. PMID: 31280675, Patel D B, Santoro M, Born L J, Fisher J P, Jay S M. Towards rationally designed biomanufacturing of therapeutic extracellular vesicles: impact of the bioproduction microenvironment. Biotechnol Adv. 2018 December; 36 (8):2051-2059 . . . doi: 10.1016/j.biotechadv.2018.09.001. Epub 2018 Sep. 12. PMID: 30218694; PMCID: PMC6250573, Ng K S, Smith J A, McAteer M P, Mead B E, Ware J, Jackson F O, Carter A, Ferreira L, Bure K, Rowley J A, Reeve B, Brindley D A, Karp J M. Bioprocess decision support tool for scalable manufacture of extracellular vesicles. Biotechnol Bioeng. 2019 February; 116 (2):307-319. doi: 10.1002/bit.26809. Epub 2018 Nov. 8. PMID: 30063243; PMCID: PMC6322973, Paganini C, Capasso Palmiero U, Pocsfalvi G, Touzet N, Bongiovanni A, Arosio P. Scalable Production and Isolation of Extracellular Vesicles: Available Sources and Lessons from Current Industrial Bioprocesses. Biotechnol J. 2019 October; 14 (10):e1800528. doi: 10.1002/biot.201800528. Epub 2019 Jul. 8. PMID: 31140717, which are incorporated herein by reference in their entireties.

In some embodiments, isolating the plurality of engineered EVs (artificial synapses) includes precipitation, centrifugation, filtration, immuno-separation, tangential flow, liquid chromatography, and/or flow fractionation. For example, differential ultracentrifugation has become a technique wherein secreted exosomes are isolated from the supernatants of cultured cells. This approach allows for separation of exosomes from non-membranous particles, by exploiting their relatively low buoyant density. Size exclusion allows for their separation from biochemically similar, but biophysically different microvesicles, which possess larger diameters of up to 1,000 nm. Differences in floatation velocity further allows for separation of differentially sized exosomes. In general, exosome sizes will possess a diameter ranging from 30-300 nm, including sizes of 30-150 nm. Further purification may rely on specific properties of the particular exosomes of interest. This includes, for example, use of immunoadsorption with a protein of interest to select specific vesicles with exoplasmic or outward orientations.

Among current methods (differential centrifugation, discontinuous density gradients, immunoaffinity, ultrafiltration and liquid chromatography (e.g., fast protein liquid chromatography (FPLC)), differential ultracentrifugation is the most commonly used for exosome isolation. This technique utilizes increasing centrifugal force from 2000×g to 10,000×g to separate the medium- and larger-sized particles and cell debris from the exosome pellet at 100,000×g. Centrifugation alone allows for significant separation/collection of exosomes from a conditioned medium, although it is insufficient to remove various protein aggregates, genetic materials, particulates from media and cell debris that are common contaminants. Enhanced specificity of exosome purification may deploy sequential centrifugation in combination with ultrafiltration, or equilibrium density gradient centrifugation in a sucrose density gradient, to provide for the greater purity of the exosome preparation (flotation density 1.1-1.2 g/ml) or application of a discrete sugar cushion in preparation.

Ultrafiltration can be used to purify exosomes without compromising their biological activity. Membranes with different pore sizes-such as 100 kDa molecular weight cut-off (MWCO) or 300 kDa MWCO and gel filtration to eliminate smaller particles—have been used to avoid the use of a nonneutral pH or non-physiological salt concentration. Currently available tangential flow filtration (TFF) systems are scalable (to >10,000 L), allowing one to not only purify, but concentrate the exosome fractions, and such approaches are less time consuming than differential centrifugation. Liquid Chromatography can also be used to purify exosomes to homogeneously sized particles and preserve their biological activity as the preparation is maintained at a physiological pH and salt concentration.

Other chemical methods have exploit differential solubility of exosomes for precipitation techniques, addition to volume-excluding polymers (e.g., polyethylene glycols (PEGs)), possibly combined additional rounds of centrifugation or filtration. For example, a precipitation reagent, ExoQuick®, can be added to conditioned cell media to quickly and rapidly precipitate a population of exosomes, although re-suspension of pellets prepared via this technique may be difficult. Flow field-flow fractionation (FIFFF) is an elution-based technique that is used to separate and characterize macromolecules (e.g., proteins) and nano- to micro-sized particles (e.g., organelles and cells) and which has been successfully applied to fractionate exosomes from culture media.

Beyond these techniques relying on general biochemical and biophysical features, focused techniques may be applied to isolated specific exosomes of interest. This includes relying on antibody immunoaffinity to recognizing certain exosome-associated antigens. Conjugation to magnetic beads, chromatography matrices, plates or microfluidic devices allows isolating of specific exosome populations of interest as may be related to their production from a parent cell of interest or associated cellular regulatory state. Other affinity-capture methods use lectins which bind to specific saccharide residues on the exosome surface.

In several embodiments, isolating a plurality of artificial synapses from the population of cells includes centrifugation of the cells and/or media conditioned by the cells. In several embodiments, ultracentrifugation is used. In several embodiments, isolating a plurality of artificial synapses from the population of cells is via size-exclusion filtration. In other embodiments, isolating a plurality of artificial synapses from the population of cells includes use of discontinuous density gradients, immunoaffinity, ultrafiltration, tangential flow and/or liquid chromatography.

In certain embodiments, differential ultracentrifugation includes using centrifugal force from 1000-2000×g, 2000-3000×g, 3000-4000×g, 4000-5000×g, 5000×g-6000×g, 6000-7000×g, 7000-8000×g, 8000-9000×g, 9000-10,000×g, to 10,000×g or more to separate larger-sized particles from a plurality of artificial synapses derived from the cells.

In other embodiments, isolating a plurality of artificial synapses from the population of cells includes use of filtration or ultrafiltration. In certain embodiments, a size exclusion membrane with different pore sizes is used. For example, a size exclusion membrane can include use of a filter with a pore size of 0.1-0.5 micron (μm), 0.5-1.0 μm, 1-2.5 μm, 2.5-5 μm, 5 or more μm. In certain embodiments, the pore size is about 0.2 μm. In certain embodiments, filtration or ultrafiltration includes size exclusion ranging from 100-500 daltons (Da), 500-1 kDa, 1-2 kDa, 2-5 kDa, 5-10 kDa, 10-25 kDa, 25-50 kDa, 50-100 kDa, 100-250 kDa, 250-500 kDa, 500 or more kDa. In certain embodi-

ments, the size exclusion is for about 2-5 kDa. In certain embodiments, the size exclusion is for about 3 kDa. In other embodiments, filtration or ultrafiltration includes size exclusion includes use of hollow fiber membranes capable of isolating particles ranging from 100-500 daltons (Da), 500-1 kDa, 1-2 kDa, 2-5 kDa, 5-10 kDa, 10-25 kDa, 25-50 kDa, 50-100 kDa, 100-250 kDa, 250-500 kDa, 500 or more kDa. In certain embodiments, the size exclusion is for about 2-5 kDa. In certain embodiments, the size exclusion is for about 3 kDa. In other embodiments, a molecular weight cut-off (MWCO) gel filtration capable of isolating particles ranging from 100-500 daltons (Da), 500-1 kDa, 1-2 kDa, 2-5 kDa, 5-10 kDa, 10-25 kDa, 25-50 kDa, 50-100 kDa, 100-250 kDa, 250-500 kDa, 500 or more kDa. In certain embodiments, the size exclusion is for about 2-5 kDa. In certain embodiments, the size exclusion is for about 3 kDa. In various embodiments, such systems are used in combination with variable fluid flow systems. In certain embodiments, a size exclusion membrane with different pore sizes is used to purify extracellular vesicles from a solution comprising undesirable proteins or nucleic acids.

In other embodiments, isolating a plurality of artificial synapses from the population of cells includes use of tangential flow filtration (TFF) systems are used purify and/or concentrate the exosome fractions. In other embodiments, isolating a plurality of artificial synapses from the population of cells includes use of liquid chromatography can also be used to purify artificial synapses to homogeneously sized particles. In various embodiments, density gradients as used, such as centrifugation in a sucrose density gradient or application of a discrete sugar cushion in preparation.

In other embodiments, isolating a plurality of artificial synapses from the population of cells includes use of a precipitation reagent. For example, a precipitation reagent, ExoQuick®, can be added to conditioned cell media to quickly and rapidly precipitate a population of artificial synapses. In other embodiments, isolating a plurality of artificial synapses from the population of cells includes use of volume-excluding polymers (e.g., polyethylene glycols (PEGs)) are used. In another embodiment, isolating a plurality of artificial synapses from the population of cells includes use of flow field-flow fractionation (FIFFF), an elution-based technique.

In certain embodiments, isolating a plurality of artificial synapses from the population of cells includes use of one or more capture agents to isolate one or more artificial synapses possessing specific biomarkers or containing particular biological molecules. In one embodiment, one or more capture agents include at least one antibody. For example, antibody immunoaffinity recognizing exosome-associated antigens is used to capture specific artificial synapses. In other embodiments, the at least one antibody are conjugated to a fixed surface, such as magnetic beads, chromatography matrices, plates or microfluidic devices, thereby allowing isolation of the specific exosome populations of interest. In other embodiments, isolating a plurality of artificial synapses from the population of cells includes use of one or more capture agents that is not an antibody. This includes, for example, use of a "bait" molecule presenting an antigenic feature complementary to a corresponding molecule of interest on the exosome surface, such as a receptor or other coupling molecule. In one embodiment, the non-antibody capture agent is a lectin capable of binding to polysaccharide residues on the exosome surface.

In other embodiments, isolating a plurality of artificial synapses from the population of cells includes use of ion exchange chromatography. In other embodiments, isolating a plurality of artificial synapses from the population of cells includes use of anion exchange chromatography. In other embodiments, isolating a plurality of artificial synapses from the population of cells includes use of caion exchange chromatography. In certain embodiments, ion exchange chromatography comprises a chromatography resin with a functional group selected from the group consisting of diethylaminoethyl (DEAE), quaternary aminoethyl (QAE), quaternary ammonium (Q), carboxymethyl (CM), sulfopropyl (SP), or methyl sulfate(S). In certain embodiments, ion exchange chromatography comprises a chromatography resin which may have properties of a weak acid, strong acid, weak base, or strong basic. In certain embodiments, ion exchange chromatography comprises a chromatography selected from the group consisting of DEAE cellulose, DEAE Sephadex, Mono Q, Mini Q, HiTrap Capto, Capto Core 700, HiPrep Q, QAE Sephadex, Q Sepharose, CM Cellulose, SP Sepharose, SOURCE S, EAH-Sepharose, sulfoxyethyl cellulose, CM Sephadex, or CM Sepharose. Isolating a plurality of artificial synapses can be prepared by any of a variety of ion exchange chromatography techniques that are known in the art.

In other embodiments, isolating a plurality of artificial synapses from the population of cells includes use of a nuclease enzyme (e.g., a DNase or RNase). For example, a working concentration of Benzonase® nuclease may be added to an extracellular vesicle sample preparation in the presence of a divalent cation, for example 1-2 mM Mg^{2+}, 2-5 mM Mg^{2+}, 10-20 mM Mg^{2+}, 20-50 mM Mg^{2+}, 50-100 mM Mg^{2+}, or more than 100 mM Mg^{2+}.

Following isolation and purification of the engineered EVs provided herein, EVs can be further evaluated for the desired structural and functional properties by methods known in the art. For example, the engineered exosomes provided herein can be assayed for functional activity on a target cell using a cell-based bioassays (e.g., those commercially available, PROMEGA® DISCOVERX®), ligand-receptor binding assays, vesicle flow cytometric assays, enzyme-linked immunosorbent assays, tunable resistive pulse sensing (TRPS), nanoparticle tracking analysis (NTA), surface plasmon resonance (SSPR), nucleotide sequencing, lipidomics, proteomics, colorimetric assays, fluorescence assays, luminescence assays, immunoblotting, radioimmunoassays, electron microscopy, or EV automated analysis (e.g., EXOVIEW®). Additional methods of characterizing EVs are found, e.g., in Zhang Y, Bi J, Huang J, Tang Y, Du S, Li P. Exosome: A Review of Its Classification, Isolation Techniques, Storage, Diagnostic and Targeted Therapy Applications. Int J Nanomedicine. 2020 Sep. 22; 15:6917-6934. doi: 10.2147/IJN.S264498. PMID: 33061359; PMCID: PMC7519827, Kluszczyńska K, Czernek L, Cypryk W, Pęczek Ł, Düchler M. Methods for the Determination of the Purity of Exosomes. Curr Pharm Des. 2019; 25(42):4464-4485. doi: 10.2174/1381612825666191206162712. PMID: 31808383, Nolan J P, Duggan E. Analysis of Individual Extracellular Vesicles by Flow Cytometry. Methods Mol Biol. 2018; 1678:79-92. doi: 10.1007/978-1-4939-7346-O_5. PMID: 29071676; Doyle L M, Wang M Z. Overview of Extracellular Vesicles, Their Origin, Composition, Purpose, and Methods for Exosome Isolation and Analysis. Cells. 2019 Jul. 15; 8(7):727. doi: 10.3390/cells8070727. PMID: 31311206; PMCID: PMC6678302, Pugholm L H, Revenfeld A L, Søndergaard E K, Jørgensen M M. Antibody-Based Assays for Phenotyping of Extracellular Vesicles. Biomed Res Int. 2015; 2015: 524817. doi: 10.1155/2015/524817. Epub 2015 Dec. 3. PMID: 26770974; PMCID: PMC4681819, Shao H, Im H,

Castro C M, Breakefield X, Weissleder R, Lee H. New Technologies for Analysis of Extracellular Vesicles. Chem Rev. 2018 Feb. 28; 118(4):1917-1950. doi: 10.1021/acs.chemrev.7b00534. Epub 2018 Jan. 31. PMID: 29384376; PMCID: PMC6029891, which are incorporated herein by reference in their entireties.

Pharmaceutical Compositions

Provided herein are compositions comprising the engineered extracellular vesicles (artificial synapses) provided herein.

In one aspect, provided herein is a composition comprising: a plurality of the engineered extracellular vesicles provided herein. In some embodiments of any of the aspects, the compositions and engineered EVs provided herein further comprise a pharmaceutically acceptable carrier.

For clinical use of the methods and compositions described herein, administration of the engineered EVs/artificial synapses provided herein can include formulation into pharmaceutical compositions or pharmaceutical formulations for parenteral administration, e.g., intravenous; mucosal, e.g., intranasal; ocular, or other mode of administration. In some embodiments, the engineered EVs described herein can be administered along with any pharmaceutically acceptable carrier compound, material, or composition which results in an effective treatment in the subject. Thus, a pharmaceutical formulation for use in the methods described herein can contain the engineered EVs described herein in combination with one or more pharmaceutically acceptable ingredients. The phrase "pharmaceutically acceptable" refers to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio. The phrase "pharmaceutically acceptable carrier" as used herein means a pharmaceutically acceptable material, composition or vehicle, such as a liquid or solid filler, diluent, excipient, solvent, media, encapsulating material, manufacturing aid (e.g., lubricant, talc magnesium, calcium or zinc stearate, or steric acid), or solvent encapsulating material, involved in maintaining the stability, solubility, or activity of, an engineered EV as described herein. Each carrier must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the patient. The terms "excipient," "carrier," "pharmaceutically acceptable carrier" or the like are used interchangeably herein.

The engineered EVs provided herein can be formulated for administration of the compound to a subject in solid, liquid, or gel form, including those adapted for the following: (1) parenteral administration, for example, by subcutaneous, intramuscular, intravenous or epidural injection as, for example, a sterile solution or suspension, or sustained-release formulation; (2) transdermally; (3) transmucosally; (4) via bronchoalveolar lavage.

In some embodiments, the compositions described herein comprise a particle or polymer-based vehicle. Exemplary particle or polymer-based vehicles include, but are not limited to, nanoparticles, microparticles, polymer microspheres, or polymer-drug conjugates.

In one embodiment of any of the aspects, the compositions described herein further comprise a lipid vehicle. Exemplary lipid vehicles include, but are not limited to, liposomes, phospholipids, micelles, lipid emulsions, and lipid-drug complexes.

Formulations can be adapted for delivery to the airway, e.g., to address respiratory inflammation. Such formulations can be adapted for delivery as an aerosol, e.g., for inhalation. In some embodiments, the compositions described herein are formulated for aerosol administration, nebulizer administration, tracheal lavage administration, or for a pulmonary delivery device.

As used herein, the term "pulmonary delivery device" refers to a device used to deliver a therapeutic dose of a composition of the present invention to the respiratory system including, but not limited to, a nebulizer, metered-dose inhaler, or dry powder inhaler.

Examples of nebulizers include, but are not limited to, soft mist inhalers (for example Respimat® Boehringer Ingelheim) jet nebulizers (use compressed gas or air), ultrasonic nebulizers (produce aerosols using a piezoelectric crystal vibrating at high frequencies), and vibrating mesh nebulizers.

As used herein, the term "jet nebulizer" refers to a device that flows compressed air or gas through a composition of the present invention for aerosolization. The aerosolized composition of the present invention may be inhaled by a patient. Jet nebulizer may include, but is not limited to, jet nebulizers with a corrugated tube, jet nebulizers with a collection bag, breath enhanced jet nebulizers, breath actuated jet nebulizers, and metered-dose inhalers. Examples of jet nebulizers include, but are not limited to, Circulaire (Westmed INC, Tucson, AZ), Pari Inhalierboy (PARI, Midlothian, VA), Pari LC Plus (PARI, Midlothian, VA), NebuTech (Salter Labs, Arvin, CA), AeroEclipse (Monoghan/Trudell Medical International, London, Ontario, Canada), and Maxin MA-2 (MA-2; Clinova Medical AB, Malmö, Sweden). Examples of ultrasonic nebulizers include, but are not limited to, De Vilbiss-Pulmosonic (Somerset, PA), Omron-Microair (Omron, Kyoto, Japan), Omron NE-U17 (Omron, Kyoto, Japan), Rhone Poulenc-Rorer-Fisoneb (Sanofi, Paris, France), and Beurer Nebulizer IH30 (Beurer GmbH, Neu-Ulm, Germany).

As used herein, the term "mesh nebulizer" refers to forcing a liquid, gel, fluid, solution, tincture, or the like through apertures in a mesh or aperture plate to generate aerosol. Mesh nebulizer may include, but is not limited to, active mesh nebulizers and passive mesh nebulizers. Examples of active mesh nebulizers include, but is not limited to, Aeroneb® (Aerogen, Galway, Ireland) and eFlow® (PARI, Midlothian, VA). Examples of passive mesh nebulizers are, but not limited to, I-neb (Philips Respironics, Newark, USA), AKITA (Activaero, Gemunden/Wohra, Germany), and Microair NE-U22® (Omron, Kyoto, Japan).

For use as aerosols, the compositions described herein can be prepared in a solution or suspension and may be packaged in a pressurized aerosol container together with suitable propellants, for example, hydrocarbon propellants like propane, butane, or isobutane with conventional excipients.

The engineered EVs provided herein can also be administered in a non-pressurized form such as in a nebulizer or atomizer that reduces a liquid to a fine spray. Preferably, by such nebulization small liquid droplets of uniform size are produced from a larger body of liquid in a controlled manner. Nebulization can be achieved by any suitable means therefor, including by using many nebulizers known and marketed today. For example, an AEROMIST™ pneumatic nebulizer available from Inhalation Plastic, Inc. of Niles, Ill.

When the active ingredients are adapted to be administered, either together or individually, via nebulizer(s) they can be in the form of a nebulized aqueous suspension or solution, with or without a suitable pH or tonicity adjustment, either as a unit dose or multi-dose device.

Furthermore, any suitable gas can be used to apply pressure during the nebulization, with preferred gases to date being those which are chemically inert. Exemplary gases including, but are not limited to, nitrogen, argon, or helium can be used to advantage.

In some embodiments, the compositions described herein can also be administered directly to the airways in the form of a dry powder. Thus, the engineered EVs can be administered via an inhaler. Exemplary inhalers include metered dose inhalers and dry powdered inhalers.

A metered dose inhaler or "MDI" is a pressure resistant canister or container filled with a product such as a pharmaceutical composition dissolved in a liquefied propellant or micronized particles suspended in a liquefied propellant. The propellants which can be used include chlorofluorocarbons, hydrocarbons or hydrofluoroalkanes. Commonly used propellants are P134a (tetrafluoroethane) and P227 (heptafluoropropane) each of which may be used alone or in combination. They are optionally used in combination with one or more other propellants and/or one or more surfactants and/or one or more other excipients, for example ethanol, a lubricant, an anti-oxidant and/or a stabilizing agent.

As used herein, the term "dry powder inhaler" refers to a device that delivers a therapeutic dose of a composition of the present invention in a powdered form without propellants to the respiratory system. A dry powder inhaler (i.e., Turbuhaler™ (Astra AB)) is a system operable with a source of pressurized air to produce dry powder particles of a pharmaceutical composition that is compacted into a very small volume. Examples of dry powder inhalers include, but are not limited to, Spinhaler® (Fisons Pharmaceuticals, Rochester, NY), Rotahaler® (GlaxoSmithKline, NC), Turbuhaler® (AstraZeneca, UK), and Diskhaler® (GlaxoSmithKline, NC).

Dry powder aerosols for inhalation therapy are generally produced with mean diameters primarily in the range of <5 μm. As the diameter of particles exceeds 3 μm, there is increasingly less phagocytosis by macrophages. However, increasing the particle size also has been found to minimize the probability of particles (possessing standard mass density) entering the airways and acini due to excessive deposition in the oropharyngeal or nasal regions.

Suitable powder compositions include, by way of illustration, powdered preparations including the engineered EVs described herein. These can be intermixed with lactose, or other inert powders acceptable for intrabronchial administration. The powder compositions can be administered via an aerosol dispenser or encased in a breakable capsule which may be inserted by the patient or clinician into a device that punctures the capsule and blows the powder out in a steady stream suitable for inhalation. The compositions can include propellants, surfactants, and co-solvents and may be filled into conventional aerosol containers that are closed by a suitable metering valve.

Aerosols for the delivery to the respiratory tract are described, for example, by Adjei, A. and Garren, J. Pharm. Res., 1:565-569 (1990); Zanen, P. and Lamm, J.-W. J. Int. J. Pharm., 114:111-115 (1995); Gonda, I. "Aerosols for delivery of therapeutic and diagnostic agents to the respiratory tract," in Critical Reviews in Therapeutic Drug Carrier Systems, 6:273-313 (1990); Anderson et al., Am. Rev. Respir. Dis., 140:1317-1324 (1989)) and have potential for the systemic delivery of peptides and proteins as well (Patton and Platz, Advanced Drug Delivery Reviews, 8:179-196 (1992)); Timsina et al., Int. J. Pharm., 101:1-13 (1995); and Tansey, I. P., Spray Technol. Market, 4:26-29 (1994); French, D. L., Edwards, D. A. and Niven, R. W., Aerosol Sci., 27:769-783 (1996); Visser, J., Powder Technology 58:1-10 (1989)); Rudt, S. and R. H. Muller, J. Controlled Release, 22:263-272 (1992); Tabata, Y, and Y. Ikada, Biomed. Mater. Res., 22:837-858 (1988); Wall, D. A., Drug Delivery, 2:10 1-20 1995); Patton, J. and Platz, R., Adv. Drug Del. Rev., 8:179-196 (1992); Bryon, P., Adv. Drug. Del. Rev., 5:107-132 (1990); Patton, J. S., et al., Controlled Release, 28:15 79-85 (1994); Damms, B. and Bains, W., Nature Biotechnology (1996); Niven, R. W., et al., Pharm. Res., 12 (9); 1343-1349 (1995); and Kobayashi, S., et al., Pharm. Res., 13 (1): 80-83 (1996), the contents of each of which are incorporated herein by reference in their entirety.

Microemulsification technology can improve bioavailability of some lipophilic (water insoluble) pharmaceutical agents. Examples include Trimetrine (Dordunoo, S. K., et al., Drug Development and Industrial Pharmacy, 17 (12), 1685-1713, 1991 and REV 5901 (Sheen, P. C., et al., J Pharm Sci 80 (7), 712-714, 1991). Among other things, microemulsification provides enhanced bioavailability by preferentially directing absorption to the lymphatic system instead of the circulatory system, which thereby bypasses the liver, and prevents destruction of the cell-based compositions in the hepatobiliary circulation.

The engineered EVs described herein can be formulated with an amphiphilic carrier. Amphiphilic carriers are saturated and monounsaturated polyethyleneglycolyzed fatty acid glycerides, such as those obtained from fully or partially hydrogenated various vegetable oils. Such oils may advantageously consist of tri-, di-, and mono-fatty acid glycerides and di- and mono-polyethyleneglycol esters of the corresponding fatty acids, with a particularly preferred fatty acid composition including capric acid 4-10, capric acid 3-9, lauric acid 40-50, myristic acid 14-24, palmitic acid 4-14 and stearic acid 5-15%. Another useful class of amphiphilic carriers includes partially esterified sorbitan and/or sorbitol, with saturated or mono-unsaturated fatty acids (SPAN-series) or corresponding ethoxylated analogs (TWEEN-series).

Commercially available amphiphilic carriers are particularly contemplated, including Gelucire-series, Labrafil, Labrasol, or Lauroglycol (all manufactured and distributed by Gattefosse Corporation, Saint Priest, France), PEG-mono-oleate, PEG-di-oleate, PEG-mono-laurate and di-laurate, Lecithin, Polysorbate 80, etc. (produced and distributed by a number of companies in USA and worldwide).

The engineered EV compositions provided herein can be formulated with hydrophilic polymers. Hydrophilic polymers are water-soluble, can be covalently attached to a vesicle-forming lipid, and which are tolerated in vivo without toxic effects (i.e., are biocompatible). Suitable polymers include polyethylene glycol (PEG), polylactic (also termed polylactide), polyglycolic acid (also termed polyglycolide), a polylactic-polyglycolic acid copolymer, and polyvinyl alcohol. Other hydrophilic polymers which may be suitable include polyvinylpyrrolidone, polymethoxazoline, polyethyloxazoline, polyhydroxypropyl methacrylamide, polymethacrylamide, polydimethylacrylamide, and derivatized celluloses such as hydroxymethylcellulose or hydroxyethylcellulose.

In certain embodiments, a pharmaceutical composition as described herein comprises a biocompatible polymer selected from the group consisting of polyamides, polycar-

bonates, polyalkylenes, polymers of acrylic and methacrylic esters, polyvinyl polymers, polyglycolides, polysiloxanes, polyurethanes and co-polymers thereof, celluloses, polypropylene, polyethylenes, polystyrene, polymers of lactic acid and glycolic acid, polyanhydrides, poly(ortho) esters, poly (butic acid), poly(valeric acid), poly(lactide-co-caprolactone), polysaccharides, proteins, polyhyaluronic acids, polycyanoacrylates, and blends, mixtures, or copolymers thereof.

In certain embodiments, a pharmaceutical composition described herein is formulated as a liposome. Liposomes can be prepared by any of a variety of techniques that are known in the art. See, e.g., U.S. Pat. No. 4,235,871; Published PCT applications WO 96/14057; New RRC, Liposomes: A practical approach, IRL Press, Oxford (1990), pages 33-104; Lasic DD, Liposomes from physics to applications, Elsevier Science Publishers BV, Amsterdam, 1993.

Therapeutic formulations of the engineered EV compositions as described herein can be prepared for storage by with optional pharmaceutically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

Vaccine or other pharmaceutical compositions comprising an engineered EV composition as described herein can contain a pharmaceutically acceptable salt, typically, e.g., sodium chloride, and preferably at about physiological concentrations. The formulations of the vaccine or other pharmaceutical compositions described herein can contain a pharmaceutically acceptable preservative. In some embodiments, the preservative concentration ranges from 0.1 to 2.0%, typically v/v. Suitable preservatives include those known in the pharmaceutical arts. Benzyl alcohol, phenol, m-cresol, methylparaben, and propylparaben are examples of preservatives. The formulations of the vaccine or other pharmaceutical compositions described herein can include a pharmaceutically acceptable surfactant at a concentration of 0.005 to 0.02%.

Therapeutic pharmaceutical compositions described herein can also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other.

In some embodiments in which the engineered EVs are formulated for use in or with a vaccine, the vaccine composition can be formulated with the engineered EVs as an adjuvant. In other embodiments the vaccine composition can be formulated with the engineered EVs and an additional adjuvant, e.g., as known in the art.

As used herein in the context of immunization, immune response and vaccination, the term "adjuvant" refers to any substance than when used in combination with a specific antigen produces a more robust immune response than the antigen alone. When incorporated into a vaccine formulation, an adjuvant acts generally to accelerate, prolong, or enhance the quality of specific immune responses to the vaccine antigen(s). Adjuvants typically promote the accumulation and/or activation of accessory cells or factors to enhance antigen-specific immune responses and thereby enhance the efficacy of vaccines, i.e., antigen-containing or encoding compositions used to induce protective immunity against the antigen.

Adjuvants, in general, include adjuvants that create a depot effect, immune-stimulating adjuvants, and adjuvants that create a depot effect and stimulate the immune system. An adjuvant that creates a depot effect is an adjuvant that causes the antigen to be slowly released in the body, thus prolonging the exposure of immune cells to the antigen. This class of adjuvants includes but is not limited to alum (e.g., aluminum hydroxide, aluminum phosphate); emulsion-based formulations including mineral oil, non-mineral oil, water-in-oil or oil-in-water-in oil emulsion, oil-in-water emulsions such as Seppic ISA series of Montanide adjuvants (e.g., Montanide ISA 720; AirLiquide, Paris, France); MF-59 (a squalene-in-water emulsion stabilized with Span 85 and Tween 80; Chiron Corporation, Emeryville, Calif.); and PROVAX™ (an oil-in-water emulsion containing a stabilizing detergent and a micelle-forming agent; IDEC Pharmaceuticals Corporation, San Diego, Calif.).

An immune-stimulating adjuvant is an adjuvant that causes activation of a cell of the immune system. It may, for instance, cause an immune cell to produce and secrete cytokines and interferons. This class of adjuvants includes but is not limited to saponins purified from the bark of the *Q. saponaria* tree, such as QS21 (a glycolipid that elutes in the 21st peak with HPLC fractionation; Aquila Biopharmaceuticals, Inc., Worcester, Mass.); poly[di(carboxylatophenoxy)phosphazene (PCPP polymer; Virus Research Institute, USA); derivatives of lipopolysaccharides such as monophosphoryl lipid A (MPL; Ribi ImmunoChem Research, Inc., Hamilton, Mont.), muramyl dipeptide (MDP; Ribi) and threonyl-muramyl dipeptide (t-MDP; Ribi); OM-174 (a glucosamine disaccharide related to lipid A; OM Pharma SA, Meyrin, Switzerland); and *Leishmania* elongation factor (a purified *Leishmania* protein; Corixa Corporation, Seattle, Wash.). This class of adjuvants also includes CpG DNA.

Adjuvants that create a depot effect and stimulate the immune system are those compounds which have both of the above-identified functions. This class of adjuvants includes but is not limited to ISCOMS (immunostimulating complexes which contain mixed saponins, lipids and form virus-sized particles with pores that can hold antigen; CSL, Melbourne, Australia); SB-AS2 (SmithKline Beecham adjuvant system #2 which is an oil-in-water emulsion containing MPL and QS21: SmithKline Beecham Biologicals [SBB], Rixensart, Belgium); SB-AS4 (SmithKline Beecham adjuvant system #4 which contains alum and MPL; SBB, Belgium); non-ionic block copolymers that form micelles such as CRL 1005 (these contain a linear chain of hydrophobic polyoxypropylene flanked by chains of polyoxyethylene; Vaxcel, Inc., Norcross, Ga.); and Syntex Adjuvant Formu-

lation (SAF, an oil-in-water emulsion containing Tween 80 and a nonionic block copolymer; Syntex Chemicals, Inc., Boulder, Colo.).

The active ingredients of the pharmaceutical compositions described herein can also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980).

In some embodiments, sustained-release preparations can be used. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing a composition described herein in which the matrices are in the form of shaped articles, e.g., films, or microcapsule. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and y ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(−)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated, the composition can remain in the body for a long time (e.g., up to about 1 hour, between 1-12 hours, 12-24 hours, 24 hours to 2 days, 2-3 days, 3-4 days, 4-5 days, 5-6 days, 6-7 days, 1-2 weeks, 3-4 weeks, 4 weeks to 2 months, 2-3 months, 3-4 months, 4-5 months, 5-6 months, or more than 6 months, or a variation thereof), denature, or aggregate as a result of exposure to moisture at 37° C., resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S—S— bond formation through thio-disulfide interchange, stabilization can be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

Administration, Dosing, Efficacy

The engineered EV compositions, pharmaceutical compositions, or vaccine compositions described herein can be formulated, dosed, and administered in a fashion consistent with good medical practice. Factors for consideration in this context include the particular disorder being treated, the particular subject being treated, the clinical condition of the individual subject, the cause of the disorder, the site of delivery of the vaccine composition, the method of administration, the scheduling of administration, and other factors known to medical practitioners.

Generally, application of artificial synapses as therapy will take into account similar parameters as other therapeutic strategies, including concentration, timing of delivery, and sustained bioavailability at injury/disease site. Extracellular vesicle can be delivered via a number of routes: intravenous, intracoronary, and intramyocardial. Extracellular vesicles (e.g., exosomes), also allow for new delivery routes that were previously infeasible for cell therapy, such as inhalation or injection. These various approaches are described below, including injection, topical application, enteral administration, and pulmonary delivery.

The engineered EV compositions provided herein can be administered to a subject in need thereof by any appropriate route which results in an effective treatment in the subject. As used herein, the terms "administering," and "introducing" are used interchangeably and refer to the placement of a composition provided herein into a subject by a method or route which results in at least partial localization of such compositions at a desired site, such as a site of inflammation or a tumor, such that a desired effect(s) is produced. The compositions can be administered to a subject by any mode of administration that delivers the composition systemically or to a desired surface or target, and can include, but is not limited to, injection, infusion, instillation, and inhalation administration. To the extent that the composition can be protected from inactivation in the gut, oral administration forms are also contemplated. "Injection" includes, without limitation, intravenous, intramuscular, intra-arterial, intrathecal, intraventricular, intracapsular, intraorbital, retro-orbital, intravitreal, intraocular, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, sub capsular, subarachnoid, intraspinal, intracerebral, intratarsal, and intrasternal, intratumoral injection, and infusion or the like as known in the art.

A therapeutic does of the present invention may be delivered to a patient by means of controlled release, for example but not limited to, implantable pump and implantable cannulas to provide continuous access to the venous or arterial system.

Topical application refers to applying or spreading a composition of the present invention onto surfaces on or in the body, both internally and/or externally, in a therapeutically effective amount for local and/or systemic treatment. Topical application may be epicutaneuos wherein a composition of the present invention may be directly applied onto a localized surface of the skin or mucous membranes. Topical application may include transdermal application wherein a composition of the present invention may be absorbed into the body to obtain systemic delivery and systemic distribution. Topical application formulations may include, but are not limited to, creams, foams, gels, lotions, solutions, ointments, dermal patch, transdermal patches, powder, solid, sponge, tape, vapor, paste, film, liposomes, balm, shampoo, spray, or tincture or the like or a combination thereof. A therapeutic dose of a composition of the present invention may be delivered vaginally (for example a vaginal suppository, vaginal ring, douche, intrauterine device, intravesical infusion, and the like) or urethra or the like or a combination thereof.

Enteral administration refers to a composition of the present invention administered via the gastrointestinal tract in a therapeutically effective amount for local or systemic treatment. Enteral administration may include, but is not limited to, delivery of a composition of the present invention via the mouth, sublingual, esophagus, gastric (for example the stomach), small intestines, large intestines or rectum. Oral delivery of the present invention may include, but is not limited to, the use of a capsule, pastille, pill, tablet, solution, gel, suspension, emulsion, syrup, elixir, tincture, mouthwash, lozenges, chewing gum, lollipop, cream, foam, solution, powder, solid, vapor, liposomes, spray, or tincture osmotic-controlled release oral delivery system, or the like. Gastric delivery may involve the use of a tube or nasal

passage that leads directly to the stomach, for example, a percutaneous endoscopic gastrostomy tube. Gastric delivery may involve direct injection made through the abdominal wall. Rectal delivery may involve, but is not limited to, the use of a suppository, ointment, enema, murphy drip, or the like. A therapeutic does of the present invention may be delivered to a patient by means of controlled release, for example but not limited to, controlled release drug delivery pellet or pill.

Inhalation (i.e., pulmonary delivery, pulmonary administration refers to delivery to the respiratory system through the respiratory route, including but not limited to, intranasal administration, oral administration, and oral inhalative administration (e.g., intratracheal instillation and intratracheal inhalation) of a therapeutically effective amount for local or systemic treatment. Pulmonary delivery of a therapeutically effective amount of a composition of the present invention may be achieved by dispersion, for example by using a syringe. Pulmonary delivery of a composition of the present invention may be achieved by aerosol administration, wherein aerosol administration may deposit a therapeutically effective amount of the present invention by gravitational sedimentation, inertial impaction, or diffusion.

Intravenous delivery technique can occur through a peripheral or central venous catheter. As the simplest delivery mode, this technique avoids the risk of an invasive procedure. However, intravenous may be regarded as a comparatively inefficient and less localized delivery method, as a high percentage of infused cell exosomes may become sequestered in organs such as the lung, liver, or spleen. Such sequestration may result in few or no cellular exosomes reaching broader circulation or have unintended systemic effects following their distribution.

In certain embodiments, administration can include delivery to a tissue or organ site that is the same as the site of diseased and/or dysfunctional tissue. In certain embodiments, administration can include delivery to a tissue or organ site that is different from the site or diseased and/or dysfunctional tissue. In certain embodiments, the delivery is via inhalation or oral administration. In various embodiments, administration of artificial synapses can include combinations of multiple delivery techniques.

In some embodiments, the compositions described herein are administered by aerosol administration, nebulizer administration, or tracheal lavage administration.

The term "effective amount" as used herein refers to the amount of an engineered EV composition needed to alleviate or prevent at least one or more symptom of a disease or disorder (e.g., autoimmune disease or cancer), and relates to a sufficient amount of pharmacological composition to provide the desired effect, e.g., reduce the pathology, or any symptom associated with or caused by a disease. The term "therapeutically effective amount" therefore refers to an amount of an engineered EV composition or vaccine composition described herein using the methods as disclosed herein, that is sufficient to affect a particular disease state when administered to a typical subject. An effective amount as used herein would also include an amount sufficient to delay the development of a symptom of the disease, alter the course of a symptom disease (for example, but not limited to, slow the progression of a symptom of the disease), or reverse a symptom of the disease. Thus, it is not possible to specify the exact "effective amount." However, for any given case, an appropriate "effective amount" can be determined by one of ordinary skill in the art using only routine experimentation.

Effective amounts, toxicity, and therapeutic efficacy can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dosage can vary depending upon the dosage form employed and the route of administration utilized. The dose ratio between toxic and therapeutic effects is the therapeutic index and can be expressed as the ratio LD50/ED50. Compositions and methods that exhibit large therapeutic indices are preferred. A therapeutically effective dose can be estimated initially from cell culture assays. Also, a dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC50 (i.e., the concentration of the engineered EVs or fusion polypeptides provided herein), which achieves a half-maximal inhibition of symptoms) as determined in cell culture, or in an appropriate animal model. Levels of therapeutic engineered Evs in plasma can be measured, for example, by high performance liquid chromatography, enzyme linked immunosorbent assay (ELISA), flow cytometry, FACS sorting, western blot, mass spectroscopy, tunable resistive pulse sensing, EXOVIEW®, qRT-PCR, next generation sequencing (NGS), or by any analysis technique known by one of ordinary skill in the art. The effects of any particular dosage can be monitored by a suitable bioassay. The dosage can be determined by a physician and adjusted, as necessary, to suit observed effects of the treatment.

The engineered EV compositions, pharmaceutical compositions, or vaccine compositions described herein can be formulated, in some embodiments, with one or more additional therapeutic agents currently used to prevent or treat the infection, for example. The effective amount of such other agents depends on the amount of an engineered EV in the formulation, the type of disorder or treatment, and other factors discussed above. These are generally used in the same dosages and with administration routes as used herein before or about from 1 to 99% of the heretofore employed dosages.

The dosage ranges for the pharmaceutical compositions described herein depend upon the potency and encompass amounts large enough to produce the desired effect. The dosage should not be so large as to cause unacceptable adverse side effects. Generally, the dosage will vary with the age, condition, health, and sex of the patient and can be determined by one of skill in the art. The dosage can also be adjusted by the individual physician in the event of any complication. In some embodiments, the dosage ranges from 0.001 mg/kg body weight to 100 mg/kg body weight. In some embodiments, the dose range is from 5 μg/kg body weight to 100 μg/kg body weight. Alternatively, the dose range can be titrated to maintain serum levels between 0.1 μg/mL and 1000 μg/mL. For systemic administration, subjects can be administered a therapeutic amount, such as, e.g., 0.1 mg/kg, 0.5 mg/kg, 1.0 mg/kg, 2.0 mg/kg, 2.5 mg/kg, 5 mg/kg, 7.5 mg/kg, 10 mg/kg, 15 mg/kg, 20 mg/kg, 25 mg/kg, 30 mg/kg, 40 mg/kg, 50 mg/kg, or more. These doses can be administered by one or more separate administrations, or by continuous infusion. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until, for example, the infection is treated, as measured by the methods described above or known in the art. However, other dosage regimens can be useful.

In various embodiments, the quantities of artificial synapses that are administered to achieve these effects range from 1×10^6 to 1×10^7, 1×10^7 to 1×10^8, 1×10^8 to 1×10^9, 1×10^9

to 1×10^{10}, 1×10^{10} to 1×10^{11}, 1×10^{11} to 1×10^{12}, 1×10^{12} to 1×10^{13}, 1×10^{13} to 1×10^{14}, 1×10^{14} to 1×10^{15}, 1×10^{15} or more Evs/artificial synapses. In other embodiments, the numbers of artificial synapses are relative to the number of cells used in a clinically relevant dose for a cell-therapy method. For example, defining an effective dose range, dosing regimen and route of administration, may be guided by studies using fluorescently labeled artificial synapses, and measuring target tissue retention, which can be >10×, >50×, or >100× background, as measured 5, 10, 15, 30, or 30 or more min as a screening criterion. In certain embodiments, >100× background measured at 30 mins is a baseline measurement for a low and high dose that is then assess for safety and bioactivity (e.g., using MRI endpoints: scar size, global and regional function of the target organ being treated). In various embodiments, single doses are compared to two, three, four, four or more sequentially-applied doses. In various embodiments, the repeated or sequentially-applied doses are provided for treatment of an acute disease and/or condition. In various embodiments, the repeated or sequentially-applied doses are provided for treatment of a chronic disease and/or condition. In other embodiments, administration of the plurality of artificial synapses is adjunctive to standard therapy.

In other embodiments, administering a composition includes 1×10^{10} or more artificial synapses in a single dose. In various embodiments, exosome quantity may be defined by protein quantity, such as dosages including 1-10, 10-25, 25-50, 50-75, 75-100, or 100 or more mg exosome protein. In other embodiments, a single dose is administered multiple times to the subject. In other embodiments, administering a composition consists of one or more of: injection, topical administration, enteral, intravenous, intra-arterial, or inhalation.

In various embodiments, exosome quantity may be defined by protein quantity, such as dosages including 1-10, 10-25, 25-50, 50-75, 75-100, or 100 or more mg exosome protein. In various embodiments, administering a composition includes multiple dosages of the artificial synapses. In various embodiments, the repeated or sequentially-applied doses are provided for treatment of an acute disease and/or condition. In various embodiments, the repeated or sequentially-applied doses are provided for treatment of a chronic disease and/or condition.

In other embodiments, administering a composition including a plurality of artificial synapses to the subject is adjunctive to standard therapy.

The duration of a therapy using the methods described herein will continue for as long as medically indicated or until a desired therapeutic effect (e.g., those described herein) is achieved. In certain embodiments, the administration of the vaccine composition described herein is continued for 1 month, 2 months, 4 months, 6 months, 8 months, 10 months, 1 year, 2 years, 3 years, 4 years, 5 years, 10 years, 20 years, or for a period of years up to the lifetime of the subject.

As will be appreciated by one of skill in the art, appropriate dosing regimens for a given composition can comprise a single administration/immunization or multiple ones. Subsequent doses may be given repeatedly at time periods, for example, about two weeks or greater up through the entirety of a subject's life, e.g., to provide a sustained preventative effect. Subsequent doses can be spaced, for example, about two weeks, about three weeks, about four weeks, about one month, about two months, about three months, about four months, about five months, about six months, about seven months, about eight months, about nine months, about ten months, about eleven months, or about one year after a primary immunization.

The precise dose to be employed in the formulation will also depend on the route of administration and should be decided according to the judgment of the practitioner and each patient's circumstances. Ultimately, the practitioner or physician will decide the amount of the engineered EV or composition thereof to administer to particular subjects.

Methods of Modulating Inflammation and Treating Autoimmune Diseases

The artificial synapses/engineered Evs and compositions thereof provided herein can be deployed in a therapeutic strategy against virtually any injury/disease, as providing a platform for altering biological signaling. This includes, for example, inflammation and immune signaling, which plays a role in virtually all injuries and diseases in living organisms.

Thus, described herein is a method of modulating inflammation, including selecting a subject afflicted with an inflammatory related disease and/or condition; and administering to the subject a composition including a plurality of artificial synapses (engineered Evs) to the subject, wherein administration of the composition modulates inflammation.

As used herein, the term "inflammation" or "inflamed" refers to activation or recruitment of the immune system or immune cells (e.g., T cells, B cells, macrophages). A tissue that has inflammation can become reddened, white, swollen, hot, painful, sensitivity, exhibit a loss of function, or have a film or mucus. Methods of identifying inflammation are well known in the art. Inflammation typically occurs following injury, infection by a microorganism, exposure to a substance (e.g., a toxin, chemical, or dust) or autoimmune dysfunction. Onset of inflammation may be rapid (e.g., immediately following injury) or slow (e.g., repeated exposure to an irritant such as a chemical over time) with a duration of minutes, hours, days, months, years, or an individual's life.

Inflammation plays a vital role in alerting the immune system of potential danger and damage within a body. Inflammation is necessary to control and repair injury. For example, acute inflammation is a response to physical trauma, infection, and stress. Acute inflammation helps prevent further injury and triggers healing and recovery. Unfortunately, inflammation can become excessive and inappropriately active, lasting beyond the typical recovery time from an injury or infection. Wherein healthy inflammation helps a body respond to injury, chronic inflammation perpetuates injury and may lead to negative consequences to one's health. In particular, autoimmune diseases are chronic diseases from a host's immune system attacking itself, often due to aberrant biological signaling in the host. Restoring normal homeostatic signaling via application of artificial synapses, particularly targeting immune checkpoints, represents a highly promising avenue. For example, surface bound immune-checkpoint proteins or fragments thereof may modulate immune cell stimulation and affect suppression of immune cell function when delivered via artificial synapses. Injection, inhalation, ingestion or topical application of artificial synapses with surface bound immune-checkpoint proteins or fragments thereof may be used to treat immune, auto-immune, inflammatory, and auto-inflammatory conditions. Examples include chronic obstructive pulmonary disease (COPD) which is an inflammatory, progressive, life-threatening lung disease, psoriasis, a common chronic noncommunicable inflammatory skin disease,

arthritis, a debilitating and painful degeneration of joints, among others well-understood to one of skill in the art.

In other embodiments, the inflammatory related disease and/or condition is acute, for example septicemia. In other embodiments, the inflammatory related disease and/or condition is chronic, for example chronic obstructive pulmonary disease. In other embodiments, the inflammatory condition is an autoimmune disease wherein the autoimmune disease and/or condition is one or more of: polymyositis, dermatomyositis, Graves' disease, Hashimoto's thyroiditis, myasthenia gravis, vasculitis, multiple sclerosis, psoriasis, rheumatoid arthritis, psoriatic arthritis, scleroderma, systemic lupus erythematosus, inflammatory bowel disease, Crohn's disease, hyperthyroidism, autoimmune adrenal insufficiency, Sjogren syndrome, type I diabetes mellitus, autoimmune hemolytic anemia, idiopathic thrombocytopeniarpura, myasthenia gravis, ulcerative colitis, uveitis, polyarteritis nodosa, relapsing polychondritis, Behcet's disease, reactive arthritis, ankylosing spondylitis, Guillain-Barre syndrome, or optic neuropathy. In other embodiments, the disease and/or condition is chronic obstructive pulmonary disease, rheumatoid arthritis, uveoretinitis, psoriasis, and eczema. In other embodiments, the disease and/or condition is irritable bowel disease, multiple sclerosis or lupus.

In other embodiments, the inflammatory related disease and/or condition is an ocular disease. As used herein, the terms "ocular disease", "eye disorder" and "eye disease" are used interchangeably and refer to a disease or disorder that affects the health and/or vision of either one or both eyes or the general area of the eye(s), eye lid(s), or area surrounding or in near proximity to the eye(s). Eye disease may include, but are not limited to, macular degeneration (e.g., age-related macular degeneration), cataracts, diabetic retinopathy, diabetic macular edema, eye floaters, eye flashes, glaucoma, amblyopia, strabismus, retinitis (e.g., CMV retinitis), color blindness, keratoconus, retinal detachment, eyelid twitching, ocular hypertension, blepharitis, uveitis, Bietti's crystalline dystrophy, blepharospasm, cornea and corneal diseases, dry eye, histoplasmosis, macular hole, macular pucker, conjunctivitis, presbyopia, retinoblastoma, retinitis pigmentosa, retinopathy, Stargardt disease, Usher syndrome, uveal Coloma, and vitreous detachment, or the like.

Described herein is a method for treatment including, selecting a subject in need of treatment, administering a composition including a plurality of artificial synapses to the individual, wherein administration of the composition treats the subject. In certain embodiments, the subject is in need to treatment for a disease and/or condition involving tissue damage or dysfunction.

Described herein is a method of treating an autoimmune disease, inflammation, inflammatory disease or condition, or cancer in a subject, the method comprising: administering to a subject an engineered EV or composition thereof as provided herein to the subject.

Measured or measurable parameters include clinically detectable markers of disease, for example, elevated or depressed levels of a clinical or biological marker, as well as parameters related to a clinically accepted scale of symptoms or markers for a disease or disorder. It will be understood, however, that the total usage of the compositions and formulations as disclosed herein will be decided by the attending physician within the scope of sound medical judgment. The exact amount required will vary depending on factors such as the type of disease being treated.

Non-limiting examples of clinical tests that can be used to assess autoimmune diseases, inflammatory conditions, or inflammation parameters include blood tests, skin biopsy, MRI, eye examination, ocular pressure tests, etc. Where necessary or desired, animal models of injury or disease can be used to gauge the effectiveness of a particular composition as described herein. For example, an EAU animal model, as demonstrated in the working examples can be used.

In various embodiments, administration of the plurality of artificial synapses alters gene expression in the damaged or dysfunctional tissue, improves viability of the damaged tissue, and/or enhances regeneration or production of new tissue in the individual. In various embodiments, administration of the plurality of artificial synapses alters gene expression in the damaged or dysfunctional tissue, improves viability of the damaged tissue, and/or enhances regeneration or production of new tissue in the individual.

In various embodiments, the damaged or dysfunctional tissue is in need of repair, regeneration, or improved function due to an acute event. Acute events include, but are not limited to, trauma such as laceration, crush or impact injury, shock, loss of blood or oxygen flow, infection, chemical or heat exposure, poison or venom exposure, drug overuse or overexposure, and the like. Other sources of damage also include, but are not limited to, injury, age-related degeneration, cancer, and infection. In several embodiments, the regenerative cells used to prepare the engineered EVs provided herein are from the same tissue type as is in need of repair or regeneration. In several other embodiments, the regenerative cells are from a tissue type other than the tissue in need of repair or regeneration. In some embodiments, the engineered EVs provided herein are derived from the subject being treated. In some embodiments, the engineered EVs are derived from a donor subject.

In other embodiments, the damaged or dysfunctional tissue is in need of repair, regeneration, or improved function due to damage from chronic disease.

Some Selected Definitions

All references cited herein are incorporated by reference in their entirety as though fully set forth. Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Allen et al., *Remington: The Science and Practice of Pharmacy* 22nd *ed.*, Pharmaceutical Press (Sep. 15, 2012); Hornyak et al., *Introduction to Nanoscience and Nanotechnology*, CRC Press (2008); Singleton and Sainsbury, *Dictionary of Microbiology and Molecular Biology* 3rd *ed., revised ed.*, J. Wiley & Sons (New York, NY 2006); Smith, *March's Advanced Organic Chemistry Reactions, Mechanisms and Structure* 7th *ed.*, J. Wiley & Sons (New York, NY 2013); Singleton, *Dictionary of DNA and Genome Technology* 3rd *ed.*, Wiley-Blackwell (Nov. 28, 2012); and Green and Sambrook, *Molecular Cloning: A Laboratory Manual* 4*th ed.*, Cold Spring Harbor Laboratory Press (Cold Spring Harbor, NY 2012), provide one skilled in the art with a general guide to many of the terms used in the present application. For references on the preparation and structure of antibodies and fusion polypeptides, see, e.g., Greenfield, *Antibodies A Laboratory Manual* 2nd *ed.*, Cold Spring Harbor Press (Cold Spring Harbor NY, 2013); Köhler and Milstein, *Derivation of specific antibody-producing tissue culture and tumor lines by cell fusion*, Eur. J. Immunol. 1976 Jul. 6 (7): 511-9; Queen and Selick, Humanized immunoglobulins, U.S. Pat. No. 5,585,089 (1996 December); and Riechmann et al., *Reshaping human antibodies for therapy*, Nature 1988 Mar. 24, 332 (6162): 323-7. See also, Kabat et

al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991), Lanzavecchia et al., Eur. J. Immunol. 17, 105 (1987)), Huston et al., Proc. Natl. Acad. Sci. U.S.A., 85, 5879-5883 (1988), Bird et al., Science 242, 423-426 (1988), Brinkman et al. mAbs Vol 9, No. 2, 182-212 (2017), Chothia & Lesk, J. Mol. Biol, 196:901-917 (1987), Chothia et al., Nature 342:877-883 (1989)), Holliger et al. (1993) Proc. Natl. Acad. Sci. USA 90:6444-6448; Poljak (1994) Structure 2:1121-1123); Kontermann and Dubel eds., Antibody Engineering, Springer-Verlag, N.Y. (2001), p. 790 (ISBN 3-540-41354-5, Zapata et al. (1995) Protein Eng. 8 (10): 1057-1062; Morrison, et al., Proc. Natl. Acad. Sci. USA, 81:6851 (1984), U.S. Pat. Nos. 4,816,567, 5,693,780, which are incorporated herein by reference in their entireties.

One skilled in the art will recognize many methods and materials similar or equivalent to those described herein, which could be used in the practice of the present invention. Indeed, the present invention is in no way limited to the methods and materials described. For purposes of the present invention, the following terms are defined below.

As used herein, the term "extracellular vesicle" and "vesicle" are used interchangeably and refer to a particle, wherein the particle comprises a phospholipid bilayer that encloses an internal space and an exterior surface and may or may not be derived from a cell. The size of extracellular vesicles can range between 20 nm to 3 μm in diameter but may be smaller than 20 nm or larger than 3 μm. Examples of extracellular vesicles include, but is not limited to, exosomes (for example small exosomes and large exosomes), ectosomes, macrovesicles, microparticles, apoptotic bodies, vesicular organelles, oncosomes (for examples large oncosomes), exospheres, exomeres, cell derived nanovesicles (CDN) (e.g., by genesis via grating or shearing cells), liposomes or the like known by one of ordinary skill in the art. Extracellular vesicles may originate naturally via known or unknown biosynthetic pathways. Extracellular vesicles may be promoted to originate by using mechanical methods such as cell grating or cell shearing wherein a cell is grated or sheared causing portions or parts of the cell membrane to from vesicles. For example, CDNs may be formed by using mechanical methods such as cell grating or cell shearing wherein a cell is grated or sheared causing portions or parts of the cell membrane to from vesicles. Additional non-limiting examples of mechanical methods that can be used to form cell derived nanovesicles are further described in detail, e.g., Goh, W. J., Zou, S., Ong, W. Y. et al. Bioinspired Cell-Derived Nanovesicles versus Exosomes as Drug Delivery Systems: a Cost-Effective Alternative. *Sci Rep* 7, 14322 (2017). doi: 10.1038/s41598-017-14725-x, the contents of which are incorporated herein by reference in their entireties.

Extracellular vesicles comprise cargo, wherein the term "cargo" refers to peptides, proteins, nucleic acids, lipids, metabolites, carbohydrates, biomolecules, small molecules, large molecules, vesicles, organelles, or fragments thereof. In some embodiments, cargo may refer to existing drugs or therapeutics known in the art. Extracellular vesicle cargo may be located within the internal space of the extracellular vesicle. Extracellular vesicle cargo may be membrane bound and span one or both layers of the extracellular vesicle phospholipid bilayer (for example a transmembrane protein). Extracellular vesicle cargo may be in contact with the external or internal surface of the extracellular vesicle, for example through a covalent bond or a non-covalent bond. The phospholipid bilayer of the extracellular vesicle may comprise one or more transmembrane proteins, wherein a portion of the one or more transmembrane membrane proteins is located within the internal space of the extracellular vesicle. The phospholipid bilayer of the extracellular vesicle may comprise one or more transmembrane proteins, wherein the one or more transmembrane membrane proteins comprises a domain on the exterior of the extracellular vesicle. The phospholipid bilayer of the extracellular vesicle may comprise one or more transmembrane proteins, wherein the one or more transmembrane membrane proteins comprises a domain on the interior of the extracellular vesicle. Cargo may refer to a protein on the luminal side (e.g., in the internal space) of the extracellular vesicle wherein said protein encodes a vesicle targeting domain that may be in contact with the interior phospholipid layer of the extracellular vesicle. Cargo may refer to a protein on the luminal side (e.g., in the internal space) of the extracellular vesicle wherein said protein encodes a vesicle targeting domain that may be in contact with the interior phospholipid layer of the extracellular vesicle and wherein said protein may be presented into the internal space of the extracellular vesicle.

As used herein, the terms "sticky binder" and "vesicle targeting domain" and "anchor protein" are used interchangeably and refer to a protein that is covalently or non-covalently attached to at least one lipid wherein the one or more lipid is embedded within a membrane (e.g., a cell membrane), and the lipid serves to anchor the protein to the membrane. The terms "sticky binder" and "vesicle targeting domain" and "anchor protein" can also mean a protein sequence that encodes for one or more transmembrane domains wherein the one or more transmembrane domains spans at least partly through a phospholipid bilayer, for example the phospholipid bilayer of an extracellular vesicle. The transmembrane domain can be of a Type I or Type II membrane protein. Transmembrane domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs that identify hydrophobic and hydrophilic domains (for example TMHMM Server, v. 2.0-DTU, Erik L. L. Sonnhammer, Gunnar von Heijne, and Anders Krogh: *A hidden Markov model for predicting transmembrane helices in protein sequences. In Proc. of Sixth Int. Conf. on Intelligent Systems for Molecular Biology, p* 175-182 Ed J. Glasgow, T. Littlejohn, F. Major, R. Lathrop, D. Sankoff, and C. Sensen Menlo Park, CA: AAAI Press, 1998, which is incorporated herein by reference in its entirety.)

A vesicle targeting domain may include, but is not limited to, one or more prenylation site, fatty acylation site, and/or glycosylphosphatidylinositol (GPI) linked protein. One preferred embodiment of a vesicle targeting domain is the GPI sequence from CD55. Another preferred embodiment of a vesicle targeting domain is the GPI sequence from CD59. Another embodiment of a vesicle targeting domain is the C1C2 domain from MFGE8. Other embodiments of sequences for vesicle targeting domains include transmembrane regions of CD9 (for example transmembrane 2 or 3 of CD9, CD9tm2 or CD9tm3, respectively), K-Ras (for example K-Ras4A and K-Ras4B), transmembrane domain from A Disintegrin and Metalloproteinase Domain-containing protein 10 (ADAM10, also known as CDw156 or CD156c) or other ADAM proteins. Vesicle targeting domains may include one or more sequences from 4F2 (for example 4F2 encoded by the solute carrier family 3 member 2 (SLC3A2) gene which makes up the heavy subunit of CD98). Vesicle targeting domains can include a sequence for one or more myristoylation sites. For example, the protein sequence for a myristoylation site from myristoylated ala-

nine-rich C-kinase substrate (MARCKS) protein. Vesicle targeting domains can include a sequence for one or more palmitoylation sites. For example, the myristoylation sequence from the MARCKS protein may be modified to encode for a palmitoylation site. All variants, isoforms, or fragments or the like known by one of ordinary skill in the art are encompassed by the present invention.

Vesicle targeting domains may include transmembrane sequences from *Homo sapiens* transferrin receptor 2 (TFR2), transcript variant 1 (transferrin receptor protein 2 isoform 1) or versions therefore. In a preferred embodiment, the vesicle targeting domain may be a transmembrane domain from CD298.

As used herein, the terms "proteins" and "peptides" and "polypeptides" are used interchangeably herein to designate a series of amino acid residues connected to the other by peptide bonds between the alpha-amino and carboxy groups of adjacent residues. Although "protein" is often used in reference to relatively large polypeptides, and "peptide" is often used in reference to small polypeptides, usage of these terms in the art overlaps and varies. The term "peptide" as used herein refers to peptides, polypeptides, proteins and fragments of proteins, unless otherwise noted. The terms "protein" and "peptide" are used interchangeably herein when referring to a gene product and fragments thereof. Thus, exemplary peptides or proteins include gene products, naturally occurring proteins, homologs, orthologs, paralogs, fragments and other equivalents, variants, fragments, and analogs of the foregoing.

As used herein, the term "linker" refers to a synthetic protein sequence of amino acids that is used to connect two polypeptide domains via peptide bonds.

As used herein, the term "fusion protein" refers to a single chimeric protein comprising a protein of interest (e.g., checkpoint protein) joined to an exogenous protein or protein fragment (e.g., an anchor protein), wherein the components of the fusion protein are linked to each other by peptide-bonds, either directly or through a peptide linker. The anchor protein of the fusion protein may enhance incorporation of the fusion protein onto and/or into the membrane of a vesicle, for example the internal and/or external leaflet of the phospholipid bilayer of an exosome membrane. The fusion protein may have at least a part of an amino acid sequence of an immune checkpoint protein or proteins involved in immune synapses. The fusion protein may have at least a part of an amino acid sequence of A2AR, VTCN1, Galectin 9, FGL-1, PECAM-1, TSG-6, STAB-1, NRP1, NRP2, SEMA3A, SEMA3F, RGMB, TIM-3, TIGIT, HLA class I, HLA class II, VISTA, HMGB1, phosphatidylserine, T-cell receptor (TCR), SHP-1, SHP-2, FBXO38, SH2D1A, B7RP1, IDO, NOX2, TNFRSF18, B7-H4, B7-H5, SISP1, B7-H6, B7-H7, APLNR, IFN y, PD-1, WNT5A, IL-6, IL-10, NKG2 family of C-type lectin receptors, ligands of NKG2 family, killer cell immunoglobulin-like receptors, CD2, CD4, CD8, CD27, CD27 ligand (CD70), CD28, CD28H, CD39, CD40, CD44, CD47, CD63, CD66a, CD80, B7-2, CD86, CD73, CD94, CD96, CD101, CD112, CD112R, CD122, CD134, CD137 (4-1BB), CD137 ligand (4-1BBL), CD152, CD154, CD155, CD158, CD158a, CD158g, CD158h, KIR2DL1, KIR2DS1, KIRDS3, KIR2DS5, CD160, CD172a, CD200, CD200R, CD223, CD226, CD252, CD270, CD272, CD273, CD274, CD275, CD276, CD278, CD279 (PD-1), CD279 ligand (PD-L1/PDL-2), CD328, CD329, and/or CD337. The fusion protein may have a polypeptide linker sequence (e.g., an Fc domain and/or a GSSG linker (SEQ ID NO: 319)), followed by an amino acid sequence coding for an anchor protein sequence (e.g., a prenylation site, fatty acylation site, or a GPI sequence) or any isoform, fragment, variation thereof, or a ligand to the aforementioned proteins thereof, or the like known by one of ordinary skill in the art. All variants are encompassed by the present invention.

As used herein, the term "immune synapse" and "cell synapse" are used interchangeably and refer to cell-to-cell interaction wherein said interaction results in activation, suppression, and/or adhesion of either one or more cells. Immune synapse or cell synapse are mediated by proteins that may be cytoplasmic, membrane bound, membrane associated, and/or secreted. Immune or cell synapses may be mediated by one or more "immune checkpoint proteins" which herein refers to any protein that is involved in maintaining immune homeostasis or plays a role in regulating immune activation or suppression. Immune checkpoint proteins may be cytoplasmic, membrane bound, membrane associated, and/or secreted.

As used herein, the term "fragment" or "active fragment" refers to a portion of a nucleic acid or polypeptide provided herein that retains the ability to be expressed by the engineered EVs provided herein. In some embodiments, the active fragment retains the ability to activate a target polypeptide, thereby increasing the activity of said target polypeptide (e.g., suppressing an immune response).

As used herein, the terms "specifically bind" and/or "specifically recognize" or "substantially binds" refers to the affinity of a binding molecule for a target molecule compared to the binding molecule's affinity for non-target molecules. A binding molecule (e.g., a POI domain) that specifically binds a target molecule (e.g., a target polypeptide provided herein) does not substantially recognize or bind non-target molecules. e.g., an antibody "specifically binds" and/or "specifically recognize" another molecule, meaning that this interaction is dependent on the presence of the binding specificity of the molecule structure, e.g., an antigenic epitope. As used herein, "non-specific binding" and "background binding" refers to the interaction that does not depend on the presence of specific structure (e.g., a specific antigenic epitopes). Methods of measuring binding of a polypeptide to a target are known in the art (e.g., differential scanning calorimetry, isothermal titration calorimetry, spectroscopy, crystallography, surface plasmon resonance, co-immunoprecipitation, pulldown assays, crosslinking, yeast two-hybrid system, tandem affinity purification-mass spectroscopy, protein microarrays, bio-layer interferometry, far-Western blots, computational prediction, analytical ultracentrifugation, light scattering, fluorescence spectroscopy, resonance energy transfer, ELISA or ELISPOT assays, or any other assays known in the art).

As used herein, the terms "treat," "treatment," "treating," or "amelioration" refer to therapeutic treatments, wherein the object is to reverse, alleviate, ameliorate, inhibit, slow down or stop the progression or severity of a condition associated with, a disease or disorder. The term "treating" includes reducing or alleviating at least one adverse effect or symptom of a condition, disease or disorder associated with an infection or a cancer. Treatment is generally "effective" if one or more symptoms or clinical markers are reduced. Alternatively, treatment is "effective" if the progression of a disease is reduced or halted. That is, "treatment" includes not just the improvement of symptoms or markers, but also a cessation or at least slowing of progress or worsening of symptoms that would be expected in absence of treatment. Beneficial or desired clinical results include, but are not limited to, alleviation of one or more symptom(s), diminishment of extent of disease, stabilized (i.e., not worsening)

state of disease, delay or slowing of disease progression, amelioration or palliation of the disease state, and remission (whether partial or total), whether detectable or undetectable. The term "treatment" of a disease also includes providing relief from the symptoms or side-effects of the disease (including palliative treatment).

As used herein "preventing" or "prevention" refers to any methodology where the disease state does not occur due to the actions of the methodology (such as, for example, administration of a composition or construct as described herein). In one aspect, it is understood that prevention can also mean that the disease is not established to the extent that occurs in untreated controls. Accordingly, prevention of a disease encompasses a reduction in the likelihood that a subject can develop the disease, relative to an untreated subject (e.g., a subject who is not treated with the methods or compositions described herein).

As used herein, the terms "autoimmune condition" and "autoimmune disease" are used interchangeably and refer to any disease characterized by abnormal functioning of the immune system and may include, but is not limited to, achalasia, Addison's disease, adult Still's disease, agammaglobulinemia, alopecia areata, amyloidosis, ankylosing spondylitis, anti-GBM/Anti-TBM nephritis, antiphospholipid syndrome, autoimmune angioedema, autoimmune dysautonomia, autoimmune encephalomyelitis, autoimmune hepatitis, autoimmune inner ear disease (AIED), autoimmune myocarditis, autoimmune oophoritis, autoimmune orchitis, autoimmune pancreatitis, autoimmune retinopathy, autoimmune urticaria, axonal & neuronal neuropathy (AMAN), Baló disease, Behcet's disease, benign mucosal pemphigoid, bullous pemphigoid, Castleman disease, celiac disease, Chagas disease, chronic inflammatory demyelinating polyneuropathy (CIDP), chronic recurrent multifocal osteomyelitis (CRMO), Churg-Strauss syndrome (CSS), eosinophilic granulomatosis (EGPA), cicatricial pemphigoid, Cogan's syndrome, cold agglutinin disease, congenital heart block, coxsackie myocarditis, CREST syndrome, Crohn's disease, dermatitis herpetiformis, dermatomyositis, Devic's disease (neuromyelitis optica), discoid lupus, Dressler's syndrome, endometriosis, eosinophilic esophagitis (EoE), eosinophilic fasciitis, erythema nodosum, essential mixed cryoglobulinemia, Evans syndrome, fibromyalgia, fibrosing alveolitis, giant cell arteritis (temporal arteritis), giant cell myocarditis, glomerulonephritis, Goodpasture's syndrome, granulomatosis with polyangiitis, Graves' disease, Guillain-Barre syndrome, Hashimoto's thyroiditis, hemolytic anemia, Henoch-Schonlein purpura (HSP), Herpes gestationis or pemphigoid gestationis (PG), hidradenitis suppurativa (HS) (acne inversa), hypogammaglobulinemia, IgA nephropathy, IgG4-related sclerosing disease, immune thrombocytopenia purpura (ITP), inclusion body myositis (IBM), interstitial cystitis (IC), juvenile arthritis, type 1 diabetes, juvenile myositis (JM), Kawasaki disease, Lambert-Eaton syndrome, leukocytoclastic vasculitis, lichen planus, lichen sclerosus, ligneous conjunctivitis, linear IgA disease (LAD), lupus, lyme disease chronic, Meniere's disease, microscopic polyangiitis (MPA), mixed connective tissue disease (MCTD), Mooren's ulcer, Mucha-Habermann disease, multifocal motor neuropathy (MMN) or MMNCB, multiple sclerosis, myasthenia gravis, myositis, narcolepsy, neonatal Lupus, neuromyelitis optica, neutropenia, ocular cicatricial pemphigoid, optic neuritis, palindromic rheumatism (PR), PANDA, paraneoplastic cerebellar degeneration (PCD), paroxysmal nocturnal hemoglobinuria (PNH), Parry Romberg syndrome, pars planitis (peripheral uveitis), Parsonage-Turner syndrome, pemphigus, peripheral neuropathy, perivenous encephalomyelitis, pernicious anemia (PA), POEMS syndrome, polyarteritis nodosa, polyglandular syndromes type I, II, III, polymyalgia rheumatica, polymyositis, postmyocardial infarction syndrome, postpericardiotomy syndrome, primary biliary cirrhosis, primary sclerosing cholangitis, progesterone dermatitis, psoriasis, psoriatic arthritis, pure red cell aplasia (PRCA), pyoderma gangrenosum, Raynaud's phenomenon, reactive arthritis, reflex sympathetic dystrophy, relapsing polychondritis, restless legs syndrome (RLS), retroperitoneal fibrosis, rheumatic fever, rheumatoid arthritis, sarcoidosis, Schmidt syndrome, scleritis, scleroderma, Sjögren's syndrome, sperm & testicular autoimmunity, stiff person syndrome (SPS), subacute bacterial endocarditis (SBE), Susac's syndrome, sympathetic ophthalmia (SO), takayasu's arteritis, temporal arteritis/Giant cell arteritis, thrombocytopenia purpura (TTP), Tolosa-Hunt syndrome (THS), transverse myelitis, type 1 diabetes, ulcerative colitis (UC), undifferentiated connective tissue disease (UCTD), uveitis, vasculitis, vitiligo, Vogt-Koyanagi-Harada disease. An autoimmune condition or autoimmune diseases may be caused by, but not limited to, a natural predisposition, an infection (e.g., bacteria or virus), drugs, vaccination, environmental triggers (e.g., toxins or chemicals such as dust, silica, oil, benzene, tri- or per-chloroethylene etc.), stress, cancer, blood or tissue or organ transplantation, or unknown etiology. Autoimmune disorders may result in but not limited to the destruction of body tissue, abnormal growth of an organ or tissue, changes in organ or tissue function (e.g., changes in blood vessels, connective tissue, function of endocrine glands, joints, muscles, blood cells, skin, etc.).

As used herein, the term "cancer" refers to a hyperproliferation of cells that exhibit a loss of normal cellular control that results in unregulated growth, lack of differentiation, local tissue invasion, and metastasis. The methods and compositions described herein can be used for the treatment of solid tumors (e.g., cancer) or non-solid tumors, such as leukemia, blood cell cancers, and the like. Solid tumors can be found in bones, muscles, the brain, or organs, and can be sarcomas or carcinomas. Where the methods and compositions described herein can overcome barriers of tumor treatment, including, but not limited to barriers to treatment or inhibition of metastases, it is contemplated that aspects of the technology described herein can be used to treat all types of solid and non-solid tumor cancers, including cancers not listed in the instant specification. The compositions and methods described herein, without limitation, include methods of treating cancer, methods of inhibiting metastases, and methods of inducing an anti-tumor immune response.

As used herein, the terms "subject", "individual", "host", and "patient" are used interchangeably and may refer to any animal, mammal, bird, fish, reptile, and amphibian, for example, human, monkey, dog, cat, horse, pig, cattle, ox, donkey, rabbit, sheep, goat, mouse, rat, guinea pig, llama, chicken, goose, duck, turkey, or the like receiving or registered to receive a therapeutic amount of a composition of the present invention for medical care or treatment.

As used herein, the term "injection" refers to any process or method which allows the person skilled in the art to administer any therapeutic to a target site by penetration. Examples of injection are, but not limited to, subcutaneous, subcuticular, subcapsular, subarachnoid, intradermal, intramuscular, intravenous, intra-arterial, intraventricular, intracapsular, intraorbital, intraocular, intrathoracic, intraperitoneal, intravitreal, retro-orbital, intranasal, intracerebral, intrathymic, intraspinal, intrasternal, intra-articular, intrac-

avernous, intracardiac, intraosseous, intrathecal, transtracheal, epidural, or the like as known in the art. A therapeutic does of the present invention may be delivered to a patient by means of controlled release, for example but not limited to, implantable pump and implantable cannulas to provide continuous access to the venous or arterial system.

As used herein, the term "topical application" refers to applying or spreading a composition of the present invention onto surfaces on or in the body, both internally and/or externally, in a therapeutically effective amount for local and/or systemic treatment. Topical application may be epicutaneuos wherein a composition of the present invention may be directly applied onto a localized surface of the skin or mucous membranes. Topical application may include transdermal application wherein a composition of the present invention may be absorbed into the body to obtain systemic delivery and systemic distribution. For example, a transdermal patch may be applied onto the body to deliver a therapeutic dose of a composition of the invention presented herein. Topical application formulations may include, but are not limited to, creams, foams, gels, lotions, solutions, ointments, dermal patch, transdermal patches, powder, solid, sponge, tape, vapor, paste, film, liposomes, balm, shampoo, spray, or tincture. A therapeutic dose of a composition of the present invention may be delivered vaginally (for example a vaginal suppository, vaginal ring, douche, intrauterine device, intravesical infusion, and the like) or urethra.

As used herein, the term "enteral administration" refers to a composition of the present invention administered via the gastrointestinal tract in a therapeutically effective amount for local or systemic treatment. Enteral administration may include, but is not limited to, delivery of a composition of the present invention via the mouth, sublingual, esophagus, gastric (for example the stomach), small intestines, large intestines or rectum. Oral delivery of the present invention may include, but is not limited to, the use of a capsule, pastille, pill, tablet, solution, gel, suspension, emulsion, syrup, elixir, tincture, mouthwash, lozenges, chewing gum, lollipop, osmotic-controlled release oral delivery system, or the like. Gastric delivery may involve the use of a tube or nasal passage that leads directly to the stomach, for example, a percutaneous endoscopic gastrostomy tube. Gastric delivery may involve direct injection made through the abdominal wall. Rectal delivery may involve, but is not limited to, the use of a suppository, ointment, enema, murphy drip, or the like. A therapeutic does of the present invention may be delivered to a patient by means of controlled release, for example but not limited to, controlled release drug delivery pellet or pill.

As used herein, the terms "pulmonary system" or "respiratory system" are used interchangeably and refer, but are not limited, to the respiratory region, conducting airways, nasal cavity, sinuses, nasopharynx, oropharynx, larynx, trachea, bronchi, bronchioles, respiratory bronchioles, alveolar ducts, alveolar sacs, respiratory epithelium (e.g., alveolar epithelial cells), endothelial cells, or the like.

As used herein, the terms "pulmonary delivery" and "pulmonary administration" are used interchangeably and refer to delivering a composition of the present invention to the respiratory system through the respiratory route, including but not limited to, intranasal administration, oral administration, and oral inhalative administration (e.g., intratracheal instillation and intratracheal inhalation) of a therapeutically effective amount for local or systemic treatment. Pulmonary delivery of a therapeutically effective amount of a composition of the present invention may be achieved by dispersion, for example by using a syringe. Pulmonary delivery of a composition of the present invention may be achieved by aerosol administration, wherein aerosol administration may deposit a therapeutically effective amount of the present invention by gravitational sedimentation, inertial impaction, or diffusion.

Pulmonary delivery of a therapeutically effective amount of a composition of the present invention may be deposited on any mucus layer of the respiratory system, for example, but not limited to, the mucus layer which coats the walls of conducting airways, the smaller airway, and/or alveolar space.

As used herein, an "appropriate control" refers to an untreated, otherwise identical cell or population (e.g., a subject who was not administered the composition described herein, or was administered by only a subset of agents provided herein, as compared to a non-control cell).

As used herein, a "reference level" can refer to one or more parameters or markers as measured for a normal, otherwise unaffected cell population or tissue (e.g., a biological sample obtained from a healthy subject, or a biological sample obtained from the subject at a prior time point, or a biological sample that has not yet been contacted with a pathogen as described herein). For measuring or monitoring therapeutic efficacy, a level determined prior to treatment or earlier in treatment can also provide a reference level for a given parameter or value.

As used herein, the term "modulates" refers to an effect including increasing or decreasing a given parameter as those terms are defined herein.

The terms "increased," "increase," "increases," or "enhance" or "activate" are all used herein to generally mean an increase of a property, level, or other parameter by a statistically significant amount; for the avoidance of any doubt, the terms "increased", "increase" or "enhance" or "activate" means an increase of at least 10% as compared to a reference level, for example an increase of at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% or up to and including a 100% increase or any increase between 10-100% as compared to a reference level, or at least about a 2-fold, or at least about a 3-fold, or at least about a 4-fold, or at least about a 5-fold or at least about a 10-fold increase, at least about a 20-fold increase, at least about a 50-fold increase, at least about a 100-fold increase, at least about a 1000-fold increase or more as compared to a reference level. For example, increasing activity can refer to activating a receptor or a signaling pathway (e.g., antibody production or inflammation).

The terms "decrease", "reduced", "reduction", or "inhibit" are all used herein to mean a decrease or lessening of a property, level, or other parameter by a statistically significant amount. In some embodiments of any of the aspects, "reduce," "reduction" or "decrease" or "inhibit" typically means a decrease by at least 10% as compared to a reference level (e.g., the absence of a given treatment) and can include, for example, a decrease by at least about 10%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or more. As used herein, "reduction" or "inhibition" does not encompass a complete inhibition or reduction as compared to a reference level. "Complete inhibition" is a 100% inhibition as compared to a reference level. A decrease can

be preferably down to a level accepted as within the range of normal for an individual without a given disorder.

As used herein the term "comprising" or "comprises" is used in reference to compositions, methods, and respective component(s) thereof, that are essential to the method or composition, yet open to the inclusion of unspecified elements, whether essential or not.

As used herein the term "consisting essentially of" refers to those elements required for a given embodiment. The term permits the presence of elements that do not materially affect the basic and novel or functional characteristic(s) of that embodiment.

The term "consisting of" refers to compositions, methods, and respective components thereof as described herein, which are exclusive of any element not recited in that description of the embodiment.

As used in this specification and the appended claims, the singular forms "a," "an," and "the" include plural references unless the context clearly dictates otherwise. Thus for example, references to "the method" includes one or more methods, and/or steps of the type described herein and/or which will become apparent to those persons skilled in the art upon reading this disclosure and so forth. Similarly, the word "or" is intended to include "and" unless the context clearly indicates otherwise. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of this disclosure, suitable methods and materials are described below.

The abbreviation, "e.g." is derived from the Latin exempli gratia, and is used herein to indicate a non-limiting example. Thus, the abbreviation "e.g." is synonymous with the term "for example."

The abbreviation, "etc." is derived from the Latin et cetera, and is used herein to indicate a non-limiting list. Thus, the abbreviation "etc.," is synonymous with the term "and other similar things", or "and so forth".

Other than in the operating examples, or where otherwise indicated, all numbers expressing quantities of ingredients or reaction conditions used herein should be understood as modified in all instances by the term "about." The term "about" when used in connection with percentages can mean±1%.

The term "statistically significant" or "significantly" refers to statistical significance and generally means a two-standard deviation (2SD) difference, above or below a reference value. Additional definitions are provided in the text of individual sections below.

It should be understood that this invention is not limited to the particular methodology, protocols, and reagents, etc., described herein and as such may vary. The terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention, which is defined solely by the claims.

As used herein and in the claims, the singular forms include the plural reference and vice versa unless the context clearly indicates otherwise. The term "or" is inclusive unless modified, for example, by "either." Other than in the operating examples, or where otherwise indicated, all numbers expressing quantities of ingredients or reaction conditions used herein should be understood as modified in all instances by the term "about."

Unless otherwise explained, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs.

It is to be understood that the foregoing description and the following examples are illustrative only and are not to be taken as limitations upon the scope of the invention. Various changes and modifications to the disclosed embodiments, which will be apparent to those of skill in the art, may be made without departing from the spirit and scope of the present invention. Further, all patents, patent applications, and publications identified are expressly incorporated herein by reference for the purpose of describing and disclosing, for example, the methodologies described in such publications that might be used in connection with the present invention. These publications are provided solely for their disclosure prior to the filing date of the present application. Nothing in this regard should be construed as an admission that the inventors are not entitled to antedate such disclosure by virtue of prior invention or for any other reason. All statements as to the date or representation as to the contents of these documents are based on the information available to the applicants and do not constitute any admission as to the correctness of the dates or contents of these documents.

All patents and other publications identified are expressly incorporated herein by reference for the purpose of describing and disclosing, for example, the methodologies described in such publications that could be used in connection with the present invention. These publications are provided solely for their disclosure prior to the filing date of the present application. Nothing in this regard should be construed as an admission that the inventors are not entitled to antedate such disclosure by virtue of prior invention or for any other reason. All statements as to the date or representation as to the contents of these documents is based on the information available to the applicants and does not constitute any admission as to the correctness of the dates or contents of these documents.

Some embodiments of the technology described herein can be defined according to any of the following numbered paragraphs:

1. An engineered extracellular vesicle comprising:
   at least one fusion polypeptide comprising:
   (i) at least one protein of interest (POI) domain or a fragment thereof; and
   (ii) at least one vesicle targeting domain,
   wherein the POI domain is in an extracellular position relative to a lipid membrane of the extracellular vesicle.
2. The engineered extracellular vesicle of paragraph 1, wherein the extracellular vesicle is an exosome.
3. The engineered extracellular vesicle of paragraph 1 or paragraph 2, wherein the protein of interest (POI) domain or a fragment thereof is a N-terminal domain of the fusion polypeptide.
4. The engineered extracellular vesicle of any one of paragraphs 1-3, wherein the vesicle targeting domain is a C-terminal domain of the fusion polypeptide.
5. The engineered extracellular vesicle of any one of paragraphs 1-4, wherein the fusion polypeptide comprises at least two POI domains and/or at least two exosome targeting domains.
6. The engineered extracellular vesicle of any one of paragraphs 1-5, wherein the fusion polypeptide further comprises a peptide linker.
7. The engineered extracellular vesicle of any one of paragraphs 1-6, wherein the fusion polypeptide further comprises a fragment crystallizable region (Fc) domain.
8. The engineered extracellular vesicle of any one of paragraphs 1-7, wherein the vesicle targeting domain is in a luminal position relative to the lipid membrane of the extracellular vesicle.

9. The engineered extracellular vesicle of any one of paragraphs 1-7, wherein the vesicle targeting domain in an exterior position relative to the lipid membrane of the extracellular vesicle.
10. The engineered extracellular vesicle of any one of paragraphs 1-9, wherein the POI domain is selected from the group consisting of: Table 1.
11. The engineered extracellular vesicle of any one of paragraphs 1-10, wherein the POI domain is PD-L1 or a fragment thereof.
12. The engineered extracellular vesicle of any one of paragraphs 1-11, wherein the POI domain is PD-L2 or a fragment thereof.
13. The engineered extracellular vesicle of any one of paragraphs 1-12, wherein the POI domain is FGL1 or a fragment thereof.
14. The engineered extracellular vesicle of any one of paragraphs 1-13, wherein the POI domain is 4-1BBL or a fragment thereof.
15. The engineered extracellular vesicle of any one of paragraphs 1-14, wherein the POI domain is CTLA-4 or a fragment thereof.
16. The engineered extracellular vesicle of any one of paragraphs 1-15, wherein the POI domain substantially binds to one or more of a target polypeptide.
17. The engineered extracellular vesicle of paragraph 16, wherein the target polypeptide is selected from the group consisting of: Table 2.
18. The engineered extracellular vesicle of any one of paragraphs 1-17, wherein the vesicle targeting domain is selected from the group consisting of: Table 3.
19. The engineered extracellular vesicle of any one of paragraphs 1-18, wherein the linker is in an exterior position relative to the lipid membrane of the extracellular vesicle.
20. The engineered extracellular vesicle of any one of paragraphs 1-18, wherein the linker is a transmembrane linker.
21. The engineered extracellular vesicle of any one of paragraphs 1-18, wherein the linker is in a luminal position relative to the lipid membrane of the extracellular vesicle.
22. The engineered extracellular vesicle of any one of paragraphs 1-21, wherein the extracellular vesicle does not comprise an endogenous POI polypeptide.
23. A composition comprising a plurality of the engineered extracellular vesicles of any one of paragraphs 1-22.
24. The composition of paragraph 23, further comprising a pharmaceutically acceptable carrier.
25. An engineered extracellular vesicle comprising:
(a) a first fusion polypeptide comprising:
(i) at least one protein of interest (POI) domain or a fragment thereof; and
(ii) at least one vesicle targeting domain,
wherein the at least one POI domain is in an extracellular position relative to a lipid membrane of the extracellular vesicle,
(b) a second fusion polypeptide comprising:
(i) at least one protein of interest (POI) domain or a fragment thereof; and
(ii) at least one vesicle targeting domain,
wherein the POI domain is in an extracellular position relative to a lipid membrane of the extracellular vesicle,
and wherein the at least one vesicle targeting domain is within a lipid membrane of the extracellular vesicle.
26. A composition comprising two or more of the engineered extracellular vesicles selected from any one of paragraphs 1-25.
27. An extracellular vesicle composition comprising:
a plurality of artificial synapses,
wherein each artificial synapse comprises (i) an extracellular vesicle; (ii) one or more sticky binders; and (iii) one or more signaling domains.
The composition of paragraph 27, wherein the extracellular vesicle comprises an exosome.
28. The composition of paragraph 27, wherein the one or more sticky binders is selected from the group consisting of: a GPI anchor, a fatty acylation site, and a prenylation site.
30. The composition of paragraph 27, wherein the signaling domain comprises one or more of: PD-L1, PD-L2, CTLA-4 (CD152), 4-1BBL (CD137L), HVEM (CD270), FGL1, OX-2 (CD200), Galectin-9, PVR (CD155), Nectin-2 (CD112) isoform alpha, Nectin-2 (CD112) isoform beta, Nectin-2 (CD112) isoform delta, IL-10, TSG-6, B7-H3 (CD276), B7-H4 (VTCN1), B7-H5 (VISTA), B7-H7 (HHLA2), BTNL1, VSIG8, VSIG3 (IGSF11), VSIG4, TIM-3 (HAVCR2), TIM-4 (TIMD4), CEACAM1, BTN3A1, BTN3A2, BTN2A1, BTNL8, BTN2A2, BTN1A1, TIGIT, CD27L (CD70), CD30L (CD153), GITRL, CD40L (CD154), LIGHT (CD258), TL1, CD80, CD86, LFA-3 (CD58), SLAM (CD150), CD40, CD28, CD28H, CD2, LFA-3 (CD58), CD48, CD226, DR3, DcR3, FasL, TIM-1 (CD365), PD-1, or active fragment thereof.
29. A method of producing the engineered extracellular vesicle or the composition of any one of paragraphs 1-30, comprising:
(a) providing a population of cells expressing a vector construct encoding one or more sticky binder and one or more signaling domains; and
(b) isolating a plurality of artificial synapses from the population of cells.
30. A method of producing the engineered extracellular vesicle or the composition of any one of paragraphs 1-30, comprising:
(a) providing a population of cells expressing a vector construct encoding one or more sticky binder and one or more signaling domains; and
(b) isolating a plurality of artificial synapses from the population of cells; and
(c) purifying the plurality of artificial synapses from the population of cells.
33. The method of paragraph 31 or paragraph 32, the isolating is via size exclusion chromatography.
34. The method of paragraph 32, wherein the purifying is via multimodal chromatography.
35. The method of any of paragraphs 31-34, further comprising performing an assay for POI binding to a target polypeptide.
36. The method of paragraph 35, wherein the vector construct further encodes a promoter.
37. The method of paragraph 36, wherein the promoter is a tissue-specific promoter or an inducible promotor.
38. A method of modulating inflammation in a subject, the method comprising:
administering a composition comprising a plurality of engineered extracellular vesicles to a subject in need thereof,

wherein the engineered extracellular vesicles comprise at least one fusion polypeptide comprising:

(i) at least one protein of interest (POI) domain or a fragment thereof; and

(ii) at least one vesicle targeting domain.

39. The method of paragraph 38, wherein the extracellular vesicle comprises an exosome.

40. The method of any one of paragraphs 38-39, further comprising selecting a subject that has or is suspected of having an autoimmune disease or an inflammatory disease or condition.

41. The method of any one of paragraphs 38-40, wherein the vesicle targeting domain is selected from the group consisting of: a Glycosylphosphatidylinositol (GPI) anchor, a fatty acylation site, and a prenylation site.

42. The method of any one of paragraphs 38-41, wherein the vesicle targeting domain is a GPI anchor.

43. The method of any one of paragraphs 38-41, wherein the vesicle targeting domain is C1C2.

44. The method of any one of paragraphs 38-43, wherein the protein of interest (POI) domain comprises one or more of: PD-L1, PD-L2, CTLA-4 (CD152), 4-1BBL (CD137L), HVEM (CD270), FGL1, OX-2 (CD200), Galectin-9, PVR (CD155), Nectin-2 (CD112) isoform alpha, Nectin-2 (CD112) isoform beta, Nectin-2 (CD112) isoform delta, IL-10, TSG-6, B7-H3 (CD276), B7-H4 (VTCN1), B7-H5 (VISTA), B7-H7 (HHLA2), BTNL1, VSIG8, VSIG3 (IGSF11), VSIG4, TIM-3 (HAVCR2), TIM-4 (TIMD4), CEACAM1, BTN3A1, BTN3A2, BTN2A1, BTNL8, BTN2A2, BTN1A1, TIGIT, CD27L (CD70), CD30L (CD153), GITRL, CD40L (CD154), LIGHT (CD258), TL1, CD80, CD86, LFA-3 (CD58), SLAM (CD150), CD40, CD28, CD28H, CD2, LFA-3 (CD58), CD48, CD226, DR3, DcR3, FasL, TIM-1 (CD365), PD-1, or active fragment thereof. 45. The method of any one of paragraphs 38-44, wherein the protein of interest (POI) domain is PD-L1 or a fragment thereof.

46. The method of any one of paragraphs 38-44, wherein the protein of interest (POI) domain is PD-L2 or a fragment thereof.

47. The method of any one of paragraphs 38-44, wherein the protein of interest (POI) domain is CTLA-4 or a fragment thereof.

48. The method of any one of paragraphs 38-44, wherein the protein of interest (POI) domain is HVEM or a fragment thereof.

49. The method of paragraph 40, wherein the inflammatory disease and/or condition is acute.

50. The method of paragraph 40, wherein the inflammatory related disease and/or condition is chronic.

51. The method of paragraph 38, wherein administering the composition comprises injection, topical administration, or inhalation.

52. Use of a composition comprising a plurality of engineered extracellular vesicles, the engineered extracellular vesicles each comprising:

at least one fusion polypeptide comprising:

(i) at least one protein of interest (POI) domain or a fragment thereof; and

(ii) at least one vesicle targeting domain

for the treatment of an inflammatory disease or condition.

53. Use of a composition comprising a plurality of engineered extracellular vesicles, the engineered extracellular vesicles each comprising:

at least one fusion polypeptide comprising:

(i) at least one protein of interest (POI) domain or a fragment thereof; and

(ii) at least one vesicle targeting domain

for the treatment of an autoimmune disease or condition.

54. Use of a composition comprising a plurality of engineered extracellular vesicles, the engineered extracellular vesicles each comprising:

at least one fusion polypeptide comprising:

(i) at least one protein of interest (POI) domain or a fragment thereof; and

(ii) at least one vesicle targeting domain

for the treatment of cancer.

EXAMPLES

The following examples are provided by way of illustration, not limitation.

Example 1

Design of Artificial Synapse

As described, artificial synapses are engineered to induce and propagate biological signaling, including for example, antagonist and agonist signaling. Artificial synapses are designed to include hallmark biophysical and biochemical features of extracellular vesicles, further including vesicle targeting domains and signaling domains. Vesicle targeting domains capable of attaching to extracellular vesicles such as exosomes, signaling domains, optionally including a linker (e.g., Fc linker), can be organized in genetic vector constructs. Designs are shown in FIG. **1**.

Sticky binders are extracellular vesicle targeting sequences. Preliminary extracellular vesicle targeting sequences of interest are from, but not limited to, 4F2 (CD98), ADAM10, CD298, TFR2, transmembrane domains of CD9, MARCKS, KRAS, etc. or the like as appreciate by one of ordinary skill in the art. The Inventors discovered high efficiency when proteins are engineered with a GPI domain. Optionally, linker regions such as an Fc linker between the vesicle targeting domains and signaling domains can be added.

A variety of signaling domains are of interest with proof-of-concept examples including PD-L1, PD-L2 and CTLA-4 (CD152). Artificial synapses including these three signaling domains are shown in FIGS. **2-5**.

Each of these elements are described in the following non-limiting examples.

Example 2

Genetic Constructs

Examples of constructs including these variable elements (e.g., sticky binders GPI or C1C2, or signaling domains including PD-L1, PD-L2 and CTLA-4 (CD152) were engineered into vectors shown in FIGS. **2-5**.

Example 3

Purification of hPD-L1 Tagged Artificial Synapses by a Multimodal Resin Marketed for Exosome Purification

Upon expression of hPD-L1-Fc-GPI in mammalian cells, artificial synapses were further purified using a size exclusion resin marketed for exosome purification. Large MW

artificial synapses elute in the first fraction as shown by the high hPD-L1 concentration and exosome quantity (2.26E9 artificial synapses/ml) in elution 1. Clean in place (CIP) fractions show bound and eliminated proteins from the Inventors' exosome elution. Results are shown in FIG. **6**.

Example 4

hPDL1-Fc-GPI Exosome Purification-Size Exclusion Chromatography Column

Artificial synapses engineered from exosomes such as hPDL1-Fc-GPI after elution from size exclusion resin marketed for exosome purification can be further purified via a size exclusion column as shown here. Using a size exclusion chromatography (SEC), artificial synapses elute in fractions 7-9. Total protein (determined by Qubit™) and hPD-L1 ng/ml (determined by ELISA) of each fraction is shown in the graph. Bars show exosome number per ml (i.e., 1E10 artificial synapses/ml etc.). Fractions 7-9 contain >99% purified artificial synapses. Fractions 7-9 are pooled and may be concentrated using a filtration device, for example a 10K MWCO Amicon® Centrifugal Filter. Final purified product is filtered through a low protein binding 0.2 μm or 0.45 μm filter, for example a PES filter. Results are shown in FIG. **7**.

Example 5

hPD-L1 Expression on Artificial Synapses

Exosome quantity and hPD-L1 concentration was determined in SEC fractions 7-9. Knowing the molecular weight of engineered hPD-L1, the Inventors can determine the number of hPD-L1 molecules per exosome to be approximately between 12 to 40 PD-L1/exosome. This value is consistent between different purification runs and constructs. Results are shown in FIG. **8**.

Example 6

Purification of hPD-L2-Fc-GPI Artificial Synapses Via Multimodal Resin Chromatography Marketed for Exosome Purification

This graph shows Abs 280 of multimodal resin chromatography fractions and quantity of hPDL2 in indicated fractions. Artificial synapses eluted in Elution 1.

Clean in place (CIP) fractions show bound and eliminated proteins from the Inventors' exosome elution. Results are shown in FIG. **9**.

Example 7

PD-L2 Purification Via Size Exclusion Chromatography

Artificial synapses engineered from artificial synapses such as hPDL2-GPI after elution from size exclusion resin size exclusion resin marketed for exosome purification are further purified via size exclusion chromatography as shown. Results are shown in FIG. **10**.

Example 8

hCTLA4-Fc-GPI Exosome Purification Via Size Exclusion Chromatography

Using size exclusion chromatography marketed for exosome purification, artificial synapses elute in fractions 7-9. Total protein (determined by Qubit™) and hPD-L1 ng/ml (determined by ELISA) of each fraction is shown in the graph. Fractions 7-9 are pooled and contain >99% purified artificial synapses. Pooled artificial synapses engineered from artificial synapses fractions may then be concentrated using a filtration device, for example a 10K MWCO Amicon®. Final purified product is filtered through a low protein binding filter, for example a 0.2 μm or 0.45 μm PES filter. Results are shown in FIG. **11**.

Example 9

PD-L1 and PD-L2 In Vitro Assay from DISCOVERX®

To perform this validation method, the Inventors modified the PathHunter® PD-1 Signaling Bioassay from DISCOVERX® Briefly, the PathHunter® PD-1 Signaling Bioassay relies on the well-established PathHunter® Enzyme Fragment Complementation (EFC) technology to interrogate receptor activity. EFC consists of a split β-galactosidase (β-gal) enzyme: the Enzyme Donor (ED) and Enzyme Acceptor (EA) fragments which independently have no β-gal activity. However, when forced to complement they form an active β-gal enzyme that will hydrolyze substrate to produce a chemiluminescent signal. The PathHunter® PD-1 Signaling Bioassay consists of human cells engineered to stably express an ED-tagged PD-1 receptor, while EA is fused to the phosphotyrosine-binding SH2 domain of the intracellular signaling protein, SHP1. Ligand or antibody-induced activation of the receptor results in phosphorylation of the receptor's cytosolic tail. The SH2-domain fused to EA binds the phosphorylated receptor, forcing complementation of ED and EA, resulting in formation of an active β-gal enzyme, which hydrolyzes the substrate to produce a chemiluminescent signal. Full-length PD-1 receptor was engineered with a small β-gal fragment (ED in red) fused to its C-terminus, and the SH2-domain of SHP1 was engineered with the complementing β-gal fragment (EA). These constructs were stably expressed in Jurkat cells (produced by DISCOVERX®), while PD-L1 and PD-L2 was stably expressed on artificial synapses produced by Diadem Biotherapeutics. Artificial synapses were engineered to have surface expressed human PD-L1 or PD-L2. Briefly, the gene sequence coding for the extracellular domain of human PD-L1 or PD-L2 was linked to the exosome via a glycosylphosphatidylinositol (GPI) linker with an Fc domain between the linker and PD-L1 or PD-L2 (PD-L1-Fc-GPI and PD-L2-Fc-GPI). Additional variations of the Inventors' PD-L1 and PD-L2 artificial synapses include cloning a C1C2 linker (from MFGE8) in place of the GPI linker, and with or without the Fc domain. The Inventors also cloned murine versions of PD-L1 and PD-L2 extracellular domains in place of the human PD-L1 and PD-L2 all variations. Ligand engagement, through addition of ligand-presenting artificial synapses, results in phosphorylation of PD-1, leading to the recruitment of SHP1-EA

The Inventors obtained approximately 1000× higher increase in Relative Light Units (RLU) in Jurkat signaling cells treated with PD-L1 or PD-L2 labeled artificial synapses when compared to soluble PD-L1-Fc or PD-L2-Fc ligand, respectively. Meaning, it took 1000× less μg/ml of PD-L1 or PD-L2 on artificial synapses than solubilized PD-L1-Fc or PD-L2 ligand to achieve the same RLU signaling. Results are shown in FIG. **12**.

Example 10

PD-L1 In Vivo Assay-Experimental Autoimmune Uveoretinitis (EAU) in Lewis Rats Bioassay

Experimental autoimmune uveoretinitis (EAU) is an organ-specific, T lymphocyte-mediated autoimmune disease, which serves as a model for several human ocular inflammations of an apparently autoimmune nature. There is a statistically significant initial reduction in EAU in mPDL1 artificial synapse treated rats via either the intravitreal and intravenous delivery modes. 2nd intravitreal and 3rd intravenous injections are performed on Day 12. There appears to be a more rapid rate of resolution in the 1× intravitreal and intravenous groups. (C) Simplified view of aforementioned results. (D) Weight of rats was monitored throughout the study. 3rd intravitreal and 4th intravenous injections are performed on Day 16. There does not appear to be any significant change in EAU in any of the test groups. The aforementioned results provide proof of principle of successfully immunizing the rats with human cell derived artificial synapses with mouse PDL1 injected into rats. Results are shown in FIG. **13**.

Example 11

Engineered Exosome Multivalent Display

The inventors have developed the following 3 types of protein display on or within exosomes:

Type I membrane proteins wherein the N-Terminus is on the luminal (interior) side of the exosome membrane and the C-Terminus is on the exterior of the exosome.

Type II membrane proteins wherein the N-Terminus is on the exterior while the C-Terminus is on the interior.

Luminal internally loaded proteins which are linked to the exosome by a Myristoylation/Palmitoylation site which attaches proteins to the interior of the exosome membrane.

FIGS. **14-21** demonstrate the various embodiments of the engineered extracellular vesicles.

Additional embodiments or ligands displayed on the exosome surface (Type I and Type II membrane proteins) and internal luminal display can include the following:

Type I: PD-L1, PD-L2, FGL1, OX40L.

Type II: 4-1BBL, GITRL, CD27L, CD30L

Luminal: NanoLuc® luciferase; Green fluorescent protein (GFP) (e.g., eGFP, etc.); Red fluorescent protein (RFP) (e.g., mScarlet, mCherry, mRuby, tdTomato, etc.); Cyan fluorescent protein (CFP); Yellow fluorescent protein (YFP); A therapeutic protein; and CRISPR/CAS-9

FIG. **20** shows an exemplary multiple protein display construct. Sequences such as P2A, E2A, F2A, and T2A induce ribosomal slippage which prevent peptide bond formation, meaning that a single mRNA transcript with a 2A sequence will result in two separate peptides after translation. This allows the expression of two separate proteins from one promoter region and thus loading of two proteins on an exosome. Any combination of the proteins of interest domains provided herein can be engineered. Furthermore, a cell line with multiple transgene inserts under separate promoter control. Either method can be used to label Type I, Type II, and luminal display proteins.

Example 12a

Designed and Engineered Human Fusion Polypeptide Constructs

The inventors have designed, engineered, and purified the following human fusion polypeptide constructs for therapeutic use (FIG. **5**A-FIG. **5**WW):

pEF5-FRT-hPDL1-C1C2 (FIG. **5**I)
pEF5-FRT-hPDL2-C1C2 (FIG. **5**J)
pEF5-FRT-hPDL1-GPI-P2A-hFGL1-GPI (FIG. **5**E)
pEF5-FRT-hCTLA4-Fc-GPI (FIG. **5**C)
pEF5-FRT-hPDL2-Fc-GPI (FIG. **5**H)
pEF5-FRT-hPD-L1-GPI-P2A-hHVEM-GPI (FIG. **5**D)
pEF5-FRT-hPDL1-GPI (FIG. **5**F)
pcDNA5-FRT-hSecPDL1-GPI (FIG. **5**O)
pcDNA5-FRT-hPDL1-GPI (FIG. **5**F)
pcDNA5-FRT-hPDL1-Link-GPI (FIG. **5**T)
pcDNA5-FRT-4F2-h41BBL (FIG. **5**K)
pcDNA5-FRT-Tfr2-h41BBL (FIG. **5**P)
pEF5-FRT-hPDL1-Fc-GPI (FIG. **5**G)
pcDNA5-FRT-CD9tm3-h41BBL (FIG. **5**Q)
pcDNA5-FRT-hPDL1-Fc-GPI (FIG. **5**G)
pcDNA5-FRT-hPDL1-4Fc-CD9tm2 (FIG. **5**RR)
pcDNA5-FRT-hPDL1-Fc-CD9tm2KRAS (FIG. **5**UU)
pcDNA5-FRT-hPDL1-4Fc-CD9tm2KRAS (FIG. **5**SS)
pcDNA5-FRT-hPDL1-4Fc-GPI (FIG. **5**L)
pcDNA5-FRT-hPDL1-ADAM10 (FIG. **5**QQ)
pcDNA5-FRT-MyrPalm-4F2-h41BBL (FIG. **5**R)
pcDNA5-FRT-MyrPalm-h41BBL (FIG. **5**S)
pcDNA5-FRT-hPDL1-Fc-CD9tm2 (FIG. **5**TT)
pcDNA5-FRT-hSecPDL1-CD9tm4 (FIG. **5**W)
pcDNA5-FRT-hSecPDL1-CD9tm2KRas (FIG. **5**V)
pcDNA5-FRT-hSecPDL1-CD9tm2 (FIG. **5**U)
pcDNA5-FRT-hSecPDL1-CD81 (FIG. **5**X)
pEF5-FRT-hCD200-Fc-GPI (FIG. **5**Y)
pEF5-FRT-hCD200-GPI (FIG. **5**BB)
pEF5-FRT-hTSG6-GPI (FIG. **5**FF)
pEF5-FRT-hPDL2-GPI (FIG. **5**EE)
pEF5-FRT-hFGL-1-GPI (FIG. **5**Z)
pEF5-FRT-hHVEM-GPI (FIG. **5**DD)
pEF5-FRT-hGal9-GPI (FIG. **5**CC)
pEF5-FRT-hHVEM-Fc-GPI (FIG. **5**GG); and
pEF5-FRT-hGal9-Fc-GPI (FIG. **5**AA)

Example 12b

Designed and Engineered Fusion Polypeptide Constructs

The inventors have designed, engineered, and purified the following mouse fusion polypeptide constructs for therapeutic use (FIG. **5**A-FIG. **5**WW):

pcDNA5-FRT-mPDL1-mFc-CD9tm2KRAS (FIG. **5**WW)
pcDNA5-FRT-mPDL1-mFc-CD9tm2 (FIG. **5**VV)
pcDNA5-FRT-mPDL1-mFc-GPI (FIG. **5**NN)
pcDNA5-FRT-mPDL1-GPI (FIG. **5**KK)
pEF5-FRT-mPDL2-GPI (FIG. **5**OO)
pEF5-FRT-mPDL1-GPI-P2A-mHVEM-GPI (FIG. **5**PP)
pEF5-FRT-mPDL1-GPI (FIG. **5**KK)
pEF5-FRT-mPDL2-Fc-GPI (FIG. **5** MM)
pEF5-FRT-mPDL1-Fc-GPI (FIG. **5**JJ)

pEF5-FRT-mCTLA4-Fc-GPI (FIG. **5**HH)
pEF5-FRT-mPDL1-C1C2 (FIG. **5**II); and
pEF5-FRT-mPDL2-C1C2 (FIG. **5**LL).

Example 12c

Designed and Engineered Luminal Loaded Fusion Polypeptide Constructs

The inventors have designed, engineered, and purified the following fusion polypeptide constructs for internal luminal loading of the fusion polypeptide:

pcDNA5-FRT-Myr-NanoLuc (FIG. **5**M)
pcDNA5-FRT-Myr-mScarlet (FIG. **5**N)

Example 13

Purification of Exosomes Labeled with Type I Membrane Fusion Polypeptides

The inventors have purified engineered EVs, including hPD-L1-GPI; hPDL1-Fc-GPI; hPDL2-Fc-GPI; hCTLA4-Fc-GPI; mPDL1-GPI; and mPD-L1-Fc-GPI. The process for purification and analytical processing of the engineered EVs are shown in the flow chart provided in FIG. **21**.

Size exclusion chromatography was performed to purify hPD-L1-GPI (no Fc) exosomes (FIG. **24**). Protein, RNA and DNA measurements in SEC fractions. Invitrogen Qubit™ fluorometric assays were used to measure biomolecules from unmodified concentrated cell media SEC fractions or hPD-L1-Exo-Tag concentrated cell media SEC fractions. PD-L1 was measured using an R&D systems PD-L1 ELISA kit. Dot-blot immunoblot analysis of SEC fractions. A 96-well dot blot apparatus was used to immobilize 50 μl of each SEC fraction onto PVDF. Exosome size and concentration was measured in fraction 7 by tunable resistive pulse sensing (TRPS). It was confirmed that GPI anchors the hPD-L1 fusion protein onto the exosomes (FIG. **25**).

Furthermore, a commercially available multimodal exosome purification resin was also used to purify and isolate PD-L1-GPI exosomes and PD-L1-Fc-GPI exosomes. Fraction 7 was further analyzed by dot blots (FIG. **28**A-**28**B). In particular, FIG. **28**B shows SEC purification results of various embodiments of human PD-L1 displayed on the surface of extracellular vesicles. One embodiment is the hPD-L1-4Fc-GPI (CMV) construct as seen in the top dot blot (stained with rabbit monoclonal anti-PD-L1 antibody). Another embodiment is the hPD-L1-4Fc-GPI (EF1a) as seen in the top dot blot (stained with rabbit monoclonal anti-PD-L1 antibody).

Large MW exosomes elute in the first fraction as shown by the high hPD-L1 concentration and exosome quantity (2.26E9 exosomes/ml) in elution 1. Clean in place (CIP) fractions show bound and eliminated proteins from our exosome elution. Exosome quantity and hPD-L1 concentration was determined in SEC fractions 7-9. Knowing the molecular weight of engineered hPD-L1, we can determine the number of hPD-L1 molecules per exosome to be approximately 12 PD-L1/exosome. This value is consistent between different purification runs and constructs (FIG. **8**).

Human hPD-L2 and hCTLA-4-Fc-GPI SEC fractions were purified. In addition, purification of the mouse PD-L1-FcGPI exosomes was performed (FIG. **29**). The mouse Fc-PD-L1 expressing exosomes have a higher valency than those that do not comprise the Fc linker.

Example 14

Comparative Proteomics Analysis of the Engineered EVs

Fc-GPI enables high density display and has a higher abundance than endogenous PTGFRN or CD81. Therefore, comparison proteomics of transprotein expression and surface labeling on the engineered exosomes, hPD-L1-Fc-GPI; hPD-L2-Fc-GPI; and hCTLA-Fc-GPI, was performed to determine the effects on endogenous protein expression in engineered exosomes. It was confirmed that the fusion polypeptide expression does not affect the relative expression of native and associated exosome proteins. However, the trans protein may crowd out abundant proteins like CD81 (data not shown).

Example 15

Scale-Up Production and Purification of mPD-L1-Fc-GPI Exosomes Using Microcarriers in a Stirred Tank Single-Use Bioreactor (STR)

1E7 HEK 293 cells were utilized for the production of mPDL1-Fc-GPI exosomes. Cells were passaged on SoloHill® Microcarriers up to Passage 4, at which point cells were expanded in a 2.5 L Stirred Tank Single-Use Bioreactor. Passage 4 cells were cultured for an additional 5 days and media was harvested on Day 5 and used for exosome purification. The general aim and process is provided below

AIM: Utilize SoloHill®'s Xeno-free microcarrier technology to scale up cells for engineering EVs and evaluate Microcarrier-stir tank bioreactor technology for production of therapeutic exosomes in the Xeno-free medium conditions.

Passage 1:

Thaw vial (1.00E+07) of cells and seed Corning® T-150 & CellSTACK®2 tissue culture treated flask at 1.00E+04 cells per cm^2 seed density.

Perform 100% medium exchange from both flasks on day 3.

Harvest Corning® T-150 & CellSTACK®2 flasks on day 4 post seeding and seed spinner microcarrier culture.

Passage 2:

Expand cells in 2×200 mL spinner flasks at 10 cm^2/mL microcarrier density using SoloHill®'s Xeno-free prototype microcarrier.

Seed microcarrier cultures at 1.00E+04 cells per cm^2 seed density and T-25 as flatware control flask.

Perform 80% batch volume medium exchange from spinners and T-25 flasks on day 3.

Harvest both microcarrier and T-25 flasks on day 4 post seeding and seed spinner microcarrier culture.

Passage 3:

Expand cells in 3×300 mL spinner flasks at 10 cm^2/mL microcarrier density using SoloHill®'s Xeno-free prototype microcarrier.

Seed microcarrier cultures at 1.00E+04 cells per cm^2 seed density and T-25 as flatware control flask.

Perform 80% batch volume medium exchange from spinners and T-25 flasks on day 3.

Harvest both microcarrier and T-25 flasks on day 4 post seeding.

Seed microcarrier-stir tank bioreactor for exosome production.

Passage 4:

Expand cells into a 2.5 L microcarrier-stir tank at 10 cm^2/mL surface area to medium ratio.

Seed cultures at 1.00E+04 cells per cm^2 seed density and T-25 as flatware control flask.

Perform 80% batch volume medium exchange on day 2.

On day 3 rinse all cultures with 2×cell culture volumes of DPBS containing Ca and Mg.

Add exosome production medium (DMEM-1% GlutaMAX™) to all cultures at 10 cm^2/mL surface area to medium volume ratio.

On day 5 collect harvest spent medium from all cultures, filter using 0.45 μm Nalgene rapid flow system and freeze at −20° C.

Procedures:

Medium Composition

DMEM 1× (Corning ref #10-013-CV)

1% GlutaMAX™ (Thermo ref #35050061)

3% Human platelet lysate (Stemulate from Cook Reagentec PG-NH-500)

Cell Harvest Protocol for Planar Culture

Settle microcarriers and remove maximum volume of spent medium without removing microcarriers.

Wash microcarrier culture with DPBS 2× time at 0.1 mL/cm^2 volume to surface area ratio.

Add 37° C. warmed TrypLE™ 5× enzyme at 0.012 mL/cm^2 and incubate flask at room temperature for ~15 minutes.

Add complete medium at 0.024 mL/cm^2 to quench TrypLE™ 5× activity.

Perform viable cell count using NC200 cell count instrument.

Nuclei Count Protocol for Microcarrier Culture

Obtain 4-5 mL of microcarrier culture from bioreactor or spinner flask

Settle microcarriers and remove maximum volume of spent medium without removing microcarriers.

Add 1.5 mL NucleoCounter® Reagent A to macrocarrier sample tube and vortex at high speed for a minute.

Add 1.5 mL NucleoCounter® Reagent B to macrocarrier sample tube and vortex at high speed for a minute.

Perform nuclei count using NC200 nuclei count instrument.

Medium Collection from STR Bioreactor

Stop all controls and settle microcarriers in the bioreactor vessel.

Pump out medium through screen bag into collection bottle at 200 mL/minute flowrate using peristaltic pump.

Inside BSC pour medium into 0.45 μm Nalgene™ Rapid-Flow™ filter system and remove free floating cells.

Freeze medium bottles in minus 20° C. freezer.

Medium Collection from Spinner Flasks

Inside BSC pour microcarrier culture into 0.45 μm Nalgene™ Rapid-Flow™ system and remove free floating cells as well as microcarriers.

Freeze medium bottles in minus 20° C. freezer.

Cell culture set points

	Temperature ° C.	Agitation rpm	Dissolved (DO) %	Oxygen pH	Incubator CO_2 setting %
T-Flask	37	n/a	n/a	n/a	5 ± 1
CellSTACK 2	37	n/a	n/a	n/a	5 ± 1

-continued

Cell culture set points

	Temperature ° C.	Agitation rpm	Dissolved (DO) %	Oxygen pH	Incubator CO_2 setting %
Spinner flask	37	35	n/a	n/a	5 ± 1
STR bioreactor	37	35	50	7.35	n/a

FIG. **31** shows mPDL1-Fc-GPI production, growth parameters, and analyte concentrations from a 2.6-L culture in a Stirred Tank Single-Use (STR) bioreactor. Day 2: 80% batch volume medium was exchanged (1st increase in glucose and decreased in lactate) Day 3: rinse culture with 2× cell culture volumes of DPBS containing Ca and Mg. (2nd increase in glucose and decreased in lactate). Add exosome production medium (DMEM-1% GlutaMAX™) to culture at 10 cm^2/mL surface area to medium volume ratio.

mPDL1 was purified using the purification process outlined above (FIGS. **32-33**).

Example 16

PD-L1-Fc-GPI and PDL2-Fc-GPI Exosomes Increase PD-1 Signaling

The purified exosomes were tested using the modified DISCOVERX® Assay in FIG. **12**A. Approximately a 1000× increase in Relative Light Units (RLU) was achieved for Jurkat signaling cells treated with PD-L1 or PD-L2 labeled exosomes when compared to soluble PD-L1-Fc or PD-L2-Fc ligands alone, respectively. Therefore, it takes 1000× less μg/ml of PD-L1 or PD-L2 on the engineered exosomes to activate PD-1 over solubilized ligands, PD-L1-Fc or PD-L2, achieve the same RLU signaling. FIG. **12**B show a dose-response curves for the PD-L1 and PD-L2 exosomes vs soluble PD-L1 and PD-L2 signaling bioassay. FIG. **12**B shows dose-response curves for the PD-L1 and PD-L2 exosomes comprising an Fc linker and GPI sticky binder vs. soluble ligands with an Fc domain linker. These results show that the PD-L1 and PD-L2 polypeptides fused with the Fc and GPI domains on EVs have a more potent effect on PD-1 signaling than the soluble ligands alone.

Example 17

In Vivo Assay—Therapeutic Effect of mPD-L1 Exosomes in an Experimental Autoimmune Uveoretinitis (EAU) Model in Lewis Rats

Lewis rats were challenged with retinal antigen interphotoreceptor retinoid-binding protein (IRBP) peptide. This model can be used to study anterior and posterior chamber dependent EAU. Rats were immunized on Day 1 with EAU presenting typically at Day 6. Clinical scores in the rat were determined. The EAU dosing schedule is shown in FIG. **13**A. EAU dosing test article are shown in the following table.

EAU dosing test articles				
	Unmodified Exosomes (IVT)	mPD-Ll-Fc-GPI Exosomes 1X (IVT)	mPD-L1-Fc-GPI Exosomes 10X (IVT)	mPD-L1 Exosomes (IV)
Dose	2 ul	2 ul	2 ul	5 ml/kg
Total protein concentration	40 ug/ml	40 ug/ml	400 ug/ml	40 ug/ml
Total protein administered	80 ng/eye	80 ng/eye	800 ng/eye	50 ug/animal
Exosome concentration	5.7×10^{10}/ml	2.34×10^{10}/ml	2.34×10^{11}/ml	2.34×10^{10}/ml
Total exosomes administered	4.7×10^{7}	4.7×10^{7}	4.7×10^{8}	2.93×10^{10}

*IVT-intravitreal, IV-intravenous

The study design is outlined below:

Group	Test Article	N	Route	Concentration	Dosage	Regimen
1	Cyclosporine	8	p.o.	1 mg/mL	10 mg/kg	BID from day 0 to Day 20
2	Negative control (PBS vehicle)	8	Intravitreal both eyes	1×	2-3 μL	Day 6, Day 12, and Day 16
3	Unmodified exosomes (Control exosomes)	8	Intravitreal both eyes	1× (~40 ug/ml)	2-3 μL	Day 6 and Day 12
4	mPD-L1-Fc-GPI (40 ug/ml)	8	Intravitreal both eyes	1× (~40 ug/ml)	2-3 μL	Day 6, Day 12, and Day 16
5	mPD-Ll-Fc-GPI (40 ug/ml)	4	Intravenous Injection	1× (~40 ug/ml)	5 mL/kg	Day 1, Day 6, Day 12, and Day 16
6	No IRBP peptide but treated with Test Agent B (for tolerability)	4	Intravitreal both eyes	1× (~40 ug/ml)	2-3 μL	Day 6, Day 12, and Day 16
7	mPD-L1-Fc-GPI (400 ug/ml)	8	Intravitreal both eyes	1× (400 ug/ml)	2-3 μL	Day 6, Day 12, and Day 16

Clinical Scores were determined as follows:

EAU Clinical Scores in Rats	
Score	Clinical Criteria
0	No disease; eye is translucent and reflects light(red reflex)
0.5 (trace)	Dilated blood vessels in the iris
1	Engorged blood vessels in the iris; abnormal pupil contraction
2	Hazy anterior chamber;decreased red reflex
3	Moderately opaque anterior chamber,but pupil still visible; dull red reflex
4	Opaque anterior chamber and obscured pupil; red reflex absent; proptosis

Each higher grade includes the criteria of the preceding one.

It was discovered that there is a statistically significant initial reduction in EAU in mPDL1 exosome treated rats via either the intravitreal and intravenous delivery modes as compared with untreated animals (FIG. **13**A). Rat weight did not change post immunization (FIG. **13**C).

Example 18

Purification of Exosomes Labeled with Type II Membrane Proteins

The inventors designed, engineered, and purified pcDNA5-FRT-4F2-4-1BBL exosomes by the methods provided herein (FIG. **34**). Several embodiments of the 4-1BBL labeled exosomes are shown in FIG. **35**. Cell expression of the 4F2-4-1BBL was confirmed (data not shown). FIGS. **92**A-**92**B shows the purification of 4F2-4-1BBL exosomes.

Example 19

Purification of Luminal Labeled Exosomes (Internal Loading)

In addition to Type I and Type II display fusion proteins on the surface of an EV, exosomes can be loaded with fusion proteins that are localized to the lumen of the phospholipid bilayer of the exosome (FIG. **37**). The Myr/Palm sequence used herein when fused to mScarlet the fusion protein into the luminal interior of extracellular vesicles. Fluorescence at an excitation wavelength 470 nm and emission wavelength of 665-720 nm peaks in SEC fractions 7, 8, and 9. SEC fractions 7, 8, and 9 contain exosomes as demonstrated by the dot blot. Fraction 8 was further analyzed for exosome quantification using an EXOVIEW® system (FIG. **38**). Unmodified exosomes do not show fluorescence. Exosomes show near 80% loading with Myr/Palm-mScarlet. The remaining 20% were out of the detection limit. Thus, nearly 100% internal loading was achieved using the specific Myr/Palm sequence.

NanoLuc® luciferase expressing exosomes were also purified with the Myr/Palm sequence incorporated into the vector encoding the fusion polypeptide. A Qubit™ fluorometer was used to measure total protein and PROMEGA® Nano-Glo® substrate and plate luminometer to measure luminescence (FIG. **39**A). Tetraspanin characterization of exosomes was performed and determined that the NanoLuc® luciferase exosomes were internally loaded and purified in fraction 8 (FIG. **39**B).

SEQUENCE LISTING

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TTSRTEGMLL NVTSSLRVNA TANDVFYCTF WRSQPGQNHT AELIIPELPA THPPQNRTHW  240
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FEATURE                 Location/Qualifiers
source                  1..2432
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                        organism = Homo sapiens
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                        mol_type = protein
                        organism = Homo sapiens
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ASYRKINTHI LKVPETDEVE LTCQATGYPL AEVSWPNVSV PANTSHSRTP EGLYQVTSVL  180
RLKPPPGRNF SCVFWNTHVR ELTLASIDLQ SQMEPRTHPT WLLHIFIPFC IIAFIFIATV  240
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source                  1..247
                        mol_type = protein
                        organism = Mus musculus
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ASYMRIDTRI LEVPGTGEVQ LTCQARGYPL AEVSWQNVSV PANTSHIRTP EGLYQVTSVL  180
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                        organism = Homo sapiens
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source 1..223
mol_type = protein
organism = Homo sapiens
SEQUENCE: 10

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AMDTGLYICK VELMYPPPYY LGIGNGTQIY VIDPEPCPDS DFLLWILAAV SSGLFFYSFL  180
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SEQ ID NO: 11 moltype = DNA length = 1933
FEATURE Location/Qualifiers
source 1..1933
mol_type = genomic DNA
organism = Mus musculus
SEQUENCE: 11

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SEQ ID NO: 12 moltype = AA length = 223
FEATURE Location/Qualifiers
source 1..223
mol_type = protein
organism = Mus musculus

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                       organism = Homo sapiens
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caatgcagcc tccagcctcg acctcccgag gctcaggtga tcctcccatc tcagcctctc  1500
gagtagctgg gaccacagtt gtgtgccacc acacttggct aactttttaa tttttttgcg  1560
gagacggtat tgctatgttg ccaaggttgt ttacatgcca gtacaattta taataaacac  1620
tcatttttcc tccc                                                    1634

SEQ ID NO: 14          moltype = AA  length = 254
FEATURE                Location/Qualifiers
source                 1..254
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 14
MEYASDASLD PEAPWPPAPR ARACRVLPWA LVAGLLLLLL LAAACAVFLA CPWAVSGARA  60
SPGSAASPRL REGPELSPDD PAGLLDLRQG MFAQLVAQNV LLIDGPLSWY SDPGLAGVSL  120
TGGLSYKEDT KELVVAKAGV YYVFFQLELR RVVAGEGSGS VSLALHLQPL RSAAGAAALA  180
LTVDLPPASS EARNSAFGFQ GRLLHLSAGQ RLGVHLHTEA RARHAWQLTQ GATVLGLFRV  240
TPEIPAGLPS PRSE                                                    254

SEQ ID NO: 15          moltype = DNA  length = 1230
FEATURE                Location/Qualifiers
source                 1..1230
                       mol_type = genomic DNA
                       organism = Mus musculus
SEQUENCE: 15
ataaagcacg ggcactggcg ggagacgtgc actgaccgac cgtggtaatg gaccagcaca  60
cacttgatgt ggaggatacc gcggatgcca gacatccagc aggtacttcg tgcccctcgg  120
atgcggcgct cctcagagat accgggctcc tcgcggacgc tgcgctcctc tcagatactg  180
tgcgccccac aaatgccgcg ctccccacgg atgctgccta ccctgcggtt aatgttcggg  240
atcgcgaggc cgcgtggccg cctgcactga acttctgttc ccgccaccca aagctctatg  300
gcctagtcgc tttggttttg ctgcttctga tcgccgcctg tgttcctatc ttcacccgca  360
ccgagcctcg gccagcgctc acaatcacca cctcgcccaa cctgggtacc cgagagaata  420
atgcagacca ggtcacccct gtttcccaca ttggctgccc caacactaca caacagggct  480
ctcctgtgtt cgccaagcta ctggctaaaa accaagcatc gttgtgcaat acaactctga  540
actggcacag ccaagatgga gctgggagct catacctatc tcaaggtctg aggtacgaag  600
aagacaaaaa ggagttggtg gtagacagtc ccgggctcta ctacgtattt ttggaactga  660
agctcagtcc aacattcaca aacacaggcc acaaggtgca gggctgggtc tctcttgttt  720
tgcaagcaaa gcctcaggta gatgactttg acaacttggc cctgacagtg gaactgttcc  780
cttgctccat ggagaacaag ttagtggacc gttcctggag tcaactgttg ctcctgaagg  840
ctggccaccg cctcagtgtg ggtctgaggg cttatctgca tggagcccag gatgcataca  900
gagactggga gctgtcttat cccaacacca ccagctttgg actctttctt gtgaaacccg  960
acaacccatg ggaatgagaa ctatccttct tgtgactcct agttgctaag tcctcaagct  1020
gctatgtttt atggggtctg agcaggggtc ccttccatga ctttctcttg tctttaactg  1080
gacttggtat ttattctgag catagctcag acaagacttt atataattca ctagatagca  1140
ttagtaaact gctgggcagc tgctagataa aaaaaaattt ctaaatcaaa gtttatattt  1200
```

```
atattaatat ataaaaataa atgtgtttgt                                    1230

SEQ ID NO: 16          moltype = AA  length = 309
FEATURE                Location/Qualifiers
source                 1..309
                       mol_type = protein
                       organism = Mus musculus
SEQUENCE: 16
MDQHTLDVED TADARHPAGT SCPSDAALLR DTGLLADAAL LSDTVRPTNA ALPTDAAYPA  60
VNVRDREAAW PPALNFCSRH PKLYGLVALV LLLLIAACVP IFTRTEPRPA LTITTSPNLG  120
TRENNADQVT PVSHIGCPNT TQQGSPVFAK LLAKNQASLC NTTLNWHSQD GAGSSYLSQG  180
LRYEEDKKEL VVDSPGLYYV FLELKLSPTF TNTGHKVQGW VSLVLQAKPQ VDDFDNLALT  240
VELFPCSMEN KLVDRSWSQL LLLKAGHRLS VGLRAYLHGA QDAYRDWELS YPNTTSFGLF  300
LVKPDNPWE                                                           309

SEQ ID NO: 17          moltype = DNA  length = 1702
FEATURE                Location/Qualifiers
source                 1..1702
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 17
ataccggccc ttcccctcgg ctttgcctgg acagctcctg cctcccgcag ggcccacctg  60
tgtcccccag cgccgctcca cccagcaggc ctgagcccct ctctgctgcc agacaccccc  120
tgctgcccac tctcctgctg ctcgggttct gaggcacagc ttgtcacacc gaggcggatt  180
ctctttctct ttctctttct cttctggccc acagccgcag caatggcgct gagttcctct  240
gctggagttc atcctgctag ctgggttccc gagctgccgg tctgagcctg aggcatggag  300
cctcctggag actgggggcc tcctccctgg agatccaccc ccaaaaccga cgtcttgagg  360
ctggtgctgt atctcacctt cctgggagcc ccctgctacg ccccagctct gccgtcctgc  420
aaggaggacg agtacccagt gggctccgag tgctgcccca agtgcagtcc aggttatcgt  480
gtgaaggagg cctgcgggga gctgacgggc acagtgtgtg aaccctgccc tccaggcacc  540
tacattgccc acctcaatgg cctaagcaag tgtctgcagt gccaaatgtg tgacccagcc  600
atgggcctgc gcgcgagccg gaactgctcc aggacagaga acgccgtgtg tggctgcagc  660
ccaggccact tctgcatcgt ccaggacggg gaccactgcg ccgcgtgccg cgcttacgcc  720
acctccagcc cgggccagag ggtgcagaag ggaggcaccg agagtcagga caccctgtgt  780
cagaactgcc ccccggggac cttctctccc aatgggaccc tggaggaatg tcagcaccag  840
accaagtgca gctggctggt gacgaaggcc ggagctggga ccagcagctc ccactgggta  900
tggtggtttc tctcagggag cctcgtcatc gtcattgttt gctccacagt tggcctaatc  960
atatgtgtga aaagaagaaa gccaaggggt gatgtagtca aggtgatcgt ctccgtccag  1020
cggaaaagac aggaggcaga aggtgaggcc acagtcattg aggccctgca ggcccctccg  1080
gacgtcacca cggtggccgt ggaggagaca ataccctcat tcacggggag gagcccaaac  1140
cactgaccca cagactctgc accccgacgc cagagatacc tggagcgacg gctgctgaaa  1200
gaggctgtcc acctggcgga accaccggag cccggaggct tgggggctcc gccctgggct  1260
ggcttccgtc tcctccagtg gagggagagg tggggcccct gctggggtag agctggggac  1320
gccacgtgcc attcccatgg gccagtgagg gcctggggcc tctgttctgc tgtggcctga  1380
gctccccaga gtcctgagga ggagcgccag ttgcccctcg ctcacagacc acacacccag  1440
ccctcctggg ccagcccaga gggcccttca gaccccagct gtctgcgcgt ctgactcttg  1500
tggcctcagc aggacaggcc ccgggcactg cctcacagcc aaggctggac tgggttggct  1560
gcagtgtggt gtttagtgga taccacatcg gaagtgattt tctaaattgg atttgaattc  1620
ggctcctgtt ttctatttgt catgaaacag tgtatttggg gagatgctgt gggaggatgt  1680
aaatatcttg tttctcctca aa                                            1702

SEQ ID NO: 18          moltype = AA  length = 283
FEATURE                Location/Qualifiers
source                 1..283
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 18
MEPPGDWGPP PWRSTPKTDV LRLVLYLTFL GAPCYAPALP SCKEDEYPVG SECCPKCSPG  60
YRVKEACGEL TGTVCEPCPP GTYIAHLNGL SKCLQCQMCD PAMGLRASRN CSRTENAVCG  120
CSPGHFCIVQ DGDHCAACRA YATSSPGQRV QKGGTESQDT LCQNCPPGTF SPNGTLEECQ  180
HQTKCSWLVT KAGAGTSSSH WVWWFLSGSL VIVIVCSTVG LIICVKRRKP RGDVVKVIVS  240
VQRKRQEAEG EATVIEALQA PPDVTTVAVE ETIPSFTGRS PNH                    283

SEQ ID NO: 19          moltype = DNA  length = 893
FEATURE                Location/Qualifiers
source                 1..893
                       mol_type = genomic DNA
                       organism = Mus musculus
SEQUENCE: 19
gctcttggcc tgaagtttct tgatcaagaa aatggaacct ctcccaggat gggggtcggc  60
accctggagc caggccccta cagacaacac cttcaggctg gtgccttgtg tcttcctttt  120
gaacttgctg cagcgcatct ctgcccagcc ctcatgcaga caggaggagt tccttgtggg  180
agacgagtgc tgccccatgt gcaacccagg ttaccatgtg aagcaggtct gcagtgagca  240
tacaggcaca gtgtgtgccc cctgtccccc acagacatat accgcccatg caaatggcct  300
gagcaagtgt ctgccctgcg gagtctgtga tccagacatg ggcctgctga cctggcagga  360
gtgctccagc tggaaggaca ctgtgtgcag atgcatccca ggctacttct gtgagaacca  420
ggatgggagc cactgttcca catgcttgca gcacaccacc tgccctccag ggcagagggt  480
agagaagaga gggactcacg accaggacac tgtatgtgct gactgcctaa cagggacctt  540
ctcacttgga gggactcagg aggaatgcct gccctggacc aactgcagtg catttcaaca  600
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ggaagtaaga cgtgggacca acagcacaga caccacctgc tcctcccagg tcgtctacta  660
cgttgtgtcc atccttttgc cacttgtgat agtgggagct gggatagctg gattcctcat  720
ctgcacgcga agacacctgc acaccagctc agtggccaag gagctggagc ctttccagga  780
acaacaggag aacaccatca ggtttccagt caccgaggtt gggtttgctg agaccgagga  840
ggagacagcc tccaactgaa caaattctgg gtgacaagac accgaggaga cgt         893

SEQ ID NO: 20          moltype = AA  length = 275
FEATURE                Location/Qualifiers
source                 1..275
                       mol_type = protein
                       organism = Mus musculus
SEQUENCE: 20
MEPLPGWGSA PWSQAPTDNT FRLVPCVFLL NLLQRISAQP SCRQEEFLVG DECCPMCNPG  60
YHVKQVCSEH TGTVCAPCPP QTYTAHANGL SKCLPCGVCD PDMGLLTWQE CSSWKDTVCR  120
CIPGYFCENQ DGSHCSTCLQ HTTCPPGQRV EKRGTHDQDT VCADCLTGTF SLGGTQEECL  180
PWTNCSAFQQ EVRRGTNSTD TTCSSQVVYY VVSILLPLVI VGAGIAGFLI CTRRHLHTSS  240
VAKELEPFQE QQENTIRFPV TEVGFAETEE ETASN                             275

SEQ ID NO: 21          moltype = DNA  length = 1237
FEATURE                Location/Qualifiers
source                 1..1237
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 21
aatgcagtta caggatcctg ggaagcagag tgtctggatg gaacctgagc tgggtctctg  60
actcacttct gactttagtt ttttcaaggg ggaacatggc aaaggtgttc agtttcatcc  120
ttgttaccac cgctctgaca atgggcaggg aaatttcggc gctcgaggac tgtgcccagg  180
agcagatgcg gctcagagcc caggtgcgcc tgcttgagac ccgggtcaaa cagcaacagg  240
tcaagatcaa gcagcttttg caggagaatg aagtccagtt ccttgataaa ggagatgaga  300
atactgtcat tgatcttgga agcaagaggc agtatgcaga ttgttcagag attttcaatg  360
atgggtataa gctcagtgga ttttacaaaa tcaaacctct ccagagccca gcagaatttt  420
ctgtttattg tgacatgtcc gatggaggag gatggactgt aattcagaga cgatctgatg  480
gcagtgaaaa ctttaacaga ggatggaaag actatgaaaa tggctttgga aattttgtcc  540
aaaaacatgg tgaatattgg ctgggcaata aaaatcttca cttcttgacc actcaagaag  600
actacacttt aaaaatcgac cttgcagatt ttgaaaaaaa tagccgttat gcacaatata  660
agaatttcaa agttggagat gaaaagaatt tctacgagtt gaatattggg gaatattctg  720
gaacagctgg agattccctt gcggggaatt ttcatcctga ggtgcagtgg tgggctagtc  780
accaaagaat gaaattcagc acgtgggaca gagatcatga caactatgaa gggaactgcg  840
cagaagaaga tcagtctggc tggtggttta acaggtgtca ctctgcaaac ctgaatggtg  900
tatactacag cggcccctac acggctaaaa cagacaatgg gattgtctgg tacacctggc  960
atgggtggtg gtattctctg aaatctgtgg ttatgaaaat taggccaaat gattttattc  1020
caaatgtaat ttaattgctg ctgttgggct ttcgtttctg caattcagct ttgtttaaag  1080
tgatttgaaa aatactcatt ctgaacatat ccatgcgcaa tcatgataac tgttgtgagt  1140
agtgcttttc attcttctca cttgcctttg ttacttaatg tgctttcagt acagcagata  1200
tgcaatattc accaaataaa tgtagactgt gttaata                           1237

SEQ ID NO: 22          moltype = AA  length = 312
FEATURE                Location/Qualifiers
source                 1..312
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 22
MAKVFSFILV TTALTMGREI SALEDCAQEQ MRLRAQVRLL ETRVKQQQVK IKQLLQENEV  60
QFLDKGDENT VIDLGSKRQY ADCSEIFNDG YKLSGFYKIK PLQSPAEFSV YCDMSDGGGW  120
TVIQRRSDGS ENFNRGWKDY ENGFGNFVQK HGEYWLGNKN LHFLTTQEDY TLKIDLADFE  180
KNSRYAQYKN FKVGDEKNFY ELNIGEYSGT AGDSLAGNFH PEVQWWASHQ RMKFSTWDRD  240
HDNYEGNCAE EDQSGWWFNR CHSANLNGVY YSGPYTAKTD NGIVWYTWHG WWYSLKSVVM  300
KIRPNDFIPN VI                                                      312

SEQ ID NO: 23          moltype = DNA  length = 1120
FEATURE                Location/Qualifiers
source                 1..1120
                       mol_type = genomic DNA
                       organism = Mus musculus
SEQUENCE: 23
gttagaagtt cctgggaggc tctgtgtgga tggactgagc ctagctaagt cctgattcat  60
tttgacttga gttctctcag tgggaagaat gggaaagatt tacagcttcg tcctggtcgc  120
cattgctctg atgatgggaa gggaaggttg ggccctcgag agtgagaact gcttgcggga  180
gcaggtgagg ctcagggctc aggtgcacca gcttgagacc cgggtcaaac aacaacagac  240
catgattgca cagctcttgc atgagaagga agtccagttt ctggataaag gatcggagaa  300
cagtttcatt gaccttggag gcaagaagca gtatgcagat tgttcagaga tttacaatga  360
cggatttaag cagagtggat tttacaaaat caaacctctt cagagcctgg cagaattctc  420
tgtttattgt gacatgtctg atggaggggg atggactgta attcagagac gatctgatgg  480
cagtgagaac tttaacaggg gttggaatga ctatgaaaat ggctttggaa actttgtcca  540
aaacaatggc gaatactggc tgggtaacaa aaacattaac ttgctaacta ttcaaggaga  600
ctacacttta aaaatcgacc tgacagattt tgagaaaaac agcagcttcg cacaatacca  660
aagttttaaa gttggtgata aaaagtcttt ttatgaacta aatattggag aatattctgg  720
cacagctgga gattccctgt caggaacttt tcatcctgaa gtacagtggt gggctagtca  780
ccaaaggatg aagttcagca cgtgggacag agataacgac aattaccaag gaaactgtgc  840
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tgaggaagag cagtctggct ggtggtttaa caggtgtcac tctgcaaacc tgaacggtgt  900
ttactaccgt ggttcctaca gggcagaaac ggataatggt gttgtgtggt acacctggca  960
tgggtggtgg tattccttga aatctgtggt tatgaaaatt aggccaagtg attttattcc  1020
aaatattatt tagttgccct cattgggatc tcctttctgt aattcatctt ggtttacttg  1080
aaaataaata tttgaaaaag atataattct gaataacaca                        1120

SEQ ID NO: 24          moltype = AA  length = 314
FEATURE                Location/Qualifiers
source                 1..314
                       mol_type = protein
                       organism = Mus musculus
SEQUENCE: 24
MGKIYSFVLV AIALMMGREG WALESENCLR EQVRLRAQVH QLETRVKQQQ TMIAQLLHEK  60
EVQFLDKGSE NSFIDLGGKK QYADCSEIYN DGFKQSGFYK IKPLQSLAEF SVYCDMSDGG  120
GWTVIQRRSD GSENFNRGWN DYENGFGNFV QNNGEYWLGN KNINLLTIQG DYTLKIDLTD  180
FEKNSSFAQY QSFKVGDKKS FYELNIGEYS GTAGDSLSGT FHPEVQWWAS HQRMKFSTWD  240
RDNDNYQGNC AEEEQSGWWF NRCHSANLNG VYYRGSYRAE TDNGVVWYTW HGWWYSLKSV  300
VMKIRPSDFI PNII                                                    314

SEQ ID NO: 25          moltype = DNA  length = 2129
FEATURE                Location/Qualifiers
source                 1..2129
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 25
agagctccag gcgcacatcc gcagtcagcc acctcgcgcg cgcctccagg agcaaggatg  60
gagaggctgg tgatcaggat gcccttctct catctgtcta cctacagcct ggtttgggtc  120
atggcagcag tggtgctgtg cacagcacaa gtgcaagtgg tgacccagga tgaaagagag  180
cagctgtaca cacctgcttc cttaaaatgc tctctgcaaa atgcccagga agccctcatt  240
gtgacatggc agaaaaagaa agctgtaagc ccagaaaaca tggtcacctt cagcgagaac  300
catggggtgg tgatccagcc tgcctataag gacaagataa acattaccca gctgggactc  360
caaaactcaa ccatcacctt ctggaatatc accctggagg atgaagggtg ttacatgtgt  420
ctcttcaata cctttggttt tgggaagatc tcaggaacgg cctgcctcac cgtctatgta  480
cagcccatag tatcccttca ctacaaattc tctgaagacc acctaaatat cacttgctct  540
gccactgccc gcccagcccc catggtcttc tggaaggtcc ctcggtcagg gattgaaaat  600
agtacagtga ctctgtctca cccaaatggg accacgtctg ttaccagcat cctccatatc  660
aaagacccta agaatcaggt ggggaaggag gtgatctgcc aggtgctgca cctggggact  720
gtgaccgact ttaagcaaac cgtcaacaaa ggctattggt tttcagttcc gctattgcta  780
agcattgttt ccctggtaat tcttctcgtc ctaatctcaa tcttactgta ctggaaacgt  840
caccggaatc aggaccgaga gccctaaata agtcacacag caccctgaaa gtgattccct  900
ggtctacttg aatttgacac aagagaaaag caggaggaaa aggggccatt ctccaaagga  960
cctgaaagag caaaagaggt gggagcgaaa gccttaagga tcccacgact ttttactgcc  1020
atctgagcta ctcagtgttt gaatcccaag aggaagtcag tttacctctc aggtctgttg  1080
taggacttga ttttgtaaag caatgccatg ttatgtggtt gaaagggcac tggacttagt  1140
tagtatcagg agcactgagc tcacagactg acttgggctc ctactggtgg ggacctctgt  1200
tagtcacttt acctcatcca aagtataaag gaattggacc aaataattta ccacatagct  1260
ctaaaactta atttaaaatg taattccaga aaaaaaaagg gaataagcaa agggggaaga  1320
attgaaagag agagagaaga aagaatacag agagcttacc ttttgccttt ctgttgatgt  1380
tacatctctt cttcctatgt tcttaggtct atgagtctgt ttccccatca tttggtatct  1440
agtccagttc ctgcttactg ctttgctaat agctggcctt gctagaatcc ttggtttcac  1500
tgctgttctt catgtgcttc tatgagattt actccaacac aaataggact gaatttattg  1560
tgaagtaaca ttggcaatct taacttattc atttaactta tttttatagc tagataaata  1620
ttgttagtct tagacaatag ctcacatttt ttgagaagca tgccctccct gtccatttgt  1680
cttataacat gacccagccc tattttacgt cattctaaat tcagcctcat ataatgaaaa  1740
tacattatga aaacagatgt ttaggagatt tcctgtatag cagtcagcca attcatatgc  1800
tttgtctctg ctggcttctt tttccatgcg ttaacttttc ccaatagcag aggaggcaaa  1860
tatgagcata caatcccttt gttctaaaga tattgttcca gctagtggaa tgatgttgaa  1920
tctttaataa ccataattag ttgctttttc agtatcttct gctttgtctg tgtctatcca  1980
gtggcctagg aattaaagtg taagttgttt tcgctgttaa attggatatt tatatatata  2040
tatagcaaga ttttcatgtg ttatttaatt ctgtattgtt tcttatattt gtagtaaaat  2100
attgaacaat taaaagtgtt gactccaaa                                    2129

SEQ ID NO: 26          moltype = AA  length = 269
FEATURE                Location/Qualifiers
source                 1..269
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 26
MERLVIRMPF SHLSTYSLVW VMAAVVLCTA QVQVVTQDER EQLYTPASLK CSLQNAQEAL  60
IVTWQKKKAV SPENMVTFSE NHGVVIQPAY KDKINITQLG LQNSTITFWN ITLEDEGCYM  120
CLFNTFGFGK ISGTACLTVY VQPIVSLHYK FSEDHLNITC SATARPAPMV FWKVPRSGIE  180
NSTVTLSHPN GTTSVTSILH IKDPKNQVGK EVICQVLHLG TVTDFKQTVN KGYWFSVPLL  240
LSIVSLVILL VLISILLYWK RHRNQDREP                                    269

SEQ ID NO: 27          moltype = DNA  length = 2363
FEATURE                Location/Qualifiers
source                 1..2363
                       mol_type = genomic DNA
                       organism = Mus musculus
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SEQUENCE: 27
gggcgtggtt ggttggtcgt ctcttcctcc acactagagg agctgtagag tctgcctgtg  60
cagtggaggg ggctctctct acggcgaata gtagtgtccc tgctcacagg tgttgcggag  120
atatcctcca tcgtggaaga gctcagaccc cgagaagctg gtgtctagct gcggcccaga  180
gcaaggatgg gcagtctggt attcaggaga cctttctgcc atctctccac ctacagcctg  240
atttggggca tggcagcagt agcgctgagc acagctcaag tggaagtggt gacccaggat  300
gaaagaaagg cgctgcacac aactgcatcc ttacgatgtt ctctaaaaac atcccaggaa  360
cccttgattg tgacatggca gaaaaagaaa gccgtgagcc cagaaaacat ggtcacctac  420
agcaaaaccc atggggttgt aatccagcct gcctacaaag acaggataaa tgtcacagag  480
ctgggactct ggaactcaag catcaccttc tggaacacaa cattggaaga tgagggctgc  540
tacatgtgtc tcttcaacac gtttggttct cagaaggtct caggaacagc ttgccttacc  600
ctctatgtac agcccatagt acaccttcac tacaactatt ttgaagacca cctaaacatc  660
acttgctctg cgactgcccg tccagcccct gccatctcct ggaagggtac tgggacagga  720
attgagaata gtaccgagag tcacttccat tcaaatggga ctacatctgt caccagcatc  780
ctccgggtca aagaccccaa aactcaagtt gggaaggaag tgatctgcca ggttttatac  840
ctggggaatg tgattgacta caagcagagt ctggacaaag gattttggtt ttcagttcca  900
ctgttgctaa gcattgtttc tctggtaatt cttctgatct tgatctccat cttactatac  960
tggaaacgtc accgaaatca ggagcggggt gaatcatcac aggggatgca aagaatgaaa  1020
taagagctct aaagaaatta tacagaaccc tgaacgtgtt tccctggtct acttgaatct  1080
gatgtgaaag aaaagcagga gggaaaaggc cattctccat aggacctaag gagagcaaaa  1140
gaccagacac gagcctgtga gggatttgac tttttgctgt tgtcccaggt cctcggtgtt  1200
tgcattccaa gaggaagtcg agtgcctcgg gtctgttgta ggacttgatt tttttttttt  1260
ttgtagagca atgcagtgcc atgctgttag aaaggctcca gacttagaac caccagtgcc  1320
aagccagctc tcagaccgac tagggctccc atcggaggaa caaatcgtag tcaacttacc  1380
tcacagagct ctctggtcct tacacaaagt agaaaggagt gggaccagaa aattggccat  1440
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agaataaaaa aaaaaaaaaa aaa                                          2363

SEQ ID NO: 28          moltype = AA  length = 278
FEATURE                Location/Qualifiers
source                 1..278
                       mol_type = protein
                       organism = Mus musculus
SEQUENCE: 28
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IVTWQKKKAV SPENMVTYSK THGVVIQPAY KDRINVTELG LWNSSITFWN TTLEDEGCYM  120
CLFNTFGSQK VSGTACLTLY VQPIVHLHYN YFEDHLNITC SATARPAPAI SWKGTGTGIE  180
NSTESHFHSN GTTSVTSILR VKDPKTQVGK EVICQVLYLG NVIDYKQSLD KGFWFSVPLL  240
LSIVSLVILL ILISILLYWK RHRNQERGES SQGMQRMK                          278

SEQ ID NO: 29          moltype = DNA  length = 1724
FEATURE                Location/Qualifiers
source                 1..1724
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 29
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SEQ ID NO: 30 moltype = AA length = 355
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mol_type = protein
organism = Homo sapiens
SEQUENCE: 30

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QYFHRVPFHR VDTISVNGSV QLSYISFQNP RTVPVQPAFS TVPFSQPVCF PPRPRGRRQK  180
PPGVWPANPA PITQTVIHTV QSAPGQMFST PAIPPMMYPH PAYPMPFITT ILGGLYPSKS  240
ILLSGTVLPS AQRFHINLCS GNHIAFHLNP RFDENAVVRN TQIDNSWGSE ERSLPRKMPF  300
VRGQSFSVWI LCEAHCLKVA VDGQHLFEYY HRLRNLPTIN RLEVGGDIQL THVQT       355
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SEQ ID NO: 31 moltype = DNA length = 1586
FEATURE Location/Qualifiers
source 1..1586
mol_type = genomic DNA
organism = Mus musculus
SEQUENCE: 31

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agtgcccagt ctccatacat taacccgatc atccccttta ctggaccaat ccaaggaggg  180
ctgcaggagg gacttcaggt gaccctccag gggactacca agagttttgc acaaaggttt  240
gtggtgaact ttcagaacag cttcaatgga aatgacattg ccttccactt caaccccggg  300
tttgaggaag gagggtatgt ggtttgcaac acgaagcaga acggacagtg gggtcctgag  360
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SEQ ID NO: 32 moltype = AA length = 353
FEATURE Location/Qualifiers
source 1..353
mol_type = protein
organism = Mus musculus
SEQUENCE: 32

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NFRPAHQAPM AQTTIHMVHS TPGQMFSTPG IPPVVYPTPA YTIPFYTPIP NGLYPSKSIM  240
ISGNVLPDAT RFHINLRCGG DIAFHLNPRF NENAVVRNTQ INNSWGQEER SLLGRMPFSR  300
GQSFSVWIIC EGHCFKVAVN GQHMCEYYHR LKNLQDINTL EVAGDIQLTH VQT         353
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SEQ ID NO: 33 moltype = DNA length = 5792
FEATURE Location/Qualifiers
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mol_type = genomic DNA
organism = Homo sapiens
SEQUENCE: 33

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SEQ ID NO: 34 moltype = AA length = 417
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mol_type = protein
organism = Homo sapiens

SEQUENCE: 34

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PVDKPINTTL ICNVTNALGA RQAELTVQVK EGPPSEHSGM SRNAIIFLVL GILVFLILLG  360
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SEQ ID NO: 35 moltype = DNA length = 2902
FEATURE Location/Qualifiers
source 1..2902
mol_type = genomic DNA
organism = Mus musculus

SEQUENCE: 35

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gtctgggcag ggccaagtgc acatcattgt taaagagaaa cctgagaata tgcagcaaaa  1140
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tatttagtta tatatatata tatttttgag actatttcat agagcccaag ctaacctcaa  1980
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tgtcaaaccc taaatcatcc ccaaaactct gtaagtccta tcagggaata aaatgtgtgt  2880
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SEQ ID NO: 36 moltype = AA length = 408
FEATURE Location/Qualifiers
source 1..408
mol_type = protein
organism = Mus musculus

SEQUENCE: 36

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MAQLARATRS PLSWLLLLFC YALRKAGGDI RVLVPYNSTG VLGGSTTLHC SLTSNENVTI  60
TQITWMKKDS GGSHALVAVF HPKKGPNIKE PERVKFLAAQ QDLRNASLAI SNLSVEDEGI  120
YECQIATFPR GSRSTNAWLK VQARPKNTAE ALEPSPTLIL QDVAKCISAN GHPPGRISWP  180
SNVNGSHREM KEPGSQPGTT TVTSYLSMVP SRQADGKNIT CTVEHESLQE LDQLLVTLSQ  240
PYPPENVSIS GYDGNWYVGL TNLTLTCEAH SKPAPDMAGY NWSTNTGDFP NSVKRQGNML  300
LISTVEDGLN NTVIVCEVTN ALGSGQGQVH IIVKEKPENM QQNTRLHLGY IFLIVFVLAV  360
VIIIAALYTI RRCRHGRALQ SNPSERENVQ YSSVNGDCRL NMEPNSTR               408
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SEQ ID NO: 37 moltype = DNA length = 1987
FEATURE Location/Qualifiers
source 1..1987
mol_type = genomic DNA
organism = Homo sapiens

SEQUENCE: 37

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ggagccggag ccggagcccc acaggcacct actaaaccgc ccagccgatc ggcccccaca  180
gagtggcccg cgggcctccg gccgggccca gtcccctccc gggccctcca tggcccgggc  240
cgctgccctc ctgccgtcga gatcgccgcc gacgccgctg ctgtggccgc tgctgctgct  300
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cgtccgcagc aacccagagc ccacgggcta tgactggagc acgacctcag gcaccttccc  1140
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ggggagcccg gggagctgag tagtggggat ccagagagga cccccgcccc cagagacttg  1920
gttttggctc cagccttccc ctggccccgt gacactcagg agttaataaa tgccttggag  1980
gaaaaca                                                            1987
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SEQ ID NO: 38 moltype = AA length = 479
FEATURE Location/Qualifiers
source 1..479
mol_type = protein
organism = Homo sapiens

SEQUENCE: 38

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MARAAALLPS RSPPTPLLWP LLLLLLLETG AQDVRVQVLP EVRGQLGGTV ELPCHLLPPV  60
PGLYISLVTW QRPDAPANHQ NVAAFHPKMG PSFPSPKPGS ERLSFVSAKQ STGQDTEAEL  120
QDATLALHGL TVEDEGNYTC EFATFPKGSV RGMTWLRVIA KPKNQAEAQK VTFSQDPTTV  180
ALCISKEGRP PARISWLSSL DWEAKETQVS GTLAGTVTVT SRFTLVPSGR ADGVTVTCKV  240
EHESFEEPAL IPVTLSVRYP PEVSISGYDD NWYLGRTDAT LSCDVRSNPE PTGYDWSTTS  300
GTFPTSAVAQ GSQLVIHAVD SLFNTTFVCT VTNAVGMGRA EQVIFVRETP RASPRDVGPL  360
VWGAVGGTLL VLLLLAGGSL AFILLRVRRR RKSPGGAGGG ASGDGGFYDP KAQVLGNGDP  420
VFWTPVVPGP MEPDGKDEEE EEEEEKAEKG LMLPPPPALE DDMESQLDGS LISRRAVYV   479
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SEQ ID NO: 39 moltype = DNA length = 2009

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FEATURE                 Location/Qualifiers
source                  1..2009
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 39
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gccgaacgaa ctgatccggg gagccgtgag cggcggaagc cggcctggag ccggacactt  180
cagacccctg actgccctcc cagccgatcg gtacacgaag agtggtccct aggcaccccc  240
tgcccgggcc cagtccctcc ccgggccccc catggcccgg gccgcagtcc tcccgccgtc  300
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ctctcagttc agcaaggacc gtctgtcctt tgtcagagcg agaccagaaa caaacgcaga  600
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tctgggtgga gaggccaaag atactcagga gccagggata caggctggca ccgtcactat  900
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agtggaacac gagagcttcg aagagccgat cctgctgcca gtgaccctct ctgtgcgcta  1020
ccctccagaa gtatccatct ccggctatga tgacaactgg taccttggcc gcagtgaggc  1080
catactgacc tgtgatgtac gaagcaaccc agagcccaca gactatgact ggagcacgac  1140
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cgatatagac actggacaca tggaaacacc aagttccacc ctcactgcca accacaccaa  1740
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ttggaagggc accgcccctg ctttcaggat agaggacaag tggaaccaca cagactccta  1860
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tcagagcttg ctttcggccc cagcctagcc ctggccccga aacactcagg agctaataaa  1980
tgccttgtcg gaaaaaaaaa aaaaaaaaa                                    2009

SEQ ID NO: 40           moltype = AA  length = 467
FEATURE                 Location/Qualifiers
source                  1..467
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 40
MARAAVLPPS RLSPTLPLLP LLLLLLQETG AQDVRVRVLP EVRGRLGGTV ELPCHLLPPT  60
TERVSQVTWQ RLDGTVVAAF HPSFGVDFPN SQFSKDRLSF VRARPETNAD LRDATLAFRG  120
LRVEDEGNYT CEFATFPNGT RRGVTWLRVI AQPENHAEAQ EVTIGPQSVA VARCVSTGGR  180
PPARITWISS LGGEAKDTQE PGIQAGTVTI ISRYSLVPVG RADGVKVTCR VEHESFEEPI  240
LLPVTLSVRY PPEVSISGYD DNWYLGRSEA ILTCDVRSNP EPTDYDWSTT SGVFPASAVA  300
QGSQLLVHSV DRMVNTTFIC TATNAVGTGR AEQVILVRDT PQASRDVGPL VWGAVGGTLL  360
VLLLAGGFLA LILLRGRRRR KSPGGGGNDG DRGSYDPKTQ VFGNGGPVFW RSASPEPMRP  420
DGREEDEEEE EEMKAEEGLM LPPHESPKDD MESHLDGSLI SRRAVYV                467

SEQ ID NO: 41           moltype = DNA  length = 2690
FEATURE                 Location/Qualifiers
source                  1..2690
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 41
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ggagccggag ccggagcccc acaggcacct actaaaccgc ccagccgatc ggcccccaca  180
gagtggcccg cgggcctccg gccgggccca gtcccctccc gggccctcca tggcccgggc  240
cgctgccctc ctgccgtcga gatcgccgcc gacgccgctg ctgtggccgc tgctgctgct  300
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cttccaccct aagatgggtc ccagcttccc cagcccgaag cctggcagcg agcggctgtc  540
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caaagagact caggtgtcag ggaccctggc cggaactgtc actgtcacca gccgcttcac  900
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cgtccgcagc aacccagagc ccacgggcta tgactggagc acgacctcag gcaccttccc  1140
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gagaagaatt tactgttaac ctggaagact actgaatcat tttacccttg cccagtggaa  2580
taggacctaa acatcccccct tccggggaaa gtgggtcatc tgaattgggg gtagcaattg  2640
atactgtttt gtaaactaca tttcctacaa aatatgaatt tatactttga             2690
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SEQ ID NO: 42          moltype = AA  length = 538
FEATURE                Location/Qualifiers
source                 1..538
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 42
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PGLYISLVTW QRPDAPANHQ NVAAFHPKMG PSFPSPKPGS ERLSFVSAKQ STGQDTEAEL  120
QDATLALHGL TVEDEGNYTC EFATFPKGSV RGMTWLRVIA KPKNQAEAQK VTFSQDPTTV  180
ALCISKEGRP PARISWLSSL DWEAKETQVS GTLAGTVTVT SRFTLVPSGR ADGVTVTCKV  240
EHESFEEPAL IPVTLSVRYP PEVSISGYDD NWYLGRTDAT LSCDVRSNPE PTGYDWSTTS  300
GTFPTSAVAQ GSQLVIHAVD SLFNTTFVCT VTNAVGMGRA EQVIFVRETP NTAGAGATGG  360
IIGGIIAAII ATAVAATGIL ICRQQRKEQT LQGAEEDEDL EGPPSYKPPT PKAKLEAQEM  420
PSQLFTLGAS EHSPLKTPYF DAGASCTEQE MPRYHELPTL EERSGPLHPG ATSLGSPIPV  480
PPGPPAVEDV SLDLEDEEGE EEEEYLDKIN PIYDALSYSS PSDSYQGKGF VMSRAMYV    538
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SEQ ID NO: 43          moltype = DNA  length = 2735
FEATURE                Location/Qualifiers
source                 1..2735
                       mol_type = genomic DNA
                       organism = Mus musculus
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gccgaacgaa ctgatccggg gagccgtgag cggcggaagc cggcctggag ccggacactt  180
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catcagccga tactccttgg tgcccgtggg ccgagcggat ggcgtcaagg tcacgtgtag  960
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gtgagggagg cacaggggct ctgacgtctc acctttcacc cttgacccat gagctttcca  1920
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tccacctgtg acttcttagt gactccacca tgacgtccaa tctatgatgt ctgaggcagg  2040
caaacctgca caactggaaa cctggagatt tttatctccc ttggcaggga gctcaccata  2100
tccttctgca ccacctgtga cccccccccc cccccccaagg actcctaaga ctacgaccct  2160
ttgaccatgc cactcagtat ctcaagaacc cttaaagtcc caaaggaatc ggaccttgca  2220
cttgtcctca ggcaatagag tccaacagat atgcaagaac gggatcaggg gctccctgtt  2280
gctcagacct gagccctcca ggcagcagaa gctcacctga tccctcccca ccctgctccc  2340
caaaggtgaa aaggagagga ttccccaatg taaggtagga cctccccatc tccacctact  2400
cctgcaggca ggaatctcag gtttctcaca ccctctcctc agcacccagg ttcctgtctc  2460
cagagcatga attccaggtc caatgctaga ggggagaacc taatgcaagt gtgccttgcc  2520
accccaagtt tgggagactc tgctcttatc ctgaggacta ctgaattctt ttaaccccta  2580
cccagtgaga tgagaactac atatccctct ttaggggatg gtgtgtgtat gtgtgtgtga  2640
tggagaatct gggcatctgg gttgggaatt ttattttgta agcatttcct acataatatg  2700
agtttctact ttgataaagt cttgtgtttt ctgtg                             2735

SEQ ID NO: 44          moltype = AA  length = 530
FEATURE                Location/Qualifiers
source                 1..530
                       mol_type = protein
                       organism = Mus musculus
SEQUENCE: 44
MARAAVLPPS RLSPTLPLLP LLLLLLQETG AQDVRVRVLP EVRGRLGGTV ELPCHLLPPT  60
TERVSQVTWQ RLDGTVVAAF HPSFGVDFPN SQFSKDRLSF VRARPETNAD LRDATLAFRG  120
LRVEDEGNYT CEFATFPNGT RRGVTWLRVI AQPENHAEAQ EVTIGPQSVA VARCVSTGGR  180
PPARITWISS LGGEAKDTQE PGIQAGTVTI ISRYSLVPVG RADGVKVTCR VEHESFEEPI  240
LLPVTLSVRY PPEVSISGYD DNWYLGRSEA ILTCDVRSNP EPTDYDWSTT SGVFPASAVA  300
QGSQLLVHSV DRMVNTTFIC TATNAVGTGR AEQVILVRES PSTAGAGATG GIIGGIIAAI  360
IATAVAGTGI LICRQQRKEQ RLQAADEEEE LEGPPSYKPP TPKAKLEEPE MPSQLFTLGA  420
SEHSPVKTPY FDAGVSCADQ EMPRYHELPT LEERSGPLLL GATGLGPSLL VPPGPNVVEG  480
VSLSLEDEEE DDEEEDFLDK INPIYDALSY PSPSDSYQSK DFFVSRAMYV             530

SEQ ID NO: 45          moltype = DNA  length = 1630
FEATURE                Location/Qualifiers
source                 1..1630
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 45
acacatcagg ggcttgctct tgcaaaacca aaccacaaga cagacttgca aaagaaggca  60
tgcacagctc agcactgctc tgttgcctgg tcctcctgac tggggtgagg gccagcccag  120
gccagggcac ccagtctgag aacagctgca cccacttccc aggcaacctg cctaacatgc  180
ttcgagatct ccgagatgcc ttcagcagag tgaagacttt ctttcaaatg aaggatcagc  240
tggacaactt gttgttaaag gagtccttgc tggaggactt taagggttac ctgggttgcc  300
aagccttgtc tgagatgatc cagttttacc tggaggaggt gatgccccaa gctgagaacc  360
aagacccaga catcaaggcg catgtgaact ccctggggga gaacctgaag accctcaggc  420
tgaggctacg gcgctgtcat cgatttcttc cctgtgaaaa caagagcaag gccgtggagc  480
aggtgaagaa tgcctttaat aagctccaag agaaaggcat ctacaaagcc atgagtgagt  540
ttgacatctt catcaactac atagaagcct acatgacaat gaagatacga aactgagaca  600
tcagggtggc gactctatag actctaggac ataaattaga ggtctccaaa atcggatctg  660
gggctctggg atagctgacc cagccccttg agaaacctta ttgtacctct cttatagaat  720
atttattacc tctgatacct caacccccat ttctatttat ttactgagct tctctgtgaa  780
cgatttagaa agaagcccaa tattataatt tttttcaata tttattattt tcacctgttt  840
ttaagctgtt tccatagggt gacacactat ggtatttgag tgttttaaga taaattataa  900
gttacataag ggaggaaaaa aaatgttctt tggggagcca acagaagctt ccattccaag  960
cctgaccacg ctttctagct gttgagctgt tttccctgac ctccctctaa tttatcttgt  1020
ctctgggctt ggggcttcct aactgctaca aatactctta ggaagagaaa ccagggagcc  1080
cctttgatga ttaattcacc ttccagtgtc tcggagggat tcccctaacc tcattcccca  1140
accacttcat tcttgaaagc tgtggccagc ttgttattta taacaaccta aatttggttc  1200
taggccgggc gcggtggctc acgcctgtaa tcccagcact ttgggaggct gaggcgggtg  1260
gatcacttga ggtcaggagt tcctaaccag cctggtcaac atggtgaaac cccgtctcta  1320
ctaaaaatac aaaaattagc cgggcatggt ggcgcgcacc tgtaatccca gctacttggg  1380
aggctgaggc aagagaattg cttgaaccca ggagatggaa gttgcagtga gctgatatca  1440
tgcccctgta ctccagcctg ggtgacagag caagactctg tctcaaaaaa taaaaataaa  1500
aataaatttg gttctaatag aactcagttt taactagaat ttattcaatt cctctgggaa  1560
tgttacattg tttgtctgtc ttcatagcag attttaattt tgaataaata aatgtatctt  1620
attcacatca                                                         1630

SEQ ID NO: 46          moltype = AA  length = 178
FEATURE                Location/Qualifiers
source                 1..178
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 46
MHSSALLCCL VLLTGVRASP GQGTQSENSC THFPGNLPNM LRDLRDAFSR VKTFFQMKDQ  60
LDNLLLKESL LEDFKGYLGC QALSEMIQFY LEEVMPQAEN QDPDIKAHVN SLGENLKTLR  120
LRLRRCHRFL PCENKSKAVE QVKNAFNKLQ EKGIYKAMSE FDIFINYIEA YMTMKIRN    178
```

```
SEQ ID NO: 47          moltype = DNA  length = 1306
FEATURE                Location/Qualifiers
source                 1..1306
                       mol_type = genomic DNA
                       organism = Mus musculus
SEQUENCE: 47
acatttagag acttgctctt gcactaccaa agccacaagg cagccttgca gaaaagagag  60
ctccatcatg cctggctcag cactgctatg ctgcctgctc ttactgactg gcatgaggat  120
cagcaggggc cagtacagcc gggaagacaa taactgcacc cacttcccag tcggccagag  180
ccacatgctc ctagagctgc ggactgcctt cagccaggtg aagactttct ttcaaacaaa  240
ggaccagctg gacaacatac tgctaaccga ctccttaatg caggacttta agggttactt  300
gggttgccaa gccttatcgg aaatgatcca gttttacctg gtagaagtga tgccccaggc  360
agagaagcat ggcccagaaa tcaaggagca tttgaattcc ctgggtgaga agctgaagac  420
cctcaggatg cggctgaggc gctgtcatcg atttctcccc tgtgaaaata agagcaaggc  480
agtggagcag gtgaagagtg attttaataa gctccaagac caaggtgtct acaaggccat  540
gaatgaattt gacatcttca tcaactgcat agaagcatac atgatgatca aaatgaaaag  600
ctaaaacacc tgcagtgtgt attgagtctg ctggactcca ggacctagac agagctctct  660
aaatctgatc cagggatctt agctaacgga aacaactcct tggaaaacct cgtttgtacc  720
tctctccgaa atatttatta cctctgatac ctcagttccc attctattta ttcactgagc  780
ttctctgtga actatttaga aagaagccca atattataat tttacagtat ttattatttt  840
taacctgtgt ttaagctgtt tccattgggg acactttata gtatttaaag ggagattata  900
ttatatgatg ggaggggttc ttccttggga agcaattgaa gcttctattc taaggctggc  960
cacacttgag agctgcaggg ccctttgcta tggtgtcctt tcaattgctc tcatccctga  1020
gttcagagct cctaagagag ttgtgaagaa actcatgggt cttgggaaga gaaaccaggg  1080
agatcctttg atgatcattc ctgcagcagc tcagagggtt cccctactgt catcccccag  1140
ccgcttcatc cctgaaaact gtggccagtt tgttatttat aaccacctaa aattagttct  1200
aatagaactc atttttaact agaagtaatg caattcctct gggaatggtg tattgtttgt  1260
ctgcctttgt agcagactct aattttgaat aaatggatct tattcg                 1306

SEQ ID NO: 48          moltype = AA  length = 178
FEATURE                Location/Qualifiers
source                 1..178
                       mol_type = protein
                       organism = Mus musculus
SEQUENCE: 48
MPGSALLCCL LLLTGMRISR GQYSREDNNC THFPVGQSHM LLELRTAFSQ VKTFFQTKDQ  60
LDNILLTDSL MQDFKGYLGC QALSEMIQFY LVEVMPQAEK HGPEIKEHLN SLGEKLKTLR  120
MRLRRCHRFL PCENKSKAVE QVKSDFNKLQ DQGVYKAMNE FDIFINCIEA YMMIKMKS    178

SEQ ID NO: 49          moltype = DNA  length = 1439
FEATURE                Location/Qualifiers
source                 1..1439
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 49
agtcacattt cagccactgc tctgagaatt tgtgagcagc ccctaacagg ctgttacttc  60
actacaactg acgatatgat catcttaatt tacttatttc tcttgctatg ggaagacact  120
caaggatggg gattcaagga tggaattttt cataactcca tatggcttga acgagcagcc  180
ggtgtgtacc acagagaagc acggtctggc aaatacaagc tcacctacgc agaagctaag  240
gcggtgtgtg aatttgaagg cggccatctc gcaacttaca agcagctaga ggcagccaga  300
aaaattggat ttcatgtctg tgctgctgga tggatggcta agggcagagt tggatacccc  360
attgtgaagc cagggcccaa ctgtggattt ggaaaaactg gcattattga ttatggaatc  420
cgtctcaata ggagtgaaag atgggatgcc tattgctaca acccacacgc aaaggagtgt  480
ggtggcgtct ttacagatcc aaagcaaatt tttaaatctc caggcttccc aaatgagtac  540
gaagataacc aaatctgcta ctggcacatt agactcaagt atggtcagcg tattcacctg  600
agttttttag attttgacct tgaagatgac ccaggttgct tggctgatta tgttgaaata  660
tatgacagtt acgatgatgt ccatggcttt gtgggaagat actgtggaga tgagcttcca  720
gatgacatca tcagtacagg aaatgtcatg accttgaagt ttctaagtga tgcttcagtg  780
acagctggag gtttccaaat caaatatgtt gcaatggatc ctgtatccaa atccagtcaa  840
ggaaaaaata caagtactac ttctactgga aataaaaact ttttagctgg aagatttagc  900
cacttataaa aaaaaaaaaa aggatgatca aaacacacag tgtttatgtt ggaatctttt  960
ggaactcctt tgatctcact gttattatta acatttattt attatttttc taaatgtgaa  1020
agcaatacat aatttaggga aaattggaaa atataggaaa ctttaaacga gaaaatgaaa  1080
cctctcataa tcccactgca tagaaataac aagcgttaac attttcatat ttttttcttt  1140
cagtcatttt tctatttgtg gtatatgtat atatgtacct atatgtattt gcatttgaaa  1200
ttttggaatc ctgctctatg tacagttttg tattatactt tttaaatctt gaactttata  1260
aacattttct gaaatcattg attattctac aaaaacatga ttttaaacag ctgtaaaata  1320
ttctatgata tgaatgtttt atgcattatt taagcctgtc tctattgttg gaatttcagg  1380
tcattttcat aaatattgtt gcaataaata tccttgaaca cacaaaaaaa aaaaaaaaaa  1439

SEQ ID NO: 50          moltype = AA  length = 277
FEATURE                Location/Qualifiers
source                 1..277
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 50
MIILIYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSGKYKLT YAEAKAVCEF  60
EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCGFGKTGI IDYGIRLNRS  120
ERWDAYCYNP HAKECGGVFT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF  180
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DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF  240
QIKYVAMDPV SKSSQGKNTS TTSTGNKNFL AGRFSHL                           277

SEQ ID NO: 51          moltype = DNA  length = 1601
FEATURE                Location/Qualifiers
source                 1..1601
                       mol_type = genomic DNA
                       organism = Mus musculus
SEQUENCE: 51
ccgctgctct gagaatttcg tgtgggcagc cccgacattg taaccggctc tgcaaccgaa  60
gagatggtcg tcctcctttg cttatgcgtc ttgctgtggg aagaggctca cggatgggga  120
ttcaagaacg ggatctttca taactccata tggcttgaac aagcagcggg cgtataccac  180
agagaagctc gggctggcag atacaagctc acctacgccg aagccaaggc cgtatgtgaa  240
tttgaaggtg gtcgtctcgc aacctacaag cagctagagg cagccagaaa aattggattc  300
catgtctgtg ctgctggatg gatggccaag ggtagagtcg gataccccat tgtgaaacct  360
gggcccaact gtggatttgg gaaaacgggt atcatcgatt atggaatccg gctcaacagg  420
agtgagcgat gggatgccta ttgctacaac ccacatgcaa aggagtgtgg tggtgtcttc  480
acagatccga agcgaatttt taaatccccg ggcttcccaa atgagtacga tgacaaccag  540
gtctgctact ggcacattcg gctcaagtac ggtcagcgaa ttcacctgag ctttttggac  600
tttgaccttg aacatgatcc aggctgcttg gctgactatg tagaaatcta tgacagttat  660
gatgacgtcc acggctttgt aggaagatac tgtggtgatg aacttccaga agacatcatt  720
agcacaggaa atgtcatgac cttgaagttt ctgagtgatg catccgtcac ggctggaggc  780
ttccagatta aatacgtcac agtggatcct gcatctaaat ccagtcaagc caaaaataca  840
agtactactg gaaataagaa gttcttacct ggaaggttta gccatctata aaaaattttt  900
tttaaaaatg ttcaaaacat ccagtacaat atttatattt gtttttgttg ttgttgttgg  960
tttttttttt tttattttgt tttgttttgt ttttttgaga cggggtttct ctgtatagcc  1020
ttggctgtcc tggaactcac tttgaagacc aggctggcct cgaactcaga aatccacctg  1080
cctccgccta ccaagtgctg ggattaaagg cgtccaccac caccgcccgg cttcaatatt  1140
tatatttgta gctcttggac ctcgtttgtt ctcttttgta tttttattat taacatgtat  1200
ttattatttt tccaaatgtg aaagccatat gtaattatgt ggaaaattga caaataaata  1260
cagagaactt caaatgagtt tttttttaa atctcataat tgtactacac agaaataact  1320
aatgttaaag tttttaaatg tttgtctttc attcattttt ctacttgtag tatatgtaca  1380
tatgtaactc tatgatttgc gtttgaattt tggcattctg ccttttgtaa cctgatattt  1440
ttaaccttga cattgtatag ctcaagcact tcccaagatc tctgagtttt ctacaaaatg  1500
ggactttgta aatatgattg ttccctgctt tatttaagct gaatttatat taggatttaa  1560
ggttgttttc ataaatattg ctgtaataaa tacttttgga t                      1601

SEQ ID NO: 52          moltype = AA  length = 275
FEATURE                Location/Qualifiers
source                 1..275
                       mol_type = protein
                       organism = Mus musculus
SEQUENCE: 52
MVVLLCLCVL LWEEAHGWGF KNGIFHNSIW LEQAAGVYHR EARAGRYKLT YAEAKAVCEF  60
EGGRLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCGFGKTGI IDYGIRLNRS  120
ERWDAYCYNP HAKECGGVFT DPKRIFKSPG FPNEYDDNQV CYWHIRLKYG QRIHLSFLDF  180
DLEHDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPEDIIS TGNVMTLKFL SDASVTAGGF  240
QIKYVTVDPA SKSSQAKNTS TTGNKKFLPG RFSHL                             275

SEQ ID NO: 53          moltype = DNA  length = 3295
FEATURE                Location/Qualifiers
source                 1..3295
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 53
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cagagtcggc gcggcgcggc aggggcagcc ttccaccacg gggagcccag ctgtcagccg  120
cctcacagga agatgctgcg tcggcggggc agccctggca tgggtgtgca tgtgggtgca  180
gccctgggag cactgtggtt ctgcctcaca ggagccctgg aggtccaggt ccctgaagac  240
ccagtggtgg cactggtggg caccgatgcc accctgtgct gctccttctc ccctgagcct  300
ggcttcagcc tggcacagct caacctcatc tggcagctga cagataccaa acagctggtg  360
cacagctttg ctgagggcca ggaccagggc agcgcctatg ccaaccgcac ggccctcttc  420
ccggacctgc tggcacaggg caacgcatcc ctgaggctgc agcgcgtgcg tgtggcggac  480
gagggcagct tcacctgctt cgtgagcatc cgggatttcg gcagcgctgc cgtcagcctg  540
caggtggccg ctccctactc gaagcccagc atgaccctgg agcccaacaa ggacctgcgg  600
ccaggggaca cggtgaccat cacgtgctcc agctaccagg gctaccctga ggctgaggtg  660
ttctggcagg atgggcaggg tgtgcccctg actggcaacg tgaccacgtc gcagatggcc  720
aacgagcagg gcttgtttga tgtgcacagc atcctgcggg tggtgctggg tgcaaatggc  780
acctacagct gcctggtgcg caaccccgtg ctgcagcagg atgcgcacag ctctgtcacc  840
atcacacccc agagaagccc cacaggagcc gtggaggtcc aggtccctga ggacccggtg  900
gtggccctag tgggcaccga tgccaccctg cgctgctcct tctcccccga gcctggcttc  960
agcctggcac agctcaacct catctggcag ctgacagaca ccaaacagct ggtgcacagt  1020
ttcaccgaag gccgggacca gggcagcgcc tatgccaacc gcacggccct cttcccggac  1080
ctgctggcac aaggcaatgc atccctgagg ctgcagcgcg tgcgtgtggc ggacgagggc  1140
agcttcacct gcttcgtgag catccgggat ttcggcagcg ctgccgtcag cctgcaggtg  1200
gccgctccct actcgaagcc cagcatgacc ctggagccca acaaggacct gcggccaggg  1260
gacacggtga ccatcacgtg ctccagctac cggggctacc ctgaggctga ggtgttctgg  1320
caggatgggc agggtgtgcc cctgactggc aacgtgacca cgtcgcagat ggccaacgag  1380
cagggcttgt ttgatgtgca cagcgtcctg cgggtggtgc tgggtgcgaa tggcacctac  1440
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agctgcctgg tgcgcaaccc cgtgctgcag caggatgcgc acggctctgt caccatcaca  1500
gggcagccta tgacattccc cccagaggcc ctgtgggtga ccgtggggct gtctgtctgt  1560
ctcattgcac tgctggtggc cctggctttc gtgtgctgga gaaagatcaa acagagctgt  1620
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gcactgtgag ccctgccccc aacagatgca tcctgctctg acaggtgggc tccttctcca  1860
aaggatgcga tacacagacc actgtgcagc cttatttctc caatggacat gattcccaag  1920
tcatcctgct gccttttttc ttatagacac aatgaacaga ccacccacaa ccttagttct  1980
ctaagtcatc ctgcctgctg ccttatttca cagtacatac atttcttagg gacacagtac  2040
actgaccaca tcaccaccct cttcttccag tgctgcgtgg accatctggc tgccttttt  2100
ctccaaaaga tgcaatattc agactgactg accccctgcc ttatttcacc aaagacacga  2160
tgcatagtca ccccggcctt gtttctccaa tggccgtgat acactagtga tcatgttcag  2220
ccctgcttcc acctgcatag aatcttttct tctcagacag ggacagtgcg gcctcaacat  2280
ctcctggagt ctagaagctg tttcctttcc cctccttcct cctcttgctc tagccttaat  2340
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cagctgtgca tggagacctg caggtgcacg tgctggaaca cgtgtggttc ccccctggcc  2460
cagcctcctc tgcagtgccc ctctcccctg cccatcctcc ccacggaagc atgtgctggt  2520
cacactggtt ctccaggggt ctgtgatggg gcccctgggg gtcagcttct gtccctctgc  2580
cttctcacct ctttgttcct ttcttttcat gtatccattc agttgatgtt tattgagcaa  2640
ctacagatgt cagcactgtg ttaggtgctg ggggccctgc gtgggaagat aaagttcctc  2700
cctcaaggac tccccatcca gctgggagac agacaactaa ctacactgca ccctgcggtt  2760
tgcagggggc tcctgcctgg ctccctgctc cacacctcct ctgtggctca aggcttcctg  2820
gatacctcac ccccatccca cccataattc ttacccagag catggggttg gggcggaaac  2880
ctggagagag ggacatagcc cctcgccacg gctagagaat ctggtggtgt ccaaaatgtc  2940
tgtccaggtg tgggcaggtg ggcaggcacc aaggccctct ggacctttca tagcagcaga  3000
aaaggcagag cctggggcag ggcagggcca ggaatgcttt ggggacaccg aggggactgc  3060
cccccacccc caccatggtg ctattctggg gctggggcag tcttttcctg gcttgcctct  3120
ggccagctcc tggcctctgg tagagtgaga cttcagacgt tctgatgcct tccggatgtc  3180
atctctccct gccccaggaa tggaagatgt gaggacttct aatttaaatg tgggactcgg  3240
agggattttg taaactgggg gtatattttg gggaaaataa atgtctttgt aaaaa       3295
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SEQ ID NO: 54          moltype = AA  length = 534
FEATURE                Location/Qualifiers
source                 1..534
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 54
MLRRRGSPGM GVHVGAALGA LWFCLTGALE VQVPEDPVVA LVGTDATLCC SFSPEPGFSL  60
AQLNLIWQLT DTKQLVHSFA EGQDQGSAYA NRTALFPDLL AQGNASLRLQ RVRVADEGSF  120
TCFVSIRDFG SAAVSLQVAA PYSKPSMTLE PNKDLRPGDT VTITCSSYQG YPEAEVFWQD  180
GQGVPLTGNV TTSQMANEQG LFDVHSILRV VLGANGTYSC LVRNPVLQQD AHSSVTITPQ  240
RSPTGAVEVQ VPEDPVVALV GTDATLRCSF SPEPGFSLAQ LNLIWQLTDT KQLVHSFTEG  300
RDQGSAYANR TALFPDLLAQ GNASLRLQRV RVADEGSFTC FVSIRDFGSA AVSLQVAAPY  360
SKPSMTLEPN KDLRPGDTVT ITCSSYRGYP EAEVFWQDGQ GVPLTGNVTT SQMANEQGLF  420
DVHSVLRVVL GANGTYSCLV RNPVLQQDAH GSVTITGQPM TFPPEALWVT VGLSVCLIAL  480
LVALAFVCWR KIKQSCEEEN AGAEDQDGEG EGSKTALQPL KHSDSKEDDG QEIA        534
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SEQ ID NO: 55          moltype = DNA  length = 3197
FEATURE                Location/Qualifiers
source                 1..3197
                       mol_type = genomic DNA
                       organism = Mus musculus
SEQUENCE: 55
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TCFVSIQDFD SAAVSLQVAA PYSKPSMTLE PNKDLRPGNM VTITCSSYQG YPEAEVFWKD  180
GQGVPLTGNV TTSQMANERG LFDVHSVLRV VLGANGTYSC LVRNPVLQQD AHGSVTITGQ  240
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QLTDAGTYTC YIRTSKGKGN ANLEYKTGAF SMPEINVDYN ASSESLRCEA PRWFPQPTVA  180
WASQVDQGAN FSEVSNTSFE LNSENVTMKV VSVLYNVTIN NTYSCMIEND IAKATGDIKV  240
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YPSSSQDSEN ITAAALATGA CIVGILCLPL ILLLVYKQRQ AASNRRAQEL VRMDSNIQGI  240
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                       mol_type = protein
                       organism = Mus musculus
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ASDHHGNFSI TLRNVTPRDS GLYCCLVIEL KNHHPEQRFY GSMELQVQAG KGSGSTCMAS  180
NEQDSDSITA AALATGACIV GILCLPLILL LVYKQRQVAS HRRAQELVRM DSSNTQGIEN  240
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RKFRVLEKNG DGYRALDFCS QNINSEEPLQ LKTRPLKIAI FLDQEDNDLS FYNMTDETHI  480
FSFAQVPFLG SPYPYFTRNS MGLSATAQP                                    509

SEQ ID NO: 69          moltype = DNA  length = 1818
FEATURE                Location/Qualifiers
source                 1..1818
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                       organism = Homo sapiens
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acctaccccc tcacacccac cactacgacc ccacgggata cccagcccag acggaggaaa  120
caccgagcct agagacatga gagttggagg agcattccac cttctactcg tgtgcctgag  180
cccagcactg ctgtctgctg tgcggatcaa cggggatgga caggaggtcc tgtacctggc  240
agaaggtgat aatgtgaggc tgggctgccc ctacgtcctg gaccctgagg actatggtcc  300
caatgggctg gacatcgagt ggatgcaggt caactcagac cccgcccacc accgagagaa  360
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gagggtccgc tttgcagcct cagacccaag ccagtacgat gcctccatca acctcatgaa  480
cctgcaggta tctgatacag ccacttatga gtgccgggtg aagaagacca ccatggccac  540
ccggaaggtc attgtcactg tccaagcacg acctgcagtg cccatgtgct ggacagaggg  600
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gaggcctggt gtccccagcc taagcagagg gccccggggg ccgggtgggt gggggtctgt  1740
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FEATURE                Location/Qualifiers
source                 1..414
                       mol_type = protein
                       organism = Homo sapiens
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EWMQVNSDPA HHRENVFLSY QDKRINHGSL PHLQQRVRFA ASDPSQYDAS INLMNLQVSD  120
TATYECRVKK TTMATRKVIV TVQARPAVPM CWTEGHMTYG NDVVLKCYAS GGSQPLSYKW  180
AKISGHHYPY RAGSYTSQHS YHSELSYQES FHSSINQGLN NGDLVLKDIS RADDGLYQCT  240
VANNVGYSVC VVEVKVSDSR RIGVIIGIVL GSLLALGCLA VGIWGLVCCC CGGSGAGGAR  300
GAFGYGNGGG VGGGACGDLA SEIREDAVAP GCKASGRGSR VTHLLGYPTQ NVSRSLRRKY  360
APPPCGGPED VALAPCTAAA ACEAGPSPVY VKVKSAEPAD CAEGPVQCKN GLLV        414

SEQ ID NO: 71          moltype = DNA  length = 1814
FEATURE                Location/Qualifiers
source                 1..1814
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                       organism = Mus musculus
SEQUENCE: 71
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SEQ ID NO: 72          moltype = AA  length = 417
FEATURE                Location/Qualifiers
source                 1..417
                       mol_type = protein
                       organism = Mus musculus
SEQUENCE: 72
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ATYECRVKKT TMATRKVIVT VQARPAVPMC WTEGHMSKGN DVVLKCFANG GSQPLSYKWA  180
KISGHSHPYR AGAYHSQHSF HSELSYQESF HSTINQGLGN GDLLLKGINA DDDGLYQCTV  240
ANHVGYSVCV VEVKVSDSQR VGMIVGAVLG SLLMLACLAL GIWGLICCCC GGGGAGGARG  300
AFGYGVGGGV GGGACGDLAS EIRVDAEAPG CKASGRGSRV THLLGYPTQN VSRSLRRKYA  360
PPPCGGPEDV ALVPRTASAS CEAGPSPVYI KVKSAEPADC ADCAQVEQRS CKDGLLV     417
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SEQ ID NO: 73          moltype = DNA  length = 3523
FEATURE                Location/Qualifiers
source                 1..3523
                       mol_type = genomic DNA
                       organism = Homo sapiens
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tcccagctct gcgcggggaa cagcggcccg gcgctgggtg tgggaggacc aggctgcccc  180
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SEQ ID NO: 74          moltype = AA  length = 431
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source                 1..431
                       mol_type = protein
                       organism = Homo sapiens
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LVNNLPDIGG RNIGVTGLTV LVPPSAPHCQ IQGSQDIGSD VILLCSSEEG IPRPTYLWEK  180
LDNTLKLPPT ATQDQVQGTV TIRNISALSS GLYQCVASNA IGTSTCLLDL QVISPQPRNI  240
GLIAGAIGTG AVIIIFCIAL ILGAFFYWRS KNKEEEEEEI PNEIREDDLP PKCSSAKAFH  300
TEISSSDNNT LTSSNAYNSR YWSNNPKVHR NTESVSHFSD LGQSFSFHSG NANIPSIYAN  360
GTHLVPGQHK TLVVTANRGS SPQVMSRSNG SVSRKPRPPH THSYTISHAT LERIGAVPVM  420
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SEQ ID NO: 75          moltype = DNA  length = 3430
FEATURE                Location/Qualifiers
source                 1..3430
                       mol_type = genomic DNA
                       organism = Mus musculus
SEQUENCE: 75
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SEQ ID NO: 76 moltype = AA length = 428
FEATURE Location/Qualifiers
source 1..428
mol_type = protein
organism = Mus musculus

SEQUENCE: 76

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SEQ ID NO: 77 moltype = DNA length = 1807
FEATURE Location/Qualifiers
source 1..1807
mol_type = genomic DNA
organism = Homo sapiens

SEQUENCE: 77

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gacagaagta gctctggctg tgatggggat cttactgggc ctgctactcc tggggcacct  120
aacagtggac acttatggcc gtcccatcct ggaagtgcca gagagtgtaa caggaccttg  180
gaaaggggat gtgaatcttc cctgcaccta tgaccccctg caaggctaca cccaagtctt  240
ggtgaagtgg ctggtacaac gtggctcaga ccctgtcacc atctttctac gtgactcttc  300
tggagaccat atccagcagg caaagtacca gggccgcctg catgtgagcc acaaggttcc  360
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cacggtgccc cagggaatga ggattagcct tcaatgccag gctcggggtt ctcctcccat  600
cagttatatt tggtataagc aacagactaa taaccaggaa cccatcaaag tagcaaccct  660
aagtacctta ctcttcaagc ctgcggtgat agccgactca ggctcctatt tctgcactgc  720
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caatggcaac tacgcccgcc tgctggacac agttcctctg gattatgagt ttctggccac  1260
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ctagtcagtc cttgccttct gcatggcctt cttccctgct acctctcttc ctggatagcc  1380
caaagtgtcc gcctaccaac actggagccg ctgggagtca ctggctttgc cctggaattt  1440
gccagatgca tctcaagtaa gccagctgct ggatttggct ctgggccctt ctagtatctc  1500
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tgccgggggc ttctggtact cctctctaaa taccagaggg aagatgccca tagcactagg  1560
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agggaggctc agctctgcca gctcagagga ccagctatat ccaggatcat ttctctttct  1680
tcagggccag acagctttta attgaaattg ttatttcaca ggccagggtt cagttctgct  1740
cctccactat aagtctaatg ttctgactct ctcctggtgc tcaataaata tctaatcata  1800
acagcaa                                                            1807

SEQ ID NO: 78          moltype = AA  length = 399
FEATURE                Location/Qualifiers
source                 1..399
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 78
MGILLGLLLL GHLTVDTYGR PILEVPESVT GPWKGDVNLP CTYDPLQGYT QVLVKWLVQR  60
GSDPVTIFLR DSSGDHIQQA KYQGRLHVSH KVPGDVSLQL STLEMDDRSH YTCEVTWQTP  120
DGNQVVRDKI TELRVQKLSV SKPTVTTGSG YGFTVPQGMR ISLQCQARGS PPISYIWYKQ  180
QTNNQEPIKV ATLSTLLFKP AVIADSGSYF CTAKGQVGSE QHSDIVKFVV KDSSKLLKTK  240
TEAPTTMTYP LKATSTVKQS WDWTTDMDGY LGETSAGPGK SLPVFAIILI ISLCCMVVFT  300
MAYIMLCRKT SQQEHVYEAA RAHAREANDS GETMRVAIFA SGCSSDEPTS QNLGNNYSDE  360
PCIGQEYQII AQINGNYARL LDTVPLDYEF LATEGKSVC                         399

SEQ ID NO: 79          moltype = DNA  length = 1434
FEATURE                Location/Qualifiers
source                 1..1434
                       mol_type = genomic DNA
                       organism = Mus musculus
SEQUENCE: 79
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ttcaaatagg atggagatct catcaggctt gctgttcctg ggccacctaa tagtgctcac  120
ctatggccac cccaccctaa aaacacctga gagtgtgaca gggacctgga aaggagatgt  180
gaagattcag tgcatctatg atcccctgag aggctacagg caagttttgg tgaaatggct  240
ggtaagacac ggctctgact ccgtcaccat cttcctacgt gactccactg gagaccatat  300
ccagcaggca aagtacagag gccgcctgaa agtgagccac aaagttccag gagatgtgtc  360
cctccaaata aataccctgc agatggatga caggaatcac tatacatgtg aggtcacctg  420
gcagactcct gatggaaacc aagtaataag agataagatc attgagctcc gtgttcggaa  480
atataatcca cctagaatca atactgaagc acctacaacc ctgcactcct ctttggaagc  540
aacaactata atgagttcaa cctctgactt gaccactaat gggactggaa aacttgagga  600
gaccattgct ggttcaggga ggaacctgcc aatctttgcc ataatcttca tcatctccct  660
ttgctgcata gtagctgtca ccatacctta tatcttgttc cgctgcagga cattccaaca  720
agagtatgtc tatggagtga gcagggtgtt tgccaggaag acaagcaact ctgaagaaac  780
cacaagggtg actaccatcg caactgatga accagattcc caggctctga ttagtgacta  840
ctctgatgat ccttgcctca gccaggagta ccaaataacc atcagatcaa caatgtctat  900
tcctgcctgc tgaacacagt ttccagaaac taagaagttc ttgctactga agaaaataac  960
atctgctaaa atgcccctac taagtcaagg tctactggcg taattacctg ttacttattt  1020
actacttgcc ttcaacatag ctttctccct ggcttccttt cttcttagac aacctaaagt  1080
atctatctag tctgccaatt ctggggccat tgagaaatcc tgggtttggc taagaatata  1140
ctacatgcac ctcaagaaat ctagcttctg ggcttcaccc agaacaattt tcttcctagg  1200
gccttcacaa ctcttctcca aacagcagag aaattccata gcagtagagg ttctttatca  1260
tgcctccaga cagcgtgagt ctcagtccta caaactcaga caagcacatg ggtctaggat  1320
tactcctctt tctctagggc cagatgactt ttaattgata ttactattgc tacattatga  1380
atctaatgca catgtattct tttgttgtta ataaatgttt aatcatgaca tcaa        1434

SEQ ID NO: 80          moltype = AA  length = 280
FEATURE                Location/Qualifiers
source                 1..280
                       mol_type = protein
                       organism = Mus musculus
SEQUENCE: 80
MEISSGLLFL GHLIVLTYGH PTLKTPESVT GTWKGDVKIQ CIYDPLRGYR QVLVKWLVRH  60
GSDSVTIFLR DSTGDHIQQA KYRGRLKVSH KVPGDVSLQI NTLQMDDRNH YTCEVTWQTP  120
DGNQVIRDKI IELRVRKYNP PRINTEAPTT LHSSLEATTI MSSTSDLTTN GTGKLEETIA  180
GSGRNLPIFA IIFIISLCCI VAVTIPYILF RCRTFQQEYV YGVSRVFARK TSNSEETTRV  240
TTIATDEPDS QALISDYSDD PCLSQEYQIT IRSTMSIPAC                        280

SEQ ID NO: 81          moltype = DNA  length = 2237
FEATURE                Location/Qualifiers
source                 1..2237
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 81
atttggagag ttaaaactgt gcctaacaga ggtgtcctct gacttttctt ctgcaagctc  60
catgttttca catcttccct ttgactgtgt cctgctgctg ctgctgctac tacttacaag  120
gtcctcagaa gtggaataca gagcggaggt cggtcagaat gcctatctgc cctgcttcta  180
caccccagcc gccccaggga acctcgtgcc cgtctgctgg ggcaaaggag cctgtcctgt  240
gtttgaatgt ggcaacgtgg tgctcaggac tgatgaaagg gatgtgaatt attggacatc  300
cagatactgg ctaaatgggg atttccgcaa aggagatgtg tccctgacca tagagaatgt  360
gactctagca gacagtggga tctactgctg ccggatccaa atcccaggca taatgaatga  420
tgaaaaattt aacctgaagt tggtcatcaa accagccaag gtcacccctg caccgactcg  480
gcagagagac ttcactgcag cctttccaag gatgcttacc accaggggac atggcccagc  540
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agagacacag acactgggga gcctccctga tataaatcta acacaaatat ccacattggc  600
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aataggcatc tacatcggag cagggatctg tgctgggctg gctctggctc ttatcttcgg  720
cgctttaatt ttcaaatggt attctcatag caaagagaag atacagaatt taagcctcat  780
ctctttggcc aacctccctc cctcaggatt ggcaaatgca gtagcagagg gaattcgctc  840
agaagaaaac atctatacca ttgaagagaa cgtatatgaa gtggaggagc ccaatgagta  900
ttattgctat gtcagcagca ggcagcaacc ctcacaacct ttgggttgtc gctttgcaat  960
gccatagatc caaccacctt atttttgagc ttggtgtttt gtctttttca gaaactatga  1020
gctgtgtcac ctgactggtt ttggaggttc tgtccactgc tatggagcag agttttccca  1080
ttttcagaag ataatgactc acatgggaat tgaactggga cctgcactga acttaaacag  1140
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tcaagcgatt ctcctgcctc agcctcctga gtggctggga ttacaggcat gcaccaccat  1560
gcccagctaa tttgttgtat ttttagtaga gacagggttt caccatgttg gccagtgtgg  1620
tctcaaactc ctgacctcat gatttgcctg cctcggcctc ccaaagcact gggattacag  1680
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attggccaag ttttgcttgt tgtgtgcttg aaagaaaata tctctgacca acttctgtat  1980
tcgtggacca aactgaagct atatttttca cagaagaaga agcagtgacg gggacacaaa  2040
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tcctttgaca gagagtggtc cctaaactta aatttcaaga cggtataggc ttgatctgtc  2160
ttgcttattg ttgccccctg cgcctagcac aattctgaca cacaattgga acttactaaa  2220
aatttttttt tactgtt                                                 2237
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SEQ ID NO: 82          moltype = AA  length = 301
FEATURE                Location/Qualifiers
source                 1..301
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 82
MFSHLPFDCV LLLLLLLLTR SSEVEYRAEV GQNAYLPCFY TPAAPGNLVP VCWGKGACPV  60
FECGNVVLRT DERDVNYWTS RYWLNGDFRK GDVSLTIENV TLADSGIYCC RIQIPGIMND  120
EKFNLKLVIK PAKVTPAPTR QRDFTAAFPR MLTTRGHGPA ETQTLGSLPD INLTQISTLA  180
NELRDSRLAN DLRDSGATIR IGIYIGAGIC AGLALALIFG ALIFKWYSHS KEKIQNLSLI  240
SLANLPPSGL ANAVAEGIRS EENIYTIEEN VYEVEEPNEY YCYVSSRQQP SQPLGCRFAM  300
P                                                                  301
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SEQ ID NO: 83          moltype = DNA  length = 2725
FEATURE                Location/Qualifiers
source                 1..2725
                       mol_type = genomic DNA
                       organism = Mus musculus
SEQUENCE: 83
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acttgcaagg tcattggaaa atgcttatgt gtttgaggtt ggtaagaatg cctatctgcc  180
ctgcagttac actctatcta cacctggggc acttgtgcct atgtgctggg gcaagggatt  240
ctgtccttgg tcacagtgta ccaacgagtt gctcagaact gatgaaagaa atgtgacata  300
tcagaaatcc agcagatacc agctaaaggg cgatctcaac aaaggagacg tgtctctgat  360
cataaagaat gtgactctgg atgaccatgg gacctactgc tgcaggatac agttccctgg  420
tcttatgaat gataaaaaat tagaactgaa attagacatc aaagcagcca aggtcactcc  480
agctcagact gcccatgggg actctactac agcttctcca agaaccctaa ccacggagag  540
aaatggttca gagacacaga cactggtgac cctccataat aacaatggaa caaaaatttc  600
cacatgggct gatgaaatta aggactctgg agaaacgatc agaactgcta tccacattgg  660
agtgggagtc tctgctgggt tgaccctggc acttatcatt ggtgtcttaa tccttaaatg  720
gtattcctgt aagaaaaaga agttatcgag tttgagcctt attacactgg ccaacttgcc  780
tccaggaggg ttggcaaatg caggagcagt caggattcgc tctgaggaaa atatctacac  840
catcgaggag aacgtatatg aagtggagaa ttcaaatgag tactactgct acgtcaacag  900
ccagcagcca tcctgaccgc ctctggactg ccacttttaa aggctcgcct tcatttctga  960
ctttggtatt tccctttttg aaaactatgt gatatgtcac ttggcaacct cattggaggt  1020
tctgaccaca gccactgaga aaagagttcc agttttctgg ggataattaa ctcacaaggg  1080
gattcgactg taactcatgc tacattgaaa tgctccattt tatccctgag tttcagggat  1140
cggatctccc actccagaga cttcaatcat gcgtgttgaa gctcactcgt gctttcatac  1200
attaggaatg gttagtgtga tgtctttgag acatagaggt ttgtggtata tctgcaaagc  1260
tcctgaacag gtagggggaa taaagggcta agataggaag gtgaggttct ttgttgatgt  1320
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aagccaggtg gcatatgctt aacactatat aacttgggaa ccttaggcag gagggtgata  1440
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aggactctcc tctgcctctg ttaagacatg agtgggagca tggcagagca gtccagtaat  1980
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aaaggaaacc ctgcgaaagg caaactttga ctgttgtgtg ctcaagggga actgactcag  2160
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gaggacagtc gtcaccaaat tgatttccaa gccggtggac ctcagtttca tctggcttac  2340
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atagaccccg agtgaaaata ttaagtgagc agaaaggtag ctttgttcaa agatttttt  2460
gcattgggga gcaactgtgt acatcagagg acatctgtta gtgaggacac caaaacctgt  2520
ggtaccgttt tttcatgtat gaattttgtt gtttaggttg cttctagcta gctgtggagg  2580
tcctggcttt cttaggtggg tatggaaggg agaccatcta acaaaatcca ttagagataa  2640
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gcaaagtact ttgagcatat ttaaa                                        2725

SEQ ID NO: 84          moltype = AA  length = 281
FEATURE                Location/Qualifiers
source                 1..281
                       mol_type = protein
                       organism = Mus musculus
SEQUENCE: 84
MFSGLTLNCV LLLLQLLLAR SLENAYVFEV GKNAYLPCSY TLSTPGALVP MCWGKGFCPW  60
SQCTNELLRT DERNVTYQKS SRYQLKGDLN KGDVSLIIKN VTLDDHGTYC CRIQFPGLMN  120
DKKLELKLDI KAAKVTPAQT AHGDSTTASP RTLTTERNGS ETQTLVTLHN NNGTKISTWA  180
DEIKDSGETI RTAIHIGVGV SAGLTLALII GVLILKWYSC KKKKLSSLSL ITLANLPPGG  240
LANAGAVRIR SEENIYTIEE NVYEVENSNE YYCYVNSQQP S                      281

SEQ ID NO: 85          moltype = DNA  length = 1330
FEATURE                Location/Qualifiers
source                 1..1330
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 85
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gattgagttt tggtggcttt acctgacacc agtcacttca gagactgttg tgacggaggt  120
tttgggtcac cgggtgactt tgccctgtct gtactcatcc tggtctcaca acagcaacag  180
catgtgctgg gggaaagacc agtgccccta ctccggttgc aaggaggcgc tcatccgcac  240
tgatggaatg agggtgacct caagaaagtc agcaaaatat agacttcagg ggactatccc  300
gagaggtgat gtctccttga ccatcttaaa ccccagtgaa agtgacagcg gtgtgtactg  360
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acagagagcc tcaacaacca cgcacagaac agcaaccacc accacacgca gaacaacaac  480
aacaagcccc accaccaccc gacaaatgac aacaacccca gctgcacttc caacaacagt  540
cgtgaccaca cccgatctca caaccggaac accactccag atgacaacca ttgccgtctt  600
cacaacagca aacacgtgcc tttcactaac cccaagcacc cttccggagg aagccacagg  660
tcttctgact cccgagcctt ctaaggaagg gcccatcctc actgcagaat cagaaactgt  720
cctccccagt gattcctgga gtagtgttga gtctacttct gctgacactg tcctgctgac  780
atccaaagag tccaaagttt gggatctccc atcaacatcc cacgtgtcaa tgtggaaaac  840
gagtgattct gtgtcttctc ctcagcctgg agcatctgat acagcagttc ctgagcagaa  900
caaaacaaca aaaacaggac agatggatgg aatacccatg tcaatgaaga atgaaatgcc  960
catctcccaa ctactgatga tcatcgcccc ctccttggga tttgtgctct tcgcattgtt  1020
tgtggcgttt ctcctgagag ggaaactcat ggaaacctat tgttcgcaga aacacacaag  1080
gctagactac attggagata gtaaaaatgt cctcaatgac gtgcagcatg gaagggaaga  1140
cgaagacggc ctttttaccc tctaacaacg cagtagcatg ttagattgag gatgggggca  1200
tgacactcca gtgtcaaaat aagtcttagt agatttcctt gtttcataaa aaagactcac  1260
ttattccatg gatgtcattg atccaggctt gctttagttt catgaatgaa gggtacttta  1320
gagaccacaa                                                         1330

SEQ ID NO: 86          moltype = AA  length = 378
FEATURE                Location/Qualifiers
source                 1..378
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 86
MSKEPLILWL MIEFWWLYLT PVTSETVVTE VLGHRVTLPC LYSSWSHNSN SMCWGKDQCP  60
YSGCKEALIR TDGMRVTSRK SAKYRLQGTI PRGDVSLTIL NPSESDSGVY CCRIEVPGWF  120
NDVKINVRLN LQRASTTTHR TATTTTRRTT TTSPTTTRQM TTTPAALPTT VVTTPDLTTG  180
TPLQMTTIAV FTTANTCLSL TPSTLPEEAT GLLTPEPSKE GPILTAESET VLPSDSWSSV  240
ESTSADTVLL TSKESKVWDL PSTSHVSMWK TSDSVSSPQP GASDTAVPEQ NKTTKTGQMD  300
GIPMSMKNEM PISQLLMIIA PSLGFVLFAL FVAFLLRGKL METYCSQKHT RLDYIGDSKN  360
VLNDVQHGRE DEDGLFTL                                                378

SEQ ID NO: 87          moltype = DNA  length = 2175
FEATURE                Location/Qualifiers
source                 1..2175
                       mol_type = genomic DNA
                       organism = Mus musculus
SEQUENCE: 87
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agatcctatc aaaatgtcca aggggcttct cctcctctgg ctggtgacgg agctctggtg  60
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aggttcatgt cccaattcca agtgcaatgc agagcttctc cgtacagatg gaacaagaat  240
catctccagg aagtcaacaa aatatacact tttggggaag gtccagtttg gtgaagtgtc  300
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tggctccttc tcacaagaaa ccacaaaagg gtccgccttc actacagaat cagaaactct  660
gcctgcatcc aatcactctc aaagaagcat gatgaccata tctacagaca tagccgtact  720
caggcccaca ggctctaacc ctgggattct cccatccact tcacagctga cgacacagaa  780
aacaacatta acaacaagtg agtctttgca gaagacaact aaatcacatc agatcaacag  840
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mol_type = protein
organism = Homo sapiens

SEQUENCE: 90

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organism = Homo sapiens

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organism = Homo sapiens

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NAKGENIPAV EAPVVADGVG LYEVAASVIM RGGSGEGVSC IIRNSLLGLE KTASISIADP 240
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PYGGVAPALK EVSMPDADGL FMVTTAVIIR DKSVRNMSCS INNTLLGQKK ESVIFIPESF  240
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FEATURE                 Location/Qualifiers
source                  1..500
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                        organism = Homo sapiens
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DVDRRKEYVT LSPDHGYWVL RLNGEHLYFT LNPRFISVFP RTPPTKIGVF LDYECGTISF  420
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SEQ ID NO: 101          moltype = DNA  length = 3583
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source                  1..3583
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                        organism = Homo sapiens
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mol_type = protein
organism = Homo sapiens

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VWRDPYGEVV PALKEVSIAD ADGLFMVTTA VIIRDKYVRN VSCSVNNTLL GQEKETVIFI  240
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KVEQEEKEIA QQLQEELRWR RTFLHAADVV LDPDTAHPEL FLSEDRRSVR RGPYRQRVPD  360
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FEATURE Location/Qualifiers
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mol_type = genomic DNA
organism = Mus musculus

SEQUENCE: 103

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mol_type = protein
organism = Mus musculus
SEQUENCE: 104

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FVPSLPLWMV AVAVTLPVVM LILLTSGSIC LVKKHRRKKS ILSAEKEAEY EEKEAARQLQ  300
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FEATURE Location/Qualifiers
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mol_type = genomic DNA
organism = Homo sapiens
SEQUENCE: 105

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                        organism = Homo sapiens
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SEQ ID NO: 107          moltype = DNA  length = 3454
FEATURE                 Location/Qualifiers
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taggctggct ttgaattcct gatcctcctg cctctacctt ccaagtgctg gaaacatagc  3060
cacatccacc acccctatcc agtccacctg gtttgattca gcaacgctca ggtagcatcg  3120
ctgtttgatc tggagctgcc agctccctcg gcccccactg caatgcttaa ccccctcaca  3180
ggcaccttcc cttgcctaac actgccatcc ttttccacac tgagccattt gctcaatgta  3240
gcctacccag gtatcctgct ttctggtccc caaagttaca ccatgatgct cagcacagct  3300
ggacagtttg tcccaatttg tgtgtgtcct cctgtttgta tgggacttct ttttgtcaat  3360
ggcctgtgtg tgtatccaag ctcttccact tctattgtat ttttccggct tctaaaacag  3420
atgttaccaa ataaagaaag agaaagaaaa aaaa                              3454

SEQ ID NO: 108          moltype = AA  length = 524
FEATURE                 Location/Qualifiers
source                  1..524
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 108
MAVPTNSCLL VCLLTLTVLQ LPTLDSAAPF DVTAPQEPVL ALVGSDAELT CGFSPNASSE  60
YMELLWFRQT RSTAVLLYRD GQEQEGQQMT EYRGRATLAT AGLLDGRATL LIRDVRVSDQ  120
GEYRCLFKDN DDFEEAAVYL KVAAVGSDPQ ISMTVQENGE MELECTSSGW YPEPQVQWRT  180
GNREMLPSTS ESKKHNEEGL FTVAVSMMIR DSSIKNMSCC IQNILLGQGK EVEISLPAPF  240
VPRLTPWIVA VAIILLALGF LTIGSIFFTW KLYKERSSLR KKEFGSKERL LEELRCKKTV  300
LHEVDVTLDP DTAHPHLFLY EDSKSVRLED SRQILPDRPE RFDSWPCVLG RETFTSGRHY  360
WEVEVGDRTD WAIGVCRENV VKKGFDPMTP DNGFWAVELY GNGYWALTPL RTSLRLAGPP  420
RRVGVFLDYD AGDISFYNMS NGSLIYTFPS ISFSGPLRPF FCLWSCGKKP LTICSTANGP  480
EKVTVIANVQ DDIPLSPLGE GCTSGDKDTL HSKLIPFSPS QAAP                   524

SEQ ID NO: 109          moltype = DNA  length = 2926
FEATURE                 Location/Qualifiers
source                  1..2926
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 109
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ggcccagggg ctgaggcagg ctcccctcgc ctcaggaatg atgacaggca caatagaaac  120
aacggggaac atttctgcag agaaaggtgg ctctatcatc ttacaatgtc acctctcctc  180
caccacggca caagtgaccc aggtcaactg ggagcagcag gaccagcttc tggccatttg  240
taatgctgac ttggggtggc acatctcccc atccttcaag gatcgagtgg ccccaggtcc  300
cggcctgggc ctcaccctcc agtcgctgac cgtgaacgat acaggggagt acttctgcat  360
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gctggtggtc atctgcacag cagtcatcgt ggtggtcgcg ttgactagaa agaagaaagc  540
cctcagaatc cattctgtgg aaggtgacct caggagaaaa tcagctggac aggaggaatg  600
gagccccagt gctccctcac ccccaggaag ctgtgtccag gcagaagctg cacctgctgg  660
gctctgtgga gagcagcggg gagaggactg tgccgagctg catgactact tcaatgtcct  720
gagttacaga agcctgggta actgcagctt cttcacagag actggttagc aaccagaggc  780
atcttctgga agatacactt ttgtctttgc tattatagat gaatatataa gcagctgtac  840
tctccatcag tgctgcgtgt gtgtgtgtgt gtgtatgtgt gtgtgtgttc agttgagtga  900
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taaacacctt caaactaact tcttcgaacc cttttattca ctccctgacg actttgtgct  1920
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tgttttagca acaagacaat tcaactattt ctcctaggat ttttattatt attatttttt  2220
cacttttcta ccaaatgggt tacataggaa gaatgaactg aaatctgtcc agagctccaa  2280
gtcctttgga agaaagatta gatgaacgta aaaatgttgt tgtttgctgt ggcagtttac  2340
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acatttataa acactattgg gatggtgata aaatacaaaa gggcctatag atgttagaaa  2580
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gaactagatt ctcctctgag aaccagagaa gaccatttca tagttggatt cctggagaca  2700
tgcgctatcc accacgtagc cactttccac atgtggccat caaccactta agatggggtt  2760
agtttaaatc aagatgtgct gttataattg gtataagcat aaaatcacac tagattctgg  2820
agatttaata tgaataataa gaatactatt tcagtagttt tggtatattg tgtgtcaaaa  2880
atgataatat tttggatgta ttgggtgaaa taaaatatta acatta                 2926

SEQ ID NO: 110          moltype = AA  length = 244
FEATURE                 Location/Qualifiers
source                  1..244
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 110
MRWCLLLIWA QGLRQAPLAS GMMTGTIETT GNISAEKGGS IILQCHLSST TAQVTQVNWE  60
QQDQLLAICN ADLGWHISPS FKDRVAPGPG LGLTLQSLTV NDTGEYFCIY HTYPDGTYTG  120
RIFLEVLESS VAEHGARFQI PLLGAMAATL VVICTAVIVV VALTRKKKAL RIHSVEGDLR  180
RKSAGQEEWS PSAPSPPGSC VQAEAAPAGL CGEQRGEDCA ELHDYFNVLS YRSLGNCSFF  240
TETG                                                               244

SEQ ID NO: 111          moltype = DNA  length = 726
FEATURE                 Location/Qualifiers
source                  1..726
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 111
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acaggagcca cagcaggcac gatagataca aagaggaaca tctctgcaga ggaaggtggc  120
tctgtcatct tacagtgtca cttctcctct gacacagctg aagtgaccca agtcgactgg  180
aagcagcagg accagcttct ggccatttat agtgttgacc tggggtggca tgtcgcttca  240
gtcttcagtg atcgggtggt cccaggcccc agcctaggcc tcaccttcca gtctctgaca  300
atgaatgaca cgggagagta cttctgtacc tatcatacgt atcctggtgg gatttacaag  360
gggagaatat tcctgaaggt ccaagaaagc tcagtggctc agttccagac tgccccgctt  420
ggaggaacca tggctgctgt gctgggactc atttgcttaa tggtcacagg agtgactgta  480
ctggctagaa agaagtctat tagaatgcat tctatagaaa gtggccttgg gagaacagaa  540
gcggagccac aggaatggaa cctgaggagt ctctcatccc ctggaagccc tgtccagaca  600
caaactgccc ctgctggtcc ctgtggagag caggcagaag atgactatgc tgacccacag  660
gaatacttta atgtcctgag ctacagaagc ctagagagct tcattgctgt atcgaagact  720
ggctaa                                                             726

SEQ ID NO: 112          moltype = AA  length = 241
FEATURE                 Location/Qualifiers
source                  1..241
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 112
MHGWLLLVWV QGLIQAAFLA TGATAGTIDT KRNISAEEGG SVILQCHFSS DTAEVTQVDW  60
KQQDQLLAIY SVDLGWHVAS VFSDRVVPGP SLGLTFQSLT MNDTGEYFCT YHTYPGGIYK  120
GRIFLKVQES SVAQFQTAPL GGTMAAVLGL ICLMVTGVTV LARKKSIRMH SIESGLGRTE  180
AEPQEWNLRS LSSPGSPVQT QTAPAGPCGE QAEDDYADPQ EYFNVLSYRS LESFIAVSKT  240
G                                                                  241

SEQ ID NO: 113          moltype = DNA  length = 911
FEATURE                 Location/Qualifiers
source                  1..911
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 113
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agggggctgc agtttccttc cttccttctc ggcagcgctc cgcgcccccca tcgcccctcc  120
tgcgctagcg gaggtgatcg ccgcggcgat gccggaggag ggttcgggct gctcggtgcg  180
gcgcaggccc tatgggtgcg tcctgcgggc tgctttggtc ccattggtcg cgggcttggt  240
gatctgcctc gtggtgtgca tccagcgctt cgcacaggct cagcagcagc tgccgctcga  300
gtcacttggg tgggacgtag ctgagctgca gctgaatcac acaggacctc agcaggaccc  360
caggctatac tggcaggggg gcccagcact gggccgctcc ttcctgcatg gaccagagct  420
ggacaagggg cagctacgta tccatcgtga tggcatctac atggtacaca tccaggtgac  480
gctggccatc tgctcctcca cgacggcctc caggcaccac cccaccaccc tggccgtggg  540
aatctgctct cccgcctccc gtagcatcag cctgctgcgt ctcagcttcc accaaggttg  600
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gcgcccctga ccactgctgc tgattagggt tttttaaatt ttattttatt ttatttaagt  780
tcaagagaaa aagtgtacac acaggggcca cccggggttg gggtgggagt gtggtggggg  840
gtagtggtgg caggacaaga gaaggcattg agctttttct ttcattttcc tattaaaaaa  900
tacaaaaatc a                                                       911

SEQ ID NO: 114          moltype = AA  length = 193
FEATURE                 Location/Qualifiers
source                  1..193
                        mol_type = protein
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                        organism = Homo sapiens
SEQUENCE: 114
MPEEGSGCSV RRRPYGCVLR AALVPLVAGL VICLVVCIQR FAQAQQQLPL ESLGWDVAEL  60
QLNHTGPQQD PRLYWQGGPA LGRSFLHGPE LDKGQLRIHR DGIYMVHIQV TLAICSSTTA  120
SRHHPTTLAV GICSPASRSI SLLRLSFHQG CTIASQRLTP LARGDTLCTN LTGTLLPSRN  180
TDETFFGVQW VRP                                                     193

SEQ ID NO: 115          moltype = DNA  length = 842
FEATURE                 Location/Qualifiers
source                  1..842
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 115
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ctgcatcgga catccccgag gttctaaggg caggtcaagg caggcagaag cttcaaaagc  120
tcggctgagg aggctacagc ttcccgctgc cttcaggccg ctgcttccgt gcagggatgc  180
cggaggaagg tcgcccttgc ccctgggttc gctggagcgg gaccgcgttc cagcgccaat  240
ggccatggct gctgctggtg gtgtttatta ctgtgttttg ctgttggttt cattgtagcg  300
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ccttgggaag gtccttcaca cacggaccag agctggagga gggccatctg cgtatccatc  480
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acctggtcca cggagatgtc ctctgtacca acctcaccct gcctctgctg ccgtcccgca  720
acgctgatga gaccttcttt ggagttcagt ggatatgccc ttgaccacaa ctccaggatg  780
acttgtgaat atttttttc ttttcaagtt ctacgtattt ataaatgtat atagtacaca  840
ta                                                                 842

SEQ ID NO: 116          moltype = AA  length = 195
FEATURE                 Location/Qualifiers
source                  1..195
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 116
MPEEGRPCPW VRWSGTAFQR QWPWLLLVVF ITVFCCWFHC SGLLSKQQQR LLEHPEPHTA  60
ELQLNLTVPR KDPTLRWGAG PALGRSFTHG PELEEGHLRI HQDGLYRLHI QVTLANCSSP  120
GSTLQHRATL AVGICSPAAH GISLLRGRFG QDCTVALQRL TYLVHGDVLC TNLTLPLLPS  180
RNADETFFGV QWICP                                                   195

SEQ ID NO: 117          moltype = DNA  length = 3779
FEATURE                 Location/Qualifiers
source                  1..3779
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 117
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acaacttaat ccctggcaat gaaaaatgaa cctctccccc acccttgctg ccgcctctcg  120
cctcacgccc ccagagaaga gtttctccac caggcagcag gtgaaggttt ttttccaagt  180
cacatgattc aggattcagg gggagaatcc ttcttggaac agagatgggc ccagaactga  240
atcagatgaa gagagataag gtgtgatgtg gggaagacta tataaagaat ggacccaggg  300
ctgcagcaag cactcaacgg aatggcccct cctggagaca cagccatgca tgtgccggcg  360
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cagaaaccca tatcaagggt gactaagccc ggcttctggt atgagaaatt aaacttgtat  2040
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aagaacaaat cagcagtggt ggtatggatg aaagggactt gagagaacaa aaatggctaa  3060
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gaataatcat taataactca actgatagat atgtagggag taggcaaccc aggaagttta  3660
aaactaaatt ctgttactct tgagggttaa ccagcccctg ggaatgttat gagcaaatga  3720
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SEQ ID NO: 118 moltype = AA length = 234
FEATURE Location/Qualifiers
source 1..234
mol_type = protein
organism = Homo sapiens

SEQUENCE: 118

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MDPGLQQALN GMAPPGDTAM HVPAGSVASH LGTTSRSYFY LTTATLALCL VFTVATIMVL  60
VVQRTDSIPN SPDNVPLKGG NCSEDLLCIL KRAPFKKSWA YLQVAKHLNK TKLSWNKDGI  120
LHGVRYQDGN LVIQFPGLYF IICQLQFLVQ CPNNSVDLKL ELLINKHIKK QALVTVCESG  180
MQTKHVYQNL SQFLLDYLQV NTTISVNVDT FQYIDTSTFP LENVLSIFLY SNSD        234
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SEQ ID NO: 119 moltype = DNA length = 2228
FEATURE Location/Qualifiers
source 1..2228
mol_type = genomic DNA
organism = Mus musculus

SEQUENCE: 119

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catgatccag gatgcagggg aaaatccttc ttggaacaga gctgggtaca gaaccgaatc  180
agatgaggag agataaggtg tgatgtggga cagactatat aaagcatgga gccagggctg  240
caacaagcag gcagctgtgg ggctccttcc cctgacccag ccatgcaggt gcagcccggc  300
tcggtagcca gcccctggag aagcacgagg ccctggagaa gcacaagtcg cagctacttc  360
tacctcagca ccaccgcact ggtgtgcctt gttgtggcag tggcgatcat tctggtactg  420
gtagtccaga aaaaggactc cactccaaat acaactgaga aggcccccct taaaggagga  480
aattgctcag aggatctctt ctgtaccctg aaaagtactc catccaagaa gtcatgggcc  540
tacctccaag tgtcaaagca tctcaacaat accaaactgt catggaacga agatggcacc  600
atccacggac tcatatacca ggacgggaac ctgatagtcc aattccctgg cttgtacttc  660
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cagctcctca tcaattccaa gatcaaaaag cagacgttgg taacagtgtg tgagtctgga  780
gttcagagta agaacatcta ccagaatctc tctcagtttt tgctgcatta cttacaggtc  840
aactctacca tatcagtcag ggtggataat ttccagtatg tggatacaaa cactttccct  900
cttgataatg tgctatccgt cttcttatat agtagctcag actgaatagt tgttcttaac  960
ctttatgaaa atgctgtcta ccatacagta cttcatctgt ccaaacatgg gccaaagaaa  1020
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aaaatacaaa cccaggattt agaaagtgga gtctccttca gatgcacaaa caggaaagaa  1140
tgtgatatgt gcacagagac ctacttgggc actagaaggg gttgagttgt cccagtataa  1200
ccactaattc actgaccttg agccattttt ccttcccctg gaacttgggg tctgaatctg  1260
gaaaagtagg agatgagatt tacatttccc caatattttc ttcaactcag aagacgagac  1320
tgtggagctg agctccctac acagatgaag gcctcccatg gcatgaggaa aatgatggta  1380
ccagtaatgt ctgtctgact gtcatctcag caagtcctaa ggacttccat gctgccttgt  1440
tgaaagatac tctaacctct tgtaatgggc aaagtgatcc tgtctctcac tgaggggagt  1500
agctgctgcc atctcctgag acatacatgg agacattttc tgcccaaatt ccattctgtg  1560
tgcagttttt aagtattccc ccaaaagttc ttgacaatga gaactttgaa tgtgggaaga  1620
gcttctggac agcaaacatt aacagcttct cctgaccaga gagaccatgc aagcttggtc  1680
ttagacccat caagcttgag gtttctacat tgtgggagac agacttttga caaaccattt  1740
gagttgatgt ctgggcccct gggagttctc cttcagtaag gagagcaagc cgttctagtg  1800
ctgtgtcaga ggatggagta aaatagacac ttttctgaag gaaaggagaa caaagttcca  1860
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gaaaaaggct agaaaatgtt taaaaggaaa agaaaaaact cagcttttct catatgagag  1920
gaacccagaa aaacaacact gaaaaagaag agtggctctg tcaacctcct cttaggtctc  1980
ctcctctcta gttattggga aaggagttgc atggtacagg acaagttctg gtgtgtggtc  2040
aaatagaatc agatgtggag aacaccatgc agagaataag gagacctgtc atatttgtgt  2100
tgtactcaaa tgaggggcaa atgaatctta ggctaaatca aataacagtc tctgtcaagc  2160
tgtgctcaga aagtcaacca ctgaagatgg agggtgaggc acgtcattta aaaaaagtga  2220
aatgtagc                                                           2228

SEQ ID NO: 120          moltype = AA  length = 239
FEATURE                 Location/Qualifiers
source                  1..239
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 120
MEPGLQQAGS CGAPSPDPAM QVQPGSVASP WRSTRPWRST SRSYFYLSTT ALVCLVVAVA  60
IILVLVVQKK DSTPNTTEKA PLKGGNCSED LFCTLKSTPS KKSWAYLQVS KHLNNTKLSW  120
NEDGTIHGLI YQDGNLIVQF PGLYFIVCQL QFLVQCSNHS VDLTLQLLIN SKIKKQTLVT  180
VCESGVQSKN IYQNLSQFLL HYLQVNSTIS VRVDNFQYVD TNTFPLDNVL SVFLYSSSD   239

SEQ ID NO: 121          moltype = DNA  length = 2744
FEATURE                 Location/Qualifiers
source                  1..2744
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 121
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ttggaaaata tgcctttaag ccattcaaga actcaaggag ctcagagatc atcctggaag  120
ctgtggctct tttgctcaat agttatgttg ctatttcttt gctccttcag ttggctaatc  180
tttatttttc tccaattaga gactgctaag gagccctgta tggctaagtt tggaccatta  240
ccctcaaaat ggcaaatggc atcttctgaa cctccttgcg tgaataaggt gtctgactgg  300
aagctggaga tacttcagaa tggcttatat ttaatttatg gccaagtggc tcccaatgca  360
aactacaatg atgtagctcc ttttgaggtg cggctgtata aaaacaaaga catgatacaa  420
actctaacaa acaaatctaa aatccaaaat gtaggaggga cttatgaatt gcatgttggg  480
gacaccatag acttgatatt caactctgag catcaggttc taaaaaataa tacatactgg  540
ggtatcattt tactagcaaa tccccaattc atctcctaga gacttgattt gatctcctca  600
ttcccttcag cacatgtaga ggtgccagtg ggtggattgg agggagaaga tattcaattt  660
ctagagtttg tctgtctaca aaaatcaaca caaacagaac tcctctgcac gtgaattttc  720
atctatcatg cctatctgaa agagactcag gggaagagcc aaagactttt ggttggatct  780
gcagagatac ttcattaatc catgataaaa caaatatgga tgacagagga catgtgcttt  840
tcaaagaatc tttatctaat tcttgaattc atgagtggaa aaatggagtt ctattcccat  900
ggaagattta cctggtatgc aaaaaggatc tggggcagta gcctggcttt gttctcatat  960
tcttgggctg ctgtaattca ttcttctcat actcccatct tctgagaccc tcccaataaa  1020
aagtagactg ataggatggc cacagatatg cctaccatac cctactttag atatggtggt  1080
gttagaagat aaagaacaat ctgagaacta ttggaataga ggtacaagtg gcataaaatg  1140
gaatgtacgc tatctggaaa tttctcttgg ttttatcttc ctcaggatgc agggtgcttt  1200
aaaaagcctt atcaaaggag tcattccgaa ccctcacgta gagctttgtg agaccttact  1260
gttggtgtgt gtgtctaaac attgctaatt gtaaagaaag agtaaccatt agtaatcatt  1320
aggtttaacc ccagaatggt attatcatta ctggattatg tcatgtaatg atttagtatt  1380
tttagctagc tttccacagt ttgcaaagtg ctttcgtaaa acagttagca attctatgaa  1440
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gccaactttc ctcaactcat aggacaagtg actacaagag gcaatgggta gtcccctgca  1560
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ttaaagtgtg tcatacatat gtgtgtgtgt gtgtgtgtgt gtgtgtatat gtgtgtgtgt  2220
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atgtaaattg gcaaacacta cacattttcc ttttggacag ctagttcacc agcacaccac  2460
tgtgaaactc tccttaatga ctcctctctg cccccgcttc attcctggga taatcatagc  2520
agactaaggg agaaaatgaa attgtaaaaa tttggcatac tggtgatttc tcagggcaag  2580
cagaggttac tacagctgca gctagaggga tgactaccaa caggtgacct ttacattttc  2640
ctgatgttat aattttagct tttgttttca atgtatactg ttttcctgtt tctccacata  2700
gtagtctgca ttttaaatct ataataaaac atgctgataa ctgg                   2744

SEQ ID NO: 122          moltype = AA  length = 177
FEATURE                 Location/Qualifiers
source                  1..177
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 122
MCLSHLENMP LSHSRTQGAQ RSSWKLWLFC SIVMLLFLCS FSWLIFIFLQ LETAKEPCMA  60
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KFGPLPSKWQ MASSEPPCVN KVSDWKLEIL QNGLYLIYGQ VAPNANYNDV APFEVRLYKN  120
KDMIQTLTNK SKIQNVGGTY ELHVGDTIDL IFNSEHQVLK NNTYWGIILL ANPQFIS     177

SEQ ID NO: 123          moltype = DNA  length = 2064
FEATURE                 Location/Qualifiers
source                  1..2064
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 123
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aggaaatgcc tttgagagaa tcaagtcctc aaagggcaga gaggtgcaag aagtcatggc  120
tcttgtgcat agtggctctg ttactgatgt tgctctgttc tttgggtaca ctgatctata  180
cttcactcaa gccaactgcc atcgagtcct gcatggttaa gtttgaacta tcatcctcaa  240
aatggcacat gacatctccc aaacctcact gtgtgaatac gacatctgat gggaagctga  300
agatactgca gagtggcaca tatttaatct acggccaagt gattcctgtg gataagaaat  360
acataaaaga caatgccccc ttcgtagtac agatatataa aaagaatgat gtcctacaaa  420
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ataacatata tctgaagttc aactctaaag accatattca gaaaactaac acatactggg  540
ggatcatctt aatgcctgat ctaccattca tctcttagag attgggtttg gtctcctcat  600
cttcttcttt gtatcccgag atgctggtgg gtgggttgga gggggatgat tgatggcaat  660
gcacacagtt tgtgagggct tacaaattga cacaatcaga gcctcttggc atataaaatt  720
ttagccctca tatctgtctg aagaggactc agcaaatggg ccaatcccta atgttgggtc  780
tgcaaatgga cttgtacaat ccatgataaa aaggagtatg ggccacagaa gacagaaact  840
cttccaaaga atgtctttct aaccttgatc cctgggtaga atgagatcct gtttccatgg  900
gagtcttact tggcttgcaa aaaagggtgt agggcagtag cttggccttt tttccatcat  960
aatttccttg agctgtttta ccttaatccc tccaaactct caccttctga gagcctccta  1020
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gtggtgtttt tagaggacag agaacattat gaagcctaga gcagcagagg tcaagatgcc  1140
acgaaatgga attgatctgg gaattttttt tttttttcat tctcaggatg caggttcatt  1200
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attttccttt tgcctggagc aagaagatcc aggatactgt tggaagagtt catctcactc  1740
aaccatgctg actttccaaa gtaataatga acatttgtgt tcaaattttg gattctgtta  1800
aatttagcca gcttgtgagt tcttgtcgaa aagtatttta aaccaattta cactatttat  1860
gggtatttgt gaaaagctat atagtgatat tttatatata actaatttaa aatattttta  1920
ttttatgtaa caaaaatact ataggctaag ctatttcttc ttattttttt atgaatactt  1980
gctgaattgc catagggcac aaagactctt ctgtttgcat atcttctcag gaaattaaaa  2040
ttgtatcaca tgtatttata agaa                                         2064

SEQ ID NO: 124          moltype = AA  length = 173
FEATURE                 Location/Qualifiers
source                  1..173
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 124
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SKWHMTSPKP HCVNTTSDGK LKILQSGTYL IYGQVIPVDK KYIKDNAPFV VQIYKKNDVL  120
QTLMNDFQIL PIGGVYELHA GDNIYLKFNS KDHIQKTNTY WGIILMPDLP FIS         173

SEQ ID NO: 125          moltype = DNA  length = 1852
FEATURE                 Location/Qualifiers
source                  1..1852
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 125
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ccagaagata ccatttcaac tttaacacag catgatcgaa acatacaacc aaacttctcc  120
ccgatctgcg gccactggac tgcccatcag catgaaaatt tttatgtatt tacttactgt  180
ttttcttatc acccagatga ttgggtcagc actttttgct gtgtatcttc atagaaggtt  240
ggacaagata gaagatgaaa ggaatcttca tgaagatttt gtattcatga aaacgataca  300
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gtttgaaggc tttgtgaagg atataatgtt aaacaaagag gagacgaaga aagaaaacag  420
ctttgaaatg caaaaaggtg atcagaatcc tcaaattgcg gcacatgtca taagtgaggc  480
cagcagtaaa acaacatctg tgttacagtg ggctgaaaaa ggatactaca ccatgagcaa  540
caacttggta accctggaaa atgggaaaca gctgaccgtt aaaagacaag gactctatta  600
tatctatgcc caagtcacct tctgttccaa tcgggaagct tcgagtcaag ctccatttat  660
agccagcctc tgcctaaagt cccccggtag attcgagaga atcttactca gagctgcaaa  720
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cactggcttc acgtcctttg gcttactcaa actctgaaca gtgtcacctt gcaggctgtg  900
gtggagctga cgctgggagt cttcataata cagcacagcg gttaagccca ccccctgtta  960
actgcctatt tataacccta ggatcctcct tatggagaac tatttattat acactccaag  1020
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ataagagctt atatatctga agcagcaacc ccactgatgc agacatccag agagtcctat  1140
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actgtattta aaggaaatct attgtatcta cctgcagtct ccattgtttc cagagtgaac  1800
ttgtaattat cttgttattt atttttgaa taataaagac ctcttaacat ta           1852

SEQ ID NO: 126          moltype = AA  length = 261
FEATURE                 Location/Qualifiers
source                  1..261
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 126
MIETYNQTSP RSAATGLPIS MKIFMYLLTV FLITQMIGSA LFAVYLHRRL DKIEDERNLH  60
EDFVFMKTIQ RCNTGERSLS LLNCEEIKSQ FEGFVKDIML NKEETKKENS FEMQKGDQNP  120
QIAAHVISEA SSKTTSVLQW AEKGYYTMSN NLVTLENGKQ LTVKRQGLYY IYAQVTFCSN  180
REASSQAPFI ASLCLKSPGR FERILLRAAN THSSAKPCGQ QSIHLGGVFE LQPGASVFVN  240
VTDPSQVSHG TGFTSFGLLK L                                            261

SEQ ID NO: 127          moltype = DNA  length = 1250
FEATURE                 Location/Qualifiers
source                  1..1250
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 127
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cttccagcga gcatgaagat ttttatgtat ttacttactg ttttccttat cacccaaatg  120
attggatctg tgctttttgc tgtgtatctt catagaagat tggataaggt cgaagaggaa  180
gtaaaccttc atgaagattt tgtattcata aaaaagctaa agagatgcaa caaaggagaa  240
ggatctttat ccttgctgaa ctgtgaggag atgagaaggc aatttgaaga ccttgtcaag  300
gatataacgt taaacaaaga agagaaaaaa gaaaacagct ttgaaatgca aagaggtgat  360
gaggatcctc aaattgcagc acacgttgta agcgaagcca acagtaatgc agcatccgtt  420
ctacagtggg ccaagaaagg atattatacc atgaaaagca acttggtaat gcttgaaaat  480
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tgctctaatc gggagccttc gagtcaacgc ccattcatcg tcggcctctg gctgaagccc  600
agcagtggat ctgagagaat cttactcaag gcggcaaata cccacagttc ctcccagctt  660
tgcgagcagc agtctgttca cttgggcgga gtgtttgaat tacaagctgg tgcttctgtg  720
tttgtcaacg tgactgaagc aagccaagtg atccacagag ttggcttctc atcttttggc  780
ttactcaaac tctgaacagt gcgctgtcct aggctgcagc agggctgatg ctggcagtct  840
tccctataca gcaagtcagt taggacctgc cctgtgttga actgcctatt tataacccta  900
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gagaattaca gggcaggcaa aaatcccaag ggaccctgct ccctaagaac ttacaatctg  1020
aaacagcaac cccactgatt cagacaacca gaaaagacaa agccataata cacagatgac  1080
agagctctga tgaaacaaca gataactaat gagcacagtt ttgttgtttt atgggtgtgt  1140
cgttcaatgg acagtgtact tgacttacca gggaagatgc agaagggcaa ctgtgagcct  1200
cagctcacaa tctgttatgg ttgacctggg ctccctgcgg ccctagtagg             1250

SEQ ID NO: 128          moltype = AA  length = 260
FEATURE                 Location/Qualifiers
source                  1..260
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 128
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EDFVFIKKLK RCNKGEGSLS LLNCEEMRRQ FEDLVKDITL NKEEKKENSF EMQRGDEDPQ  120
IAAHVVSEAN SNAASVLQWA KKGYYTMKSN LVMLENGKQL TVKREGLYYV YTQVTFCSNR  180
EPSSQRPFIV GLWLKPSSGS ERILLKAANT HSSSQLCEQQ SVHLGGVFEL QAGASVFVNV  240
TEASQVIHRV GFSSFGLLKL                                              260

SEQ ID NO: 129          moltype = DNA  length = 4778
FEATURE                 Location/Qualifiers
source                  1..4778
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 129
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ttgctgttgt tcattgctgc atcccccaca ccgagagcag agcctggcat gggcagaaag  180
tcctcagtcg atatttggtg gccccaagcg aatgaagcat ccaagaaggg aaagctgggg  240
gctccccact gcacttgcca cctgagtcac attttcagaa gcctctggaa agtcgtgcac  300
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tcagtgggca ccaccaaggc gagatgaagc cccagcaggc accttcagaa gacccacgta  1620
gactgcagac cctgccacgg acaatactaa ggacaaaaac ccagagactt ggggtctgtg  1680
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                        mol_type = protein
                        organism = Homo sapiens
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ELNAINTTVS QDPETELYAV SSKLDFNMTT NHSFMCLIKY GHLRVNQTFN WNTTKQEHFP  240
DNLLPSWAIT LISVNGIFVI CCLTYCFAPR CRERRRNERL RRESVRPV                288

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ctggctctaa ggtgggatca ctaagggatg gggcagtctc tgcccaaaca taaagagaac  2520
tctggggagc ctgagccaca aaaatgttcc tttattttat gtaaaccctc aagggttata  2580
gactgccatg ctagacaagc ttgtccatgt aatattccca tgtttttacc ctgcccctgc  2640
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ataaatgctt gttacattca                                              2720

SEQ ID NO: 142          moltype = AA  length = 329
FEATURE                 Location/Qualifiers
source                  1..329
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 142
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ENLVLNEVYL GKEKFDSVHS KYMGRTSFDS DSWTLRLHNL QIKDKGLYQC IIHHKKPTGM  120
IRIHQMNSEL SVLANFSQPE IVPISNITEN VYINLTCSSI HGYPEPKKMS VLLRTKNSTI  180
EYDGVMQKSQ DNVTELYDVS ISLSVSFPDV TSNMTIFCIL ETDKTRLLSS PFSIELEDPQ  240
PPPDHIPWIT AVLPTVIICV MVFCLILWKW KKKKRPRNSY KCGTNTMERE ESEQTKKREK  300
IHIPERSDEA QRVFKSSKTS SCDKSDTCF                                    329

SEQ ID NO: 143          moltype = DNA  length = 2539
FEATURE                 Location/Qualifiers
source                  1..2539
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 143
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gacttgaaca accagactcc tgtagacgtg ttccagaact tacggaagca cccacgatgg  120
accccagatg caccatgggc ttggcaatcc ttatctttgt gacagtcttg ctgatctcag  180
atgctgtttc cgtggagacg caagcttatt tcaatgggac tgcatatctg ccgtgcccat  240
ttacaaaggc tcaaaacata agcctgagtg agctggtagt attttggcag gaccagcaaa  300
agttggttct gtacgagcac tatttgggca cagagaaact tgatagtgtg aatgccaagt  360
acctgggccg cacgagcttt gacaggaaca actggactct acgacttcac aatgttcaga  420
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ataacatgca gatatcacaa gataatgtca cagaactgtt cagtatctcc aacagcctct  720
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agactcttaa gatctggcca gttaccaaca tgttctgtac agagtggatt tcaataaagt  2520
tttcttgaat tttttcaag                                               2539

SEQ ID NO: 144          moltype = AA  length = 309
FEATURE                 Location/Qualifiers
source                  1..309
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 144
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QKLVLYEHYL GTEKLDSVNA KYLGRTSFDR NNWTLRLHNV QIKDMGSYDC FIQKKPPTGS  120
IILQQTLTEL SVIANFSEPE IKLAQNVTGN SGINLTCTSK QGHPKPKKMY FLITNSTNEY  180
GDNMQISQDN VTELFSISNS LSLSFPDGVW HMTVVCVLET ESMKISSKPL NFTQEFPSPQ  240
TYWKEITASV TVALLLVMLL IIVCHKKPNQ PSRPSNTASK LERDSNADRE TINLKELEPQ  300
IASAKPNAE                                                          309

SEQ ID NO: 145          moltype = DNA  length = 1086
FEATURE                 Location/Qualifiers
source                  1..1086
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 145
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ttagacactg tgtcaggtag cctcactatc tacaacttaa catcatcaga tgaagatgag  360
tatgaaatgg aatcgccaaa tattactgat accatgaagt tctttcttta tgtgcttgag  420
tctcttccat ctcccacact aacttgtgca ttgactaatg gaagcattga agtccaatgc  480
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atggagcaat gtaaacgtaa ctcaaccagt atatatttta agatggaaaa tgatcttcca  600
caaaaaatac agtgtactct tagcaatcca ttatttaata caacatcatc aatcattttg  660
acaacctgta tcccaagcag cggtcattca agacacagat atgcacttat acccatacca  720
ttagcagtaa ttacaacatg tattgtgctg tatatgaatg gtattctgaa atgtgacaga  780
aaaccagaca gaaccaactc caattgattg gtaacagaag atgaagacaa cagcataact  840
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caactgttgg aaatgtaact tgaagcagct gctttaagaa gaaataccca ctaacaaaga  960
acaagcatta gttttggctg tcatcaactt attatatgac taggtgcttg ctttttttgt  1020
cagtaaattg tttttactga tgatgtagat acttttgtaa ataaatgtaa atatgtacac  1080
aagtga                                                             1086

SEQ ID NO: 146          moltype = AA  length = 250
FEATURE                 Location/Qualifiers
source                  1..250
                        mol_type = protein
                        organism = Homo sapiens
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DKVAELENSE FRAFSSFKNR VYLDTVSGSL TIYNLTSSDE DEYEMESPNI TDTMKFFLYV  120
LESLPSPTLT CALTNGSIEV QCMIPEHYNS HRGLIMYSWD CPMEQCKRNS TSIYFKMEND  180
LPQKIQCTLS NPLFNTTSSI ILTTCIPSSG HSRHRYALIP IPLAVITTCI VLYMNGILKC  240
DRKPDRTNSN                                                         250

SEQ ID NO: 147          moltype = DNA  length = 3749
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source                  1..3749
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 147
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acccccttctg gtgatacatt cacaactctc tagtttcccc caaatggcac tatggggagc  3420
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gacgcttcct ccattcacac agcggggatg tgattgttac agcgggtggt gtgtgctggc  3660
tgagaagcca ctgtgaattg attcttcttc tgaagtttat gtttctactt tttggaaatg  3720
aataaattac agccagtcca tcaaggaaa                                    3749

SEQ ID NO: 148          moltype = AA  length = 335
FEATURE                 Location/Qualifiers
source                  1..335
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 148
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HIVVTMAKSL ENSVENKIVS LDPSEAGPPR YLGDRYKFYL ENLTLGIRES RKEDEGWYLM  120
TLEKNVSVQR FCLQLRLYEQ VSTPEIKVLN KTQENGTCTL ILGCTVEKGD HVAYSWSEKA  180
GTHPLNPANS SHLLSLTLGP QHADNIYICT VSNPISNNSQ TFSPWPGCRT DPSETKPWAV  240
YAGLLGGVIM ILIMVVILQL RRRGKTNHYQ TTVEKKSLTI YAQVQKPGPL QKKLDSFPAQ  300
DPCTTIYVAA TEPVPESVQE TNSITVYASV TLPES                             335

SEQ ID NO: 149          moltype = DNA  length = 2688
FEATURE                 Location/Qualifiers
source                  1..2688
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 149
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gtaacaaaga acaccaactg cctggctcaa aactctcatg tcccattact ctgtaccttt  2580
ctgtatttag ataatttaca gtgtgagttc tgctgttcca tgtatcctat ttgtgttact  2640
aacttatgtc aaagtatttc taattataat caacaaaagc taactttg               2688

SEQ ID NO: 150          moltype = AA  length = 343
FEATURE                 Location/Qualifiers
source                  1..343
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 150
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VRILVTMATS PGSKSNKKIV SFDLSKGSYP DHLEDGYHPQ SKNLSLKILG NRRESEGWYL  120
VSVEENVSVQ QFCKQLKLYE QVSPPEIKVL NKTQENENGT CSLLLACTVK KGDHVTYSWS  180
DEAGTHLLSR ANRSHLLHIT LSNQHQDSIY NCTASNPVSS ISRTFNLSSQ ACKQESSSES  240
SPWMQYTLVP LGVVIIFILV FTAIIMMKRQ GKSNHCQPPV EEKSLTIYAQ VQKSGPQEKK  300
LHDALTDQDP CTTIYVAATE PAPESVQEPN PTTVYASVTL PES                    343

SEQ ID NO: 151          moltype = DNA  length = 1682
FEATURE                 Location/Qualifiers
source                  1..1682
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 151
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tggggctgct tgctgaccgc tgtccatcca gaaccaccca ctgcatgcag agaaaaacag  120
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LHRSCSPGFG VKQIATGVSD TICEPCPVGF FSNVSSAFEK CHPWTSCETK DLVVQQAGTN  180
KTDVVCGPQD RLRALVVIPI IFGILFAILL VLVFIKKVAK KPTNKAPHPK QEPQEINFPD  240
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source                  1..203
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QHTPCIPGFG VMEMATETTD TVCHPCPVGF FSNQSSLFEK CYPWTRFKVP DASPAGHSCR  180
DGHPHHHFRG VSLYQKGGQE TKG                                          203

SEQ ID NO: 155          moltype = DNA  length = 4721
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source                  1..4721
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source                  1..220
                        mol_type = protein
                        organism = Homo sapiens
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PYLDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR  180
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                        organism = Mus musculus
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ttcctaaatc tacaccggat ctccaaaggg aaagaactcc atttgctttg attttattgc  4260
tgtatcccca gtgcctagaa taatgcttag cctgcaataa atatttattc attgact     4317
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SEQ ID NO: 158          moltype = AA  length = 218
FEATURE                 Location/Qualifiers
source                  1..218
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 158
MTLRLLFLAL NFFSVQVTEN KILVKQSPLL VVDSNEVSLS CRYSYNLLAK EFRASLYKGV  60
NSDVEVCVGN GNFTYQPQFR SNAEFNCDGD FDNETVTFRL WNLHVNHTDI YFCKIEFMYP  120
PPYLDNERSN GTIIHIKEKH LCHTQSSPKL FWALVVVAGV LFCYGLLVTV ALCVIWTNSR  180
RNRLLQSDYM NMTPRRPGLT RKPYQPYAPA RDFAAYRP                          218

SEQ ID NO: 159          moltype = DNA  length = 1282
FEATURE                 Location/Qualifiers
source                  1..1282
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 159
ggaagtctgt caactgggag ggggagaggg gggtgatggg ccaggaatgg ggtccccggg  60
catggtgctg ggcctcctgg tgcagatctg ggccctgcaa gaagcctcaa gcctgagcgt  120
gcagcagggg cccaacttgc tgcaggtgag gcagggcagt caggcgaccc tggtctgcca  180
ggtggaccag gccacagcct gggaacggct ccgtgttaag tggacaaagg atggggccat  240
cctgtgtcaa ccgtacatca ccaacggcag cctcagcctg ggggtctgcg ggccccaggg  300
acggctctcc tggcaggcac ccagccatct caccctgcag ctggaccctg tgagcctcaa  360
ccacagcggg gcgtacgtgt gctgggcggc cgtagagatt cctgagttgg aggaggctga  420
gggcaacata acaaggctct ttgtggaccc agatgacccc acacagaaca gaaaccggat  480
cgcaagcttc ccaggattcc tcttcgtgct gctgggggtg ggaagcatgg gtgtggctgc  540
gatcgtgtgg ggtgcctggt tctggggccg ccgcagctgc cagcaaaggg actcaggtaa  600
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cagcccagga aatgcattct acagcaacgt cctataccgg ccccgggggg ccccaaagaa  660
gagtgaggac tgctctggag aggggaagga ccagaggggc cagagcattt attcaacctc  720
cttcccgcaa ccggcccccc gccagccgca cctggcgtca agaccctgcc ccagcccgag  780
accctgcccc agccccaggc ccggccaccc cgtctctatg gtcagggtct ctcctagacc  840
aagccccacc cagcagccga ggccaaaagg gttccccaaa gtgggagagg agtgagagat  900
cccaggagac ctcaacagga ccccacccat aggtacacac aaaaaagggg ggatcgaggc  960
cagacacggt ggctcacgcc tgtaatccca gcagtttggg aagccgaggc gggtggaaca  1020
cttgaggtca ggggtttgag accagcctgg cttgaacctg ggaggcggag gttgcagtga  1080
gccgagattg cgccactgca ctccagcctg ggcgacagag tgagactccg tctcaaaaaa  1140
aacaaaaagc aggaggattg ggagcctgtc agccccatcc tgagaccccg tcctcatttc  1200
tgtaatgatg gatctcgctc ccactttccc ccaagaacct aataaaggct tgtgaagaaa  1260
aagcaaaaaa aaaaaaaaaa aa                                           1282

SEQ ID NO: 160          moltype = AA  length = 282
FEATURE                 Location/Qualifiers
source                  1..282
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 160
MGSPGMVLGL LVQIWALQEA SSLSVQQGPN LLQVRQGSQA TLVCQVDQAT AWERLRVKWT  60
KDGAILCQPY ITNGSLSLGV CGPQGRLSWQ APSHLTLQLD PVSLNHSGAY VCWAAVEIPE  120
LEEAEGNITR LFVDPDDPTQ NRNRIASFPG FLFVLLGVGS MGVAAIVWGA WFWGRRSCQQ  180
RDSGNSPGNA FYSNVLYRPR GAPKKSEDCS GEGKDQRGQS IYSTSFPQPA PRQPHLASRP  240
CPSPRPCPSP RPGHPVSMVR VSPRPSPTQQ PRPKGFPKVG EE                     282

SEQ ID NO: 161          moltype = DNA  length = 1643
FEATURE                 Location/Qualifiers
source                  1..1643
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 161
agtctcactt cagttccttt tgcatgaaga gctcagaatc aaaagaggaa accaacccct  60
aagatgagct ttccatgtaa atttgtagcc agcttccttc tgattttcaa tgtttcttcc  120
aaaggtgcag tctccaaaga gattacgaat gccttggaaa cctggggtgc cttgggtcag  180
gacatcaact tggacattcc tagttttcaa atgagtgatg atattgacga tataaaatgg  240
gaaaaaactt cagacaagaa aaagattgca caattcagaa aagagaaaga gactttcaag  300
gaaaaagata catataagct atttaaaaat ggaactctga aaattaagca tctgaagacc  360
gatgatcagg atatctacaa ggtatcaata tatgatacaa aaggaaaaaa tgtgttggaa  420
aaaatatttg atttgaagat tcaagagagg gtctcaaaac caaagatctc ctggacttgt  480
atcaacacaa ccctgacctg tgaggtaatg aatggaactg accccgaatt aaacctgtat  540
caagatggga aacatctaaa actttctcag agggtcatca cacacaagtg gaccaccagc  600
ctgagtgcaa aattcaagtg cacagcaggg aacaaagtca gcaaggaatc cagtgtcgag  660
cctgtcagct gtccaggagg cagcatcctt ggccagagta atgggctctc tgcctggacc  720
cctcccagcc atcccacttc tcttcctttt gcagagaaag gtctggacat ctatctcatc  780
attggcatat gtggaggagg cagcctcttg atggtctttg tggcactgct cgttttctat  840
atcaccaaaa ggaaaaaaca gaggagtcgg agaaatgatg aggagctgga gacaagagcc  900
cacagagtag ctactgaaga aaggggccgg aagccccacc aaattccagc ttcaacccct  960
cagaatccag caacttccca acatcctcct ccaccacctg gtcatcgttc ccaggcacct  1020
agtcatcgtc ccccgcctcc tggacaccgt gttcagcacc agcctcagaa gaggcctcct  1080
gctccgtcgg gcacacaagt tcaccagcag aaaggcccgc ccctccccag acctcgagtt  1140
cagccaaaac ctccccatgg ggcagcagaa aactcattgt ccccttcctc taattaaaaa  1200
agatagaaac tgtctttttc aataaaaagc actgtggatt tctgccctcc tgatgtgcat  1260
atccgtactt ccatgaggtg ttttctgtgt gcagaacatt gtcacctcct gaggctgtgg  1320
gccacagcca cctctgcatc ttcgaactca gccatgtggt caacatctgg agtttttggt  1380
ctcctcagag agctccatca caccagtaag gagaagcaat ataagtgtga ttgcaagaat  1440
ggtagaggac cgagcacaga aatcttagag atttcttgtc ccctctcagg tcatgtgtag  1500
atgcgataaa tcaagtgatt ggtgtgcctg ggtctcacta caagcagcct atctgcttaa  1560
gagactctgg agtttcttat gtgccctggt ggacacttgc ccaccatcct gtgagtaaaa  1620
gtgaaataaa agctttgact aga                                          1643

SEQ ID NO: 162          moltype = AA  length = 377
FEATURE                 Location/Qualifiers
source                  1..377
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 162
MSFPCKFVAS FLLIFNVSSK GAVSKEITNA LETWGALGQD INLDIPSFQM SDDIDDIKWE  60
KTSDKKKIAQ FRKEKETFKE KDTYKLFKNG TLKIKHLKTD DQDIYKVSIY DTKGKNVLEK  120
IFDLKIQERV SKPKISWTCI NTTLTCEVMN GTDPELNLYQ DGKHLKLSQR VITHKWTTSL  180
SAKFKCTAGN KVSKESSVEP VSCPGGSILG QSNGLSAWTP PSHPTSLPFA EKGLDIYLII  240
GICGGGSLLM VFVALLVFYI TKRKKQRSRR NDEELETRAH RVATEERGRK PHQIPASTPQ  300
NPATSQHPPP PPGHRSQAPS HRPPPPGHRV QHQPQKRPPA PSGTQVHQQK GPPLPRPRVQ  360
PKPPHGAAEN SLSPSSN                                                 377

SEQ ID NO: 163          moltype = DNA  length = 1144
FEATURE                 Location/Qualifiers
source                  1..1144
                        mol_type = genomic DNA
                        organism = Mus musculus
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SEQUENCE: 163
gcctcaccac agtcctgaca gaaagaactc agagtcaccc ctgggaaaag aactctaaag  60
atgaaatgta aattcctggg tagcttcttt ctgctcttca gcctttccgg caaaggggcg  120
gactgcagag acaatgagac catctggggt gtcttgggtc atggcatcac cctgaacatc  180
cccaactttc aaatgactga tgatattgat gaggtgcgat gggtaaggag gggcaccctg  240
gtcgcagagt ttaaaaggaa gaagccacct tttttgatat cagaaacgta tgaggtctta  300
gcaaacggat ccctgaagat aaagaagccg atgatgagaa acgacagtgg cacctataat  360
gtaatggtgt atggcacaaa tgggatgact aggctggaga aggacctgga cgtgaggatt  420
ctggagaggg tctcaaagcc catgatccac tgggaatgcc ccaacacaac cctgacctgt  480
gcggtcttgc aagggacaga ttttgaactg aagctgtatc aaggggaaac actactcaat  540
agtctccccc agaagaacat gagttaccag tggaccaacc tgaacgcacc attcaagtgt  600
gaggcgataa acccggtcag caaggagtct aagatggaag ttgttaactg tccagagaaa  660
ggtctgtcct tctatgtcac agtgggggtc ggtgcaggag gactcctctt ggtgctcttg  720
gtggcgcttt ttattttctg tatctgcaag aggagaaaac ggaacaggag gagaaaagat  780
gaagagctgg aaataaaagc ttccagaaca agcactgtgg aaaggggccc caagccgcac  840
tcaaccccag ccgcagcagc gcagaattca gtggcgctcc aagctcctcc tccacctggc  900
catcacctcc agacacctgg ccatcgtccc ttgcctccag gccaccgtac ccgtgagcac  960
cagcagaaga agagacctcc tccatcaggc acacagattc accagcagaa aggccctcct  1020
ttacccagac cccgagttca gccaaaacct ccctgtggga gtggagatgg tgtttcactg  1080
ccgcccccta attaagaagg cagagttcgt catttccaat aaaaagctgt gtggatttat  1140
cttc                                                               1144

SEQ ID NO: 164          moltype = AA  length = 344
FEATURE                 Location/Qualifiers
source                  1..344
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 164
MKCKFLGSFF LLFSLSGKGA DCRDNETIWG VLGHGITLNI PNFQMTDDID EVRWVRRGTL  60
VAEFKRKKPP FLISETYEVL ANGSLKIKKP MMRNDSGTYN VMVYGTNGMT RLEKDLDVRI  120
LERVSKPMIH WECPNTTLTC AVLQGTDFEL KLYQGETLLN SLPQKNMSYQ WTNLNAPFKC  180
EAINPVSKES KMEVVNCPEK GLSFYVTVGV GAGGLLLVLL VALFIFCICK RRKRNRRRKD  240
EELEIKASRT STVERGPKPH STPAAAAQNS VALQAPPPPG HHLQTPGHRP LPPGHRTREH  300
QQKKRPPPSG TQIHQQKGPP LPRPRVQPKP PCGSGDGVSL PPPN                   344

SEQ ID NO: 165          moltype = DNA  length = 1086
FEATURE                 Location/Qualifiers
source                  1..1086
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 165
gaacttaggg ctgcttgtgg ctgggcactc gcgcagaggc cggcccgacg agccatggtt  60
gctgggagcg acgcggggcg ggccctgggg gtcctcagcg tggtctgcct gctgcactgc  120
tttggtttca tcagctgttt ttcccaacaa atatatggtg ttgtgtatgg gaatgtaact  180
ttccatgtac caagcaatgt gcctttaaaa gaggtcctat ggaaaaaaca aaaggataaa  240
gttgcagaac tggaaaattc tgaattcaga gctttctcat cttttaaaaa tagggtttat  300
ttagacactg tgtcaggtag cctcactatc tacaacttaa catcatcaga tgaagatgag  360
tatgaaatgg aatcgccaaa tattactgat accatgaagt tctttcttta tgtgcttgag  420
tctcttccat ctcccacact aacttgtgca ttgactaatg gaagcattga agtccaatgc  480
atgataccag agcattacaa cagccatcga ggacttataa tgtactcatg ggattgtcct  540
atggagcaat gtaaacgtaa ctcaaccagt atatatttta agatggaaaa tgatcttcca  600
caaaaaatac agtgtactct tagcaatcca ttatttaata caacatcatc aatcattttg  660
acaacctgta tcccaagcag cggtcattca agacacagat atgcacttat acccatacca  720
ttagcagtaa ttacaacatg tattgtgctg tatatgaatg gtattctgaa atgtgacaga  780
aaaccagaca gaaccaactc caattgattg gtaacagaag atgaagacaa cagcataact  840
aaattatttt aaaaactaaa aagccatctg atttctcatt tgagtattac aatttttgaa  900
caactgttgg aaatgtaact tgaagcagct gctttaagaa gaaataccca ctaacaaaga  960
acaagcatta gttttggctg tcatcaactt attatatgac taggtgcttg ctttttttgt  1020
cagtaaattg tttttactga tgatgtagat acttttgtaa ataaatgtaa atatgtacac  1080
aagtga                                                             1086

SEQ ID NO: 166          moltype = AA  length = 250
FEATURE                 Location/Qualifiers
source                  1..250
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 166
MVAGSDAGRA LGVLSVVCLL HCFGFISCFS QQIYGVVYGN VTFHVPSNVP LKEVLWKKQK  60
DKVAELENSE FRAFSSFKNR VYLDTVSGSL TIYNLTSSDE DEYEMESPNI TDTMKFFLYV  120
LESLPSPTLT CALTNGSIEV QCMIPEHYNS HRGLIMYSWD CPMEQCKRNS TSIYFKMEND  180
LPQKIQCTLS NPLFNTTSSI ILTTCIPSSG HSRHRYALIP IPLAVITTCI VLYMNGILKC  240
DRKPDRTNSN                                                         250

SEQ ID NO: 167          moltype = DNA  length = 1097
FEATURE                 Location/Qualifiers
source                  1..1097
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 167
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ctttttctag ccaggctctc aactgtctcc tgcgttgctg ggaagttctg gaaggaagca  60
tgtgctccag aggttgggat tcgtgtctgg ctctggaatt gctactgctg cctctgtcac  120
tcctggtgac cagcattcaa ggtcacttgg tacatatgac cgtggtctcc ggcagcaacg  180
tgactctgaa catctctgag agcctgcctg agaactacaa acaactaacc tggttttata  240
ctttcgacca gaagattgta gaatgggatt ccagaaaatc taagtacttt gaatccaaat  300
ttaaaggcag ggtcagactt gatcctcaga gtggcgcact gtacatctct aaggtccaga  360
aagaggacaa cagcacctac atcatgaggg tgttgaaaaa gactgggaat gagcaagaat  420
ggaagatcaa gctgcaagtg cttgaccctg tacccaagcc tgtcatcaaa attgagaaga  480
tagaagacat ggatgacaac tgttatctga aactgtcatg tgtgatacct ggcgagtctg  540
taaactacac ctggtatggg gacaaaaggc ccttcccaaa ggagctccag aacagtgtgc  600
ttgaaaccac ccttatgcca cataattact ccaggtgtta tacttgccaa gtcagcaatt  660
ctgtgagcag caagaatggc acggtctgcc tcagtccacc ctgtaccctg gcccggtcct  720
ttggagtaga atggattgca agttggctag tggtcacggt gcccaccatt cttggcctgt  780
tacttacctg agatgagctc ttttaactca agcgaaactt caaggccaga agatcttgcc  840
tgttggtgat catgctcctc accaggacag agactgtata ggctgaccag aagcatgctg  900
ctgaattatc aacgaggatt ttcaagttaa cttttaaata ctggttatta tttaatttta  960
tatccctttg ttgttttcta gtacacagag atatagagat acacatgctt ttttcccacc  1020
caaaattgtg acaacattat gtgaatgttt tattattttt taaaataaac atttgatata  1080
attgtcaatt aactgaa                                                 1097

SEQ ID NO: 168          moltype = AA  length = 243
FEATURE                 Location/Qualifiers
source                  1..243
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 168
MCSRGWDSCL ALELLLLPLS LLVTSIQGHL VHMTVVSGSN VTLNISESLP ENYKQLTWFY  60
TFDQKIVEWD SRKSKYFESK FKGRVRLDPQ SGALYISKVQ KEDNSTYIMR VLKKTGNEQE  120
WKIKLQVLDP VPKPVIKIEK IEDMDDNCYL KLSCVIPGES VNYTWYGDKR PFPKELQNSV  180
LETTLMPHNY SRCYTCQVSN SVSSKNGTVC LSPPCTLARS FGVEWIASWL VVTVPTILGL  240
LLT                                                                243

SEQ ID NO: 169          moltype = DNA  length = 1205
FEATURE                 Location/Qualifiers
source                  1..1205
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 169
atacgacttc cggttttggg ttttgcttcc tgattgaagg gcaggcgccc tgacttctct  60
tacagttgtc tccagtgttc tggggaagct tctctaagta ttatgtgctt cataaaacag  120
ggatggtgtc tggtcctgga actgctactg ctgcccttgg gaactggatt tcaaggtcat  180
tcaataccag atataaatgc caccaccggc agcaatgtaa ccctgaaaat ccataaggac  240
ccacttggac catataaacg tatcacctgg cttcatacta aaaatcagaa gattttagag  300
tacaactata atagtacaaa gacaatcttc gagtctgaat ttaaaggcag ggtttatctt  360
gaagaaaaca atggtgcact tcatatctct aatgtccgga aagaggacaa aggtacctac  420
tacatgagag tgctgcgtga aactgagaac gagttgaaga taaccctgga agtatttgat  480
cctgtgccca agccttccat agaaatcaat aagactgaag cgtcgactga ttcctgtcac  540
ctgaggctat cgtgtgaggt aaaggaccag catgttgact atacttggta tgagagctcg  600
ggacctttcc ccaaaaagag tccaggatat gtgctcgatc tcatcgtcac accacagaac  660
aagtctacat tttacacctg ccaagtcagc aatcctgtaa gcagcaagaa cgacacagtg  720
tacttcactc taccttgtga tctagccaga tcttctggag tatgttggac tgcaacttgg  780
ctagtggtca caacactcat cattcacagg atcctgttaa cctgacaaga actcttctca  840
cccaagaagg caacttggaa gcacagagtc ttgccttcat ccctagcagt gttcctagcc  900
agcgaagcaa ctctggctct attggacaaa ggaaaatgtg ttactgaacg tctgcgagag  960
tttgcatgca tgctctatga aacaagcaca ggaccttgta cagtgctcca ccactgacct  1020
gtgtgcccag tcctttacaa agatttcaaa tcaacctttt aaaaactgtg cataatatct  1080
aattttatat accctagttg tttcccaaca tatattaaag ataaatgcat tctttttacc  1140
aaaatgtgac tatattattt tcatgttttc atatctcttt ttaaaataaa ttcttttaaa  1200
aaact                                                              1205

SEQ ID NO: 170          moltype = AA  length = 240
FEATURE                 Location/Qualifiers
source                  1..240
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 170
MCFIKQGWCL VLELLLLPLG TGFQGHSIPD INATTGSNVT LKIHKDPLGP YKRITWLHTK  60
NQKILEYNYN STKTIFESEF KGRVYLEENN GALHISNVRK EDKGTYYMRV LRETENELKI  120
TLEVFDPVPK PSIEINKTEA STDSCHLRLS CEVKDQHVDY TWYESSGPFP KKSPGYVLDL  180
IVTPQNKSTF YTCQVSNPVS SKNDTVYFTL PCDLARSSGV CWTATWLVVT TLIIHRILLT  240

SEQ ID NO: 171          moltype = DNA  length = 12123
FEATURE                 Location/Qualifiers
source                  1..12123
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 171
gcagatggga agaagcgtta gagcgagcag cactcacatc tcaagaacca gcctttcaaa  60
cagtttccag agatggatta tcctacttta cttttggctc ttcttcatgt atacagagct  120
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ctatgtgaag aggtgctttg gcatacatca gttccctttg ccgagaacat gtctctagaa  180
tgtgtgtatc catcaatggg catcttaaca caggtggagt ggttcaagat cgggacccag  240
caggattcca tagccatttt cagccctact catggcatgg tcataaggaa gccctatgct  300
gagagggttt actttttgaa ttcaacgatg gcttccaata acatgactct tttctttcgg  360
aatgcctctg aagatgatgt tggctactat tcctgctctc tttacactta cccacaggga  420
acttggcaga aggtgataca ggtggttcag tcagatagtt ttgaggcagc tgtgccatca  480
aatagccaca ttgtttcgga acctggaaag aatgtcacac tcacttgtca gcctcagatg  540
acgtggcctg tgcaggcagt gaggtgggaa aagatccagc cccgtcagat cgacctctta  600
acttactgca acttggtcca tggcagaaat ttcacctcca agttcccaag acaaatagtg  660
agcaactgca gccacggaag gtggagcgtc atcgtcatcc ccgatgtcac agtctcagac  720
tcggggcttt accgctgcta cttgcaggcc agcgcaggag aaaacgaaac cttcgtgatg  780
agattgactg tagccgaggg taaaaccgat aaccaatata ccctctttgt ggctggaggg  840
acagttttat tgttgttgtt tgttatctca attaccacca tcattgtcat tttccttaac  900
agaaggagaa ggagagagag aagagatcta tttacagagt cctgggatac acagaaggca  960
cccaataact atagaagtcc catctctacc agtcaaccta ccaatcaatc catggatgat  1020
acaagagagg atatttatgt caactatcca accttctctc gcagaccaaa gactagagtt  1080
taagcttatt cttgacatga gtgcattagt aatgactctt atgtactcat gcatggatct  1140
ttatgcaatt tttttccact acccaaggtc taccttagat actagttgtc tgaattgagt  1200
tactttgata ggaaaaatac ttcattacct aaaatcattt ttcatagaac tgtttcagaa  1260
aacctgactc taactggttt atatacaaaa gaaaacttac tgtatcatat aacagaatga  1320
tccaggggag attaagcttt gggcaagggc tatttaccag ggcttaaatg ttgtgtctag  1380
aattaagtat gggcataaac tggcttctga atccctttcc agagtgttgg atccatttcc  1440
ctggtcttgg cctcactctc atgcaggctt tcctcttgtg ttggcaagat ggctgccaac  1500
tcttggcaat tcatacatcc ttgtttctgt ctggtagaga gtttgcttct caaatggagc  1560
aaacaaattt gattattttt tcattgttaa ataggcaaca tgaccagaaa ggatggaatg  1620
gcttaagtaa actaagggtt cacttctaga gctgagaagc agggtcaaag cacaatactg  1680
ggcaattcag agcatggtta gaagaggaaa ggggagtctc aaagctggag agtttaccaa  1740
caaatattga ctgcagtgat taaccaagac atttttgtta actaaaaagt gaaatatggg  1800
atggattcta gaaatggggt atctctgtcc atacttctag aatccactct atcagcatag  1860
tccagaagaa tacctggcag tagaagaaat gaatattcaa gaggaagata aatgcgagag  1920
ggcaatcctt tactattctc atatttattt atctctcatt ctgtatagaa ttcttgccgc  1980
catcccaggt ctagccttag gagcaaatgt agtagatagt cgaataataa ataacttaat  2040
gttttggaca tattttgtct acttttgaga attattttta atatgtaaat tctctcaaaa  2100
gggtcaggca cctagttatt atttttaat gattatgtga aagttgaata taatatacca  2160
ctaaaagtga cagttgaaag tggtggcata ggacggtagg gtagaaattt gggagggaaa  2220
aaagaaattg ggagggtaca ggcaacagga gaaaggaatc aaaccacaga aaaatacaaa  2280
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ctgctggggg cccgggccca gggcggcact cgtagcccca ggtgtgactg tgccggtgac  180
ttccacaaga agattggtct gttttgttgc agaggctgcc cagcggggca ctacctgaag  240
gccccttgca cggagccctg cggcaactcc acctgccttg tgtgtcccca agacaccttc  300
ttggcctggg agaaccacca taattctgaa tgtgcccgct gccaggcctg tgatgagcag  360
gcctcccagg tggcgctgga gaactgttca gcagtggccg acacccgctg tggctgtaag  420
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tcttgtcacc ccgggatctg gcacccatgg tggagtccag tgtggcctta gctcccaagc  1740
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cacagcgagt gagtgaaccg gagcccagat gagagcgctt taatggggct gcgaggtggc  1860
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ctattcactc caccggggca gtgaaagggt cccggcagcg agtgggtc               1968
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SEQ ID NO: 176          moltype = AA  length = 417
FEATURE                 Location/Qualifiers
source                  1..417
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 176
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CTEPCGNSTC LVCPQDTFLA WENHHNSECA RCQACDEQAS QVALENCSAV ADTRCGCKPG  120
WFVECQVSQC VSSSPFYCQP CLDCGALHRH TRLLCSRRDT DCGTCLPGFY EHGDGCVSCP  180
TSTLGSCPER CAAVCGWRQM FWVQVLLAGL VVPLLLGATL TYTYRHCWPH KPLVTADEAG  240
MEALTPPPAT HLSPLDSAHT LLAPPDSSEK ICTVQLVGNS WTPGYPETQE ALCPQVTWSW  300
DQLPSRALGP AAAPTLSPES PAGSPAMMLQ PGPQLYDVMD AVPARRWKEF VRTLGLREAE  360
IEAVEVEIGR FRDQQYEMLK RWRQQQPAGL GAVYAALERM GLDGCVEDLR SRLQRGP     417

SEQ ID NO: 177          moltype = DNA  length = 1611
FEATURE                 Location/Qualifiers
source                  1..1611
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 177
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ggagcctgag aactgagctt actcgggcaa atgctagggc ttcagaaatg gaggagctgc  180
ctaggaggga gaggtcacct cctggggcag ccacaccagg gtcaactgca cgtgttctcc  240
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gcggcatgtc tggcaggtgt gactgtgcca gtgagtccca gaagaggtat ggcccgtttt  360
gttgcagggg ctgcccaaag ggacactaca tgaaggcccc ctgcgcagaa ccctgtggca  420
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ccgagccatg tgggaaaagc tcacctttct cttgtgtccc atgcggggct acaacaccag  660
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tagcccgagt ttggacttgg tattaaattt cgtaagaaaa gcagctgctt g           1611

SEQ ID NO: 178          moltype = AA  length = 387
FEATURE                 Location/Qualifiers
source                  1..387
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 178
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YGPFCCRGCP KGHYMKAPCA EPCGNSTCLP CPSDTFLTRD NHFKTDCTRC QVCDEEALQV  120
TLENCSAKSD THCGCQSGWC VDCSTEPCGK SSPFSCVPCG ATTPVHEAPT PLFWVQVLLG  180
VAFLFGAILI CAYCRWQPCK AVVTADTAGT ETLASPQTAH LSASDSAHTL LAPPSSTGKI  240
CTTVQLVGNN WTPGLSQTQE VVCGQASQPW DQLPNRTLGT PLASPLSPAP PAGSPAAVLQ  300
PGPQLYDVMD AVPARRWKEF VRTLGLREAE IEAVEVEICR FRDQQYEMLK RWRQQQPAGL  360
GAIYAALERM GLEGCAEDLR SRLQRGP                                      387

SEQ ID NO: 179          moltype = DNA  length = 1140
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source                  1..1140
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 179
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gggcgctgga ggggccaggc ctgtcgctgc tgtgcctggt gttggcgctg cctgccctgc  180
tgccggtgcc ggctgtacgc ggagtggcag aaacacccac ctacccctgg cgggacgcag  240
agacagggga gcggctggtg tgcgcccagt gcccccccagg cacctttgtg cagcggccgt  300
gccgccgaga cagccccacg acgtgtggcc cgtgtccacc gcgccactac acgcagttct  360
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acgctggttt ctgcttggag cacgcatcgt gtccacctgg tgccggcgtg attgccccgg  540
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gctccagctc agagcagtgc cagccccacc gcaactgcac ggccctgggc ctggccctca  660
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gcaccagggt accaggagct gaggagtgtg agcgtgccgt catcgacttt gtggctttcc  780
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cctggccccc tcttatttat tctacatcct tggcacccca cttgcactga aagaggcttt  1080
tttttaaata gaagaaatga ggtttcttaa agcttatttt tataaagctt tttcataaaa  1140

SEQ ID NO: 180          moltype = AA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 180
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PCRRDSPTTC GPCPPRHYTQ FWNYLERCRY CNVLCGEREE EARACHATHN RACRCRTGFF  120
AHAGFCLEHA SCPPGAGVIA PGTPSQNTQC QPCPPGTFSA SSSSSEQCQP HRNCTALGLA  180
LNVPGSSSHD TLCTSCTGFP LSTRVPGAEE CERAVIDFVA FQDISIKRLQ RLLQALEAPE  240
GWGPTPRAGR AALQLKLRRR LTELLGAQDG ALLVRLLQAL RVARMPGLER SVRERFLPVH  300

SEQ ID NO: 181          moltype = DNA  length = 1805
FEATURE                 Location/Qualifiers
source                  1..1805
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 181
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ccatatcccc agatctactg ggtggacagc agtgccagct ctccctgggc ccctccaggc  180
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ccaccgccac cgccaccact accacctccg ccgccgccgc caccactgcc tccactaccg  300
ctgccacccc tgaagaagag agggaaccac agcacaggcc tgtgtctcct tgtgatgttt  360
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ggttcaaaat gtctgtagct cctcaactca cctaatgttt atgagccaga caaatggagg  1140
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gcttaaaaat cattgattgt cagctactaa tgatgttttc ctataatata ataaatattt  1740
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aataa                                                              1805

SEQ ID NO: 182          moltype = AA  length = 281
FEATURE                 Location/Qualifiers
source                  1..281
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 182
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MHTASSLEKQ IGHPSPPPEK KELRKVAHLT GKSNSRSMPL EWEDTYGIVL LSGVKYKKGG  180
LVINETGLYF VYSKVYFRGQ SCNNLPLSHK VYMRNSKYPQ DLVMMEGKMM SYCTTGQMWA  240
RSSYLGAVFN LTSADHLYVN VSELSLVNFE ESQTFFGLYK L                      281

SEQ ID NO: 183          moltype = DNA  length = 1935
FEATURE                 Location/Qualifiers
source                  1..1935
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 183
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cttttattat cagctactga tgctgttttt ctttaataca actagtattt atgctctgaa  1860
catcctaatg aggaaaagac aaataaaatt atgttataga atacagaaat gccttaagga  1920
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SEQ ID NO: 184 moltype = AA length = 279
FEATURE Location/Qualifiers
source 1..279
mol_type = protein
organism = Mus musculus

SEQUENCE: 184

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KVSSFEKQIA NPSTPSEKKE PRSVAHLTGN PHSRSIPLEW EDTYGTALIS GVKYKKGGLV  180
INETGLYFVY SKVYFRGQSC NNQPLNHKVY MRNSKYPEDL VLMEEKRLNY CTTGQIWAHS  240
SYLGAVFNLT SADHLYVNIS QLSLINFEES KTFFGLYKL                         279
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SEQ ID NO: 185 moltype = DNA length = 1713
FEATURE Location/Qualifiers
source 1..1713
mol_type = genomic DNA
organism = Homo sapiens

SEQUENCE: 185

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ccttctgatc attgcagttt tctctcaaat atgaacactt tataattgta tgttcttttt  1680
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agaccccata aatcctgtat acatcaaaga gaa                                1713

SEQ ID NO: 186          moltype = AA  length = 364
FEATURE                 Location/Qualifiers
source                  1..364
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 186
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IVWTNGTHVT YRKDTRYKLL GDLSRRDVSL TIENTAVSDS GVYCCRVEHR GWFNDMKITV  120
SLEIVPPKVT TTPIVTTVPT VTTVRTSTTV PTTTTVPMTT VPTTTVPTTM SIPTTTTVLT  180
TMTVSTTTSV PTTTSIPTTT SVPVTTTVST FVPPMPLPRQ NHEPVATSPS SPQPAETHPT  240
TLQGAIRREP TSSPLYSYTT DGNDTVTESS DGLWNNNQTQ LFLEHSLLTA NTTKGIYAGV  300
CISVLVLLAL LGVIIAKKYF FKKEVQQLSV SFSSLQIKAL QNAVEKEVQA EDNIYIENSL  360
YATD                                                                364

SEQ ID NO: 187          moltype = DNA  length = 1909
FEATURE                 Location/Qualifiers
source                  1..1909
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 187
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acttactcaa catatcgtgg aatcacaacg acatgttggg gccgagggca atgcccatct  180
tctgcttgtc aaaatacact tatttggacc aatggacatc gtgtcaccta tcagaagagc  240
agtcggtaca acttaaaggg gcatatttca gaaggagatg tgtccttgac gatagagaac  300
tctgttgaga gtgacagtgg tctgtattgt tgtcgagtgg agattcctgg atggtttaat  360
gatcagaaag tgaccttttc attgcaagtt aaaccagaga ttcccacacg tcctccaaga  420
agacccacaa ctacaaggcc cacagctaca ggaagaccca cgactatttc aacaagatcc  480
acacatgtac caacatcaac cagagtctct acctccactc ctccaacatc tacacacaca  540
tggactcaca aaccagaacc cactacattt tgtccccatg agacaacagc tgaggtgaca  600
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tatagttaaa ttcatttccg aaagacatag catcttcccc aatgggtcag tttgtcaaaa  1860
tcaataaaat attttgtttt gctaagaatt aaaaaaaaaa aaaaaaaaa              1909

SEQ ID NO: 188          moltype = AA  length = 305
FEATURE                 Location/Qualifiers
source                  1..305
                        mol_type = protein
                        organism = Mus musculus
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VTFSLQVKPE IPTRPPRRPT TTRPTATGRP TTISTRSTHV PTSTRVSTST PPTSTHTWTH  180
KPEPTTFCPH ETTAEVTGIP SHTPTDWNGT VTSSGDTWSN HTEAIPPGKP QKNPTKGFYV  240
GICIAALLLL LLVSTVAITR YILMKRKSAS LSVVAFRVSK IEALQNAAVV HSRAEDNIYI  300
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SEQ ID NO: 189          moltype = DNA  length = 2097
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source                  1..2097
                        mol_type = genomic DNA
                        organism = Homo sapiens
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gatggttctt agactcccca gacaggccct ggaacccccc caccttctcc ccagccctgc  180
tcgtggtgac cgaaggggac aacgccacct tcacctgcag cttctccaac acatcggaga  240
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ctagtacccc cgccgtggcc tatccactcc tcacatccac acactgcacc cccactcctg  1980
gggcagggcc accagcatcc aggcggccag caggcacctg agtggctggg acaagggatc  2040
ccccttccct gtggttctat tatattataa ttataattaa atatgagagc atgctaa     2097
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FEATURE                 Location/Qualifiers
source                  1..288
                        mol_type = protein
                        organism = Homo sapiens
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YLCGAISLAP KAQIKESLRA ELRVTERRAE VPTAHPSPSP RPAGQFQTLV VGVVGGLLGS  180
LVLLVWVLAV ICSRAARGTI GARRTGQPLK EDPSAVPVFS VDYGELDFQW REKTPEPPVP  240
CVPEQTEYAT IVFPSGMGTS SPARRGSADG PRSAQPLRPE DGHCSWPL               288
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SEQ ID NO: 191          moltype = DNA  length = 1933
FEATURE                 Location/Qualifiers
source                  1..1933
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 191
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gcctggctca cagtgtcaga gggagcaaat gccaccttca cctgcagctt gtccaactgg  240
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ccaaaagctt taa                                                     1933

SEQ ID NO: 192          moltype = DNA  length = 696
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misc_feature            1..696
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..696
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 192
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ggcacccaga ccgccaagct gaaggtgacc aagggtggcc ccctgccctt ctcctgggac  180
atcctgtccc ctcagttcat gtacggctcc agggccttca ccaagcaccc cgccgacatc  240
cccgactact ataagcagtc cttccccgag ggcttcaagt gggagcgcgt gatgaacttc  300
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acaatgggct gggaagcgtc caccgagcgg ttgtaccccg aggacggcgt gctgaagggc  480
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gacatcacct cccacaacga ggactacacc gtggtggaac agtacgaacg ctccgagggc  660
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SEQ ID NO: 193          moltype = AA  length = 232
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REGION                  1..232
                        note = Description of Artificial Sequence: Synthetic
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source                  1..232
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 193
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ILSPQFMYGS RAFTKHPADI PDYYKQSFPE GFKWERVMNF EDGGAVTVTQ DTSLEDGTLI  120
YKVKLRGTNF PPDGPVMQKK TMGWEASTER LYPEDGVLKG DIKMALRLKD GGRYLADFKT  180
TYKAKKPVQM PGAYNVDRKL DITSHNEDYT VVEQYERSEG RHSTGGMDEL YK          232

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misc_feature            1..3861
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                         polynucleotide
source                  1..3861
                        mol_type = other DNA
                        organism = synthetic construct
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tattttcatt acatctgtgt gttggttttt tgtgtgaatc gatagtacta acatacgctc  3780
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caggtgccag aacatttctc t                                            3861
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SEQ ID NO: 195          moltype = AA  length = 171
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REGION                  1..171
                        note = Description of Artificial Sequence: Synthetic
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source                  1..171
                        mol_type = protein
                        organism = synthetic construct
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IIPYEGLSGD QMGQIEKIFK VVYPVDDHHF KVILHYGTLV IDGVTPNMID YFGRPYEGIA  120
VFDGKKITVT GTLWNGNKII DERLINPDGS LLFRVTINGV TGWRLCERIL A           171
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SEQ ID NO: 196          moltype = DNA  length = 2590
FEATURE                 Location/Qualifiers
source                  1..2590
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 196
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tgacaatgga ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta  840
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aacttctcag aaaaccacca caaaaaccac cacaccaaat gctcaagcaa cacggagtac  1080
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acacaagtat acagactgtt cctagtttct tagacttatc tgcatattgg ataaaataaa  1320
tgcaattgtg ctcttcattt aggatgcttt cattgtcttt aagatgtgtt aggaatgtca  1380
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gaggaatata gaatgaaaga ctgaatcttc ctttgttgca caaatagagt ttggaaaaag  1860
cctgtgaaag gtgtcttctt tgacttaatg tctttaaaag tatccagaga tactacaata  1920
ttaacataag aaaagattat atattatttc tgaatcgaga tgtccatagt caaatttgta  1980
aatcttattc ttttgtaata tttatttata tttatttatg acagtgaaca ttctgatttt  2040
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tcctccttaa                                                         2590
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SEQ ID NO: 197 moltype = AA length = 381
FEATURE Location/Qualifiers
source 1..381
mol_type = protein
organism = Homo sapiens
SEQUENCE: 197

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ITYKCEESFV KIPGEKDSVI CLKGSQWSDI EEFCNRSCEV PTRLNSASLK QPYITQNYFP  120
VGTVVEYECR PGYRREPSLS PKLTCLQNLK WSTAVEFCKK KSCPNPGEIR NGQIDVPGGI  180
LFGATISFSC NTGYKLFGST SSFCLISGSS VQWSDPLPEC REIYCPAPPQ IDNGIIQGER  240
DHYGYRQSVT YACNKGFTMI GEHSIYCTVN NDEGEWSGPP PECRGKSLTS KVPPTVQKPT  300
TVNVPTTEVS PTSQKTTTKT TTPNAQATRS TPVSRTTKHF HETTPNKGSG TTSGTTRLLS  360
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SEQ ID NO: 198 moltype = AA length = 128
FEATURE Location/Qualifiers
source 1..128
mol_type = protein
organism = Homo sapiens
SEQUENCE: 198

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YNKCWKFEHC NFNDVTTRLR ENELTYYCCK KDLCNFNEQL ENGGTSLSEK TVLLLVTPFL  120
AAAWSLHP                                                           128
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SEQ ID NO: 199 moltype = DNA length = 1936
FEATURE Location/Qualifiers
source 1..1936
mol_type = genomic DNA
organism = Homo sapiens
SEQUENCE: 199

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atttcccaag aagtgcgagg agatgtcttc ccctcgtaca cctgcacgtg ccttaagggc  240
tacgcgggca accactgtga gacgaaatgt gtcgagccac tgggcctgga gaatgggaac  300
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gagtttgtgg gtaactggaa caaaaacgcg gtgcatgtca acctgtttga gacccctgtg  660
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ggtctatggg gagaaaggga gcgaggtcag aggagggcat gggttggcag ggtgggcgtt  1860
tggggccctc tatgctggct tttcacccca gaggacacag gcagcttcca aaatatattt  1920
atcttcttca cgggaa                                                  1936

SEQ ID NO: 200          moltype = AA  length = 387
FEATURE                 Location/Qualifiers
source                  1..387
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 200
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YAGNHCETKC VEPLGLENGN IANSQIAASS VRVTFLGLQH WVPELARLNR AGMVNAWTPS  120
SNDDNPWIQV NLLRRMWVTG VVTQGASRLA SHEYLKAFKV AYSLNGHEFD FIHDVNKKHK  180
EFVGNWNKNA VHVNLFETPV EAQYVRLYPT SCHTACTLRF ELLGCELNGC ANPLGLKNNS  240
IPDKQITASS SYKTWGLHLF SWNPSYARLD KQGNFNAWVA GSYGNDQWLQ VDLGSSKEVT  300
GIITQGARNF GSVQFVASYK VAYSNDSANW TEYQDPRTGS SKIFPGNWDN HSHKKNLFET  360
PILARYVRIL PVAWHNRIAL RLELLGC                                      387

SEQ ID NO: 201          moltype = DNA  length = 2221
FEATURE                 Location/Qualifiers
source                  1..2221
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 201
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cttgcccaca caccccaaac ctgtgtgcag gatccgcctc catggagcta cagcctcctg  180
aagcctcgat cgccgtcgtg tcgattccgc gccagttgcc tggctcacat tcggaggctg  240
gtgtccaggg tctcagcgcg ggggacgact cagagttggg gtctcactgt gttgcccaga  300
ctggtctcga actcttggcc tcaggtgatc ctcttccctc agcttcccag aatgccgaga  360
tgatagagac ggggtctgac tgtgttaccc aggctggtct tcaactcttg gcctcaagtg  420
atcctcctgc cttagcttcc aagaatgctg aggttacagg caccatgagc caggacaccg  480
aggtggatat gaaggaggtg gagctgaatg agttagagcc cgagaagcag ccgatgaacg  540
cggcgtctgg ggcggccatg tccctggcgg gagccgagaa gaatggtctg gtgaagatca  600
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ccctttggct tctgattttt ctctttttta aaaacaaaca aacaaactgt tgcagattat  2160
gagtgaaccc ccaaataggg tgttttctgc cttcaaataa aagtcacccc tgcatggtga  2220
a                                                                  2221

SEQ ID NO: 202          moltype = AA  length = 630
FEATURE                 Location/Qualifiers
source                  1..630
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 202
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EKQPMNAASG AAMSLAGAEK NGLVKIKVAE DEAEAAAAAK FTGLSKEELL KVAGSPGWVR  180
TRWALLLLFW LGWLGMLAGA VVIIVRAPRC RELPAQKWWH TGALYRIGDL QAFQGHGAGN  240
LAGLKGRLDY LSSLKVKGLV LGPIHKNQKD DVAQTDLLQI DPNFGSKEDF DSLLQSAKKK  300
SIRVILDLTP NYRGENSWFS TQVDTVATKV KDALEFWLQA GVDGFQVRDI ENLKDASSFL  360
AEWQNITKGF SEDRLLIAGT NSSDLQQILS LLESNKDLLL TSSYLSDSGS TGEHTKSLVT  420
QYLNATGNRW CSWSLSQARL LTSFLPAQLL RLYQLMLFTL PGTPVFSYGD EIGLDAAALP  480
```

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GQPMEAPVML WDESSFPDIP GAVSANMTVK GQSEDPGSLL SLFRRLSDQR SKERSLLHGD  540
FHAFSAGPGL FSYIRHWDQN ERFLVVLNFG DVGLSAGLQA SDLPASASLP AKADLLLSTQ  600
PGREEGSPLE LERLKLEPHE GLLLRFPYAA                                   630

SEQ ID NO: 203          moltype = DNA  length = 2886
FEATURE                 Location/Qualifiers
source                  1..2886
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 203
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gccctgggac ctggccagct ctgttagtgg gagagatcgc tggcaccata gccttatggc  2820
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caataa                                                             2886

SEQ ID NO: 204          moltype = AA  length = 801
FEATURE                 Location/Qualifiers
source                  1..801
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 204
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DVNYEPDLDF HQGRLYWSDL QAMFLQFLGE GRLEDTIRQT SLRERVAGSA GMAALTQDIR  180
AALSRQKLDH VWTDTHYVGL QFPDPAHPNT LHWVDEAGKV GEQLPLEDPD VYCPYSAIGN  240
VTGELVYAHY GRPEDLQDLR ARGVDPVGRL LLVRVGVISF AQKVTNAQDF GAQGVLIYPE  300
PADFSQDPPK PSLSSQQAVY GHVHLGTGDP YTPGFPSFNQ TQFPPVASSG LPSIPAQPIS  360
ADIASRLLRK LKGPVAPQEW QGSLLGSPYH LGPGPRLRLV VNNHRTSTPI NNIFGCIEGR  420
SEPDHYVVIG AQRDAWGPGA AKSAVGTAIL LELVRTFSSM VSNGFRPRRS LLFISWDGGD  480
FGSVGSTEWL EGYLSVLHLK AVVYVSLDNA VLGDDKFHAK TSPLLTSLIE SVLKQVDSPN  540
HSGQTLYEQV VFTNPSWDAE VIRPLPMDSS AYSFTAFVGV PAVEFSFMED DQAYPFLHTK  600
EDTYENLHKV LQGRLPAVAQ AVAQLAGQLL IRLSHDRLLP LDFGRYGDVV LRHIGNLNEF  660
SGDLKARGLT LQWVYSARGD YIRAAEKLRQ EIYSSEERDE RLTRMYNVRI MRVEFYFLSQ  720
YVSPADSPFR HIFMGRGDHT LGALLDHLRL LRSNSSGTPG ATSSTGFQES RFRRQLALLT  780
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WTLQGAANAL SGDVWNIDNN F                                                801

SEQ ID NO: 205          moltype = DNA  length = 11158
FEATURE                 Location/Qualifiers
source                  1..11158
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 205
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tgtgctgctg ttaacccgtg aggaggcggc ggcggcggca gcggcagcgg aagatggtgt  180
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accaaaaaca ccagcgtgcc aaaagagcag tctcacatga agaccaattt ttacgtctag  360
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acactggaca tatttatggt gaagaaggaa gttttagcca tgggtctgtt attgatggaa  540
gatttgaagg attcatccag actcgtggtg gcacatttta tgttgagcca gcagagagat  600
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cagccattgg ttgctgttca ggtcagcttt gctcctaaca acactgggaa agaagtaaca  900
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SEQ ID NO: 210          moltype = AA  length = 279
FEATURE                 Location/Qualifiers
source                  1..279
                        mol_type = protein
                        organism = Homo sapiens
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MLQTLNDEVP KYRDQIPSPG LMVFPKPVTA LEYTFSRSDP TSYAGYIEDL KKFLKPYTLE  120
EQKNLTVCPD GALFEQKGPV YVACQFPISL LQACSGMNDP DFGYSQGNPC ILVKMNRIIG  180
LKPEGVPRID CVSKNEDIPN VAVYPHNGMI DLKYFPYYGK KLHVGYLQPL VAVQVSFAPN  240
NTGKEVTVEC KIDGSANLKS QDDRDKFLGR VMFKITARA                         279

SEQ ID NO: 211          moltype = DNA  length = 5306
FEATURE                 Location/Qualifiers
source                  1..5306
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 211
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cctgctgaaa atgactgaat ataaacttgt ggtagttgga gctggtggcg taggcaagag  240
tgccttgacg atacagctaa ttcagaatca ttttgtggac gaatatgatc caacaataga  300
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gtgaagtgat ctaaaatttg taatattttt gtcatgaact gtactactcc taattattgt  5280
aatgtaataa aaatagttac agtgac                                       5306

SEQ ID NO: 212          moltype = AA  length = 188
FEATURE                 Location/Qualifiers
source                  1..188
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 212
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QEEYSAMRDQ YMRTGEGFLC VFAINNTKSF EDIHHYREQI KRVKDSEDVP MVLVGNKCDL  120
PSRTVDTKQA QDLARSYGIP FIETSAKTRQ GVDDAFYTLV REIRKHKEKM SKDGKKKKKK  180
SKTKCVIM                                                           188

SEQ ID NO: 213          moltype = DNA  length = 42
FEATURE                 Location/Qualifiers
misc_feature            1..42
                        note = Description of Artificial Sequence: Synthetic
                         oligonucleotide
source                  1..42
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 213
aaaaagaaga aaaagaagaa gaagacaaag tgtgtaatta tg                     42

SEQ ID NO: 214          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Description of Artificial Sequence: Synthetic peptide
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 214
KKKKKKKKTK CVIM                                                    14

SEQ ID NO: 215          moltype = DNA  length = 4296
FEATURE                 Location/Qualifiers
source                  1..4296
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 215
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SEQ ID NO: 216 moltype = AA length = 332
FEATURE Location/Qualifiers
source 1..332
mol_type = protein
organism = Homo sapiens

SEQUENCE: 216

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AAEGEAASAA SSTSSPKAED GATPSPSNET PKKKKKRFSF KKSFKLSGFS FKKNKKEAGE  180
GGEAEAPAAE GGKDEAAGGA AAAAAEAGAA SGEQAAAPGE EAAAGEEGAA GGDPQEAKPQ  240
EAAVAPEKPP ASDETKAAEE PSKVEEKKAE EAGASAAACE APSAAGPGAP PEQEAAPAEE  300
PAAAAASSAC AAPSQEAQPE CSPEAPPAEA AE                                332
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SEQ ID NO: 217 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
note = Description of Artificial Sequence: Synthetic
oligonucleotide
source 1..24
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 217

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SEQ ID NO: 218 moltype = AA length = 8
FEATURE Location/Qualifiers
REGION 1..8
note = Description of Artificial Sequence: Synthetic peptide
source 1..8
mol_type = protein
organism = synthetic construct

SEQUENCE: 218

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SEQ ID NO: 219 moltype = DNA length = 2079
FEATURE Location/Qualifiers
misc_feature 1..2079
note = Description of Artificial Sequence: Synthetic
polynucleotide
source 1..2079
mol_type = other DNA
organism = synthetic construct

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aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca  480
tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat  540
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc  600
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac  660
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcacga ggctctgcac  720
aaccactaca cgcagaagag cctctccctg tctccgggta aagccagcgg aagtggcgga  780
ggaggcggtc ctggagaagg tgcctatgta taccgctcag cattcagtgt gggattggag  840
acttacgtta ctatccccaa catgcccatt cgctttacca agatcttcta caatcagcaa  900
aaccactatg atggctccac tggtaaattc cactgcaaca ttcctgggct gtactacttt  960
gcctaccaca tcacagtcta tatgaaggat gtgaaggtca gcctcttcaa gaaggacaag  1020
gctatgctct tcacctatga tcagtaccag gaaaataatg tggaccaggc ctccggctct  1080
gtgctcctgc atctggaggt gggcgaccaa gtctggctcc aggtgtatgg ggaaggagag  1140
cgtaatggac tctatgctga taatgacaat gactccacct tcacaggctt tcttctctac  1200
catgacacca actctagaaa gcttcctgga gaaggtgcct atgtataccg ctcagcattc  1260
agtgtgggat tggagactta cgttactatc cccaacatgc ccattcgctt taccaagatc  1320
ttctacaatc agcaaaacca ctatgatggc tccactggta aattccactg caacattcct  1380
gggctgtact actttgccta ccacatcaca gtctatatga aggatgtgaa ggtcagcctc  1440
ttcaagaagg acaaggctat gctcttcacc tatgatcagt accaggaaaa taatgtggac  1500
caggcctccg gctctgtgct cctgcatctg gaggtgggcg accaagtctg gctccaggtg  1560
tatggggaag gagagcgtaa tggactctat gctgataatg acaatgactc caccttcaca  1620
ggctttcttc tctaccatga caccaacact agtcctggag aaggtgccta tgtataccgc  1680
tcagcattca gtgtgggatt ggagacttac gttactatcc ccaacatgcc cattcgcttt  1740
accaagatct tctacaatca gcaaaaccac tatgatggct ccactggtaa attccactgc  1800
aacattcctg ggctgtacta ctttgcctac cacatcacag tctatatgaa ggatgtgaag  1860
gtcagcctct tcaagaagga caaggctatg ctcttcacct atgatcagta ccaggaaaat  1920
aatgtggacc aggcctccgg ctctgtgctc ctgcatctgg aggtgggcga ccaagtctgg  1980
ctccaggtgt atggggaagg agagcgtaat ggactctatg ctgataatga caatgactcc  2040
accttcacag gctttcttct ctaccatgac accaactaa                         2079

SEQ ID NO: 220          moltype = AA  length = 227
FEATURE                 Location/Qualifiers
REGION                  1..227
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..227
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 220
DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD  60
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK  120
GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS  180
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK                227

SEQ ID NO: 221          moltype = DNA  length = 27
FEATURE                 Location/Qualifiers
misc_feature            1..27
                        note = Description of Artificial Sequence: Synthetic
                         oligonucleotide
source                  1..27
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 221
gctactaact tcagcctgct gaagcag                                      27

SEQ ID NO: 222          moltype = AA  length = 17
FEATURE                 Location/Qualifiers
REGION                  1..17
                        note = Description of Artificial Sequence: Synthetic peptide
source                  1..17
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 222
ATNFSLKQAG DVENPGP                                                 17

SEQ ID NO: 223          moltype = DNA  length = 1290
FEATURE                 Location/Qualifiers
misc_feature            1..1290
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1290
                        mol_type = other DNA
```

```
                        organism = synthetic construct
SEQUENCE: 223
atggcttgcc ttggatttca gcggcacaag gctcagctga acctggctac caggacctgg  60
ccctgcactc tcctgttttt tcttctcttc atccctgtct tctgcaaagc aatgcacgtg  120
gcccagcctg ctgtggtact ggccagcagc cgaggcatcg ccagctttgt gtgtgagtat  180
gcatctccag gcaaagccac tgaggtccgg gtgacagtgc ttcggcaggc tgacagccag  240
gtgactgaag tctgtgcggc aacctacatg atggggaatg agttgacctt cctagatgat  300
tccatctgca cgggcacctc cagtggaaat caagtgaacc tcactatcca aggactgagg  360
gccatggaca cgggactcta catctgcaag gtggagctca tgtacccacc gccatactac  420
ctgggcatag gcaacggaac ccagatttat gtaattgatc cagaaccgtg cccagattct  480
gacatcgatg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga  540
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct  600
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg  660
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac  720
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag  780
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc  840
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag  900
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc  960
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg  1020
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg  1080
cagcagggga acgtcttctc atgctccgtg atgcacgagg ctctgcacaa ccactacacg  1140
cagaagagcc tctccctgtc tccgggtaaa atcgatccaa ataaaggaag tggaaccact  1200
tcaggtacta cccgtcttct atctgggcac acgtgtttca cgttgacagg tttgcttggg  1260
acgctagtaa ccatgggctt gctgacttag                                   1290

SEQ ID NO: 224          moltype = AA  length = 429
FEATURE                 Location/Qualifiers
REGION                  1..429
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..429
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 224
MACLGFQRHK AQLNLATRTW PCTLLFFLLF IPVFCKAMHV AQPAVVLASS RGIASFVCEY  60
ASPGKATEVR VTVLRQADSQ VTEVCAATYM MGNELTFLDD SICTGTSSGN QVNLTIQGLR  120
AMDTGLYICK VELMYPPPYY LGIGNGTQIY VIDPEPCPDS DIDDKTHTCP PCPAPELLGG  180
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  240
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE  300
MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  360
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK IDPNKGSGTT SGTTRLLSGH TCFTLTGLLG  420
TLVTMGLLT                                                          429

SEQ ID NO: 225          moltype = DNA  length = 828
FEATURE                 Location/Qualifiers
misc_feature            1..828
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..828
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 225
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc agaactacct ctggcacatc ctccaaatga aaggccaaat  720
aaaggaagtg gaaccacttc aggtactacc cgtcttctat ctgggcacac gtgtttcacg  780
ttgacaggtt tgcttgggac gctagtaacc atgggcttgc tgacttag               828

SEQ ID NO: 226          moltype = AA  length = 275
FEATURE                 Location/Qualifiers
REGION                  1..275
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..275
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 226
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
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TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERPN  240
KGSGTTSGTT RLLSGHTCFT LTGLLGTLVT MGLLT                             275

SEQ ID NO: 227         moltype = DNA  length = 1518
FEATURE                Location/Qualifiers
misc_feature           1..1518
                       note = Description of Artificial Sequence: Synthetic
                        polynucleotide
source                 1..1518
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 227
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc agaactacct ctggcacatc ctccaaatga aaggatcgat  720
gtcgagccac tgggcatgga gaatgggaac attgccaact cacagatcgc cgcctcatct  780
gtgcgtgtga ccttcttggg tttgcagcat tgggtcccgg agctggcccg cctgaaccgc  840
gcaggcatgg tcaatgcctg gacacccagc agcaatgacg ataacccctg gatccaggtg  900
aacctgctgc ggaggatgtg ggtaacaggt gtggtgacgc agggtgccag ccgcttggcc  960
agtcatgagt acctgaaggc cttcaaggtg gcctacagcc ttaatggaca cgaattcgat  1020
ttcatccatg atgttaataa aaaacacaag gagtttgtgg gtaactggaa caaaaacgcg  1080
gtgcatgtca acctgtttga gacccctgtg gaggctcagt acgtgagatt gtaccccacg  1140
agctgccaca cggcctgcac tctgcgcttt gagctactgg gctgtgagct gaacggatgc  1200
gccaatcccc tgggcctgaa gaataacagc atccctgaca agcagatcac ggcctccagc  1260
agctacaaga cctggggctt gcatctcttc agctggaacc cctcctatgc acggctggac  1320
aagcagggca acttcaacgc ctgggttgcg gggagctacg gtaacgatca gtggctgcag  1380
atcttccctg gcaactggga caaccactcc cacaagaaga acttgtttga gacgcccatc  1440
ctggctcgct atgtgcgcat cctgcctgta gcctggcaca accgcatcgc cctgcgcctg  1500
gagctgctgg gctgttag                                                1518

SEQ ID NO: 228         moltype = AA  length = 505
FEATURE                Location/Qualifiers
REGION                 1..505
                       note = Description of Artificial Sequence: Synthetic
                        polypeptide
source                 1..505
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 228
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERID  240
VEPLGMENGN IANSQIAASS VRVTFLGLQH WVPELARLNR AGMVNAWTPS SNDDNPWIQV  300
NLLRRMWVTG VVTQGASRLA SHEYLKAFKV AYSLNGHEFD FIHDVNKKHK EFVGNWNKNA  360
VHVNLFETPV EAQYVRLYPT SCHTACTLRF ELLGCELNGC ANPLGLKNNS IPDKQITASS  420
SYKTWGLHLF SWNPSYARLD KQGNFNAWVA GSYGNDQWLQ IFPGNWDNHS HKKNLFETPI  480
LARYVRILPV AWHNRIALRL ELLGC                                        505

SEQ ID NO: 229         moltype = DNA  length = 1521
FEATURE                Location/Qualifiers
misc_feature           1..1521
                       note = Description of Artificial Sequence: Synthetic
                        polynucleotide
source                 1..1521
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 229
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc agaactacct ctggcacatc ctccaaatga aaggatcgat  720
```

```
gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc  780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca  840
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac  900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac  960
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag  1020
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa  1080
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag  1140
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag  1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc  1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg  1320
aacgtcttct catgctccgt gatgcacgag gctctgcaca accactacac gcagaagagc  1380
ctctccctgt ctccgggtaa aatcgatcca aataaaggaa gtggaaccac ttcaggtact  1440
acccgtcttc tatctgggca cacgtgtttc acgttgacag gtttgcttgg gacgctagta  1500
accatgggct tgctgactta g                                            1521
```

SEQ ID NO: 230 moltype = AA length = 506
FEATURE Location/Qualifiers
REGION 1..506
note = Description of Artificial Sequence: Synthetic polypeptide
source 1..506
mol_type = protein
organism = synthetic construct
SEQUENCE: 230

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MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERID  240
DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD  300
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK  360
GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS  420
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGKIDP NKGSGTTSGT  480
TRLLSGHTCF TLTGLLGTLV TMGLLT                                       506
```

SEQ ID NO: 231 moltype = DNA length = 1464
FEATURE Location/Qualifiers
misc_feature 1..1464
note = Description of Artificial Sequence: Synthetic polynucleotide
source 1..1464
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 231

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atgatcttcc tcctgctaat gttgagcctg gaattgcagc ttcaccagat agcagcttta  60
ttcacagtga cagtccctaa ggaactgtac ataatagagc atggcagcaa tgtgaccctg  120
gaatgcaact ttgacactgg aagtcatgtg aaccttggag caataacagc cagtttgcaa  180
aaggtggaaa atgatacatc cccacaccgt gaaagagcca ctttgctgga ggagcagctg  240
cccctaggga aggcctcgtt ccacatacct caagtccaag tgagggacga aggacagtac  300
caatgcataa tcatctatgg ggtcgcctgg gactacaagt acctgactct gaaagtcaaa  360
gcttcctaca ggaaaataaa cactcacatc ctaaaggttc cagaaacaga tgaggtagag  420
ctcacctgcc aggctacagg ttatcctctg gcagaagtat cctggccaaa cgtcagcgtt  480
cctgccaaca ccagccactc caggacccct gaaggcctct accaggtcac cagtgttctg  540
cgcctaaagc cacccccctgg cagaaacttc agctgtgtgt tctggaatac tcacgtgagg  600
gaacttactt tggccagcat tgaccttcaa agtcagatgg aacccaggac ccatccaact  660
atcgatgtcg agccactggg catggagaat gggaacattg ccaactcaca gatcgccgcc  720
tcatctgtgc gtgtgacctt cttgggtttg cagcattggg tcccggagct ggcccgcctg  780
aaccgcgcag gcatggtcaa tgcctggaca cccagcagca atgacgataa cccctggatc  840
caggtgaacc tgctgcggag gatgtgggta acaggtgtgg tgacgcaggg tgccagccgc  900
ttggccagtc atgagtacct gaaggccttc aaggtggcct acagccttaa tggacacgaa  960
ttcgatttca tccatgatgt taataaaaaa cacaaggagt ttgtgggtaa ctggaacaaa  1020
aacgcggtgc atgtcaacct gtttgagacc cctgtggagg ctcagtacgt gagattgtac  1080
cccacgagct gccacacggc ctgcactctg cgctttgagc tactgggctg tgagctgaac  1140
ggatgcgcca atcccctggg cctgaagaat aacagcatcc ctgacaagca gatcacggcc  1200
tccagcagct acaagacctg gggcttgcat ctcttcagct ggaacccctc ctatgcacgg  1260
ctggacaagc agggcaactt caacgcctgg gttgcgggga gctacggtaa cgatcagtgg  1320
ctgcagatct tccctggcaa ctgggacaac cactcccaca agaagaactt gtttgagacg  1380
cccatcctgg ctcgctatgt gcgcatcctg cctgtagcct ggcacaaccg catcgccctg  1440
cgcctggagc tgctgggctg ttag                                         1464
```

SEQ ID NO: 232 moltype = AA length = 487
FEATURE Location/Qualifiers
REGION 1..487
note = Description of Artificial Sequence: Synthetic polypeptide
source 1..487
mol_type = protein
organism = synthetic construct
SEQUENCE: 232

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MIFLLLMLSL ELQLHQIAAL FTVTVPKELY IIEHGSNVTL ECNFDTGSHV NLGAITASLQ  60
```

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KVENDTSPHR ERATLLEEQL PLGKASFHIP QVQVRDEGQY QCIIIYGVAW DYKYLTLKVK  120
ASYRKINTHI LKVPETDEVE LTCQATGYPL AEVSWPNVSV PANTSHSRTP EGLYQVTSVL  180
RLKPPPGRNF SCVFWNTHVR ELTLASIDLQ SQMEPRTHPT IDVEPLGMEN GNIANSQIAA  240
SSVRVTFLGL QHWVPELARL NRAGMVNAWT PSSNDDNPWI QVNLLRRMWV TGVVTQGASR  300
LASHEYLKAF KVAYSLNGHE FDFIHDVNKK HKEFVGNWNK NAVHVNLFET PVEAQYVRLY  360
PTSCHTACTL RFELLGCELN GCANPLGLKN NSIPDKQITA SSSYKTWGLH LFSWNPSYAR  420
LDKQGNFNAW VAGSYGNDQW LQIFPGNWDN HSHKKNLFET PILARYVRIL PVAWHNRIAL  480
RLELLGC                                                            487

SEQ ID NO: 233          moltype = DNA  length = 1467
FEATURE                 Location/Qualifiers
misc_feature            1..1467
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1467
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 233
atgatcttcc tcctgctaat gttgagcctg gaattgcagc ttcaccagat agcagcttta  60
ttcacagtga cagtccctaa ggaactgtac ataatagagc atggcagcaa tgtgaccctg  120
gaatgcaact ttgacactgg aagtcatgtg aaccttggag caataacagc cagtttgcaa  180
aaggtggaaa atgatacatc cccacaccgt gaaagagcca ctttgctgga ggagcagctg  240
cccctaggga aggcctcgtt ccacatacct caagtccaag tgagggacga aggacagtac  300
caatgcataa tcatctatgg ggtcgcctgg gactacaagt acctgactct gaaagtcaaa  360
gcttcctaca ggaaaataaa cactcacatc ctaaaggttc cagaaacaga tgaggtagag  420
ctcacctgcc aggctacagg ttatcctctg gcagaagtat cctggccaaa cgtcagcgtt  480
cctgccaaca ccagccactc caggacccct gaaggcctct accaggtcac cagtgttctg  540
cgcctaaagc cacccccctgg cagaaacttc agctgtgtgt tctggaatac tcacgtgagg  600
gaacttactt tggccagcat tgaccttcaa agtcagatgg aacccaggac ccatccaact  660
atcgatgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg  720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag  780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac  840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc  900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag  960
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa  1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg  1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc  1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg  1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag  1260
caggggaacg tcttctcatg ctccgtgatg cacgaggctc tgcacaacca ctacacgcag  1320
aagagcctct ccctgtctcc gggtaaaatc gatccaaata aaggaagtgg aaccacttca  1380
ggtactaccc gtcttctatc tgggcacacg tgtttcacgt tgacaggttt gcttgggacg  1440
ctagtaacca tgggcttgct gacttag                                      1467

SEQ ID NO: 234          moltype = AA  length = 488
FEATURE                 Location/Qualifiers
REGION                  1..488
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..488
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 234
MIFLLLMLSL ELQLHQIAAL FTVTVPKELY IIEHGSNVTL ECNFDTGSHV NLGAITASLQ  60
KVENDTSPHR ERATLLEEQL PLGKASFHIP QVQVRDEGQY QCIIIYGVAW DYKYLTLKVK  120
ASYRKINTHI LKVPETDEVE LTCQATGYPL AEVSWPNVSV PANTSHSRTP EGLYQVTSVL  180
RLKPPPGRNF SCVFWNTHVR ELTLASIDLQ SQMEPRTHPT IDDKTHTCPP CPAPELLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSREEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ  420
QGNVFSCSVM HEALHNHYTQ KSLSLSPGKI DPNKGSGTTS GTTRLLSGHT CFTLTGLLGT  480
LVTMGLLT                                                           488

SEQ ID NO: 235          moltype = DNA  length = 930
FEATURE                 Location/Qualifiers
misc_feature            1..930
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..930
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 235
atgagccagg acaccgaggt ggatatgaag gaggtggagc tgaatgagtt agagcccgag  60
aagcagccga tgaacgcggc gtctggggcg gccatgtccc tggcgggagc cgagaagaat  120
ggtctggtga agatcaaggt ggcggaagac gaggcggagg cggcagccgc ggctaagttc  180
acgggcctgt ccaaggagga gctgctgaag gtggcaggca gccccggctg ggtacgcacc  240
cgctgggcac tgctgctgct cttctggctc ggctggctcg gcatgcttgc tggtgccgtg  300
gtcataatcg tggcctgccc ctgggccgtg tccggggctc gcgcctcgcc cggctccgcg  360
gccagcccga gactccgcga gggtcccgag ctttcgcccg acgatcccgc cggcctcttg  420
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gacctgcggc agggcatgtt tgcgcagctg gtggcccaaa atgttctgct gatcgatggg  480
cccctgagct ggtacagtga cccaggcctg gcaggcgtgt ccctgacggg gggcctgagc  540
tacaaagagg acacgaagga gctggtggtg gccaaggctg gagtctacta tgtcttcttt  600
caactagagc tgcggcgcgt ggtggccggc gagggctcag gctccgtttc acttgcgctg  660
cacctgcagc cactgcgctc tgctgctggg gccgccgccc tggctttgac cgtggacctg  720
ccacccgcct cctccgaggc tcggaactcg gccttcggtt tccagggccg cttgctgcac  780
ctgagtgccg gccagcgcct gggcgtccat cttcacactg aggccagggc acgccatgcc  840
tggcagctta cccagggcgc cacagtcttg ggactcttcc gggtgacccc cgaaatccca  900
gccggactcc cttcaccgag gtcggaataa                                   930
```

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SEQ ID NO: 236          moltype = AA  length = 309
FEATURE                 Location/Qualifiers
REGION                  1..309
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..309
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 236
MSQDTEVDMK EVELNELEPE KQPMNAASGA AMSLAGAEKN GLVKIKVAED EAEAAAAAKF  60
TGLSKEELLK VAGSPGWVRT RWALLLLFWL GWLGMLAGAV VIIVACPWAV SGARASPGSA  120
ASPRLREGPE LSPDDPAGLL DLRQGMFAQL VAQNVLLIDG PLSWYSDPGL AGVSLTGGLS  180
YKEDTKELVV AKAGVYYVFF QLELRRVVAG EGSGSVSLAL HLQPLRSAAG AAALALTVDL  240
PPASSEARNS AFGFQGRLLH LSAGQRLGVH LHTEARARHA WQLTQGATVL GLFRVTPEIP  300
AGLPSPRSE                                                          309
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SEQ ID NO: 237          moltype = DNA  length = 1515
FEATURE                 Location/Qualifiers
misc_feature            1..1515
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1515
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 237
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc agaactacct ctggcacatc ctccaaatga aagggagtcc  720
aaatatggtc ccccatgccc atcatgccca gcacctgagt tcctgggggg accatcagtc  780
ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg  840
tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat  900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac  960
cgtgtggtca gggtcctcac cgtcctgcac caggactggc tgaacggtaa ggagtacaag  1020
tgcaaggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa  1080
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag  1140
aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag  1200
tgggagagca atgggcagcc ggaggacaac tacaagacca cgcctcccgt gctggactcc  1260
gacggctcct tcttcctcta cagcaggcta accgtggaca agagcaggtg gcaggagggg  1320
aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc  1380
ctctccctgt ctccgggtaa accaaataaa ggaagtggaa ccacttcagg tactacccgt  1440
cttctatctg ggcacacgtg tttcacgttg acaggtttgc ttgggacgct agtaaccatg  1500
ggcttgctga cttag                                                   1515
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SEQ ID NO: 238          moltype = AA  length = 504
FEATURE                 Location/Qualifiers
REGION                  1..504
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..504
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 238
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERES  240
KYGPPCPSCP APEFLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD  300
GVEVHNAKTK PREEQFNSTY RVVRVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK  360
GQPREPQVYT LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPEDN YKTTPPVLDS  420
DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE ALHNHYTQKS LSLSPGKPNK GSGTTSGTTR  480
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LLSGHTCFTL TGLLGTLVTM GLLT                                          504

SEQ ID NO: 239          moltype = DNA  length = 1941
FEATURE                 Location/Qualifiers
misc_feature            1..1941
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1941
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 239
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc agaactacct ctggcacatc ctccaaatga aaggccaaat  720
aaaggaagtg gaaccacttc aggtactacc cgtcttctat ctgggcacac gtgtttcacg  780
ttgacaggtt tgcttgggac gctagtaacc atgggcttgc tgactggaag cggagctact  840
aacttcagcc tgctgaagca ggctggcgac gtggaggaga accctggacc tatggcaaag  900
gtgttcagtt tcatccttgt taccaccgct ctgacaatgg gcagggaaat ttcggcgctc  960
gaggactgtg cccaggagca gatgcggctc agagcccagg tgcgcctgct tgagacccgg  1020
gtcaaacagc aacaggtcaa gatcaagcag cttttgcagg agaatgaagt ccagttcctt  1080
gataaaggag atgagaatac tgtcattgat cttggaagca agaggcagta tgcagattgt  1140
tcagagattt tcaatgatgg gtataagctc agtggatttt acaaaatcaa acctctccag  1200
agcccagcag aattttctgt ttattgtgac atgtccgatg gaggaggatg gactgtaatt  1260
cagagacgat ctgatggcag tgaaaacttt aacagaggat ggaaagacta tgaaaatggc  1320
tttggaaatt ttgtccaaaa acatggtgaa tattggctgg gcaataaaaa tcttcacttc  1380
ttgaccactc aagaagacta cactttaaaa atcgaccttg cagattttga aaaaaatagc  1440
cgttatgcac aatataagaa tttcaaagtt ggagatgaaa agaatttcta cgagttgaat  1500
attggggaat attctggaac agctggagat tcccttgcgg ggaattttca tcctgaggtg  1560
cagtggtggg ctagtcacca aagaatgaaa ttcagcacgt gggacagaga tcatgacaac  1620
tatgaaggga actgcgcaga agaagatcag tctggctggt ggtttaacag gtgtcactct  1680
gcaaacctga atggtgtata ctacagcggc ccctacacgg ctaaaacaga caatgggatt  1740
gtctggtaca cctggcatgg gtggtggtat tctctgaaat ctgtggttat gaaaattagg  1800
ccaaatgatt ttattccaaa tgtaattcca aataaaggaa gtggaaccac ttcaggtact  1860
acccgtcttc tatctgggca cacgtgtttc acgttgacag gtttgcttgg gacgctagta  1920
accatgggct tgctgactta g                                             1941

SEQ ID NO: 240          moltype = AA  length = 646
FEATURE                 Location/Qualifiers
REGION                  1..646
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..646
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 240
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERPN  240
KGSGTTSGTT RLLSGHTCFT LTGLLGTLVT MGLLTGSGAT NFSLLKQAGD VEENPGPMAK  300
VFSFILVTTA LTMGREISAL EDCAQEQMRL RAQVRLLETR VKQQQVKIKQ LLQENEVQFL  360
DKGDENTVID LGSKRQYADC SEIFNDGYKL SGFYKIKPLQ SPAEFSVYCD MSDGGGWTVI  420
QRRSDGSENF NRGWKDYENG FGNFVQKHGE YWLGNKNLHF LTTQEDYTLK IDLADFEKNS  480
RYAQYKNFKV GDEKNFYELN IGEYSGTAGD SLAGNFHPEV QWWASHQRMK FSTWDRDHDN  540
YEGNCAEEDQ SGWWFNRCHS ANLNGVYYSG PYTAKTDNGI VWYTWHGWWY SLKSVVMKIR  600
PNDFIPNVIP NKGSGTTSGT TRLLSGHTCF TLTGLLGTLV TMGLLT                 646

SEQ ID NO: 241          moltype = DNA  length = 729
FEATURE                 Location/Qualifiers
misc_feature            1..729
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..729
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 241
atgggttgct gtttctccaa gaccggctcg agcggcgtga gcaagggcga ggcagtgatc  60
aaggagttca tgcggttcaa ggtgcacatg gagggctcca tgaacggcca cgagttcgag  120
atcgagggcg agggcgaggg ccgcccctac gagggcaccc agaccgccaa gctgaaggtg  180
accaagggtg gccccctgcc cttctcctgg gacatcctgt cccctcagtt catgtacggc  240
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tccagggcct tcaccaagca ccccgccgac atccccgact actataagca gtccttcccc  300
gagggcttca agtgggagcg cgtgatgaac ttcgaggacg gcggcgccgt gaccgtgacc  360
caggacacct ccctggagga cggcaccctg atctacaagg tgaagctccg cggcaccaac  420
ttccctcctg acggccccgt aatgcagaag aagacaatgg gctgggaagc gtccaccgag  480
cggttgtacc ccgaggacgg cgtgctgaag ggcgacatta agatggccct gcgcctgaag  540
gacggcggcc gctacctggc ggacttcaag accacctaca aggccaagaa gcccgtgcag  600
atgcccggcg cctacaacgt cgaccgcaag ttggacatca cctcccacaa cgaggactac  660
accgtggtgg aacagtacga acgctccgag ggccgccact ccaccggcgg catggacgag  720
ctgtacaag                                                          729

SEQ ID NO: 242          moltype = AA  length = 243
FEATURE                 Location/Qualifiers
REGION                  1..243
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..243
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 242
MGCCFSKTGS SGVSKGEAVI KEFMRFKVHM EGSMNGHEFE IEGEGEGRPY EGTQTAKLKV  60
TKGGPLPFSW DILSPQFMYG SRAFTKHPAD IPDYYKQSFP EGFKWERVMN FEDGGAVTVT  120
QDTSLEDGTL IYKVKLRGTN FPPDGPVMQK KTMGWEASTE RLYPEDGVLK GDIKMALRLK  180
DGGRYLADFK TTYKAKKPVQ MPGAYNVDRK LDITSHNEDY TVVEQYERSE GRHSTGGMDE  240
LYK                                                                243

SEQ ID NO: 243          moltype = DNA  length = 549
FEATURE                 Location/Qualifiers
misc_feature            1..549
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..549
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 243
atgggttgct gtttctccaa gaccggctcg agcggcgtct tcacactcga agatttcgtt  60
ggggactggc gacagacagc cggctacaac ctggaccaag tccttgaaca gggaggtgtg  120
tccagtttgt ttcagaatct cggggtgtcc gtaactccga tccaaaggat tgtcctgagc  180
ggtgaaaatg ggctgaagat cgacatccat gtcatcatcc cgtatgaagg tctgagcggc  240
gaccaaatgg gccagatcga aaaaattttt aaggtggtgt accctgtgga tgatcatcac  300
tttaaggtga tcctgcacta tggcacactg gtaatcgacg gggttacgcc gaacatgatc  360
gactatttcg gacggccgta tgaaggcatc gccgtgttcg acggcaaaaa gatcactgta  420
acagggaccc tgtggaacgg caacaaaatt atcgacgagc gcctgatcaa ccccgacggc  480
tccctgctgt tccgagtaac catcaacgga gtgaccggct ggcggctgtg cgaacgcatt  540
ctggcgtaa                                                          549

SEQ ID NO: 244          moltype = AA  length = 182
FEATURE                 Location/Qualifiers
REGION                  1..182
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..182
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 244
MGCCFSKTGS SGVFTLEDFV GDWRQTAGYN LDQVLEQGGV SSLFQNLGVS VTPIQRIVLS  60
GENGLKIDIH VIIPYEGLSG DQMGQIEKIF KVVYPVDDHH FKVILHYGTL VIDGVTPNMI  120
DYFGRPYEGI AVFDGKKITV TGTLWNGNKI IDERLINPDG SLLFRVTING VTGWRLCERI  180
LA                                                                 182

SEQ ID NO: 245          moltype = DNA  length = 849
FEATURE                 Location/Qualifiers
misc_feature            1..849
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..849
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 245
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
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acagctgaat tggtcatccc aggtaatatt ctgaatgtgt ccattaaaat atgtctaaca  720
ctgtccccta gcaccccaaa taaaggaagt ggaaccactt caggtactac ccgtcttcta  780
tctgggcaca cgtgtttcac gttgacaggt ttgcttggga cgctagtaac catgggcttg  840
ctgacttag                                                          849

SEQ ID NO: 246          moltype = AA  length = 282
FEATURE                 Location/Qualifiers
REGION                  1..282
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..282
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 246
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPGNI LNVSIKICLT  240
LSPSTPNKGS GTTSGTTRLL SGHTCFTLTG LLGTLVTMGL LT                     282

SEQ ID NO: 247          moltype = DNA  length = 939
FEATURE                 Location/Qualifiers
misc_feature            1..939
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..939
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 247
atggagcggc tttggggtct attccagaga gcgcaacaac tgtccccaag atcctctcag  60
accgtctacc agcgtgtgga aggcccccgg aaagggcacc tggaggagga agaggaagac  120
ggggaggagg gggcggagac attggcccac ttctgcccca tggagctgag gggccctgag  180
cccctgggct ctagacccag gcagccaaac ctcattccct gggcggcagc aggacggagg  240
gctgcccccct acctggtcct gacggccctg ctgatcttca ctggggcctt cctactgggc  300
tacgtcgcct tccgagggtc cgcctgcccc tgggccgtgt ccggggctcg cgcctcgccc  360
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ggcctcttgg acctgcggca gggcatgttt gcgcagctgg tggcccaaaa tgttctgctg  480
atcgatgggc ccctgagctg gtacagtgac ccaggcctgg caggcgtgtc cctgacgggg  540
ggcctgagct acaaagagga cacgaaggag ctggtggtgg ccaaggctgg agtctactat  600
gtcttctttc aactagagct gcggcgcgtg gtggccggcg agggctcagg ctccgtttca  660
cttgcgctgc acctgcagcc actgcgctct gctgctgggg ccgccgccct ggctttgacc  720
gtggacctgc cacccgcctc ctccgaggct cggaactcgg ccttcggttt ccagggccgc  780
ttgctgcacc tgagtgccgg ccagcgcctg ggcgtccatc ttcacactga ggccagggca  840
cgccatgcct ggcagcttac ccagggcgcc acagtcttgg gactcttccg ggtgaccccc  900
gaaatcccag ccggactccc ttcaccgagg tcggaataa                         939

SEQ ID NO: 248          moltype = AA  length = 311
FEATURE                 Location/Qualifiers
REGION                  1..311
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..311
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 248
MERLWGLFQR AQQLSPRSSQ TVYQRVEGPR KGHLEEEEED GEEGAETLAH FCPMELRGPE  60
PLGSRPRQPN LIPWAAAGRR AAPYLVLTAL LIFTGAFLLG YVAFRGSACP WAVSGARASP  120
GSAASPRLRG PELSPDDPAG LLDLRQGMFA QLVAQNVLLI DGPLSWYSDP GLAGVSLTGG  180
LSYKEDTKEL VVAKAGVYYV FFQLELRRVV AGEGSGSVSL ALHLQPLRSA AGAAALALTV  240
DLPPASSEAR NSAFGFQGRL LHLSAGQRLG VHLHTEARAR HAWQLTQGAT VLGLFRVTPE  300
IPAGLPSPRS E                                                       311

SEQ ID NO: 249          moltype = DNA  length = 741
FEATURE                 Location/Qualifiers
misc_feature            1..741
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..741
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 249
atgggctgct gcggggctgt gcaggagtcc cagtgcatgc tgggactgtt cttcggcttc  60
ctcttggtga tattcgccat tgaaatagct gcggccatct ggggatattc ccacaaggat  120
gaggcctgcc cctgggccgt gtccggggct cgcgcctcgc ccggctccgc ggccagcccg  180
agactccgcg agggtcccga gctttcgccc gacgatcccg ccggcctctt ggacctgcgg  240
cagggcatgt ttgcgcagct ggtggcccaa aatgttctgc tgatcgatgg gcccctgagc  300
tggtacagtg acccaggcct ggcaggcgtg tccctgacgg ggggcctgag ctacaaagag  360
gacacgaagg agctggtggt ggccaaggct ggagtctact atgtcttctt tcaactagag  420
ctgcggcgcg tggtggccgg cgagggctca ggctccgttt cacttgcgct gcacctgcag  480
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ccactgcgct ctgctgctgg ggccgccgcc ctggctttga ccgtggacct gccacccgcc  540
tcctccgagg ctcggaactc ggccttcggt ttccagggcc gcttgctgca cctgagtgcc  600
ggccagcgcc tgggcgtcca tcttcacact gaggccaggg cacgccatgc ctggcagctt  660
acccagggcg ccacagtctt gggactcttc cgggtgaccc ccgaaatccc agccggactc  720
ccttcaccga ggtcggaata a                                            741

SEQ ID NO: 250          moltype = AA  length = 246
FEATURE                 Location/Qualifiers
REGION                  1..246
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..246
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 250
MGCCGAVQES QCMLGLFFGF LLVIFAIEIA AAIWGYSHKD EACPWAVSGA RASPGSAASP  60
RLREGPELSP DDPAGLLDLR QGMFAQLVAQ NVLLIDGPLS WYSDPGLAGV SLTGGLSYKE  120
DTKELVVAKA GVYYVFFQLE LRRVVAGEGS GSVSLALHLQ PLRSAAGAAA LALTVDLPPA  180
SSEARNSAFG FQGRLLHLSA GQRLGVHLHT EARARHAWQL TQGATVLGLF RVTPEIPAGL  240
PSPRSE                                                             246

SEQ ID NO: 251          moltype = DNA  length = 963
FEATURE                 Location/Qualifiers
misc_feature            1..963
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..963
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 251
atgggttgct gtttctccaa gaccggctcg agcggcagcc aggacaccga ggtggatatg  60
aaggaggtgg agctgaatga gttagagccc gagaagcagc cgatgaacgc ggcgtctggg  120
gcggccatgt ccctggcggg agccgagaag aatggtctgg tgaagatcaa ggtggcggaa  180
gacgaggcgg aggcggcagc cgcggctaag ttcacgggcc tgtccaagga ggagctgctg  240
aaggtggcag gcagccccgg ctgggtacgc acccgctggg cactgctgct gctcttctgg  300
ctcggctggc tcggcatgct tgctggtgcc gtggtcataa tcgtggcctg cccctgggcc  360
gtgtccgggg ctcgcgcctc gcccggctcc gcggccagcc cgagactccg cgagggtccc  420
gagctttcgc ccgacgatcc cgccggcctc ttggacctgc ggcagggcat gtttgcgcag  480
ctggtggccc aaaatgttct gctgatcgat gggcccctga gctggtacag tgacccaggc  540
ctggcaggcg tgtccctgac gggggggcctg agctacaaag aggacacgaa ggagctggtg  600
gtggccaagg ctggagtcta ctatgtcttc tttcaactag agctgcggcg cgtggtggcc  660
ggcgagggct caggctccgt ttcacttgcg ctgcacctgc agccactgcg ctctgctgct  720
ggggccgccg ccctggcttt gaccgtggac ctgccacccg cctcctccga ggctcggaac  780
tcggccttcg gtttccaggg ccgcttgctg cacctgagtg ccggccagcg cctgggcgtc  840
catcttcaca ctgaggccag ggcacgccat gcctggcagc ttacccaggg cgccacagtc  900
ttgggactct tccgggtgac ccccgaaatc ccagccggac tcccttcacc gaggtcggaa  960
taa                                                                963

SEQ ID NO: 252          moltype = AA  length = 320
FEATURE                 Location/Qualifiers
REGION                  1..320
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..320
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 252
MGCCFSKTGS SGSQDTEVDM KEVELNELEP EKQPMNAASG AAMSLAGAEK NGLVKIKVAE  60
DEAEAAAAAK FTGLSKEELL KVAGSPGWVR TRWALLLLFW LGWLGMLAGA VVIIVACPWA  120
VSGARASPGS AASPRLREGP ELSPDDPAGL LDLRQGMFAQ LVAQNVLLID GPLSWYSDPG  180
LAGVSLTGGL SYKEDTKELV VAKAGVYYVF FQLELRRVVA GEGSGSVSLA LHLQPLRSAA  240
GAAALALTVD LPPASSEARN SAFGFQGRLL HLSAGQRLGV HLHTEARARH AWQLTQGATV  300
LGLFRVTPEI PAGLPSPRSE                                              320

SEQ ID NO: 253          moltype = DNA  length = 717
FEATURE                 Location/Qualifiers
misc_feature            1..717
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..717
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 253
atgggttgct gtttctccaa gaccggctcg agcggctggg ccctggtcgc ggggctgctg  60
ctgctgctgc tgctcgctgc cgcctgcgcc gtcttcctcg cctgcccctg ggccgtgtcc  120
ggggctcgcg cctcgcccgg ctccgcggcc agcccgagac tccgcgaggg tcccgagctt  180
tcgcccgacg atcccgccgg cctcttggac ctgcggcagg gcatgtttgc gcagctggtg  240
gcccaaaatg ttctgctgat cgatgggccc ctgagctggt acagtgaccc aggcctggca  300
ggcgtgtccc tgacgggggg cctgagctac aaagaggaca cgaaggagct ggtggtggcc  360
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aaggctggag tctactatgt cttctttcaa ctagagctgc ggcgcgtggt ggccggcgag  420
ggctcaggct ccgtttcact tgcgctgcac ctgcagccac tgcgctctgc tgctggggcc  480
gccgccctgg ctttgaccgt ggacctgcca cccgcctcct ccgaggctcg gaactcggcc  540
ttcggtttcc agggccgctt gctgcacctg agtgccggcc agcgcctggg cgtccatctt  600
cacactgagg ccagggcacg ccatgcctgg cagcttaccc agggcgccac agtcttggga  660
ctcttccggg tgacccccga aatcccagcc ggactccctt caccgaggtc ggaataa     717

SEQ ID NO: 254          moltype = AA  length = 238
FEATURE                 Location/Qualifiers
REGION                  1..238
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..238
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 254
MGCCFSKTGS SGWALVAGLL LLLLLAAACA VFLACPWAVS GARASPGSAA SPRLREGPEL  60
SPDDPAGLLD LRQGMFAQLV AQNVLLIDGP LSWYSDPGLA GVSLTGGLSY KEDTKELVVA  120
KAGVYYVFFQ LELRRVVAGE GSGSVSLALH LQPLRSAAGA AALALTVDLP PASSEARNSA  180
FGFQGRLLHL SAGQRLGVHL HTEARARHAW QLTQGATVLG LFRVTPEIPA GLPSPRSE    238

SEQ ID NO: 255          moltype = DNA  length = 798
FEATURE                 Location/Qualifiers
misc_feature            1..798
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..798
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 255
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tgggctcgag cggcccaaat aaaggaagtg gaaccacttc aggtactacc  720
cgtcttctat ctgggcacac gtgtttcacg ttgacaggtt tgcttgggac gctagtaacc  780
atgggcttgc tgacttag                                                798

SEQ ID NO: 256          moltype = AA  length = 265
FEATURE                 Location/Qualifiers
REGION                  1..265
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..265
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 256
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELGSSGPN KGSGTTSGTT  240
RLLSGHTCFT LTGLLGTLVT MGLLT                                        265

SEQ ID NO: 257          moltype = DNA  length = 834
FEATURE                 Location/Qualifiers
misc_feature            1..834
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..834
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 257
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
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acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc aggtaatatt ctgaatgtgt ccattaaaat atgtctaaca  720
ctgtccccta gcaccttcta cacaggagtc tatattctga tcggagccgg cgccctcatg  780
atgctggtgg gcttcctggg ctgctgcggg gctgtgcagg agtcccagtg ctag        834

SEQ ID NO: 258          moltype = AA  length = 277
FEATURE                 Location/Qualifiers
REGION                  1..277
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..277
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 258
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPGNI LNVSIKICLT  240
LSPSTFYTGV YILIGAGALM MLVGFLGCCG AVQESQC                           277

SEQ ID NO: 259          moltype = DNA  length = 876
FEATURE                 Location/Qualifiers
misc_feature            1..876
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..876
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 259
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc aggtaatatt ctgaatgtgt ccattaaaat atgtctaaca  720
ctgtccccta gcaccttcta cacaggagtc tatattctga tcggagccgg cgccctcatg  780
atgctggtgg gcttcctggg ctgctgcggg gctgtgcagg agtcccagtg caaaaagaag  840
aaaaagaagt caaagacaaa gtgtgtaatt atgtaa                            876

SEQ ID NO: 260          moltype = AA  length = 291
FEATURE                 Location/Qualifiers
REGION                  1..291
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..291
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 260
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPGNI LNVSIKICLT  240
LSPSTFYTGV YILIGAGALM MLVGFLGCCG AVQESQCKKK KKKSKTKCVI M           291

SEQ ID NO: 261          moltype = DNA  length = 837
FEATURE                 Location/Qualifiers
misc_feature            1..837
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..837
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 261
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
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acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc aggtaatatt ctgaatgtgt ccattaaaat atgtctaaca  720
ctgtccccta gcaccatcgg cgcagtgggc atcggcattg ccgtggtcat gatatttggc  780
atgatcttca gtatgatctt gtgctgtgct atccgcagga accgcgagat ggtctag     837

SEQ ID NO: 262          moltype = AA  length = 278
FEATURE                 Location/Qualifiers
REGION                  1..278
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..278
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 262
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPGNI LNVSIKICLT  240
LSPSTIGAVG IGIAVVMIFG MIFSMILCCA IRRNREMV                          278

SEQ ID NO: 263          moltype = DNA  length = 843
FEATURE                 Location/Qualifiers
misc_feature            1..843
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..843
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 263
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc aggtaatatt ctgaatgtgt ccattaaaat atgtctaaca  720
ctgtccccta gcaccctgta cctcatcggc attgctgcca tcgtggtcgc tgtgatcatg  780
atcttcgaga tgatcctgag catggtgctg tgctgtggca tccggaacag ctccgtgtac  840
tga                                                                843

SEQ ID NO: 264          moltype = AA  length = 280
FEATURE                 Location/Qualifiers
REGION                  1..280
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..280
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 264
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPGNI LNVSIKICLT  240
LSPSTLYLIG IAAIVVAVIM IFEMILSMVL CCGIRNSSVY                        280

SEQ ID NO: 265          moltype = DNA  length = 1503
FEATURE                 Location/Qualifiers
misc_feature            1..1503
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1503
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 265
atggagaggc tggtgatcag gatgcccttc tctcatctgt ctacctacag cctggtttgg  60
gtcatggcag cagtggtgct gtgcacagca caagtgcaag tggtgaccca ggatgaaaga  120
gagcagctgt acacacctgc ttccttaaaa tgctctctgc aaaatgccca ggaagccctc  180
attgtgacat ggcagaaaaa gaaagctgta agcccagaaa acatggtcac cttcagcgag  240
aaccatgggg tggtgatcca gcctgcctat aaggacaaga taaacattac ccagctggga  300
ctccaaaact caaccatcac cttctggaat atcaccctgg aggatgaagg gtgttacatg  360
tgtctcttca ataccttttgg ttttgggaag atctcaggaa cggcctgcct caccgtctat  420
gtacagccca tagtatccct tcactacaaa ttctctgaag accacctaaa tatcacttgc  480
tctgccactg cccgcccagc ccccatggtc ttctggaagg tccctcggtc agggattgaa  540
aatagtacag tgactctgtc tcacccaaat gggaccacgt ctgttaccag catcctccat  600
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atcaaagacc ctaagaatca ggtggggaag gaggtgatct gccaggtgct gcacctgggg  660
actgtgaccg actttaagca aaccgtcaac aaaggcatcg atgacaaaac tcacacatgc  720
ccaccgtgcc cagcacctga actcctgggg ggaccgtcag tcttcctctt ccccccaaaa  780
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg  840
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat  900
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc  960
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa  1020
gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca  1080
caggtgtaca ccctgccccc atcccgggag gagatgacca agaaccaggt cagcctgacc  1140
tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag  1200
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc  1260
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc  1320
gtgatgcacg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt  1380
aaaatcgatc caaataaagg aagtggaacc acttcaggta ctacccgtct tctatctggg  1440
cacacgtgtt tcacgttgac aggtttgctt gggacgctag taaccatggg cttgctgact  1500
tag                                                                1503
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SEQ ID NO: 266          moltype = AA  length = 500
FEATURE                 Location/Qualifiers
REGION                  1..500
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..500
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 266
MERLVIRMPF SHLSTYSLVW VMAAVVLCTA QVQVVTQDER EQLYTPASLK CSLQNAQEAL  60
IVTWQKKKAV SPENMVTFSE NHGVVIQPAY KDKINITQLG LQNSTITFWN ITLEDEGCYM  120
CLFNTFGFGK ISGTACLTVY VQPIVSLHYK FSEDHLNITC SATARPAPMV FWKVPRSGIE  180
NSTVTLSHPN GTTSVTSILH IKDPKNQVGK EVICQVLHLG TVTDFKQTVN KGIDDKTHTC  240
PPCPAPELLG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN  300
AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP  360
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL  420
YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG KIDPNKGSGT TSGTTRLLSG  480
HTCFTLTGLL GTLVTMGLLT                                              500
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SEQ ID NO: 267          moltype = DNA  length = 1050
FEATURE                 Location/Qualifiers
misc_feature            1..1050
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1050
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 267
atggcaaagg tgttcagttt catccttgtt accaccgctc tgacaatggg cagggaaatt  60
tcggcgctcg aggactgtgc ccaggagcag atgcggctca gagcccaggt gcgcctgctt  120
gagacccggg tcaaacagca acaggtcaag atcaagcagc ttttgcagga gaatgaagtc  180
cagttccttg ataaaggaga tgagaatact gtcattgatc ttggaagcaa gaggcagtat  240
gcagattgtt cagagatttt caatgatggg tataagctca gtggatttta caaaatcaaa  300
cctctccaga gcccagcaga attttctgtt tattgtgaca tgtccgatgg aggaggatgg  360
actgtaattc agagacgatc tgatggcagt gaaaacttta acagaggatg gaaagactat  420
gaaaatggct ttggaaattt tgtccaaaaa catggtgaat attggctggg caataaaaat  480
cttcacttct tgaccactca agaagactac actttaaaaa tcgaccttgc agattttgaa  540
aaaaatagcc gttatgcaca atataagaat ttcaaagttg gagatgaaaa gaatttctac  600
gagttgaata ttggggaata ttctggaaca gctggagatt cccttgcggg gaattttcat  660
cctgaggtgc agtggtgggc tagtcaccaa agaatgaaat tcagcacgtg ggacagagat  720
catgacaact atgaagggaa ctgcgcagaa gaagatcagt ctggctggtg gtttaacagg  780
tgtcactctg caaacctgaa tggtgtatac tacagcggcc cctacacggc taaaacagac  840
aatgggattg tctggtacac ctggcatggg tggtggtatt ctctgaaatc tgtggttatg  900
aaaattaggc caaatgattt tattccaaat gtaattccaa ataaaggaag tggaaccact  960
tcaggtacta cccgtcttct atctgggcac acgtgtttca cgttgacagg tttgcttggg  1020
acgctagtaa ccatgggctt gctgacttag                                   1050
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SEQ ID NO: 268          moltype = AA  length = 349
FEATURE                 Location/Qualifiers
REGION                  1..349
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..349
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 268
MAKVFSFILV TTALTMGREI SALEDCAQEQ MRLRAQVRLL ETRVKQQQVK IKQLLQENEV  60
QFLDKGDENT VIDLGSKRQY ADCSEIFNDG YKLSGFYKIK PLQSPAEFSV YCDMSDGGGW  120
TVIQRRSDGS ENFNRGWKDY ENGFGNFVQK HGEYWLGNKN LHFLTTQEDY TLKIDLADFE  180
KNSRYAQYKN FKVGDEKNFY ELNIGEYSGT AGDSLAGNFH PEVQWWASHQ RMKFSTWDRD  240
HDNYEGNCAE EDQSGWWFNR CHSANLNGVY YSGPYTAKTD NGIVWYTWHG WWYSLKSVVM  300
KIRPNDFIPN VIPNKGSGTT SGTTRLLSGH TCFTLTGLLG TLVTMGLLT              349
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SEQ ID NO: 269          moltype = DNA  length = 1872
FEATURE                 Location/Qualifiers
misc_feature            1..1872
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1872
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 269
atggccttca gcggttccca ggctccctac ctgagtccag ctgtcccctt ttctgggact  60
attcaaggag gtctccagga cggacttcag atcactgtca atgggaccgt tctcagctcc  120
agtggaacca ggtttgctgt gaactttcag actggcttca gtggaaatga cattgccttc  180
cacttcaacc ctcggtttga agatggaggg tacgtggtgt gcaacacgag gcagaacgga  240
agctgggggc ccgaggagag gaagacacac atgcctttcc agaaggggat gccctttgac  300
ctctgcttcc tggtgcagag ctcagatttc aaggtgatgg tgaacgggat cctcttcgtg  360
cagtacttcc accgcgtgcc cttccaccgt gtggacacca tctccgtcaa tggctctgtg  420
cagctgtcct acatcagctt ccagaacccc cgcacagtcc ctgttcagcc tgccttctcc  480
acggtgccgt tctcccagcc tgtctgtttc ccacccaggc ccagggggcg cagacaaaaa  540
cctcccggcg tgtggcctgc caacccggct cccattaccc agacagtcat ccacacagtg  600
cagagcgccc ctggacagat gttctctact cccgccatcc cacctatgat gtacccccac  660
cccgcctatc cgatgccttt catcaccacc attctgggag ggctgtaccc atccaagtcc  720
atcctcctgt caggcactgt cctgcccagt gctcagaggt tccacatcaa cctgtgctct  780
gggaaccaca tcgccttcca cctgaacccc cgttttgatg agaatgctgt ggtccgcaac  840
acccagatcg acaactcctg ggggtctgag gagcgaagtc tgccccgaaa aatgcccttc  900
gtccgtggcc agagcttctc agtgtggatc ttgtgtgaag ctcactgcct caaggtggcc  960
gtggatggtc agcacctgtt tgaatactac catcgcctga ggaacctgcc caccatcaac  1020
agactggaag tgggggcga catccagctg acccatgtgc agacaatcga tgacaaaact  1080
cacacatgcc caccgtgccc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc  1140
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg  1200
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag  1260
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc  1320
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc  1380
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc  1440
cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc  1500
agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc  1560
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc  1620
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc  1680
tcatgctccg tgatgcacga ggctctgcac aaccactaca cgcagaagag cctctccctg  1740
tctccgggta aaatcgatcc aaataaagga agtggaacca cttcaggtac tacccgtctt  1800
ctatctgggc acacgtgttt cacgttgaca ggtttgcttg ggacgctagt aaccatgggc  1860
ttgctgactt ag                                                      1872

SEQ ID NO: 270          moltype = AA  length = 623
FEATURE                 Location/Qualifiers
REGION                  1..623
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..623
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 270
MAFSGSQAPY LSPAVPFSGT IQGGLQDGLQ ITVNGTVLSS SGTRFAVNFQ TGFSGNDIAF  60
HFNPRFEDGG YVVCNTRQNG SWGPEERKTH MPFQKGMPFD LCFLVQSSDF KVMVNGILFV  120
QYFHRVPFHR VDTISVNGSV QLSYISFQNP RTVPVQPAFS TVPFSQPVCF PPRPRGRRQK  180
PPGVWPANPA PITQTVIHTV QSAPGQMFST PAIPPMMYPH PAYPMPFITT ILGGLYPSKS  240
ILLSGTVLPS AQRFHINLCS GNHIAFHLNP RFDENAVVRN TQIDNSWGSE ERSLPRKMPF  300
VRGQSFSVWI LCEAHCLKVA VDGQHLFEYY HRLRNLPTIN RLEVGGDIQL THVQTIDDKT  360
HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE  420
VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP  480
REPQVYTLPP SREEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS  540
FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGKIDPNKG SGTTSGTTRL  600
LSGHTCFTLT GLLGTLVTMG LLT                                          623

SEQ ID NO: 271          moltype = DNA  length = 810
FEATURE                 Location/Qualifiers
misc_feature            1..810
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..810
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 271
atggagaggc tggtgatcag gatgcccttc tctcatctgt ctacctacag cctggtttgg  60
gtcatggcag cagtggtgct gtgcacagca caagtgcaag tggtgaccca ggatgaaaga  120
gagcagctgt acacacctgc ttccttaaaa tgctctctgc aaaatgccca ggaagccctc  180
attgtgacat ggcagaaaaa gaaagctgta agcccagaaa acatggtcac cttcagcgag  240
aaccatgggg tggtgatcca gcctgcctat aaggacaaga taaacattac ccagctggga  300
ctccaaaact caaccatcac cttctggaat atcaccctgg aggatgaagg gtgttacatg  360
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tgtctcttca ataccttttgg ttttgggaag atctcaggaa cggcctgcct caccgtctat  420
gtacagccca tagtatccct tcactacaaa ttctctgaag accacctaaa tatcacttgc  480
tctgccactg cccgcccagc ccccatggtc ttctggaagg tccctcggtc agggattgaa  540
aatagtacag tgactctgtc tcacccaaat gggaccacgt ctgttaccag catcctccat  600
atcaaagacc ctaagaatca ggtggggaag gaggtgatct gccaggtgct gcacctgggg  660
actgtgaccg actttaagca aaccgtcaac aaaggcccaa ataaaggaag tggaaccact  720
tcaggtacta cccgtcttct atctgggcac acgtgtttca cgttgacagg tttgcttggg  780
acgctagtaa ccatgggctt gctgacttag                                   810

SEQ ID NO: 272          moltype = AA  length = 269
FEATURE                 Location/Qualifiers
REGION                  1..269
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..269
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 272
MERLVIRMPF SHLSTYSLVW VMAAVVLCTA QVQVVTQDER EQLYTPASLK CSLQNAQEAL  60
IVTWQKKKAV SPENMVTFSE NHGVVIQPAY KDKINITQLG LQNSTITFWN ITLEDEGCYM  120
CLFNTFGFGK ISGTACLTVY VQPIVSLHYK FSEDHLNITC SATARPAPMV FWKVPRSGIE  180
NSTVTLSHPN GTTSVTSILH IKDPKNQVGK EVICQVLHLG TVTDFKQTVN KGPNKGSGTT  240
SGTTRLLSGH TCFTLTGLLG TLVTMGLLT                                    269

SEQ ID NO: 273          moltype = DNA  length = 1179
FEATURE                 Location/Qualifiers
misc_feature            1..1179
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1179
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 273
atggccttca gcggttccca ggctccctac ctgagtccag ctgtcccctt ttctgggact  60
attcaaggag gtctccagga cggacttcag atcactgtca atgggaccgt tctcagctcc  120
agtggaacca ggtttgctgt gaactttcag actggcttca gtggaaatga cattgccttc  180
cacttcaacc ctcggtttga agatggaggg tacgtggtgt gcaacacgag gcagaacgga  240
agctgggggc ccgaggagag gaagacacac atgcctttcc agaaggggat gccctttgac  300
ctctgcttcc tggtgcagag ctcagatttc aaggtgatgg tgaacgggat cctcttcgtg  360
cagtacttcc accgcgtgcc cttccaccgt gtggacacca tctccgtcaa tggctctgtg  420
cagctgtcct acatcagctt ccagaacccc cgcacagtcc ctgttcagcc tgccttctcc  480
acggtgccgt tctcccagcc tgtctgtttc ccacccaggc ccagggggcg cagacaaaaa  540
cctcccggcg tgtggcctgc caacccggct cccattaccc agacagtcat ccacacagtg  600
cagagcgccc ctggacagat gttctctact cccgccatcc cacctatgat gtacccccac  660
cccgcctatc cgatgccttt catcaccacc attctgggag ggctgtaccc atccaagtcc  720
atcctcctgt caggcactgt cctgcccagt gctcagaggt tccacatcaa cctgtgctct  780
gggaaccaca tcgccttcca cctgaacccc cgttttgatg agaatgctgt ggtccgcaac  840
acccagatcg acaactcctg ggggtctgag gagcgaagtc tgccccgaaa aatgcccttc  900
gtccgtggcc agagcttctc agtgtggatc ttgtgtgaag ctcactgcct caaggtggcc  960
gtggatggtc agcacctgtt tgaatactac catcgcctga ggaacctgcc caccatcaac  1020
agactggaag tgggggggcga catccagctg acccatgtgc agacaccaaa taaaggaagt  1080
ggaaccactt caggtactac ccgtcttcta tctgggcaca cgtgtttcac gttgacaggt  1140
ttgcttggga cgctagtaac catgggcttg ctgacttag                         1179

SEQ ID NO: 274          moltype = AA  length = 392
FEATURE                 Location/Qualifiers
REGION                  1..392
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..392
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 274
MAFSGSQAPY LSPAVPFSGT IQGGLQDGLQ ITVNGTVLSS SGTRFAVNFQ TGFSGNDIAF  60
HFNPRFEDGG YVVCNTRQNG SWGPEERKTH MPFQKGMPFD LCFLVQSSDF KVMVNGILFV  120
QYFHRVPFHR VDTISVNGSV QLSYISFQNP RTVPVQPAFS TVPFSQPVCF PPRPRGRRQK  180
PPGVWPANPA PITQTVIHTV QSAPGQMFST PAIPPMMYPH PAYPMPFITT ILGGLYPSKS  240
ILLSGTVLPS AQRFHINLCS GNHIAFHLNP RFDENAVVRN TQIDNSWGSE ERSLPRKMPF  300
VRGQSFSVWI LCEAHCLKVA VDGQHLFEYY HRLRNLPTIN RLEVGGDIQL THVQTPNKGS  360
GTTSGTTRLL SGHTCFTLTG LLGTLVTMGL LT                                392

SEQ ID NO: 275          moltype = DNA  length = 720
FEATURE                 Location/Qualifiers
misc_feature            1..720
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..720
                        mol_type = other DNA
                        organism = synthetic construct
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SEQUENCE: 275
atggagcctc ctggagactg ggggcctcct ccctggagat ccacccccaa aaccgacgtc  60
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tcctgcaagg aggacgagta cccagtgggc tccgagtgct gccccaagtg cagtccaggt  180
tatcgtgtga aggaggcctg cggggagctg acgggcacag tgtgtgaacc ctgccctcca  240
ggcacctaca ttgcccacct caatggccta agcaagtgtc tgcagtgcca aatgtgtgac  300
ccagccatgg gcctgcgcgc gagccggaac tgctccagga cagagaacgc cgtgtgtggc  360
tgcagcccag gccacttctg catcgtccag gacggggacc actgcgccgc gtgccgcgct  420
tacgccacct ccagcccggg ccagagggtg cagaagggag gcaccgagag tcaggacacc  480
ctgtgtcaga actgcccccc ggggaccttc tctcccaatg ggaccctgga ggaatgtcag  540
caccagacca agtgcagctg gctggtgacg aaggccggag ctgggaccag cagctcccac  600
tgggtaccaa ataaaggaag tggaaccact tcaggtacta cccgtcttct atctgggcac  660
acgtgtttca cgttgacagg tttgcttggg acgctagtaa ccatgggctt gctgacttag  720

SEQ ID NO: 276          moltype = AA  length = 239
FEATURE                 Location/Qualifiers
REGION                  1..239
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..239
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 276
MEPPGDWGPP PWRSTPKTDV LRLVLYLTFL GAPCYAPALP SCKEDEYPVG SECCPKCSPG  60
YRVKEACGEL TGTVCEPCPP GTYIAHLNGL SKCLQCQMCD PAMGLRASRN CSRTENAVCG  120
CSPGHFCIVQ DGDHCAACRA YATSSPGQRV QKGGTESQDT LCQNCPPGTF SPNGTLEECQ  180
HQTKCSWLVT KAGAGTSSSH WVPNKGSGTT SGTTRLLSGH TCFTLTGLLG TLVTMGLLT   239

SEQ ID NO: 277          moltype = DNA  length = 774
FEATURE                 Location/Qualifiers
misc_feature            1..774
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..774
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 277
atgatcttcc tcctgctaat gttgagcctg gaattgcagc ttcaccagat agcagcttta  60
ttcacagtga cagtccctaa ggaactgtac ataatagagc atggcagcaa tgtgaccctg  120
gaatgcaact ttgacactgg aagtcatgtg aaccttggag caataacagc cagtttgcaa  180
aaggtggaaa atgatacatc cccacaccgt gaaagagcca ctttgctgga ggagcagctg  240
cccctaggga aggcctcgtt ccacatacct caagtccaag tgagggacga aggacagtac  300
caatgcataa tcatctatgg ggtcgcctgg gactacaagt acctgactct gaaagtcaaa  360
gcttcctaca ggaaaataaa cactcacatc ctaaaggttc cagaaacaga tgaggtagag  420
ctcacctgcc aggctacagg ttatcctctg gcagaagtat cctggccaaa cgtcagcgtt  480
cctgccaaca ccagccactc caggaccccct gaaggcctct accaggtcac cagtgttctg  540
cgcctaaagc cacccccctgg cagaaacttc agctgtgtgt tctggaatac tcacgtgagg  600
gaacttactt tggccagcat tgaccttcaa agtcagatgg aacccaggac ccatccaact  660
ccaaataaag gaagtggaac cacttcaggt actacccgtc ttctatctgg gcacacgtgt  720
ttcacgttga caggtttgct tgggacgcta gtaaccatgg gcttgctgac ttag        774

SEQ ID NO: 278          moltype = AA  length = 257
FEATURE                 Location/Qualifiers
REGION                  1..257
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..257
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 278
MIFLLLMLSL ELQLHQIAAL FTVTVPKELY IIEHGSNVTL ECNFDTGSHV NLGAITASLQ  60
KVENDTSPHR ERATLLEEQL PLGKASFHIP QVQVRDEGQY QCIIIYGVAW DYKYLTLKVK  120
ASYRKINTHI LKVPETDEVE LTCQATGYPL AEVSWPNVSV PANTSHSRTP EGLYQVTSVL  180
RLKPPPGRNF SCVFWNTHVR ELTLASIDLQ SQMEPRTHPT PNKGSGTTSG TTRLLSGHTC  240
FTLTGLLGTL VTMGLLT                                                 257

SEQ ID NO: 279          moltype = DNA  length = 951
FEATURE                 Location/Qualifiers
misc_feature            1..951
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..951
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 279
atgatcatct taatttactt atttctcttg ctatgggaag acactcaagg atggggattc  60
aaggatggaa tttttcataa ctccatatgg cttgaacgag cagccggtgt gtaccacaga  120
gaagcacggt ctggcaaata caagctcacc tacgcagaag ctaaggcggt gtgtgaattt  180
gaaggcggcc atctcgcaac ttacaagcag ctagaggcag ccagaaaaat tggatttcat  240
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gtctgtgctg ctggatggat ggctaagggc agagttggat accccattgt gaagccaggg  300
cccaactgtg gatttggaaa aactggcatt attgattatg gaatccgtct caataggagt  360
gaaagatggg atgcctattg ctacaaccca cacgcaaagg agtgtggtgg cgtctttaca  420
gatccaaagc aaatttttaa atctccaggc ttcccaaatg agtacgaaga taaccaaatc  480
tgctactggc acattagact caagtatggt cagcgtattc acctgagttt tttagatttt  540
gaccttgaag atgacccagg ttgcttggct gattatgttg aaatatatga cagttacgat  600
gatgtccatg gctttgtggg aagatactgt ggagatgagc ttccagatga catcatcagt  660
acaggaaatg tcatgacctt gaagtttcta agtgatgctt cagtgacagc tggaggtttc  720
caaatcaaat atgttgcaat ggatcctgta tccaaatcca gtcaaggaaa aaatacaagt  780
actacttcta ctggaaataa aaacttttta gctggaagat ttagccactt aatcgatcca  840
aataaaggaa gtggaaccac ttcaggtact acccgtcttc tatctgggca cacgtgtttc  900
acgttgacag gtttgcttgg gacgctagta accatgggct tgctgactta g           951
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SEQ ID NO: 280 moltype = AA length = 316
FEATURE Location/Qualifiers
REGION 1..316
note = Description of Artificial Sequence: Synthetic polypeptide
source 1..316
mol_type = protein
organism = synthetic construct
SEQUENCE: 280

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MIILIYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSGKYKLT YAEAKAVCEF  60
EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCGFGKTGI IDYGIRLNRS  120
ERWDAYCYNP HAKECGGVFT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF  180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF  240
QIKYVAMDPV SKSSQGKNTS TTSTGNKNFL AGRFSHLIDP NKGSGTTSGT TRLLSGHTCF  300
TLTGLLGTLV TMGLLT                                                  316
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SEQ ID NO: 281 moltype = DNA length = 1413
FEATURE Location/Qualifiers
misc_feature 1..1413
note = Description of Artificial Sequence: Synthetic polynucleotide
source 1..1413
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 281

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atggagcctc ctggagactg ggggcctcct ccctggagat ccacccccaa aaccgacgtc  60
ttgaggctgg tgctgtatct caccttcctg ggagcccccct gctacgcccc agctctgccg  120
tcctgcaagg aggacgagta cccagtgggc tccgagtgct gccccaagtg cagtccaggt  180
tatcgtgtga aggaggcctg cggggagctg acgggcacag tgtgtgaacc ctgccctcca  240
ggcacctaca ttgcccacct caatggccta agcaagtgtc tgcagtgcca aatgtgtgac  300
ccagccatgg gcctgcgcgc gagccggaac tgctccagga cagagaacgc cgtgtgtggc  360
tgcagcccag gccacttctg catcgtccag gacggggacc actgcgccgc gtgccgcgct  420
tacgccacct ccagcccggg ccagagggtg cagaagggag gcaccgagag tcaggacacc  480
ctgtgtcaga actgcccccc ggggaccttc tctcccaatg ggaccctgga ggaatgtcag  540
caccagacca agtgcagctg gctggtgacg aaggccggag ctgggaccag cagctcccac  600
tgggtaatcg atgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg  660
ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc  720
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac  780
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac  840
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc  900
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc  960
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggag  1020
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac  1080
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  1140
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg  1200
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcacg aggctctgca caaccactac  1260
acgcagaaga gcctctccct gtctccgggt aaaatcgatc caaataaagg aagtggaacc  1320
acttcaggta ctacccgtct tctatctggg cacacgtgtt tcacgttgac aggtttgctt  1380
gggacgctag taaccatggg cttgctgact tag                               1413
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SEQ ID NO: 282 moltype = AA length = 470
FEATURE Location/Qualifiers
REGION 1..470
note = Description of Artificial Sequence: Synthetic polypeptide
source 1..470
mol_type = protein
organism = synthetic construct
SEQUENCE: 282

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MEPPGDWGPP PWRSTPKTDV LRLVLYLTFL GAPCYAPALP SCKEDEYPVG SECCPKCSPG  60
YRVKEACGEL TGTVCEPCPP GTYIAHLNGL SKCLQCQMCD PAMGLRASRN CSRTENAVCG  120
CSPGHFCIVQ DGDHCAACRA YATSSPGQRV QKGGTESQDT LCQNCPPGTF SPNGTLEECQ  180
HQTKCSWLVT KAGAGTSSSH WVIDDKTHTC PPCPAPELLG GPSVFLFPPK PKDTLMISRT  240
PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY NSTYRVVSVL TVLHQDWLNG  300
KEYKCKVSNK ALPAPIEKTI SKAKGQPREP QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD  360
IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY  420
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TQKSLSLSPG KIDPNKGSGT TSGTTRLLSG HTCFTLTGLL GTLVTMGLLT            470

SEQ ID NO: 283          moltype = DNA  length = 1611
FEATURE                 Location/Qualifiers
misc_feature            1..1611
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1611
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 283
atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact  60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc agaactacct ctggcacatc ctccaaatga aaggccaaat  720
aaaggaagtg gaaccacttc aggtactacc cgtcttctat ctgggcacac gtgtttcacg  780
ttgacaggtt tgcttgggac gctagtaacc atgggcttgc tgactggaag cggagctact  840
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cctggagact gggggcctcc tccctggaga tccaccccca aaaccgacgt cttgaggctg  960
gtgctgtatc tcaccttcct gggagccccc tgctacgccc cagctctgcc gtcctgcaag  1020
gaggacgagt acccagtggg ctccgagtgc tgccccaagt gcagtccagg ttatcgtgtg  1080
aaggaggcct gcggggagct gacgggcaca gtgtgtgaac cctgccctcc aggcacctac  1140
attgcccacc tcaatggcct aagcaagtgt ctgcagtgcc aaatgtgtga cccagccatg  1200
ggcctgcgcg cgagccggaa ctgctccagg acagagaacg ccgtgtgtgg ctgcagccca  1260
ggccacttct gcatcgtcca ggacggggac cactgcgccg cgtgccgcgc ttacgccacc  1320
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aataaaggaa gtggaaccac ttcaggtact acccgtcttc tatctgggca cacgtgtttc  1560
acgttgacag gtttgcttgg gacgctagta accatgggct tgctgactta g           1611

SEQ ID NO: 284          moltype = AA  length = 536
FEATURE                 Location/Qualifiers
REGION                  1..536
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..536
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 284
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERPN  240
KGSGTTSGTT RLLSGHTCFT LTGLLGTLVT MGLLTGSGAT NFSLLKQAGD VEENPGPMEP  300
PGDWGPPPWR STPKTDVLRL VLYLTFLGAP CYAPALPSCK EDEYPVGSEC CPKCSPGYRV  360
KEACGELTGT VCEPCPPGTY IAHLNGLSKC LQCQMCDPAM GLRASRNCSR TENAVCGCSP  420
GHFCIVQDGD HCAACRAYAT SSPGQRVQKG GTESQDTLCQ NCPPGTFSPN GTLEECQHQT  480
KCSWLVTKAG AGTSSSHWVP NKGSGTTSGT TRLLSGHTCF TLTGLLGTLV TMGLLT      536

SEQ ID NO: 285          moltype = DNA  length = 1289
FEATURE                 Location/Qualifiers
misc_feature            1..1289
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1289
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 285
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ccttttgtag ccctgctcac tcttcttttc atcccagtct tctctgaagc catacaggtg  120
acccaacctt cagtggtgtt ggctagcagc catggtgtcg ccagctttcc atgtgaatat  180
tcaccatcac acaacactga tgaggtccgg gtgactgtgc tgcggcagac aaatgaccaa  240
atgactgagg tctgtgccac gacattcaca gagaagaata cagtgggctt cctagattac  300
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gctgttgaca cgggactgta cctctgcaag gtggaactca tgtacccacc gccatacttt  420
gtgggcatgg gcaacgggac gcagatttat gtcattgatc cagaaccatg cccggattct  480
gaatcgatga caaaactcac acatgcccac cgtgcccagc acctgaactc ctgggggac  540
cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc cggacccctg  600
aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt  660
acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag cagtacaaca  720
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gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg aatggcaagg  780
agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa accatctcca  840
aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc cgggaggaga  900
tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc agcgacatcg  960
ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg cctcccgtgc  1020
tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag agcaggtggc  1080
agcaggggaa cgtcttctca tgctccgtga tgcacgaggc tctgcacaac cactacacgc  1140
agaagagcct ctccctgtct ccgggtaaaa tcgatccaaa taaaggaagt ggaaccactt  1200
caggtactac ccgtcttcta tctgggcaca cgtgtttcac gttgacaggt ttgcttggga  1260
cgctagtaac catgggcttg ctgacttag                                    1289

SEQ ID NO: 286          moltype = AA  length = 429
FEATURE                 Location/Qualifiers
REGION                  1..429
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..429
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 286
MACLGLRRYK AQLQLPSRTW PFVALLTLLF IPVFSEAIQV TQPSVVLASS HGVASFPCEY  60
SPSHNTDEVR VTVLRQTNDQ MTEVCATTFT EKNTVGFLDY PFCSGTFNES RVNLTIQGLR  120
AVDTGLYLCK VELMYPPPYF VGMGNGTQIY VIDPEPCPDS DIDDKTHTCP PCPAPELLGG  180
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  240
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE  300
MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  360
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK IDPNKGSGTT SGTTRLLSGH TCFTLTGLLG  420
TLVTMGLLT                                                          429

SEQ ID NO: 287          moltype = DNA  length = 1518
FEATURE                 Location/Qualifiers
misc_feature            1..1518
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1518
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 287
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agattccctg tagaacggga gctggacctg cttgcgttag tggtgtactg ggaaaaggaa  180
gatgagcaag tgattcagtt tgtggcagga gaggaggacc ttaagcctca gcacagcaac  240
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atcacagacg tcaagctgca ggacgcaggc gtttactgct gcataatcag ctacggtggt  360
gcggactaca agcgaatcac gctgaaagtc aatgccccat accgcaaaat caaccagaga  420
atttccgtgg atccagccac ttctgagcat gaactaatat gtcaggccga gggttatcca  480
gaagctgagg taatctggac aaacagtgac caccaacccg tgagtgggaa gagaagtgtc  540
accacttccc ggacagaggg gatgcttctc aatgtgacca gcagtctgag ggtcaacgcc  600
acagcgaatg atgttttcta ctgtacgttt tggagatcac agccagggca aaaccacaca  660
gcggagctga tcatcccaga actgcctgca acacatcctc cacagaacag gactatcgat  720
gtcgagccac tgggcatgga gaatgggaac attgccaact cacagatcgc cgcctcatct  780
gtgcgtgtga ccttcttggg tttgcagcat tgggtcccgg agctggcccg cctgaaccgc  840
gcaggcatgg tcaatgcctg gacacccagc agcaatgacg ataacccctg gatccaggtg  900
aacctgctgc ggaggatgtg ggtaacaggt gtggtgacgc agggtgccag ccgcttggcc  960
agtcatgagt acctgaaggc cttcaaggtg gcctacagcc ttaatggaca cgaattcgat  1020
ttcatccatg atgttaataa aaaacacaag gagtttgtgg gtaactggaa caaaaacgcg  1080
gtgcatgtca acctgtttga gacccctgtg gaggctcagt acgtgagatt gtaccccacg  1140
agctgccaca cggcctgcac tctgcgcttt gagctactgg gctgtgagct gaacggatgc  1200
gccaatcccc tgggcctgaa gaataacagc atccctgaca agcagatcac ggcctccagc  1260
agctacaaga cctggggctt gcatctcttc agctggaacc cctcctatgc acggctggac  1320
aagcagggca acttcaacgc ctgggttgcg gggagctacg gtaacgatca gtggctgcag  1380
atcttccctg gcaactggga caaccactcc cacaagaaga acttgtttga gacgcccatc  1440
ctggctcgct atgtgcgcat cctgcctgta gcctggcaca accgcatcgc cctgcgcctg  1500
gagctgctgg gctgttag                                                1518

SEQ ID NO: 288          moltype = AA  length = 505
FEATURE                 Location/Qualifiers
REGION                  1..505
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..505
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 288
MRIFAGIIFT ACCHLLRAFT ITAPKDLYVV EYGSNVTMEC RFPVERELDL LALVVYWEKE  60
DEQVIQFVAG EEDLKPQHSN FRGRASLPKD QLLKGNAALQ ITDVKLQDAG VYCCIISYGG  120
ADYKRITLKV NAPYRKINQR ISVDPATSEH ELICQAEGYP EAEVIWTNSD HQPVSGKRSV  180
TTSRTEGMLL NVTSSLRVNA TANDVFYCTF WRSQPGQNHT AELIIPELPA THPPQNRTID  240
VEPLGMENGN IANSQIAASS VRVTFLGLQH WVPELARLNR AGMVNAWTPS SNDDNPWIQV  300
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NLLRRMWVTG VVTQGASRLA SHEYLKAFKV AYSLNGHEFD FIHDVNKKHK EFVGNWNKNA  360
VHVNLFETPV EAQYVRLYPT SCHTACTLRF ELLGCELNGC ANPLGLKNNS IPDKQITASS  420
SYKTWGLHLF SWNPSYARLD KQGNFNAWVA GSYGNDQWLQ IFPGNWDNHS HKKNLFETPI  480
LARYVRILPV AWHNRIALRL ELLGC                                        505

SEQ ID NO: 289          moltype = DNA  length = 1521
FEATURE                 Location/Qualifiers
misc_feature            1..1521
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1521
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 289
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agattccctg tagaacggga gctggacctg cttgcgttag tggtgtactg ggaaaaggaa  180
gatgagcaag tgattcagtt tgtggcagga gaggaggacc ttaagcctca gcacagcaac  240
ttcaggggga gagcctcgct gccaaaggac cagcttttga agggaaatgc tgcccttcag  300
atcacagacg tcaagctgca ggacgcaggc gtttactgct gcataatcag ctacggtggt  360
gcggactaca agcgaatcac gctgaaagtc aatgccccat accgcaaaat caaccagaga  420
atttccgtgg atccagccac ttctgagcat gaactaatat gtcaggccga gggttatcca  480
gaagctgagg taatctggac aaacagtgac caccaacccg tgagtgggaa gagaagtgtc  540
accacttccc ggacagaggg gatgcttctc aatgtgacca gcagtctgag ggtcaacgcc  600
acagcgaatg atgttttcta ctgtacgttt tggagatcac agccagggca aaaccacaca  660
gcggagctga tcatcccaga actgcctgca acacatcctc cacagaacag gactatcgat  720
gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc  780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca  840
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac  900
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cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag  1020
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa  1080
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag  1140
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag  1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc  1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg  1320
aacgtcttct catgctccgt gatgcacgag gctctgcaca accactacac gcagaagagc  1380
ctctccctgt ctccgggtaa aatcgatcca aataaaggaa gtggaaccac ttcaggtact  1440
acccgtcttc tatctgggca cacgtgtttc acgttgacag gtttgcttgg gacgctagta  1500
accatgggct tgctgactta g                                            1521

SEQ ID NO: 290          moltype = AA  length = 506
FEATURE                 Location/Qualifiers
REGION                  1..506
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..506
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 290
MRIFAGIIFT ACCHLLRAFT ITAPKDLYVV EYGSNVTMEC RFPVERELDL LALVVYWEKE  60
DEQVIQFVAG EEDLKPQHSN FRGRASLPKD QLLKGNAALQ ITDVKLQDAG VYCCIISYGG  120
ADYKRITLKV NAPYRKINQR ISVDPATSEH ELICQAEGYP EAEVIWTNSD HQPVSGKRSV  180
TTSRTEGMLL NVTSSLRVNA TANDVFYCTF WRSQPGQNHT AELIIPELPA THPPQNRTID  240
DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD  300
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK  360
GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS  420
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGKIDP NKGSGTTSGT  480
TRLLSGHTCF TLTGLLGTLV TMGLLT                                       506

SEQ ID NO: 291          moltype = DNA  length = 828
FEATURE                 Location/Qualifiers
misc_feature            1..828
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..828
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 291
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agattccctg tagaacggga gctggacctg cttgcgttag tggtgtactg ggaaaaggaa  180
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atcacagacg tcaagctgca ggacgcaggc gtttactgct gcataatcag ctacggtggt  360
gcggactaca agcgaatcac gctgaaagtc aatgccccat accgcaaaat caaccagaga  420
atttccgtgg atccagccac ttctgagcat gaactaatat gtcaggccga gggttatcca  480
gaagctgagg taatctggac aaacagtgac caccaacccg tgagtgggaa gagaagtgtc  540
accacttccc ggacagaggg gatgcttctc aatgtgacca gcagtctgag ggtcaacgcc  600
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acagcgaatg atgttttcta ctgtacgttt tggagatcac agccagggca aaaccacaca  660
gcggagctga tcatcccaga actgcctgca acacatcctc cacagaacag gactccaaat  720
aaaggaagtg gaaccacttc aggtactacc cgtcttctat ctgggcacac gtgtttcacg  780
ttgacaggtt tgcttgggac gctagtaacc atgggcttgc tgacttag               828

SEQ ID NO: 292          moltype = AA  length = 275
FEATURE                 Location/Qualifiers
REGION                  1..275
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..275
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 292
MRIFAGIIFT ACCHLLRAFT ITAPKDLYVV EYGSNVTMEC RFPVERELDL LALVVYWEKE  60
DEQVIQFVAG EEDLKPQHSN FRGRASLPKD QLLKGNAALQ ITDVKLQDAG VYCCIISYGG  120
ADYKRITLKV NAPYRKINQR ISVDPATSEH ELICQAEGYP EAEVIWTNSD HQPVSGKRSV  180
TTSRTEGMLL NVTSSLRVNA TANDVFYCTF WRSQPGQNHT AELIIPELPA THPPQNRTPN  240
KGSGTTSGTT RLLSGHTCFT LTGLLGTLVT MGLLT                             275

SEQ ID NO: 293          moltype = DNA  length = 1464
FEATURE                 Location/Qualifiers
misc_feature            1..1464
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1464
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 293
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gcttcttaca tgaggataga cactaggatc ctggaggttc caggtacagg ggaggtgcag  420
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gagctgactt cagccatcat tgaccctctg agtcggatgg aacccaaagt ccccagaacg  660
atcgatgtcg agccactggg catggagaat gggaacattg ccaactcaca gatcgccgcc  720
tcatctgtgc gtgtgacctt cttgggtttg cagcattggg tcccggagct ggcccgcctg  780
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caggtgaacc tgctgcggag gatgtgggta acaggtgtgg tgacgcaggg tgccagccgc  900
ttggccagtc atgagtacct gaaggccttc aaggtggcct acagccttaa tggacacgaa  960
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aacgcggtgc atgtcaacct gtttgagacc cctgtggagg ctcagtacgt gagattgtac  1080
cccacgagct gccacacggc ctgcactctg cgctttgagc tactgggctg tgagctgaac  1140
ggatgcgcca atcccctggg cctgaagaat aacagcatcc ctgacaagca gatcacggcc  1200
tccagcagct acaagacctg gggcttgcat ctcttcagct ggaacccctc ctatgcacgg  1260
ctggacaagc agggcaactt caacgcctgg gttgcgggga gctacggtaa cgatcagtgg  1320
ctgcagatct tccctggcaa ctgggacaac cactcccaca agaagaactt gtttgagacg  1380
cccatcctgg ctcgctatgt gcgcatcctg cctgtagcct ggcacaaccg catcgccctg  1440
cgcctggagc tgctgggctg ttag                                         1464

SEQ ID NO: 294          moltype = AA  length = 487
FEATURE                 Location/Qualifiers
REGION                  1..487
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..487
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 294
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KVENDTSLQS ERATLLEEQL PLGKALFHIP SVQVRDSGQY RCLVICGAAW DYKYLTVKVK  120
ASYMRIDTRI LEVPGTGEVQ LTCQARGYPL AEVSWQNVSV PANTSHIRTP EGLYQVTSVL  180
RLKPQPSRNF SCMFWNAHMK ELTSAIIDPL SRMEPKVPRT IDVEPLGMEN GNIANSQIAA  240
SSVRVTFLGL QHWVPELARL NRAGMVNAWT PSSNDDNPWI QVNLLRRMWV TGVVTQGASR  300
LASHEYLKAF KVAYSLNGHE FDFIHDVNKK HKEFVGNWNK NAVHVNLFET PVEAQYVRLY  360
PTSCHTACTL RFELLGCELN GCANPLGLKN NSIPDKQITA SSSYKTWGLH LPSWNPSYAR  420
LDKQGNFNAW VAGSYGNDQW LQIFPGNWDN HSHKKNLFET PILARYVRIL PVAWHNRIAL  480
RLELLGC                                                            487

SEQ ID NO: 295          moltype = DNA  length = 1467
FEATURE                 Location/Qualifiers
misc_feature            1..1467
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
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source                  1..1467
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 295
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gagtgcgatt ttgaccgcag agaatgcact gaactggaag ggataagagc cagtttgcag  180
aaggtagaaa atgatacgtc tctgcaaagt gaaagagcca ccctgctgga ggagcagctg  240
cccctgggaa aggctttgtt ccacatccct agtgtccaag tgagagattc cgggcagtac  300
cgttgcctgg tcatctgcgg ggccgcctgg gactacaagt acctgacggt gaaagtcaaa  360
gcttcttaca tgaggataga cactaggatc ctggaggttc caggtacagg ggaggtgcag  420
cttacctgcc aggctagagg ttatccccta gcagaagtgt cctggcaaaa tgtcagtgtt  480
cctgccaaca ccagccacat caggaccccc gaaggcctct accaggtcac cagtgttctg  540
cgcctcaagc ctcagcctag cagaaacttc agctgcatgt tctggaatgc tcacatgaag  600
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atcgatgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg  720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag  780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac  840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc  900
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tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa  1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg  1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc  1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg  1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag  1260
caggggaacg tcttctcatg ctccgtgatg cacgaggctc tgcacaacca ctacacgcag  1320
aagagcctct ccctgtctcc gggtaaaatc gatccaaata aaggaagtgg aaccacttca  1380
ggtactaccc gtcttctatc tgggcacacg tgtttcacgt tgacaggttt gcttgggacg  1440
ctagtaacca tgggcttgct gacttag                                      1467

SEQ ID NO: 296          moltype = AA  length = 488
FEATURE                 Location/Qualifiers
REGION                  1..488
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..488
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 296
MLLLLPILNL SLQLHPVAAL FTVTAPKEVY TVDVGSSVSL ECDFDRRECT ELEGIRASLQ  60
KVENDTSLQS ERATLLEEQL PLGKALFHIP SVQVRDSGQY RCLVICGAAW DYKYLTVKVK  120
ASYMRIDTRI LEVPGTGEVQ LTCQARGYPL AEVSWQNVSV PANTSHIRTP EGLYQVTSVL  180
RLKPQPSRNF SCMFWNAHMK ELTSAIIDPL SRMEPKVPRT IDDKTHTCPP CPAPELLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSREEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ  420
QGNVFSCSVM HEALHNHYTQ KSLSLSPGKI DPNKGSGTTS GTTRLLSGHT CFTLTGLLGT  480
LVTMGLLT                                                           488

SEQ ID NO: 297          moltype = DNA  length = 1494
FEATURE                 Location/Qualifiers
misc_feature            1..1494
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1494
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 297
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atcacggctc caaaggactt gtacgtggtg gagtatggca gcaacgtcac gatggagtgc  120
agattccctg tagaacggga gctggacctg cttgcgttag tggtgtactg ggaaaaggaa  180
gatgagcaag tgattcagtt tgtggcagga gaggaggacc ttaagcctca gcacagcaac  240
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atcacagacg tcaagctgca ggacgcaggc gtttactgct gcataatcag ctacggtggt  360
gcggactaca agcgaatcac gctgaaagtc aatgccccat accgcaaaat caaccagaga  420
atttccgtgg atccagccac ttctgagcat gaactaatat gtcaggccga gggttatcca  480
gaagctgagg taatctggac aaacagtgac caccaacccg tgagtgggaa gagaagtgtc  540
accacttccc ggacagaggg gatgcttctc aatgtgacca gcagtctgag ggtcaacgcc  600
acagcgaatg atgttttcta ctgtacgttt tggagatcac agccagggca aaaccacaca  660
gcggagctga tcatcccaga actgcctgca acacatcctc cacagaacag gactggttgt  720
aagccttgca tatgtacagt cccagaagta tcatctgtct tcatcttccc cccaaagccc  780
aaggatgtgc tcaccattac tctgactcct aaggtcacgt gtgttgtggt agacatcagc  840
aaggatgatc ccgaggtcca gttcagctgg tttgtagatg atgtggaggt gcacacagct  900
cagacgcaac cccgggagga gcagttcaac agcactttcc gctcagtcag tgaacttccc  960
atcatgcacc aggactggct caatggcaag gagttcaaat gcagggtcaa cagtgcagct  1020
ttccctgccc ccatcgagaa aaccatctcc aaaaccaaag gcagaccgaa ggctccacag  1080
gtgtacacca ttccacctcc caaggagcag atggccaagg ataaagtcag tctgacctgc  1140
atgataacag acttcttccc tgaagacatt actgtggagt ggcagtggaa tgggcagcca  1200
gcggagaact acaagaacac tcagcccatc atggacacag atggctctta cttcgtctac  1260
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agcaagctca atgtgcagaa gagcaactgg gaggcaggaa atactttcac ctgctctgtg  1320
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ccaaataaag gaagtggaac cacttcaggt actacccgtc ttctatctgg gcacacgtgt  1440
ttcacgttga caggtttgct tgggacgcta gtaaccatgg gcttgctgac ttag        1494

SEQ ID NO: 298          moltype = AA  length = 497
FEATURE                 Location/Qualifiers
REGION                  1..497
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..497
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 298
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DEQVIQFVAG EEDLKPQHSN FRGRASLPKD QLLKGNAALQ ITDVKLQDAG VYCCIISYGG  120
ADYKRITLKV NAPYRKINQR ISVDPATSEH ELICQAEGYP EAEVIWTNSD HQPVSGKRSV  180
TTSRTEGMLL NVTSSLRVNA TANDVFYCTF WRSQPGQNHT AELIIPELPA THPPQNRTGC  240
KPCICTVPEV SSVFIFPPKP KDVLTITLTP KVTCVVVDIS KDDPEVQFSW FVDDVEVHTA  300
QTQPREEQFN STFRSVSELP IMHQDWLNGK EFKCRVNSAA FPAPIEKTIS KTKGRPKAPQ  360
VYTIPPPKEQ MAKDKVSLTC MITDFFPEDI TVEWQWNGQP AENYKNTQPI MDTDGSYFVY  420
SKLNVQKSNW EAGNTFTCSV LHEGLHNHHT EKSLSHSPGK PNKGSGTTSG TTRLLSGHTC  480
FTLTGLLGTL VTMGLLT                                                 497

SEQ ID NO: 299          moltype = DNA  length = 774
FEATURE                 Location/Qualifiers
misc_feature            1..774
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..774
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 299
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ttcaccgtga cagcccctaa agaagtgtac accgtagacg tcggcagcag tgtgagcctg  120
gagtgcgatt ttgaccgcag agaatgcact gaactggaag ggataagagc cagtttgcag  180
aaggtagaaa atgatacgtc tctgcaaagt gaaagagcca ccctgctgga ggagcagctg  240
cccctgggaa aggctttgtt ccacatccct agtgtccaag tgagagattc cgggcagtac  300
cgttgcctgg tcatctgcgg ggccgcctgg gactacaagt acctgacggt gaaagtcaaa  360
gcttcttaca tgaggataga cactaggatc ctggaggttc caggtacagg ggaggtgcag  420
cttacctgcc aggctagagg ttatccccta gcagaagtgt cctggcaaaa tgtcagtgtt  480
cctgccaaca ccagccacat caggaccccc gaaggcctct accaggtcac cagtgttctg  540
cgcctcaagc ctcagcctag cagaaacttc agctgcatgt tctggaatgc tcacatgaag  600
gagctgactt cagccatcat tgaccctctg agtcggatgg aacccaaagt ccccagaacg  660
ccaaataaag gaagtggaac cacttcaggt actacccgtc ttctatctgg gcacacgtgt  720
ttcacgttga caggtttgct tgggacgcta gtaaccatgg gcttgctgac ttag        774

SEQ ID NO: 300          moltype = AA  length = 257
FEATURE                 Location/Qualifiers
REGION                  1..257
                        note = Description of Artificial Sequence: Synthetic
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source                  1..257
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 300
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KVENDTSLQS ERATLLEEQL PLGKALFHIP SVQVRDSGQY RCLVICGAAW DYKYLTVKVK  120
ASYMRIDTRI LEVPGTGEVQ LTCQARGYPL AEVSWQNVSV PANTSHIRTP EGLYQVTSVL  180
RLKPQPSRNF SCMFWNAHMK ELTSAIIDPL SRMEPKVPRT PNKGSGTTSG TTRLLSGHTC  240
FTLTGLLGTL VTMGLLT                                                 257

SEQ ID NO: 301          moltype = DNA  length = 1623
FEATURE                 Location/Qualifiers
misc_feature            1..1623
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1623
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 301
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agattccctg tagaacggga gctggacctg cttgcgttag tggtgtactg ggaaaaggaa  180
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atcacagacg tcaagctgca ggacgcaggc gtttactgct gcataatcag ctacggtggt  360
gcggactaca agcgaatcac gctgaaagtc aatgccccat accgcaaaat caaccagaga  420
atttccgtgg atccagccac ttctgagcat gaactaatat gtcaggccga gggttatcca  480
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gaagctgagg taatctggac aaacagtgac caccaacccg tgagtgggaa gagaagtgtc  540
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acagcgaatg atgttttcta ctgtacgttt tggagatcac agccagggca aaaccacaca  660
gcggagctga tcatcccaga actgcctgca acacatcctc cacagaacag gactccaaat  720
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ttgacaggtt tgcttgggac gctagtaacc atgggcttgc tgactggaag cggagctact  840
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ctcccaggat gggggtcggc accctggagc caggccccta cagacaacac cttcaggctg  960
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caggaggagt tccttgtggg agacgagtgc tgccccatgt gcaacccagg ttaccatgtg  1080
aagcaggtct gcagtgagca tacaggcaca gtgtgtgccc cctgtccccc acagacatat  1140
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tgccctccag ggcagagggt agagaagaga gggactcacg accaggacac tgtatgtgct  1380
gactgcctaa cagggacctt ctcacttgga gggactcagg aggaatgcct gccctggacc  1440
aactgcagtg catttcaaca ggaagtaaga cgtgggacca acagcacaga caccacctgc  1500
tcctcccagc caaataaagg aagtggaacc acttcaggta ctacccgtct tctatctggg  1560
cacacgtgtt tcacgttgac aggtttgctt gggacgctag taaccatggg cttgctgact  1620
tag                                                                1623
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SEQ ID NO: 302          moltype = AA  length = 540
FEATURE                 Location/Qualifiers
REGION                  1..540
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..540
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 302
MRIFAGIIFT ACCHLLRAFT ITAPKDLYVV EYGSNVTMEC RFPVERELDL LALVVYWEKE  60
DEQVIQFVAG EEDLKPQHSN FRGRASLPKD QLLKGNAALQ ITDVKLQDAG VYCCIISYGG  120
ADYKRITLKV NAPYRKINQR ISVDPATSEH ELICQAEGYP EAEVIWTNSD HQPVSGKRSV  180
TTSRTEGMLL NVTSSLRVNA TANDVFYCTF WRSQPGQNHT AELIIPELPA THPPQNRTPN  240
KGSGTTSGTT RLLSGHTCFT LTGLLGTLVT MGLLTGSGAT NFSLLKQAGD VEENPGPMEP  300
LPGWGSAPWS QAPTDNTFRL VPCVFLLNLL QRISAQPSCR QEEFLVGDEC CPMCNPGYHV  360
KQVCSEHTGT VCAPCPPQTY TAHANGLSKC LPCGVCDPDM GLLTWQECSS WKDTVCRCIP  420
GYFCENQDGS HCSTCLQHTT CPPGQRVEKR GTHDQDTVCA DCLTGTFSLG GTQEECLPWT  480
NCSAFQQEVR RGTNSTDTTC SSQPNKGSGT TSGTTRLLSG HTCFTLTGLL GTLVTMGLLT  540
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SEQ ID NO: 303          moltype = DNA  length = 1584
FEATURE                 Location/Qualifiers
misc_feature            1..1584
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1584
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 303
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aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc agaactacct ctggcacatc ctccaaatga aaggtgtgga  720
aatggaatgg tagaacaagg tgaagaatgt gattgtggct atagtgacca gtgtaaagat  780
gaatgctgct tcgatgcaaa tcaaccagag ggaagaaaat gcaaactgaa acctgggaaa  840
cagtgcagtc caagtcaagg tccttgttgt acagcacagt gtgcattcaa gtcaaagtct  900
gagaagtgtc gggatgattc agactgtgca agggaaggaa tatgtaatgg cttcacagct  960
ctctgcccag catctgaccc taaaccaaac ttcacagact gtaataggca tacacaagtg  1020
tgcattaatg ggcaatgtgc aggttctatc tgtgagaaat atggcttaga ggagtgtacg  1080
tgtgccagtt ctgatggcaa agatgataaa gaattatgcc atgtatgctg tatgaagaaa  1140
atggacccat caacttgtgc cagtacaggg tctgtgcagt ggagtaggca cttcagtggt  1200
cgaaccatca ccctgcaacc tggatcccct tgcaacgatt ttagaggtta ctgtgatgtt  1260
ttcatgcggt gcagattagt agatgctgat ggtcctctag ctaggcttaa aaaagcaatt  1320
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ttacttatgg gaattgctct gatcatgcta atggctggat ttattaagat atgcagtgtt  1440
catactccaa gtagtaatcc aaagttgcct cctcctaaac cacttccagg cactttaaag  1500
aggaggagac ctccacagcc cattcagcaa ccccagcgtc agcggccccg agagagttat  1560
caaatgggac acatgagacg ctaa                                         1584
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SEQ ID NO: 304          moltype = AA  length = 527
FEATURE                 Location/Qualifiers
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REGION                  1..527
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..527
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 304
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DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERCG  240
NGMVEQGEEC DCGYSDQCKD ECCFDANQPE GRKCKLKPGK QCSPSQGPCC TAQCAFKSKS  300
EKCRDDSDCA REGICNGFTA LCPASDPKPN FTDCNRHTQV CINGQCAGSI CEKYGLEECT  360
CASSDGKDDK ELCHVCCMKK MDPSTCASTG SVQWSRHFSG RTITLQPGSP CNDFRGYCDV  420
FMRCRLVDAD GPLARLKKAI FSPELYENIA EWIVAHWWAV LLMGIALIML MAGFIKICSV  480
HTPSSNPKLP PPKPLPGTLK RRRPPQPIQQ PQRQRPRESY QMGHMRR                527

SEQ ID NO: 305          moltype = DNA  length = 1497
FEATURE                 Location/Qualifiers
misc_feature            1..1497
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1497
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 305
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aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
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atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc agaactacct ctggcacatc ctccaaatga aagggagtcc  720
aaatatggtc ccccatgccc atcatgccca gcacctgagt tcctgggggg accatcagtc  780
ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg  840
tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat  900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac  960
cgtgtggtca gggtcctcac cgtcctgcac caggactggc tgaacggtaa ggagtacaag  1020
tgcaaggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa  1080
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag  1140
aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag  1200
tgggagagca atgggcagcc ggaggacaac tacaagacca cgcctcccgt gctggactcc  1260
gacggctcct tcttcctcta cagcaggcta accgtggaca agagcaggtg gcaggagggg  1320
aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc  1380
ctctccctgt ctccgggtaa attctacaca ggagtctata ttctgatcgg agccggcgcc  1440
ctcatgatgc tggtgggctt cctgggctgc tgcggggctg tgcaggagtc ccagtgc     1497

SEQ ID NO: 306          moltype = AA  length = 502
FEATURE                 Location/Qualifiers
REGION                  1..502
                        note = Description of Artificial Sequence: Synthetic
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source                  1..502
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 306
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DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERES  240
KYGPPCPSCP APEFLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD  300
GVEVHNAKTK PREEQFNSTY RVVRVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK  360
GQPREPQVYT LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPEDN YKTTPPVLDS  420
DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE ALHNHYTQKS LSLSPGKFYT GVYILIGAGA  480
LMMLVGFLGC CGAVQESQCV IM                                           502

SEQ ID NO: 307          moltype = DNA  length = 1542
FEATURE                 Location/Qualifiers
misc_feature            1..1542
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1542
                        mol_type = other DNA
                        organism = synthetic construct
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SEQUENCE: 307
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gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc  120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc agaactacct ctggcacatc ctccaaatga aagggagtcc  720
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aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag  1200
tgggagagca atgggcagcc ggaggacaac tacaagacca cgcctcccgt gctggactcc  1260
gacggctcct tcttcctcta cagcaggcta accgtggaca agagcaggtg gcaggagggg  1320
aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc  1380
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ctcatgatgc tggtgggctt cctgggctgc tgcggggctg tgcaggagtc ccagtgcaaa  1500
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SEQ ID NO: 308          moltype = AA  length = 513
FEATURE                 Location/Qualifiers
REGION                  1..513
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..513
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 308
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DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERES  240
KYGPPCPSCP APEFLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD  300
GVEVHNAKTK PREEQFNSTY RVVRVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK  360
GQPREPQVYT LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPEDN YKTTPPVLDS  420
DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE ALHNHYTQKS LSLSPGKFYT GVYILIGAGA  480
LMMLVGFLGC CGAVQESQCK KKKKKKKTKC VIM                               513

SEQ ID NO: 309          moltype = DNA  length = 1515
FEATURE                 Location/Qualifiers
misc_feature            1..1515
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1515
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 309
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aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag  180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag  300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
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accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
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gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc  780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca  840
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac  900
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cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag  1020
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gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag  1140
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag  1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc  1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg  1320
aacgtcttct catgctccgt gatgcacgag gctctgcaca accactacac gcagaagagc  1380
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ctctccctgt ctccgggtaa aatcgatttc tacacaggag tctatattct gatcggagcc  1440
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tgcgtaatta tgtaa                                                   1515

SEQ ID NO: 310          moltype = AA  length = 504
FEATURE                 Location/Qualifiers
REGION                  1..504
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..504
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 310
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ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERID  240
DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD  300
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK  360
GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS  420
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGKIDF YTGVYILIGA  480
GALMMLVGFL GCCGAVQESQ CVIM                                         504

SEQ ID NO: 311          moltype = DNA  length = 1548
FEATURE                 Location/Qualifiers
misc_feature            1..1548
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1548
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 311
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gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc  240
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atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt  360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga  420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac  480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc  540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac  600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat  660
acagctgaat tggtcatccc agaactacct ctggcacatc ctccaaatga aaggatcgat  720
gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc  780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca  840
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ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac  960
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag  1020
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gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag  1140
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag  1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc  1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg  1320
aacgtcttct catgctccgt gatgcacgag gctctgcaca accactacac gcagaagagc  1380
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SEQ ID NO: 312          moltype = AA  length = 515
FEATURE                 Location/Qualifiers
REGION                  1..515
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..515
                        mol_type = protein
                        organism = synthetic construct
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ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERID  240
DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD  300
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK  360
GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS  420
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGKIDF YTGVYILIGA  480
GALMMLVGFL GCCGAVQESQ CKKKKKKKKT KCVIM                             515

SEQ ID NO: 313          moltype = DNA  length = 1488
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misc_feature            1..1488
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1488
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 313
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gatgagcaag tgattcagtt tgtggcagga gaggaggacc ttaagcctca gcacagcaac  240
ttcaggggga gagcctcgct gccaaaggac cagcttttga agggaaatgc tgcccttcag  300
atcacagacg tcaagctgca ggacgcaggc gtttactgct gcataatcag ctacggtggt  360
gcggactaca agcgaatcac gctgaaagtc aatgccccat accgcaaaat caaccagaga  420
atttccgtgg atccagccac ttctgagcat gaactaatat gtcaggccga gggttatcca  480
gaagctgagg taatctggac aaacagtgac caccaacccg tgagtgggaa gagaagtgtc  540
accacttccc ggacagaggg gatgcttctc aatgtgacca gcagtctgag ggtcaacgcc  600
acagcgaatg atgttttcta ctgtacgttt tggagatcac agccagggca aaaccacaca  660
gcggagctga tcatcccaga actgcctgca acacatcctc cacagaacag gactggttgt  720
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aaggatgtgc tcaccattac tctgactcct aaggtcacgt gtgttgtggt agacatcagc  840
aaggatgatc ccgaggtcca gttcagctgg tttgtagatg atgtggaggt gcacacagct  900
cagacgcaac cccgggagga gcagttcaac agcactttcc gctcagtcag tgaacttccc  960
atcatgcacc aggactggct caatggcaag gagttcaaat gcagggtcaa cagtgcagct  1020
ttccctgccc ccatcgagaa aaccatctcc aaaaccaaag gcagaccgaa ggctccacag  1080
gtgtacacca ttccacctcc caaggagcag atggccaagg ataaagtcag tctgacctgc  1140
atgataacag acttcttccc tgaagacatt actgtggagt ggcagtggaa tgggcagcca  1200
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agcaagctca atgtgcagaa gagcaactgg gaggcaggaa atactttcac ctgctctgtg  1320
ttacatgagg gcctgcacaa ccaccatact gagaagagcc tctcccactc tcctggtaaa  1380
ttctacacag gagtctatat tctgatcgga gccggcgccc tcatgatgct ggtgggcttc  1440
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SEQ ID NO: 314          moltype = AA  length = 495
FEATURE                 Location/Qualifiers
REGION                  1..495
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..495
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 314
MRIFAGIIFT ACCHLLRAFT ITAPKDLYVV EYGSNVTMEC RFPVERELDL LALVVYWEKE  60
DEQVIQFVAG EEDLKPQHSN FRGRASLPKD QLLKGNAALQ ITDVKLQDAG VYCCIISYGG  120
ADYKRITLKV NAPYRKINQR ISVDPATSEH ELICQAEGYP EAEVIWTNSD HQPVSGKRSV  180
TTSRTEGMLL NVTSSLRVNA TANDVFYCTF WRSQPGQNHT AELIIPELPA THPPQNRTGC  240
KPCICTVPEV SSVFIFPPKP KDVLTITLTP KVTCVVVDIS KDDPEVQFSW FVDDVEVHTA  300
QTQPREEQFN STFRSVSELP IMHQDWLNGK EFKCRVNSAA FPAPIEKTIS KTKGRPKAPQ  360
VYTIPPPKEQ MAKDKVSLTC MITDFFPEDI TVEWQWNGQP AENYKNTQPI MDTDGSYFVY  420
SKLNVQKSNW EAGNTFTCSV LHEGLHNHHT EKSLSHSPGK FYTGVYILIG AGALMMLVGF  480
LGCCGAVQES QCVIM                                                   495

SEQ ID NO: 315          moltype = DNA  length = 1521
FEATURE                 Location/Qualifiers
misc_feature            1..1521
                        note = Description of Artificial Sequence: Synthetic
                         polynucleotide
source                  1..1521
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 315
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gatgagcaag tgattcagtt tgtggcagga gaggaggacc ttaagcctca gcacagcaac  240
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atcacagacg tcaagctgca ggacgcaggc gtttactgct gcataatcag ctacggtggt  360
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aaggatgtgc tcaccattac tctgactcct aaggtcacgt gtgttgtggt agacatcagc  840
aaggatgatc ccgaggtcca gttcagctgg tttgtagatg atgtggaggt gcacacagct  900
cagacgcaac cccgggagga gcagttcaac agcactttcc gctcagtcag tgaacttccc  960
atcatgcacc aggactggct caatggcaag gagttcaaat gcagggtcaa cagtgcagct  1020
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atgataacag acttcttccc tgaagacatt actgtggagt ggcagtggaa tgggcagcca  1200
gcggagaact acaagaacac tcagcccatc atggacacag atggctctta cttcgtctac  1260
agcaagctca atgtgcagaa gagcaactgg gaggcaggaa atactttcac ctgctctgtg  1320
ttacatgagg gcctgcacaa ccaccatact gagaagagcc tctcccactc tcctggtaaa  1380
ttctacacag gagtctatat tctgatcgga gccggcgccc tcatgatgct ggtgggcttc  1440
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acaaagtgtg taattatgta a                                            1521

SEQ ID NO: 316          moltype = AA  length = 506
FEATURE                 Location/Qualifiers
REGION                  1..506
                        note = Description of Artificial Sequence: Synthetic
                         polypeptide
source                  1..506
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 316
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DEQVIQFVAG EEDLKPQHSN FRGRASLPKD QLLKGNAALQ ITDVKLQDAG VYCCIISYGG  120
ADYKRITLKV NAPYRKINQR ISVDPATSEH ELICQAEGYP EAEVIWTNSD HQPVSGKRSV  180
TTSRTEGMLL NVTSSLRVNA TANDVFYCTF WRSQPGQNHT AELIIPELPA THPPQNRTGC  240
KPCICTVPEV SSVFIFPPKP KDVLTITLTP KVTCVVVDIS KDDPEVQFSW FVDDVEVHTA  300
QTQPREEQFN STFRSVSELP IMHQDWLNGK EFKCRVNSAA FPAPIEKTIS KTKGRPKAPQ  360
VYTIPPPKEQ MAKDKVSLTC MITDFFPEDI TVEWQWNGQP AENYKNTQPI MDTDGSYFVY  420
SKLNVQKSNW EAGNTFTCSV LHEGLHNHHT EKSLSHSPGK FYTGVYILIG AGALMMLVGF  480
LGCCGAVQES QCKKKKKKKK TKCVIM                                       506

SEQ ID NO: 317          moltype = AA  length = 288
FEATURE                 Location/Qualifiers
source                  1..288
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 317
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EDLMLNWNRL SPSNQTEKQA AFCNGLSQPV QDARFQIIQL PNRHDFHMNI LDTRRNDSGI  120
YLCGAISLHP KAKIEESPGA ELVVTERILE TSTRYPSPSP KPEGRFQGMV IGIMSALVGI  180
PVLLLLAWAL AVFCSTSMSE ARGAGSKDDT LKEEPSAAPV PSVAYEELDF QGREKTPELP  240
TACVHTEYAT IVFTEGLGAS AMGRRGSADG LQGPRPPRHE DGHCSWPL               288

SEQ ID NO: 318          moltype = DNA  length = 7796
FEATURE                 Location/Qualifiers
source                  1..7796
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 318
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What is claimed is:

1. An engineered extracellular vesicle comprising a fusion protein, the fusion protein comprising:

at least two signaling domains, each of the at least two signaling domains being a same signaling domain and selected from the group consisting of either full length or active fragments of 4-1BBL (CDI37L), CD27L (CD70), CD30L (CD153), mCD30L, GITRL, CD40L (CD154), mCD140L, LIGHT (CD258), TL1, mTL1, FasL, NKG2 family, CD94, CD98, OX40L (CD252), and 4-1BB/TNFRSF4/CD137;

at least one linker, and

at least one vesicle targeting domain linked to the at least two signaling domains;

wherein the at least one linker comprises a fragment crystallizable region (Fc) domain,

wherein the at least one vesicle targeting domain comprises a Type II transmembrane domain, and

wherein the at least two signaling domains are in an extracellular position relative to a lipid membrane of the extracellular vesicle.

2. The engineered extracellular vesicle of claim **1**, wherein the at least one vesicle targeting domain comprises a fatty acylation site or a prenylation site, whereby the at least one vesicle targeting domain is embedded in a phospholipid bilayer of the engineered extracellular vesicle through covalent lipid attachment to the fatty acylation site or the prenylation site.

3. The engineered extracellular vesicle of claim **1**, wherein the at least one vesicle targeting domain is selected from the group consisting of sequences encoding peptides or protein domains from ADAM10, TFR2, and MARCKS comprising modified myristoylation and palmitoylation tags; sequences encoding prenylation sites and fatty acylation sites; and sequences encoding lipid affinity tags derived from KRAS, CD81, CD63, ALIX, TSG101, CD98, CD298, GPI, CD9, and CD105.

4. The engineered extracellular vesicle of claim **1**, wherein the at least one vesicle targeting domain comprises at least two exosome targeting domains.

5. The engineered extracellular vesicle of claim **1**, further comprising a tetraspanin selected from the group consisting of CD9, CD63, CD81, CD82, CD53, and CD37.

6. The engineered extracellular vesicle of claim **5**, wherein the at least two signaling domains comprise three identical signaling domains.

7. The engineered extracellular vesicle of claim **1**, comprising a plurality of the fusion protein, and wherein the density of the plurality of fusion protein is configured to support receptor clustering on a target cell.

8. The engineered extracellular vesicle of claim **1**, wherein the at least two signaling domains substantially bind to one or more of a target polypeptide.

9. The engineered extracellular vesicle of claim **1**, further comprising one or more secondary fusion proteins, each comprising a secondary signaling domain different from the at least two signaling domains of the fusion protein.

10. The engineered extracellular vesicle of claim **9**, wherein the secondary signaling domains are each independently selected from the group consisting of either full-length or active fragments of PD-L1 (CD274), PD-L2 (CD273), CTLA-4 (CD152), 4-1BBL (CD137L), HVEM

(CD270), FGL1, OX-2 (CD200), Galectin-9, PVR (CD155), Nectin-2 (CD112) isophorm alpha, Nectin-2 (CD112) isophorm delta, mNectin-2 beta, IL-10, TSG-6, B7-H3 (CD276), B7-H4 (VTCN1), B7-H5 (VISTA), B7-H7 (HHLA2), VSIG8, VSIG3 (IGSF11), VSIG4, Tim-3 (HAVCR2), Tim-4, CEACAM1 (CD66a), BTN3A1, BTN3A2, BTN2A1, BTNLR, BTN2A2, mBTN2A2, BTN1A1, TIGIT, CD27L (CD70), CD30L (CD153), mCD30L, GITRL, CD40L (CD154), mCD140L, LIGHT (CD258), TL1, mTL1, B7-1 (CD80), B7-2 (CD86), LFA-3 (CD58), SLAM (CD150), mSLAM, CD40, CD28, mCD28, CD28H/TMIGD2/IGPR1, CD2, CD48, CD226, DR3, DcR3, FasL, Tim-1 (CD365), PD-1 (CD279), mScarlet, Nanoluciferase, A2AR, PECAM-1, STAB-1, Clever-I, NRP1, NRP2, SEMA3A, SEMA3F, RGMB/DRG11, HLA DII, HMGB1, TCR, SHP-1, SHP-2, FBOX38, SH2DIA, B7RP1, IDO, NOX2, TNFRSF18/GITR/CD357, SISP1, B7-H6/NCR3LG1, APLNR, IFNg receptor, WNTSA, PAK4, IL-6, NKG2 family, NKG2 family ligands, Killer cell Ig-like receptors, CD4, CD5, CD27, CD39, CD44, CD47, CD73, CD94, CD96, CD98, 1GSF2/CD101, PVIRG/CD112R, IL5RB/CD122, OX40L (CD252), 4-1BB/TNFRSF4/CD137, KIRs/CD158 family, CD160, SIRP alpha/CD172a, CD200R, LAG-3/CD223, CD244, BTLA/CD272, B7H2/ICOSLG/B7RP1/CD275, ICOS/CD278, LIAR-1/CD305, Collagen family members, SIGLEC7/CD328, SIGLEC9/CD329, NKp30/CD337, TNFR superfamily, Nectin-like binding receptors, Nectin, IL10RA, IL10RB, TNFRSF25, TNFRSF6B, CDI13, CD30, TRAF family members, and TIM family members.

11. The engineered extracellular vesicle of claim **9**, wherein the one or more secondary fusion proteins each comprises a secondary vesicle targeting domain linked to its secondary signaling domain.

12. The engineered extracellular vesicle of claim **11**, wherein the one or more secondary vesicle targeting domains are each independently selected from the group consisting of sequence prides or protein domains from ADAM10, TFR2, and MARCKS comprising modified myristoylation and palmitoylation tags; sequences encoding prenylation sites and fatty acylation sites; and sequences encoding lipid affinity tags derived from KRAS, CD81, CD63, ALIX, TSG101, CD98, CD298, GPL CD9, and CD105.

13. An engineered extracellular vesicle comprising a fusion protein, the fusion protein comprising:

at least two signaling domains, each of the at least two signaling domains being a same signaling domain and selected from the group consisting of either full-length of active fragments of 4-1BBL (CD137L), CD27L (CD70), CD30L (CD153), mCD30L, GITRL, CD40L (CD154), mCD140L, LIGHT (CD258), TL1, mTL1 FasL, NKG2 family, CD94, CD98, OX40L (CD252), and 4-1BB/TNFRSF4/CD137;

at least one linker, and

at least one vesicle targeting domain linked to the at least two signaling domains;

wherein the at least one linker comprises a fragment crystallizable region (Fc) domain and is between the at lea st two signaling domains and the at least one vesicle targeting domain, wherein the at least one vesicle targeting domain comprises a Type II transmembrane domain, and

wherein the at least two signaling domains are in an extracellular position relative to a lipid membrane of the extracellular vesicle.

14. The engineered extracellular vesicle of claim **13**, wherein the linker is an Fc from IgG1, Fc from IgG2, Fc from IgG3, or Fc from IgG4, or wherein the linker further comprises Gly-Ser-Ser-Gly (SEQ ID NO: 319), a cleavable 2A sequence, P2A, E2A, F2A, T2A, or (GGGGS (SEQ ID NO: 320)) n.

15. The engineered extracellular vesicle of claim **13**, wherein the at least one vesicle targeting domain comprises a sequence encoding a fatty acylation site or a prenylation site, whereby the at least one vesicle targeting domain is embedded in a phospholipid bilayer of the engineered extracellular vesicle through covalent lipid attachment to the fatty acylation site or the prenylation site.

16. The engineered extracellular vesicle of claim **13**, wherein the at least one vesicle targeting domain is selected from the group consisting of sequences encoding peptides or protein domains from ADAM10, TFR2, and MARCKS comprising modified myristoylation and palmitoylation tags; sequences encoding prenylation sites and fatty acylation sites; and sequences encoding lipid affinity tags derived from KRAS, CD81, CD63, ALIX, TSG101, CD98, CD298, GPI, CD9, and CD105.

17. The engineered extracellular vesicle of claim **13**, further comprising a tetraspanin selected from the group consisting of CD9, CD63, CD81, CD82, CD53, and CD37.

18. The engineered extracellular vesicle of claim **17**, wherein the at least two signaling domains comprise three identical signaling domains.

19. The engineered extracellular vesicle of claim **13**, comprising a plurality of the fusion protein, and wherein the density of the plurality of fusion protein is configured to support receptor clustering on a target cell.

20. The engineered extracellular vesicle of claim **13**, further comprising one or more secondary fusion proteins, each comprising a secondary signaling domain different from the signaling domain of the fusion protein.

21. The engineered extracellular vesicle of claim **20**, wherein the secondary signaling domains are each independently selected from the group consisting of either full-length or active fragments of PD-L1, PD-L2, CTLA-4 (CD152), 4-1BBL (CD137L), HVEM (CD270), FOL1, OX-2 (CD200), Galectin-9, PVR (CD155), Nectin-2 (CD112) isophorm alpha, Nectin-2 (CD112) isophorm delta, mNectin-2 beta, IL-10, TSG-6, B7-H3 (CD276), B7-H4 (VTCN1), B7-H5 (VISTA), B7-H7 (HHLA2), VSIG8, VSIG3 (IGSF11), VSIG4, Tim-3 (HAVCR2), Tim-4, CEACAM1 (CD66a), BTN3A1, BTN3A2, BTN2A1, BTNL8, BTN2A2, mBTN2A2, BTN1A1, TIGIT, CD27L (CD70), CD30L (CD153), mCD30L, GITRL, CD40L (CD154), mCD140L, LIGHT (CD258), TL1, mTL1, B7-1 (CD80), B7-2 (CD86), LFA-3 (CD58), SLAM (CD150), mSLAM, CD40, CD28, mCD28, CD28H/TMIGD2/IGPR1, CD2, CD48, CD226, DR3, DcR3, FasL, Tim-1 (CD365), PD-1 (CD279), mScarlet, Nanoluciferase, AZAR, PECAM-I, STAB-1, Clever-1, NRP1, NRP2, SEMA3A, SEMA3F, RGMB/DRG11, HLA I/II, HMGB1, TCR, SHP-1, SHP-2, FBOX38, SH2D1A, B7RP1, IDO, NOX2, TNERSF18/GITR/CD357, SISP1, B7-H6/NCR3LG1, APLNR, IFNg receptor, WNTSA, PAK4, IL-6, NKG2 family, NKG2 family ligands, Killer cell Ig-like receptors, CD4, CD8, CD27, CD39, CD44, CD47, CD73, CD94, CD96, CD98, IGSF2/CD101, NECTIN2/CD112, PVIRO/CD112R, ILSRB/CD122, OX40L (CD252), 4-1BB/TNFRSF4/CD137, CTLA-4/CD152, KIRs/CD158 family, CD160, SIRP alpha/CD172a, CD200R, LAG-3/CD223, CD244, BTLA/CD272, B7H2/ICOSLG/B7RP1/CD275, ICOS/CD278, LIAR-1/CD305, Collagen family members, SIGLEC7/CD328,

SIGLEC9/CD329, NKp30/CD337, TNER superfamily, Nectin-like binding receptors, Nectin, IL10RA, IL10RB, TNERSF25, TNFRSF6B, CD113, CD30, TRAF family members, and TIM family members.

22. The engineered extracellular vesicle of claim **20**, wherein the one or more secondary fusion proteins each comprises a secondary vesicle targeting domain linked to its secondary signaling domain.

23. The engineered extracellular vesicle of claim **22**, wherein the one or more secondary vesicle targeting domains are each independently selected from the group consisting of sequences encoding peptides or protein domains from ADAM10, TFR2, and MARCKS comprising modified myristoylation and palmitoylation tags; sequences encoding prenylation sites and fatty acylation sites; and sequences encoding lipid affinity s derived from KRAS, CD81, CD63, ALIX, TSG101, CD98, CD298, GPI, CD9, and CD105.

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