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(54) ANTIBODIES TO OX-2/CD200 AND USES
THEREOF

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(57) ABSTRACT

This application provides methods and compositions for modulating and/or depleting CD200 positive cells.

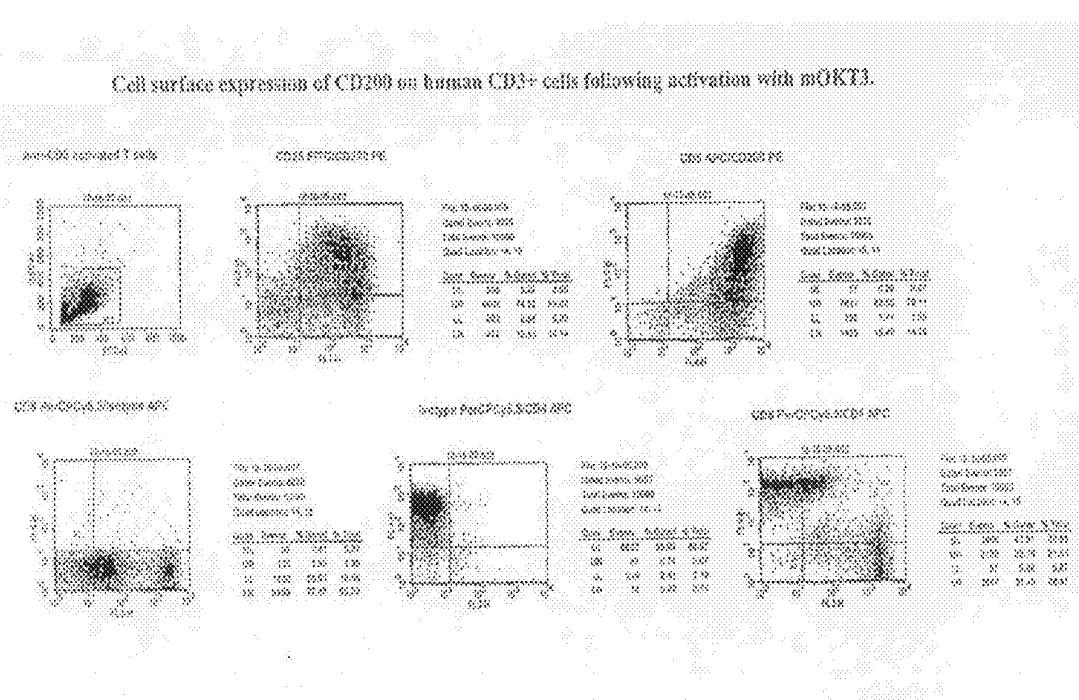


FIGURE 1

Primer C7mhHF (SEQ ID NO: 1)
TCCTCAGCCTCCACCAAGGGCC

FIGURE 2

Primer Rev Age Pri (SEQ ID NO: 2)
GGGCGCCTGAGTTCCACGAC

FIGURE 3

Primer C2aB7 rev (SEQ ID NO: 3)
GGCCCTTGGTGGAGGGCTGAGGAAACTGTGAGAGTGTTGC

FIGURE 4

lacpri (SEQ ID NO: 4)
GCTCCCGGCTCGTATGTTGTGT

FIGURE 5

LeadVHpAX (SEQ ID NO: 5)
ATATGAAATATCTGCTGCCGACCG

FIGURE 6A Note: Figs. 6-15, leader sequences (AA) are underlined and constant regions are in bold.

chC2aB7-hG1

Heavy chain (introns in hG1) (SEQ ID NO. 7)

MGWSCIILFLVATATGVHSLEVQLQQSGPELVKGASLKM**SCKASGY**SFT
DYIILWVKQNHGKSLEWIGHIDPYYGSSNYNL**KFKGKATLTVDKSS**STAY
MQLNSLTSEDSAVYYCGRSKRDYFDYWGQGTTLVSSAST**KGPSVF**PLA
PSSK**STSGGT**AALGCLVKDYFPEPVTVSWNSGALTSGVHTFP**AVLQSS**
GLYSLSSVVTPSSSLGTQTYICNVNH**KPSNTKVDRVEPKSCDKTHT**
CPPCPAPELLGGPSVFLFPPKP**KDTLMISRTPEVTCVVVDVSHEDPEV**
KFNWYVDGVEVHNAKT**KPREEQYNSTYRVVSVLTVLHQDWLNGKE**
YKCKVSNKALPAPIEKTISKAKGQP**REPQVYTLPPSREEMTKNQVS**LT
CLVK**GFYPSDI**AVEWESNGQP**EENNYKTTPVLDSDGSFFLYSKLTV**DK
SRWQQGNVFSCSVM**HEALHNHYTQKSLSLSPGK**

FIGURE 6B

(SEQ ID NO. 6) (genomic sequence hG1)

ATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGTGTCCACTCCCTCGAG
GTCCAGCTGCAACAGTCTGGACCTGAGCTGGTGAAGCCTGGGCTTCACTGAAGATGTCTGC
AAGGCTTCTGGTATTCACTCACTACATCATACTCTGGTGAAGCAGAACCATGGAAAG
AGCCTTGAGTGGATTGGACATATTGATCCTACTATGGTAGTTCTAACTACAATCTGAAATTCA
AGGGCAAGGCCACATTGACTGTAGACAAATCTCCAGCACAGCCTACATGCAGCTAACAGT
CTGACATCTGAGGACTCTGAGTCTATTACTGTGGAAGATCTAAGAGGGACTACTTGACTAC
TGGGCCAAGGCACCACTCTCACAGTTCTCAGCCTCCACCAAGGGCCATCGTCTTCCCC
CTGGCACCCCTCCTCCAAGAGCACCTCTGGCGGCACAGCGCCCTGGCTGCCTGGTCAAGGAC
TACTTCCCCGAACCGGTGACGGTGTGAGACTCAGGGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCA
GCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG
GACAAGAGAGTTGGTAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTC
AGCGCTCCTGCCTGGACGCATCCCGCTATGCAGTCCAGTCCAGGGCAGCAAGGCAGGCC
CGTCTGCCTCTCACCCGGAGGCCCTGCCCCCCCCACTCATGTCAGGGAGAGGGTCTCTG
GCTTTTCCCCAGGCTCTGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAA
AGGGGCAGGTGCTGGCTCAGACCTGCCAAGAGCCATATCCGGAGGGACCCCTGCCCTGACC
TAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCGGACACCTCTCTCCTCCCAGA
TTCCAGTAACTCCAACTTCTCTGCAGAGCCAAATCTGTGACAAAACTCACACATGCC
ACCGTGCCAGGTAAAGCCAGGCCAGGCCCTGCCCTCAGCTCAAGGGGACAGGTGCCCTA
GAGTAGCCTGCATCCAGGGACAGGCCAGGCCAGCCGGTGTGACACGTCACCTCCATCTCITCC
TCAGCACCTGAACTCCTGGGGGACCGTCAGTCTCTCTCITCCCCAAAACCCAAAGGACACC
CTCATGATCTCCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGGCCAGAAGACCC
GAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCG
GGAGGAGCAGTACAACAGCACGTACCGTGTGGTACAGCGTCCCTACGGTCTGCACCCAGGACT
GGCTGAATGGCAAGGAGTACAAGTGCAGGGCTCCAAACAAAGCCCTCCCAGCCCCATCGAG
AAAACCATCTCCAAAGCCAAAGGTGGACCCGTGGGGTGCAGGGCCACATGGACAGAGGCC
GGCTCGGCCCCACCCCTGCCCCGTGAGGTACAGCGTCCCTACGGTCTGCACCCAGGACT
CCCGAGAACCAAGGTGTACACCCCTGCCCTACAGGGAGGAGATGACCAAGAACCAAGGTC
AGCCTGACCTGCCTGGTCAAAGGCTCTATCCAGCGACATGCCGTGGAGTGGAGAGCAAT
GGCAGCCGGAGAACAAACTACAAGACCACGCCCTCCCGTGTGGACTCCGACGGCTCCCTCTC
CTCTATAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGAAACGTCTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCAACTACACGCAGAAGAGCAGCTCCCTGTCCCCGGTAAA
TGA

FIGURE 6C: A schematic representation of the heavy chain of antibody chC2aB7-hG1.

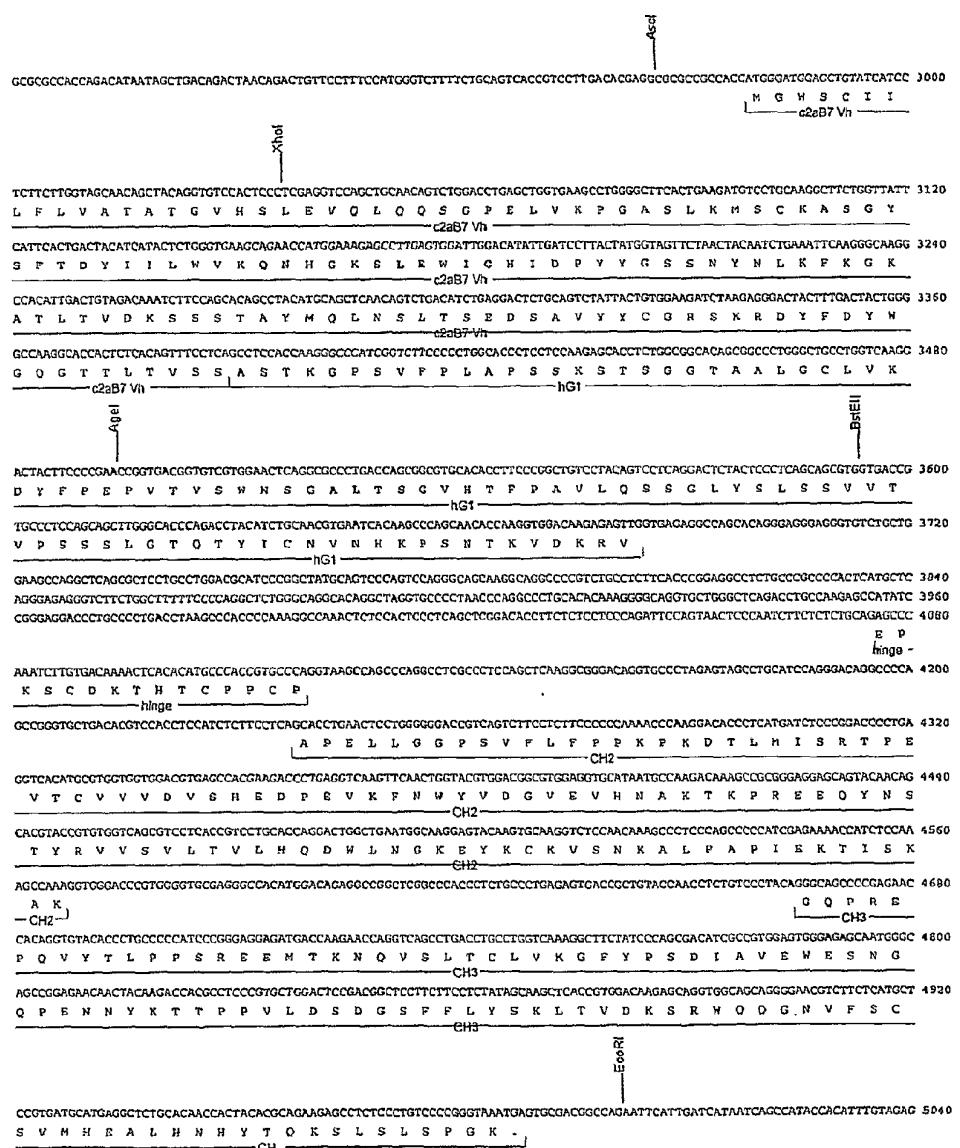


FIGURE 6D

Light Chain (human Ck) (SEQ ID NO. 24)

MGWSCIILFLVATATGVHSRDIQMTQSPSSMYASLGERVTITCKASQDINSYL
SWFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGQDYSLTISSLEYEDMGIY
YCLQYDEFPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN
FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 6E

(SEQ ID NO. 23)

ATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGTGT
CCACTCTAGAGACATCCAGATGACACAGTCATCCATCTCCATGTATGCATC
TCTAGGAGAGAGAGTCACTATCACTTGCAAGGCGAGTCAGGACATTAATA
GCTATTAAAGCTGGTCCAGCAGAAACCAGGGAAATCTCCTAACAGACCCCTG
ATCTATCGTCAAACAGATTGGTAGATGGGTTCCATCAAGGTTCAAGTGG
CAGTGGATCTGGCAAGATTATTCTCTACCACAGCAGCCTGGAGTATG
AAGATATGGAAATTATTATTGTCTACAGTATGATGAGTTCCGTACACGT
TCGGAGGGGGGACCAAGCTGGAATAAAAACGGACTGTGGCTGCACCATC
TGTCTCATCTTCCC GCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTC
TGTTGTGCGCTGCTGAATAACTCTATCCCAGAGAGGCCAAAGTACAGT
GGAAGGTGGATAACGCCCTCCAATGGGTAACTCCCAGGAGAGTGTCA
AGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACG
CTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCA
CCCATCAGGGCCTGAGCTGCCGTACAAAGAGCTTCAACAGGGAGA
GTGTTAA

FIGURE 6F: A schematic representation of the light chain of antibody chC2aB7-hG1.

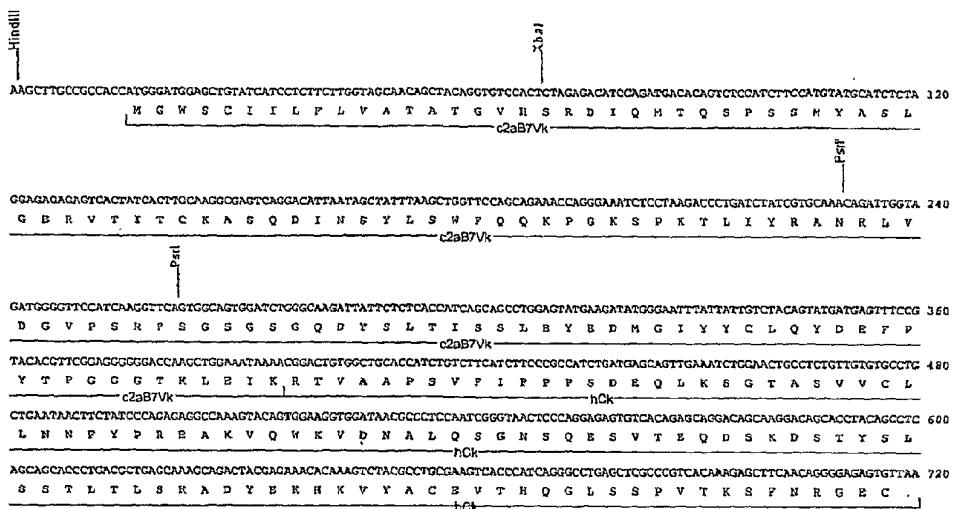


FIGURE 7A

hB7V4V1-hG1

Heavy chain (SEQ ID NO. 9)

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M G W S W I F L F L L S V T A G V F S E V Q L V E S G P E V K K P G A S V K V S C K A S G Y S F D
Y I I L W I R Q H S G K G L E W I G H I D P Y Y G S S N Y N L K F K G R V T I T A D K S T R T T Y M E
L T S L T S E D T A V Y Y C G R S K R D Y F D Y W G Q G T T L V S S A S T K G P S V F P L A P S S
K S T S G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L
Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V D K R V E P K S C D K T H T C P
P C P A P E L L G G P S V F L F P P K P K D T L M I S R T P E V T C V V D V S H E D P E V K F
N W Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y K
C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L
V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D G S F F L Y S K L T V D K S R
W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K

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FIGURE 7B

(SEQ ID NO. 8) (cDNA hG1)

ATGGGATGGAGCTGGATCTTCTCTTCCTGTCACTGCAGGTG
TGTTCTCTGAGGTCCAGCTGGTGGAGTCCGGACCTGAGGTGAAGAAC
CTGGGGCTTCAGTGAAGGTGTCCTGCAAGGCTCTGGTTATTCAATTAC
TGACTACATCATACTCTGGATCAGGCAGCATAGCGAAAGGGCCTGA
GTGGATTGGACATATTGATCCTTACTATGGTAGTTCTAACTACAATCTG
AAATTCAAGGGCAGGGTCACAATCACTGCAGACAAATCTACCAGGAC
AACCTACATGGAGCTCACCACTGACATCTGAGGACACTGCAGTCTA
TTACTGTGGAAGATCTAAGAGGGACTACTTGACTACTGGGGCCAAGG
CACCACTCTCACAGTTCTCAGCCTCCACCAAGGGCCCACCGGTCTTC
CCGCTAGCACCTCCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTG
GGCTGCCTGGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGTTGG
AACTCAGGCGCCCTGACCAGCGCGTGCACACCTCCGGCTGCTCTA
CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCCTCC
AGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGGCCAAATCTGTGACAA
AACTCACACATGCCACCGTGCCAGCACCTGAACCTGGGGACC
GTCAGTCTCCTCTTCCCCAAAACCAAGGACACCCCTATGATCTCC
CGGACCCCTGAGGTACATGCGTGGTGGACGTGAGGCCACGAAGA
CCCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA
TGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG
TGGTCAGCGTCTCACCGTCTGCACCAAGGACTGGCTGAATGGCAAGG
AGTACAAGTGCAAGGTCTCAAACAAAGCCCTCCAGCCCCATCGAG
AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTA
CACCCCTGCCCTCCATCCGGGAGGAGATGACCAAGAACCAAGGTG
TGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATGCCGTGGAGT
GGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCAAGGTG
GTGCTGGACTCCGACGGCTCCTCTTCTACAGCAAGCTCACCCTG
GACAAGAGCAGGTGGCAGCAGGGAACGTCTTCTATGCTCCGTGAT
GCATGAGGCTCTGCACAACCAACTACACGCAGAAGAGCCTCTCCGTG
TCCGGTAAATGA

FIGURE 7C: A schematic representation of the heavy chain of antibody hB7V4V1-hG1.

The diagram illustrates the heavy chain of antibody hB7V4V1-hG1. It features a top section labeled "V4V1" with a leader sequence, followed by a hinge region, and a bottom section labeled "G1". The hinge region contains restriction sites for BstEII, KpnI, and SmaI. The G1 domain contains restriction sites for Bpu111I and AgeI.

Sequence details from the patent:

- V4V1 Domain:**
 - 5160: CNTGGATGGAAGCTGGATCTTTCCTCCGTCACTGACGGTGTTCTGAGGTCAGCTGGTAGAGTCGGACCTGAGGTGAAAGAGCCGGGCTTCAGTGAAGGTGTC
 - 5280: CTCGAACTCTCTGGTTAATCATTCAGTCACTACATCATCTCTGGATCAGGCCAGATAAGCCAABGGGCTCTGGATGGACATATGGATCTACTATGGTAGTTCTAACTACAA
- Hinge Region:**
 - 5400: TCTGAAATTCAAGCCACGGCTCACATCACTGGACACAAATCTAACCGGACAACCTACATGGACTCAGCCAGTCTGACATCTGACGACACTGCTATTA
 - 5520: CGACTACTTTGACTACTGGGCCACGGCACCACTCTCACAGCTTCTCAAGCTCCACCAACGGCCACCTCTCCACGACCCACCTCTGGGGCACACGGGC
- G1 Domain:**
 - 5640: CCTGGGCTGCCGCTGGCAAGGACTACTTCCCCGAAACGGTCACTGGTGGACTACGGGCCCCTGACCAAGGGCCGTCACACACCTCCCGGCTGCTCACAGTCCTGAGGACTCTACTC
 - 5760: 5880: CTCAAGCTCACATGCCACCGCTGCCAGACCTGAACTCTGGGGGGAACGGCTGCTTCACCTTCCCAAAACCCAGGAACCCCTGATGATCTCCGGACCCCTGAGGTCACATG
 - 6000: CGTGGGAGTGGACGTGAGCCACGARGAACCTGAGGTCAACTTCACTGGTACGGTACGGGGGGGGGCTTAATGCCAACACAAAGCCGGGAGGGCACTACACAGCACGTACCG
 - 6120: TGTGGTCAAGCTCTCACCTCTCTGCCACAGGACTCTGCTGATGCCAGGAACTACAGCTGCTCACAAACCCCTCCAGGCCCATGGRANACCATCTCCAAAGCCAAAGG
 - 6240: GCAGCCCCGAGAACCAACAGGTGTACACCCCTGCCCCTACACCGGGAGGAGATGCCAGAACAGGTGAGCTGACCTGCTGGTCAGGGCTCTATCCAGCACCTGGGGAGTG
 - 6360: CGAGACGAACTGGCGAGAACACACTACAGGACCAACGCCCTGGCTGGACTCCAGGCTCTCTGCTCACAGGACTCACCGTGACAGAGCAGGTOGCAGGGGAA
 - 6442: CGCTCTCTCATGCTCTGGTGTGAGGCTCTGACAGAACCTACAGGAGAGACGGCTCTCCCTGCTCCGGGTAAATGCA

FIGURE 7D

Light chain (human Ck) (SEQ ID NO. 26)

**MDMRVSAQLLGLLLWLSGARCDIQMTQSPSSLSASIGDRVVTITCKASQD
INSYLSWYQQKPGKAPKSLIYRANLVDGVPSSRSGSGSGTDYTLTISSLQ
PEDFAVYYCLQYDEFPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC**

FIGURE 7E

(SEQ ID NO. 25)

ATGGACATGAGGGTCTCTGCTCAGCTCCTGGGGCTCCTGCTGCTCTGG
CTCTCAGGAGCCAGATGTGACATCCAGATGACACAGTCTCCATCTTCC
CTGTCTGCATCTATAGGAGACAGAGTCACTATCACTTGCAAGGCGAGT
CAGGACATTAATAGCTATTAAAGCTGGTACCAAGCAGAAACCAGGGAA
AGCTCCTAAGTCCCTGATCTATCGTCAAACAGATTGGTAGATGGGT
TCCATCAAGGTTCAGTGGCAGTGGATCTGGACAGATTATACTCTCAC
CATCAGCAGCCTGCAGCCTGAAGATTGCAGTTATTATTGTCTACA
GTATGATGAGTTCCGTACACGTTGGAGGGGGGACCAAGCTGGAAAT
AAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCACATCTGAT
GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGCTGCTGAATAAC
TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTC
CAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACT
ACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTG
AGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAG

FIGURE 7F: A schematic representation of the light chain of antibody hB7V4V1-hG1.

FIGURE 8A
hB7V3V1-hG1 (SEQ ID NO. 11)
Heavy chain

MGWSRIFLFLLSIIAGVHCQVQLQQSGSELKKPGASVKISCKASGYSFTDY
IIIWVRQNPGKGLEWIGHIDPYYGSSNNLKFGRVTITADQSTTTAYME
LSSLRSEDTAVYYCGRSKRDYFDYWQGQTTLVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL
YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP
PCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTIASKAKGQPREPQVYTLPPSREEMTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 8B

(SEQ ID NO. 10) (cDNA hG1)

ATGGGATGGAGCCGGATCTTCTTCCTCTGTCAATAATTGCAGGTG
TCCATTGCCAGGTCCAGCTGCAACAGTCTGGATCTGAGCTGAAGAAGC
CTGGGGCTTCAGTGAAGATCTCCTGCAAGGCTCTGGTTATTCAATTAC
TGACTACATCATACTCTGGGTGAGGCAGAACCCCTGGAAAGGGCCTG
GTGGATTGGACATATTGATCCTTACTATGGTAGTTCAACTACAATCTG
AAATTCAAGGGCAGAGTGACAATCACCGCCGACCAGTCTACCAC
AGCCTACATGGAGCTCTCAGTCTGAGATCTGAGGACACTGCAGTCTA
TTACTGTGGAAGATCTAAGAGGGACTACTTGACTACTGGGGCCAAGG
CACCACTCTCACAGTTCTCAGCCTCCACCAAGGGCCCATCGGTCTC
CCGCTAGCACCCCTCCCAAGAGCACCTCTGGGGCACAGCGGCCCTG
GGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGG
AACTCAGGCGCCCTGACCAGCGCGTGACACCTCCGGCTGTCCTA
CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCC
AGCAGCTGGCACCCAGACCTACATCTGCAACGTGAATACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
AACTCACACATGCCACCGTGCCAGCACCTGAACCTCTGGGGGACC
GTCAGTCTTCCTCTCCCCAAAACCCAAGGACACCCCTCATGATCTCC
CGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCACGAAGA
CCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA
TGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG
TGGTCAGCGTCTCACCCTGCAACAGGACTGGCTGAATGGCAAGG
AGTACAAGTGCAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAG
AAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCCACAGGTGTA
CACCCCTGCCCATCCCCGGAGGAGATGACCAAGAACCAAGGTGAGC
TGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATGCCGTGGAGT
GGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCAAGGTGAGC
GTGCTGGACTCCGACGGCTCTTCTTACAGCAAGCTCACCCTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTCATGCTCCGTGAT
GCATGAGGCTCTGCACAACCAACTACACGCAGAAGAGCCTCTCCCTGTC
TCCGGGTAAATGA

FIGURE 8C: A schematic representation of the heavy chain of antibody hB7V3V1-hG1.

FIGURE 8D
Light chain (human Ck) (SEQ ID NO. 26)

MDMRVSAQLLGLLLLWLSGARCDIQMTQSPSSLASIGDRVITICKASQD
INSYLSWYQQKPGKAPKSLIYRANRLVDGVPSRFSGSGSGTDYTLTISSLQ
PEDFAVYYCLQYDEFPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGT
ASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 8E

(SEQ ID NO. 25)

ATGGACATGAGGGTCTTGCTCAGCTCCTGGGCTCTGCTGCTCTGG
CTCTCAGGAGCCAGATGTGACATCCAGATGACACAGTCTCCATCTTCC
CTGTCATCTATAGGAGACAGAGTCACTATCACTGCAAGGCAGT
CAGGACATTAATAGCTATTAAAGCTGGTACCGAGCAGAAACCAGGGAA
AGCTCCTAAGCTTCAAGGTTCAAGTGGCAGTGGATCTGGACAGATTAGTGGTAGATGGGGT
TCCATCAAGGTTCAAGTGGCAGTGGATCTGGACAGATTAGTGGTAGATGGGGT
CATCAGCAGCCTGCAGCCTGAAGATTTCGAGTTATTATTGTCTACA
GTATGATGAGTTCCGTACACGTTGGAGGGGGACCAAGCTGGAAAT
AAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGAT
GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGCCTGCTGAATAAAC
TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTC
CAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCCGTACGCTGAGCAAAGCAGACT
ACGAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCTG
AGCTCGCCCGTCACAAAGAGCTAACAGGGGAGAGTGTAG.

FIGURE 8F: A schematic representation of the light chain of antibody hB7V3V1-hG1.

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TTCATGGCTTTCTCAGTCACUTCTTGACAG/AGCT/GCCACATGACAGGGCTCTGCTACCTCTSGGCCCTGCTGCTGCTAGGGAGCCAGGT 11400
M D H R V S A Q L L G L L L H L S G A R C
leader
GACATCCAGATGAAACAGCTCCTCACTCTCCCCTGCTGCACTATAGGAGACAGAGCTACTAATCTGCAGAGGCGTACAGSACRITATAGCTATTAGCTGCTACAGGAGAACCA 11520
D I Q M T O S P E S L S A S I G D R V T I T C K A S Q D I N S Y L S W Y Q Q K P
VIVK

GCGAAAGCTCTAAGTCCCTGATCTATCOTGCAAACAGATTGGTAGATGGGGTCCATCAAGGTGAGSTGGAGCTGGAGCAGATTAACTCTCACCATCACGAGCCIGCAGCT 11640
G K A P K S L I Y R A N R L V D G V P S R F S G S G S G T D Y T L T I S S L O P
VIVK

GAGAGTTCCGAGTTATATATCTACAGTAATGAGTTCCGTACA CGTTCCGAGGGGGGACCAAGCTGGAAATAAGCTACCGTGGCTGCACCATCTGCTCTTCACTCTCCCCCA 11760
E D F A V Y Y C L Q Y D S F P Y T F G G G T K L E I K R T V A A P S V F I F P P
VIVK
hCk
TCTGATGAGCAGTGAAATCTGAACTCTGCTGTGCTGCTGCTGAGATACCTCTATCCCGAGGAGGCGAAGCTACAGTGGAGGTGGTAAAGCCCTCCGATCGGTAATCTCCAG 11880
S D E O L K S G T A S V V C L L R N F Y P R E A K V Q W R V D N A L O S G N S Q
hCk
GAGAGTGTCAAGAGCAGGAGCAAGGAGCAAGCACTACAGGCTCAGCAAGCAGCTGAGCTGAAGAGCAGCTACAGCAAGCTAAGCTAACCCCTGGAGCTACCCATCAAGGC 12000
E S V T E D D S K D S T Y S L S T L T L S K A D Y E H H K V Y A C E V T H Q G
hCk
CTGAGCTCCCGTGAGCAAGAGCTCAACAGGGAGCTGCTTAG 12045
L S S P V T K S F N R G E C
hCk

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FIGURE 9A

hB7V3V2-hG1

Heavy chain (SEQ ID NO. 11)

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MGWSRIFLFLLSIAGVHCVQLQQSGSELKPGASVKISCKASGYSFTDY
IIIWVRQNPNGKGLEWIGHIDPYYGSSNYNLKFKGRTVTITADQSTTAYME
LSSLRSEDTAVYYCGRSKRDYFDYWQGTTLTVSSASTKGPSVFPLAPSS
KSTSGGTAAALGCLVKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGL
YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTCP
PCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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FIGURE 9B

(SEQ ID NO. 10) (cDNA hG1)

ATGGGATGGAGCCGGATTTCTCTCCTCTGTCAATAATTGCAGGTG
TCCATTGCCAGGTCCAGCTGCAACAGTCTGGATCTGAGCTGAAGAACG
CTGGGGCTTCAGTGAAGATCTCCTGCAAGGCTCTGGTATTCAATTAC
TGACTACATCATACTCTGGGTGAGGCAGAACCTGGAAAGGGCCTTGA
GTGGATTGGACATATTGATCCTTACTATGGTAGTTCTAACTACAATCTG
AAATTCAAGGGCAGAGTACAATCACCGCCGACCAGTCTACCAAC
AGCCTACATGGAGCTCTCAGTCTGAGATCTGAGGACACTGCAGTCTA
TTACTGTGGAAGATCTAACAGAGGGACTACTTGACTACTGGGGCCAAGG
CACCACTCTCACAGTTCTCAGCCTCCACCAAGGGCCATCGGTCTTC
CCGCTAGCACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTG
GGCTGCCTGGTCAAGGACTACTCCCCGAACCGGTACGGTGTGCGTGG
AACTCAGGCGCCCTGACCAGCGCGTGCACACCTCCCGTGTCTTA
CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCCTCC
AGCAGCTGGGACCCAGACCTACATGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTTGACAA
AACTCACACATGCCACCCTGCCCCAGCACCTGAACCTCTGGGGGACC
GTCAGTCTCCTCTTCCCCAAAACCCAAGGACACCCCTCATGATCTCC
CGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCACGAAGA
CCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA
TGCCAAGACAAAGCCGGGGAGGAGCAGTACAACACAGCACGTACCGTG
TGGTCAGCGCCTCACCGCCTGCACCAGGACTGGCTGAATGGCAAGG
AGTACAAGTGAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAG
AAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCAACAGGTGTA
CACCCCTGCCCCCATCCCCGGAGGAGATGACCAAGAACCAACAGGTGAGC
TGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATGCCGTGGAGT
GGGAGAGCAATGGGAGCCGGAGAACAAACTACAAGACCAACGCCCTCCC
GTGCTGGACTCCGACGGCTCCTCTTACAGCAAGCTCACCGTG
GACAAGAGCAGGGTGGCAGCAGGGGAACGTCTCTCATGCTCCGTGAT
GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTC
TCCGGGTAAATGA

FIGURE 9C: A schematic representation of the heavy chain of antibody hB7V3V2-hG1.

FIGURE 9D
Light Chain (human Ck) (SEQ ID NO. 28)

FIGURE 9E

(SEQ ID NO. 27)

ATGGACATGAGGGTCTTGCTCAGCTCCTGGGCTCCTGCTGCTCTGG
CTCTCAGGGGCCAGGTGTGACATCCAGATGACACAGTCTCCATCTTCC
CTGTCTGCATCTATAGGAGACAGAGTCACTATCACTGCAAGGCGAGT
CAGGACATTAATAGCTATTAAAGCTGGTCCAGCAGAAACCAGGGAA
AGCTCCTAACAGCTGCTGATCTATCGTCAAACAGATTGGTAGATGGGT
TCCATCAAGGTTAGTGGCAGTGGATCTGGACAGATTATACTCTCAC
CATCAGCAGCCTGCAGCCTGAAGATTTCGCAGTTATTATTGTCTACA
GTATGATGAGTTCCGTACACGTTGGAGGGGGACCAAGCTGGAAAT
AAAACGTACGGTGGCTGCACCATCTGTCTCATCTCCGCCATCTGAT
GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGCCTGCTGAATAAC
TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTC
CAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACT
ACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTG
AGCTCGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGTAG

FIGURE 9F: A schematic representation of the light chain of antibody hB7V3V2-hG1.

TTTCCATGGGCTTCTCGCTGCAAGCTTGACAGCAGCTTGGGCCACATTGAGCAGGGGCTCTGGCTCAGCTCTGGGCTCTGGCTCTGGCTCTGGCTCTCAAGGCGGAGGTG 11400
 H D M R V S A Q L L G L L L W L S C A R C
 leader
 GACATCAGAGAACAGACTCTTCATCTTCCCCTGCTGCACTCTATAGGAGACAGAGCTACTATCACTCTGGCAGAGGAGTCAGGAGCATTAATAGCTTAAAGCTGTTCCAGGAGAGCCA 11520
 D I Q M T Q S P S S L S A S I G D R V T T C K A S O D I N S Y L S H F Q Q K P
 V2V
 P5'
 5'
 GGGAAAGCTCTTAACTCTGATCTATCGTCACAAAGATTTGCTAGATGGGGTCCATCAAGGTCAAGTGGGATGGATCTGGGACAGAATTATACTCTCACCCATCACGAGCTGCAGGCT 11640
 G K A P K L L I Y R A N R L V D G V P S R F S G S G S G T D Y T L T I S S L Q P
 V2V
 P5'
 5'
 GAAGATTTGCGAGTTTTATTTCTACAGTATGATGAGTTTCCTGATACACGTCGGAGGGGGGAGACAGCTGGGAATTAACGCTACGTTGGCTTGACAOATCTGCTTCACTTCCCGC 11760
 B D F A V Y Y C L Q Y D E F P Y T F G G G T K L B E I K R T V A A P S V F I F P P
 V2V
 hCK
 S D E O L K S G T A S V Y N F Y P R E A K V Q W K V D N A L O S G N S O
 hCK
 TCTGAAGGAGCTGAACTCTGGAACCTGGCCCTTGTGCTCTGATANACTCTTACCGAGACAGGCOVAGTACGAGTGGATAAGCCCTCCTACGGCTTACCTCCCG 11880
 S D E O L K S G T A S V Y N F Y P R E A K V Q W K V D N A L O S G N S O
 hCK
 GAGAGTCTCACAGGAGGAGCACGAGCACAGCACCTTCAGCTTCAAGCAGACAGAGCTACGAGCAACAGAGCTACGAGAGAACACAAAGTCTACGGCTGGGAAGTCAACGAGC 12000
 E S V T E O D S K P D S T Y S L S S T L Y T L S K A D Y E K K H V Y A C E V T H O G
 hCK
 CTGACCTGCGCGCTACAACAGCTTCAACAGGGAGAGTGTAG 12045
 L S S P V T K S F N R G E C
 hCK

FIGURE 10A

hB7V3V2-hG2G4
Heavy chain (SEQ ID NO. 13)

MGWSRIFLFLLSIAGVHCQVLQQSGSELKKPGASVKISCKASGYSFTDY
ILWVRQNPGKGLEWIGHIDPYGGSSYNLKFGRVTITADQSTTTAYME
LSSLRSEDTAVYYCGRSKRDYFDYWQGTTLVSSASTIKGPSVFPLAPC
SRSTSESTAALGCLVKDVFPEPVTVSWNSGALTSGVHTFPAVLQSSGL
YSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCP
APPVAGPSVLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV
DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTPPVLDSDGSFLYSRLTVDKSRWQEG
NVFSCSVMHEALHNHYTQKSLSLSGK

FIGURE 10B

(SEQ ID NO. 12) (genomic sequence hG2G4)

ATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGTGTCCACTCCCTCGAG
GTCCAGCTGCAACAGCTGGACCTGAGCTGGTAGCAGGCTGGGCTTCACTGAAGATGTCCCTGC
AAGGCTCTGGTTATTCACTCACTGACTACATCATACTCTGGGTGAAGCAGAACCATGAAAG
AGCCTTGAGTGGATTGGACATATTGATCCTTAATGGTAGITCTAACTACAATCTGAAATTCA
AGGGCAAGGCCACATTGACTGTAGACAAATCTTCCAGCACAGCCTACATGCAGCTAACAGT
CTGACATCTGAGGACTCTGCAGTCTATTACTGTGGAAAGATCTAAGAGGGACTACTTGACTAC
TGGGCCAAGGCACCACTCTCACAGTTCCAGCAGCTCCAGGAGCACAGCCGCTGGCTGCCGTCAAGGA
CTACTTCCCCGAACCGGTGACGGTGTGGAACTCAGGCGCCCTGACCAGCGCGTGCACAC
CTTCCCGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCCTCC
AGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGT
GGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTC
AGCCCTCCTGCCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCC
CATCTGTCTCCTCACCCGGAGGGCTCTGCCGCCACTCATGCTCAGGGAGAGGGTCTCTG
GCTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCTACCCAGGCCCTCACACA
CAGGGGCAGGTGCTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCCTGCCCTGAC
CTAACCGACCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGAACCTCTCTCCCTCCAG
ATCCGAGTAACTCCCAATCTCTCTGCAAGCGCAAATGTTGTGTCAGTGCCACCGTGC
CCAGGTAAGCCAGCCAGGCCCTGCCCTCAGCTCAAGGCGGACAGGTGCCCTAGAGTAGC
CTGCATCCAGGGACAGGCCCTAGCTGGGTGCTGACACGTCCACCTCCATCTCTCCCTCAGCAC
CACCTGTGGCAGGACCGTCAGTCTCTCTTCCCCAAAACCCAAGGACACCCCTCATGATCT
CCCGGACCCCTGAGGTACGTGCGTGGTACGGTACGGTACGGTACGGTACGGTACGGTACGG
TTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGGAGGAGCA
GTTCAACAGCACGTACCGTGTGGTCAGCGCTCCTCACCGTCTGCACCGAGACTGGCTGAACGG
CAAGGAGTACAAGTCAAGGTCTCAACAAAGGCCCTCCCGCCTCCATCGAGAAAACCATCT
CCAAAGCCAAGGTGGGACCCACGGGTGCGAGGGCCACATGGACAGAGGTACGCTCGGCC
ACCCCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGCTCCCTACAGGGCAGCCCCGAGAGCC
ACAGGTGTACCCCTGCCCTACCCAGGAGGAGATGACCAAGAACCAAGGTACGCCCTGACCT
GCCCTGGTCAAAGGCTCTACCCAGCGACATGCCGTGGAGTGGAGAGCAATGGCAGGCC
GAGAACAAACTACAAGACCACGCCCTCCCGTGTGGACTCCGACGGCTCCCTTCCCTACAGC
AGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGAAATGTCTCTCATGCTCCGTGATGCA
TGAGGCTCTGCACAACCACTACACACAGAACAGCCTCCCTGTCTGGTAAATGATGA

FIGURE 10C: A schematic representation of the heavy chain of antibody hB7V3V2-hG2G4.

FIGURE 10D

Light Chain (human Ck) (SEQ ID NO. 28)

MDMRVSAQLLGLLLWLSGARCDIQMTQSPSSLSASIGDRVITCKASQD
INSYLSWFQQKPGKAPKLLIYRANRLVDGVPSRFSGSGSGTDYTLTISSLQ
PEDFAVYYCLQYDEFPYTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE

FIGURE 10E

(SEQ ID NO. 27)

ATGGACATGAGGGTCTCTGCTCAGCTCCTGGGGCTCCTGCTGCTCTGG
CTCTCAGGGGCCAGGTGTGACATCCAGATGACACAGTCTCCATCTCC
CTGTCTGCATCTATAGGAGACAGAGTCACTATCACTTGCAAGGCGAGT
CAGGACATTAATAGCTATTAAAGCTGGTCCAGCAGAAACCAGGGAA
AGCTCCTAACGCTGCTGATCTATCGTCAAACAGATTGGTAGATGGGGT
TCCATCAAGGTTCAGTGGCAGTGGATCTGGACAGATTATACTCTCAC
CATCAGCAGCCTGCAGCCTGAAGATTGGCAGTTATTATTGTCTACA
GTATGATGAGTTCCGTACACGTCGGAGGGGGACCAAGCTGGAAAT
AAAACGTACGGTGGCTGCACCATCTGTCTCATCTCCGCCATCTGAT
GAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGCGCTGCTGAATAAC
TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTC
CAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACT
ACGAGAAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTG
AGCTCGCCCCGTACAAAGAGCTTCAACAGGGAGAGTGTAG

FIGURE 10F: A schematic representation of the light chain of antibody hB7V3V2-hG2G4.

TTCCATGGGCTTTCTGCACTACCGTCCTGACACGAGCTTCCGCCACCATGAGCTCAGGCTCTGGGCTCTGGCTCTGCTCTGGGCTCAGGGGCAAGGTGT 11400
 M D M R V S A O L L G L L L W L S G A R C
 leader
 GACATCCAGATGACAGTCATCTTCCCTGCACTATAGAGAACAGTACTAATCTTGCAAGGGCAGAGCAAGGAACTTACAGCTTACAGGCTCTGGGCTCAGGGGCAAGGTGT 11520
 D I O M T Q S P S S L S A S I G D R V T I T C K A S O D I N S Y L S R F O O K P
 V2V
 PstI PstI
 GGAAACCTCTAAGCTGCTGATCTATCGTCAAACAGATTGGTAGAGTGGGCTCCATCAAGGTCTAGTGGGAGTGGATCTGGGACAGATTATACTCTCACCTCACCGAGCTGCAGCCT 11640
 G K A P K L L I Y R A N R L V D G V P R F S G S G S G T D Y T L T I S S L O P
 V2V
 BsmBI
 GAAGATTTCGCAAGTTTATTATGCTCTACAGTATGATGAGTTCTCGTACACTTCCGGAGGGGGAGCAAGCTGAAATAAAACGTCGGTGGCTGACCCCTGCTCTTCATCTTCCGGCA 11760
 E D F A V Y Y C L Q Y D E F P Y T F G G G G T K L E I K R T V A A P S V F I F P P
 V2V
 hCk
 TCTGATGAGCAAGTGTGAATCTGGACTGCTCTGCTGTTGCTGCTGTAATANACTCTATCCAGGAGGGCCAGCTGAAAGTACAGTGGAGGTGGATACCCCTCCATCGGGTAACCTCCCG 11880
 S D E O L K S G T A S V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q
 hCk
 GAGAGTCTCACAGAGCAGGAGCAGCAAGGAGCACACCTACAGGCTGAGCAAGCTGAGCTGAGCAAGGAGACTACGGAGRAACAAAGCTACCCGCTGCGAGTCACCCATCAGGGC 12000
 E S V T B O D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C S V T H Q G
 hCk
 CTAGGCTGCGCCGTCAACAGAGCTTCACAGGGGAGAGTGTGAG 12045
 L S S P V T K S F N R G E C .
 hCk

FIGURE 11A
chC2aB7-hG2G4
Heavy chain (SEQ ID NO. 15)

MGWSCIILFLVATATGVHSLEVQLQQSGPELVKPGASLKMSCKASGYSFT
DYIILWVKQNHGKSLEWIGHIDPYYGSSNYNLKFKGKATLTVDKSSSTAY
MQLNSLTSEDSA^VYYCGRSKRDYFDYWGQGTTLVSSASTKGPSVFPLA
PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPALQSS
GLYSLSSVVTPSSNFGTQTYTNCVDHKPSNTKVDKTVERKCCVECP
PCPAPPVAGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFN
WYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTPVLDSDGSFFLYSRLTVDKSR
WQEGNVFSCSVMHEALHNHYTQKSLSLSGK

FIGURE 11B

(SEQ ID NO. 14) (genomic sequence hG2G4)

ATGGGATGGAGCTGTATCATCCTCITCTTGGTAGCAACAGCTACAGGTGTCCACTCCCTCGAG
GTCCAGCTGCAACAGTCTGGACCTGAGCTGGTGAAGCCTGGGCTTCAGTGAAGATGTCTGC
AAGGCTTCTGGTTATTCAATTCACTGACTACATCATACTCTGGGTGAAGCAGAACCATGGAAAG
AGCCTGAGTGGATTGGACATATTGATCCTTACTATGGTAGTTCTAACTACAATCTGAAATTCA
AGGGCAAGGCCACATTGACTGTAGACAAATCTTCAGCACAGCCTACATGCAGCTAACAGT
CTGACATCTGAGGACTCTGCAGTCTATTACTGTGGAAGATCTAAGAGGGACTACTTGACTAC
TGGGCCAAGGCACCACTCTCACAGTTCTCAGCCTCCACCAAGGGCCATCCGTCTCCCC
CTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGCTGCCCTGGTCAAGGA
CTACTCCCCGAACGGTGACGGTGTGAACTCAGGCCCTGACCAGCGCGTGCACAC
CTTCCCGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCTGGTGACCGTGCCCTCC
AGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGT
GGACAAGACAGTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTC
AGCCCTCCTGCCCTGGACCGCACCCCGCTGTGAGCCCCAGCCAGGGCAGCAAGGCAGGCC
CATCTGTCTCCTCACCCGGAGGCCTCTGCCGCCACTCATGCTCAGGGAGAGGGTCTCTG
GCTTTTCCACCGGCTCAGGCAGGCACAGGCTGGGTGCCCTACCCAGGCCCTCACACA
CAGGGGCAGGTGCTGGCTCAGACCTGCCAAAAGCCATATCCGGAGGACCTGCCCCGTGAC
CTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTGGACACCTCTCCTCCCTCCAG
ATCCGAGTAACTCCAATCTCTCTGCAGAGCGAAATGTTGTGTCAGTGCCCACCGTG
CCAGGTAAAGCCAGGCCAGGCCCTGCCCTCCAGCTGGTGCTGACACGTCACCTCCATCTCTCAGCAC
CTGCATCCAGGGACAGGCCAGCTGGTGCTGACACGTCACCTCCATCTCTCAGCAC
CACCTGTGGCAGGACCGTCAGTCTCCTCTCCCCAAAACCCAAGGACACCTCATGATCT
CCCCGACCCCTGAGGTACGTGCGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAG
TTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCA
GTTCAACAGCAGTACCGTGTGGTCAGCGTCTCACCCTGCCATCGACAGGACTGGCTGAACGG
CAAGGAGTACAAGTGAAGGTCTCCAACAAAGGCCCTCCGTCCTCCATCGAGAAAACCATCT
CCAAAGCCAAAGGTGGGACCCACGGGGTGCAGGGCCACATGGACAGAGGTCAAGCTGGGCC
ACCCCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCTACAGGGCAGGCCAGAGGCC
ACAGGTGTACACCCCTGCCCTACCCAGGAGGAGATGACCAAGAACCAAGGTCAAGCTGCC
GCCTGGTCAAAGGCTTCTACCCAGCGACATGCCGTGGAGTGGAGAGCAATGGCAGGCC
GAGAACAACTACAAGACCAAGGCCCTCCGTGCTGGACTCCGACGGCTCCCTCTACAGC
AGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGAAATGCTCTCATGCTCCGTGATGCA
TGAGGCTCTGCACAACCACTACACACAGAACAGCCTCTCCCTGTCTGGTAAATGA

FIGURE 11C: A schematic representation of the heavy chain of antibody chC2aB7-hG2G4 (amino acids 1-337).

CC T G A C A S A T A A C A G A C T G I F C C Y T T C A T G G G I C T T T C T G C A R T C A C C G T C C T T G A C A C D A Q R G D E R C C C C C A C C L T C C G A T Q G A C C U T G T A T C A F C C 100
Lender H G W S C I I

XbaI

T C T C T T C G T A R C A C A G C I A K A R G T G I C C A C T C G C A T C G A C G C A C T G C N A A C T C T C G A C C T G A C G T C T G A C C C T G S G C T T C A C T C A A R A T O I C 200
Lender re VH
L F L V A I A T C V H S L E V G L O O S C P E L V K P C A S I L X M S
C I G C A A U D C T T E C T T F T T C A T C A C I G A C T A C T C A T C T G G C T G A A C C A G A C C A T / C A A A R G C C I T G A T T G G A T T G G A C A I A T T G A I A U C T A C 300
VH
C K A G G Y S F T O Y I I L K W V K O N H R K S L E W I G H I D P Y
T A T G G T A G T T C I A A C T A C A T T G A A I T C A A G G D C A A R G C C A C A T T G A C I G T A G A G A A A I C T T G C A C C A G A C C T A C A T / G C A G C T C A A C A C T C T G A C A T 400
VH
T C S S H Y N L K F X G R A T I L V D K S S S T A Y H Q L N S L T
C I G A G A C T C T G A R G T C T A I C I G T G B A A A G A C T A C T T G A C T A C T C C G C C E A A G G C A C C A E T C I C A C A G T T I C C T G A C C C I P C A E M A 500
VH
S E D S A V Y Y C G R S K R O Y F D Y W G O C T T I L T V S S A S I X
G G G C C A T C C C G I T C C C C C G T A G C G G C R C T A C T C G A G G A R C A C E T C C G A G A R C A L A R T C C C C T G C G G T I R C T G C T A C C A G A C T A T T T C C C C C A A E C C G T G 600
G2G4 CH1
G P S V F P L A P C S R S T S E S T A A L G C L V K D Y F P E P V
A C C C I G T C G G A A C T C A G H R E R C C T T G A C C A C C E U G G C I I C C C C C G I G F C C T A C A G T C C T G A B G A C T C T A C T C C C U T C A G G A U C G T O U T G A C C G 700
G2G4 CH1
T V S W N S C A L T S C V H T F P A V L O S S C L Y S L R S V V T
T G C C I C C E A C C A A C E T C C G G A C C C A B A C C T A C C E F G C A A A E R T G A G A T C A C A A A G C C A C E A A C C A A A B G T B G A L A A G A C A G T / G G I C A G A N D E C A G C F A 800
G2G4 CH1
V P S S N F G T D T Y T C N V D H K P S N T K V D K T Y
G G G A G G G A G G G I C I C T G C T G G A A G C C A G G C T I C A G C C E C T C T C C C T G A C G C A C C C U G G C T I G T C A G G C C C A C C C C A C C C C A C C C C A C C E T T G 900
T C T C C T C A C C C G G A G G C C T C T C C C C C C C A C T A F G C T C A G G C A A G G G I C T T C Y U C C T T Y T C C A C C A G G C T C C A G G C A R G C A C A G C T C G G G T C C C C C 1000
T A C C C A G I N C T I C A C A L A C A C A U D D C A G G D I D T I C G C T C A G G C T C A G G C T C C C A A A G G C A T A T C G C G G A B G A C C T C C C C U I G A C T A A G C C B A C / C C A A G G 1100
C C A A A C T U C C A C T Y C C T C A G G C T C G G A A C C C I C T C T C C T C C C A G A I C C G A C T A A R T C C C A A I C T C G C I V I C G C A G G G C C A A A T G T T D T G I C D A C I R G C 1200
F R K C F V E C
G2G4 Hinge

C A C C C I G R C C C A G R I T A A G G C A G G C C A G G C C T C C C C F C C A G C T C A A G G C C C G A C C G T C A D T C C C A G G C A C A G G C C C A C C C T C C C C 1300
P P C P
G2G4 Hinge

C T G A C A G G T G G A G E T C C A T C T C T T C C T C A G A C C A C C T G T G C A G G A C C C T G A C G T C A G T T C C T C T F C C C C C A A A A C C C C A A G R A C A C C C T C A Y G A T E T C C C 1400
A P P V A G P S V F L F P P X P K D I L H I S R
G2G4 CH2

G A C C C T G A G G T C A C R F C C G T R G T R G F G B A C G T I G A B C A C G G A A G A C C C C G A G G G T C A G G T C A C T G G T A C R T G A T G R C G T G G A G R T G C A T A A T G C C A A G 1500
T P E V T C V V V D Y S Q E D P E V O F N W Y V D G V E V H N A K
G2G4 CH2

A C A A A C C C C C C C G G A G G C A G T I C A A L A G C A C G T A C C G T G I G G I C A C G G T C C T C A C C G T C C C A C C G A G T G G C T H A A C C G G A A A G G A G T A C A A G T G C A 1600
T X P R E E O F N S T T R V V S Y L T V L H O O W L N G K E V K C
G2G4 CH2

FIGURE 11D

Light Chain (human Ck) (SEQ ID NO. 24)

MGWSCIIFLVATATGVHSRDIQMTQSPSSMYASLGERVTITCKASQDINS
YLSWFQQKPGKSPKTLIYRANRLVDGVPSPSGSGSGQDYSLTISSLEYED
MGIYYCLQYDEFPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL
TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 11E

(SEQ ID NO. 23)

ATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGT
GTCCACTCTAGAGACATCCAGATGACACAGTCATCCATCTCCATGTAT
GCATCTCTAGGAGAGAGAGTCACTATCACTGCAAGGCGAGTCAGGA
CATTAATAGCTATTAAGCTGGTCCAGCAGAAACCAGGGAAATCTCC
TAAGACCTGTATCGTCAAACAGATTGGTAGATGGGTCCATC
AAGGTTAGTGGCAGTGGATCTGGCAAGATTATTCTCTCACCATCAG
CAGCCTGGAGTATGAAGATATGGGAATTATTATTGTCTACAGTATGA
TGAGTTCCGTACACGTTGGAGGGGGACCAAGCTGGAAATAAAAAC
GGACTGTGGCTGCACCCTGTCTTCATCTTCCCCTGCATCTGATGAGCA
GTTGAAATCTGGAACTGCCTCTGTTGTGCCTGCTGAATAACTCTAT
CCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATC
GGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCA
CCTACAGCCTCAGCAGCACCCGTGACGCTGAGCAAAGCAGACTACGAG
AAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
GCCCGTCACAAAGAGCTCAACAGGGAGAGTGTAA

FIGURE 11F: A schematic representation of the light chain of antibody chC2aB7-hG2G4.

FIGURE 12A

hB7V3V2-cG2G4

Heavy Chain (SEQ ID NO. 13)

MGWSRIFLFLSIIAGVHCQVQLQQSGSELKKPGASVKISCKASGYSTDY
IILWVRQNPKGKLEWIGHIDPYYGSSNYNLKFGRVTITADQSTTAYME
LSSLRSEDTAVYYCGRSKRDYFDYWQGTTLTVSSASTKGPSVFPLAPC
SRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL
YSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV
DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG
NVFSCSVMHEALHNHYTQKSLSLGK

FIGURE 12B

(SEQ ID NO. 16) (cDNA G2G4)

ATGGGATGGAGCCGGATCTTCTCTCCTGTCAATAATTGCAGGTG
TCCATTGCCAGGTCCAGCTGCAACAGTCTGGATCTGAGCTGAAGAAC
CTGGGGCTTCAGTGAAGATCTCCTGCAAGGCTCTGGTTATTCATTCA
TGACTACATCATACTCTGGGTGAGGCAGAACCCCTGGAAAGGGCCTG
GTGGATTGGACATATTGATCCTTACTATGGTAGTTCTAACTACAATCTG
AAATTCAAGGGCAGAGTGACAATCACCGCCGACCAGTCTACCACCA
AGCCTACATGGAGCTCTCAGTCTGAGATCTGAGGACACTGCAGTCTA
TTACTGTGGAAGATCTAAGAGGGACTACTTGACTACTGGGGCCAAGG
CACCACTCTCACAGTTCTCAGCCTCCACCAAGGGCCATCCGTCTTC
CCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTG
GGCTGCCTGGTCAAGGACTACTCCCCGAACCGGTGACGGTGTGTTGG
AACTCAGGCGCCCTGACCAGCGCGTGCACACCTCCGGCTGTCTTA
CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
AGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCC
AGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTGTGTCGA
GTGCCACCAGTGGCCAGCACCTGTGGCAGGACCGTCAGTCTTCT
CTTCCCCCCTAAACCCAAGGACACCCCTCATGATCTCCGGACCCCTGA
GGTCACGTGCGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCC
AGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGGAGGGAGCAGTCAACAGCACGTACCGTGTGGTCAGCGT
CCTCACCGTCCCTGACCAGGACTGGCTAACGGCAAGGAGTACAAGT
GCAAGGTCTCCAACAAAGGCCTCCGTCCATCGAGAAAACCATCT
CCAAAGCCAAGGGCAGCCCCGAGAGGCCACAGGTGTACACCCCTGCC
CCATCCCAGGAGGGAGATGACCAAGAACCCAGGTCAAGCCTGACCTGCCT
GGTCAAAGGCTTCTACCCCTACAGCGACATGCCGTGGAGTGGAGAGCA
ATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCCGTGTGGAC
TCCGACGGCTCCTCTTCTACAGCAGGCTAACCGTGGACAAGAGC
AGGTGGCAGGAGGGAAATGTCTCTCATGCTCCGTGATGCATGAGGCT
CTGCACAACCAACTACACACAGAACAGCCTCTCCGTCTGGTAAA
TGATG

FIGURE 12C: A schematic representation of the heavy chain of antibody hB7V3V2-cG2G4.

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CCACCCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTCCATGGGCTTTCTGCAGTCACCGTCCCTTGACACAGAAGCTGCCGCCACCATGGGATGGAGCCGGATCTTCTCTC 2260
M G H S R I F L F
leader

CTCCTGTCATAATTGCGAGGTCCATTGCCAGGTCCAGCTGCAACAGCTGGATCTGAGCTGAAGAAGCCCTGGGCTTCAGTAAGAATCTCTGCAAGGCTTCGGTTATTCACT 2400
L D S T I A G V H C Q V O L Q Q S C S E L K K P G A S V K I S C K A S G Y S F T
leader V3 VH

GACTACATCATACTCTGGTGGAGGAGAACCTGAAAGCAGCTGGATGGACATATTGATCTTACTATGGTAGTACTCTACATACAACTGAAATTCAAGGGAGAGTGACAAATC 2520
D Y I X L H V R O N P G K G L E W I G H I D P Y Y G S S N Y N L K F K G R V T I
V3 VH

ACCGCCGACCAAGTCTACCCACACGGCTACATGGAGCTCCAGTCTGAGATCTGAGGACACTCAGCTATTACTGTGGAAGATCTAAGAGGGACTACTTGACTACTGGGGCAAGGC 2640
T A D Q S T T T A R Y M E L S S L R S E T A V Y Y C G R S K R D Y F D Y W G Q G
V3 VH

ACCCTCTCACAGTTCTCAGCCTCCACAGGGCCCATCCGTCCTCCCTCTGGGCCCTCTCTCAGGAGCAGCCCTCCAGAGCACAGGCCCTGGGCTGCCCTCAAGGACTACTTC 2760
T T L T V S S A S T K G P S V F P L A P C S R S T S E S T A A L G C L V K D Y F
V3 VH G2G4 cDNA

CCCGAACCGGUTGACCGTGTCTGDAACTCAAGGCCCTGACCAACGGCTGGCTGCTGAGCTCTCAGGACTCTACTCCAGGACTCTACTCCAGGACTCTACTCCAGGACTCTCC 2880
P E P V T V S H N S G A L T S G V H T F F P A V L Q S S G L Y S L S S V V T V P S
G2G4 cDNA

ACCAACTCTGGGACCCAGACCTACACCTGCAACAGTAGATCACAGGCCAGCACCAGGACAGTGAGCTGGCAATGTCGAGTGCCCACCGTGCCAGAACCCCTCC 3000
S N F G T Q T Y T C N V D H K P S N T K V D K T V E R K C C V E C P P C P A P P
G2G4 cDNA

GTGGCAGGGACCTGTCAGTCTTCTTCCCCAAAACCCAAGGAACCCCTCAAGATCTCCCGGCCCTTGAGGTCAGCTGCGCTGGTGCTGGACGTGAGCCAGGAGACCCCGAGGTCCAG 3120
V A G P S V F L F P P K P K D T L M I S R T P E V T C V V V D V S O E D P E V O
G2G4 cDNA

TTCAACTGGTACGTGGATGGCGTGGAGGTGCATATGCCAAGAACAAAGCCGCGAGGAGCAGTCAACAGCACGTACGGCTGTGCTCAGCCTCTACCGCTCTGACCTGGACTGGCTG 3240
F N W Y V D G V E V H N A K T K P R E E D F N S T Y R V V S V L T V L H Q D W L
G2G4 cDNA

AACGGCAAGGACTACAGTCAGCTCCAAACAAAGCCCTCCCTCTCTCTGAGAAAACCTCTGCAAGAACGGCAGCCCGAGAGCCACAGGTGACACCCCTGCCCTCATCC 3360
M G K E Y K C K V S N K G L P S S I E K T I S K A K G Q P R E P O V Y T L P P S
G2G4 cDNA

CAGCAGGAGATGACCAAGAACCAAGGTCAAGCTGACCTGGCTGGTCAAAGGCTTCTACCCAGGCTACGGCTGGAGTGCGAGGACATGGCAGCCGGAGAACACTACAGGACCC 3480
O G E M T K N Q V S L T C L V K G F Y P S D X A V E W E S N G Q P E N N Y K T T
G2G4 cDNA

CTCCCGCTGGACTCCAGGCTCCCTCTCTCTACAGGCTAACGGTGGACAAGAGCAGGCTGGCAGGAGGGGAATGTCCTCTCATGCTCCGATGCAATGGCTCTGCACAC 3600
P P V L D S D G S P F L Y S R L T V D K S R H O E G N V F S C S V M H E A L H N
G2G4 cDNA

CACTACACAGAAGAGGCTCTCCCTGTCCTGGGTAATGAGAGAAATCTTGTGATCATATACTGACCTACACATTGTAGAGGTTTACTTGCTTTAAAAACCTCCACCC 3720
H Y T Q K S L S L S L G K . .
G2G4 cDNA

```

FIGURE 12D

Light Chain (human Ck) (SEQ ID NO. 28)

MDMRVSAQLLGLLLWLSGARCDIQMTQSPSSLSASIGDRVITCKASQD
INSYLSWFQQKPGKAPKLLIYRANRLVDGVPSRFSGSGSGTDYTLTISSLQ
PEDFAVYYCLQYDEFPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 12E

(SEQ ID NO. 27)

ATGGACATGAGGGTCTCTGCTCAGCTCCTGGGCTCCTGCTGCTCTGG
CTCTCAGGGGCCAGGTGTGACATCCAGATGACACAGACTCCATCTTC
CTGTCTGCATCTATAGGAGACAGAGTCACTATCACTTGCAAGGCGAGT
CAGGACATTAATAGCTATTAAGCTGGTCCAGCAGAAACCAGGGAA
AGCTCCTAACGCTGCTGATCTATCGTCAAACAGATTGGTAGATGGGGT
TCCATCAAGGTTCAAGTGGCAGTGGATCTGGACAGATTATACTCTCAC
CATCAGCAGCCTGCAGCCTGAAGATTCTCAGTTATTATTGTCTACA
GTATGATGAGTTCCGTACACGTTGGAGGGGGACCAAGCTGGAAAT
AAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC GCCATCTGAT
GAGCAGTTGAAATCTGGAAC TGCTCTGTTGTGCCTGCTGAATAAC
TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTC
CAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACT
ACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTG
AGCTCGCCCGTACAAAGAGCTTCAACAGGGAGAGTGTAG

FIGURE 12F: A schematic representation of the light chain of antibody hB7V3V2-eG2G4.

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CTGGTCCCTTCATGGGCTTTCTGCAGTCACCGCTCTTGACACGAAGCTTCCGCCACCATGGACATGAGGCTCTGTGCTCAQCTCCCTGGGCTCCCTGCTCTGGCTCTAGGGCC 10800
M D M R V S A Q L L G L L L W L S G A
                            leader

CAGGTGTGACATCCAGATGACAGTCAGTCATCTTCCCTGCTGCTGATCTATAGGACAGGACTACATCACTTGCAACGCCAGTCAGGACATAAAGCTATTAAAGCTGTTCCAGGCA 10920
R C P I Q N T Q S P S S L S A S I G D R V T T I T C K A R S Q D I N S Y L S H F Q Q
                            V2 VL

GAAACCGGAAAGCTCCCTAGCTGCTGATCTATCGCCAPACAGRTTGGATGGGGTTCACATCAAGGTTCAAGGGCTGGGAGCTGGGACAGNTTAACTCTCACCATCRGCAGGCT 11040
K P G K A P K L L I Y R A N R L V D G V P S R F S G S G S G T D Y T L T I S S L
                            V2 VL

GCAGCCCTGAGAATTTCAGTTTATTATTCAGTACAGTAATGAGGTTTCGTTACAGCTTCCGGAGGGGGGACCAAGCTGGRANTAAACCTAACGGTACGGTGGCTGCACCCNTCTGTCATCTT 11160
O P E D F A V Y Y C L O Y D E F P Y T F G G G T X L B I K R T V A A P S V F I F
                            V2 VL
                            huCK

CCCGCCATCTCACTGAGCACTTCAATTCTGGAACTGCCCTCTGTTGCTGCTCTGATAACTCTTATCCAGAGGGCCAACTACAGTGCAAGGTTGGATAACGCCCTCCATCGGTAA 11280
P P S D E Q L K S G T A S V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N
                            huCK

CTCCCAGGAGAGTGTACACAGCAGGACAGCAAGCCAGCCTACAGCCCTAGCAGCACCCCTAGCCAGCTGACCCAAAGCTAACGGCTCCATCGGTAAAGTCACCCCTCCATCGGTAA 11400
S Q E S V T E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H
                            huCK

TCAGGGCTGAGCTCGCCGTCAAGAGCTTCAACAGGGAGACTCTAG 11452
Q G L S S P V T K S F N R G E C
                            huCK

```

FIGURE 13A

ChC7-hG2G4

Heavy chain (genomic sequence hG2G4) (SEQ ID NO. 18)

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MGWSCIILFLVATATGVHSLEVQLQQSGPELEKPGASVKISCKASGYSFTG
YNMNWVKQSSGKSLEWIGNFDPYYGVITYNQFKKGKATLTVDKSSSTAY
MQLKSLTSEDSAVYYCARTATALYTMDYWGQGTSVTSSASTKGPSVF
PLAPCSRSTSESTAALGCLVKDYFPEPVWSWNSALTSGVHTFPALV
QSSGLYSLSSVTVPSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVE
CPPCPGKPAPPVAGPSVLFPPPKDLMISRTPEVTCVVVDVSQEDP
EVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVS
LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTV
DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLLGK

```

FIGURE 13B

(SEQ ID NO. 17)

ATGGGATGGAGCTGTATCATCCTCTTCTTGTAGCAACAGCTACAGGTGTCCACTCCCTCGAG
GTCCAACGTGAGCAGTCTGGACCTGAGCTGGAGAAGGCCTGGCGCTTCAGTGAAGATACTCTGC
AAGGCTTCTGGTACTCATTCACTGGCTACAACATGAACCTGGGTGAAGCAGAGCAGTGGAAA
GAGCCTTGAGTGGATTGAAATTTGATCCTACTATGGTGTATTACCTACAACCAGAAGTTC
AAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAAGAG
CCTGACATCTGAGGACTCTGAGTCTATTACTGTGCAAGAACGGCTACGGCTCTCTATACTAT
GGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCCGT
CTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGCTGCCTGGT
CAAGGACTACTCCCCGAACCGGTACGGTGTGTTGAACTCAGGCGCCCTGACCAGCGGCG
TGCACACCTTCCCAGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
GCCCTCCAGCAACTCGGACCCAGACCTACACCTGCAACGTAGATCACAAGGCCAGCAACA
CCAAGGTGGACAAGACAGTTGGTGGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAAGC
CAGGCTCAGCCCTCTGCCTGGACGCACCCGGCTGTGCAGCCCCAGCCAGGGCAGCAAGG
CAGGCCCCATCTGTCCTCACCAGGAGGCCCTGTGCCCCCCCCACTCATGCTCAGGGAGAGGG
TCTTCTGGCTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGTGGCCCTACCCAGGCCCTT
CACACACAGGGGCAGGTGCTGGCTCAGACCTGCCAAAGCCATATCGGGAGGACCCCTGCC
CTGACCTAAGCCGACCCAAAGGCCAAACTGTCCACTCCCTCAGCTGGACACCTTCTCTCC
TCCCAGATCCGAGTAACTCCCAATCTCTCTGCAAGCGCAAATGTTGTGTCAGTGCCCA
CCGTGCCAGGTAAAGCCAGGCCAGGCCCTCCAGCTCAAGGCAGGGACAGGTGCCCTAG
AGTAGCCTGCACTCCAGGGACAGGCCAGCTGGTGTGACACGTCACCTCCATCTCTCC
CAGCACCACTGTGGCAGGACCCGTCAAGTCTCTCTGCAAGGCCCTACAGGGCAGGCC
TGATCTCCGGACCCCTGAGGTACGTGCTGGTGGAGGTGACATGCAAGAACAAAGCCGGGA
GTCCAGTCAACTGGTACGTGGATGGCGTGGAGGTGACATGCAAGAACAAAGCCGGGA
GGAGCAGTCAACAGCACGTACCGTGTGGTCAGCGTCTCAGCGTCTGCACCCAGGACTGGCT
GAACGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGGCCCTCCGTCTCCATCGAGAAAA
CCATCTCAAAGCCAAAGGTGGACCCACGGGTGCGAGGGCACATGGACAGAGGTCACT
CGGCCACCCCTCTGCCCTGGAGTACCGCTGTGCAACCTCTGTCCTACAGGGCAGGCC
AGAGCCACAGGTGTACACCTGCCCTACAGGAGGAGTACCGTCAAGAACCCAGGTCA
TGACCTGCCCTGGTCAAAGGCTCTACCCAGCGACATGCCGTGGAGTGGAGAGCAATGG
CAGCCGGAGAACAACTACAAGACCAACGCCCTCCGTGCTGGACTCCGACGGCTCCCTCTC
TACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGAAATGTCTCTCATGCTCGT
GATGCATGAGGCTCTGCACAACCAACTACACACAGAAGAGCCTCTCCCTGTCTGGTAAATG

A

FIGURE 13C

Light Chain (human C_k) (SEQ ID NO. 30)

**MGWSCIILFLVATATGVHSREIVLTQSPAIMSASPGEKVTMTCRASSVSS
SYLHWYQQKSGASPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISSVEAE
DAATYYCQQYSGYPLTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTAS
VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC**

FIGURE 13D

(SEQ ID NO. 29)

**ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT
GTCCACTCTAGAGAAATTGTGCTCACCCAGTCTCCAGCAATCATGTCT
GCATCTCCAGGGAAAAGGTACCACATGACCTGCAGGCCAGCTCAAG
TGTAAGTCCAGTTACTGCACGGTACCGAGCAGAAGTCAGGTGCCTC
CCCCAAACTCTGGATTATAGCACATCCAACCTGGCTCTGGAGTCCCT
GCTCGCTTCAGTGGCAGTGGCTGGGACCTCTTACTCTCACAATCA
GCAGTGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTACA
GTGGTTACCCACTCACGTTGGCTCGGGACAAAGTTGGAAATAAAAC
GGACTGTGGCTGCACCATCTGTCTCATCTTCCC GCCATCCGATGAGC
AGTTGAAATCTGGAACTGCCCTGTTGTGCTGCTGAATAACTCTA
TCCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAAT
CGGGTAACTCCCAGGAGAGGTGTCACAGAGCAGGACAGCAAGGACAGC
ACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGA
GAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCT
CGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGTAA**

FIGURE 14A

D1B5-hG1

Heavy Chain (SEQ ID NO. 20)

**MGWSCILFLVATATGVHSLEVQLQQPGAEVRSGASVKLSCKASGFNIK
DYYIHWVKQRPEQGLEWIGWIDPEIGATKYVPKFQGKATMTTDTSNTA
YLQLSSLTSEDTAVYYCNALYGNYDRYYAMDYWGQGTSVTVSSASTKG
PSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTWSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPDKTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNGKEYKCKVSNKALPAPIEKTIASKAKGQPREPQVYTLPPSREEMT
KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK**

FIGURE 14B

(SEQ ID NO. 19) (genomic sequence hG1 constant region)

ATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGTGTCCACTCCCTCGAG
GTC CA ACT GC AG CAG CG CT GGG CAG AG CTT GT GAG GT CAG GGG C CT CAG T CA AG IT GT CCT GC
AA AG CT IT GG CT T CA AC AT AA AG ACT ACT AT AT AC ACT GGG T GA AG CAG AG GGC TGA ACA
GGG C CT GG AG T GG ATT GG AT GG ATT GAT CCT GAG ATT GGT GCT ACT AA AT AT GT CCC GAA GT TT
CC AG GG CA AGG CC ACT AT GACT ACAG ACAC AT CCT CC A AC AC AG C CT AC CT GC AG CT CAG CA
GC CT GAC AT CT GAG GAC ACT GCC GT CT ATT ACT GT A AT GCC CT AT GGT A ACT AC G ACC GT
ACT AT GCT AT GG ACT ACT GGG GT CA AGG A AC CT CAG T CAC CG T CT CAG C CT CC ACCA AGG
GCC CAT CG GT CT TCCC CT GG C ACC T CCT CC AAG AG CAC CT CT GG CGG CAC AG CG CC CT GG
GCT GCT GG T CA AGG ACT ACT TCCC GA ACC GG T GAC GG T GT CG T GG A ACT CAG GCG CC CT GA
CC AG CG GCG T GCA CAC ACC TCCC GG CT GT CCT AC AG T CCT CAG G ACT CT ACT CCT CAG CAG CG
TG GT GAC CG T GCC CT CC AG CAG CT TGG C ACCA GAC CT AC AT CT GCA AC GT GA AT CA AAG C
CC AG CA AC ACCA AGG T GG GACA AG AG AG T GT GAG AG GGC AG CAC AG GG AG GG AG GG TG
TG CT GG AAG CC AGG CT CAG CG CT CCT GCT GG AC G C AT CCC GG CT AT G CAG T CCT CAG T CC AGG
GC AG CA AGG CAG GCCC CT GCT CCT CTC ACC CG GAG GGC T CT G CCG GCCC ACT CAT G CT CA
GG GAG AGG GT CT TGG CT TTTCCCAGG CT TGG CAGG CAC AGG CT AGG T GCG CC TA ACC
CAG GCC CT GCA CAC AAAAGGG CAG GT GCT GGG CT CAG AC CT GCA AG AG CC AT AT CGG GAG
GAC CCT GCC CT GAC CT AAG CCC ACC CAAAGG CCA AAC T CT CC ACT CCT CAG CT CG GAC AC
CT T CT CCT CCC AG AT T CC AG T AACT CCT CA T CT GCA AG GCC AA AT CT T GT GACA
AA ACT CAC AC AT GCC ACC CG T GCC CAG GT AAG CC AG GCC ACC G C T CG CCG T CC AG CT CA AGG C
GG GAC AGG T GCC CT AG AG T AG C CT GCA TCC AGG GAC AG G C C C AG G C G C T G C G C A C G T C
CAC CT CC AT CT CCT CAG CAC CT GAA CT CCT GGG GAC CG T CAG T CCT CCT T T CCCCC
AA ACC CA AGG AC ACC CT CAT GAT CT CCC GG ACC C CT GAG GT CAC AT GCG T GGT GGT GG AC GT
AG CC AC GA AG ACC CT GAG GT CA AG IT CA ACT GGT AC GT GG AC GG CG T GG AG GT GCA TA AT GC
CA AG AC AA AG CG C GGG AGG AG CAG T AC A AC AG CAC CG T ACC GT GT GG T CAG CG T CCT CAC CG
TC CT GCA CC AGG ACT GG CT GA AT GG CA AGG AGT AC A AGT GCA AGG T CT CA AC AA AG CC CT C
CC AG G C C C AT CG AG AAA ACC AT CCT CA AAG CCA AGG T GGG ACC CG T GGG GT GCG AGG G C C
AC AT GG AC AG AG G C C G CT CG G C C C ACC C T CT G C C T GAG AG T GAC CG C T GT ACC A AC CT TG
T C C CT AC AG GG CAG C C C GAG A ACC AC AGG T GT AC ACC CT G C C C C AT C C C G G GAG GAG AT G
ACCA AG A ACC AGG T CAG C CT GAC CT G C C T GGT CAA AGG CT T CT AT C C C AG CG C AC AT CG C C G T
GAG T GGG AG AG CA AT GGG CAG CG GAG A ACA ACT AC A AG ACC ACC CG C T C C G T G C T G G A C T C
CG AC GG C T C C T CT T C C T CT AT AG CA AG C T CAC CG T GG AC A AG G CAG GT GG CAG CAG GGG A
AC GT CT T CT CAT G C T C C G T GAT G C AT GAG G C T CT G CACA ACC ACT AC AG CAG A AG AG C C T C T
CC CT G T C C C C G G G T AA AT GA

FIGURE 14C: A schematic representation of the heavy chain of antibody DIB5-hG1.

FIGURE 14D

Light chain (human Ck) (SEQ ID NO. 32)

MGWSCILFLVATATGVHSR DIVMTQSQKFMSTSVGDRVSITCKASQNVR
TAVAWYQQKPGQSPKALIYLASNRHTGVPDFRTGSGSGTDFTLTISNVQS
EDLADYFCLQHWNYPLTFGAGTKLEKRTVAAPSVFIPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
NTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC

FIGURE 14E

(SEQ ID NO. 31)

ATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGT
GTCCACTCTAGAGACATTGTGATGACCCAGTCTAAAAATTGATGTCC
ACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGAA
TGTTCGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGGCAGTCTCC
TAAAGCACTGATTACTGGCATCCAACCGGCACACTGGAGTCCCTGA
TCGCTTCACAGGCAGTGGATCTGGGACAGATTCACTCTCACCATTAG
CAATGTGCAACTGAAAGACCTGGCAGATTATTCTGTCTGCAACATTG
GAATTATCCTCTCACGTCGGTGGACCAAGCTGGAGCTGAAACAG
GACTGTGGCTGCACCATCTGTCTCATCTTCCC GCCATCTGATGAGCAG
TTGAAATCTGGA ACTGCCTCTGTTGTGCGCTGCTGAATAACTTCTATC
CCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCAATCG
GGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAC
CTACAGCCTCAGCAACACCCTGACGCTGAGCAAAGCAGACTACGAGA
AACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC
CCGTCACAAAGAGCTCAACAGGGGAGAGTGTAA

FIGURE 14F: A schematic representation of the light chain of antibody D1B5-hG1.

AGCTTGGCCCACTATGGATGAGCTGTATCATCCTCTCTGGTAGCARACGTCAGGGTGTCACCTAGAGACATTGIGATGCCAGTCARAAATTICATGTCACATCAGTA
 M G W S C I I L F L V A T A T G V H S R , D I V H T Q S O K F M S T S V
 -leader-
 d1B5VK
 GGAGACAGGTGCGCATCCTGCAGGCCAGTCAGAATTTCTGACTGCTGTAGCCCTGGTATCACAGAACCCAGGGCAGTCCTAAAGCAGTATTACTGGCATCAACGGCAC
 G D R V S I T C K A S O N V R T A V A N Y Q Q K P G Q S P K A L I Y L A S N R H
 d1B5VK
 ACTGGAGCTCTATGCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACCTTCACCATTTGGCATGTCATACTGAAACCTCTGGCAGAGTTATTCTCTGCAACNTGGAATTATCTC
 T G V P D R F T G S G S G T D E D F T L T I S N V Q S E D L A D Y F C L Q H N N Y P
 d1B5VK
 CTCACTGGTGGCTGGGACAGCTGGAGCTGAACAGGCTGTGGCTGGACCATCTGGCTCTCATCTGGCCATCTGGAGCTGATGAGCAGITGAAACTGGAACTGGCTCTGTTGCTGCGCTC
 L T F G A G T K L E L K R T V R A P S F F P P S D E O L K S G T T A S V V C L
 d1B5VK
 -HCK-
 CTGAAATACTCTCCAGAGGCGCAAGTACAGCTGGAGCTGGTATGCCCTCCBAGTCGGTAACTCCCGAGGAGTGTCAAGAGCAGGACAGCAGGRCAGCAGCTCAGCGCTC
 L N N F Y P R E A K V Q W K V D N A L O S G N S O E S V T E Q D S K D S T Y S L
 d1B5VK
 -HCK-
 AGCAACACCCCTGAGCTGGAGCAAAGCAACTACAGAGAACACRAAGTCAGCTGGGAAGTCACCCATCAGGGCTGAGTCAGGCTGGCTGAGTCACAAAGCTTCACAGGGAGACTGTTAA
 S N T L T L S K A D Y E K H K V Y A C E V U T H O G L S S P V T K T S F N R G E C .
 d1B5VK

FIGURE 15A

G2G4 63L1D

Heavy chain (SEQ ID NO. 22)

MGWSCILFLVATATGVHSQMQLVQSGAEVKPGSSVKVSCKASGGTFS
NYATSWVRQAPGQGLEWLGIIIPVFGTANYAQKFQGRVTITADESTSTAY
MELNSLTFFDTAVYYCARGGGGWGGRNYYYYYMDVWGKGTTVTVSS
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVVDHKPSNTKVDK
TVERKCCVECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVD
VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEM
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL
YSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

FIGURE 15B

(SEQ ID NO. 21) (genomic sequence hG2G4)

ATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGTGTCCACTCCCAGATG
CAGCTGGTGCGAGTCTGGGCTGAGGTGAAGAAGCCTGGTCCTCGGTGAAGGTCTCCTGCAA
GGCCTCTGGAGGCACCTTCAGCAACTATGCTACCAGTTGGGTGCGACAGGCCCTGGACAAG
GTCTTGAGTGGCTGGAGGATCATCCCCGTCTCGGTACTGCAAACACTACGCACAGAAGTTTC
AGGGCAGAGTCACCATTACCGCGACGAGTCCACGAGCACAGCCTACATGGAGTTGAATAGT
CTGACATTGACGACACGGCCGTCTTAACTGTGCGAGAGGGGGTGGGGATGGGAGGCCG
GAACTACTACTACTACTACATGGACGTCTGGGCAAAGGGACCACGTACCGTCTCCTC
AGCCTCCACCAAGGGCCCATCGTCTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAG
CACAGCCGCCCTGGCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTGGAA
CTCAGGCGCCCTGACCAGCGCGTGCACACCTCCCGGTGCTCCTACAGTCCTCAGGACTCTA
CTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAA
CGTAGATACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTAGAGGCCAGCTCAGG
GAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCGTGGACGCACCCGGCTGTGC
AGCCCCAGCCCAGGGCAGCAAGGCAGGCCATCTGTCTOCTCACCCGGAGGCCTCTGCCCGC
CCCACCTCATGCTCAGGGAGAGGGTCTCTGGTTTTCCACCCAGGCTCCAGGCAGGCACAGGC
TGGGTGCCCTACCCCAGGCCCTACACACAGGGCAGGTGCTGGCTCAGACCTGCCAAA
GCCATATCCGGAGGACCCCTGCCCTGACCTAACGCCACCCAAAGGCCAAACTGTCCACTCC
CTCAGCTCGGACACCTCTCTCCCTCCAGATCCGAGTAACCTCCAATCTCTCTGAGAGCG
CAAATGTTGTCGAGTGCCTCACCGTGCAGGTAAGCCAGGCCAGGCTCGCCCTCCAGCTC
AAGGCAGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCAGCTGGGTGCTGAC
ACGTCCACCTCCATCTCTCTCAGCACCCACTGTGGCAGGACCGTCAGTCITCTCTTCCCCC
AAAAACCCAAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACCGTGCAGGCTGGTGGAC
GTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAA
TGCCAAGACAAAGCCGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCTCA
CCGTCTGCACCAAGGACTGGCTAACGGCAAGGAGTACAAGTGCAGGTCTCCAACAAAGGC
CTCCCGTCTCCATCGAGAAAACCATCTCAAAGCCAAAGGTGGACCCACGGGTGCGAGG
GCCACATGGACAGAGGTCACTGGCCCACCCCTGCCCCCTGGAGTGCAGGCTGTGCCAACCT
CTGTCCCTACAGGGCAGCCCCGAGAGCCACAGGTGTACACCCCTGCCCTACCCAGGAGGAG
ATGACCAAGAACCAAGGTCACTGGCTAACGGCAAGGAGTACAAGTGCAGGTCTCCAACAAAGGC
GTGGAGTGGGAGAGCAATGGGAGCCGGAGAACAAACTACAAGACCCACGCCCTCCGTGCTGGA
CTCCGACGGCTCTCTCAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGG
GGAATGTCTCTCATGCTCCGTATGCTGAGGCTCTGCACAAACCAACTACACACAGAACGCC
TCTCCCTGTCTGGTAAATGA

FIGURE 15C

Light chain (human CL) (SEQ ID NO. 34)

**MGWSCIILFLVATATGVHSSYVLTQPPSEVAPGQTARISCGGSNIGSYGV
HWYQQKAGQAPVLVVHDDSDRPSGIPERFSGSNSGNTATLTISSVEAGDE
ADYYCQVWDNSAVIFGGGTKLTVLSQPKAAPSVTLFPPSSEELQANKA
TLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNNKYAASSYL
SLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS**

FIGURE 15D

(SEQ ID NO. 33)

**ATGGGATGGAGCTGTATCATCCTCTTGGTAGCAACAGCTACAGGT
GTCCACTCTCCTATGTGCTGACTCAGCCACCCTCGGAGTCAGTGGCC
CCAGGACAGACGCCAGGATTCTGTGGGGGGAGCAACATTGGAAG
TTACGGTGTGCACTGGTACCAGCAGAAGGCAGGACAGGCCCTGTGCT
GGTCGTCCATGATGATTCCGACCGGCCCTCAGGGATTCTGAGCGATT
CTCTGGCTCCAATTCTGGAACACGCCACCCCTGACCATCAGCAGTGT
CGAAGCCGGCGATGAGGCCGACTATTACTGTCAGGTGTGGATAATA
GTGCTGTGATATTGGCGGAGGGACCAAACTAACCGTCCTAAGTCAGC
CCAAGGCTGCCCTCGGTACTCTGTTCCGCCCTCTGAGGAGCT
TCAAGCCAACAAGGCCACACTGGTGTCTCATAAGTGACTTCTACCC
GGGAGCTGTGACAGTGGCTTGGAAAGCAGATAGCAGCCCCGTCAAGG
CGGGAGTGGAGACCACCCACCCCTCAAACAAAGCAACAACAAGTAC
GCGGCCAGCAGCTATCTGAGCCTGACGCCAGCAGTGGAAAGTCCA
CAGAAGCTACAGCTGCCAGGTACCGCATGAAGGGAGCACCGTGGAGA
AGACAGTGGCCCTACAGAATGTTCTAA**

FIGURE 16

5'-GACAAGCTTGCAAGGATGGAGAGGCTGGTGA-3' (SEQ ID NO: 35)

FIGURE 17

5'-GACGGATCCGCCCTTTCCCTGCTTTCTC-3' (SEQ ID NO: 36)

FIGURE 18

Efficacy of humanized anti CD200 antibodies (C2aB7) in the RAI_CD200/PBL model.

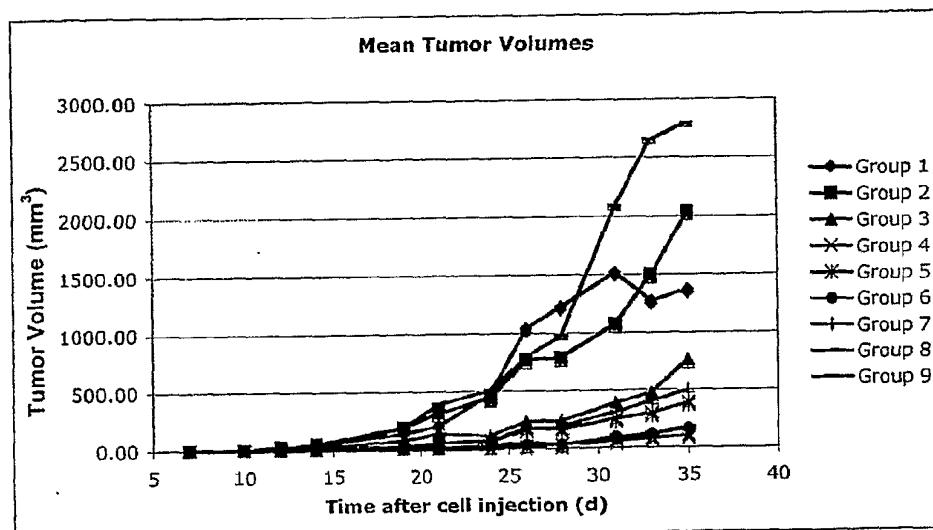


FIGURE 19

Comparison of mean tumor volumes in C2aB7-G1 versus C2aB7-G2G4 treated animals in the Namalwa_CD200 model.

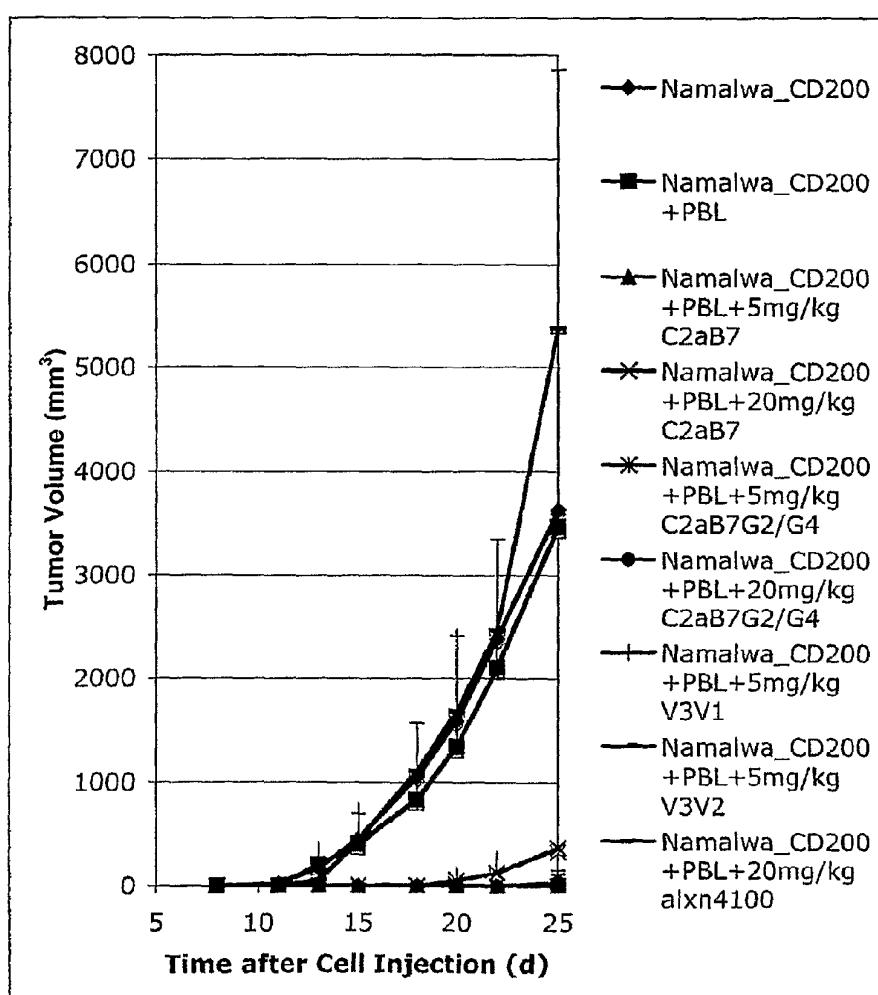


FIGURE 20

FACS analysis of CD200 expression on B-CLL cells in comparison to normal B cells.

Donor ID	CLL sample		Healthy donor	
	B-CLL	Normal B	CD200 (GMFI)	Ratio(CLL/normal B)
	CD200 (GMFI)			
RC011731	93	58		1.6
RF020934	659	185		3.6
JA073031	334	64		5.2
GR011846	156	64		2.4
BB101735	420	95		4.4
DM6988172	290	97		2.9
MR8074020	403	97		4.2
CB8267677	300	97		3.1
GB1325248	178	77(7)		2.3
VN7029373	154	77(7)		2.0
DG8942820	146	77(7)		1.9
MM8451869	237	77(7)		3.1
JR4539931	215	77(7)		2.8
HS6787771	305	77(7)		4.0
VB040439	123	41		3.0
				MEAN= 3.1
				STDEV= 1.0

FIGURE 21

Tumor type	Cell line	CD200 staining
Melanoma	SK-MEL2	-
	SK-MEL28	++
	SK-MEL1	+
	SK-MEL5	+/-
	SK-MEL24	+++
Ovarian	OVCAR3	++
	SKOV3	+/-
Renal	CAKI-1	+
	ACHN	-
	SN12C	+
Neuroblastoma	IMR-32	+++
	SK-N-SH	++
Breast cancer	MDA-MB-435	+/-
	MCF7	-
	MDA-MB-231	-

FIGURE 22

RTQ-PCR of primary ovarian cancer samples.

RT-QPCR: CD200 on Ovarian Cancer samples

Number	Sample	norm/#51	sd/#51
51	PBL	1.00	0.03
124	normal ovary	5.82	0.16
125	normal ovary	19.45	1.33
127	ov. adenocarc, serous	10.93	0.47
128	ov. adenocarc, serous met	10.08	0.60
134	ov. adenocarc, serous met	21.24	0.69
129	ov. adenocarc, papill. serous	13.33	1.26
130	ov. adenocarc, papill. serous	8.71	0.42
126	ov. adenocarc, endometroid	11.02	0.54
131	ov. adenocarc, endometroid	1.38	0.20
135	ov. adenocarc, endometroid	2.42	0.02
132	ov. adenocarc, mucinous	1.61	0.00
133	ov. adenocarc, mucinous	2.46	0.23
136	ov. adenocarc, clear cell	6.51	1.14
137	ov. adenocarc, clear cell	0.70	0.04

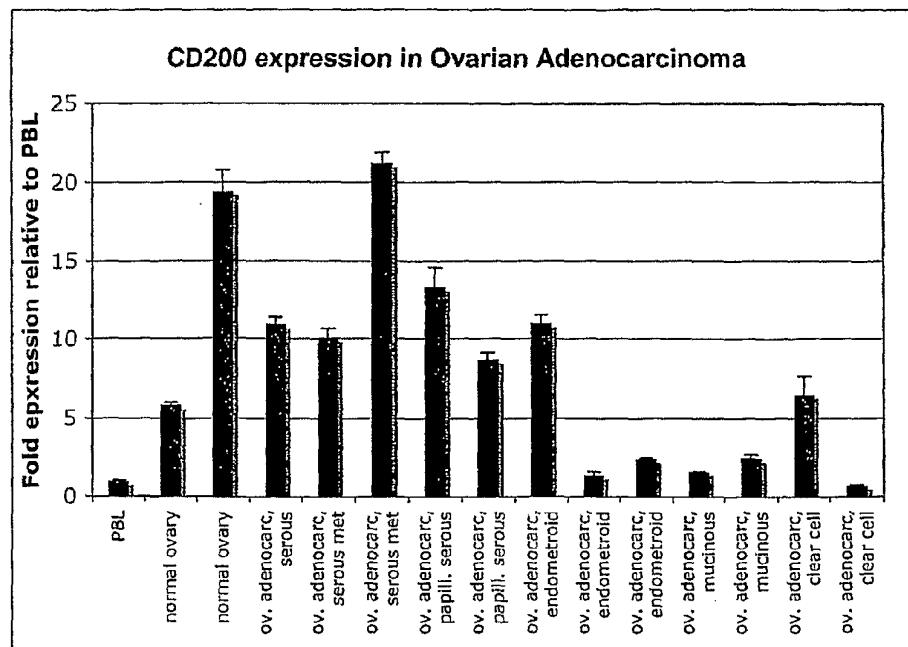


FIGURE 23

RT-QPCR: CD200 on Melanoma samples

Number	Sample	norm#51	sd#51
81	PBL	1.00	0.28
139	norm jejunum -1	2.60	0.15
138	jejunum met -1	8.32	0.24
147	norm jejunum -2	1.37	0.31
146	jejunum met -2	14.66	3.38
143	norm small intestine -1	3.57	1.21
142	small intestine met -1	4.81	0.35
141	norm lymph node -1	8.82	1.00
140	lymph node met -1	8.23	0.53
151	norm lymph node -2	4.80	1.40
150	lymph node met -2	12.94	0.51
153	lymph node met -3	0.89	0.21
166	lymph node met -4	2.72	1.72
145	norm lung -1	14.87	1.14
144	lung met -1	8.63	0.83
169	norm lung -2	4.25	0.64
143	lung met -2	3.83	1.04
111	norm skin -1	1.68	0.26
152	melanoma metastatic, skin -2	0.38	0.08
158	melanoma metastatic, skin -3	3.22	0.61
169	malign. melanoma, brain met -3	22.92	3.30
182	malign. melanoma, lung met	15.16	1.14
183	malign. melanoma, LN met	15.16	1.14
187	malign. melanoma, LN met	15.16	1.14
186	malign. melanoma, skin	15.16	1.14
180-No RT	malign. melanoma, skin	0.00	0.00

values from Q1003 plate

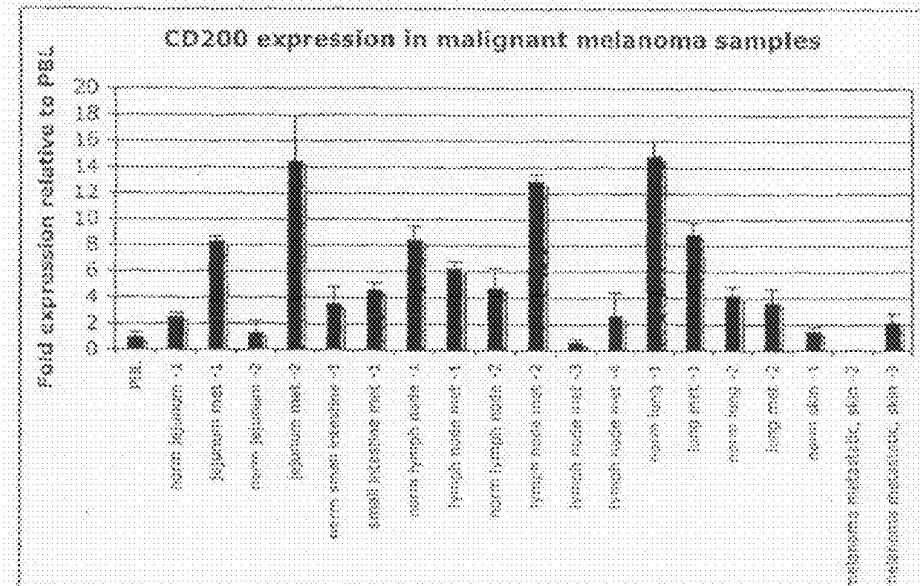


FIGURE 24

Immunohistochemistry staining of melanoma patient samples.

Frozen Skin, Melanoma - Positive Control

Sample 3: This sample of melanoma was obtained from an 83-year-old female.

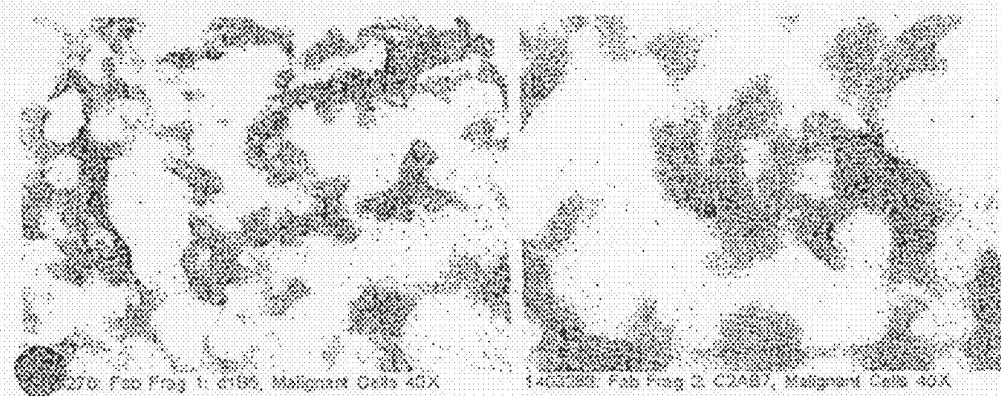
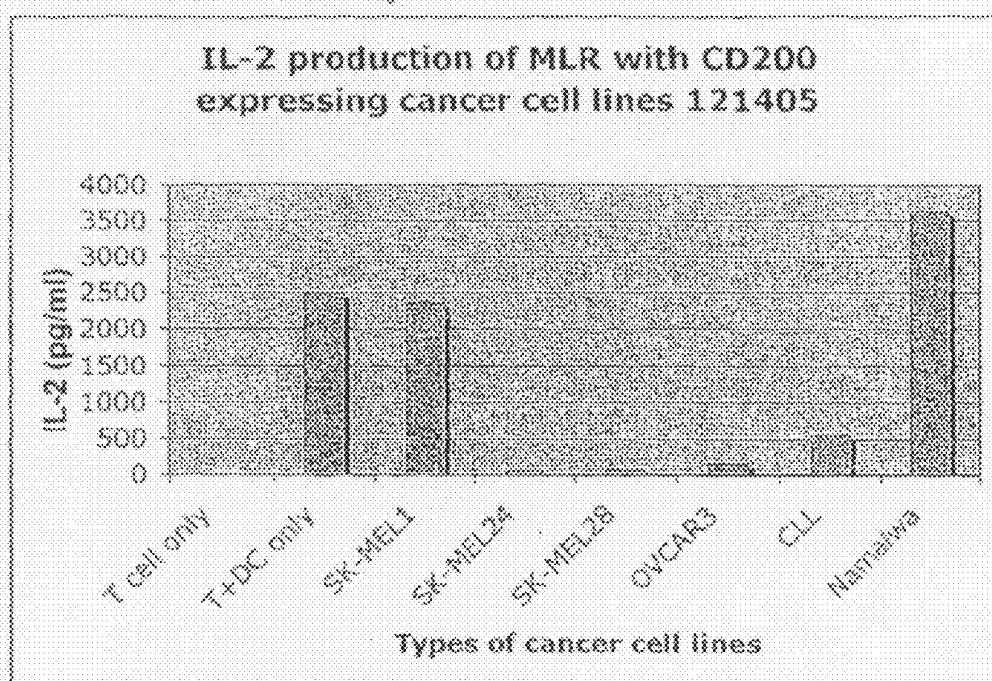


FIGURE 25

IL-2 production in MLR with cancer cell lines.

A. In the absence of antibody



B. In the presence of antibody

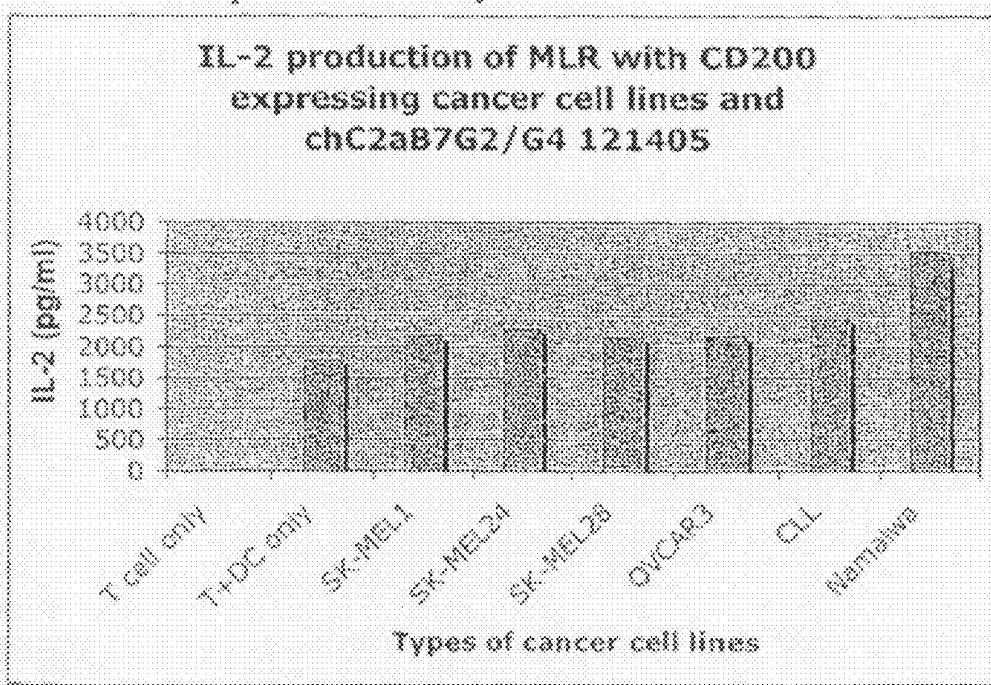


FIGURE 26

Tumor volumes in the Namalwa/PBL model (no CD200 expression) comparing anti-CD200 G1 or G2G4 construct treated groups.

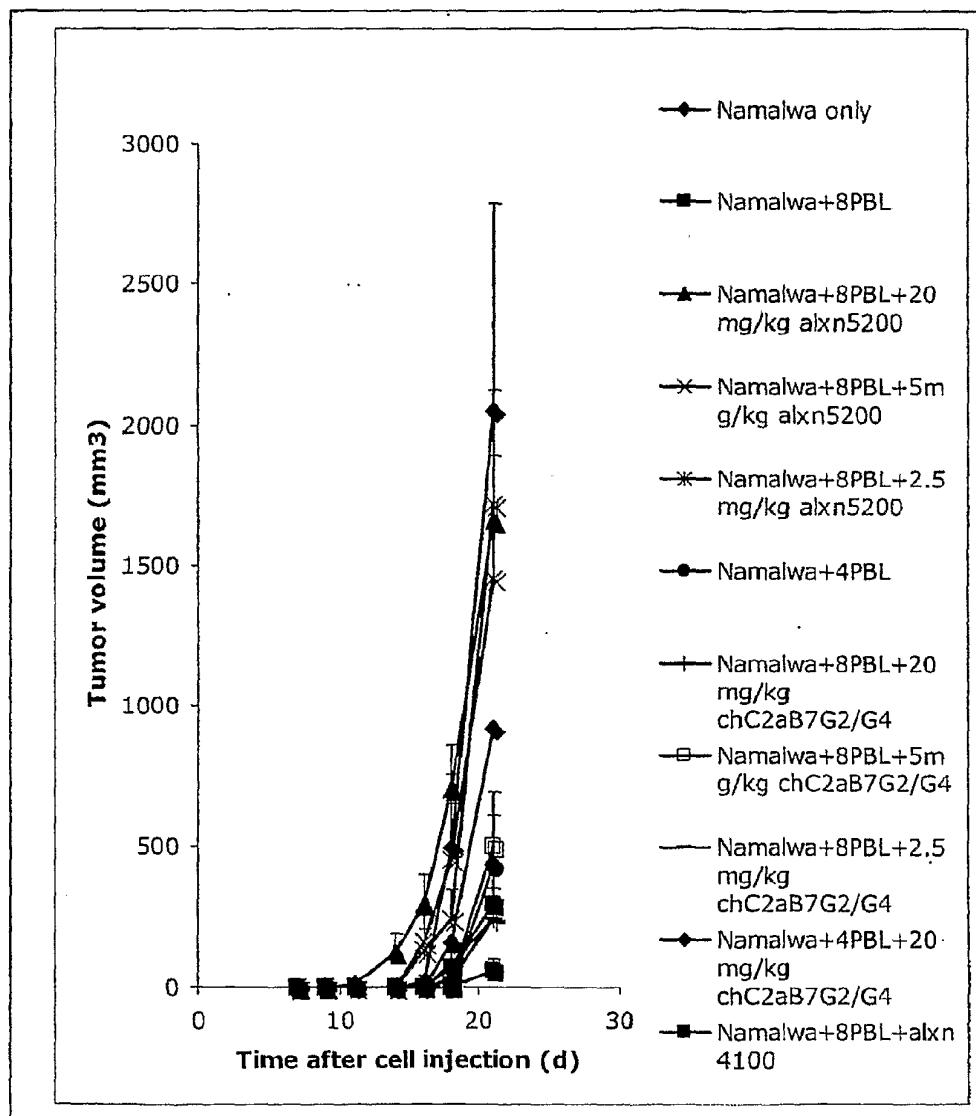


FIGURE 27 Cell surface expression of CD200 on human CD3+ cells following activation with mOKT3.

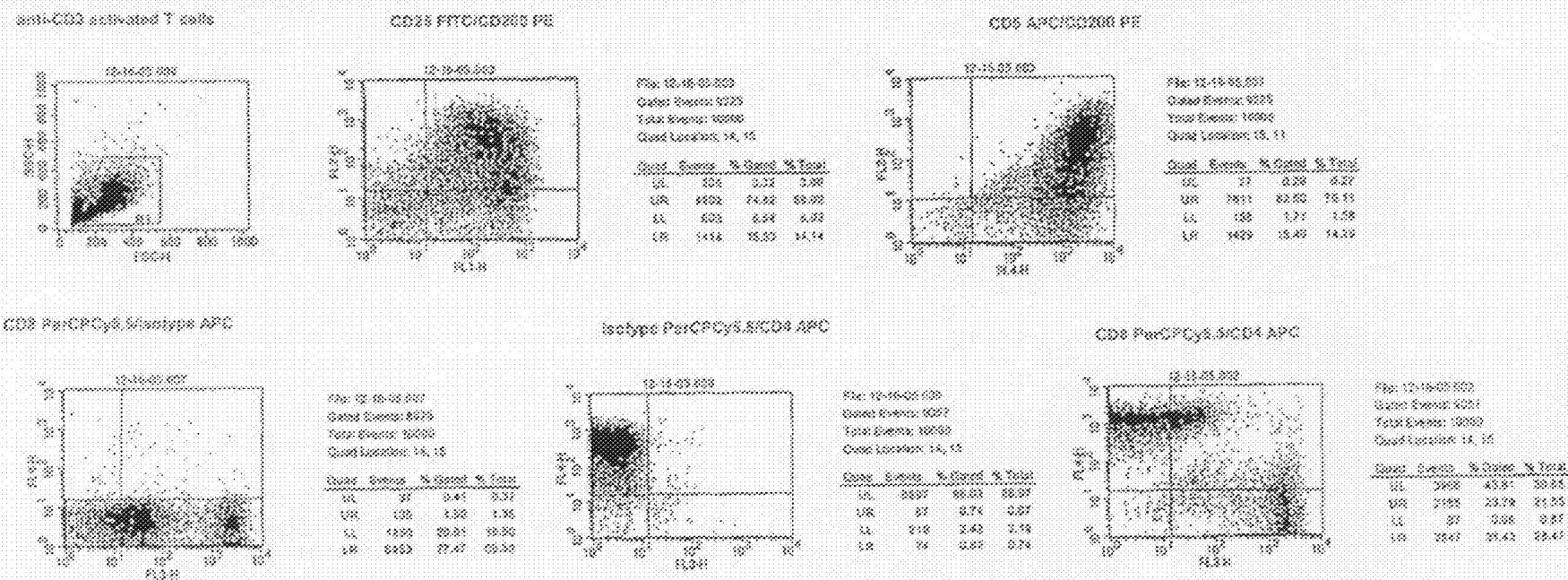
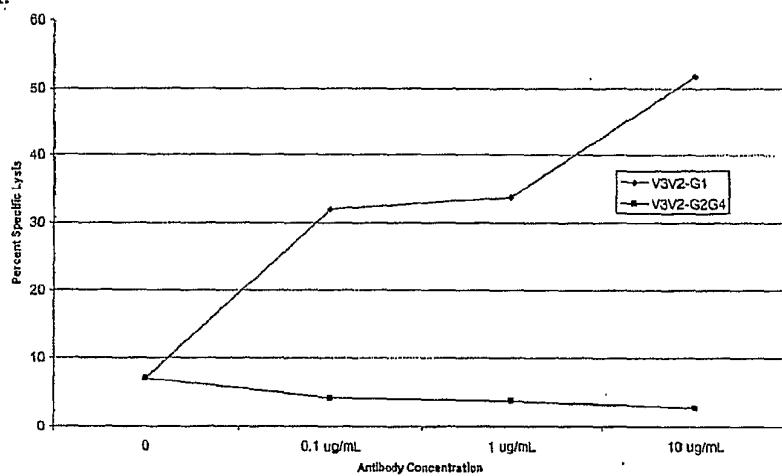


FIGURE 28 Human T cells activated through T cell receptor signaling serve as sensitive targets for anti-CD200 mediated ADCC.

A.



B.

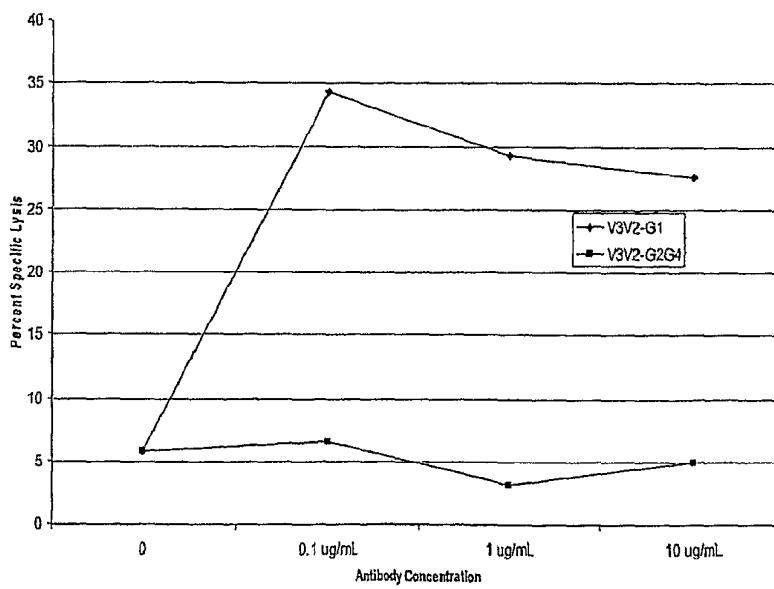


FIGURE 29

Sample	Status	Light Chain Isotype	CD200 Expression on CD30+ Bright Cells (Plasma cells)		Current Clinical Treatment
			Threshold Set Through Isotype Control (Expressed as %)	Threshold Set Through Isotype Control (Expressed as Geometric Mean Intensity)	
1	Normal	Polyclonal	48	6575	NA
2	Normal	Polyclonal	48	19411	NA
3	Normal	Polyclonal	33	87084	NA
4	M Myeloma	Kappa	12	4056	Velcade, Melphalan
5	M Myeloma	Kappa	12	3001	Velcade, ATO
6	M Myeloma	Negative	14	2162	Aranesp, Zometa, Coumadin
7	M Myeloma	Polyclonal	37	3419	DVD (Dox, Vin, Dex)
8	M Myeloma	Kappa	71	4024	None
9	M Myeloma	Kappa	76	1506	Zometa, Prednisone
10	M Myeloma	Kappa	82	9056	Aranesp, Zometa
11	M Myeloma	Kappa	85	5388	HTN, PCTA
12	M Myeloma	Kappa	89	23269	Prednisone, Zometa
13	M Myeloma	Lambda	95	1535	Zometa, Coumadin, IVIG, Biaxin, Medrol

ANTIBODIES TO OX-2/CD200 AND USES THEREOF**RELATED APPLICATIONS**

[0001] This application claims the benefit of U.S. Provisional Application Nos. 60/758,426, filed Jan. 12, 2006, 60/759,085, filed Jan. 12, 2006, and 60/801,991, filed May 18, 2006, which applications are hereby incorporated by reference in their entireties.

TECHNICAL FIELD

[0002] The disclosure relates to OX-2/CD200 (herein referred to as CD200) antagonists and methods of depleting or eliminating cells overexpressing CD200 in a subject with cancer or autoimmune disease. The methods of therapy for the treatment of cancer provide a combination of two mechanisms. More specifically, this disclosure relates to treating cancer using a therapy that: (1) interferes with the interaction between CD200 and its receptor to block immune suppression thereby promoting eradication of the cancer cells; and/or (2) directly kills the cancer cells either by (a) antibody-dependent cellular cytotoxicity or complement-mediated cytotoxicity or by (b) targeting cells using a fusion molecule that includes a CD200-targeting portion. The disclosure also relates to a method of treating autoimmune disorders by a therapy that increases the antibody-dependent cellular cytotoxicity and/or complement-mediated cytotoxicity of CD200-positive immune cells.

BACKGROUND

[0003] Various mechanisms play a role in the body's response to a disease state, including cancer. For example, CD⁺ T helper cells play a crucial role in an effective immune response against various malignancies by providing stimulatory factors to effector cells. Cytotoxic T cells are believed to be the most effective cells to eliminate cancer cells, and T helper cells prime cytotoxic T cells by secreting Th1 cytokines such as IL-2 and IFN- γ . In various malignancies, T helper cells have been shown to have an altered phenotype compared to cells found in healthy individuals. One of the prominent altered features is decreased Th1 cytokine production and a shift to the production of Th2 cytokines. (See, e.g., Kiani, et al., *Haematologica* 88:754-761 (2003); Maggio, et al., *Ann Oncol* 13 Suppl 1:52-56 (2002); Ito, et al., *Cancer* 85:2359-2367 (1999); Podhorecka, et al., *Leuk Res* 26:657-660 (2002); Tatsumi, et al., *J Exp Med* 196:619-628 (2002); Agarwal, et al., *Immunol Invest* 32:17-30 (2003); Smyth, et al., *Ann Surg Oncol* 10:455-462 (2003); Contasta, et al., *Cancer Biother Radiopharm* 18:549-557 (2003); Lauerova, et al., *Neoplasma* 49:159-166 (2002).) Reversing that cytokine shift to a Th1 profile has been demonstrated to augment anti-tumor effects of T cells. (See Winter, et al., *Immunology* 108:409-419 (2003); Inagawa, et al., *Anticancer Res* 18:3957-3964 (1998).)

[0004] Mechanisms underlying the capacity of tumor cells to drive the cytokine expression of T helper cells from Th1 to Th2 include the secretion of cytokines such as IL-10 or TGF- β as well as the expression of surface molecules interacting with cells of the immune system. CD200, a molecule expressed on the surface of dendritic cells which possesses a high degree of homology to molecules of the immunoglobulin gene family, has been implicated in immune suppression (Gorczynski et al., *Transplantation* 65:1106-1114 (1998)). It

has been shown, for example, that CD200-expressing cells can inhibit the stimulation of Th1 cytokine production.

[0005] Although immune cells can help attack and eliminate cancer cells, in certain instances, such as in autoimmune disorders, allergies, and the rejection of tissue or organ transplants, the immune system can be the cause of illness. In order to inhibit harmful immune reactions in such instances, immunosuppressive agents such as corticosteroids and cytokine antagonists may be administered to patients. However these general immunosuppressives can elicit undesirable side effects including toxicity and reduced resistance to infection. Thus alternative, and perhaps more specific, methods of treating autoimmunity are needed.

[0006] Several immunomodulatory therapies, including antibody therapies, have proven successful in the treatment of certain cancers and autoimmune disorders. However there is a clinical need for additional antibody therapies for the treatment of both cancer and autoimmune disorders. Furthermore, there is a related need for humanized or other chimeric human/mouse monoclonal antibodies. In well publicized studies, patients administered murine anti-TNF (tumor necrosis factor) monoclonal antibodies developed anti-murine antibody responses to the administered antibody. (Exley A. R., et al., *Lancet* 335:1275-1277 (1990)). This type of immune response to the treatment regimen, commonly referred to as the human anti-mouse antibody (HAMA) response (Mirick et al. *Q J Nucl Med Mol Imaging* 2004; 48: 251-7), decreases the effectiveness of the treatment and may even render the treatment completely ineffective. Humanized or chimeric human/mouse monoclonal antibodies have been shown to significantly decrease the HAMA response and to increase the therapeutic effectiveness of antibody treatments. See, for example, LoBuglio et al., *P.N.A.S.* 86:4220-4224 (June 1989). Furthermore, antibodies in which particular functionalities are either enhanced or reduced may find useful applications in the clinic.

SUMMARY

[0007] This disclosure relates to agents and methods for modulating the function of CD200. Agents that modulate the function of CD200 include agents that modulate the activity and/or expression of CD200 and/or its receptor (CD200R). In some embodiments, the agents inhibit the function or activity of CD200. Thus in certain aspects, said agents act as antagonists to CD200. Certain antagonists may bind to CD200 and inhibit or disrupt the interaction of CD200 with its receptor. Other antagonists may bind to CD200 but may not block the CD200:CD200R interaction. Thus CD200 antagonists include any agent that is capable of modulating the effects of CD200 by mechanisms that may or may not include blocking the CD200:CD200R interaction. CD200 antagonists include but are not limited to polypeptides, small molecules, organometallic compounds, oligonucleotide constructs, RNAi constructs, aptamers, spiegelmers, antisense nucleic acids, locked nucleic acid (LNA) inhibitors, peptide nucleic acid (PNA) inhibitors, immunomodulatory agents, antibodies, antigen-binding fragments, prodrugs, and/or peptidomimetic compounds.

[0008] In certain embodiments, the said antagonist is an anti-CD200 antibody. Antibodies, as referred to herein, include antigen-binding fragments, Fab, Fv, scFv, Fab' and F(ab')₂, monoclonal and polyclonal antibodies, engineered antibodies (including chimeric, single chain, CDR-grafted,

humanized, fully human antibodies, and artificially selected antibodies), and synthetic or semi-synthetic antibodies.

[0009] In certain aspects, the present disclosure relates to chimeric, humanized, human and de-immunized anti-CD200 antibodies and antigen-binding fragments thereof. In further embodiments, an antibody of the disclosure comprises a heavy chain comprising an amino acid sequence that is at least 90% identical to an amino acid sequence selected from among SEQ ID NOS: 7, 9, 11, and 20, or fragments thereof. Included is an antibody comprising an amino acid sequence that is about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical or similar to an amino acid sequence provided in SEQ ID NOS: 7, 9, 11, and 20, or fragments thereof (including but not limited to fragments corresponding to the sequences without the leader sequences). The said antibody may additionally comprise a light chain comprising an amino acid sequence that is at least about 90% identical or similar to an amino acid sequence selected from among SEQ ID NOS: 24, 26, 28, and 32, or fragments thereof. Likewise, the aforementioned amino acid sequence may be about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical or similar to an amino acid sequence provided in SEQ ID NOS: 24, 26, 28, and 32, including fragments thereof (including but not limited to fragments corresponding to the sequences without the leader sequences).

[0010] In one embodiment, the disclosure relates to an anti-CD200 antibody comprising a heavy chain comprising an amino acid sequence that is at least about 90% identical to the amino acid sequence of SEQ ID NO: 7 and also comprising a light chain comprising an amino acid sequence that is at least about 90% identical to SEQ ID NO: 24. Also included are anti-CD200 antibodies comprising amino acid sequences that are about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical or similar to one or more amino acid sequence provided in SEQ ID NOS: 7 and 24 or fragments thereof. Fragments include, but are not limited to, sequences corresponding to the sequences set forth in SEQ ID NOS: 7 and 24 without the leader sequences. Accordingly, the disclosure relates to an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 6 (including fragments thereof and complements thereto) and also comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 23 (including fragments thereof and complements thereto). Also included is an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous or similar to a nucleic acid sequence provided in SEQ ID NO: 6, including fragments thereof and complements thereto, and also comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous or similar to a nucleic acid sequence provided in SEQ ID NO: 23, including fragments thereof and complements thereto. The invention also relates to anti-CD200 antibodies comprising an amino acid sequence encoded by a nucleic acid sequence that is about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous or similar to a nucleic acid sequence provided in SEQ ID NOS: 6 or 23, including fragments thereof and complements thereto.

[0011] In another embodiment, the disclosure relates to an anti-CD200 antibody comprising a heavy chain comprising

an amino acid sequence that is at least about 90% identical to the amino acid sequence of SEQ ID NO: 9 and also comprising an amino acid sequence that is at least about 90% identical to SEQ ID NO: 26. Also included are anti-CD200 antibodies comprising amino acid sequences that are about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical or similar to one or more amino acid sequence provided in SEQ ID NOS: 9 and 26 or fragments thereof. Fragments include, but are not limited to, sequences corresponding to the sequences set forth in SEQ ID NOS: 9 and 26 without the leader sequences. Accordingly, the disclosure relates to an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 8 (including fragments thereof and complements thereto) and also comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 25 (including fragments thereof and complements thereto). Also included is an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous or similar to a nucleic acid sequence provided in SEQ ID NO: 8, including fragments thereof and complements thereto, and also comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous or similar to a nucleic acid sequence provided in SEQ ID NO: 25, including fragments thereof and complements thereto. The invention also relates to anti-CD200 antibodies comprising an amino acid sequence encoded by a nucleic acid sequence that is about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous or similar to a nucleic acid sequence provided in SEQ ID NOS: 8 or 25, including fragments thereof and complements thereto.

[0012] In a further embodiment, the disclosure relates to an anti-CD200 antibody comprising an amino acid sequence that is at least about 90% identical to the amino acid sequence of SEQ ID NO: 11 and also comprising an amino acid sequence that is at least about 90% identical to SEQ ID NO: 26. Also included are anti-CD200 antibodies comprising amino acid sequences that are about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical or similar to one or more amino acid sequence provided in SEQ ID NOS: 11 and 26 or fragments thereof. Fragments include, but are not limited to, sequences corresponding to the sequences set forth in SEQ ID NOS: 11 and 26 without the leader sequences. Accordingly, the disclosure relates to an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 10 (including fragments thereof and complements thereto) and also comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 25 (including fragments thereof and complements thereto). Also included is an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous or similar to a nucleic acid sequence provided in SEQ ID NO: 10, including fragments thereof and complements thereto, and also comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous or similar to a nucleic acid sequence provided in SEQ ID NO: 25, including fragments thereof and complements thereto. The invention also relates

to anti-CD200 antibodies comprising an amino acid sequence encoded by a nucleic acid sequence that is about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous or similar to a nucleic acid sequence provided in SEQ ID NOS: 10 or 25, including fragments thereof and complements thereto.

[0013] In an additional embodiment, the disclosure relates to an anti-CD200 antibody comprising an amino acid sequence that is at least about 90% identical to the amino acid sequence of SEQ ID NO: 11 and also comprising an amino acid sequence that is at least about 90% identical to SEQ ID NO: 28. Also included are anti-CD200 antibodies comprising amino acid sequences that are about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical or similar to one or more amino acid sequence provided in SEQ ID NOS: 11 and 28 or fragments thereof. Fragments include, but are not limited to, sequences corresponding to the sequences set forth in SEQ ID NOS: 11 and 28 without the leader sequences. Accordingly, the disclosure relates to an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 10 (including fragments thereof and complements thereto) and also comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 27 (including fragments thereof and complements thereto). Also included is an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous or similar to a nucleic acid sequence provided in SEQ ID NO: 10, including fragments thereof and complements thereto, and also comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous or similar to a nucleic acid sequence provided in SEQ ID NO: 27, including fragments thereof and complements thereto. The invention also relates to anti-CD200 antibodies comprising an amino acid sequence encoded by a nucleic acid sequence that is about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous or similar to a nucleic acid sequence provided in SEQ ID NOS: 10 or 27, including fragments thereof and complements thereto.

[0014] In yet another embodiment, the disclosure relates to an anti-CD200 antibody, comprising an amino acid sequence that is at least about 90% identical to the amino acid sequence of SEQ ID NO: 20 and also comprising an amino acid sequence that is at least about 90% identical to SEQ ID NO: 32. Also included are anti-CD200 antibodies comprising amino acid sequences that are about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical or similar to one or more amino acid sequence provided in SEQ ID NOS: 20 and 32 or fragments thereof. Fragments include, but are not limited to, sequences corresponding to the sequences set forth in SEQ ID NOS: 20 and 32 without the leader sequences. Accordingly, the disclosure relates to an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 19 (including fragments thereof and complements thereto) and also comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 31 (including fragments thereof and complements thereto). Also included is an anti-CD200 antibody comprising an amino

acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous or similar to a nucleic acid sequence provided in SEQ ID NO: 19, including fragments thereof and complements thereto, and also comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous or similar to a nucleic acid sequence provided in SEQ ID NO: 31, including fragments thereof and complements thereto. Included, therefore, are anti-CD200 antibodies comprising an amino acid sequence encoded by a nucleic acid sequence that is about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous or similar to a nucleic acid sequence provided in SEQ ID NOS: 19 or 31, including fragments thereof and complements thereto.

[0015] Anti-CD200 antibodies provided in the present disclosure include antibodies and antigen-binding fragments with altered or no effector function(s). Included are antibodies that comprise an altered constant or Fc region with either increased or decreased effector functions. The disclosure also relates to antibodies with altered or no effector functions due to increased or decreased binding affinity, which may arise from changes in the variable regions. Altered effector functions include, for example, an increased or decreased ability to bind one or more Fc receptor (FcR) or effector cell, increased or decreased antigen-dependent cytotoxicity (ADCC), and/or increased or decreased complement-dependent cytotoxicity (CDC). Variant antibodies include but are not limited to antibodies in which the constant region or Fc region contains one or more amino acid insertions, deletions, and/or substitutions. In additional embodiments, these variant antibodies comprise a constant region wherein the CH1 and hinge region are derived from human IgG2 and the CH2 and CH3 regions are derived from human IgG4. Also included are antibodies in which the constant or Fc region exhibits altered glycosylation. The aforementioned antibodies and antigen-binding fragments (including single-chain antibodies) may be murine, chimeric, humanized, fully human, or de-immunized; included are antibodies comprising the IgG1, IgG2, IgG3, IgG4, IgM, IgA1, IgA2, IgA, IgD, or IgE frameworks. Furthermore, the said antibodies, including fragments and variants thereof, may be blocking or non-blocking antibodies or fragments thereof.

[0016] In certain aspects, the disclosure provides anti-CD200 antibodies that exhibit decreased or no effector function. Antibodies with decreased or no effector function may comprise a variant or altered Fc or constant region, such as, for example, a constant region with one or more amino acid substitutions, insertions, and/or deletions, or a constant region with one or more changes in glycosylation. A variant constant region includes, for example, a region wherein one or more amino acids are substituted with alanine, such as in the Ala-Ala mutation described herein, or wherein one or more carbohydrate groups is changed, added, or removed. An alteration in the number and/or location of carbohydrate groups may be achieved by producing the said antibody in particular cell types for which post-translational modifications would be reduced, absent, or increased. In one embodiment, effector function of anti-CD200 antibodies is eliminated by swapping the IgG1 constant domain for an IgG2/4 fusion domain. Other ways of eliminating effector function can be envisioned such as, e.g., mutation of the sites known to interact with an FcR or insertion of a peptide in the hinge region, thereby eliminating critical sites required for an FcR interaction.

[0017] In certain aspects and methods of the present disclosure, anti-CD200 antibodies with altered or no effector functions comprise anti-CD200 antibodies with one or more amino acid substitutions, insertions, and/or deletions. In certain embodiments, such a variant anti-CD200 antibody exhibits its reduced or no effector function. In certain embodiments, the variant constant region (of said variant antibody) possesses at least about 70% homology with the native sequence constant or Fc region and/or with a constant or Fc region of the parent antibody or fragment thereof; in other embodiments the variant constant or Fc region possesses at least about 80% homology or similarity therewith; in other embodiments at least about 90% homology or similarity therewith and in additional embodiments at least about 95% homology or similarity therewith. In particular embodiments, a variant antibody comprises a G2/G4 construct. Accordingly, the present disclosure relates to a constant or Fc region of an anti-CD200 antibody with reduced or no effector function, wherein said constant region comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 13, 15, 18, 22, and fragments thereof. The present disclosure also relates to variant constant regions of an anti-CD200 antibody wherein an antibody comprises an amino acid sequence that is at least about 90% identical or similar to an amino acid sequence selected from among SEQ ID NOS: 13, 15, 18, 22, and fragments thereof. Also included in the disclosure are antibodies comprising an amino acid sequence that is about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical or similar to an amino acid sequence provided in SEQ ID NOS: 13, 15, 18, 22, and fragments thereof. Fragments include, but are not limited to, sequences without the leader sequences. Additionally, in some embodiments a constant region of an anti-CD200 antibody with reduced or no effector function and comprising the G2/G4 construct is encoded by a nucleic acid selected from the group consisting of SEQ ID NOS: 12, 14, 16, 17, and 21, or fragments thereof and complements thereto. In certain embodiments, an anti-CD200 antibody with reduced or no effector function is encoded by a nucleic acid comprising a nucleic acid sequence that is at least about 80% homologous or similar to a sequence selected from SEQ ID NOS: 12, 14, 16, 17, and 21, including fragments thereof and complements thereto. In other embodiments, a variant anti-CD200 antibody is encoded by a nucleic acid sequence comprising a sequence that is about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous or similar to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 12, 14, 16, 17, and 21, including fragments thereof and complements thereto. In still other embodiments, the nucleic acid encoding a variant anti-CD200 antibody comprises a nucleic acid sequence that hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 12, 14, 16, 17, and 21, including fragments thereof and complements thereto. Included are antigen-binding fragments and both blocking and non-blocking antibodies or fragments thereof.

[0018] In one embodiment, the present disclosure relates to a variant anti-CD200 antibody comprising an amino acid sequence that is at least about 90% identical to the amino acid sequence of SEQ ID NO: 13 and also comprising an amino acid sequence that is at least about 90% identical to SEQ ID NO: 28. Also included is an anti-CD200 antibody comprising one or more amino acid sequence that is about 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to an amino acid sequence provided in SEQ ID NOS: 13 and 28 or fragments thereof. Fragments include, but are not limited to, sequences corresponding to the sequences set forth in SEQ ID NOS: 13 and 28 without the leader sequences. Accordingly, the disclosure relates to a variant anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 12 (including fragments thereof and complements thereto) and also comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 27 (including fragments thereof and complements thereto). Also included is an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous to a nucleic acid sequence provided in SEQ ID NO: 12, including fragments thereof and complements thereto, and also comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous to a nucleic acid sequence provided in SEQ ID NO: 27, including fragments thereof and complements thereto. Included, therefore, are anti-CD200 antibodies comprising an amino acid sequence encoded by a nucleic acid sequence that is about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to a nucleic acid sequence provided in SEQ ID NOS: 12 or 27, including fragments thereof and complements thereto.

[0019] In another embodiment, the disclosure relates to a variant anti-CD200 antibody comprising an amino acid sequence that is at least about 90% identical to the amino acid sequence of SEQ ID NO: 15 and also comprising an amino acid sequence that is at least about 90% identical to SEQ ID NO: 24. Also included is an anti-CD200 antibody comprising an amino acid sequence that is about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to one or more amino acid sequence provided in SEQ ID NOS: 15 and 24 or fragments thereof. Fragments include, but are not limited to, sequences corresponding to the sequences set forth in SEQ ID NOS: 15 and 24 without the leader sequences (e.g., the fragment of SEQ ID NO: 15 beginning at amino acid 20 or 21). Accordingly, the disclosure relates to a variant anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 14 (including fragments thereof and complements thereto) and also comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 23 (including fragments thereof and complements thereto). Also included is an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous to a nucleic acid sequence provided in SEQ ID NO: 14, including fragments thereof and complements thereto, and also comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous to a nucleic acid sequence provided in SEQ ID NO: 23, including fragments thereof and complements thereto. Included, therefore, are anti-CD200 antibodies comprising an amino acid sequence encoded by a nucleic acid sequence that is about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to a nucleic acid sequence provided in SEQ ID NOS: 14 or 23, including fragments thereof and complements thereto.

[0020] In an additional embodiment, the disclosure relates to a variant anti-CD200 antibody comprising an amino acid sequence that is at least about 90% identical to the amino acid sequence of SEQ ID NO: 13 and also comprising an amino acid sequence that is at least 90% identical to SEQ ID NO: 28. Also included is an anti-CD200 antibody comprising one or more amino acid sequence that is about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to an amino acid sequence provided in SEQ ID NOS: 13 and 28 or fragments thereof. Fragments include, but are not limited to, sequences corresponding to the sequences set forth in SEQ ID NOS: 13 and 28 without the leader sequences. Accordingly, the disclosure relates to a variant anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 16 (including fragments thereof and complements thereto) and also comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 27 (including fragments thereof and complements thereto). Also included is an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous to a nucleic acid sequence provided in SEQ ID NO: 16, including fragments thereof and complements thereto, and also comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous to a nucleic acid sequence provided in SEQ ID NO: 27, including fragments thereof and complements thereto. Included, therefore, are anti-CD200 antibodies comprising an amino acid sequence encoded by a nucleic acid sequence that is about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to a nucleic acid sequence provided in SEQ ID NOS: 16 or 27, including fragments thereof and complements thereto.

[0021] In still another embodiment, the disclosure relates to a variant anti-CD200 antibody comprising an amino acid sequence that is at least about 90% identical to the amino acid sequence of SEQ ID NO: 18 and also comprising an amino acid sequence that is at least about 90% identical to SEQ ID NO: 30. Also included is an anti-CD200 antibody comprising an amino acid sequence that is about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to an amino acid sequence provided in SEQ ID NOS: 18 and 30 or fragments thereof. Accordingly, the disclosure relates to a variant anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 17 (including fragments thereof and complements thereto) and also comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 29 (including fragments thereof and complements thereto). Also included is an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous to a nucleic acid sequence provided in SEQ ID NO: 17, including fragments thereof and complements thereto, and also comprising an amino acid sequence encoded by a nucleic acid sequence that is at least 80% homologous to a nucleic acid sequence provided in SEQ ID NO: 29, including fragments thereof and complements thereto. Included, therefore, are anti-CD200 antibodies comprising an amino acid sequence encoded by a nucleic acid sequence that is about 80%, 85%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to a nucleic acid sequence provided in SEQ ID NOS: 17 or 29, including fragments thereof and complements thereto.

[0022] In another embodiment, the disclosure relates to a variant anti-CD200 antibody comprising an amino acid sequence that is at least about 90% identical to the amino acid sequence of SEQ ID NO: 22 and also comprising an amino acid sequence that is at least about 90% identical to SEQ ID NO: 34: Also included is an anti-CD200 antibody comprising an amino acid sequence that is about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to an amino acid sequences provided in SEQ ID NOS: 22 and 34 or fragments thereof. Accordingly, the disclosure relates to a variant anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 21 (including fragments thereof and complements thereto) and also comprising an amino acid sequence encoded by a nucleic acid sequence that hybridizes under stringent conditions to the nucleic acid sequence of SEQ ID NO: 33 (including fragments thereof and complements thereto). Also included is an anti-CD200 antibody comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous to a nucleic acid sequence provided in SEQ ID NO: 21, including fragments thereof and complements thereto, and also comprising an amino acid sequence encoded by a nucleic acid sequence that is at least about 80% homologous to a nucleic acid sequence provided in SEQ ID NO: 33, including fragments thereof and complements thereto. Included, therefore, are anti-CD200 antibodies comprising an amino acid sequence encoded by a nucleic acid sequence that is about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to a nucleic acid sequence provided in SEQ ID NOS: 21 and 33, including fragments thereof and complements thereto.

[0023] Anti-CD200 antibodies with altered effector function may also exhibit increased effector function. Increased effector functions include but are not limited to increased binding to one or more Fc receptors, increased ability to elicit ADCC, and/or increased ability to elicit CDC. Anti-CD200 antibodies with increased effector function may also comprise a variant Fc or constant region as described herein. The aforementioned anti-CD200 antibodies with altered effector functions may furthermore be blocking or non-blocking antibodies. For example, an anti-CD200 antibody with increased effector function may bind to CD200 but may not block the CD200:CD200R interaction. Such an antibody may be useful when targeting an effector function (e.g., ADCC or CDC) to a CD200-expressing cell. As mentioned previously, antibodies described herein, including the aforementioned anti-CD200 antibodies with altered effector function(s), include murine, chimeric, humanized, fully human and de-immunized antibodies, all in their blocking and non-blocking forms, and fragments thereof.

[0024] In certain aspects, this disclosure provides methods and compositions for modulating or depleting CD200-positive cells. CD200-positive cells may be modulated or depleted by administering a CD200 antagonist to a subject. The said antagonist may target CD200-positive cells for effector function and/or may disrupt the CD200:CD200R interaction. In certain embodiments, the said antagonist is an anti-CD200 antibody. The said anti-CD200 antibody may be

an antibody described herein, including any fragments and variants thereof. Included are antibodies and antigen-binding fragments with altered effector function(s), such as, for example, anti-CD200 antibodies with decreased or no effector function. Also included are murine, chimeric, humanized, fully human and de-immunized antibodies and antigen-binding fragments, including single-chain antibodies. The aforementioned antibodies may be non-blocking or blocking antibodies and include antibodies comprising the IgG1, IgG2, IgG3, IgG4, IgM, IgA1, IgA2, IgA, IgD, or IgE frameworks.

[0025] CD200-positive cells are implicated in certain types of cancers and certain autoimmune diseases. Accordingly, CD200-positive cells include but are not limited to immune cells (such as, e.g., B-cells and T-cells) and cancer cells (such as, e.g., cancer cells of ovarian, skin, lung, renal, breast, prostate, neuroblastoma, lymphoma, myeloma, leukemia, thyroid, and plasma cell cancers). Also included are cancer cells from any tissue or organ derived from neural crest cells. Thus the subject in need of a method of modulating or depleting CD200-positive cells may be a patient with cancer or autoimmune disease, or a patient who has received or is expected to receive an organ transplant.

[0026] In one aspect this disclosure provides methods and compositions for treating autoimmune disease. Autoimmune diseases that may be treated by the methods and compositions provided herein include but are not limited to rheumatoid arthritis, inflammatory bowel disease (including ulcerative colitis and Crohn's disease), systemic lupus erythematosus, multiple sclerosis, Hashimoto's thyroiditis, pernicious anemia, Addison's disease, type I diabetes, dermatomyositis, Sjogren's syndrome, lupus erythematosus, myasthenia gravis, Reiter's syndrome, Grave's disease, psoriasis, and autoimmune hemolytic diseases. In some embodiments, a patient with autoimmune disease is given an antagonist to CD200, and in certain embodiments, the antagonist is an anti-CD200 antibody. The anti-CD200 antibody may comprise a variant constant region as described herein. Accordingly, the anti-CD200 antibody may exhibit altered effector function(s), such as, for example, increased effector function (s). The said antibody may exhibit, for example, increased binding to one or more Fc receptors. Additionally, the said antibody may elicit increased ADCC and/or CDC. The said antibody may furthermore be either a blocking or non-blocking antibody or fragment thereof and may be either a murine, chimeric, humanized, fully human or de-immunized antibody or fragment thereof.

[0027] Cancers for which the disclosed methods may be used include but are not limited to melanoma, ovarian cancer, renal cancer, neuroblastoma, lung cancer, breast cancer, prostate cancer, lymphoma, myeloma, leukemia, and plasma cell cancers. Also included are cancers derived from neural crest cells and any cancers that express CD200. In certain embodiments, this disclosure provides a method for treating hematological malignancies, such as, for example, leukemias including chronic lymphocytic leukemia.

[0028] In a particularly useful embodiment, a cancer therapy in accordance with this disclosure comprises (1) administering an anti-CD200 antibody or antagonist that interferes with the interaction between CD200 and its receptor to block immune suppression, thereby promoting eradication of the cancer cells; and/or (2) administering a fusion molecule that includes a CD-200 targeting portion to directly kill cancer cells. Alternatively, the antibody directly kills cancer cells through complement-mediated and/or antibody-

dependent cellular cytotoxicity. In various embodiments, the effector function of the anti-CD200 antibody is altered. In one particular embodiment, the anti-CD200 antibody contains a variant or altered constant region for which the effector function is decreased or eliminated; such an antibody may be useful for the methods described above in (1) and (2), for example.

[0029] In certain embodiments, the disclosure relates to fusion molecules wherein an anti-CD200 antibody or antigen-binding fragment is linked to a second molecule. The said fusion molecule may comprise, for example, a small molecule, polypeptide, peptidomimetic, heterocyclic peptide, a chemotherapeutic agent, an immunomodulatory agent, a targeting moiety, or a nucleic acid construct (e.g., antisense, RNAi, or gene-targeting construct). The disclosure also includes antigen-binding fragments to CD200 wherein the fragment is fused or otherwise linked to a polypeptide, protein domain, serum protein, albumin, PEG (polyethylene glycol), or any other molecule that will increase the half-life of the said fragment in vivo. Said antigen-binding fragments include Fab, Fv, single-chain fragments or scFv, Fab', and F(ab')₂, for example.

[0030] The present disclosure also relates to methods employing anti-CD200 antibodies to determine the CD200 expression status of a cell or tissue sample obtained from a patient. Such methods include but are not limited to immunohistochemical staining of tissue samples and flow cytometry analysis of CD200-stained cells from a patient. The patient may be a patient with cancer, for example.

[0031] In accordance with the methods and compositions described herein, the disclosure also relates to methods of treating a transplant or allograft patient. An anti-CD200 antibody or other CD200 antagonist of the present disclosure may be administered to a patient prior to a transplant or allograft procedure or after the procedure in order to decrease or eliminate CD200-positive immune cells that could reduce the patient's acceptance of the transplanted organ or tissue. In a particular embodiment, an anti-CD200 antibody with increased effector function is given to a transplant patient.

[0032] In further embodiments, methods are provided for combination therapies comprising anti-CD200 therapy. For example, a patient receiving a first therapy comprising a CD200 antagonist (e.g., an anti-CD200 antibody described herein) may also be given a second therapy. The CD200 antagonist may be given simultaneously with the second therapy. Alternatively, the CD200 antagonist may be given prior to or following the second therapy. Second therapies include but are not limited to chemotherapeutic agents, radiation therapy, vaccines, antibiotics and anti-viral agents, and immunomodulatory therapies.

[0033] In another embodiment of the present disclosure, methods are provided for monitoring the progress of a therapeutic treatment. The method involves administering a therapy (e.g. an immunomodulatory therapy, a chemotherapeutic therapy, etc.) and determining CD200 levels in a subject at least twice to determine the effectiveness of the therapy. Other methods to determine the effectiveness of a therapy include but are not limited to detection of cancer cells, total lymphocyte count, spleen, liver, and/or lymph node size, number of regulatory T cells, intracellular or serum cytokine profiles, or secretion of cytokines by T or B cells as measured by ELISPOT—an assay system that allows the detection of cytokines or other secreted molecules on a per cell basis.

[0034] According to the compositions and methods set forth in the present embodiments, the disclosure also relates to any pharmaceutical composition comprising an anti-CD200 antibody. Included are chimeric, humanized, human and de-immunized anti-CD200 antibodies and antigen-binding fragments, including single-chain antibodies. Also included are murine, chimeric, humanized, human and de-immunized variant anti-CD200 antibodies and antigen-binding fragments with altered effector function(s) as described herein. The aforementioned antibodies and variant antibodies may either be blocking or non-blocking antibodies or antigen-binding fragments.

[0035] In certain embodiments, patients for whom anti-CD200 therapy is useful or patients who expect to receive a therapy comprising a CD200 antagonist therapy (including, for example, an anti-CD200 antibody) may be screened for certain previously received treatments and procedures or for current medical status. In one embodiment for example, female patients may be pre-screened for pregnancy and agree to contraception, since CD200 plays an important role in protection against abortion. Accordingly, patients receiving said therapy may agree to practice one or more methods of contraception. The said patient may agree to use one or more methods of contraception for a designated period prior to starting the said therapy and/or for the duration of the said therapy. In certain embodiments, female patients receive counseling concerning the risks with respect to fetal exposure to such anti-CD200 therapy. In additional embodiments, such patients may be expected to sign informed consent forms prior to such treatment. In other aspects, physicals counseling patients regarding anti-CD200 therapy may require such patients to use contraceptive devices or formulations prior to administering the anti-CD200 therapy (see, for example, U.S. Pat. No. 6,908,432 and related patents, the contents of which are incorporated herein by reference). Similarly, in other embodiments, patients may be screened to identify patients who have previously received brain surgery and/or radiation therapy to the brain; anti-CD200 therapy would not be prescribed for such patients.

BRIEF DESCRIPTION OF THE FIGURES

[0036] FIG. 1 provides the nucleic acid sequence for the primer C7 mhHF (SEQ ID NO:1) used in generating the G2/G4 construct.

[0037] FIG. 2 provides the nucleic acid sequence for the Primer Rev Age Pri (SEQ ID NO: 2) used in generating the G2/G4 construct.

[0038] FIG. 3 provides the nucleic acid sequence for the primer C2aB7 rev (SEQ ID NO: 3) used in generating the G2/G4 construct.

[0039] FIG. 4 provides the nucleic acid sequence for the Iacpri (SEQ ID NO: 4) used in generating the G2/G4 construct.

[0040] FIG. 5 provides the nucleic acid sequence for Lead-VHpAX (SEQ ID NO: 5).

[0041] FIGS. 6A-F depict the amino acid sequences and nucleotide sequences for the heavy and light chains of antibody chC2aB7-hG1 (SEQ ID NOS: 6, 7, 23, 24, 37, and 38). FIG. 6C shows SEQ ID NO: 37 (nucleic acid sequence) and SEQ ID NO: 7 (amino acid sequence). SEQ ID NO: 7 as shown in the schematic is contiguous but is depicted with a corresponding nucleotide sequence that includes introns. FIG. 6F shows SEQ ID NO: 38 (nucleic acid sequence) and SEQ ID NO: 24 (amino acid sequence).

[0042] FIGS. 7A-F depict the amino acid sequences and nucleotide sequences for the heavy and light chains of antibody hB7V4V1-hG1(SEQ ID NOS: 8, 9, 25, 26, 39, and 40). FIG. 7C shows SEQ ID NO: 39 (nucleic acid sequence) and SEQ ID NO: 9 (amino acid sequence). FIG. 7F shows SEQ ID NO: 40 (nucleic acid sequence) and SEQ ID NO: 26 (amino acid sequence).

[0043] FIGS. 8A-F depict the amino acid sequences and nucleotide sequences for the heavy and light chains of antibody hB7V3V1-hG1 (SEQ ID NOS: 10, 11, 25, 26, 40, and 41). FIG. 8C shows SEQ ID NO: 41 (nucleic acid sequence) and SEQ ID NO: 11 (amino acid sequence). FIG. 8F shows SEQ ID NO: 41 (nucleic acid sequence) and SEQ ID NO: 26 (amino acid sequence).

[0044] FIGS. 9A-F depict the amino acid sequences and nucleotide sequences for the heavy and light chains of antibody hB7V3V2-hG1(SEQ ID NOS: 10, 11, 27, 28, 41, and 42). FIG. 9C shows SEQ ID NO: 41 (nucleic acid sequence) and SEQ ID NO: 11 (amino acid sequence). FIG. 9F shows SEQ ID NO: 42 (nucleic acid sequence) and SEQ ID NO: 28 (amino acid sequence).

[0045] FIGS. 10A-F depict the amino acid sequences and nucleotide sequences for the heavy and light chains of antibody hB7V3V2-hG2G4 (SEQ ID NOS: 12, 13, 27, 28, 42, and 43). FIG. 10C shows SEQ ID NO: 43 (nucleic acid sequence) and SEQ ID NO: 13 (amino acid sequence). SEQ ID NO: 13 as shown in the schematic is contiguous but is depicted with a corresponding nucleotide sequence that includes introns. FIG. 10F shows SEQ ID NO: 42 (nucleic acid sequence) and SEQ ID NO: 28 (amino acid sequence).

[0046] FIGS. 11A-F depict the amino acid sequences and nucleotide sequences for the heavy and light chains of antibody chC2aB7-hG2G4 (SEQ ID NOS: 14, 15, 23, 24, 44, 45, 46, and 47). FIG. 11C shows SEQ ID NO: 44 (nucleic acid sequence) and SEQ ID NO: 45 (amino acid sequence). SEQ ID NO: 45 corresponds to amino acids 1-337 of SEQ ID NO: 15. As shown in the schematic, SEQ ID NO: 45 is contiguous but is depicted with a corresponding nucleotide sequence that includes introns. FIG. 11F shows SEQ ID NO: 46 (nucleic acid sequence) and SEQ ID NO: 47 (amino acid sequence).

[0047] FIGS. 12A-F depict the amino acid sequences and nucleotide sequences for the heavy and light chains of antibody hB7V3V2-cG2G4 (SEQ ID NOS: 13, 16, 27, 28, 48, and 49). FIG. 12C shows SEQ ID NO: 48 (nucleic acid sequence) and SEQ ID NO: 13 (amino acid sequence). FIG. 12F shows SEQ ID NO: 49 (nucleic acid sequence) and SEQ ID NO: 28 (amino acid sequence).

[0048] FIGS. 13A-D depict the amino acid sequences and nucleotide sequences for the heavy and light chains of antibody chC7-hG2G4 (SEQ ID NOS: 17, 18, 29, and 30).

[0049] FIGS. 14A-F depict the amino acid sequences and nucleotide sequences for the heavy and light chains of antibody D1B5-hG1 (SEQ ID NOS: 19, 20, 31, 32, 50, and 51). FIG. 14C shows SEQ ID NO: 50 (nucleic acid sequence) and SEQ ID NO: 20 (amino acid sequence). SEQ ID NO: 20 as shown in the schematic is contiguous but is depicted with a corresponding nucleotide sequence that includes introns. FIG. 14F shows SEQ ID NO: 51 (nucleic acid sequence) and SEQ ID NO: 32 (amino acid sequence).

[0050] FIGS. 15A-D depict the amino acid sequences and nucleotide sequences for the heavy and light chains of antibody G2G4 63L1D (SEQ ID NOS: 21, 22, 33, and 34).

[0051] FIG. 16 provides the nucleic acid sequence for the forward primer for cloning CD200 cDNA (SEQ ID NO: 35).

[0052] FIG. 17 provides the nucleic acid sequence for the reverse primer for cloning CD200 cDNA (SEQ ID NO: 36).
 [0053] FIG. 18 shows the effects of administering humanized CD200 antibodies in the RAJI-CD200/PBL model. Humanized anti-CD200 antibodies resulted in an inhibition of tumor growth.

[0054] FIG. 19 demonstrates the effects of administering humanized CD200 antibodies with and without effector function in the Namaiwa CD200 animal model. Antibodies without effector function exhibited efficacy in inhibiting tumor growth.

[0055] FIG. 20 is a table showing the expression level of CD200 in chronic lymphocytic leukemia (CLL) patient samples compared to normal samples.

[0056] FIG. 21 depicts the relative levels of CD200 expression detected in cancer cell lines.

[0057] FIG. 22 shows the expression level of CD200 antigen in human ovarian cancer samples relative to the expression level detected in human peripheral blood lymphocytes (PBL).

[0058] FIG. 23 shows the expression level of CD200 antigen in human melanoma patient samples relative to the expression level detected in PBL.

[0059] FIG. 24 shows immunohistochemical staining of CD200 of melanoma patient samples.

[0060] FIG. 25 demonstrates the effects of anti-CD200 antibody in cytokine production. The levels of IL-2 production in mixed cell population assays were measured in the absence and presence of CD200 antibody. The antibody used is a chimeric anti-CD200 antibody with no effector function.

[0061] FIG. 26 shows the effects of administering anti-CD200 antibodies, with or without effector function, in the Namalwa/PBL model in which the tumors do not express CD200.

[0062] FIG. 27 shows flow cytometric analysis of CD200 expression on activated T-cells. CD3+ cells were activated with mOKT3, harvested, washed and subjected to staining with the indicated conjugated antibodies specific for human CD25, CD200, CD5, CD4 and CD8. Cells were washed and analyzed for immunofluorescence on a FacsCaliber flow cytometer using CellQuest software.

[0063] FIG. 28 demonstrates the effects of anti-CD200 antibodies on ADCC of activated T-cells. CD3+ human T cells were stimulated with 10 µg/mL immobilized (plate-coated) mOKT3 for 72 hrs. Activated T cells were then chromatized for use as targets and incubated with purified autologous CD56+ (NK) cells as effector cells. Cells were coincubated for 4 hours at 37° C. at 25:1 (A) or 10:1 (B) effector: target cell ratios in the presence or absence of a humanized anti-CD200 antibody capable of mediating effector function (V3V2-G1) or engineered to lack effector function (V3V2-G2G4). Data is represented as percent specific lysis. Anti-CD200 antibody increased ADCC of activated T-cells, whereas the anti-CD200 antibody with no effector function failed to induce ADCC.

[0064] FIG. 29 is a table showing the expression level of CD200 on plasma cells.

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

I. CD200 Antagonists

[0065] CD200 is a highly conserved type I transmembrane glycoprotein expressed on various cell types including cells

of the immune system (e.g., T-cells, B-cells, and dendritic cells (Barclay et al., *TRENDS Immunol.* 2002; 23)) as well as certain cancer cells as shown herein. The protein interacts with its receptor CD200R on myeloid cells and sub-populations of T cells (Wright et al. *J. Immunol.* 2003 (171): 3034-3046 and Wright et al., *Immunity* 2000 (13):233-242); the CD200:CD200R interaction delivers an immunomodulatory signal to cells and induces immunosuppression including apoptosis-associated immune tolerance (Rosenblum et al. 2004 *Blood* (103): 2691-2698). Thus agents that interfere with the function or activity of CD200 and/or its receptor may inhibit or reverse the immunosuppressive effects of the CD200:CD200R interaction. In addition, agents that specifically bind CD200 (but that may or may not inhibit the CD200:CD200R interaction) may trigger downstream events that reverse or abolish the effects of CD200.

[0066] In certain aspects, the present disclosure relates to CD200 antagonists. As used herein, the term antagonist includes any agent that is capable of inhibiting the activity, function and/or the expression of CD200 or its receptor. Examples include but are not limited to polypeptides, antibodies, small molecules, aptamers, spiegelmers, locked nucleic acid (LNA) inhibitors, peptide nucleic acid (PNA) inhibitors, nucleic acid constructs (e.g., gene-targeting constructs, antisense constructs, RNA interference (RNAi) constructs, etc.) and peptidomimetics. In certain embodiments, the antagonist disrupts the interaction of CD200 and CD200R. In other embodiments, the CD200 antagonists are capable of decreasing the immunosuppressive effects of CD200 or are capable of targeting CD200-expressing cells for depletion or elimination.

[0067] In certain aspects, the CD200 antagonists are polypeptides. Polypeptides utilized in the present disclosure can be constructed using different techniques which are known to those skilled in the art. In one embodiment, the polypeptides are obtained by chemical synthesis. In other embodiments, the polypeptides are antibodies constructed from a fragment or several fragments of one or more antibodies. In further embodiments, the polypeptide is an anti-CD200 antibody as described herein.

[0068] Thus in certain embodiments, the CD200 antagonists are anti-CD200 antibodies. As used herein, the term "antibodies" refers to complete antibodies or antibody fragments capable of binding to CD200 or CD200R. Included are Fab, Fv, scFv, Fab' and F(ab')₂, monoclonal and polyclonal antibodies, engineered antibodies (including chimeric, single chain, CDR-grafted, humanized, fully human antibodies, and artificially selected antibodies), and synthetic or semi-synthetic antibodies produced using phage display or alternative techniques. Also included are antibodies engineered or produced in ways to contain variant or altered constant or Fc regions with either increased or decreased ability to bind one or more effector cell; such variant antibodies include but are not limited to antibodies in which the constant or Fc region contains altered glycosylation patterns. Small fragments, such as Fv and scFv, possess advantageous properties for diagnostic and therapeutic applications on account of their small size and consequent superior tissue distribution. Antibodies with engineered or variant constant or Fc regions can be useful in modulating effector functions, such as, for example, ADCC and CDC. Such antibodies with engineered or variant constant or Fc regions may be useful in instances where CD200 is expressed in normal tissue, for example; variant anti-CD200 antibodies without effector function in

these instances may elicit the desired therapeutic response while not damaging normal tissue. Furthermore, antibodies, variant antibodies, and fragments thereof may be blocking (i.e., the said antibodies or fragments inhibit the interaction of CD200 and CD200R) or non-blocking (i.e., the said antibodies or fragments bind to CD200 but do not block its interaction with CD200R).

[0069] The disclosure also relates to anti-CD200 antibodies comprising heavy and light chains as provided herein, including heavy and light chains that are homologous or similar to the heavy and/or light chains provided herein. "Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology and identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When an equivalent position in the compared sequences is occupied by the same base or amino acid, then the molecules are identical at that position; when the equivalent site occupied by the same or a similar amino acid residue (e.g., similar in steric and/or electronic nature), then the molecules can be referred to as homologous (similar) at that position. Expression as a percentage of homology/similarity or identity refers to a function of the number of identical or similar amino acids at positions shared by the compared sequences. The term "homology" describes a mathematically based comparison of sequence similarities which is used to identify genes or proteins with similar functions or motifs. As used herein, "identity" means the percentage of identical nucleotide or amino acid residues at corresponding positions in two or more sequences when the sequences are aligned to maximize sequence matching, i.e., taking into account gaps and insertions. Thus methods to determine identity are designed to give the largest match between the sequences tested (see Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heijne, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., SIAM J. Applied Math., 48: 1073 1988, Devereux, J., et al., Nucleic Acids Research 12(1): 387 (1984), BLASTP, BLASTN, FASTA (Altschul, S. F. et al., J. Molec. Biol. 215: 403-410 (1990) and Altschul et al. Nuc. Acids Res. 25: 3389-3402 (1997)) and BLAST X (BLAST Manual, Altschul, S., et al., NCBI NLM NIH Bethesda, Md. 20894; Altschul, S., et al., J. Mol. Biol. 215: 403-410 (1990). A sequence which is "unrelated" or "non-homologous" shares less than 40% identity, though preferably less than 25% identity with a sequence of the present disclosure. In comparing two sequences, the absence of residues (amino acids or nucleic acids) or presence of extra residues also decreases the identity and homology/similarity.

[0070] Accordingly, the disclosure relates to antibodies as described herein without the leader sequences. Thus antibodies of the disclosure may comprise heavy and light chains (as described herein) in which the leader sequence is either absent or replaced by a different leader sequence. If host cells are used to produce antibodies of the present disclosure, appropriate leader sequences may therefore be selected according to the particular host cell used.

[0071] Antibodies may be produced by methods well known in the art. For example, monoclonal anti-CD200 antibodies may be generated using CD200 positive cells, CD200 polypeptide, or a fragment of CD200 polypeptide, as an immunogen, thus raising an immune response in animals from which antibody-producing cells and in turn monoclonal antibodies may be isolated. The sequence of such antibodies may be determined and the antibodies or variants thereof produced by recombinant techniques. Recombinant techniques may be used to produce chimeric, CDR-grafted, humanized and fully human antibodies based on the sequence of the monoclonal antibodies as well as polypeptides capable of binding to CD200.

[0072] Moreover, antibodies derived from recombinant libraries ("phage antibodies") may be selected using CD200-positive cells, or polypeptides derived therefrom, as bait to isolate the antibodies or polypeptides on the basis of target specificity. The production and isolation of non-human and chimeric anti-CD200 antibodies are well within the purview of the skilled artisan.

[0073] Recombinant DNA technology is used to improve the antibodies produced in non-human cells. Thus, chimeric antibodies may be constructed in order to decrease the immunogenicity thereof in diagnostic or therapeutic applications. Moreover, immunogenicity may be minimized by humanizing the antibodies by CDR grafting and, optionally, framework modification. See, U.S. Pat. No. 5,225,539, the contents of which are incorporated herein by reference.

[0074] Antibodies may be obtained from animal serum or, in the case of monoclonal antibodies or fragments thereof, produced in cell culture. Recombinant DNA technology may be used to produce the antibodies according to established procedure, including procedures in bacterial or preferably mammalian cell culture. The selected cell culture system preferably secretes the antibody product.

[0075] In another embodiment, a process for the production of an antibody disclosed herein includes culturing a host, e.g. *E. coli* or a mammalian cell, which has been transformed with a hybrid vector. The vector includes one or more expression cassettes containing a promoter operably linked to a first DNA sequence encoding a signal peptide linked in the proper reading frame to a second DNA sequence encoding the antibody protein. The antibody protein is then collected and isolated. Optionally, the expression cassette may include a promoter operably linked to polycistronic, for example bicistronic, DNA sequences encoding antibody proteins each individually operably linked to a signal peptide in the proper reading frame.

[0076] Multiplication of hybridoma cells or mammalian host cells in vitro is carried out in suitable culture media, which include the customary standard culture media (such as, for example Dulbecco's Modified Eagle Medium (DMEM) or RPMI 1640 medium), optionally replenished by a mammalian serum (e.g. fetal calf serum), or trace elements and growth sustaining supplements (e.g. feeder cells such as normal mouse peritoneal exudate cells, spleen cells, bone marrow macrophages, 2-aminoethanol, insulin, transferrin, low density lipoprotein, oleic acid, or the like). Multiplication of host cells which are bacterial cells or yeast cells is likewise carried out in suitable culture media known in the art. For example, for bacteria suitable culture media include medium LE, NZCYM, NZYM, NZM, Terrific Broth, SOB, SOC, 2xYT, or M9 Minimal Medium. For yeast, suitable culture

media include medium YPD, YEPD, Minimal Medium, or Complete Minimal Dropout Medium.

[0077] In vitro production provides relatively pure antibody preparations and allows scale-up production to give large amounts of the desired antibodies. Techniques for bacterial cell, yeast, plant, or mammalian cell cultivation are known in the art and include homogeneous suspension culture (e.g. in an airlift reactor or in a continuous stirrer reactor), and immobilized or entrapped cell culture (e.g. in hollow fibres, microcapsules, on agarose microbeads or ceramic cartridges).

[0078] Large quantities of the desired antibodies can also be obtained by multiplying mammalian cells *in vivo*. For this purpose, hybridoma cells producing the desired antibodies are injected into histocompatible mammals to cause growth of antibody-producing tumors. Optionally, the animals are primed with a hydrocarbon, especially mineral oils such as pristane (tetramethyl-pentadecane), prior to the injection. After one to three weeks, the antibodies are isolated from the body fluids of those mammals. For example, hybridoma cells obtained by fusion of suitable myeloma cells with antibody-producing spleen cells from Balb/c mice, or transfected cells derived from hybridoma cell line Sp2/0 that produce the desired antibodies are injected intraperitoneally into Balb/c mice optionally pre-treated with pristane. After one to two weeks, ascitic fluid is taken from the animals.

[0079] The foregoing, and other, techniques are discussed in, for example, Kohler and Milstein, (1975) *Nature* 256:495-497; U.S. Pat. No. 4,376,110; Harlow and Lane, *Antibodies: a Laboratory Manual*, (1988) Cold Spring Harbor, the disclosures of which are all incorporated herein by reference. Techniques for the preparation of recombinant antibody molecules are described in the above references and also in, for example WO97/08320; U.S. Pat. No. 5,427,908; U.S. Pat. No. 5,508,717; Smith, 1985, *Science*, Vol. 225, pp 1315-1317; Parmley and Smith, 1988, *Gene* 73, pp 305-318; De La Cruz et al., 1988, *Journal of Biological Chemistry*, 263 pp 4318-4322; U.S. Pat. No. 5,403,484; U.S. Pat. No. 5,223,409; WO88/06630; WO92/15679; U.S. Pat. No. 5,780,279; U.S. Pat. No. 5,571,698; U.S. Pat. No. 6,040,136; Davis et al., 1999, *Cancer Metastasis Rev.*, 18(4):421-5; Taylor, et al., *Nucleic Acids Research* 20 (1992): 6287-6295; Tomizuka et al., *Proc. Natl. Academy of Sciences USA* 97(2) (2000): 722-727. The contents of all these references are incorporated herein by reference.

[0080] The cell culture supernatants are screened for the desired antibodies, preferentially by immunofluorescent staining of CD200-positive cells, by immunoblotting, by an enzyme immunoassay, e.g. a sandwich assay or a dot-assay, or a radioimmunoassay.

[0081] For isolation of the antibodies, the immunoglobulins in the culture supernatants or in the ascitic fluid may be concentrated, e.g. by precipitation with ammonium sulfate, dialysis against hygroscopic material such as polyethylene glycol, filtration through selective membranes, or the like. If necessary and/or desired, the antibodies are purified by the customary chromatography methods, for example gel filtration, ion-exchange chromatography, chromatography over DEAE-cellulose and/or (immuno-) affinity chromatography, e.g. affinity chromatography with one or more surface polypeptides derived from a CD200-positive cell line, or with Protein-A or -G.

[0082] Another embodiment provides a process for the preparation of a bacterial cell line secreting antibodies

directed against CD200 in a suitable mammal. For example a rabbit is immunized with pooled samples from CD200-positive tissue or cells or CD200 polypeptide or fragments thereof. A phage display library produced from the immunized rabbit is constructed and panned for the desired antibodies in accordance with methods well known in the art (such as, for example, the methods disclosed in the various references incorporated herein by reference).

[0083] Hybridoma cells secreting the monoclonal antibodies are also disclosed. The preferred hybridoma cells are genetically stable, secrete monoclonal antibodies described herein of the desired specificity, and can be activated from deep-frozen cultures by thawing and recloning.

[0084] In another embodiment, a process is provided for the preparation of a hybridoma cell line secreting monoclonal antibodies against CD200. In that process, a suitable mammal, for example a Balb/c mouse, is immunized with one or more polypeptides or antigenic fragments of CD200 or with one or more polypeptides or antigenic fragments derived from a CD200-positive cell, the CD200-positive cell itself, or an antigenic carrier containing a purified polypeptide as described. Antibody-producing cells of the immunized mammal are grown briefly in culture or fused with cells of a suitable myeloma cell line. The hybrid cells obtained in the fusion are cloned, and cell clones secreting the desired antibodies are selected. For example, spleen cells of Balb/c mice immunized with a CD200-positive Chronic Lymphocytic Leukemia (CLL) cell line are fused with cells of the myeloma cell line PAI or the myeloma cell line Sp2/0-Ag 14. The obtained hybrid cells are then screened for secretion of the desired antibodies and positive hybridoma cells are cloned.

[0085] Preferred is a process for the preparation of a hybridoma cell line, characterized in that Balb/c mice are immunized by injecting subcutaneously and/or intraperitoneally between 10^6 and 10^7 cells of a CD200-positive cell line several times, e.g. four to six times, over several months, e.g. between two and four months. Spleen cells from the immunized mice are taken two to four days after the last injection and fused with cells of the myeloma cell line PAI in the presence of a fusion promoter, preferably polyethylene glycol. Preferably, the myeloma cells are fused with a three- to twenty-fold excess of spleen cells from the immunized mice in a solution containing about 30% to about 50% polyethylene glycol of a molecular weight around 4000. After the fusion, the cells are expanded in suitable culture media as described hereinbefore, supplemented with a selection medium, for example HAT medium, at regular intervals in order to prevent normal myeloma cells from overgrowing the desired hybridoma cells.

[0086] The antibodies and fragments thereof can be "chimeric". Chimeric antibodies and antigen-binding fragments thereof comprise portions from two or more different species (e.g., mouse and human). Chimeric antibodies can be produced with mouse variable regions of desired specificity spliced into human constant domain gene segments (for example, U.S. Pat. No. 4,816,567). In this manner, non-human antibodies can be modified to make them more suitable for human clinical application.

[0087] The monoclonal antibodies of the present disclosure include "humanized" forms of the non-human (i.e., mouse) antibodies. Humanized or CDR-grafted mAbs are particularly useful as therapeutic agents for humans because they are not cleared from the circulation as rapidly as mouse antibodies and do not typically provoke an adverse immune reaction.

Generally, a humanized antibody has one or more amino acid residues introduced into it from a non-human source. These non-human amino acid residues are often referred to as “import” residues, which are typically taken from an “import” variable domain. Methods of preparing humanized antibodies are generally well known in the art. For example, humanization can be essentially performed following the method of Winter and co-workers (Jones et al., *Nature* 321: 522-525 (1986); Reichmann et al., *Nature*, 332:323-327 (1988); Verheggen et al., *Science*, 239: 1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Also see Staelens et al. 2006 *Mol Immunol* 43: 1243-1257. In particular embodiments, humanized forms of non-human (e.g., mouse) antibodies are human antibodies (recipient antibody) in which hypervariable (CDR) region residues of the recipient antibody are replaced by hypervariable region residues from a non-human species (donor antibody) such as a mouse, rat, rabbit, or non-human primate having the desired specificity, affinity, and binding capacity. In some instances, framework region residues of the human immunoglobulin are also replaced by corresponding non-human residues (so called “back mutations”). In addition, phage display libraries can be used to vary amino acids at chosen positions within the antibody sequence. The properties of a humanized antibody are also affected by the choice of the human framework. Furthermore, humanized and chimerized antibodies can be modified to comprise residues that are not found in the recipient antibody or in the donor antibody in order to further improve antibody properties, such as, for example, affinity or effector function.

[0088] Fully human antibodies are also provided in the disclosure. The term “human antibody” includes antibodies having variable and constant regions (if present) derived from human germline immunoglobulin sequences. Human antibodies can include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo). However, the term “human antibody” does not include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences (i.e., humanized antibodies). Fully human or human antibodies may be derived from transgenic mice carrying human antibody genes (carrying the variable (V), diversity (D), joining (J), and constant (C) exons) or from human cells. For example, it is now possible to produce transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production (see, e.g., Jakobovits et al., *PNAS*; 90:2551 (1993); Jakobovits et al., *Nature*, 362:255-258 (1993); Brugemann et al., *Year in Immuno.*, 7:33 (1993); and Duchosal et al. *Nature* 355:258 (1992). Transgenic mice strain can be engineered to contain gene sequences from unrearranged human immunoglobulin genes. The human sequences may code for both the heavy and light chains of human antibodies and would function correctly in the mice, undergoing rearrangement to provide a wide antibody repertoire similar to that in humans. The transgenic mice can be immunized with the target protein (e.g., CD200, fragments thereof, or cells expressing CD200) to create a diverse array of specific antibodies and their encoding RNA. Nucleic acids encoding the antibody chain components of such antibodies may then be cloned from the animal

into a display vector. Typically, separate populations of nucleic acids encoding heavy and light chain sequences are cloned, and the separate populations then recombined on insertion into the vector, such that any given copy of the vector receives a random combination of a heavy and a light chain. The vector is designed to express antibody chains so that they can be assembled and displayed on the outer surface of a display package containing the vector. For example, antibody chains can be expressed as fusion proteins with a phage coat protein from the outer surface of the phage. Thereafter, display packages can be screened for display of antibodies binding to a target.

[0089] In addition, human antibodies can be derived from phage-display libraries (Hoogenboom et al., *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581-597 (1991); Vaughan et al. *Nature Biotech* 14:309 (1996)). Synthetic phage libraries can be created which use randomized combinations of synthetic human antibody V-regions. By selection on antigen fully human antibodies can be made in which the V-regions are very human-like in nature. See U.S. Pat. Nos. 6,794,132, 6,680,209, 4,634,666, and Ostberg et al. (1983), *Hybridoma* 2:361-367, the contents of which are incorporated by reference.

[0090] For the generation of human antibodies, also see Mendez et al. *Nature Genetics* 15:146-156 (1997), Green and Jakobovits *J. Exp. Med.* 188:483-495 (1998), the disclosures of which are hereby incorporated by reference. Human antibodies are further discussed and delineated in U.S. Pat. Nos. 5,939,598 and 6,673,986. Also see U.S. Pat. Nos. 6,114,598, 6,075,181, and 6,162,963, all filed Jun. 5, 1995. Also see U.S. Pat. No. 6,150,584, filed Oct. 2, 1996 and U.S. Pat. Nos. 6,713,610 and 6,657,103 as well as U.S. patent application Ser. Nos. 10/421,011 (US 2003-0229905 A1), 10/455,013 (US 2004-0010810 A1), 10/627,250 (US 2004-0093622 A1), 10/656,623 (US 2006-0040363 A1), 10/658,521 (US 2005-0054055 A1), 10/917,703 (US 2005-0076395 A1) and 10/978,297 (US 2005-0287630 A1). See also PCT/US93/06926 filed on Jul. 23, 1993, European Patent No., EP 0 463 151 B1, grant published Jun. 12, 1996, International Patent Application No., WO 94/02602, published Feb. 3, 1994, International Patent Application No., WO 96/34096, published Oct. 31, 1996, and WO 98/24893, published Jun. 11, 1998. The disclosures of each of the above-cited patents, applications, and references are hereby incorporated by reference in their entirety.

[0091] In an alternative approach, others, including GenPharm International, Inc., have utilized a “minilocus” approach. In the minilocus approach, an exogenous Ig locus is mimicked through the inclusion of pieces (individual genes) from the Ig locus. Thus, one or more V_H genes, one or more D_H genes, one or more J_H genes, a mu constant region, and a second constant region (preferably a gamma constant region) are formed into a construct for insertion into an animal. This approach is described in U.S. Pat. No. 5,545,807 to Surani et al. and U.S. Pat. Nos. 5,545,806, 5,625,825, 5,625,126, 5,633,425, 5,661,016, 5,770,429, 5,789,650, and 5,814,318 each to Lonberg and Kay, U.S. Pat. No. 5,591,669 to Krimpenfort and Berns, U.S. Pat. Nos. 5,612,205, 5,721,367, 5,789,215 to Berns et al., and U.S. Pat. No. 5,643,763 to Choi and Dunn, and GenPharm International. Also see U.S. Pat. Nos. 5,569,825, 5,877,397, 6,300,129, 5,874,299, 6,255,458, and 7,041,871, the disclosures of which are hereby incorporated by reference. See also European Patent No. 0 546 073 B1, International Patent Application Nos. WO 92/03918, WO

92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852, and WO 98/24884, the disclosures of which are hereby incorporated by reference in their entirety. See further Taylor et al. (1992 Nuc. Acids. Res., 20: 6287), Chen et al. (1993 Int. Immunol. 5: 647), Tuailon et al. (1993 PNAS USA. 90: 3720-4), Choi et al., (1993 Nature Genetics 4: 117), Lonberg et al. (1994 Nature 368: 856-859), Taylor et al. (1994 International Immunology 6: 579-591), and Tuailon et al. (1995 J. Immunol. 154: 6453-65), Fishwild et al. (1996 Nature Biotechnology 14: 845), and Tuailon et al. (2000 Eur J. Immunol. 10: 2998-3005), the disclosures of which are hereby incorporated by reference in their entirety.

[0092] In certain embodiments, de-immunized anti-CD200 antibodies or antigen-binding fragments thereof are provided. De-immunized antibodies or antigen-binding fragments thereof may be modified so as to render the antibody or antigen-binding fragment thereof non-immunogenic, or less immunogenic, to a given species. De-immunization can be achieved by modifying the antibody or antigen-binding fragment thereof utilizing any of a variety of techniques known to those skilled in the art (see e.g., PCT Publication Nos. WO 04/108158 and WO 00/34317). For example, an antibody or antigen-binding fragment thereof may be de-immunized by identifying potential T cell epitopes and/or B cell epitopes within the amino acid sequence of the antibody or antigen-binding fragment thereof and removing one or more the potential T cell epitopes and/or B cell epitopes from the antibody or antigen-binding fragment thereof, for example, using recombinant techniques. The modified antibody or antigen-binding fragment thereof may then optionally be produced and tested to identify antibodies or antigen-binding fragments thereof that have retained one or more desired biological activities, such as, for example, binding affinity, but have reduced immunogenicity. Methods for identifying potential T cell epitopes and/or B cell epitopes may be carried out using techniques known in the art, such as, for example, computational methods (see e.g., PCT Publication No. WO 02/069232), in vitro or in silico techniques, and biological assays or physical methods (such as, for example, determination of the binding of peptides to MHC molecules, determination of the binding of peptide:MHC complexes to the T cell receptors from the species to receive the antibody or antigen-binding fragment thereof, testing of the protein or peptide parts thereof using transgenic animals with the MHC molecules of the species to receive the antibody or antigen-binding fragment thereof, or testing with transgenic animals reconstituted with immune system cells from the species to receive the antibody or antigen-binding fragment thereof, etc.). In various embodiments, the de-immunized anti-CD200 antibodies described herein include de-immunized antigen-binding fragments, Fab, Fv scFv, Fab' and F(ab')₂, monoclonal antibodies, murine antibodies, engineered antibodies (such as, for example, chimeric, single chain, CDR-grafted, humanized, fully human antibodies, and artificially selected antibodies), synthetic antibodies and semi-synthetic antibodies.

[0093] In a further embodiment, recombinant DNA comprising an insert coding for a heavy chain variable domain and/or for a light chain variable domain of antibodies directed to CD200 or a CD200-positive cell line are produced. The term DNA includes coding single stranded DNAs, double stranded DNAs consisting of said coding DNAs and of

complementary DNAs thereto, or these complementary (single stranded) DNAs themselves.

[0094] Furthermore, DNA encoding a heavy chain variable domain and/or a light chain variable domain of antibodies directed to CD200 or the CD200-positive cell line can be enzymatically or chemically synthesized DNA having the authentic DNA sequence coding for a heavy chain variable domain and/or for the light chain variable domain, or a mutant thereof. A mutant of the authentic DNA is a DNA encoding a heavy chain variable domain and/or a light chain variable domain of the above-mentioned antibodies in which one or more amino acids are deleted, inserted, or exchanged with one or more other amino acids. Preferably said modification(s) are outside the CDRs of the heavy chain variable domain and/or of the light chain variable domain of the antibody in humanization and expression optimization applications. The term mutant DNA also embraces silent mutants wherein one or more nucleotides are replaced by other nucleotides with the new codons coding for the same amino acid(s). The term mutant sequence also includes a degenerate sequence. Degenerate sequences are degenerate within the meaning of the genetic code in that an unlimited number of nucleotides are replaced by other nucleotides without resulting in a change of the amino acid sequence originally encoded. Such degenerate sequences may be useful due to their different restriction sites and/or frequency of particular codons which are preferred by the specific host, particularly *E. coli*, to obtain an optimal expression of the heavy chain murine variable domain and/or a light chain murine variable domain.

[0095] The term mutant is intended to include a DNA mutant obtained by in vitro mutagenesis of the authentic DNA according to methods known in the art.

[0096] For the assembly of complete tetrameric immunoglobulin molecules and the expression of chimeric antibodies, the recombinant DNA inserts coding for heavy and light chain variable domains are fused with the corresponding DNAs coding for heavy and light chain constant domains, then transferred into appropriate host cells, for example after incorporation into hybrid vectors.

[0097] Recombinant DNAs including an insert coding for a heavy chain murine variable domain of an antibody directed to CD200 or a CD200-positive cell line fused to a human constant domain IgG, for example $\gamma 1$, $\gamma 2$, $\gamma 3$ or $\gamma 4$; in particular embodiments $\gamma 1$ or $\gamma 4$ may be used. Recombinant DNAs including an insert coding for a light chain murine variable domain of an antibody directed to the cell line disclosed herein fused to a human constant domain κ or λ , preferably κ are also provided.

[0098] Another embodiment pertains to recombinant DNAs coding for a recombinant polypeptide wherein the heavy chain variable domain and the light chain variable domain are linked by way of a spacer group, optionally comprising a signal sequence facilitating the processing of the antibody in the host cell and/or a DNA sequence encoding a peptide facilitating the purification of the antibody and/or a cleavage site and/or a peptide spacer and/or an agent. The DNA coding for an agent is intended to be a DNA coding for the agent useful in diagnostic or therapeutic applications. Thus, agent molecules which are toxins or enzymes, especially enzymes capable of catalyzing the activation of pro-drugs, are particularly indicated. The DNA encoding such an agent has the sequence of a naturally occurring enzyme or toxin encoding DNA, or a mutant thereof, and can be prepared by methods well known in the art.

[0099] Accordingly, the monoclonal antibodies or antigen-binding fragments of the disclosure can be naked antibodies or antigen-binding fragments that are not conjugated to other agents, for example, a therapeutic agent or detectable label. Alternatively, the monoclonal antibody or antigen-binding fragment can be conjugated to an agent such as, for example, a cytotoxic agent, a small molecule, a hormone, an enzyme, a growth factor, a cytokine, a ribozyme, a peptidomimetic, a chemical, a prodrug, a nucleic acid molecule including coding sequences (such as antisense, RNAi, gene-targeting constructs, etc.), or a detectable label (e.g., an NMR or X-ray contrasting agent, fluorescent molecule, etc.). In certain embodiments, an anti-CD200 polypeptide or antigen-binding fragment (e.g., Fab, Fv, single-chain scFv, Fab' and F(ab')₂) is linked to a molecule that increases the half-life of the said polypeptide or antigen-binding fragment. Molecules that may be linked to said anti-CD200 polypeptide or antigen-binding fragment include but are not limited to serum proteins including albumin, polypeptides, other proteins or protein domains, and PEG.

[0100] Several possible vector systems are available for the expression of cloned heavy chain and light chain genes in mammalian cells. One class of vectors relies upon the integration of the desired gene sequences into the host cell genome. Cells which have stably integrated DNA can be selected by simultaneously introducing drug resistance genes such as *E. coli* gpt (Mulligan, R. C. and Berg, P., Proc. Natl. Acad. Sci., USA, 78: 2072 (1981)) or Tn5 neo (Southern, P. J. and Berg, P., J. Mol. Appl. Genet., 1: 327 (1982)). The selectable marker gene can be either linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection (Wigler, M. et al., Cell, 16: 77 (1979)). A second class of vectors utilizes DNA elements which confer autonomously replicating capabilities to an extrachromosomal plasmid. These vectors can be derived from animal viruses, such as bovine papillomavirus (Sarver, N. et al., Proc. Natl. Acad. Sci., USA, 79: 7147 (1982)), polyoma virus (Deans, R. J. et al., Proc. Natl. Acad. Sci., USA, 81: 1292 (1984)), or SV40 virus (Lusky, M. and Botchan, M., Nature, 293: 79 (1981)).

[0101] Since an immunoglobulin cDNA is comprised only of sequences representing the mature mRNA encoding an antibody protein, additional gene expression elements regulating transcription of the gene and processing of the RNA are required for the synthesis of immunoglobulin mRNA. These elements may include splice signals, transcription promoters, including inducible promoters enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama, H. and Berg, P., Mol. Cell. Biol., 3: 280 (1983); Cepko, C. L. et al., Cell, 37: 1053 (1984); and Kaufman, R. J., Proc. Natl. Acad. Sci., USA, 82: 689 (1985).

[0102] In certain embodiments, an anti-CD200 antibody may be a blocking or non-blocking antibody. As used herein, a blocking antibody is one that blocks the interaction between CD200 and CD200R. A non-blocking antibody binds and/or interacts with CD200 but does not block its interaction with CD200R. Thus in certain embodiments, an anti-CD200 antibody is either a blocking or non-blocking murine, chimeric, humanized human or de-immunized antibody.

II. CD200 Antagonists with Altered Effector Functions

[0103] CD200 antagonists may be altered to elicit increased or decreased effects relative to the original or parent

antagonist. For example, an antagonist that binds CD200 may elicit secondary functions following binding to CD200 and, in some instances, inhibiting the CD200:CD200R interaction. For example, an antagonist may contain additional binding sites for other ligands, including receptors or extracellular proteins. Binding to these other ligands may trigger other events, such as the attraction or recruitment of other cells and the activation of various events including cell death. Thus in certain aspects, the present disclosure relates to CD200 antagonists that elicit altered secondary functions (or effector functions as referred to below). In certain embodiments, the CD200 antagonist with altered secondary or effector function(s) exhibits increased, decreased, or no secondary or effector function(s), and further may or may not block the CD200:CD200R interaction. In particular embodiments, the CD200 antagonist with altered secondary or effector function(s) is an anti-CD200 antibody.

[0104] A) Effector Functions

[0105] The interaction of antibodies and antibody-antigen complexes with cells of the immune system affects a variety of responses, referred to herein as effector functions. Exemplary effector functions include Fc receptor binding, phagocytosis, down-regulation of cell surface receptors (e.g. B cell receptor; BCR), etc. Other effector functions include ADCC, whereby antibodies bind Fc receptors on natural killer (NK) cells or macrophages leading to cell death, and CDC, which is cell death induced via activation of the complement cascade (reviewed in Daeron, Annu. Rev. Immunol. 15:203-234 (1997); Ward and Ghiette, Therapeutic Immunol. 2:77-94 (1995); and Ravetch and Kinet, Annu. Rev. Immunol. 9:457-492 (1991)). Such effector functions generally require the Fc region to be combined with a binding domain (e.g. an antibody variable domain) and can be assessed using various assays as herein disclosed, for example.

[0106] Several antibody effector functions, including ADCC, are mediated by Fc receptors (FcRs), which bind the Fc region of an antibody. In ADCC, NK cells or macrophages bind to the Fc region of the antibody complex and promote lysis of the target cell. The cross-linking of FcRs on NK cells triggers perforin/granzyme-mediated cytotoxicity, whereas in macrophages this cross-linking promotes the release of mediators such as nitric oxide (NO), TNF- α , and reactive oxygen species. For CD200-positive target cells, an anti-CD200 antibody binds to the target cell and the Fc region directs effector function to the target cell. The affinity of an antibody for a particular FcR, and hence the effector activity mediated by the antibody, may be modulated by altering the amino acid sequence and/or post-translational modifications of the Fc and/or constant region of the antibody.

[0107] FcRs are defined by their specificity for immunoglobulin isotypes; Fc receptors for IgG antibodies are referred to as Fc γ R, for IgE as Fc ϵ R, for IgA as Fc α R and so on. Three subclasses of Fc γ R have been identified: Fc γ RI (CD64), Fc γ RII (CD32) and Fc γ RIII (CD16). Because each Fc γ R subclass is encoded by two or three genes, and alternative RNA splicing leads to multiple transcripts, a broad diversity in Fc γ R isoforms exists. The three genes encoding the Fc γ RI subclass (Fc γ RIA, Fc γ RB and Fc γ RC) are clustered in region 1821.1 of the long arm of chromosome 1; the genes encoding Fc γ RII isoforms (Fc γ RIIA, Fc γ RIIB and Fc γ RIIC) and the two genes encoding Fc γ RIII (Fc γ RIIA and Fc γ RIIB) are all clustered in region 1q22. These different FcR subtypes are expressed on different cell types (reviewed in Ravetch and Kinet, Arum. Rev. Immunol. 9:457-492

(1991)). For example, in humans, Fc γ RIIIB is found only on neutrophils, whereas Fc γ RIIIA is found on macrophages, monocytes, natural killer (NK) cells, and a subpopulation of T-cells. Notably, Fc γ RIIIA is the only FcR present on NK cells, one of the cell types implicated in ADCC.

[0108] Fc γ RI, Fc γ RII and Fc γ RIII are immunoglobulin superfamily (IgSF) receptors; Fc γ RI has three IgSF domains in its extracellular domain, while Fc γ RII and Fc γ RIII have only two IgSF domains in their extracellular domains. Another type of Fc receptor is the neonatal Fc receptor (FcRn). FcRn is structurally similar to major histocompatibility complex (MHC) and consists of an α -chain noncovalently bound to β 2-microglobulin.

[0109] The binding site on human and murine antibodies for Fc γ R have been previously mapped to the so-called "lower hinge region" consisting of residues 233-239 (EU index numbering as in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)). Woof et al. Molec. Immunol. 23:319-330 (1986); Duncan et al. Nature 332:563 (1988); Canfield and Morrison, J. Exp. Med. 173:1483-1491 (1991); Chappel et al., Proc. Natl. Acad. Sci. USA 88:9036-9040 (1991). Of residues 233-239, P238 and S239 have been cited as possibly being involved in binding.

[0110] Other previously cited areas possibly involved in binding to Fc γ R are: G316-K338 (human IgG) for human Fc γ RI (by sequence comparison only; no substitution mutants were evaluated) (Woof et al. Molec. Immunol. 23:319-330 (1986)); K274-R301 (human IgG1) for human Fc γ RIII (based on peptides) (Sarmay et al. Molec. Immunol. 21:43-51 (1984)); Y407-R416 (human IgG) for human Fc γ RIII (based on peptides) (Gergely et al. Biochem. Soc. Trans. 12:739-743 (1984)); as well as N297 and E318 (murine IgG2b) for murine Fc γ RII (Lund et al., Molec. Immunol., 29:53-59 (1992)).

[0111] Human effector cells are leukocytes which express one or more FcRs and perform effector functions. In certain embodiments, the cells express at least Fc γ RIII and perform ADCC effector function. Examples of human leukocytes which mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils. Effector cells may be isolated from a native source thereof, e.g. from blood or PBMCs.

[0112] In CDC, the antibody-antigen complex binds complement, resulting in the activation of the complement cascade and generation of the membrane attack complex. Activation of the classical complement pathway is initiated by the binding of the first component of the complement system (C1q) to antibodies (of the appropriate subclass) which are bound to their cognate antigen; thus the activation of the complement cascade is regulated in part by the binding affinity of the immunoglobulin to C1q protein. C1q and two serine proteases, C1r and C1s, form the complex C1, the first component of the CDC pathway. C1q is a hexavalent molecule with a molecular weight of approximately 460,000 and a structure in which six collagenous "stalks" are connected to six globular head regions. Burton and Woof, Advances in Immunol. 51:1-84 (1992). To activate the complement cascade, it is necessary for C1q to bind to at least two molecules of IgG1, IgG2, or IgG3, but only one molecule of IgM, attached to the antigenic target (Ward and Ghetie, Therapeutic Immunology 2:77-94 (1995) p. 80). To assess complement

activation, a CDC assay, e.g. as described in Gazzano-Santoro et al., J. Immunol. Methods 202:163 (1996), may be performed.

[0113] It has been proposed that various residues of the IgG molecule are involved in binding to C1q including the G1u318, Lys320 and Lys322 residues on the CH2 domain, amino acid residue 331 located on a turn in close proximity to the same beta strand, the Lys235 and Gly237 residues located in the lower hinge region, and residues 231 to 238 located in the N-terminal region of the CH2 domain (see e.g., Xu et al., J. Immunol. 150:152 A (Abstract) (1993) WO94/29351; Tao et al., J. Exp. Med., 178:661-667 (1993); Brekke et al., Eur. J. Immunol. 24:2542-47 (1994); Burton et al.; Nature, 288:338-344 (1980); Duncan and Winter, Nature 332:738-40 (1988); U.S. Pat. No. 5,648,260, and U.S. Pat. No. 5,624,821). It has further been proposed that the ability of IgG to bind C1q and activate the complement cascade also depends on the presence, absence or modification of the carbohydrate moiety positioned between the two CH2 domains (which is normally anchored at Asn297) (Ward and Ghetie, Therapeutic Immunology 2:77-94 (1995)). In certain embodiments, one or more of these residues may be modified, substituted, or removed or one or more amino acid residues may be inserted so as to enhance or decrease CDC activity of the anti-CD200 antibodies provided herein.

[0114] B) Anti-CD200 Antibodies with Modulated Effector Function(s)

[0115] Effector functions involving the constant region of the target-specific antibody may be modulated by altering properties of the constant or Fc region. Altered effector functions include, for example, a modulation in one or more of the following activities: ADCC, CDC, apoptosis, binding to one or more Fc-receptors, and pro-inflammatory responses. Modulation refers to an increase, decrease, or elimination of an activity compared to the activity of a second antibody. In certain embodiments, the second antibody is an antibody with effector function. The second antibody may be an engineered antibody or a naturally occurring antibody and may be referred to as a non-variant, native, or parent antibody. In particular embodiments, modulation includes situations in which an activity is abolished or completely absent. Further, in some instances, a non-variant antibody may exhibit effector function activity similar or equivalent to the activity of the chC2aB7-hG1 or the hB7V3V2-hG1 antibodies disclosed herein. Likewise, a functional or non-variant constant or Fc region may possess an effector function of a native constant or Fc domain; in some instances, the constant or Fc region of chC2aB7-hG1 or hB7V3V2-hG1 may represent the non-variant domains. For present purposes, chC2aB7-hG1 and hB7V3V2-hG1 are the standards against which the activities of other antibodies are compared, with hB7V3V2-hG1 being the preferred standard.

[0116] A polypeptide variant with altered FcR binding affinity and/or ADCC activity and/or altered CDC activity is a polypeptide which has either enhanced or diminished FcR binding activity and/or ADCC activity and/or CDC activity compared to the native or parent polypeptide or to a polypeptide comprising a native sequence Fc or constant region. A polypeptide variant which displays increased binding to an FcR binds at least one FcR with greater affinity than the parent polypeptide. A polypeptide variant which displays decreased binding to an FcR binds at least one FcR with lower affinity than a parent polypeptide. Such variants which display decreased binding to an FcR may possess little or no appre-

ciable binding to an FcR, e.g., 0-20% binding to the FcR compared to the level of binding of a native sequence immunoglobulin constant or Fc region to the FcR. Similarly a polypeptide variant which displays altered ADCC and/or CDC activity may exhibit either increased or reduced ADCC and/or CDC activity compared to the native or parent polypeptide. A polypeptide variant which displays reduced ADCC and/or CDC may exhibit reduced or no ADCC and/or CDC activity as shown herein by example. In certain embodiments, the parent or native polypeptide and its variant are antibodies or antigen-binding fragments. In particular embodiments, the said antibody or antigen-binding fragment binds CD200 and may or may not block the CD200:CD200R interaction.

[0117] A native sequence Fc or constant region comprises an amino acid sequence identical to the amino acid sequence of a Fc or constant chain region found in nature. A variant or altered Fc or constant region comprises an amino acid sequence which differs from that of a native sequence heavy chain region by virtue of at least one amino acid modification, insertion, or deletion, for example. In certain embodiments, the variant or altered constant region has at least one amino acid substitution, insertion, and/or deletion, compared to a native sequence constant region or to the constant region of a parent polypeptide, e.g. from about one to about one hundred amino acid substitutions, insertions, and/or deletions in a native sequence constant region or in the constant region of the parent polypeptide. In some embodiments, the variant or altered constant region herein will possess at least about 70% homology (similarity) or identity with a native sequence constant region and/or with a constant region of a parent polypeptide, and in some instances at least about 75% and in other instances at least about 80% homology or identity therewith, and in other embodiments at least about 85%, 90% or 95% homology or identity therewith. The variant or altered constant region may also contain one or more amino acid deletions or insertions. Additionally, the variant constant region may contain one or more amino acid substitutions, deletions, or insertions that results in altered post-translational modifications, including, for example, an altered glycosylation pattern.

[0118] Variant anti-CD200 antibodies as presently disclosed may be encoded by a nucleic acid sequence that encodes a polypeptide with one or more amino acid insertions, deletions, or substitutions relative to the native or parent polypeptide sequence. Furthermore, variant antibodies may be encoded by nucleic acid sequences that hybridize under stringent conditions to a nucleic acid sequence encoding a variant anti-CD200 antibody. A variety of conditions may be used to detect hybridization, and the stringency is determined primarily by the wash stage of the hybridization assay. Generally high temperatures and low salt concentrations give high stringency, while low temperatures and high salt concentrations give low stringency. Low stringency hybridization is achieved by washing in, for example, about 2.0×SSC at 50° C., and high stringency is achieved with about 0.2×SSC at 50° C.

[0119] Antibodies or antigen-binding fragments thereof with altered or no effector functions may be generated by engineering or producing antibodies with variant constant, Fc, or heavy chain regions; recombinant DNA technology and/or cell culture and expression conditions may be used to produce antibodies with altered function and/or activity. For example, recombinant DNA technology may be used to engi-

neer one or more amino acid substitutions, deletions, or insertions in regions (such as, for example, Fc or constant regions) that affect antibody function including effector functions. Alternatively, changes in post-translational modifications, such as, e.g. glycosylation patterns, may be achieved by manipulating the cell culture and expression conditions by which the antibody is produced.

[0120] Accordingly, certain aspects and methods of the present disclosure relate to anti-CD200 antibodies with altered effector functions that comprise one or more amino acid substitutions, insertions, and/or deletions. In certain embodiments, such a variant anti-CD200 antibody exhibits reduced or no effector function. In particular embodiments, a variant antibody comprises a G2/G4 construct in place of the G1 domain (see FIGS. 10, 11, 12, 13, and 15, for example).

[0121] In addition to swapping the G1 domain with a G2/G4 construct as presented herein, anti-CD200 antibodies with reduced effector function may be produced by introducing other types of changes in the amino acid sequence of certain regions of the antibody. Such amino acid sequence changes include but are not limited to the Ala-Ala mutation described by Bluestone et al. (see WO 94/28027 and WO 98/47531; also see Xu et al. 2000 Cell Immunol 200; 16-26). Thus in certain embodiments, anti-CD200 antibodies with mutations within the constant region including the Ala-Ala mutation may be used to reduce or abolish effector function. According to these embodiments, the constant region of an anti-CD200 antibody comprises a mutation to an alanine at position 234 or a mutation to an alanine at position 235. Additionally, the constant region may contain a double mutation: a mutation to an alanine at position 234 and a second mutation to an alanine at position 235. In one embodiment, the anti-CD200 antibody comprises an IgG4 framework, wherein the Ala-Ala mutation would describe a mutation(s) from phenylalanine to alanine at position 234 and/or a mutation from leucine to alanine at position 235. In another embodiment, the anti-CD200 antibody comprises an IgG1 framework, wherein the Ala-Ala mutation would describe a mutation(s) from leucine to alanine at position 234 and/or a mutation from leucine to alanine at position 235. An anti-CD200 antibody may alternatively or additionally carry other mutations, including the point mutation K322A in the CH2 domain (Hezareh et al. 2001 J. Virol. 75: 12161-8). An antibody with said mutation(s) in the constant region may furthermore be a blocking or non-blocking antibody.

[0122] Changes within the hinge region also affect effector functions. For example, deletion of the hinge region may reduce affinity for Fc receptors and may reduce complement activation (Klein et al. 1981 PNAS USA 78: 524-528). The present disclosure therefore also relates to antibodies with alterations in the hinge region.

[0123] In particular embodiments, anti-CD200 antibodies may be modified to either enhance or inhibit complement dependent cytotoxicity (CDC). Modulated CDC activity may be achieved by introducing one or more amino acid substitutions, insertions, or deletions in an Fc region of the antibody (see, e.g., U.S. Pat. No. 6,194,551). Alternatively or additionally, cysteine residue(s) may be introduced in the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved or reduced internalization capability and/or increased or decreased complement-mediated cell killing. See Caron et al., J. Exp Med. 176:1191-1195 (1992) and Shope, B. J. Immunol. 148:2918-2922 (1992), WO99/

51642, Duncan & Winter Nature 322: 738-40 (1988); U.S. Pat. No. 5,648,260; U.S. Pat. No. 5,624,821; and WO94/29351. Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research 53:2560-2565 (1993). Alternatively, an antibody can be engineered which has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al. Anti-Cancer Drug Design 3:219-230 (1989).

[0124] Another potential means of modulating effector function of antibodies includes changes in glycosylation. This topic has been recently reviewed by Raju who summarized the proposed importance of the oligosaccharides found on human IgGs with their degree of effector function (Raju, T S. BioProcess International April 2003. 44-53). According to Wright and Morrison, the microheterogeneity of human IgG oligosaccharides can affect biological functions such as CDC and ADCC, binding to various Fc receptors, and binding to C1q protein (Wright A. & Morrison SL. TIBTECH 1997, 15 26-32). It is well documented that glycosylation patterns of antibodies can differ depending on the producing cell and the cell culture conditions (Raju, T S. BioProcess International April 2003. 44-53). Such differences can lead to changes in both effector function and pharmacokinetics (Israel et al. Immunology. 1996; 89(4):573-578; Newkirk et al. P. Clin. Exp. 1996; 106(2):259-64). Differences in effector function may be related to the IgGs ability to bind to the Fc γ receptors (Fc γ Rs) on the effector cells. Shields, et al., have shown that IgG, with variants in amino acid sequence that have improved binding to Fc γ R, can exhibit up to 100% enhanced ADCC using human effector cells (Shields et al. J Biol. Chem. 2001 276(9):6591-604). While these variants include changes in amino acids not found at the binding interface, both the nature of the sugar component as well as its structural pattern may also contribute to the differences observed. In addition, the presence or absence of fucose in the oligosaccharide component of an IgG can improve binding and ADCC (Shields et al. J Biol. Chem. 2002; 277(30):26733-40). An IgG that lacked a fucosylated carbohydrate linked to Asn²⁹⁷ exhibited normal receptor binding to the Fc γ receptor. In contrast, binding to the Fc γ RIIA receptor was improved 50% and accompanied by enhanced ADCC, especially at lower antibody concentrations.

[0125] Work by Shinkawa, et al., demonstrated that an antibody to the human IL-5 receptor produced in a rat hybridoma showed more than 50% higher ADCC when compared to the antibody produced in Chinese hamster ovary cells (CHO) (Shinkawa et al. J Biol. Chem. 2003 278(5):3466-73). Monosaccharide composition and oligosaccharide profiling showed that the rat hybridoma-produced IgG had a lower content of fucose than the CHO-produced protein. The authors concluded that the lack of fucosylation of an IgG 1 has a critical role in enhancement of ADCC activity.

[0126] A different approach was taken by Umana, et al., who changed the glycosylation pattern of chCE7, a chimeric IgG1 anti-neuroblastoma antibody (Umana et al. Nat. Biotechnol. 1999 February; 17(2): 176-80). Using tetracycline, they regulated the activity of a glycosyltransferase enzyme (GnnU) which bisects oligosaccharides that have been implicated in ADCC activity. The ADCC activity of the parent antibody was barely above background level. Measurement of ADCC activity of the chCE7 produced at different tetracycline levels showed an optimal range of GnTIH expression for maximal chCE7 in vitro ADCC activity. This activity

correlated with the level of constant region-associated, bisected complex oligosaccharide. Newly optimized variants exhibited substantial ADCC activity. Similarly, Wright and Morrison produced antibodies in a CHO cell line deficient in glycosylation (1994 J Exp Med 180: 1087-1096) and showed that antibodies produced in this cell line were incapable of complement-mediated cytotoxicity. Thus as known alterations that affect effector function include modifications in the glycosylation pattern or a change in the number of glycosylated residues, the present disclosure relates to a CD200 antibody wherein glycosylation is altered to either enhance or decrease effector function(s) including ADCC and CDC. Altered glycosylation includes a decrease or increase in the number of glycosylated residues as well as a change in the pattern or location of glycosylated residues.

[0127] Still other approaches exist for the altering effector function of antibodies. For example, antibody-producing cells can be hypermutagenic, thereby generating antibodies with randomly altered nucleotide and polypeptide residues throughout an entire antibody molecule (see WO 2005/011735). Hyperrmutagenic host cells include cells deficient in DNA mismatch repair. Antibodies produced in this manner may be less antigenic and/or have beneficial pharmacokinetic properties. Additionally, such antibodies may be selected for properties such as enhanced or decreased effector function(s).

[0128] It is further understood that effector function may vary according to the binding affinity of the antibody. For example, antibodies with high affinity may be more efficient in activating the complement system compared to antibodies with relatively lower affinity (Marzocchi-Machado et al. 1999 Immunol Invest 28: 89-101). Accordingly, an antibody may be altered such that the binding affinity for its antigen is reduced (e.g., by changing the variable regions of the antibody by methods such as substitution, addition, or deletion of one or more amino acid residues). An anti-CD200 antibody with reduced binding affinity may exhibit reduced effector functions, including, for example, reduced ADCC and/or CDC.

III. Methods of Depleting or Eliminating Cells Overexpressing CD200

[0129] In accordance with the present disclosure, methods are provided for depleting cells that express CD200 in a subject by administering to the subject a therapy comprising a CD200 antagonist. As mentioned above, CD200 is expressed on certain immune cells; and as demonstrated in the present disclosure, CD200 is also expressed on certain malignant cells. The disparate expression of CD200 provides an avenue by which to target cancer cells (i.e., CD200-positive cells) for therapy. Likewise, CD200-positive immune cells may be targeted for depletion in methods of treating autoimmune disorders.

[0130] CD200, through its interaction with CD200R on myeloid cells, modulates immunosuppression by delivering an inhibitory signal for myeloid activity and/or migration. CD200-knockout mice, for example, demonstrate a more active immune response following immunogenic stimuli (Hoek et al. Science 2000), and CD200-expressing cells elicit immunosuppression by inducing a shift in the cytokine profile of stimulated immune cells (see data shown herein). Specifically, CD200-positive cells are capable of inducing a shift from Th1 to Th2 cytokine production in mixed cell population assays. While CD200-positive cells are capable of suppressing the immune response, CD200-positive cancer cells,

accordingly, may be capable of escaping immune cell attack. However expression of CD200 on the membrane of cancer cells as well as immune cells can be exploited to target these cells in therapy. For example, an anti-CD200 antagonist can specifically target CD200-positive cells and disrupt the CD200:CD200R interaction, thereby inhibiting immune suppression, as well as target CD200-positive cells to immune effector cells. The embodiments of this disclosure, therefore, relate to methods of targeting CD200-positive cells for depletion comprising an antagonist that binds to CD200 and, in some instances, disrupts the CD200:CD200R interaction.

[0131] In certain embodiments, the present disclosure relates to methods of enhancing the immune response. Such methods include administering a therapy comprising a CD200 antagonist, and in particular embodiments the antagonist is an anti-CD200 antibody or antigen-binding fragment as set forth herein. While not wishing to be bound by any particular mechanism(s), a blocking anti-CD200 antibody, antigen-binding fragment, polypeptide, or other antagonist may eliminate CD200-positive cells by blocking immune suppression, thereby allowing immune cells to attack and eliminate CD200-positive cells. Alternatively or in combination with the aforementioned mechanism, an anti-CD200 antibody (either blocking or non-blocking) or other antagonist may recruit effector cells or other ligands (e.g., complement component) to the CD200-positive cell to which the antibody or antagonist is bound and target the CD200-positive cell for effector-mediated cell death.

[0132] In one aspect, the present disclosure relates to methods of modulating ADCC and/or CDC of CD200-positive target cells by administering a murine, chimeric, humanized, or human anti-CD200 antibody to a subject in need thereof. The disclosure relates to variant anti-CD200 antibodies that elicit increased ADCC and/or CDC and to variant anti-CD200 antibodies that exhibit reduced or no ADCC and/or CDC activity.

[0133] In one embodiment, the variant anti-CD200 antibody comprises a variant or altered Fc or constant region, wherein the variant Fc or constant region exhibits increased effector function. Such said variant region may contain one or more amino acid substitutions, insertions, or deletions. Alternatively or additionally, the variant or altered Fc or constant region may comprise altered post-translational modifications, including, for example, an altered glycosylation pattern. An altered glycosylation pattern includes an increase or decrease in the number of glycosydic bonds and/or a modification in the location (i.e., amino acid residue number) of one or more glycosydic bonds.

[0134] In another embodiment, the disclosure relates to methods of depleting or eliminating CD200-positive cells comprising variant anti-CD200 antibodies that exhibit reduced or no ADCC and/or CDC activity. In one embodiment, the variant anti-CD200 antibody comprises a variant or altered Fc or constant region, wherein the variant Fc or constant region exhibits decreased or no effector function. Such said variant or altered Fc or constant region may contain one or more amino acid substitutions, insertions, or deletions. Alternatively or additionally, the variant Fc or constant region may comprise altered post-translational Modifications, including but not limited to an altered glycosylation pattern. Examples of altered glycosylation patterns are described above.

[0135] In a further embodiment, a murine, chimeric, humanized, human or de-immunized anti-CD200 antibody

administered to a patient is a non-blocking antibody. The non-blocking anti-CD200 antibody may be a variant antibody as described above and may consequently exhibit modulated effector function(s). For example, a variant anti-CD200 antibody may not block the CD200:CD200R interaction and may also comprise a variant constant region that elicits increased effector function, such as, e.g., increased ADCC.

[0136] A) Methods of Treating Patients with Autoimmune Disorders

[0137] In certain aspects, the disclosure relates to treating patients with autoimmune disorders with a therapy comprising a CD200 antagonist. In certain embodiments, the antagonist is an anti-CD200 antibody or antigen-binding fragment thereof. In other embodiments, the anti-CD200 antibody or fragment thereof is a variant anti-CD200 antibody that exhibits modulated effector activity. For example, the variant antibody may comprise a variant or altered constant region capable of eliciting increased or enhanced effector function, such as, for example, ADCC. Additionally, the said antibody may be a non-blocking antibody and may be a murine, chimeric, humanized, human or de-immunized anti-CD200 antibody. Thus, methods of treating patients with autoimmune disorders may comprise any of the CD200 antagonists and antibodies as set forth in the present disclosure.

[0138] In certain embodiments, anti-CD200 antibodies or CD200 antagonists may be used for depleting any type of cell that expresses CD200 on its surface, including for example, immune cells such as T-cells, B-cells, and dendritic cells. In one embodiment, anti-CD200 antibodies may be useful for targeted destruction of immune cells involved in an unwanted immune response, such as, for example, immune responses associated with an autoimmune disorder, transplants, allergies, or inflammatory disorders. Exemplary autoimmune diseases and disorders that may be treated with the anti-CD200 antibodies provided herein include, for example, inflammatory responses such as inflammatory skin diseases including psoriasis and dermatitis (e.g. atopic dermatitis); dermatomyositis; systemic scleroderma and sclerosis; responses associated with inflammatory bowel disease (such as Crohn's disease and ulcerative colitis); respiratory distress syndrome (including adult respiratory distress syndrome; ARDS); dermatitis; meningitis; encephalitis; uveitis; colitis; glomerulonephritis; allergic conditions such as eczema and asthma and other conditions involving infiltration of T cells and chronic inflammatory responses; atherosclerosis; leukocyte adhesion deficiency; rheumatoid arthritis; systemic lupus erythematosus (SLE); diabetes mellitus (e.g. Type I diabetes mellitus or insulin dependent diabetes mellitus); multiple sclerosis; Reynaud's syndrome; autoimmune thyroiditis; allergic encephalomyelitis; Sjogren's syndrome; juvenile onset diabetes; and immune responses associated with acute and delayed hypersensitivity mediated by cytokines and T-lymphocytes typically found in tuberculosis, sarcoidosis, polymyositis, granulomatosis and vasculitis; pernicious anemia (Addison's disease); diseases involving leukocyte diapedesis; central nervous system (CNS) inflammatory disorder; multiple organ injury syndrome; hemolytic anemia (including, but not limited to cryoglobulinemia or Coombs positive anemia); myasthenia gravis; antigen-antibody complex mediated diseases; anti-glomerular basement membrane disease; antiphospholipid syndrome; allergic neuritis; Graves' disease; Lambert-Eaton myasthenic syndrome; pemphigoid bullous; pemphigus; autoimmune polyendocrinopathies; Reiter's disease; stiff-man syndrome; Bechet disease; giant cell arteritis;

immune complex nephritis; IgA nephropathy; IgM polyneuropathies; immune thrombocytopenic purpura (ITP) or autoimmune thrombocytopenia and autoimmune hemolytic diseases, Hashimoto's thyroiditis, etc.

[0139] In accordance with the methods and compositions described herein, the disclosure also relates to methods of treating a transplant or allograft patient. An anti-CD200 antibody or other CD200 antagonist of the present disclosure may be administered to a patient prior to a transplant or allograft procedure or after the procedure in order to decrease or eliminate CD200-positive immune cells that could reduce the patient's acceptance of the transplanted organ or tissue. In a particular embodiment, an anti-CD200 antibody with increased effector function is given to a transplant patient. In addition, an anti-CD200 antibody is a non-blocking antibody.

[0140] Therapies comprising CD200 antagonists or antibodies may be administered to patients in combination therapies. Accordingly, targeted killing of certain populations of immune cells for treating or preventing autoimmune disorders, enhancing or extending transplant survival, treating or preventing allergies, or treating or preventing inflammatory disorders, may be administered as part of a combination therapy. For example, a patient receiving a first therapy comprising a CD200 antagonist (e.g., an anti-CD200 antibody described herein) may also be given a second therapy. The CD200 antagonist may be given simultaneously with the second therapy. Alternatively, the CD200 antagonist may be given prior to or following the second therapy. Second therapies include but are not limited to anti-inflammatory agents, immunosuppressive agents, and/or anti-infective agents.

[0141] Combination therapies of the present disclosure include, for example, a CD200 antagonist as described herein administered concurrently or sequentially in series with steroids, anti-malarials, aspirin, non-steroidal anti-inflammatory drugs, immunosuppressants, or cytotoxic drugs. Included are corticosteroids (e.g. prednisone, dexamethasone, and prednisolone), methotrexate, methylprednisolone, macrolide immunosuppressants (e.g. sirolimus and tacrolimus), mitotic inhibitors (e.g. azathioprine, cyclophosphamide, and methotrexate), fungal metabolites that inhibit the activity of T lymphocytes (e.g. cyclosporine), mycophenolate mofetil, glatiramer acetate, and cytotoxic and DNA-damaging agents (e.g. chlorambucil). For autoimmune disorders and allograft or transplant patients, anti-CD200 therapy may be combined with antibody treatments including daclizumab, a genetically engineered human IgG1 monoclonal antibody that binds specifically to the α -chain of the interleukin-2 receptor, as well as various other antibodies targeting immune cells or other cells. Such combination therapies may be useful in the treatment of type 1 diabetes, rheumatoid arthritis, lupus, and idiopathic thrombocytopenic purpura, and other autoimmune indications. The disclosure also relates to therapies for autoimmune disorders and for transplant patients comprising a CD200 antagonist (such as, for example, the antibodies and variants thereof described in the present disclosure) conjugated to one or more agent.

[0142] B) Methods of Treating Patients with Cancer

[0143] In one aspect, the disclosure provides a method of treating cancer in which an agent that disrupts or inhibits the interaction of CD200 with its receptor is administered to a subject. Disruption of the CD200:CD200R interaction subsequently reverses or inhibits immune suppression, thus enhancing the immune response. Possible agents for the disruption of the CD200:CD200R interaction include, for

example, small molecules, chemicals, polypeptides, inorganic molecules, and organometallic compounds. The CD200:CD200R interaction may also be inhibited by reducing the expression of either the membrane protein or its receptor via antisense, RNAi, or gene therapy. Additionally, a polypeptide specific for CD200 or CD200R, such as an anti-CD200- or anti-CD200R-specific antibody or fragments thereof, may inhibit the immunosuppressive effects of the CD200:CD200R interaction.

[0144] Cancer cells that may be treated by a CD200 antagonist include any cancer cells that exhibit CD200 expression or CD200 up-regulation. Cancers for which anti-CD200 therapy may be used include, for example, ovarian, melanoma, myeloma, neuroblastoma, renal, breast, prostate, hematological malignancies (e.g., lymphomas and leukemias), and plasma cell cancer. Also included are any cancer cells derived from neural crest cells. In some embodiments, the CD200 antagonist is an anti-CD200 antibody. Such antibodies used as anti-cancer therapeutics are capable of interfering with the interaction of CD200 and its receptors. This interference can block the immune-suppressing effect of CD200. By improving the immune response in this manner, such antibodies can promote the eradication of cancer cells. Anti-CD200 antibodies may also target cancer cells for effector-mediated cell death.

[0145] In one embodiment, a variant anti-CD200 antibody that exhibits modulated ADCC and/or CDC activity may be administered to a subject with CD200-positive cancer cells. For example, a variant anti-CD200 antibody used in cancer therapy may exhibit enhanced effector activity compared to the parent or native antibody. In another embodiment, the variant anti-CD200 antibody exhibits reduced effector function, including reduced ADCC, relative to the native antibody. The said antibody may be a murine, chimeric, humanized, human or de-immunized antibody. Cancers for which the variant anti-CD200 antibody may be used in treatment include but are not limited to neural crest cell cancers. Also included are plasma cell cancer, ovarian cancer, skin cancer, lung cancer, renal cancer, breast cancer, prostate cancer, neuroblastoma, lymphoma, myeloma, and leukemia.

[0146] The present antibodies can be administered as a therapeutic to cancer patients, especially, but not limited to, patients with CLL, plasma cell cancer, ovarian cancer, skin cancer, lung cancer, renal cancer, breast cancer, prostate cancer, neuroblastoma, lymphoma, myeloma, leukemia, and any cancer derived from neural crest cells. In a particularly useful embodiment, a cancer therapy in accordance with this disclosure comprises (1) administering an anti-CD200 antibody or antagonist that interferes with the interaction between CD200 and its receptor to block immune suppression, thereby promoting eradication of the cancer cells; and/or (2) administering a fusion molecule that includes a CD200 targeting portion to directly kill cancer cells. Alternatively, the antibody directly kills the cancer cells through complement-mediated or antibody-dependent cellular cytotoxicity. Since CD200 is also expressed on normal cells such as endothelial cells, albeit at lower levels than on cancer cells, it could also be advantageous to administer an anti-CD200 antibody with a constant region modified to reduce or eliminate ADCC or CDC to limit damage to normal cells. For example, if CD200 expression is upregulated on some activated normal cells (e.g., activated T cells), rendering such cells vulnerable to killing by an anti-CD200 antibody with effector function, it may therefore also

be advantageous to use an anti-CD200 antibody lacking effector function to avoid depletion of these cells which aid in destroying cancer cells.

[0147] In a particular embodiment, effector function of anti-CD200 antibodies is eliminated by swapping the IgG1 constant domain for an IgG2/4 fusion domain. Other ways of eliminating effector function can be envisioned such as, e.g., mutation of the sites known to interact with FcR or insertion of a peptide in the hinge region, thereby eliminating critical sites required for FcR interaction. Variant anti-CD200 antibodies with reduced or no effector function also include variants as described previously herein.

[0148] The aforementioned agents for the inhibition or prevention of the CD200:CD200R interaction may be used in combination with other therapies or with other agents. Other agents include but are not limited to polypeptides, small molecules, chemicals, metals, organometallic compounds, inorganic compounds, nucleic acid molecules, oligonucleotides, aptamers, spiegelmers, antisense nucleic acids, locked nucleic acid (LNA) inhibitors, peptide nucleic acid (PNA) inhibitors, immunomodulatory agents, antigen-binding fragments, prodrugs, and peptidomimetic compounds.

[0149] In certain aspects, the present disclosure relates to combination treatments comprising a CD200 antagonist including the antibodies described herein and immunomodulatory compounds, vaccines or chemotherapy. Illustrative examples of suitable immunomodulatory agents that may be used in such combination therapies include agents that block negative regulation of T cells or antigen presenting cells (e.g., anti-CTLA4 antibodies, anti-PD-L1 antibodies, anti-PDL-2 antibodies, anti-PD-1 antibodies and the like) or agents that enhance positive co-stimulation of T cells (e.g., anti-CD40 antibodies or anti 4-1BB antibodies) or agents that increase NK cell number or T-cell activity (e.g., anti-CD200 antibodies alone or in combination with inhibitors such as IMiDs, thalidomide, or thalidomide analogs). Furthermore, immunomodulatory therapy could include cancer vaccines such as dendritic cells loaded with tumor cells, proteins, peptides, RNA, or DNA derived from such cells, patient derived heat-shocked proteins (hsp's) or general adjuvants stimulating the immune system at various levels such as CpG, Luivac, Biostim, Ribominyl, Imudon, Bronchovaxom or any other compound or other adjuvant activating receptors of the innate immune system (e.g., toll like receptor agonist, anti-CTLA-4 antibodies, etc.). Also, immunomodulatory therapy could include treatment with cytokines such as IL-2, GM-CSF and IFN-gamma.

[0150] In additional embodiments, elimination of existing regulatory T cells with reagents such as anti-CD25, fludarabine, or cyclophosphamide is achieved before starting anti-CD200 treatment. Also, therapeutic efficacy of myeloablative therapies followed by bone marrow transplantation or adoptive transfer of T cells reactive with CLL cells is enhanced by anti-CD200 therapy. In yet other embodiments, efficacy of anti-CD200 treatment is improved by blocking immunosuppressive mechanisms with agents such as anti-PDL1 and/or 2 antibodies, anti-IL-10 antibodies, anti-IL-6 antibodies, and the like. Furthermore, it could be advantageous to eliminate plasmacytoid dendritic cells, shown to be immunosuppressive in the cancer environment. In these embodiments in which delivery of an anti-CD200 antibody is intended to augment an immune response by blocking immune suppression, for example, a variant anti-CD200 antibody lacking effector function may also be used.

[0151] In particularly useful embodiments, the therapy that enhances immune response is the administration of a polypeptide that binds to CD200, alone or in combination with one of the previously mentioned immunomodulatory therapies. Accordingly, a CD200 antagonist (including an anti-CD200 antibody as described herein) may be used in combination with a monoclonal antibody (e.g., rituximab, trastuzumab, alemtuzumab, cetuximab, or bevacizumab), including a conjugated monoclonal antibody (e.g., gemtuzumab ozogamicin, ibritumomab tiuxetan, or tositumomab).

[0152] Furthermore, combination of anti-CD200 therapy with chemotherapeutics could be particularly useful to reduce overall tumor burden, to limit angiogenesis, to enhance tumor accessibility, to enhance susceptibility to ADCC, to result in increased immune function by providing more tumor antigen, or to increase the expression of the T cell attractant LIGHT. When anti-CD200 therapy is administered to a subject in combination with another conventional anti-neoplastic agent, either concomitantly or sequentially, anti-CD200 therapy may be shown to enhance the therapeutic effect of either agent alone. Pharmaceutical compounds that may be used for combinatory anti-tumor therapy include, merely to illustrate: amnoglutethimide, amsacrine, anastrozole, asparaginase, bcg, bicalutamide, bleomycin, buserelin, busulfan, camptothecin, capecitabine, carboplatin, carbustine, chlorambucil, cisplatin, cladribine, clodronate, colchicine, cyclophosphamide, cyproterone, cytarabine, dacarbazine, dactinomycin, daunorubicin, dienestrol, diethylstilbestrol, docetaxel, doxorubicin, epirubicin, estradiol, estramustine, etoposide, exemestane, filgrastim, fludarabine, fludrocortisone, fluorouracil, fluoxymesterone, flutamide, gemcitabine, genistein, goserelin, hydroxyurea, idarubicin, ifosfamide, imatinib, interferon, irinotecan, letrozole, leucovorin, leuprolide, levamisole, lomustine, mechlorethamine, medroxyprogesterone, megestrol, melphalan, mercaptopurine, mesna, methotrexate, mitomycin, mitotane, mitoxantrone, nilutamide, nocodazole, octreotide, oxaliplatin, paclitaxel, pamidronate, pentostatin, plicamycin, porfimer, procarbazine, raltitrexed, rituximab, streptozocin, suramin, tamoxifen, temozolomide, teniposide, testosterone, thioguanine, thiotepa, titanocene dichloride, topotecan, trastuzumab, tretinoin, vinblastine, vincristine, vindesine, and vinorelbine.

[0153] These chemotherapeutic anti-tumor compounds may be categorized by their mechanism of action into groups, including, for example, the following classes of agents: anti-metabolites/anti-cancer agents, such as pyrimidine analogs (5-fluorouracil, floxuridine, capecitabine, gemcitabine and cytarabine) and purine analogs, folate antagonists and related inhibitors (mercaptopurine, thioguanine, pentostatin and 2-chlorodeoxyadenosine (cladribine)); antiproliferative/anticancer agents including natural products such as vinca alkaloids (vinblastine, vincristine, and vinorelbine), microtubule disruptors such as taxane (paclitaxel, docetaxel), vincristine, vinblastine, nocodazole, epithilones and navelbine, epipodophyllotoxins (etoposide, teniposide), DNA damaging agents (actinomycin, amsacrine, anthracyclines, bleomycin, busulfan, camptothecin, carboplatin, chlorambucil, cisplatin, cyclophosphamide, cytoxin, dactinomycin, daunorubicin, doxorubicin, epirubicin, hexamethylmelamineoxaliplatin, iphosphamide, melphalan, mechlorethamine, mitomycin, mitoxantrone, nitrosourea, plicamycin, procarbazine, taxol, taxotere, teniposide, triethylenethiophosphoramide and etoposide (VP16)); antibiotics such as dactinomycin (actinomycin D), daunorubicin, doxorubicin (adriamycin), idarubicin,

anthracyclines, mitoxantrone, bleomycins, plicamycin (mithramycin) and mitomycin; enzymes (L-asparaginase which systemically metabolizes L-asparagine and deprives cells which do not have the capacity to synthesize their own asparagine); antiplatelet agents; antiproliferative/antimitotic alkylating agents such as nitrogen mustards (mechlorethamine, cyclophosphamide and analogs, melphalan, chlorambucil), ethylenimines and methylmelamines (hexamethylmelamine and thiotepa), alkyl sulfonates-busulfan, nitrosoureas (carmustine (BCNU) and analogs, streptozocin), trazenes-dacarbazine (DTIC); antiproliferative/antimitotic antimetabolites such as folic acid analogs (methotrexate); platinum coordination complexes (cisplatin, carboplatin), procarbazine, hydroxyurea, mitotane, aminoglutethimide; hormones, hormone analogs (estrogen, tamoxifen, goserelin, bicalutamide, nilutamide) and aromatase inhibitors (letrozole, anastrozole); anticoagulants (heparin, synthetic heparin salts and other inhibitors of thrombin); fibrinolytic agents (such as tissue plasminogen activator, streptokinase and urokinase), aspirin, dipyridamole, ticlopidine, clopidogrel, abciximab; antimigratory agents; antisecretory agents (breveldin); immunosuppressives (cyclosporine, tacrolimus (FK-506), sirolimus (rapamycin), azathioprine, mycophenolate mofetil); immunomodulatory agents (thalidomide and analogs thereof such as lenalidomide (Revlimid, CC-5013) and CC-4047 (Actimid)), cyclophosphamide; anti-angiogenic compounds (TNP-470, genistein) and growth factor inhibitors (vascular endothelial growth factor (VEGF) inhibitors, fibroblast growth factor (FGF) inhibitors); angiotensin receptor blocker; nitric oxide donors; anti-sense oligonucleotides; antibodies (trastuzumab); cell cycle inhibitors and differentiation inducers (tretinoin); mTOR inhibitors, topoisomerase inhibitors (doxorubicin (adriamycin), amsacrine, camptothecin, daunorubicin, dactinomycin, eniposide, epirubicin, etoposide, idarubicin and mitoxantrone, topotecan, irinotecan), corticosteroids (cortisone, dexamethasone, hydrocortisone, methylprednisolone, prednisone, and prenisolone); growth factor signal transduction kinase inhibitors; mitochondrial dysfunction inducers and caspase activators; and chromatin disruptors.

[0154] In certain embodiments, pharmaceutical compounds that may be used for combinatory anti-angiogenesis therapy include: (1) inhibitors of release of "angiogenic molecules," such as bFGF (basic fibroblast growth factor); (2) neutralizers of angiogenic molecules, such as anti- β bFGF antibodies; and (3) inhibitors of endothelial cell response to angiogenic stimuli, including collagenase inhibitor, basement membrane turnover inhibitors, angiostatic steroids, fungal-derived angiogenesis inhibitors, platelet factor 4, thrombospondin, arthritis drugs such as D-penicillamine and gold thiomolate, vitamin D₃ analogs, alpha-interferon, and the like. For additional proposed inhibitors of angiogenesis, see Blood et al., *Biochim. Biophys. Acta*, 1032:89-118 (1990), Moses et al., *Science*, 248:1408-1410 (1990), Ingber et al., *Lab. Invest.*, 59:44-51 (1988), and U.S. Pat. Nos. 5,092,885, 5,112,946, 5,192,744, 5,202,352, and 6,573,256. In addition, there are a wide variety of compounds that can be used to inhibit angiogenesis, for example, peptides or agents that block the VEGF-mediated angiogenesis pathway, endostatin protein or derivatives, lysine binding fragments of angiostatin, melanin or melanin-promoting compounds, plasminogen fragments (e.g., Kringles 1-3 of plasminogen), troponin subunits, antagonists of vitronectin $\alpha_v\beta_3$, peptides derived from Saposin B, antibiotics or analogs (e.g., tetracycline, or neo-

mycin), dienogest-containing compositions, compounds comprising a MetAP-2 inhibitory core coupled to a peptide, the compound EM-138, chalcone and its analogs, and naaladase inhibitors. See, for example, U.S. Pat. Nos. 6,395,718, 6,462,075, 6,465,431, 6,475,784, 6,482,802, 6,482,810, 6,500,431, 6,500,924, 6,518,298, 6,521,439, 6,525,019, 6,538,103, 6,544,758, 6,544,947, 6,548,477, 6,559,126, and 6,569,845.

[0155] Depending on the nature of the combinatory therapy, administration of the anti-CD200 antibody may be continued while the other therapy is being administered and/or thereafter. Administration of the antibody may be made in a single dose, or in multiple doses. In some instances, administration of the anti-CD200 antibody is commenced at least several days prior to the conventional therapy, while in other instances, administration is begun either immediately before or at the time of the administration of the conventional therapy. In some cases, the anti-CD200 antibody will be administered after other therapies, or it could be administered alternating with other therapies.

[0156] The present antibodies can be utilized to directly kill or ablate cancerous cells *in vivo*. Direct killing involves administering the antibodies (which are optionally fused to a cytotoxic drug) to a subject requiring such treatment. Since the antibodies recognize CD200 on cancer cells, any such cells to which the antibodies bind are destroyed. Where the antibodies are used alone to kill or ablate cancer cells, such killing or ablation can be effected by initiating endogenous host immune functions, such as CDC and/or ADCC. Assays for determining whether an antibody kills cells in this manner are within the purview of those skilled in the art.

[0157] Accordingly in one embodiment, the antibodies of the present disclosure may be used to deliver a variety of cytotoxic compounds. Any cytotoxic compound can be fused to the present antibodies. The fusion can be achieved chemically or genetically (e.g., via expression as a single, fused molecule). The cytotoxic compound can be a biological, such as a polypeptide, or a small molecule. As those skilled in the art will appreciate, for small molecules, chemical fusion is used, while for biological compounds, either chemical or genetic fusion can be employed.

[0158] Non-limiting examples of cytotoxic compounds include therapeutic drugs, a compound emitting radiation, molecules of plants, fungal, or bacterial origin, biological proteins, and mixtures thereof. The cytotoxic drugs can be intracellularly acting cytotoxic drugs, such as short-range radiation emitters, including, for example, short-range, high-energy α -emitters. Enzymatically active toxins and fragments thereof are exemplified by diphtheria toxin A fragment, nonbinding active fragments of diphtheria toxin, exotoxin A (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sacrin, certain Aleurites fordii proteins, certain Dianthin proteins, *Phytolacca americana* proteins (PAP, PAPII and PAP-S), *Morodica charantia* inhibitor, curcin, crotin, *Saponaria officinalis* inhibitor, gelonin, mitogillin, restrictocin, phenomycin, and enomycin, for example. Procedures for preparing enzymatically active polypeptides of the immunotoxins are described in WO84/03508 and WO85/03508, which are hereby incorporated by reference. Certain cytotoxic moieties are derived from adriamycin, chlorambucil, daunomycin, methotrexate, neocarzinostatin, and platinum, for example.

[0159] Procedures for conjugating the antibodies with the cytotoxic agents have been previously described and are within the purview of one skilled in the art.

[0160] Alternatively, the antibody can be coupled to high energy radiation emitters, for example, a radioisotope, such as ^{131}I , a γ -emitter, which, when localized at the tumor site, results in a killing of several cell diameters. See, e.g., S. E. Order, "Analysis, Results, and Future Prospective of the Therapeutic Use of Radiolabeled Antibody in Cancer Therapy", Monoclonal Antibodies for Cancer Detection and Therapy, R. W. Baldwin et al. (eds.), pp 303-316 (Academic Press 1985), which is hereby incorporated by reference. Other suitable radioisotopes include α -emitters, such as ^{212}Bi , ^{213}Bi , and ^{211}At , and β -emitters, such as ^{186}Re and ^{90}Y .

[0161] In some embodiments, present CD200 binding antibodies provide the benefit of blocking immune suppression in CLL by targeting the leukemic cells directly through CD200. Specifically, stimulating the immune system can allow the eradication of CLL cells from the spleen and lymph nodes. Applicants are unaware of any successful eradication of CLL cells from these microenvironments having been achieved with agents that simply target B cells (such as alemtuzumab). In contrast, CLL reactive T cells can have better access to these organs than antibodies. In other embodiments, direct cell killing is achieved by tagging the CLL cells with anti-CD200 Abs.

[0162] According to the compositions and methods of the present disclosure, in particularly useful embodiments, the combination of direct cell killing and driving the immune response towards a Th1 profile provides a particularly powerful approach to cancer treatment. Thus, in one embodiment, a cancer treatment is provided wherein an antibody or antibody fragment, which binds to CD200 and both a) blocks the interaction between CD200 and its receptor and b) directly kills the cancer cells expressing CD200, is administered to a cancer patient. The mechanism by which the cancer cells are killed can include, but are not limited to ADCC and/or CDC; fusion with a toxin; fusion with a radiolabel; fusion with a biological agent involved in cell killing, such as granzyme B or perforin; fusion with a cytotoxic virus; fusion with a cytokine such as TNF- α or IFN- α . In an alternative embodiment, a cancer treatment involves administering an antibody that both a) blocks the interaction between CD200 and its receptor and b) enhances cytotoxic T cell or NK cell activity against the tumor. Such enhancement of the cytotoxic T cell or NK cell activity may, for example, be combined by fusing the antibody with cytokines such as e.g. IL-2, IL-12, IL-18, IL-13, and IL-5. In addition, such enhancement may be achieved by administration of an anti-CD200 antibody in combination with inhibitors such as IMIDs, thalidomide, or thalidomide analogs.

[0163] In yet another embodiment, the cancer treatment involves administering an antibody that both (1) blocks the interaction between CD200 and its receptor and (2) attracts T cells to the tumor cells. T cell attraction can be achieved by fusing the Ab with chemokines such as MIG, IP-10, I-TAC, CCL21, CCL5 or LIGHT. Also, treatment with therapeutics can result in the desired upregulation of LIGHT. The combined action of blocking immune suppression and killing directly through antibody targeting of the tumor cells is a unique approach that provides increased efficacy.

[0164] Anti-CD200 antibodies in accordance with the present disclosure can also be used as a diagnostic tool. Biopsies or cancer cell tissue samples may be tested for CD200

expression prior to treatment in order to predict the efficacy of anti-CD200 therapy, alone or in combination with other agents or methods (such as chemotherapeutic agents, radiation therapy, immunomodulatory therapy, etc.). For example, using blood obtained from patients with hematopoietic cancers, expression of CD200 can be evaluated on cancer cells by FACS analysis using anti-CD200 antibodies in combination with the appropriate cancer cell markers such as, e.g., CD38 and CD19 on CLL cells. Patients with CD200 levels at least 1.4-fold above the levels found on normal B cells can be selected for treatment with anti-CD200 antibodies. As another example, tissue samples from a patient may be stained with anti-CD200 antibody to determine the expression of CD200 in the patient's malignant and normal cells.

[0165] In another example of using the present anti-CD200 antibodies as a diagnostic or prognostic tool, biopsies from patients with malignancies are obtained and expression of CD200 is determined by FACS analysis using anti-CD200 antibodies or by immunohistochemistry using anti-CD200. If tumor cells express CD200 at levels that are at least 1.4-fold higher compared to corresponding normal tissue, cancer patients are selected for immunomodulatory therapy (including but not limited to a therapy comprising anti-CD200 therapy). For cancer derived from cells that normally do not express CD200, any detectable CD200 on cancer biopsies indicates potential usefulness of anti-CD200 therapy. Immunomodulatory therapy can be anti-CD200 therapy, but can also be any other therapy affecting the patient's immune system. Examples of suitable immunomodulatory therapies include the administration of agents that block negative regulation of T cells or antigen presenting cells (e.g., anti-CTLA4, anti-PD-L1, anti-PDL-2, anti-PD-1) or the administration of agents that enhance positive co-stimulation of T cells (e.g., anti-CD40 or anti 4-1BB). Furthermore, immunomodulatory therapy could be cancer vaccines such as heteroclitic peptides or tumor cell peptides that generate cytotoxic T cells or dendritic cells loaded with tumor cells, or the administration of agents that increase NK cell number or T-cell activity (e.g., anti-CD200 antibodies alone or in combination with inhibitors such as IMIDs, thalidomide, or thalidomide analogs), or the administration of agents that deplete regulatory T cells (e.g. anti-CD200 antibodies alone or in combination with ONTAK), or plasmacytoid dendritic cells. Combination with agents increasing T cell or dendritic cell migration is also advantageous, such as e.g. any agent blocking SPARC. Furthermore, immunomodulatory therapy could be cancer vaccines such as dendritic cells loaded with tumor cells, patient derived exosomes tumor RNA or tumor DNA, tumor protein or tumor peptides, patient derived heat-shocked proteins (hsp's), hsp's loaded with tumor antigens or general adjuvants stimulating the immune system at various levels such as CpG, Luivac, Biostim, Ribomimyl, Imudon, Bronchovaxom or any other compound activating receptors of the innate immune system (e.g., toll like receptors). Also, therapy could include treatment with cytokines such as IL-2, GM-CSF and IFN-gamma. Combination with agents restoring compromised activity of dendritic cells in the tumor environment such as e.g. MAP kinase inhibitors are also contemplated.

[0166] In one embodiment, the present antibodies also may be utilized to detect cancerous cells in vivo. Detection in vivo is achieved by labeling the antibody, administering the labeled antibody to a subject, and then imaging the subject. Examples of labels useful for diagnostic imaging in accordance with the present disclosure are radiolabels such as ^{131}I ,

^{111}In , ^{123}I , ^{99m}Tc , ^{32}P , ^{125}I , ^3H , ^{14}C , and ^{188}Rh , fluorescent labels such as fluorescein and rhodamine, nuclear magnetic resonance active labels, positron emitting isotopes detectable by a positron emission tomography (“PET”) scanner, chemiluminescers such as luciferin, and enzymatic markers such as peroxidase or phosphatase. Short-range radiation emitters, such as isotopes detectable by short-range detector probes, such as a transrectal probe, can also be employed. The antibody can be labeled with such reagents using techniques known in the art. For example, see Wensel and Meares, Radioimmunoimaging and Radioimmunotherapy, Elsevier, N.Y. (1983), which is hereby incorporated by reference, for techniques relating to the radiolabeling of antibodies. See also, D. Colcher et al., “Use of Monoclonal Antibodies as Radiopharmaceuticals for the Localization of Human Carcinoma Xenografts in Athymic Mice”, Meth. Enzymol. 121: 802-816 (1986), which is hereby incorporated by reference.

[0167] A radiolabeled antibody in accordance with this disclosure can be used for in vitro diagnostic tests. The specific activity of an antibody, binding portion thereof, probe, or ligand, depends upon the half-life, the isotopic purity of the radioactive label, and how the label is incorporated into the biological agent. In immunoassay tests, the higher the specific activity, in general, the better the sensitivity. Procedures for labeling antibodies with the radioactive isotopes are generally known in the art.

[0168] The radiolabeled antibody can be administered to a patient where it is localized to cancer cells bearing the antigen with which the antibody reacts, and is detected or “imaged” in vivo using known techniques such as radionuclear scanning using e.g., a gamma camera or emission tomography. See e.g., A. R. Bradwell et al., “Developments in Antibody Imaging”, Monoclonal Antibodies for Cancer Detection and Therapy, R. W. Baldwin et al., (eds.), pp. 65-85 (Academic Press 1985), which is hereby incorporated by reference. Alternatively, a positron emission transaxial tomography scanner, such as designated Pet VI located at Brookhaven National Laboratory, can be used where the radiolabel emits positrons (e.g., ^{11}C , ^{18}F , ^{15}O , and ^{13}N).

[0169] Fluorophore and chromophore labeled biological agents can be prepared from standard moieties known in the art. Since antibodies and other proteins absorb light having wavelengths up to about 310 nm, the fluorescent moieties should be selected to have substantial absorption at wavelengths above 310 nm and preferably above 400 nm. A variety of suitable fluorescers and chromophores are described by Shyer, Science, 162:526 (1968) and Brand, L. et al., Annual Review of Biochemistry, 41:843-868 (1972), which are hereby incorporated by reference. The antibodies can be labeled with fluorescent chromophore groups by conventional procedures such as those disclosed in U.S. Pat. Nos. 3,940,475, 4,289,747, and 4,376,110, which are hereby incorporated by reference.

[0170] In another embodiment in accordance with the present disclosure, methods are provided for monitoring the progress and/or effectiveness of a therapeutic treatment. The method involves administering an immunomodulatory therapy and determining CD200 levels in a subject at least twice to determine the effectiveness of the therapy. For example, pre-treatment levels of CD200 can be ascertained

and, after at least one administration of the therapy, levels of CD200 can again be determined. A decrease in CD200 levels is indicative of an effective treatment. Measurement of CD200 levels can be used by the practitioner as a guide for increasing dosage amount or frequency of the therapy. It should of course be understood that CD200 levels can be directly monitored or, alternatively, any marker that correlates with CD200 can be monitored. Other methods to determine the effectiveness of this therapy include but are not limited to detection of cancer cells, total lymphocyte count, lymph node size, number of regulatory T cells, cytokine profiles in the serum or intracellular, or secretion of cytokines by T or B cells as measured by ELISPOT.

[0171] C. Other CD200 Antagonists

[0172] The CD200 antagonists and polypeptides and/or antibodies utilized in the present disclosure are especially indicated for diagnostic and therapeutic applications as described herein. Accordingly CD200 antagonists and anti-CD200 antibodies and variants thereof may be used in therapies, including combination therapies, in the diagnosis and prognosis of disease, as well as in the monitoring of disease progression.

[0173] In the therapeutic embodiments of the present disclosure, bispecific antibodies are contemplated. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the CD200 antigen on a cell (such as, e.g., a cancer cell or immune cell), the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

[0174] Methods for making bispecific antibodies are within the purview of those skilled in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, including at least part of the hinge, CH2, and CH3 regions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of illustrative currently known methods for generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986); WO 96/27011; Brennan et al., Science 229:81 (1985); Shalaby et al., J. Exp. Med. 175:217-225 (1992); Kostelny et al., J. Immunol. 148(5):1547-1553 (1992); Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993); and Gruber et al., J. Immunol. 152:5368 (1994); and Tutt et al., J. Immunol. 147:60 (1991). Bispecific antibodies also include cross-linked or heteroconjugate antibodies. Heteroconjugate antibodies may be made using any convenient cross-linking methods. Suitable cross-linking agents are well known in the art, and are disclosed in U.S. Pat. No. 4,676,980, along with a number of cross-linking techniques.

[0175] Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell cul-

ture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol., 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins may be linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers may be reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (scFv) dimers has also been reported. See Gruber et al., J. Immunol., 152:5368 (1994). Alternatively, the antibodies can be "linear antibodies" as described in Zapata et al. Protein Eng. 8(10):1057-1062 (1995). Briefly, these antibodies comprise a pair of tandem Fd segments (V_H -C_H1-V_H-C_H1) which form a pair of antigen binding regions. Linear antibodies can be bispecific or monospecific.

[0176] D. Modes of Administration and Formulations

[0177] The route of antibody administration of the antibodies of the present disclosure (whether the pure antibody, a labeled antibody, an antibody fused to a toxin, etc.) is in accord with known methods, e.g., injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, subcutaneous, intraocular, intraarterial, intrathecal, inhalation or intralesional routes, or by sustained release systems. The antibody is preferably administered continuously by infusion or by bolus injection. One may administer the antibodies in a local or systemic manner.

[0178] The present antibodies may be prepared in a mixture with a pharmaceutically acceptable carrier. Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, Pa., latest edition. This therapeutic composition can be administered intravenously or through the nose or lung, preferably as a liquid or powder aerosol (lyophilized). The composition may also be administered parenterally or subcutaneously as desired. When administered systemically, the therapeutic composition should be sterile, substantially pyrogen-free and in a parenterally acceptable solution having due regard for pH, isotonicity, and stability. For example, a pharmaceutical preparation is substantially free of pyrogenic materials so as to be suitable for administration as a human therapeutic. These conditions are known to those skilled in the art.

[0179] Pharmaceutical compositions suitable for use include compositions wherein one or more of the present antibodies are contained in an amount effective to achieve their intended purpose. More specifically, a therapeutically effective amount means an amount of antibody effective to prevent, alleviate or ameliorate symptoms of disease or prolong the survival of the subject being treated. Determination of a therapeutically effective amount is well within the capability of those skilled in the art, especially in light of the

detailed disclosure provided herein. Therapeutically effective dosages may be determined by using in vitro and in vivo methods.

[0180] While the above disclosure has been directed to antibodies, in some embodiments polypeptides derived from such antibodies can be utilized in accordance with the present disclosure.

EXEMPLIFICATION

Mouse Model and CD200+ Cell Construction

Raji/PBL Model

[0181] NOD.CB17-Prkdc<scid> mice (Jackson Laboratory) were injected with 200 μ l RPMI containing 4×10^6 Raji cells (ATCC) s.c. along with 0, 1, 5 or 10 million PBLs. Nine or ten mice were included per group. PBLs were isolated from 250 ml whole blood on a histopaque gradient followed by red blood cell lysis using 0.9% ammonium chloride. Tumor growth was monitored three times a week by measuring length and width with a caliper. Tumor volume was calculated based on length \times width \times width/2.

[0182] Differences between the groups that were injected with PBLs compared to the group that received tumor cells only were analyzed by 2-tailed unpaired Student's t-test. Significant differences were observed in the groups that received 5 or 10 million PBLs, but not in the group that received 1 million PBLs from Day 32 on.

Namalwa PBL Model

[0183] NOD.CB17-Prkdc<scid> mice (Jackson Laboratory, Bar Harbor, Me.) were injected with 200 μ l RPMI containing 4×10^6 Namalwa cells (ATCC) s.c. along with 0, 2 or 10 million PBLs. 9-10 mice were included per group. PBLs were isolated from 250 ml whole blood on a histopaque gradient followed by red blood cell lysis using 0.9% ammonium chloride. Tumor growth was monitored three times a week by measuring length and width with a caliper. Tumor volume was calculated based on length \times width \times width/2.

[0184] Creation of Stable CD200-Expressing Cell Lines

[0185] Stable CD200-expressing Raji and Namalwa cell lines were generated using the Virapower Lentiviral Expression System (Invitrogen, Carlsbad, Calif.). A CD200 cDNA was isolated from primary CLL cells by RT-PCR using forward primer 5'-GACAAGCTTGCAAGGATGGAGAG-GCTGGTGA-3' (SEQ ID NO: 34) and reverse primer 5'-GACGGATCCGCCCTTTCTCTGCTTTCTC-3' (SEQ ID NO: 35). The PCR product was cloned into the Gateway entry vector pCR8/GW/TOPO-TA and individual clones were sequenced. Clones with the correct sequence were recombined in both the sense and antisense orientations into the lentiviral vectors pLenti6/V5/DEST and pLenti6/UbC/V5/DEST using Gateway technology (Invitrogen, Carlsbad, Calif.). The primary difference between these two vectors is the promoter used to drive CD200 expression: pLenti6/V5/DEST contains the human CMV immediate early promoter, whereas pLenti6/UbC/V5/DEST contains the human ubiquitin C promoter.

[0186] High-titer, VSV-G pseudotyped lentiviral stocks were produced by transient cotransfection of 293-FT cells as recommended by the manufacturer. Raji or Namalwa cells were transduced by resuspending 10^6 cells in 1 ml of growth medium containing 12 μ g/ml Polybrene and adding 1 ml of lentiviral stock. After incubating the cells overnight at 37° C.,

the medium containing virus was removed and replaced with 4 ml of fresh medium. Two days later, the infected cells were analyzed for CD200 expression by flow cytometry. In all experiments, $\geq 70\%$ of the cells were CD200⁺, whereas CD200 was undetectable in the parental cell lines and in cells transduced with the negative control (antisense CD200) viruses.

[0187] To isolate clonal cell lines that overexpress CD200, the infected cells were selected with blasticidin for 13 days. The concentrations of blasticidin used were 6 $\mu\text{g}/\text{ml}$ for Raji cells or 2 $\mu\text{g}/\text{ml}$ for Namalwa cells. Stable clones were then isolated by limiting dilution of the blasticidin-resistant cells into 96-well plates. Clones were screened in 96-well format by flow cytometry using PE-conjugated Mouse Anti-Human CD200 (clone MRC OX104, Serotec) and a BD FACSCalibur equipped with a High Throughput Sampler. After screening a total of 2000 Raji and 2000 Namalwa clones, those clones with the highest CD200 expression were expanded for further characterization using conventional techniques.

Example 1

Efficacy of Humanized Versions of C2aB7 in the RAJI_CD200/PBL Model

[0188] A) To evaluate whether humanized versions of C2aB7 retain their efficacy in in vivo tumor models, chimeric C2aB7 (see U.S. patent application publication number 2005/0129690) and 3 humanized versions (C2aB7V4V1, C2aB7V3V1 and C2aB7V3V2) as well as the negative control antibody alxn4100 were tested in the RAJI_CD200/PBL model. RAJI cells transduced with CD200 were injected s.c. into NOD.CB17-Prkdc<scid> mice, and the ability of PBLs to reduce tumor growth in the presence or absence of chimeric or humanized C2aB7 antibodies or control antibody alxn4100 (which does not bind tumor cells) was assessed. Antibodies at concentrations indicated below were administered initially with the tumor cells, and then twice/week i.v. The following groups were set up with 10 mice each:

Group 1: 4×10^6 RAJI_CD200 s.c.

Group 2: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL

[0189] Group 3: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+5 mg/kg C2aB7

Group 4: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+20 mg/kg C2aB7V4V1

Group 5: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+5 mg/kg C2aB7V4V1

Group 6: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+20 mg/kg C2aB7V3V1

Group 7: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+5 mg/kg C2aB7V3V1

Group 8: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+5 mg/kg C2aB7V3V2

Group 9: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+20 mg/kg alxn4100

[0190] Tumor length and width were measured 3 times a week, and the tumor volume was calculated by tumor length*width*width/2. FIG. 18 shows that, as expected, CD200 expression on the tumor cells prevented the immune cells from reducing tumor growth. All humanized versions of C2aB7 blocked tumor growth by up to 97% at doses of 20 mg/kg. The control antibody alxn4100 did not affect tumor

growth. These data demonstrate that all the humanized antibodies are highly efficacious in blocking tumor growth.

B) Immune Evasion by CD200

[0191] Although the human immune system is capable of raising an immune response against many cancer types, that response is insufficient to eradicate the cancer in most patients, possibly due to immune evasion through negative regulation of the immune system by the tumor. We identified the immune-suppressive molecule CD200 to be upregulated 1.5-5.4-fold on chronic lymphocytic leukemia (CLL) cells in all patients examined (n=80). Interaction of CD200 with its receptor is known to alter cytokine profiles from Th1 to Th2 in mixed lymphocyte reactions, and to result in the induction of regulatory T cells, which are thought to hamper tumor-specific effector T cell immunity. In the present study we addressed whether CD200 expression on tumor cells plays a role in immune evasion, thereby preventing elimination of tumor cells by the immune system in a xenograft hu/SCID mouse model, and whether treatment with an antagonistic anti-CD200 antibody affects tumor growth in this model.

[0192] The human non-Hodgkin's lymphoma cell lines RAH and Namalwa were transduced with human CD200 and were injected subcutaneously together with human peripheral blood lymphocytes (PBMC) into NOD/SCID mice. Tumor growth in mice that received CD200 expressing tumor cells was compared to tumor growth in mice that received tumor cells not expressing CD200 over time. In subsequent experiments, mice were treated with chimeric, or humanized anti-CD200 antibodies (dose range 1 mg/kg to 20 mg/kg) by intravenous injection. Treatment was either started immediately or 7 days after tumor cell injection.

[0193] PBMCs reduced RAJI or Namalwa tumor growth by up to 75% in the absence of CD200 expression. In contrast, growth of RAH or Namalwa tumors expressing CD200 at levels comparable to CLL was not reduced by PBMCs. Administration of anti-CD200 antibodies at 5 mg/kg resulted in nearly complete tumor growth inhibition ($\frac{1}{10}$ mice developed a small tumor) over the course of the study even when treatment was started 7 days after tumor cell injection.

[0194] The presence of human CD200 on tumor cells inhibits the ability of human lymphocytes to eradicate tumor cells. Treatment of CD200-expressing tumors with antagonistic anti-CD200 antibodies inhibits tumor growth, indicating the potential for anti-CD200 therapy as a promising approach for CLL.

C) Efficacy of C2aB7G1 Versus C2aB7G2/G4 Constructs

[0195] To evaluate whether anti-CD200 antibodies without effector function (G2/G4 fusion constructs of C2aB7 as described below) are equally or more efficacious than the G1 constructs, G1 and G2/G4 versions as well as the humanized version of C2aB7 (alxn5200) were tested in the Raji_CD200/PBL model. RAJI cells transduced with CD200 as described above were injected s.c. into NOD.CB17-Prkdc<scid> mice, and the ability of PBLs to reduce tumor growth in the presence or absence of chimeric anti-CD200 antibodies c2aB7G1 (c2aB7), c2aB7G2/G4 or the humanized versions hC2aB7V3V1G1 (V3V1), or hC2aB7V3V2G1 (V3V2) or control antibody alxn4100 was assessed. Antibodies at concentrations indicated below were administered initially with

the tumor cells and then twice/week i.v. The following groups were set up with 10 mice each:

Group 1: 4×10^6 RAJI_CD200 s.c.

Group 2: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL

[0196] Group 3: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+20 mg/kg hV3V2-G1

Group 4: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+5 mg/kg alxn 5200

Group 5: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+2.5 mg/kg alxn 5200

Group 6: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+1 mg/kg alxn 5200

Group 7: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+20 mg/kg chC2aB7G2/G4

Group 8: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+5 mg/kg chC2aB7G2/G4

Group 9: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+2.5 mg/kg chC2aB7G2/G4

Group 10: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+1 mg/kg chC2aB7G2/G4

Group 11: 4×10^6 RAJI_CD200 s.c.+ 6×10^6 PBL+20 mg/kg alxn4100

[0197] Tumor length and width were measured three times a week, and the tumor volume was calculated by tumor length*width*width/2. FIG. 19 shows that, as expected, CD200 expression on the tumor cells prevented the immune cells from reducing tumor growth. However, addition of anti-CD200 antibodies reduced the tumor volume by up to 100%. While 20 mg/kg C2aB7G1 resulted in growth of small tumors in 6/10 mice, only 1 mouse grew tumors in the group treated with 20 mg/kg C2aB7G2/G4, suggesting that the G2/G4 version might result in better or at least equal efficacy as the G1 version. All anti-CD200 antibodies, including the humanized versions, completely blocked tumor growth at 5 mg/kg. Treatment with the control antibody did not reduce the tumor growth. These data prove that the G2/G4 version of C2aB7 is highly efficacious in blocking tumor growth of CD200 expressing tumors. These data further confirm that the humanized versions of C2aB7 are highly efficacious in blocking tumor growth in this model.

D) Generation of G2/G4 Construct

[0198] Plasmids were altered in two steps, first replacing the IgG1 region from an Age I site in the human CH1 region through the stop codon to a BamH I site located after the SV40 poly A signal. C2aB7-6 and cC7 G2G4 (L-SIGN antibody) were digested with Age I and BamH I, and C2aB7-6 was treated with CIP. A 10,315 bp fragment from C2AB7-6 and a 1752 bp fragment from cC7 G2G4 were purified by electrophoresis and gel extraction. These fragments were ligated, electroporated into XL1 Blue *E. coli*, and plated on LB/carb/gluc plates. Colonies were grown in solution and DNA was isolated using Qiagen miniprep columns. The presence of the IgG2G4 Age I/BamH I fragment, as opposed to the IgG1 fragment, was determined by Pvu II digestion which results in the presence of two bands of 267 and 1152 bp as opposed to one band of 1419 bp. Clone 21 was selected for further use.

[0199] The remainder of the CH1 region from the end of the variable region to the Age I site was generated in an IgG2/G4 format by using overlap PCR. The PCR fragment containing the beginning of the CH1 region through the Age I site had

previously been generated in the production of plasmid cC7 G2G4. Primers C7 mhHF (TCCTCAGCCTCCAC-CAAGGGGCC, SEQ ID NO:1) and Rev Age Pri (GGGCGC-CTGAGTCCACGAC, SEQ ID NO: 2) were used in a PCR reaction with G2G4 63L1D as template to generate a 142 bp fragment. Primers C2aB7 rev (GGCCCTTGGTGGAGGCT-GAGGAAACTGTGAGAGTGGTGC, SEQ ID NO: 3) and lacpri (GCTCCCGGCTCGTATGTTGTGT, SEQ ID NO: 4) were used with Fab C2aB7 as template to generate the murine heavy chain variable region (and upstream material) in a fragment of about 1250 bp. These fragments were purified by electrophoresis and gel extraction and were used in overlap PCR with the primers Rev Age Pri (GGGCGCCTGAGTTC-CACGAC, SEQ ID NO: 2) and LeadVHpAX (ATAT-GAAATATCTGCTGCCGACCG, SEQ ID NO: 5) to generate a 558 bp fragment that was purified on a PCR purification column. This 558 bp fragment and clone 21 were digested with Xho I and Age I to generate a 458 bp fragment that was purified by electrophoresis and gel extraction. Clone 21 was also digested with Xho I and Age I, treated with CIP, and an 11.6 kb fragment was purified by electrophoresis and gel extraction. These fragments were ligated and electroporated into XL1 Blue *E. coli* and plated on LB/carb/gluc plates. Clone C2aB7G2G4.11 was seen to have the expected restriction fragments when digested with Pvu II.

[0200] The final construct C2AB7G2G4.11 was sequenced. It was discovered that the TAA stop codon of the light chain had been mutated to the sequence TCA such that an additional 6 amino acids would be added to the carboxy terminus of the light chain. It was found to have been present in the IgG1 version clone C2AB7-6 that was the parent for C2AB7G2G4.11. Antibodies containing the G2G4 construct are depicted in FIGS. 10, 11, 12, 13, and 15.

Example 2

CD200 Expression on Cancer Cells

A. Determination of CD200 Upregulation in CLL Patients

[0201] Lymphocytes from 15 CLL patients were stained with FITC-conjugated anti-CD5 (e-bioscience), APC-conjugated anti-CD19 (e-bioscience) and PE-conjugated anti-CD200 (Serotec). Lymphocytes from healthy donors were stained accordingly. CD200 expression on CD5+CD19+ cells was determined. As shown in FIG. 20, although the level of CD200 expression varied among CLL patient samples, all CLL samples showed elevated levels (1.6-4-fold range) higher CD200 expression compared to CD200 expression on normal B cells. The CLL patients showing elevated levels of CD200 expression are selected for anti-CD200 treatment in accordance with the methods described herein.

B. FACS Analysis on Cancer Cell Lines

[0202] CD200 expression was evaluated by FACS analysis using a panel of NCI60 cell lines from melanoma cancer patients, prostate cancer patients, glioblastoma patients, astrocytoma patients, neuroblastoma patients, ovarian cancer patients, lung cancer patients and renal cancer patients. C2aB7 was labeled with Zenon-Alexa488 according to the manufacturer's instructions (Invitrogen). One half million to 1 million cells were stained with 1 μ g of the labeled antibody for 20 min, followed by a PBS wash. Cell staining was assessed using a FACSCalibur (Becton Dickinson). Staining of antibody-labeled cells was compared with samples that

remained unlabeled and the ratio of stained/unstained was determined. In FIG. 21, a ratio greater than 1 but smaller than 2 is indicated as +/-, a ratio between 2 and 3 is +, between 3 and 10 is ++, >10 is ++++. None of the cell lines tested for glioblastoma, astrocytoma, prostate or lung cancer expressed CD200, and are not listed below. Four out of 5 tested melanoma cell lines, 2/2 ovarian cancer cell lines, 2/3 renal cell lines, 2/2 neuroblastoma cell lines and 1/3 breast cancer cell lines expressed CD200 at detectable levels on the cell surface, suggesting that solid tumors might use CD200 as an immune escape mechanism as well.

C. RT-QPCR on Patient Samples

[0203] To verify whether CD200 is upregulated not only on cell lines, but also on primary patient samples, RT-QPCR and immunohistochemistry (IHC) were performed on primary patient samples. RNA samples from ovarian and melanoma patients were obtained from Cytomix. cDNA was prepared and samples were diluted 1:100 and 1:1000 in 10 ng/ml yeast RNA. Samples were run for QPCR with CD200 assay Hs00245978_ml as provided by ABI. For 18S normalization, 18S assay (ABI) was run with samples diluted 1:10,000. Each dilution was run in duplicate. Ovarian and melanoma patient samples, along with CLL patient samples were normalized to 18S, then fold expression relative to normal PBL was determined. FIG. 22 shows CD200 expression on ovarian cancer samples. Serous/serous metastatic/papillary serous appeared to have the highest expression of CD200 at approximately 10- to 20-fold higher than normal PBL. CD200 expression was relatively low in endometroid, mucinous, and clear cell samples, all at or below normal ovary expression levels (1-5 fold higher than normal PBL). FIG. 23 shows the CD200 expression levels of several melanoma metastases samples: jejunum, small intestine, lymph node, lung, skin, and brain). Several of these samples are matched normal/tumor, indicated by the number (-1 pair or -2 pair). Other additional samples without matched normals were also run for comparison. Jejunum samples showed significantly higher CD200 expression levels than the normal organ, with the metastatic samples about 4-7-fold higher than normal jejunum.

D. Immunohistochemistry on Primary Patient Samples

[0204] IHC was performed on 2 frozen melanoma patient samples (LifeSpan). D1B5 and C2aB7 Fab fragments were used for staining. An IgG1 antibody was used as isotype control. Binding of the primary antibodies was detected with an anti-mouse secondary antibody and DAB chromagen.

[0205] As shown in FIG. 24, both melanoma samples tested showed strong membrane staining with the anti-CD200 antibodies, but no staining with the isotype control. Normal skin tissue did not show CD200 staining. These data demonstrate that CD200 is not only upregulated on melanoma and ovarian cancer cell lines, but also on primary patient samples.

E. Immune Evasion of Melanoma and Ovarian Tumor Cells Through Upregulation of the Immunosuppressive Molecule CD200

[0206] Immune escape is a critical feature of cancer progression. Tumors can evade the immune system by multiple

mechanisms, each a significant barrier to immunotherapy. Implementing new and more effective forms of immunotherapy will require understanding of these processes as well as their similarities and differences across cancers. We previously identified the immunosuppressive molecule CD200 to be upregulated on chronic lymphocytic leukemia cells. Presence of CD200 downregulates Th1 cytokine production required for an effective cytotoxic T cell response. We demonstrated in animal models that CD200 expression by human tumor cells prevents human lymphocytes from rejecting the tumor, and treatment with an antagonistic anti-CD200 antibody inhibited tumor growth. In this study, we evaluated whether CD200 upregulation is found on other cancers, and whether CD200 expression on these cancer cells affects the immune response.

[0207] Relative CD200 message levels were quantitated by RT-QPCR in ovarian adenocarcinoma (serous/serous metastatic/papillary serous, endometroid, mucinous, clear cell) and malignant melanoma metastatic patient samples.

[0208] Cell surface expression of CD200 was evaluated by IHC in two melanoma and three ovarian carcinoma (serous) patient frozen tissue samples in comparison with normal skin and normal ovaries. CD200 expression on the cell surface of the melanoma cancer cell lines SK-MEL-5, SK-MEL-24 and SK-MEL-28 and the ovarian cancer cell line OV-CAR-3 was assessed by FACS analysis using a PE-labeled anti-CD200 antibody. The effect of the CD200-expressing cancer cell lines on cytokine profile mixed in lymphocyte reactions were assessed by adding the cells to a culture of human monocyte-derived dendritic cells with allogeneic human T cells. Cytokine production (IL-2 and IFN- γ for Th1, IL4 and IL10 for Th2) was detected in the supernatant by ELISA.

[0209] Quantitative PCR showed CD200 expression levels in serous ovarian adenocarcinoma samples at up to 20 fold higher than normal PBL, and equal to or up to 4-fold higher than normal ovary. CD200 expression was at or below normal ovary levels in endometroid, mucinous, and clear cell ovarian adenocarcinoma samples. In malignant melanoma metastases to the jejunum, CD200 expression levels appeared to be significantly higher than normal samples. In malignant melanoma lung metastases, 2/6 showed higher CD200 expression than normal samples.

[0210] IHC showed strong, specific, membrane-associated CD200 staining on malignant cells of both melanoma patients. The normal skin sample showed faint staining of endothelial cells. Among three ovarian cancer patients, one showed strong CD200 staining, one was moderately positive, and one showed subsets of faintly stained tumor cells. In all three cases, the stroma showed strong staining.

[0211] CD200 was highly expressed on the cell surface of the melanoma cancer cell lines SK-MEL-24 and SK-MEL-28 as well as on the ovarian cancer cell line OV-CAR-3, and moderately expressed on the melanoma cell line SK-MEL-5. Addition of any of these cell lines to a mixed lymphocyte reaction downregulated the production of Th1 cytokines, while cell lines not expressing CD200 did not, demonstrating a direct correlation. Inclusion of an antagonistic anti-CD200 antibody during the culture abrogated the effect.

[0212] Melanoma and ovarian tumor cells can upregulate CD200, thereby potentially suppressing an effective immune response. Therapy with an antagonistic anti-CD200 might allow the immune system to mount an effective cytotoxic response against the tumor cells.

F. Effect of CD200-Expressing Cancer Cell Lines on Cytokine Profiles in Mixed Lymphocyte Reactions

[0213] The capability of cells overexpressing CD200 to shift the cytokine response from a TH1 response (IL-2, IFN- γ) to a Th2 response (IL-4, IL-10) was assessed in a mixed lymphocyte reaction. As a source of CD200-expressing cells, either CD200 transfected cells or cells from CD200 positive cancer cell lines were used.

[0214] Mixed lymphocyte reactions were set up in 24 well plates using 250,000 dendritic cells matured from human peripheral monocytes using IL-4, GM-CSF and IFN- γ and 1×10^6 responder cells. Responder cells were T cell enriched lymphocytes purified from peripheral blood using Ficoll. T cells were enriched by incubating the cells for 1 hour in tissue culture flasks and taking the non-adherent cell fraction. 500,000 cells from the melanoma cancer cell lines SK-MEL-1, SK-MEL-24, SK-MEL-28, the ovarian cancer cell line OVCAR3 and the non-Hodgkin's lymphoma cell line Namalwa or primary CLL cells as positive control were added to the dendritic cells in the presence or absence of 30 μ g/ml anti-CD200 antibody. Supernatants were collected after 48 and 68 hours and analyzed for the presence of cytokines.

[0215] Cytokines such as IL-2, IFN- γ , and IL-10 found in the tissue culture supernatant were quantified using ELISA. Matched capture and detection antibody pairs for each cytokine were obtained from R+D Systems (Minneapolis, Minn.), and a standard curve for each cytokine was produced using recombinant human cytokine. Anti-cytokine capture antibody was coated on the plate in PBS at the optimum concentration. After overnight incubation, the plates were washed and blocked for 1 hour with PBS containing 1% BSA and 5% sucrose. After 3 washes with PBS containing 0.05% Tween, supernatants were added at dilutions of two-fold or ten-fold in PBS containing 1% BSA. Captured cytokines were detected with the appropriate biotinylated anti-cytokine antibody followed by the addition of alkaline phosphatase conjugated streptavidin and SigmaS substrate. Color development was assessed with an ELISA plate reader (Molecular Devices).

[0216] As shown in FIG. 25A, the presence of cell lines with high CD200 expression (MEL-24, MEL-28, OVCAR-3) resulted in down-regulation of Th1 cytokines such as IL-2 and IFN- γ . In contrast, addition of MEL-1 (low CD200 expression) or Namalwa (no CD200 expression) did not affect the cytokine profile. Addition of the anti-CD200 antibody hB7VH3VL2 at 50 μ g/ml fully restored the Th1 response (FIG. 25B), indicating that anti-CD200 antibody treatment of melanoma or ovarian cancer patients might be therapeutically beneficial.

Example 3

Elimination of Activated T Cells by C2aB7-G1 and its Derivatives

[0217] To evaluate whether anti-CD200 treatment has an effect in a cancer model using tumor cells not expressing CD200, Namalwa cells and human PBLs were injected into NOD/SCID mice, and mice were treated as outlined below. In

this model, CD200 is only present on immune cells naturally expressing CD200 such as B cells and follicular T-helper cells.

Group Design:

[0218] 10 animals/group

Group 1: 4×10^6 Namalwa s.c.

Group 2: 4×10^6 Namalwa s.c.+ 8×10^6 PBL

[0219] Group 3: 4×10^6 Namalwa s.c.+ 8×10^6 PBL+20 mg/kg hV3V2-G1

Group 4: 4×10^6 Namalwa s.c.+ 8×10^6 PBL+5 mg/kg hV3V2-G1

Group 5: 4×10^6 Namalwa s.c.+ 8×10^6 PBL+2.5 mg/kg hV3V2-G1

Group 6: 4×10^6 Namalwa s.c.+ 4×10^6 PBL

[0220] Group 7: 4×10^6 Namalwa s.c.+ 8×10^6 PBL+20 mg/kg chC2aB7-G2G4

Group 8: 4×10^6 Namalwa s.c.+ 8×10^6 PBL+5 mg/kg chC2aB7-G2G4

Group 9: 4×10^6 Namalwa s.c.+ 8×10^6 PBL+2.5 mg/kg chC2aB7-G2G4

Group 10: 4×10^6 Namalwa s.c.+ 4×10^6 PBL+20 mg/kg chC2aB7-G2G4

Group 11: 4×10^6 Namalwa s.c.+ 8×10^6 PBL+20 mg/kg alxn4100 $^{1/10}$ th of the dose was included in the injection mixture. Subsequent dosing was 2x/week i.v. for 3 weeks.

[0221] Tumor length (L) and width (W) were measured 3 times/week and tumor volumes were calculated by $L^*W^*W/2$. FIG. 26 shows that as previously established, simultaneous injection of human PBLs with Namalwa cells inhibits tumor growth. No effect of chC2aB7-G2G4 on PBL-mediated tumor growth inhibition was observed. In contrast, administration of ALXN5200 (hB7VH3VL2-G 1) blocked PBL mediated tumor growth inhibition. In the absence of CD200 on tumor cells, it appears that anti-CD200 antibody treatment with an antibody that mediates effector function such as G1 constructs, critical effector cells in the PBL population are eliminated. These data suggest that anti-CD200 cancer therapy is less effective when an antibody with effector function is being used as compared to using the antibody without effector function. However, anti-CD200 treatment using a construct with effector function could be therapeutically beneficial in situations where elimination of immune cells is desirable such as in the transplantation setting or autoimmune diseases.

Example 4

T Cell Killing by hB7VH3VL2

[0222] To evaluate whether incubation of activated T cells with anti-CD200 antibodies containing a constant region mediating effector function (e.g. G1) results in the killing of the T cells, T cells were activated and killing assays were set up as described below.

A). CD3+T Cell Isolation

[0223] Human peripheral blood lymphocytes (PBLs) were obtained from normal healthy volunteers by density gradient centrifugation of heparinized whole blood using the Accuspin™ System. Fifteen ml of Histopaque-1077 (Sigma, St.

Louis, Mo.; cat# H8889) was added to each Accuspin tube (Sigma, St. Louis, Mo.; cat# A2055) which was then centrifuged at 1500 rpm for 2 minutes so that the Histopaque was allowed to pass through the frit. Thirty ml of whole blood was layered over the frit and the tubes were centrifuged for 15 minutes at 2000 rpm at room temperature with no brake. The PBL interface was collected and mononuclear cells were washed twice in PBS with 2% heat-inactivated fetal bovine serum (FBS) (Atlas Biologicals, Ft. Collins, Colo.; cat# F-0500-D) with 1200 rpm centrifugation for 10 minutes. CD3+T cells were isolated by passage over a HTCC-5 column (R&D Systems) according to the manufacturer's instructions. Eluted cells were washed, counted and resuspended in RPMI 1640 containing 5% heat-inactivated single donor serum, 2 mM L-glutamine, 10 mM Hepes and penicillin/streptomycin.

B. Activation with Plate-Bound mOKT3

[0224] Wells of 12-well plates (Falcon) were coated by overnight incubation at 4° C. with 10 µg/mL mOKT3 (Orthoclone) diluted in PBS. Residual antibody was removed and the plates gently rinsed with PBS. Purified CD3+T cells, isolated as described above, were added to the plates at a final concentration of 2×10^6 /well in RPMI 1640 containing 5% heat-inactivated single donor serum, 2 mM L-glutamine, 10 mM Hepes and penicillin/streptomycin. Cells were maintained for 72 hours at 37° C. in a humidified incubator containing 5% CO₂.

C. ⁵¹Chromium Labeling of mOKT3-Activated CD3+Target Cells

[0225] At the end of the culture period, mOKT3-activated CD3+ cells were harvested, washed and resuspended at 10^7 cells/mL in RPMI 1640 without serum. Cells were chromatated by the addition of 125 µCi of ⁵¹Chromium (Perkin Elmer, Billerica, Mass.)/ 10^6 cells for 2 hours at 37° C. Labeled cells were harvested, washed in RPMI containing 5% heat-inactivated single donor serum and resuspended at a final concentration of 2×10^5 cells/mL in the same medium.

D. Preparation of Autologous NK Effector Cells

[0226] Human peripheral blood lymphocytes (PBLs) from the same individual were obtained as described above by density gradient centrifugation. The PBL interface was collected and mononuclear cells were washed twice in PBS with 2% heat-inactivated fetal bovine serum (FBS) (Atlas Biologicals, Ft. Collins, Colo.; cat# F-0500-D) with 1200 rpm centrifugation for 10 minutes. CD56+ cells were isolated by positive selection over anti-CD56-conjugated magnetic beads (Miltenyi Biotec, Auburn, Calif., Cat # 120-000-307) according to the manufacturer's instructions. Eluted cells were washed, counted and resuspended at 1.3×10^6 cells/mL in RPMI 1640 containing 5% heat-inactivated single donor serum, 2 mM L-glutamine, 10 mM Hepes and penicillin/streptomycin. Cells were incubated overnight at 37° C. in a humidified incubator containing 5% CO₂ at a final concentration of 4×10^6 cells/well in 3 mL of the same medium. At the end of the culture period, the cells were harvested, washed, counted and resuspended in serum-free RPMI containing 2 mM L-glutamine, 10 mM Hepes, 2×10^{-5} M 2-mercaptoethanol and penicillin/streptomycin.

E. ADCC Assay

[0227] ⁵¹Cr-labelled mOKT3-activated CD3+ target cells prepared as described above were distributed in wells of a

96-well plate at 10^4 cells/well in 50 µL. CD56+ effector cells were harvested, washed, counted and resuspended at either 2.5×10^6 cells/mL (for an effector:target cell ratio of 25:1) or 10^6 cells/mL (for an effector:target cell ratio of 10:1) and were distributed (100 µL/well) to wells containing the target cells. Ten-fold dilutions of anti-CD200 antibodies (V3V2-G1 or V3V2-G2/G4) were added to the effectors and targets at final concentrations of 10, 1, 0.1 and 0.01 µg/mL. Assay controls included the following: 1) effectors and targets in the absence of antibody (0 Ab); 2) target cells in the absence of effectors (spontaneous lysis) and 3) effectors and targets incubated with 0.2% Tween-80 (maximum release). All cell culture conditions were performed in triplicate. Cells were incubated at 37° C. for 4 hours in a humidified incubator containing 5% CO₂. At the end of the culture period, the plates were centrifuged to pellet the cells and 150 µL of cell supernatant was transferred to scintillation vials and counted in a gamma scintillation counter (Wallac). The results are expressed as percent specific lysis according to the following formula:

$$\frac{(\text{Mean sample counts per minute (cpm)} - \text{mean spontaneous lysis})}{\text{Mean sample counts per minute (cpm)}} \times 100$$

[0228] (mean maximum lysis-mean spontaneous lysis)

F. Flow Cytometry

[0229] One hundred µL of cell suspensions (mOKT3-activated CD3+ cells or purified CD56+NK cells) prepared as described above were distributed to wells of a 96-well round bottom plate (Falcon, Franklin Lakes N.J.; cat# 353077). Cells were incubated for 30 minutes at 4° C. with the indicated combinations of the following fluorescein isothiocyanate (FITC)-, Phycoerythrin (PE)-, PerCP-Cy5.5-, or allophycocyanin (APC)-conjugated antibodies (all from Becton-Dickinson, San Jose, Calif.); anti-human CD25-FITC (cat# 555431); anti-human CD3-APC (cat# 555335); anti-human CD200-PE (cat #552475); anti-human CD8-PerCP-Cy5.5 (cat# 341051); anti-human CD4-APC (cat# 555349); anti-human CD5-APC (cat# 555355) and anti-human CD56-APC (cat# 341025). Isotype controls for each labeled antibody were also included. After washing cells twice with FACS buffer (1800 rpm centrifugation for 3 minutes), cells were resuspended in 300 µL of PBS (Mediatech, Herndon, Va.; cat# 21-031-CV) and analyzed by flow cytometry using a Facs-Caliber machine and CellQuest Software (Becton Dickinson, San Jose, Calif.).

[0230] As shown in FIG. 27, activated T cells show high CD200 expression on their surface. Activated T cells are efficiently killed in the presence of VH3VL2-G1 but not VH3VL2-G2G4 when NK cells are used as effector cells (FIG. 28). These data demonstrate that anti-CD200 antibodies with effector function can eliminate activated T cells. Such an antibody could be of therapeutic use in the transplantation setting or for the treatment of autoimmune diseases.

[0231] In addition to regulatory T cells, plasmacytoid dendritic cells have been shown to play a negative immunoregulatory role in human cancer (Wei S, Kryczek I, Zou L, Daniel B, Cheng P, Mottram P, Curiel T, Lange A, Zou W Plasmacytoid dendritic cells induce CD8+ regulatory T cells in human ovarian carcinoma. Cancer Res. 2005 Jun. 15; 65(12): 5020-6). Combination of a therapy eliminating plasmacytoid dendritic cells with anti-CD200 therapy could therefore be advantageous.

Example 5 CD200 on Plasma Cells

[0232] Bone marrow cells from 10 multiple myeloma patients and 3 normal donors were prepared by first lysing red

blood cells using ammonium chloride. Cells were resuspended in FACS buffer and labeled with the following antibody cocktails:

- [0233] Kappa-FITC/CD38-PE/CD138-PerCP-Cy5.5
- [0234] Lambda-FITC/CD38-PE/CD138-PerCP-Cy5.5
- [0235] Isotype Control-FITC/CD38-PE
- [0236] CD200-FITC/CD38-PE

[0237] Data were collected using a BD FACS Canto and analyzed using BD DiVA software. Expression of CD200 on CD38 bright cells (plasma cells) was analyzed. As shown in FIG. 29, a portion of plasma cells expresses CD200 at high intensity in normal donors. In multiple myeloma patients, the majority of plasma cells express CD200.

[0238] In the multiple myeloma setting, similar to CLL or other cancers expressing CD200, CD200 expression by the tumor cells might prevent the immune system from eradicating the tumor cells. Antagonistic anti-CD200 therapy might subsequently allow the immune system to eliminate cancer cells. Ablative anti-CD200 therapy targeting plasma cells could be therapeutically beneficial in the autoimmune or transplantation setting.

Example 6

CD200 on Viruses

[0239] CD200 is also expressed on a number of viruses such as myxoma virus M141R or human herpesvirus 8. Similar to expression of CD200 on tumor cells, CD200 on viruses might prevent the immune system from effectively clearing the virus. Treatment with an antagonistic anti-CD200 antibody could be therapeutically beneficial in an infection with a CD200 expressing virus, allowing the immune system to eradicate the virus. Alternatively, an ablative anti-CD200 antibody could be used.

[0240] It will be understood that various modifications may be made to the embodiments disclosed herein. For example, as those skilled in the art will appreciate, the specific sequences described herein can be altered slightly without necessarily adversely affecting the functionality of the polypeptide, antibody or antibody fragment used in binding OX-2/CD200. For instance, substitutions of single or multiple amino acids in the antibody sequence can frequently be made without destroying the functionality of the antibody or fragment. Thus, it should be understood that polypeptides or antibodies having a degree of identity greater than 70% to the specific antibodies described herein are within the scope of this disclosure. In particularly useful embodiments, antibodies having an identity greater than about 80% to the specific antibodies described herein are contemplated. In other useful embodiments, antibodies having an identity greater than about 90% to the specific antibodies described herein are contemplated. Therefore, the above description should not be construed as limiting, but merely as exemplifications of preferred embodiments. Those skilled in the art will envision other modifications within the scope and spirit of this disclosure.

REFERENCES

[0241] The following references are incorporated herein by reference to more fully describe the state of the art to which the present invention pertains. Any inconsistency between these publications below or those incorporated by reference above and the present disclosure shall be resolved in favor of the present disclosure.

- [0242] 1) Agarwal, et al., (2003). Disregulated expression of the Th2 cytokine gene in patients with intraoral squamous cell carcinoma. *Immunol Invest* 32:17-30.
- [0243] 2) Almasri, N M et al. (1992). *Am J Hemato* 140: 259-263.
- [0244] 3) Contasta, et al., (2003). Passage from normal mucosa to adenoma and colon cancer: alteration of normal sCD30 mechanisms regulating TH1/TH2 cell functions. *Cancer Biother Radiopharm* 18:549-557.
- [0245] 4) Gorczynski, et al., (1998). Increased expression of the novel molecule OX-2 is involved in prolongation of murine renal allograft survival. *Transplantation* 65:1106-1114.
- [0246] 5) Gorczynski, et al., (2001). Evidence of a role for CD200 in regulation of immune rejection of leukaemic tumour cells in C57BU6 mice. *Clin Exp Immunol* 126: 220-229.
- [0247] 6) Hainsworth, J D (2000). *Oncologist* 2000; 5(5): 376-84.
- [0248] 7) Inagawa, et al., (1998). Mechanisms by which chemotherapeutic agents augment the antitumor effects of tumor necrosis factor: involvement of the pattern shift of cytokines from Th2 to Th1 in tumor lesions. *Anticancer Res* 18:3957-3964.
- [0249] 8) Ito, et al., (1999). Lung carcinoma: analysis of T helper type 1 and 2 cells and T cytotoxic type 1 and 2 cells by intracellular cytokine detection with flow cytometry. *Cancer* 85:2359-2367.
- [0250] 9) Kiani, et al., (2003). Normal intrinsic Th1/Th2 balance in patients with chronic phase chronic myeloid leukemia not treated with interferon-alpha or imatinib. *Haematologica* 88:754-761.
- [0251] 10) Laurová, et al., (2002). Malignant melanoma associates with Th1/Th2 imbalance that coincides with disease progression and immunotherapy response. *Neoplasma* 49:159-166.
- [0252] 11) Maggio, et al., (2002). Chemokines, cytokines and their receptors in Hodgkin's lymphoma cell lines and tissues. *Ann Oncol* 13 Suppl 1:52-56.
- [0253] 12) Nilsson, K (1992). *Burn Cell*. 5(1):25-41.
- [0254] 13) Podhorecka, et al., (2002). T type 1/type 2 subsets balance in B-cell chronic lymphocytic leukemia—the three-color flow cytometry analysis. *Leuk Res* 26:657-660.
- [0255] 14) Pu, Q Q and Bezwoda, W (2000). *Anticancer Res*. 20(4):2569-78
- [0256] 15) Smyth, et al., (2003). Renal cell carcinoma induces prostaglandin E2 and T-helper type 2 cytokine production in peripheral blood mononuclear cells. *Ann Surg Oncol* 10:455-462.
- [0257] 16) Tatsumi, et al., (2002). Disease-associated bias in T helper type 1 (Th1)/Th2 CD4(+) T cell responses against MAGE-6 in HLA-DRB10401(+) patients with renal cell carcinoma or melanoma. *J Exp Med* 196:619-628.
- [0258] 17) Walls A Vet al. (1989). *Int. J. Cancer* 44:846-853.
- [0259] 18) Winter, et al., (2003). Tumour-induced polarization of tumour vaccine-draining lymph node T cells to a type 1 cytokine profile predicts inherent strong immunogenicity of the tumour and correlates with therapeutic efficacy in adoptive transfer studies. *Immunology* 108:409-419.
- [0260] 19) Cameron, C. M., J. W. Barrett, L. Liu, A. R. Lucas, and G. McFadden. 2005. Myxoma virus M141R

expresses a viral CD200 (vOX-2) that is responsible for down-regulation of macrophage and T-cell activation in vivo. *J Virol* 79:6052.

- [0261] 20) Foster-Cuevas, M., G. J. Wright, M. J. Puklavec, M. H. Brown, and A. N. Barclay. 2004. Human herpesvirus 8 K14 protein mimics CD200 in down-regulating macrophage activation through CD200 receptor. *J Virol* 78:7667.
- [0262] 21) Nicholas, J. 2003. Human herpesvirus-8-encoded signalling ligands and receptors. *J Biomed Sci* 10:475.
- [0263] 22) Shiratori, I., M. Yamaguchi, M. Suzukawa, K. Yamamoto, L. L. Lanier, T. Saito, and H. Arase. 2005.

Down-regulation of basophil function by human CD200 and human herpesvirus-8 CD200. *J Immunol* 175:4441.

- [0264] 23) Voigt, S., G. R. Sandford, G. S. Hayward, and W. H. Burns. 2005. The English strain of rat cytomegalovirus (CMV) contains a novel captured CD200 (vOX2) gene and a spliced CC chemokine upstream from the major immediate-early region: further evidence for a separate evolutionary lineage from that of rat CMV Maastricht. *J Gen Virol* 86:263.

- [0265] 24) Zhang, J., J. Wang, C. Wood, D. Xu, and L. Zhang. 2005. Kaposi's sarcoma-associated herpesvirus/human herpesvirus 8 replication and transcription activator regulates viral and cellular genes via interferon-stimulated response elements. *J Virol* 79:5640.

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tgcaaggctt	ctggttattc	attcaactgac	tacatcatac	tctggatcag	gcagcatagc	180
ggaaagggcc	ttgagtggat	tggacatatt	gatcctact	atggtagttc	taactacaat	240
ctgaaattca	agggcagggt	cacaatca	gcagacaaat	ctaccaggac	aacctacatg	300
gagctcacca	gtctgacatc	tgaggacact	gcagtctatt	actgtggaa	atctaagagg	360
gactacttg	actactgggg	ccaaggcacc	actctcacag	tttcctcagc	ctccaccaag	420
ggcccatcg	tctccccgt	agcacccctcc	tccaagagca	cctctgggg	cacagcggcc	480
ctgggtgcc	tggtcaagga	ctacttcccc	gaaccgggtga	cggtgtcgtg	gaactcaggc	540
gccctgacca	gccccgtgc	cacccccc	gtgtcctac	agtccctagg	actctactcc	600
ctcagcagcg	tggtgaccgt	gccctccagc	agcttggca	cccagaccta	catctgcaac	660
gtgaatcaca	agcccgacaa	caccaagggt	gacaagagag	ttgagccaa	atcttgac	720
aaaactcaca	catgcccacc	gtgcccagca	cctgaactcc	tggggggacc	gtcagtcttc	780
ctcttcccc	caaacccaa	ggacaccctc	atgatctccc	ggaccctga	ggtcacatgc	840
gtgggttgtgg	acgtgagcca	cgaagaccct	gaggtcaagt	tcaactggta	cgtggacggc	900
gtggaggtgc	ataatgccaa	gacaagccg	cgggaggagc	agtacaacag	cacgtaccgt	960
gtggtcagcg	tcctcaccgt	cctgcaccag	gactggctga	atggcaagga	gtacaagtgc	1020

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aaggctcca acaaagccct cccagcccc atcgagaaaa ccacatccaa agccaaaggg	1080
cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac	1140
caggtcagcc tgacacctg ggtcaaaaggc ttctatccca gcgcacatcg cgtggagtgg	1200
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccggtct ggactccgac	1260
ggcttccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaaac	1320
gtcttctcat gctccgtgtat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1380
tccctgtctc cgggttaaatg a	1401

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<210> SEQ ID NO 9
<211> LENGTH: 466
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hB7V4V1-hG1 Heavy chain

<400> SEQUENCE: 9

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

Val Phe Ser Glu Val Gln Leu Val Glu Ser Gly Pro Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
35 40 45

Thr Asp Tyr Ile Ile Leu Trp Ile Arg Gln His Ser Gly Lys Gly Leu
50 55 60

Glu Trp Ile Gly His Ile Asp Pro Tyr Tyr Gly Ser Ser Asn Tyr Asn
65 70 75 80

Leu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Arg
85 90 95

Thr Thr Tyr Met Glu Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Gly Arg Ser Lys Arg Asp Tyr Phe Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145 150 155 160

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
165 170 175

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
195 200 205

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225 230 235 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu

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275	280	285	
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His			
290	295	300	
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg			
305	310	315	320
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys			
325	330	335	
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu			
340	345	350	
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr			
355	360	365	
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu			
370	375	380	
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp			
385	390	395	400
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val			
405	410	415	
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp			
420	425	430	
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His			
435	440	445	
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro			
450	455	460	
Gly Lys			
465			

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<210> SEQ ID NO 10
<211> LENGTH: 1401
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hB7V3V1-hG1 Heavy chain (cDNA hG1)

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<400> SEQUENCE: 10
atggatgga gccggatctt tctttcctc ctgtcaataa ttgcaggtgt ccattgccag 60
gtccagctgc aacagtctgg atctgagctg aagaaggctg gggcttcagt gaagatctcc 120
tgcaaggctt ctgggttattc attcaactgac tacatcatac tctgggttag gcagaaccct 180
ggaaagggcc ttgagtgat tggacatatt gatccttaact atggtagttc taactacaat 240
ctgaaattca agggcagagt gacaatcacc gccgaccagt ctaccaccac agcctacatg 300
gagctctcca gtctgagatc tgaggacact gcagtctatt actgtggaa atctaagagg 360
gactactttg actactgggg ccaaggcacc actctcacag tttcctcagc ctccaccaag 420
ggcccatcggt tcttcccgtc agcaccctcc tccaagagca cctctgggg cacagggcc 480
ctgggctgcc tggtcaagga ctacttcccc gaaccgggtga cggtgtcggtg gaactcaggc 540
gccctgacca gccccgtgca cacttcccg gctgtctac agtccctcagg actctactcc 600
ctcagcagcg tggtgaccgt gcccctccagc agcttgggc cccagaccta catctgcaac 660
gtgaatcaca agcccagcaa caccaagggtg gacaagagag ttgagccaa atcttgcac 720
aaaactcaca catgcccacc gtgccccagca cctgaactcc tggggggacc gtcagtcattc 780
ctcttccccca caaaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

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gtgggtgtgg acgtgagcca cgaagacccct gaggtcaagt tcaactggta cgtggacggc	900
gtggagggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt	960
gtggtcagecg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	1020
aaggctcca acaaagccct cccagcccc atcgagaaaa ccatactccaa agccaaagg	1080
cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac	1140
caggtcagcc tgacacctgcct ggtcaaaggc ttctatccca ggcacatcgc cgtggagtgg	1200
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctccctgtgc ggactccgac	1260
ggctccctct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaa	1320
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1380
tccctgtctc cgggtaaatg a	1401

<210> SEQ ID NO 11

<211> LENGTH: 466

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: hB7V3V1-hG1 Heavy chain

<400> SEQUENCE: 11

Met Gly Trp Ser Arg Ile Phe Leu Phe Leu Ser Ile Ile Ala Gly			
1	5	10	15

Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Ser Glu Leu Lys Lys			
20	25	30	

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe			
35	40	45	

Thr Asp Tyr Ile Ile Leu Trp Val Arg Gln Asn Pro Gly Lys Gly Leu			
50	55	60	

Glu Trp Ile Gly His Ile Asp Pro Tyr Tyr Gly Ser Ser Asn Tyr Asn			
65	70	75	80

Leu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Gln Ser Thr Thr			
85	90	95	

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val			
100	105	110	

Tyr Tyr Cys Gly Arg Ser Lys Arg Asp Tyr Phe Asp Tyr Trp Gly Gln			
115	120	125	

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val			
130	135	140	

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala			
145	150	155	160

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser			
165	170	175	

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val			
180	185	190	

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro			
195	200	205	

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys			
210	215	220	

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp			
225	230	235	240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly

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245	250	255
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile		
260	265	270
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu		
275	280	285
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His		
290	295	300
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg		
305	310	315
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys		
325	330	335
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu		
340	345	350
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr		
355	360	365
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu		
370	375	380
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp		
385	390	395
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val		
405	410	415
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp		
420	425	430
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His		
435	440	445
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro		
450	455	460
Gly Lys		
465		

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<210> SEQ ID NO 12
<211> LENGTH: 2002
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hB7V3V2-hG2G4 Heavy chain (genomic sequence
hG2G4)

<400> SEQUENCE: 12

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atgggatgga gctgttatcat ccttttcttg gtagcaacag ctacagggtgt ccactccctc	60
gagggtccagc tgcaaacagtc tggacctgag ctggtaaaggc ctggggcttc actgaagatgc	120
tccctgcaagg cttctggta ttcatctact gactacatca tactctgggt gaagcagaac	180
catggaaaga gcctttagtg gattggacat attgtaccc ttatgttagt ttctaaactac	240
aatctgaaat tcaaggccaa ggcccacattg actgttagaca aatcttccag cacagcctac	300
atgcagctca acagtctgac atctgaggac tctgcagtctt attactgtgg aagatctaag	360
aggggactact ttgactactg gggccaaggc accactctca cagttccctc agcctccacc	420
aagggcccat ccgttcccc cctggcgccc tgctccagga gcacccctcg gacacagcc	480
gcctggct gcctggtaa ggactacttc cccgaaaccgg tgacgggtgc gtggactca	540
ggcgccctga ccagccccgt gcacaccccttc cccgctgtcc tacagtcctc aggactctac	600
tccctcagca gcgtggtgac cgtgccctcc agcaacttcg gcacccagac ctacacccgtc	660

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aacgttagatc acaagccag caacaccaag gtggacaaga cagttggta gaggccagct	720
cagggaggga gggtgtctgc tggaagccag gtcagccct cctgcctgga cgcaccccg	780
ctgtgcagcc ccagcccagg gcagcaaggc aggccccatc tgtctctca cccggaggcc	840
tctgcccgc ccactcatgc tcagggagag ggttcttg cttttccac caggctccag	900
gcagggacag gctgggtgcc cctacccag gccctcaca cacagggca ggtgcttggc	960
tcagacctgc caaaagccat atccgggagg accctgcccc tgacctaagc cgaccccaa	1020
ggccaaactg tccactccct cagctcgac accttctctc ctcccaagatc cgagtaactc	1080
ccaatcttct ctctgcagag cgcaaatgtt gtgtcgagtg cccaccgtgc ccaggtaagc	1140
cagccaggc ctgcctcc agctcaaggc gggacaggtg ccctagagta gcctgcattcc	1200
agggacaggc cccagctggg tgctgacacg tccacctcca tctcttctc agcaccac	1260
gtggcaggac cgtcagtctt cctttcccc caaaaaccca aggacaccct catgatctcc	1320
cggaccctg aggtcacgtg cgtgggtgt gacgtgagcc aggaagaccc cgaggtccag	1380
ttcaactggt acgtggatgg cgtggaggtg cataatgcca agacaaaagcc gcggggaggag	1440
cagttcaaca gcacgtaccg tgggtcagc gtcctcaccc tcctgcacca ggactggctg	1500
aacggcaagg agtacaatgt caaggtctcc aacaaaggcc tcccttcctc catcgagaaa	1560
accatctcca aagccaaagg tgggacccac ggggtgcgag ggccacatgg acagaggta	1620
gctggccca ccctctgccc tgggagtgtac cgctgtgcca acctctgtcc ctacaggc	1680
gccccgagag ccacaggtgt acaccctgcc cccatccag gaggagatga ccaagaacca	1740
ggtcagccctg acctgcctgg tcaaaggctt ctacccagc gacatgcggc tggagtggg	1800
gagcaatggg cagccggaga acaactacaa gaccacgcct cccgtgtgg actccgacgg	1860
ctccttcttc ctctacagca ggctaaccgt ggacaagagc aggtggcagg agggaaatgt	1920
cttctcatgc tccgtatgc atgaggctct gcacaaccac tacacacaga agaccccttc	1980
cctgtctctg ggtaaatgtat ga	2002

<210> SEQ ID NO 13

<211> LENGTH: 462

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: hB7V3V2-hG2G4 Heavy chain

<400> SEQUENCE: 13

Met	Gly	Trp	Ser	Arg	Ile	Phe	Leu	Phe	Leu	Leu	Ser	Ile	Ile	Ala	Gly
1															15

Val	His	Cys	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys
														20	30

Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe
														35	45

Thr	Asp	Tyr	Ile	Ile	Leu	Trp	Val	Arg	Gln	Asn	Pro	Gly	Lys	Gly	Leu
														50	60

Glu	Trp	Ile	Gly	His	Ile	Asp	Pro	Tyr	Tyr	Gly	Ser	Ser	Asn	Tyr	Asn	
														65	75	80

Leu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Ile	Asp	Gln	Ser	Thr	Thr			
														85	90	95

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
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100	105	110	
Tyr Tyr Cys Gly Arg Ser Lys Arg Asp Tyr Phe Asp Tyr Trp Gly Gln			
115	120	125	
Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val			
130	135	140	
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala			
145	150	155	160
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser			
165	170	175	
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val			
180	185	190	
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro			
195	200	205	
Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys			
210	215	220	
Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val			
225	230	235	240
Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe			
245	250	255	
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro			
260	265	270	
Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val			
275	280	285	
Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr			
290	295	300	
Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val			
305	310	315	320
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys			
325	330	335	
Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser			
340	345	350	
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro			
355	360	365	
Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val			
370	375	380	
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly			
385	390	395	400
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp			
405	410	415	
Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp			
420	425	430	
Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His			
435	440	445	
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys			
450	455	460	

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<210> SEQ ID NO 14
<211> LENGTH: 1999
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: chC2aB7-hG2G4 Heavy chain (genomic sequence
hG2G4)

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<400> SEQUENCE: 14

atggatgga gctgtatcat cctttcttg gtagcaacag ctacagggt ccactccctc	60
gagggtccagc tgcaacagtc tggacctgag ctggtaago ctggggcttc actgaagatg	120
tcttgcagg cttctggta ttcatctact gactacatca tactctgggt gaaggcagaac	180
catggaaaga gccttgagtg gattggacat attgatcctt actatggtag ttctaactac	240
aatctgaaat tcaagggcaa ggccacattt actgttagaca aatcttccag cacgcctac	300
atgcagctca acagtcgtac atctgaggac tctgcagtc attactgtgg aagatctaag	360
agggactact ttgactactg gggccaaggc accactctca cagtttccctc agcctccacc	420
aaggcccatt ccgtttcccc cctggcgccc tgctccagga gcacccctcgaa gggcacagcc	480
gccttggct gcctggtaaa ggactacttc cccgaaccgg tgacgggtgc gtggactca	540
ggcgcctgtc ccagcggcgt gcacaccccttc cggctgttc tacagtcctc aggactctac	600
tccctcagca cgctgggtac cgtgccttc agcaacttcg gcacccagac ctacacccctc	660
aacgttagatc acaagcccag caacaccaag gtggacaaga cagttgggtga gggccagct	720
caggggaggga ggggtctgc tggaagccag gtcagccctt cctgcctggaa cgaccccccgg	780
ctgtgcagcc ccagccaggc gcagcaaggc agggccatctc tgtctccatca cccggaggcc	840
tctgcggccccc ccactcatgc tcagggagag ggtttctgg cttttccac caggctccag	900
gcaggcacag gctgggtgcc cctaccccaag gcccctcaca cacagggca ggtgtttggc	960
tcagacctgc caaaagccat atccggagg accctgccttc tgacctaagc cgaccccaaa	1020
ggccaaactg tccactccct cagctcgac accttctctc ctcccaatgc ctagtaactc	1080
ccaatcttct ctctgcagag cgcaaatgtt gtgtcgagtg cccaccgtgc ccaggtaagc	1140
cagcccaaggc ctgcggccccc agctcaaggc gggacagggtg ccctagagta gcctgcatacc	1200
agggacaggc cccagctggg tgctgacacg tccacccctca tctttccctc agcaccaccc	1260
gtggcaggac cgtcagtc tctttcccccc ccaaaaccca aggacaccct catgatctcc	1320
cggacccctg aggtcacgtg cgtgggtggc gacgtgagcc aggaagaccc cgagggtccag	1380
ttcaacttgtt acgtggatgg cgtggagggtg cataatgcca agacaaagcc gggggaggag	1440
cagttcaaca gcacgttaccg tgggtcagc gtcctcaccc tcctgcacca ggactggctg	1500
aacggcaagg agtacaatgtt caaggcttcc aacaaaggcc tccctgccttc catcgagaaa	1560
accatctcca aagccaaagg tgggacccac ggggtgcgag ggccacatgg acagaggta	1620
gctggccca ccctctgccc tggggtggc acgtgtgcaccc ctacaggccaa	1680
gccccggagag ccacagggtt acaccctgc cccatccag gaggagatga ccaagaacca	1740
ggtcagccctg acctgcctgg tcaaaggctt ctaccccaacgacatcgccg tggagttggg	1800
gagcaatggg cagccggaga acaactacaa gaccacgcct cccgtgtgg actccgcgg	1860
ctctttcttc ctctacagca ggctaaccgt ggacaagagc aggtggcagg agggaaatgt	1920
cttctcatgc tcgggtatgc atgaggcttgc acacaaccac tacacacaga agaccccttc	1980
cctgtctctg ggttaatga	1999

<210> SEQ ID NO 15

<211> LENGTH: 463

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:

<223> OTHER INFORMATION: chC2aB7-hG2G4 Heavy chain

<400> SEQUENCE: 15

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5          10          15

Val His Ser Leu Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val
20          25          30

Lys Pro Gly Ala Ser Leu Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser
35          40          45

Phe Thr Asp Tyr Ile Ile Leu Trp Val Lys Gln Asn His Gly Lys Ser
50          55          60

Leu Glu Trp Ile Gly His Ile Asp Pro Tyr Tyr Gly Ser Ser Asn Tyr
65          70          75          80

Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
85          90          95

Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala
100         105         110

Val Tyr Tyr Cys Gly Arg Ser Lys Arg Asp Tyr Phe Asp Tyr Trp Gly
115         120         125

Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130         135         140

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145         150         155         160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165         170         175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180         185         190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195         200         205

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
210         215         220

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
225         230         235         240

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
245         250         255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260         265         270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
275         280         285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290         295         300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
305         310         315         320

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325         330         335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
340         345         350

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
355         360         365

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370         375         380

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Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
385															400
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
															415
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
															430
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
															445
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
450															460

<210> SEQ ID NO 16
<211> LENGTH: 1391
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hB7V3V2-cG2G4 Heavy chain (cDNA G2G4)

<400> SEQUENCE: 16

atgggatgga	gcgggatctt	tcttttcctc	ctgtcaataa	ttgcaggtgt	ccattgccag	60
gtccagctgc	aacagtctgg	atctgagctg	aagaaggcctg	gggcttcagt	gaagatctcc	120
tgcaaggcct	ctggttattc	attcaactgac	tacatcatac	tctgggtgag	gcagaaccct	180
ggaaagggcc	ttgagtggat	tggaatattt	gatcctact	atggtagttc	taactacaat	240
ctgaaattca	agggcagagt	gacaatcacc	gccgaccagt	ctaccaccac	agcctacatg	300
gagctctcca	gtctgagatc	tgaggacact	gcagtttattt	actgttggaa	atctaagagg	360
gactactttg	actactgggg	ccaaggcacc	actctcacag	tttccctcagc	ctccaccaag	420
ggcccatccg	tcttccccct	ggcgccctgc	tccaggagca	cctccgagag	cacagccgcc	480
ctgggtgcc	tggtcaagga	ctacttcccc	gaaccgggtg	cggtgtcggt	gaactcaggc	540
gcccctgacca	ggggcggtgca	caccccccgg	gctgttctac	agtcctcagg	actctactcc	600
ctcagcagcg	tggtgaccgt	gccctccagc	aacttcggca	cccagaccta	cacctgcaac	660
gtagatcaca	agcccgacaa	caccaagggt	gacaagacag	ttgagcgcac	atgttgtgtc	720
gagtgccccac	cgtgccccagc	accacctgtg	gcaggaccgt	cagtcttccct	cttccccccca	780
aaaccccaagg	acaccctcat	gatctccgg	accctggagg	tcacgtgcgt	gggtggggac	840
gtgagccagg	aagaccccgaa	ggtccagttc	aactggtacg	tggatggcg	ggaggtgcat	900
aatgccaaga	caaagcccg	ggaggaggcag	ttcaacagca	cgtaccgtgt	ggtcagcgtc	960
ctcacccgtcc	tgcaccagga	ctggctgaac	ggcaaggagt	acaagtgcac	ggcttccaa	1020
aaaggcctcc	cgtccctccat	cgagaaaaacc	atctccaaag	ccaaaggggca	gccccgagag	1080
ccacagggtgt	acaccctggcc	cccatcccaag	gaggagatga	ccaagaacca	ggtcagcgctg	1140
acctgcctgg	tcaaaggctt	ctaccccagc	gacatcgccg	tggagtggga	gagcaatggg	1200
cagccggaga	acaactacaa	gaccacgct	cccggtgtgg	actccgacgg	ctccttcttc	1260
ctctacagca	ggctaaccgt	ggacaagagc	aggtggcagg	aggggaatgt	cttctcatgc	1320
tccgtatgc	atgaggctct	gcacaaccac	tacacacaga	agagcctctc	cctgtctctg	1380
ggttaatgtat	g					1391

<210> SEQ ID NO 17

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<211> LENGTH: 2005
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: ChC7-hG2G4 Heavy chain (genomic sequence hG2G4)

<400> SEQUENCE: 17

atggatgga	gctgtatcat	cctttcttg	gtagcaacag	ctacagggt	ccactccctc	60
gagggtccaac	tgcagcagtc	tggacctgag	ctggagaagc	ctggcgcttc	agtgaagata	120
tcctgcaagg	cttctggta	ctcattcact	ggctacaaca	tgaactgggt	gaagcagagc	180
agtggaaaga	gcctttagtg	gattggaaat	tttgatcctt	actatgggt	tattacctac	240
aaccagaagt	tcaagggcaa	ggccacattt	actgttagaca	aatcctccag	cacagcctac	300
atgcagctca	agagcctgac	atctgaggac	tctgcagtt	attactgtgc	aagaacggct	360
acggctctct	atactatgga	ctactgggt	caaggaacct	cagtcaccgt	ctccctcagcc	420
tccaccaagg	gccccatccgt	cttcccccgt	gcccctgtct	ccaggagcac	ctccgagagc	480
acagccgccc	tgggctgcct	ggtcaaggac	tacttcccg	aaccgggtac	ggtgtcggt	540
aactcaggcg	ccctgaccag	cggegtgcac	accttcccg	ctgtcctaca	gtcctcagga	600
ctctactccc	tcagcagcgt	ggtgaccgt	ccctccagca	acttcggcac	ccagacctac	660
acctgcaacg	tagatcacaa	gcccagcaac	accaagggtgg	acaagacagt	ttggtgagagg	720
ccagctcagg	gagggagggt	gtctgctgga	agccaggctc	agccctctg	cctggacgcac	780
ccccggctgt	gcagccccag	cccagggcag	caaggcaggc	cccatctgtc	tcctcaccgg	840
gaggcctctg	cccgccccac	tcatgctcag	ggaggggtc	ttctggcttt	ttccaccagg	900
ctccaggcag	gcacaggctg	ggtgccctca	ccccaggccc	ttcacacaca	ggggcagggt	960
cttggctcag	acctgcca	agccatatcc	gggaggaccc	tgccctgac	ctaagccac	1020
cccaaaggcc	aaactgtcca	ctccctcagc	tcggacacct	tctctctcc	cagatccqag	1080
taactcccaa	tcttctctct	gcagagcgca	aatgttgtgt	cgagtgcaca	ccgtgcccag	1140
gtaagccagc	ccaggcctcg	ccctccagct	caaggcggga	caggtgccct	agagtagcct	1200
gcattccagg	acaggccccca	gctgggtgt	gacacgtcca	cctccatctc	ttctcagca	1260
ccacctgtgg	caggaccgtc	agtcttcctc	ttccccccaa	aacccaagga	caccctcatg	1320
atctcccgga	ccccctgagg	cacgtgcgt	gtgggtggac	tgagccagga	agaccccgag	1380
gtccagttca	actggta	ggatggcgt	gaggtgcata	atgccaagac	aaagccgegg	1440
gaggagcagt	tcaacagcac	gtaccgtgt	gtcagcgtcc	tcaccgtct	gcaccaggac	1500
tggctgaacg	gcaaggagta	caagtgcag	gtctccaaca	aaggcctccc	gtccctccatc	1560
gagaaaacca	tctccaaagc	caaagggtgg	acccacgggg	tgcgagggcc	acatggacag	1620
aggtcagctc	ggcccaccc	ctgcctctgg	agtggcgt	gtgccaaacct	ctgtccctac	1680
aggcagccc	cgagagccac	aggtgtacac	cctgccccca	tcccaggagg	agatgacca	1740
gaaccagg	tcgacgtac	gcctggtaa	aggcttctac	cccagcaca	tcgcgtgg	1800
gtggggagagc	aatgggcagc	cgagaaacaa	ctacaagacc	acgcctccc	tgctggactc	1860
cgacggctcc	ttcttcctct	acagcaggct	aaccgtggac	aagagcagg	ggcaggagg	1920
gaatgtctc	tcatgctcgg	tgtatgcata	ggctgtgcac	aaccactaca	cacagaagag	1980
cctctccctg	tctctggta	aatga				2005

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<210> SEQ ID NO 18
<211> LENGTH: 468
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: ChC7-hG2G4 Heavy chain (genomic sequence hG2G4)

<400> SEQUENCE: 18

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5          10          15

Val His Ser Leu Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu
20          25          30

Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser
35          40          45

Phe Thr Gly Tyr Asn Met Asn Trp Val Lys Gln Ser Ser Gly Lys Ser
50          55          60

Leu Glu Trp Ile Gly Asn Phe Asp Pro Tyr Tyr Gly Val Ile Thr Tyr
65          70          75          80

Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
85          90          95

Ser Thr Ala Tyr Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala
100         105         110

Val Tyr Tyr Cys Ala Arg Thr Ala Thr Ala Leu Tyr Thr Met Asp Tyr
115         120         125

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130         135         140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145         150         155         160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165         170         175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180         185         190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195         200         205

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
210         215         220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
225         230         235         240

Cys Cys Val Glu Cys Pro Pro Cys Pro Gly Lys Pro Ala Pro Pro Val
245         250         255

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
260         265         270

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275         280         285

Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
290         295         300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
305         310         315         320

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
325         330         335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
340         345         350
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Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
355 360 365

Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
370 375 380

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
420 425 430

Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
450 455 460

Ser Leu Gly Lys
465

<210> SEQ ID NO 19
<211> LENGTH: 2025
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: D1B5-hG1 Heavy chain (genomic sequence hG1
constant region)

<400> SEQUENCE: 19

atgggatgga	gctgtatcat	cctttcttg	gttagcaacag	ctacagggtgt	ccactccctc	60
gagggtccaaac	tgcagcagcc	tggggcagag	cttgtgaggt	caggggcctc	agtcaagttt	120
tcctgcaaag	ttctctggctt	caacattaaa	gactactata	tacactgggt	gaagcagagg	180
cctgaacagg	gcctggagtg	gattggatgg	attgtatcctg	agattgggtgc	tactaaatat	240
gtccccaaagt	tccaggggaa	ggccactatg	actacagaca	catcctccaa	cacagcctac	300
ctgcagctca	gcagcctgac	atctgaggac	actgcctgt	attactgtaa	tgcctcttat	360
ggtaactacg	accgttacta	tgctatggac	tactgggtc	aaggAACCTC	agtccaccgtc	420
tcctcagcct	ccaccaaggg	cccacggc	ttccccctgg	caccctcttc	caagagcacc	480
tctggggca	cagcggccct	gggctgcctg	gtcaaggact	acttccccga	accgggtgacg	540
gtgtcggtga	actcaggcgc	cctgaccgc	ggcgtgcaca	ccttccggc	tgtcctacag	600
tcctcaggac	tctactccct	cagcagcgtg	gtgaccgtgc	cctccagcag	cttgggcacc	660
cagacctaca	tctgcaacgt	gaatcacaag	cccagcaaca	ccaagggtgga	caagaggtt	720
ggtgagaggc	cagcacaggg	agggagggtg	tctgctggaa	gccaggetca	gcgtccctgc	780
ctggacgcac	cccggtatg	cagtccctgt	ccagggcago	aaggcaggcc	ccgtctgcct	840
cttcacccgg	aggcctctgc	ccgccccact	catgtcagg	gagagggtct	tctggcttt	900
tccccaggct	ctggggcaggc	acaggctagg	tgcctcta	ccaggccctg	cacacaaagg	960
ggcaggtgct	gggctcagac	ctgccaagag	ccatatccgg	gaggaccctg	ccctgtacat	1020
aagcccaccc	caaaggccaa	actctccact	ccctcagctc	ggacacccctc	tctctccca	1080
gatccagta	actcccaatc	ttctctctgc	agagccaaa	tcttgcaca	aaactcacac	1140
atgcccaccc	tgcccaggta	agccagccca	ggcctcgccc	tccagctaa	ggcgggacag	1200
gtgcctaga	gtagcctgca	tccagggaca	ggccccagcc	gggtgctgac	acgtccaccc	1260

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ccatctcttc	ctcagcacct	gaactcctgg	ggggaccgtc	agtcttctc	ttcccccaa	1320
aacccaagga	caccctcatg	atctcccgg	cccctgagggt	cacatgcgtg	gtggtgtggacg	1380
tgagccacga	agaccctgag	gtcaagttca	actggtacgt	ggacggcgtg	gagggtgcata	1440
atgccaagac	aaagccgcgg	gaggagcagt	acaacagcac	gtaccgtgtg	gtcagcgtcc	1500
tcaccgtct	gcaccaggac	tggctgaatg	gcaaggagta	caagtgcag	gtctccaaca	1560
aagccctccc	agccccatc	gagaaaacca	tctccaaagc	caaagggtggg	acccgtgggg	1620
tgcgagggcc	acatggacag	aggeccggctc	ggcccccacct	ctgcccgtag	agtgaccgct	1680
gtaccaacct	ctgtccctac	agggcagccc	cgagaaccac	aggtgtacac	cctgccccca	1740
tcccgggagg	agatgaccaa	gaaccaggtc	agcctgacct	gcctggtcaa	aggcttctat	1800
cccagcgaca	tcgccgtgga	gtgggagagc	aatgggcagc	cgggagaacaa	ctacaagacc	1860
acgcctcccc	tgctggactc	cgacggctcc	ttcttctct	atagcaagct	caccgtggac	1920
aagagcaggt	ggcagcaggg	gaacgtcttc	tcatgctccg	tgatgcata	ggctctgcac	1980
aaccactaca	cgcagaagag	cctctccctg	tcccccggta	aatga		2025

<210> SEQ ID NO 20

<211> LENGTH: 472

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: D1B5-hG1 Heavy chain

<400> SEQUENCE: 20

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1					5										15

Val	His	Ser	Leu	Glu	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val
					20										30

Arg	Ser	Gly	Ala	Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Phe	Asn
						35									45

Ile	Lys	Asp	Tyr	Tyr	Ile	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly
50					55										60

Leu	Glu	Trp	Ile	Gly	Trp	Ile	Asp	Pro	Glu	Ile	Gly	Ala	Thr	Lys	Tyr
65					70					75					80

Val	Pro	Lys	Phe	Gln	Gly	Lys	Ala	Thr	Met	Thr	Thr	Asp	Thr	Ser	Ser
						85			90						95

Asn	Thr	Ala	Tyr	Leu	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala
						100			105						110

Val	Tyr	Tyr	Cys	Asn	Ala	Leu	Tyr	Gly	Asn	Tyr	Asp	Arg	Tyr	Tyr	Ala
						115			120						125

Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Ala	Ser
							130		135						140

Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr
145						150				155					160

Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro
						165			170						175

Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val
						180			185						190

His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser
						195			200						205

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Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
210          215          220

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
225          230          235          240

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
245          250          255

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
260          265          270

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
275          280          285

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
290          295          300

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305          310          315          320

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
325          330          335

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
340          345          350

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
355          360          365

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
370          375          380

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385          390          395          400

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
405          410          415

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
420          425          430

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
435          440          445

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
450          455          460

Ser Leu Ser Leu Ser Pro Gly Lys
465          470

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<210> SEQ ID NO 21
<211> LENGTH: 2026
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: G2G4 63L1D Heavy chain (genomic sequence hG2G4)

<400> SEQUENCE: 21

atgggatgga gctgtatcat cctttcttg gtagcaacag ctacagggtt ccactcccg 60
atgcagctgg tgcaagtctgg ggctgagggtg aagaagcctg ggtcctcggt gaagggtctcc 120
tgcaaggcct ctggaggcac cttcagcaac tatgctacca gttgggtgcg acaggcccc 180
ggacaaggctc ttgagtggtt gggagggttc atccccgtct tccgtactgc aaactacgca 240
cagaagtttc agggcagagt caccattacc gcccacgact ccacgacgac agcctacatg 300
gagttgaata gtctgacatt tgacgacacg gccgtctatt actgtgcgag aggggggtggg 360
ggatggggag gccgaaacta ctactactac tactacatgg acgtctgggg caaaggggacc 420
actgtcaccg tctcctcagc ctccaccaag ggcccatccg tcttccccct ggcccccgtc 480

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tccaggagca cctccgagag cacagccgcc	ctgggtgcc	tttgtcaagga	ctacttcccc	540
gaaccgggtga cgggtgcgtg	gaactcaggc	gcccgtacca	gccccgtgca	600
gctgtcctac agtcctcagg	actctactcc	ctcagcagcg	tttgtgaccgt	660
aacttcggca cccagaccta	cacctgcaac	gtagatcaca	agccccagcaa	720
gacaagacag ttggtgagag	gccagctcg	ggagggaggg	tgtctgtgg	780
cagccctctt gcctggacgc	accccggtg	tgcagcccc	gcccaggggca	840
ccccatctgt ctctcaccc	ggaggccct	gcccggccca	ctcatgtca	900
cttctggctt tttccaccag	gctccaggca	ggcacaggct	gggtgcccct	960
cttcacacac aggggcagg	gcttggctca	gacctgcca	aagccatatac	1020
ctgccccctga cctaagccga	ccccaaaggc	caaactgtcc	actccctcag	1080
ttctctccctc ccagatccga	gttaactccca	atcttotctc	tgcagagcgc	1140
tcgagtgccc accgtgccc	ggtaagccag	cccaggcctc	gcccctccag	1200
acaggtgccc tagagtagcc	tgcattccagg	gacaggcccc	agctgggtgc	1260
acctccatct cttccctcagc	accacctgtg	gcaggaccgt	cagtcttcc	1320
aaacccaaagg acaccctcat	gatctcccg	acccctgagg	tcacgtgcgt	1380
gtgagccagg aagaccccg	ggtccagttc	aactggtacg	tggatggcgt	1440
aatgccaaga caaagccgcg	ggaggagcag	ttcaacagca	cgtaccgtgt	1500
ctcaccgtcc tgcaccagga	ctggctgaac	ggcaaggagt	acaagtgcaa	1560
aaaggccctcc cgccctccat	cgaaaaacc	atctccaaag	ccaaagggtgg	1620
gtgcgagggc cacatggaca	gaggtcagct	cggcccaccc	tctgcccgg	1680
tgtgccaacc tctgtcccta	cagggcagcc	ccgagagcca	caggtgtaca	1740
atcccaggag gagatgacca	agaaccagg	cagcctgacc	tgcctggta	1800
ccccagcgcac atgcgcgtgg	agtggagag	caatggcag	ccggagaaca	1860
cacgcctccc gtgctggact	ccgacggc	cttctccctc	tacagcaggc	1920
caagagcagg tggcaggagg	ggaatgtctt	ctcatgtcc	gtgatgtcatg	1980
caaccactac acacagaaga	gcctctccct	gtctctgggt	aaatgta	2026

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<210> SEQ ID NO 22
<211> LENGTH: 472
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: G2G4 63L1D Heavy chain

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<400> SEQUENCE: 22

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1					5				10					15	

Val	His	Ser	Gln	Met	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
				20				25					30		

Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe
				35				40				45			

Ser	Asn	Tyr	Ala	Thr	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
50					55				60						

Glu Trp Leu Gly Gly Ile Ile Pro Val Phe Gly Thr Ala Asn Tyr Ala

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65	70	75	80
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser			
85	90	95	
Thr Ala Tyr Met Glu Leu Asn Ser Leu Thr Phe Asp Asp Thr Ala Val			
100	105	110	
Tyr Tyr Cys Ala Arg Gly Gly Trp Gly Gly Arg Asn Tyr Tyr			
115	120	125	
Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val			
130	135	140	
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys			
145	150	155	160
Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys			
165	170	175	
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu			
180	185	190	
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu			
195	200	205	
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr			
210	215	220	
Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val			
225	230	235	240
Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro			
245	250	255	
Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro			
260	265	270	
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val			
275	280	285	
Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val			
290	295	300	
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln			
305	310	315	320
Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln			
325	330	335	
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly			
340	345	350	
Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro			
355	360	365	
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr			
370	375	380	
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser			
385	390	395	400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr			
405	410	415	
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr			
420	425	430	
Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe			
435	440	445	
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys			
450	455	460	
Ser Leu Ser Leu Ser Leu Gly Lys			
465	470		

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<210> SEQ ID NO 23
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Light Chain chC2aB7-hG1, human Ck

<400> SEQUENCE: 23

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atgggatgga gctgttatcat cctttcttg gtagcaacag ctacagggtgt ccactctaga      60
gacatccaga tgacacagtc tccatcttcc atgtatgcat ctctaggaga gagagtact      120
atcacttgca aggcgagtca ggacattaat agctatttaa gctggttcca gcagaaacca      180
gggaaatctc ctaagaccct gatctatcgt gcaaacagat tggtagatgg ggttccatca      240
aggttcagtg cgagtggatc tggcaagat tattctctca ccatcagcag cctggagat      300
gaagatatgg gaatttatta ttgtctacag tatgtatgat ttccgtacac gttcggaggg      360
gggaccaagc tggaaataaa acggactgtg gctgcaccat ctgtcttcat ctcccccca      420
tctgtatgac agttgaaatc tggaaactgcc tctgttgtgt gcctgctgaa taacttctat      480
cccagagagg ccaaagtaca gtggaaagggtg gataacgccc tccaatcggt taactccag      540
gagagtgtca cagacgagga cagcaaggac agcacctaca gcctcagcag caccctgacg      600
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcaggc      660
ctgagctcgc ccgtcacaaa gagttcaac agggagagt gttaa                         705

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<210> SEQ ID NO 24
<211> LENGTH: 234
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Light Chain chC2aB7-hG1, human Ck

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<400> SEQUENCE: 24
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10          15

Val His Ser Arg Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Met Tyr
20          25           30

Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
35          40           45

Ile Asn Ser Tyr Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro
50          55           60

Lys Thr Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser
65          70           75           80

Arg Phe Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser
85          90           95

Ser Leu Glu Tyr Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp
100         105          110

Glu Phe Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg
115         120          125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130         135          140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145         150          155           160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser

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165	170	175
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Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr		
180	185	190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys		
195	200	205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro		
210	215	220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
225	230	

<210> SEQ ID NO 25

<211> LENGTH: 711

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: hB7V4V1-hG1 light chain

<400> SEQUENCE: 25

atggacatga gggctctgc tcagctcctg gggctctgc tgctctggct ctcaggagcc	60
agatgtgaca tccagatgac acagtctcca tttccctgt ctgcatactat aggagacaga	120
gtcaatatca cttgcaaggc gagtcaggac attaatagct attaaagctg gtaccagcag	180
aaaccaggga aagctcttaa gtccctgatc tatcgtgcaa acagattgg agatggggtt	240
ccatcaaggt tcagtggcag tggatctggg acagattata ctctcaccat cagcagcctg	300
cagcctgaag atttcgcagt ttattattgt ctacagtatg atgagttcc gtacacgttc	360
ggagggggga ccaagctgga aataaacgt acggtggtg caccatctgt cttcatcttc	420
ccgccccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac	480
ttctatccca gagaggccaa agtacagtgg aagggtggata acgcctccca atcgggtAAC	540
tcccaggaga qtgtcacaga gcaggacagc aaggacagca cttacagcct cagcagcacc	600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgca agtcacccat	660
cagggcctga gctcgccctg cacaaagagc ttcaacaggg gagagtgtta g	711

<210> SEQ ID NO 26

<211> LENGTH: 236

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: hB7V4V1-hG1 Light chain (human Ck)

<400> SEQUENCE: 26

Met Asp Met Arg Val Ser Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp			
1	5	10	15

Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser		
20	25	30

Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser		
35	40	45

Gln Asp Ile Asn Ser Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys		
50	55	60

Ala Pro Lys Ser Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val			
65	70	75	80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr		
85	90	95

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Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Leu	Gln
100						105							110		
Tyr	Asp	Glu	Phe	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile
115						120							125		
Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp
130						135							140		
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn
145						150							155		160
Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu
													165		175
Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp
													180		190
Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr
													195		205
Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
													210		220
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
													225		235

<210> SEQ ID NO 27																
<211> LENGTH: 711																
<212> TYPE: DNA																
<213> ORGANISM: Artificial Sequence																
<220> FEATURE:																
<223> OTHER INFORMATION: hB7V3V2-hG1 Light Chain																
<400> SEQUENCE: 27																
atggacatga gggtctctgc tcagtcctg gggctcctgc tgcgtctggct ctcaggggcc															60	
aggtgtgaca tccagatgac acagtctcca tcttccctgt ctgcatactat aggagacaga															120	
gtcactatca cttgcaaggc gagtcaggac attaatagct atttaagctg gttccagcag															180	
aaaccaggga aagctctaa gctgctgatc tatcgatgaa acagattgg agatggggtt															240	
ccatcaaggt tcagtgccag tggatctggg acagattata ctctcaccat cagcagcctg															300	
cagcctgaag atttcgcagt ttattattgt ctacagttatc atgagttcc gtacacgttc															360	
ggagggggga ccaagctgaa aataaaaacgt acggtggtc caccatctgt cttcatcttc															420	
ccgccccatctg atgagcgtt gaaatctggc actgcctctg ttgtgtgcct gctgaataac															480	
ttcttatccca gagaggccaa agtacagtgg aaggtggata acggccctcca atcgggttaac															540	
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc															600	
ctgacgcgtg ccaaaggcaga ctacgagaaa cacaaggct acgcctgcga agtcacccat															660	
cagggcctga gctcgcccgat cacaaggcgc ttcaacaggg gagagtgtta g															711	

<210> SEQ ID NO 28																
<211> LENGTH: 236																
<212> TYPE: PRT																
<213> ORGANISM: Artificial Sequence																
<220> FEATURE:																
<223> OTHER INFORMATION: hB7V3V2-hG1 Light Chain (human Ck)																
<400> SEQUENCE: 28																

Met	Asp	Met	Arg	Val	Ser	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	
1				5				10						15		
Leu	Ser	Gly	Ala	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	
														20	25	30

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Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
 35           40           45

Gln Asp Ile Asn Ser Tyr Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys
 50           55           60

Ala Pro Lys Leu Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val
65           70           75           80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
85           90           95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln
100          105          110

Tyr Asp Glu Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
115          120          125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130          135          140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145          150          155          160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165          170          175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180          185          190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195          200          205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
210          215          220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225          230          235

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<210> SEQ ID NO 29
<211> LENGTH: 708
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: ChC7-hG2G4 Light chain

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<400> SEQUENCE: 29

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atgggatgga gctgtatcat cctttcttg gtagcaacag ctacagggtgt ccactctaga   60
gaaattgtgc tcacccagtc tccagcaatc atgtctgcattt ctccaggggaa aaaggtcacc 120
atgacctgca gggccagctc aagtgttaatc tccagttact tgcaactggta ccagcagaag 180
tcaggtgcct cccccaaact ctggatttat agcacatcca acttggcttc tggagtccct 240
gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagtgtggag 300
gctgaagatg ctgccactta ttactgccag cagtagtgcgtt gttacccact cacgttcggc 360
tcggggacaa agttggaaat aaaacggact gtggctgcac catctgtctt catcttcccg 420
ccatccgatg agcagttgaa atctggaaact gctctgttg tggctgtctt gaataacttc 480
tatcccagag aggccaaatg acagtggaaat gtggataacg ccctccaatc gggtaactcc 540
caggagatgt tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaatgtt caccatcag 660
ggcctgatgtt cggccgtcac aaagagcttc aacaggggag agtgtttaa 708

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<210> SEQ ID NO 30

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<211> LENGTH: 235
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: ChC7-hG2G4 Light chain (human Ck)

<400> SEQUENCE: 30

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5          10          15

Val His Ser Arg Glu Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser
20          25          30

Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser
35          40          45

Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Lys Ser Gly Ala Ser
50          55          60

Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
65          70          75          80

Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85          90          95

Ser Ser Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr
100         105         110

Ser Gly Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
115         120         125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130         135         140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145         150         155         160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165         170         175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180         185         190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195         200         205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210         215         220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225         230         235

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<210> SEQ ID NO 31
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: D1B5-hG1 Light chain

<400> SEQUENCE: 31

atgggatgga gctgttatcat cctttcttg gtagcaacag ctacagggtt ccactctaga    60
gacattgtga tgacccagtc tcaaaaattc atgtccacat cagtaggaga cagggtcagc   120
atcacctgca aggccagtca gaatgttcgt actgtctgt tagctggatca acagaaacca   180
gggcagtctc ctaaagcaact gatttacttg gcataccaacc ggcacactgg agtccctgat  240
cgcttcacag gcagtggatc tgggacagat ttcaactctca ccatttagcaa tgtgcaatct 300
gaagacctgg cagatttattt ctgtctgcaa cattggaatt atcctctcac gttcggtgct  360
gggaccaagc tggagctgaa acggactgtg gctgcaccat ctgtcttcat cttcccgcca  420

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tctgatggc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttcat	480
cccaagaggc ccaaagtaca gtggaaagggtg gataacgcgg tccaatcgaaa taactccagg	540
gagagtgtca cagagcaggaa cagcaaggac agcacctaca gcctcagcaa caccctgacg	600
ctgagcaaaggc cagactacgaa gaaacacaaaa gtctacgccc gcgaagtcac ccatcaggc	660
ctgagctcgcc cccgtccaaaa gagcttcaac agggggagagt gttaa	705

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<210> SEQ ID NO 32
<211> LENGTH: 234
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: D1B5-hG1 Light chain (human Ck)
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<400> SEQUENCE: 32

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10          15

Val His Ser Arg Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser
20          25          30

Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn
35          40          45

Val Arg Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
50          55          60

Lys Ala Leu Ile Tyr Leu Ala Ser Asn Arg His Thr Gly Val Pro Asp
65          70          75          80

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85          90          95

Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Leu Gln His Trp
100         105         110

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Asn Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
 115 120 125
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 180 185 190

Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

225 230

```
<210> SEQ ID NO 33
<211> LENGTH: 696
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
  333 OTHER INFORMATION: GCG4-6CL1D_Light_chain
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<400> SEQUENCE: 33

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atgggatgga gctgttatcat ccttttttg gtagcaacag ctacagggtt ccactttcc	60
tatgtgctga ctcageccacc ctcggagtca gtggccccag gacagacggc caggattcc	120
tgtggggggaa gcaacattgg aagttacggt gtgcactggt accagcgaa ggcaggacag	180
gcccctgtgc tggtcgtcca tcatgattcc gaccggccct cagggattcc tgagcgattc	240
tctggctcca attctggaa cacggccacc ctgaccatca gcagtgtcga agccggcgat	300
gaggccgact attactgtca ggtgtggat aatagtgtc tgatattcgg cggagggacc	360
aaactaaccg tcctaagtca gcccaaggct gccccctcg tcaactctgtt cccgcctcc	420
tctgaggagc ttcaagccaa caaggccaca ctgggtgtc tcatatagtga cttctacccg	480
ggagctgtga cagtggcttg gaaagcagat agcagcccg tcaaggcggg agtggagacc	540
accacaccct ccaaacaag caacaacaag tacggggcca gcagctatct gagectgacg	600
cctgagcagt ggaagtccca cagaagctac agctgccagg tcacgcattga agggagcacc	660
gtggagaaga cagtggcccc tacagaatgt tcataaa	696

<210> SEQ ID NO 34
<211> LENGTH: 231
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: G2G4 63L1D Light chain (human CL)

<400> SEQUENCE: 34

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15
Val His Ser Ser Tyr Val Leu Thr Gln Pro Pro Ser Glu Ser Val Ala			
20	25	30	
Pro Gly Gln Thr Ala Arg Ile Ser Cys Gly Gly Ser Asn Ile Gly Ser			
35	40	45	
Tyr Gly Val His Trp Tyr Gln Gln Lys Ala Gly Gln Ala Pro Val Leu			
50	55	60	
Val Val His Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe			
65	70	75	80
Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Ser Val			
85	90	95	
Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Ser			
100	105	110	
Ala Val Ile Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro			
115	120	125	
Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu			
130	135	140	
Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro			
145	150	155	160
Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala			
165	170	175	
Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala			
180	185	190	
Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg			
195	200	205	
Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr			
210	215	220	

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Val Ala Pro Thr Glu Cys Ser
225 230

<210> SEQ ID NO 35
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: forward primer

<400> SEQUENCE: 35

gacaagcttg caaggatgga gaggctggta a 31

<210> SEQ ID NO 36
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: reverse primer

<400> SEQUENCE: 36

gacggatccg cccctttcc tcctgtttt ctc 33

<210> SEQ ID NO 37
<211> LENGTH: 2160
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: chC2aB7-hG1 Heavy chain

<400> SEQUENCE: 37

gcgcgcacc	agacataata	gctgacagac	taacagactg	tccctttcca	tgggtctttt	60
ctgcagtca	cgtccttgac	acgaggcgcg	ccgccaccat	gggatggagc	tgtatcatcc	120
tcttcttgtt	agcaacagct	acagggtgtcc	actccctcga	ggtccagctg	caacagtctg	180
gacctgagct	ggtgaagcct	ggggcttac	tgaagatgtc	ctgcaaggct	tctggttatt	240
cattcactga	ctacatcata	ctctgggtga	agcagaacca	tggaaagagc	cttgagtgga	300
ttggacatat	tgtatcattac	tatggtagtt	ctaactacaa	tctgaaattc	aaggcaagg	360
ccacattgac	tgttagacaaa	tcttccagca	cagcctacat	gcagctcaac	agtctgacat	420
ctgaggactc	tgcagtctat	tactgtggaa	gatctaagag	ggactacttt	gactactggg	480
gccaaggcac	cactctcaca	gtttcctcag	cctccaccaa	gggccatcg	gtttcccccc	540
tggcacccctc	ctccaagagc	acctctggcg	gcacagcgcc	cctgggctgc	ctggtaagg	600
actaattccc	cgaaccggtg	acgggtgttgt	ggaactcagg	cgcctgacc	agcggcggtc	660
acaccttccc	ggctgtctca	cagtcctcag	gactctactc	cctcagcagc	gtggtgaccg	720
tgccctccag	cagcttgggc	acccagacct	acatctgcaa	cgtgaatcac	aagcccagca	780
acaccaaggt	ggacaagaga	gttggtgaga	ggccagcaca	gggagggagg	gtgtctgtcg	840
gaagccaggc	tcaagcgctcc	tgcctggacg	catcccggt	atgcagtccc	agtccagggc	900
agcaaggcag	gccccgtctg	cctcttcacc	cggaggcctc	tgcctggccc	actcatgctc	960
agggagaggg	tcttctggct	ttttccccag	gctctggcga	ggcacaggct	aggtgcct	1020
aaccaggccc	ctgcacacaa	agggcaggt	gctgggctca	gacctgccaa	gagccatatc	1080
cgggaggacc	ctgccccctga	cctaagccca	ccccaaaggc	caaactctcc	actccctcag	1140
ctcggacacc	ttctctcctc	ccagattcca	gtaactccca	atcttctctc	tgcagagccc	1200

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aaatcttgtg	acaaaactca	cacatgccca	ccgtgcccag	gtaagccagc	ccaggcctcg	1260
ccctccagct	caaggcggga	caggtgcct	agagtgcct	gcatccagg	acaggcccc	1320
gcccgggtct	gacacgtcca	cctccatctc	ttcctcagca	cctgaactcc	tgggggacc	1380
gtcagtcttc	ctttcccc	caaaaaccaa	ggacacccct	atgatctccc	ggacccctga	1440
ggtcacatgc	gtgggtgtgg	acgtgagcc	cgaagaccc	gaggtaagt	tcaactggta	1500
cgtggacggc	gtggaggtgc	ataatgccaa	gacaaagccg	cgggaggagc	agtacaacag	1560
cacgtaccgt	gtggtcagcg	tcctcaccgt	cctgcaccag	gactggctga	atggcaagg	1620
gtacaagtgc	aaggctccca	acaaagccct	cccagcccc	atcgagaaaa	ccatctccaa	1680
agccaaaggt	gggacccgtg	gggtgcgagg	gccacatgga	cagaggccgg	ctcgccccac	1740
cctctgcct	gagagtgacc	gctgtaccaa	cctctgtccc	tacagggcag	ccccgagaac	1800
cacaggtgt	caccctgccc	ccatccccc	aggagatgac	caagaaccag	gtcagcctga	1860
cctgccttgt	caaaggcttc	tatcccagcg	acatcccg	ggagtgggag	agcaatggc	1920
agccggagaa	caactacaag	accacgcctc	ccgtgctgga	ctccgacggc	tccttctcc	1980
tctatagcaa	gctcaccgtg	gacaagagca	ggtggcagca	ggggAACGTC	ttctcatgct	2040
ccgtgtatgca	tgaggctctg	cacaaccact	acacgcagaa	gagcctctcc	ctgtccccgg	2100
gtaaatgagt	gcgacggcca	gaattcattt	atcataatca	gccataccac	attttagag	2160

<210> SEQ ID NO 38
<211> LENGTH: 720
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: chC2aB7-hG1 Light chain

<400> SEQUENCE: 38

aagcttgcgg	ccaccatggg	atggagctgt	atcatcctct	tcttggtagc	aacagctaca	60
ggtgtccact	ctagagacat	ccagatgaca	cagtctccat	cttccatgt	tgcatactcta	120
ggagagagag	tcactatcac	ttgcaaggcg	agtcaggaca	ttaatagcta	tttaagctgg	180
ttccagcaga	aaccaggaa	atctcctaag	accctgatct	atcgtcAAA	cagattggta	240
gatggggttc	catcaagggtt	cagtggcagt	ggatctgggc	aagattatttc	tctcaccatc	300
agcagcctgg	agtatgaaga	tatggaaatt	tattattgtc	tacagtgat	tgagtttccg	360
tacacgttcg	gaggggggac	caagctggaa	ataaaacgga	ctgtggctgc	accatctgtc	420
ttcatcttcc	cgccatctga	tgagcagttg	aatctggaa	ctgcctctgt	tgtgtgcctg	480
ctgaataact	tctatcccag	agaggccaaa	gtacagtgg	aggtggataa	cgcctccaa	540
tcggtaact	cccaggagag	tgtcacagag	caggacagca	aggacagcac	ctacagcctc	600
agcagcaccc	tgacgctgag	caaagcagac	tacgagaaac	acaaagtcta	cgcctgcgaa	660
gtcaccctatc	agggcctgag	ctcgccccgt	acaaagagct	tcaacagggg	agagtgttaa	720

<210> SEQ ID NO 39
<211> LENGTH: 1402
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hB7V4V1-hG1 Heavy chain

<400> SEQUENCE: 39

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catggatgg agctggatct ttctttct cctgtcagta actgcaggta tggttctctga	60
ggtccagctg gtggagtcgg gacctgaggt gaagaaggct ggggcttcag tgaagggtgc	120
ctgcaaggct tctggatttatt cattcaactga ctacatcata ctctggatca ggcagcatag	180
cggaaaggcg cttgagtgga ttggacatat tgatccttac tatggtagtt ctaactacaa	240
tctgaaattc aaggcgagg tcacaatcac tgcaagacaaa tctaccaggaa caacctacat	300
ggagctcacc agtctgacat ctgaggacac tgcaagtctat tactgtggaa gatctaagag	360
ggactacttt gactactggg gccaaaggcac cacttcaca gtttccctcag cctccaccaa	420
ggggccatcg gtcttcccgc tagcaccctc ctccaagagc acctctgggg gcacagcggc	480
cctgggctgc ctggtaagg actactccc cgaaccggtg acgggtgcgt ggaactcagg	540
cgcctgacc agcggcgtgc acacccccc ggctgtccta cagtcctcag gactctactc	600
cctcagcago gtggtgaccg tgccctccag cagcttgggc acccagaccc acatctgcaa	660
cgtgaatcac aagccccagca acaccaaggt ggacaagaga gttgagccca aatcttgta	720
caaaaactcac acatgcccac cgtccccagc acctgaactc ctggggggac cgtcagtctt	780
cctttcccc ccaaaaccca aggacacccct catgatctcc cggacccctg aggtcacatg	840
cgtggtggtg gacgtgagcc acgaagaccc tgaggtaag ttcaactggt acgtggacgg	900
cgtggagggtg cataatgcca agacaaagcc gcggggaggag cagtacaaca gcacgtaccc	960
tgtggtcago gtcttcaccc tcctgcacca ggactggctg aatggcaagg agtacaagt	1020
caaggctctcc aacaaagccc tcccgcccc catcgagaaa accatctcca aagccaaagg	1080
gcagccccga gaaccacagg tgtacaccct gccccatcc cgggaggaga tgaccaagaa	1140
ccaggtcagc ctgacctgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg	1200
ggagagcaat gggcagccgg agaacaacta caagaccacg cctccctgc tggactccga	1260
cggtcccttc ttctctaca gcaagctcac cggtgacaag agcagggcgc agcaggggaa	1320
cgtttctca tgctccgtga tgcatgaggc tctgcacaaac cactacacgc agaagagect	1380
ctccctgtct ccgggtaaat ga	1402

<210> SEQ ID NO 40
<211> LENGTH: 765
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hB7V4V1-hG1 and hB7V3V1-hG1 Light chains

<400> SEQUENCE: 40	
tttccatggg tcttttctgc agtacccgtc cttgacacga agcttgcgc caccatggac	60
atgagggtct ctgctcagct cctggggctc ctgctctct ggctctcagg agccagatgt	120
gacatccaga tgacacagtc tccatcttcc ctgtctgcat ctataggaga cagagtca	180
atcacttgca aggcgagtca ggacattaat agctatattaa gctggatcca gcagaaacca	240
gggaaagctc ctaagtcct gatctatcgt gcaaacagat tggtagatgg ggttccatca	300
aggttcagtg gcagtggatc tggacagat tatactctca ccatcagcag cctgcagect	360
gaagatttcg cagtttatta ttgtctacag tatgtatgtt ttccgtacac gtccggagg	420
gggaccaagc tggaaataaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca	480
tctgtatgac agttgaaatc tggaaactgcc tctgttgttgc gcctgctgaa taacttctat	540

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cccaagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggt taactcccag	600
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg	660
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtac ccacaggc	720
ctgagctgc ccgtcacaaa gagttcaac aggggagagt gttag	765

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<210> SEQ ID NO 41
<211> LENGTH: 1402
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hB7V3V1-hG1 and hB7V3V2-hG1 Heavy chains

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<400> SEQUENCE: 41	
catgggatgg agccggatct ttcttttctt cctgtcaata attgcagggtg tccattgc	60
ggtccagctg caacagtctg gatctgagct gaagaaggct ggggcttcag tgaagatctc	120
ctgcaaggct tctggttatt cattcactga ctacatcata ctctgggtga ggcagaaccc	180
tggaaagggc cttgagtgga ttggacatat tgatccttac tatggtagtt ctaactacaa	240
tctgaaattc aagggcagag tgacaatcac cgccgaccag tctaccacca cagcctacat	300
ggagctctcc agtctgagat ctgaggacac tgcagtctat tactgtggaa gatctaagag	360
ggactacttt gactactggg gccaaggcac cacttcaca gttcctcag cttccaccaa	420
ggggccatcg gtottccgc tagcaccctc ctccaagago acctctgggg gcacagcggc	480
cctgggctgc ctggcaggacttccc cgaaccgggtg acgggtgcgt ggaactcagg	540
cgccctgacc agccggcgtgc acaccttccc ggctgtccata cagtcctcag gactctactc	600
cctcagcagc gtgggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa	660
cgtgaatcac aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgta	720
caaaaactcac acatgcccac cgtcccccgc acctgaactc ctggggggac cgtcagtctt	780
cctttccccc caaaaaccca aggacacccct catgatctcc cggaccctcg aggtcacatg	840
cgtgggtggtg gacgtgagcc acgaagaccc tgaggcataag ttcaactggt acgtggacgg	900
cgtggagggtg cataatgccca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg	960
tgtggtcagc gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg	1020
caaggctctcc aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg	1080
gcagccccga gaaccacagg tgtacaccct gccccatcc cgggaggaga tgaccaagaa	1140
ccaggtcagc ctgacccgtcc tggtaaaagg cttctatccc agcgcacatcg ccgtggagtg	1200
ggagagcaat gggcagccgg agaacaacta caagaccacg cttcccggtc tggactccga	1260
cggctcccttc ttcccttaca gcaagctcac cgtggacaag agcaggtggc agcagggaa	1320
cgtcttcata tgctccgtga tgcataggc tctgcacaaac cactacacgc agaagagcct	1380
ctccctgtct ccgggtaat ga	1402

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<210> SEQ ID NO 42
<211> LENGTH: 765
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hB7V3V2-hG1 and hB7V3V2-hG2G4 Light chains

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<400> SEQUENCE: 42

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tttccatggg tctttctgc agtcaccgtc cttgacacga agttgccgc caccatggac	60
atgagggtct ctgctcagct cctggggctc ctgctgcct ggctctcagg ggccaggtgt	120
gacatccaga tgacacagtc tccatcttcc ctgtctgcat ctataggaga cagagtca	180
atcacttgca aggcgagtca ggacattaat agctattaa gctggttcca gcagaaacca	240
gggaaaagctc ctaagctgct gatctatcgt gcaaacagat tggtagatgg ggttccatca	300
aggttcagtg gcagtggtac tgggacagat tatactctca ccatcagcag cctgcagecct	360
gaagatttcg cagtttatta ttgtctacag tatgtatgatg ttccgtacac gtccggaggg	420
gggaccaagc tgaaataaaa acgtacggtg gctgcaccat ctgtcttcat ctccccgcca	480
tctgtatgac agttgaaatc tggaaactgcc tctgttgtgt gcctgctgaa taacttctat	540
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactccag	600
gagagtgtca cagagcagga cagaaggac agcacotaca gcctcagcag caccctgacg	660
ctgagcaaag cagactacga gaaacacaaa gtctacgct gcgaagtca ccatcaggc	720
ctgagctcgc ccgtcacaaa gagcttcaac agggagagt gttag	765

<210> SEQ ID NO 43

<211> LENGTH: 2159

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: hB7V3V2-hG2G4 Heavy chain

<400> SEQUENCE: 43

ccaccagaca taatagctga cagactaaca gactgttctt ttccatgggt cttttctgca	60
gtcacccgtcc ttgacacgaa gcttgccgcc accatggat ggagccggat ctttctttc	120
ctcctgtcaa taattgcagg tgtccattgc caggtccagc tgcaacagtc tggatctgag	180
ctgaagaagc ctggggcttc agtgaagatc tcctgcaagg cttctggta ttcatctact	240
gactacatca tactctgggt gaggcagaac cctggaaagg gccttgatgt gattggacat	300
attgatccctt actatggtag ttctaactac aatctgaaat tcaagggcag agtgacaatc	360
accggccgacc agtctaccac cacagcctac atggagctct ccagtcgtag atctgaggac	420
actgcagtct attactgtgg aagatctaag agggactact ttgactactg gggccaaggc	480
accactctca cagtttcttc agcctccacc aaggggccat ccgtcttccc cctggcgccc	540
tgctccagga gcacccctca gagcacagcc gccctgggt gcctggtcaa ggactacttc	600
cccgaaaccgg tgacgggtgc gtggaactca ggcgccttgc ccagcggcgt gcacaccttc	660
ccggctgtcc tacagtcttc aggactctac tccctcagca gcgtggtgac cgtccctcc	720
agcaacttcg gcacccagac ctacacctgc aacgttagatc acaagcccag caacaccaag	780
gtggacaaga cagttggta gaggccagct cagggaggga gggtgtctgc tggaaagccag	840
gctcagccct cctgccttgc cgaccccccgg ctgtcagcc ccagccagg gcagcaaggc	900
aggccccatc tgtctctca cccggaggcc tctgcccggcc ccactcatgc tcagggagag	960
ggtcttctgg cttttccac caggctccag gcaggcacag gctgggtgcc cctacccca	1020
gcccttcaca cacagggca ggtcttggc tcagacctgc caaaagccat atccggagg	1080
accctgcccc tgacctaagc cgacccaaa ggccaaactg tccactccct cagtcggac	1140
accttctctc ctcccagatc cgagtaactc ccaatcttct ctctgcagag cgcaaatgtt	1200

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gtgtcgagtgc	cccacccgtgc	ccaggtaagc	cagccccaggc	ctcgccctcc	agctcaaggc	1260
gggacagggtgc	cccttagagta	gcctgcatcc	agggacaggc	cccgctgggt	gctgacacgt	1320
ccacacctccat	cttttcctca	gcaccacctg	tggcaggacc	gtcagtttcc	ctttcccccc	1380
caaaaacccaa	ggacacccctc	atgatctccc	ggacccctga	ggtaacgtgc	gtggtggtgg	1440
acgtgagccaa	ggaagacccc	gaggtccagt	tcaactggta	cgtggatggc	gtggaggtgc	1500
ataatgcca	gacaaagccg	cgggaggaggc	agttcaacag	cacgtaccgt	gtggtcagcg	1560
tcctcaccgt	cctgcaccag	gactggctga	acggcaagg	gtacaagtgc	aaggcttcca	1620
acaaaaggcct	cccgcttcc	atcgagaaaa	ccatctccaa	agccaaaggt	gggacccacg	1680
gggtgcgagg	gccacatgga	cagaggtcag	ctcgcccad	cctctgcctt	gggagtgacc	1740
gctgtccaa	cctctgtccc	tacagggcag	ccccgagago	cacaggtgt	caccctgccc	1800
ccatcccagg	aggagatgac	caagaaccag	gtcagoctga	cctgcctgg	caaaggcttc	1860
taccccagcg	acatgcgcgt	ggagtgggag	agcaatggc	agccggagaa	caactacaag	1920
accacgcctc	ccgtgctgga	ctccgacggc	tccttcttcc	tctacagcag	gctaaccgtg	1980
gacaagagca	ggtggcagga	ggggaatgtc	ttctcatgt	ccgtgatgca	tgaggctctg	2040
cacaaccact	acacacagaa	gagcctctcc	ctgtctctgg	gtaaatgtat	agaatttcatt	2100
gatcataatc	agccatacca	catttgtaga	ggttttactt	gctttaaaaa	acctcccac	2159

<210> SEQ ID NO: 44
 <211> LENGTH: 1600
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: chC2aB7-hG2G4 Heavy chain

<400> SEQUENCE: 44						
gctgacagac	taacagactg	ttccttcca	tgggtctttt	ctgcagtcac	cgtccttgac	60
acgaggcgcg	ccgcccacat	gggatggagc	tgtatcatcc	tcttcttgg	agcaacagct	120
acaggtgtcc	actccctcg	ggtccagctg	caacagtctg	gacctgagct	ggtgaagecct	180
ggggcttac	tgaagatgtc	ctgcaaggct	tctggattt	cattca	ctacatcata	240
ctctgggtga	agcagaacca	tggaaagagc	ctttagtgg	ttggacat	tgatccttac	300
tatggtagtt	ctaactacaa	tctgaaattc	aaggcaagg	ccacattgac	tgtagacaaa	360
tcttccagca	cagcctacat	gcagctcaac	agtctgacat	ctgaggactc	tgcagtctat	420
tactgtggaa	gatctaagag	ggactacttt	gactactgg	gccaaggcac	cactctcaca	480
gtttcctcag	cctccaccaa	gggeccatcc	gtcttcccc	tggcgccctg	ctccaggagc	540
acctccgaga	gcacagccgc	cctgggctgc	ctggtaagg	actactccc	cgaaccggtg	600
acgggtgtcgt	ggaactcagg	cgcctgtacc	agcggcgtgc	acacccccc	ggctgtccta	660
cagtccctcag	gactctactc	cctcagcagc	gtggtgaccg	tgcctccag	caacttcggc	720
acccagaccc	acacctgaa	cgtagatcac	aagcccagca	acaccaaggt	ggacaagaca	780
gttggtgaga	ggccagctca	gggagggagg	gtgtctgt	gaagccaggc	tcagccctcc	840
tgcctggacg	caccccggt	gtgcagcccc	agcccaggc	agcaaggcag	gccccatctg	900
tctcctcacc	cggaggcctc	tggccgcccc	actcatgctc	agggagaggg	tcttctggct	960
ttttccacca	ggctccaggc	aggcacaggc	tgggtgcccc	taccccaggc	cttcacaca	1020

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caggggcagg tgcttggctc agacctgcca aaagccatat ccgggaggac cctgccccctg 1080
acctaagccg accccaaagg ccaaactgtc cactccctca gctcgacac ctttcctct 1140
cccagatccg agtaactccc aatcttctct ctgcagagcg caaatgtgt gtgcagtgcc 1200
cacctgtgcc aggttaagcca gcccaggcct cgccctccag ctcaggcg gacaggtgcc 1260
cttagatgtc ctgcacatccag ggacagggccc cagctgggtg ctgcacacgtc cacctccatc 1320
tcttcctcag caccacctgt ggcaggaccg tcagtcttcc tcttcccccc aaaacccaag 1380
gacaccctca tgatctcccg gaccctcgag gtcacgtcg tggtgggtga cgtgagccag 1440
gaagaccccg aggtccagtt caactggta cttggatggcg tggaggtgca taatgccaag 1500
acaaagccgc gggaggagca gttcaaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1560
ctgcaccagg actggctgaa cggcaaggag tacaagtgc 1600
```

<210> SEQ ID NO 45

<211> LENGTH: 337

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: chC2aB7-hG2G4 Heavy chain

<400> SEQUENCE: 45

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1					5						10				15

Val	His	Ser	Leu	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val
					20				25				30		

Lys	Pro	Gly	Ala	Ser	Leu	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser
35					40					45					

Phe	Thr	Asp	Tyr	Ile	Ile	Leu	Trp	Val	Lys	Gln	Asn	His	Gly	Lys	Ser
50					55				60						

Leu	Glu	Trp	Ile	Gly	His	Ile	Asp	Pro	Tyr	Tyr	Gly	Ser	Ser	Asn	Tyr
65					70				75			80			

Asn	Leu	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser
						85			90			95			

Ser	Thr	Ala	Tyr	Met	Gln	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala
					100				105			110			

Val	Tyr	Tyr	Cys	Gly	Arg	Ser	Lys	Arg	Asp	Tyr	Phe	Asp	Tyr	Trp	Gly
115					120				125						

Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
130					135				140						

Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
145					150				155			160			

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
						165			170			175			

Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
						180			185			190			

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
						195			200			205			

Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
210					215				220						

Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Arg	Lys	Cys	Cys
225					230				235			240			

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Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val
245															255

Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
260															270

Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
275															285

Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
290															300

Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
305															320

Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
325															335

Cys

<210> SEQ ID NO 46

<211> LENGTH: 735

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: chC2aB7-hG2G4 Light chain

<400> SEQUENCE: 46

aagcttgccg	ccaccatggg	atggagctgt	atcatcctct	tcttggtagc	aacagctaca	60
ggtgtccact	cttagagacat	ccagatgaca	cagtctccat	cttccatgtta	tgcatactagg	120
agagagagtc	actatcaccc	gcaaggcgag	tcaggacatt	aataagctatt	aagctggttc	180
cagcagaaac	cagggaaatc	tcctaagacc	ctgatctatac	gtgcaaacag	attggtagat	240
ggggttccat	caagggttcag	tggcagtgga	tctggcaag	attattctct	caccatcagc	300
agcctggagt	atgaagatat	gggaatttat	tattgtctac	agtatgtga	gtttccgtac	360
acgttccggag	gggggaccaa	gctggaaata	aaacggactg	tggctgcacc	atctgtcttc	420
atcttcccgc	catctgatga	gcagttgaaa	tctggactg	cctctgttgt	gtgcctgtcg	480
aataacttct	atcccagaga	ggccaaagta	cagtggaaagg	tggataaacgc	cctccaaatcg	540
ggtaactccc	aggagagtgt	cacagagcag	gacagcaagg	acagcaccta	cagcctcagc	600
agcacccctga	cgttgagcaa	agcagactac	gagaaacaca	aagtctacgc	ctgcaagtc	660
acccatcagg	gcctgagctc	gcccgatcaca	aagagcttca	acaggggaga	gtgttcagcg	720
gccgcaattc	attga					735

<210> SEQ ID NO 47

<211> LENGTH: 240

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: chC2aB7-hG2G4 Light chain

<400> SEQUENCE: 47

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1															15

Val	His	Ser	Arg	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Met	Tyr
20															30

Ala	Ser	Leu	Gly	Glu	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp
35															45

Ile Asn Ser Tyr Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro

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50	55	60	
Lys Thr Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser			
65	70	75	80
Arg Phe Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser			
85	90	95	
Ser Leu Glu Tyr Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp			
100	105	110	
Glu Phe Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg			
115	120	125	
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln			
130	135	140	
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr			
145	150	155	160
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser			
165	170	175	
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr			
180	185	190	
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys			
195	200	205	
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro			
210	215	220	
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Ser Ala Ala Ala Ile His			
225	230	235	240

<210> SEQ ID NO 48
<211> LENGTH: 1560
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hB7V3V2-cG2G4 Heavy chain

<400> SEQUENCE: 48

ccaccagaca	taatagctga	cagactaaca	gactgttctt	ttccatgggt	cttttctgca	60
gtcacccgtcc	ttgacacgaa	gcttgccgcc	accatggat	ggagccggat	ctttctcttc	120
ctcctgtcaa	taattgcagg	tgtccattgc	caggtccago	tgcaacagtc	tggatcttag	180
ctgaagaagc	ctggggcttc	agtgaagata	tcctgcaagg	cttctggta	ttcattcact	240
gactacatca	tactctgggt	gaggcagaac	cctggaaagg	gccttgatgt	gattggacat	300
attgatccctt	actatggtag	ttctaactac	aatctgaaat	tcaagggcag	agtgacaatc	360
accggccgacc	agtctaccac	cacagcctac	atggagctct	ccagtctgag	atctgaggac	420
actgcagtct	attactgtgg	aagatctaag	agggactact	ttgactactg	gggccaaggc	480
accactctca	cagtttcctc	agcctccacc	aagggccat	ccgtttcccc	ctggcgcccc	540
tgctccagga	gcacccctcg	gagcacagcc	gcccctgggt	gcctggtaa	ggactacttc	600
cccgaaacctg	tgacgggtgtc	gtggaaactca	ggcgccctga	ccagcggcg	gcaccccttc	660
ccggctgtcc	tacagtcttc	aggactctac	tccctcagca	cgctggtgac	cgtccccctcc	720
agcaacttcg	gcacccagac	ctacacccctgc	aacgttagata	acaagcccag	caacaccaag	780
gtggacaaga	cagttgagcg	caaatagttgt	gtcgagtgtcc	caccgtgccc	agcaccaccc	840
gtggcaggac	cgtcagtcgtt	cctcttcccc	caaaaaccca	aggacaccct	catgatctcc	900
cggaccctcg	aggtcacgtg	cgtgggtggtg	gacgtgagcc	aggaagaccc	cgagggtccag	960

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ttcaactgg	acgtggatgg	cgtggagggtg	cataatgcc	agacaaagcc	gcggggaggag	1020
cagttcaaca	gcacgttaccg	tgtggtcagc	gtcctcaccc	tcctgcacca	ggactggctg	1080
aacggcaagg	agtacaagtg	caaggcttcc	aacaaaggcc	tcccgttctc	catcgagaaa	1140
accatctcca	aagccaaagg	gcagccccga	gagccacagg	tgtacaccct	gccccatcc	1200
caggaggaga	tgaccaagaa	ccaggttcgc	ctgacotgco	tggtaaagg	cttcttacccc	1260
agcgacatcg	ccgtggagt	ggagagcaat	gggcagccgg	agaacaacta	caagaccacg	1320
cctccgtgc	tggactccga	cggctcttc	ttcctctaca	gcaggcta	cgtggacaag	1380
agcaggtggc	aggaggggaa	tgtttctca	tgctccgtga	tgcatgaggc	tctgcacaac	1440
cactacacac	agaagagcct	ctccctgtct	ctgggtaat	gatgagaatt	cattgatcat	1500
aatcagccat	accacatgg	tagaggttt	acttgctta	aaaaacctcc	cacacccccc	1560

<210> SEQ ID NO 49

<211> LENGTH: 772

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: hB7V3V2-cG2G4 Light chain

<400> SEQUENCE: 49

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catggacatg	agggtctctg	ctcagtcct	ggggctcctg	ctgtctggc	tctcaggggc	120
caggtgtgac	atccagatga	cacagtctcc	atcttccctg	tctgcacatca	taggagacag	180
agtcaatc	acttgcaagg	cgagtcagga	cattaatagc	tatthaagct	ggttccagca	240
gaaaccagg	aaagctccta	agctgctgat	ctatcgtgca	aacagattgg	tagatgggg	300
tccatcaagg	ttcagtgca	gtggatctgg	gacagattat	actctcacca	tcagcagcct	360
gcagectgaa	atttcgcag	tttattattg	tctacagtat	gatgagttc	cgtacacgtt	420
cgaggggggg	accaagctgg	aaataaaacg	tacggtggt	gcaccatctg	tcttcatctt	480
ccgcacatct	gatgagcagt	tgaatctgg	aactgcctct	gttgtgtgcc	tgctgaataa	540
cttctatccc	agagaggcca	aagtacatgt	gaaggtggat	aacgcctcc	aatcggttaa	600
ctcccaggag	agtgtcacag	agcaggacag	caaggacago	acctacagcc	tcagcagcac	660
cctgacgctg	accaaagcag	actacgagaa	acacaaagtc	tacgcctgco	aagtccaccca	720
tcagggcctg	agctcgcccg	tcacaaagag	cttcaacagg	ggagagtgtt	ag	772

<210> SEQ ID NO 50

<211> LENGTH: 2158

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: DIB5-hG1 Heavy chain

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ctgcagtcac	cgtccttgac	acgaggcgcg	cgcgcaccat	gggatggagc	tgtatcatcc	120
tcttcttgg	agcaacagct	acagggtgtcc	actccctcga	ggtccaaactg	cagcagcctg	180
gggcagagct	tgtgaggtca	ggggcctcag	tcaagttgtc	ctgcaaaagct	tctggcttca	240
acattaaaga	ctactatata	cactgggtga	agcagaggcc	tgaacaggcc	ctggagtgga	300

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ttggatggat tgatcctgag attggtgcta ctaaatatgt cccgaagtgc caggcaagg	360
ccactatgac tacagacaca tcctccaaca cagcctacct gcagctcagc agcctgacat	420
ctgaggacac tgccgtctat tactgtatgc ccctctatgg taactacgac cgttactatg	480
ctatggacta ctggggtcaa ggaacctcag tcaccgtctc ctcagcctcc accaagggcc	540
catcggtctt cccctggca ccctcttca agagcacctc tggcggcaca gcccgcctgg	600
gctgcctggt caaggactac ttccccgaaac cggtgacgggt gtctggaac tcaggcgc	660
tgaccagcgg cgtgcacacc ttccggctg tcctacagtc ctcaggactc tactccctca	720
gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc tgcaacgtga	780
atcacaagcc cagcaacacc aagggtggaca agagagttgg tgagaggcca gcacaggag	840
ggagggtgtc tgctggaacg caggctcagc gtcctgcct ggacgcattcc cggtatgtca	900
gtcccagtcc agggcagcaa ggcaggcccc gtctgacatc tcaccggag gcctctgccc	960
gccccactca tgctcaggga gagggtcttc tggcttttc cccaggtct gggcaggcac	1020
aggcttaggtg cccctaacc cagccctgca cacaaagggg caggtgtgg gctcagaccc	1080
gccaagagcc atatccggga ggaccctgccc cctgacctaa gcccacccca aaggccaaac	1140
tctccactcc ctcagctcgg acaccccttc tcctcccaga ttccagtaac tcccaatctt	1200
ctctctgcag agcccaaatac ttgtgacaaa actcacat gcccaccgtg cccaggtaa	1260
ccageccagg cctcgccctc cagtcaggc cgggacgggt gcccctagatc agcctgcattc	1320
cagggacagg ccccaaggccg gtgtgacac gtcaccccttc atctcttcct cagcacctga	1380
actctctgggg ggaccgtcag tcttcctt cccccaaaaa cccaaggaca ccctcatgtat	1440
ctcccgacc cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt	1500
caagttcaac tggtagtgg acggcggtgg ggtgcataat gccaagacaa agccgcgggaa	1560
ggagcgtac aacagcacgt accgtgttgt cagcgtccctc accgtctgc accaggactg	1620
gctgaatggc aaggagtaca agtgcaaggt ctccaaacaaa gcccctccag ccccatcgaa	1680
gaaaaccatc tccaaagcca aagggtggac ccgtgggtg cggggccac atggacagag	1740
gcccggctcg cccacccttc gcccgtggag tgaccgtgtt accaacccttc gtcctacag	1800
ggcagccccc agaaccacag gtgtacaccc tgccccatc ccggggaggag atgaccaaga	1860
accagggtcag cctgacctgc ctggtaaaag gtttatcc cagcgtacatc gcccgtggagt	1920
gggagagcaa tgggcagccg gagaacaact acaagaccac gcccggctgt ctggactccg	1980
acggctccctt ctccctat agcaagctca ccgtggacaa gagcagggtgg cagcaggggaa	2040
acgtttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg cagaagagcc	2100
tctccctgtc cccggtaaa tgagtgcac ggcagaatt cattgatcat aatcagcc	2158

<210> SEQ ID NO 51
<211> LENGTH: 720
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: DIB5-hG1 Light chain

<400> SEQUENCE: 51	
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ggtgtccact ctagagacat tgtgtatgacc cagtcataaa aattcatgtc cacatcgtat	120

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ggagacaggg tcagcatcac ctgcaaggcc agtcagaatg ttctgtactgc tgtagcctgg	180
tatcaacaga aaccaggggca gtctccctaaa gcactgatt acttggcatc caaccggcac	240
actggagtcc ctgatcgctt cacaggcagt ggatctggga cagatttcac tctcaccatt	300
agcaatgtgc aatctgaaga cctggcagat tattttgtc tgcaacatgg gaattatctt	360
ctcacgttcg gtgctggac caagctggag ctgaaacggg ctgtggctgc accatctgtc	420
ttcatcttcc cgccatctga tgagcagttt aaatctggaa ctgcctctgt ttttgtgcctg	480
ctgaataact tctatcccag agaggccaaa gtacagtggaa aggtggataa cgccctccaa	540
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc	600
agcaacaccc tgacgcttag caaaggcagac tacgagaaac acaaagtcta cgcctgcgaa	660
gtcaccatc agggccttag ctcgccccgtc acaaagatcttca acacagggg agagtgttaa	720

1. An anti-CD200 antibody or antigen-binding fragment thereof comprising an altered constant region, wherein said antibody or antigen-binding fragment exhibits decreased effector function relative to a non-variant anti-CD200 antibody.

2. The antibody or antigen-binding fragment of claim 1, wherein decreased effector function comprises one or more of the following:

- a. decreased antibody-dependent cell-mediated cytotoxicity (ADCC);
- b. decreased complement dependent cytotoxicity (CDC) compared to a non-variant anti-CD200 antibody.

3. The antibody or antigen-binding fragment of claim 1, wherein the antibody is a murine antibody, a chimeric antibody, a humanized antibody, a single chain antibody, or a human antibody.

4. The antibody or antigen-binding fragment of claim 1, wherein the antibody or antigen-binding fragment thereof is selected from the group consisting of IgG 1, IgG2, IgG3, IgG4, IgM, IgA1, IgA2, IgA, IgD, and IgE.

5. The antibody or antigen-binding fragment of claim 1, wherein the constant region has been engineered to comprise at least one amino acid substitution, insertion, or deletion.

6. The antibody or antigen-binding fragment of claim 1, comprising an amino acid sequence that is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 12, 14, 16, 17, and 21, or to fragments thereof.

7. The antibody or antigen-binding fragment of claim 1 comprising an amino acid sequence that is at least 90% identical to an amino acid sequence of SEQ ID NOS: 13, 15, 18, or 22, or to fragments thereof.

8. The antibody or antigen-binding fragment of claim 1, wherein said constant region comprises one or more of the following characteristics:

- i) altered glycosylation;
- ii) an Ala-Ala mutation;
- iii) a G2/G4 construct selected from the group consisting of SEQ ID NOS: 13, 15, 18, and 22.

9. The antibody of claim 8, wherein the altered glycosylation comprises one or more of the following: (i) a change in one or more sugar components; (ii) presence of one or more sugar components; and (iii) absence of sugar components.

10. The antibody of claim 9, wherein said antibody is expressed in a host cell selected from the group consisting of a mammalian cell, a bacterial cell, and a plant cell.

11. The antibody of claim 10, wherein the host cell is *E. coli*.

12. The antibody of claim 10, wherein the host cell is a rat-hybridoma cell.

13. The antibody of claim 10, wherein the host cell is a CHO cell.

14. The antibody or antigen-binding fragment of claim 1, comprising one or more of the following characteristics:

- a) decreased binding to one or more Fc receptors;
- b) decreased ADCC activity; and
- c) decreased CDC activity

relative to a non-variant anti-CD200 antibody.

15. The antibody or antigen-binding fragment of claim 1, wherein the antibody is a blocking anti-CD200 antibody.

16. The antibody or antigen-binding fragment of claim 15, wherein the antibody is a murine antibody, a chimeric antibody, a humanized antibody, a single chain antibody, or a human antibody.

17. An antibody or antigen-binding fragment thereof comprising:

- (i) one or more amino acid sequence(s) that is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 10 and 25 or fragments thereof;
- (ii) one or more amino acid sequence(s) that is at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 26, the fragment of SEQ ID NO: 11 beginning at amino acid 20, the fragment of SEQ ID NO: 26 beginning at amino acid 23, and other fragments of SEQ ID NOS: 11 and 26;
- (iii) one or more amino acid sequence(s) that is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 10 and 27 or fragments thereof;
- (iv) one or more amino acid sequence(s) that is at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 28, the fragment of SEQ ID NO: 11 beginning at amino acid 20,

- the fragment of SEQ ID NO: 28 beginning at amino acid 23, and other fragments of SEQ ID NOS: 11 and 28;
- (v) one or more amino acid sequence(s) that is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 8 and 25 or fragments thereof;
- (vi) one or more amino acid sequence(s) that is at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 26, the fragment of SEQ ID NO: 9 beginning at amino acid 20, the fragment of SEQ ID NO: 26 beginning at amino acid 23, and other fragments of SEQ ID NOS: 9 and 26;
- (vii) one or more amino acid sequence(s) that is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 12 and 27 or fragments thereof;
- (viii) one or more amino acid sequence(s) that is at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO: 13, SEQ ID NO: 28, the fragment of SEQ ID NO: 13 beginning at amino acid 20, the fragment of SEQ ID NO: 28 beginning at amino acid 23, and other fragments of SEQ ID NOS: 13 and 28;
- (ix) one or more amino acid sequence(s) that is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 14 and 23 or fragments thereof;
- (x) an amino acid sequence that is at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO: 15, SEQ ID NO: 24, the fragment of SEQ ID NO: 15 beginning at amino acid 21, the fragment of SEQ ID NO: 24 beginning at amino acid 21, and other fragments of SEQ ID NOS: 15 and 24;
- (xi) one or more amino acid sequence(s) that is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 16 and 27 or fragments thereof;
- (xii) one or more amino acid sequence(s) that is at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO: 13, SEQ ID NO: 28, the fragment of SEQ ID NO: 13 beginning at amino acid 20, the fragment of SEQ ID NO: 28 beginning at amino acid 23, and other fragments of SEQ ID NOS: 13 and 28;
- (xiii) one or more amino acid sequence(s) that is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 17 and 29 or fragments thereof;
- (xiv) one or more amino acid sequence(s) that is at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO: 18, SEQ ID NO: 30, the fragment of SEQ ID NO: 18 beginning at amino acid 21, the fragment of SEQ ID NO: 30 beginning at amino acid 21, and other fragments of SEQ ID NOS: 18 and 30;
- (xv) one or more amino acid sequence(s) that is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 19 and 31 or fragments thereof;
- (xvi) one or more amino acid sequence(s) that is at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO: 20, SEQ ID NO: 32, the fragment of SEQ ID NO: 20 beginning at amino acid 21, the fragment of SEQ ID NO: 32 beginning at amino acid 21, and other fragments of SEQ ID NOS: 20 and 32;
- (xvii) one or more amino acid sequence(s) that is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 21 and 33 or fragments thereof; or
- (xviii) one or more amino acid sequence(s) that is at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO: 22, SEQ ID NO: 34, the fragment of SEQ ID NO: 22 beginning at amino acid 20, the fragment of SEQ ID NO: 34 beginning at amino acid 20, and other fragments of SEQ ID NOS: 22 and 34.
- 18-34.** (canceled)
- 35.** The antigen-binding fragment of claim **17**, wherein the antigen-binding fragment exhibits reduced effector function.
- 36.** An antibody or antigen-binding fragment of claim **1**, wherein said antibody or antigen-binding fragment is conjugated to an agent.
- 37.** The antibody or antigen-binding fragment of claim **36**, wherein the agent is selected from the group consisting of a toxin, enzyme, therapeutic agent, diagnostic agent, and imaging agent.
- 38.** An antigen-binding fragment of an anti-CD200 antibody, wherein the antigen-binding fragment is modified to exhibit increased half-life in a subject.
- 39-43.** (canceled)
- 44.** A method of decreasing the number of CD200 positive cells in a patient, comprising administering to said patient an anti-CD200 antibody or antigen-binding fragment thereof.
- 45.** (canceled)
- 46.** A method of inhibiting the interaction of CD200 with its receptor comprising administering a CD200 antagonist.
- 47-56.** (canceled)
- 57.** A method of treating a patient with cancer, comprising administering to said patient a CD200 antagonist, wherein said antagonist is selected from the group consisting of polypeptide, small molecule, chemical, metal, organometallic compound, inorganic compound, nucleic acid, oligonucleotide, aptamer, immunomodulatory agent, antigen-binding fragment, prodrug, and peptidomimetic compound.
- 58.** A method for treating a patient with cancer, said method comprising administering an antibody or antigen-binding fragment of claim **1** to said patient.
- 59-60.** (canceled)
- 61.** A method of treating a patient with cancer, comprising administering to said patient an antibody or antigen-binding fragment of claim **17**.
- 62.** A method of treating cancer comprising administering an anti-CD200 antibody or fragment thereof in combination with a second agent or therapy.
- 63-81.** (canceled)
- 82.** A method of treating a viral infection in a patient comprising administering an anti-CD200 antibody or antigen-binding fragment thereof to said patient.
- 83-84.** (canceled)
- 85.** An anti-CD200 antibody or antigen-binding fragment thereof comprising a variant constant region, wherein said antibody exhibits increased effector function compared to a non-variant anti-CD200 antibody.
- 86-109.** (canceled)
- 110.** An agent that inhibits the interaction of CD200 with its receptor wherein said agent does not elicit effector function.
- 111.** (canceled)

112. A pharmaceutical composition comprising an agent that binds to CD200.

113-116. (canceled)

117. A method of monitoring the progress of a therapy comprising the collection of tissue samples or cells from a patient receiving or planning to receive said therapy at least twice and determining the expression of CD200 on said collected samples.

118-122. (canceled)

123. A de-immunized anti-CD200 antibody or antigen-binding fragment thereof comprising an altered constant

region, wherein said antibody or antigen-binding fragment exhibits decreased effector function relative to a non-variant anti-CD200 antibody.

124. A de-immunized anti-CD200 antibody or antigen-binding fragment thereof comprising a variant constant region, wherein said de-immunized antibody or antigen-binding fragment thereof exhibits increased effector function compared to a non-variant anti-CD200 antibody.

125-126. (canceled)

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