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(54) **ANTI-CD28 ANTIBODIES AND METHODS OF USE THEREOF**

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(73) Assignee: **ADAGENE PTE. LTD.**, Singapore (SG)

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C07K 16/32	(2006.01)

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

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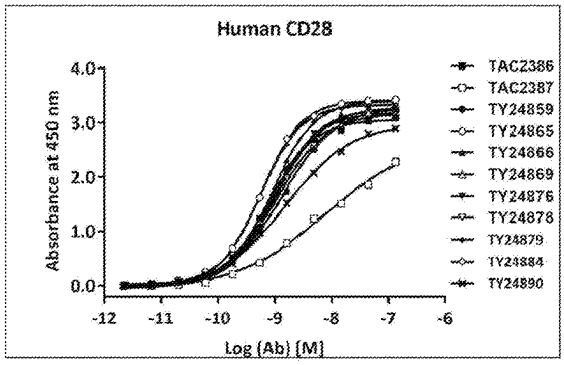
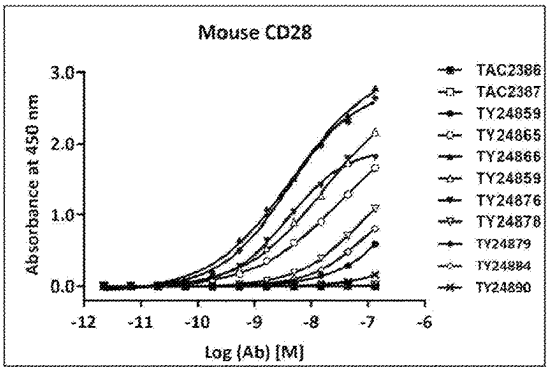
(57) **ABSTRACT**

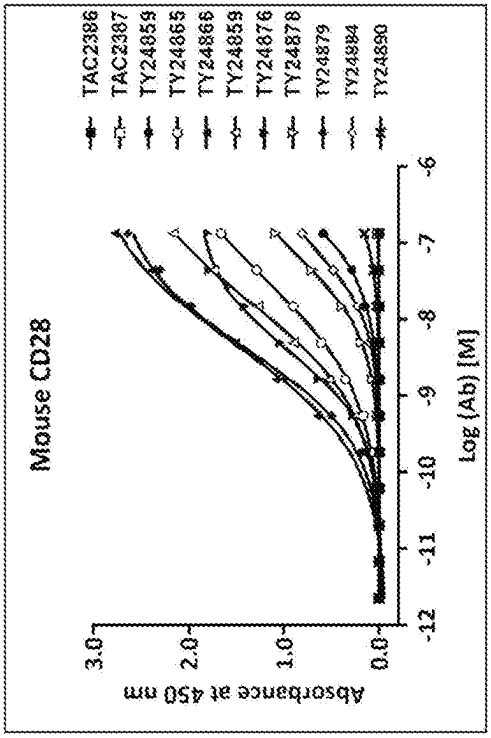
The present disclosure relates to anti-CD28 antibodies that bind to human CD28 and antigen-binding fragments thereof, compositions comprising same, and uses thereof in delaying and/or preventing tumor growth.

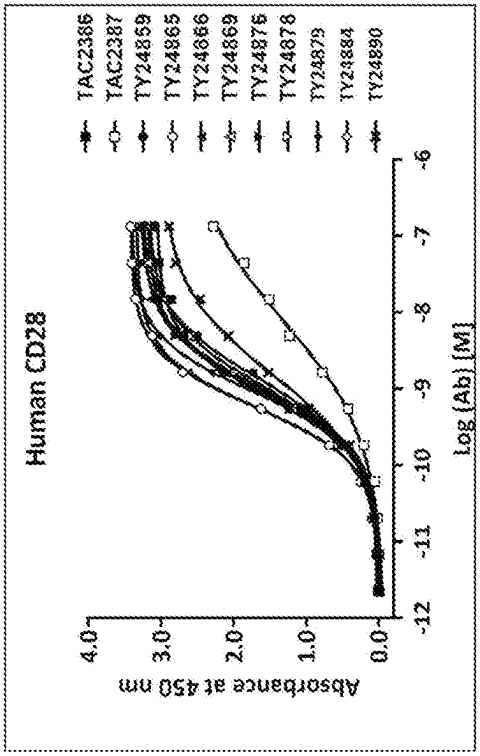
Specification includes a Sequence Listing.



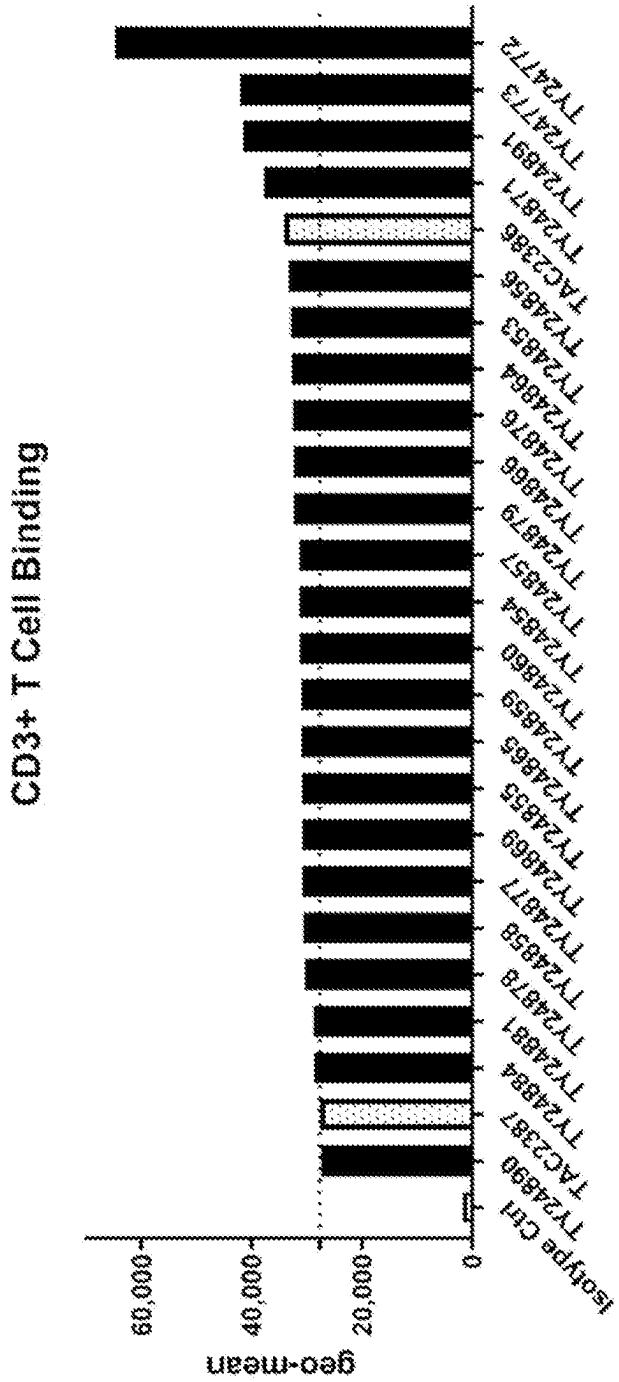


[Fig. 1]

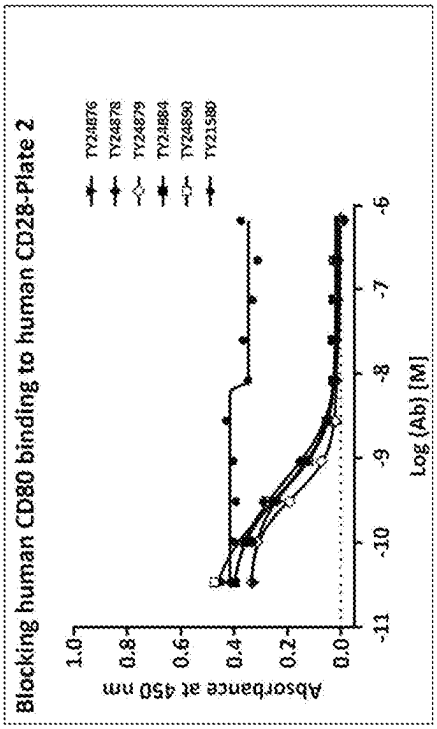

Mouse CD28
Absorbance at 450 nm
3.0
2.0
1.0
0.0
-12
-11
-10
-9
-8
-7
-6
Log (Ab) [M]
TAC2386
TAC2387
TY24859
TY24865
TY24866
TY24869
TY24876
TY24878
TY24879
TY24884
TY24890

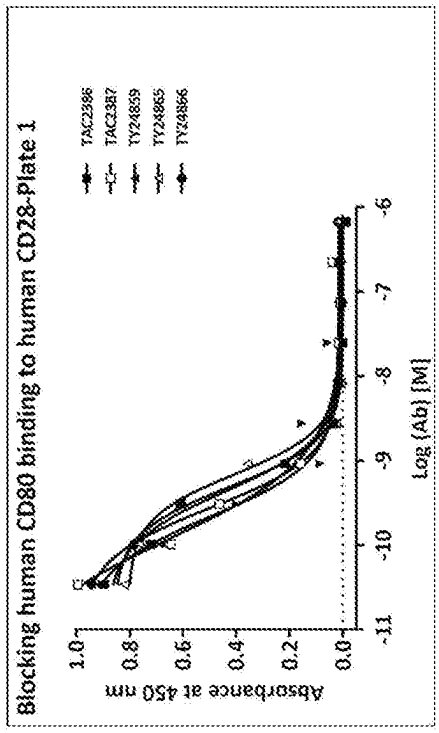

Human CD28
Absorbance at 450 nm
4.0
3.0
2.0
1.0
0.0
-12
-11
-10
-9
-8
-7
-6
Log (Ab) [M]
TAC2386
TAC2387
TY24859
TY24865
TY24866
TY24869
TY24876
TY24878
TY24879
TY24884
TY24890

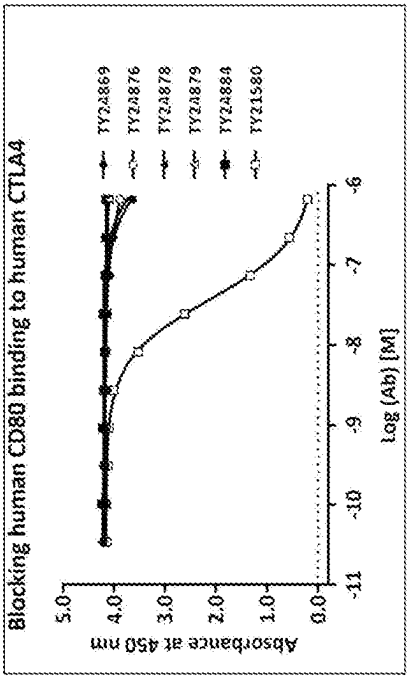
[Fig. 2]


CD3+ T Cell Binding
geo-mean
60,000
40,000
20,000
0
Isotype Ctrl
TY24890
TAC2387
TY24884
TY24881
TY24879
TY24858
TY24871
TY24869
TY24855
TY24865
TY24859
TY24860
TY24854
TY24857
TY24879
TY24866
TY24876
TY24864
TY24853
TY24866
TAC2386
TY24871
TY24891
TY24873
TY24872

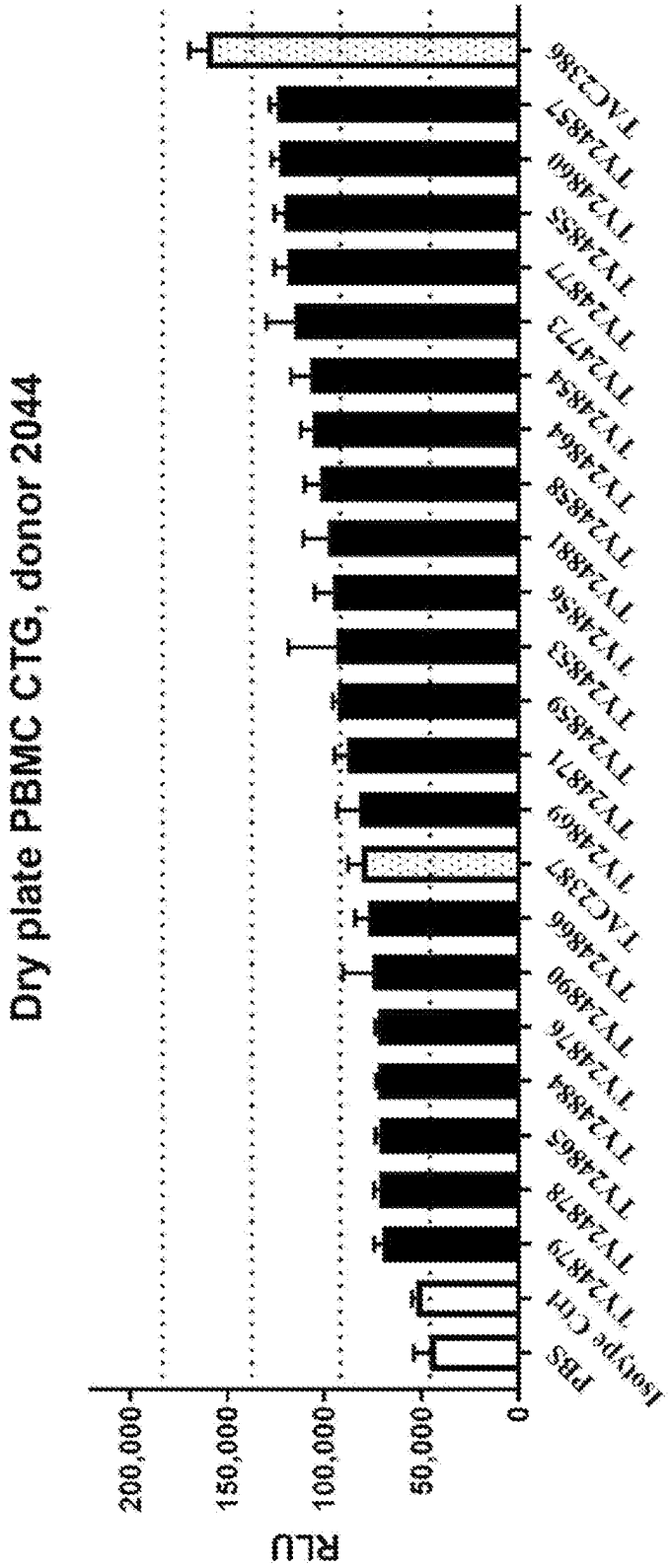
[Fig. 3]


Blocking human CD80 binding to human CD28-Plate 2
Absorbance at 450 nm
1.0
0.8
0.6
0.4
0.2
0.0
-11
-10
-9
-8
-7
-6
Log (Ab) [M]
TY24876
TY24878
TY24879
TY24884
TY24890
TY21580

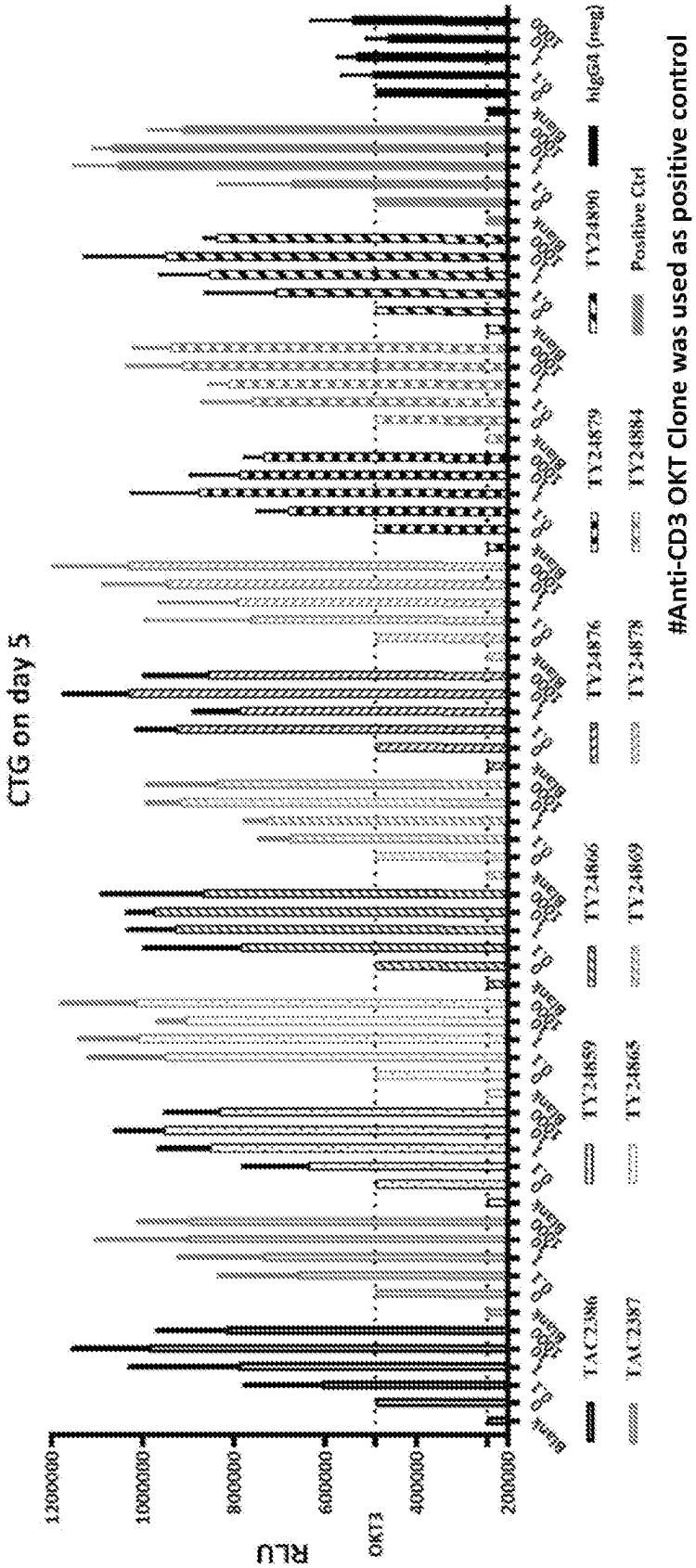

Blocking human CD80 binding to human CD28-Plate 1
Absorbance at 450 nm
1.0
0.8
0.6
0.4
0.2
0.0
-11
-10
-9
-8
-7
-6
Log (Ab) [M]
TAC2386
TAC2387
TY24859
TY24865
TY24866


Blocking human CD80 binding to human CTLA4
Absorbance at 450 nm
5.0
4.0
3.0
2.0
1.0
0.0
-11
-10
-9
-8
-7
-6
Log (Ab) [M]
TY24869
TY24876
TY24878
TY24879
TY24884
TY21580

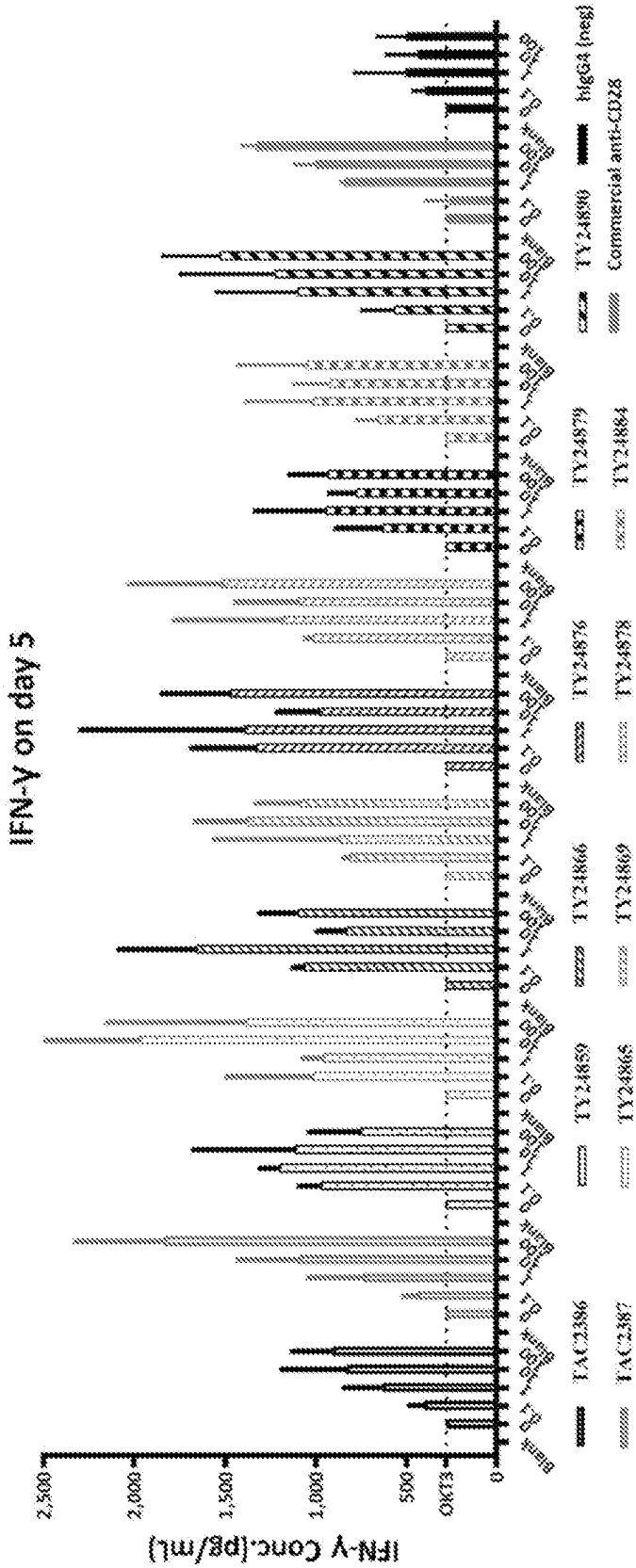
[Fig. 4A]


Dry plate PBMC CTG, donor 2044
RLU
200,000
150,000
100,000
50,000
0
FBS
Isotype Ctrl
TV24879
TV24878
TV24865
TV24884
TV24876
TV24890
TV24866
TAC2387
TV24869
TV24871
TV24859
TV24853
TV24856
TV24881
TV24858
TV24864
TV24854
TV24873
TV24877
TV24855
TV24860
TV24857
TAC2386

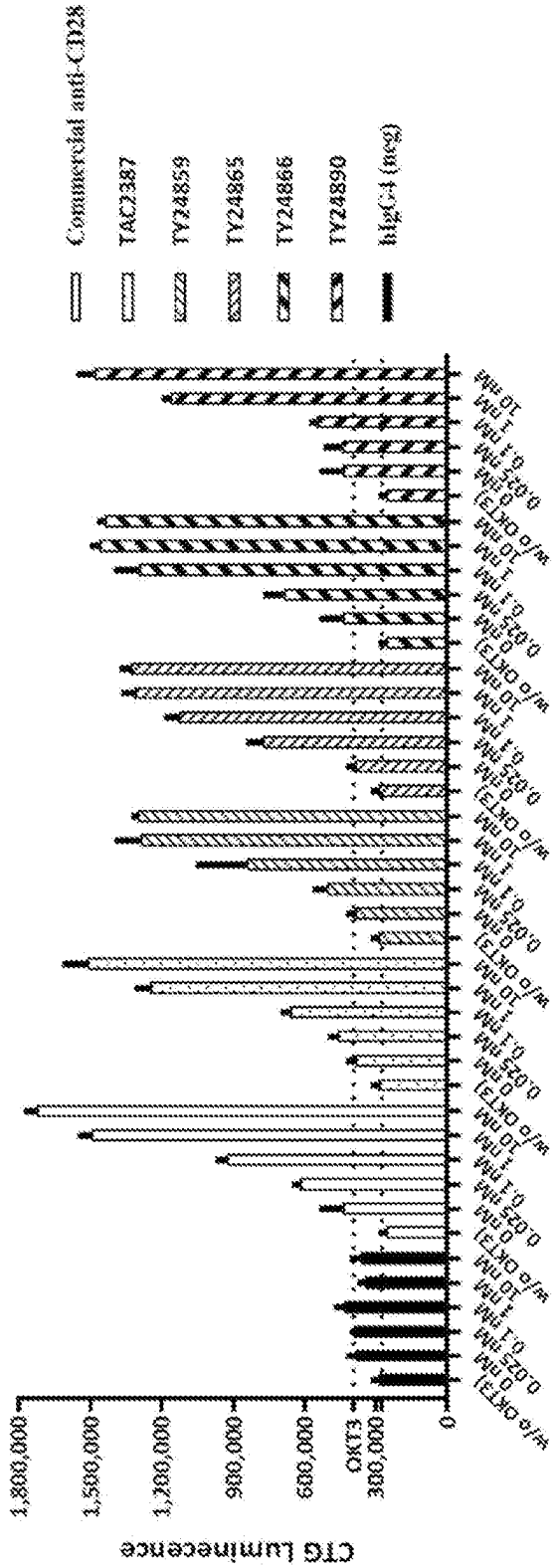
[Fig. 4B]


CTG on day 5
RLU
1200000
1000000
800000
600000
400000
200000
OKT3
TAC2386
TAC2387
TY24859
TY24865
TY24866
TY24869
TY24876
TY24878
TY24879
TY24884
TY24896
Positive Ctrl
hIgG4 (neg)
#Anti-CD3 OKT Clone was used as positive control

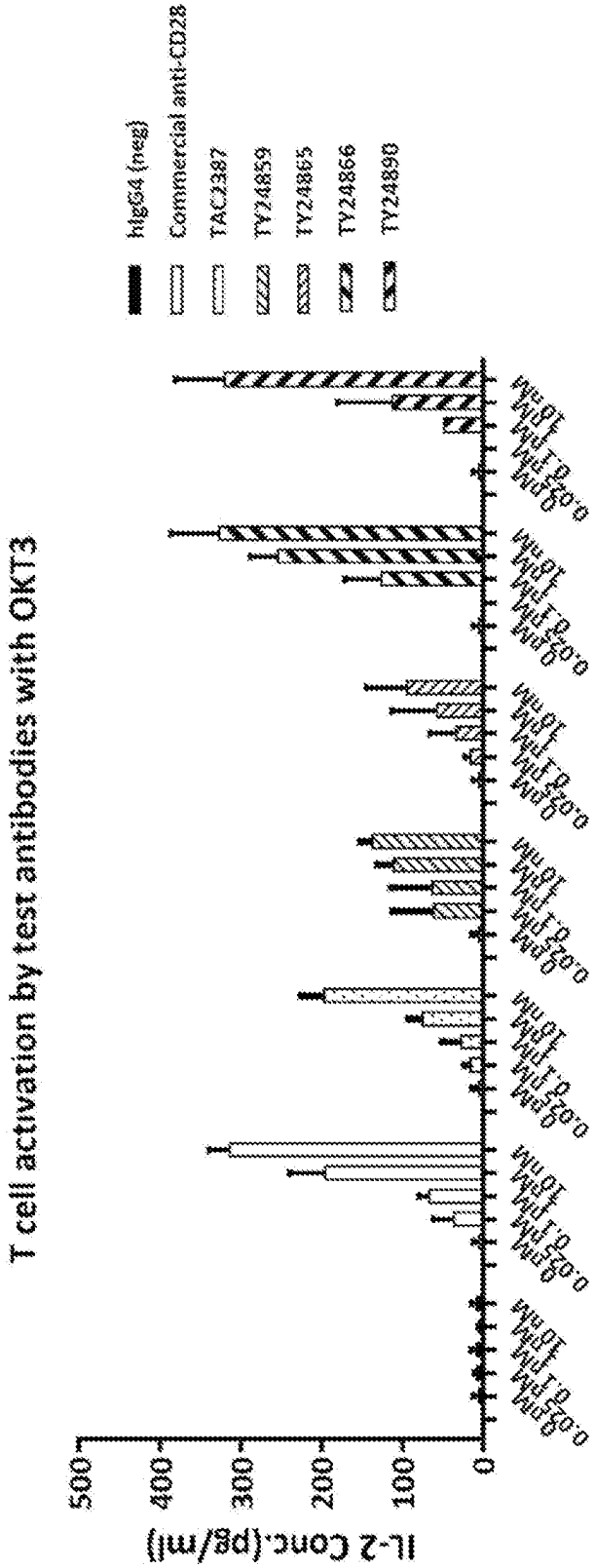
[Fig. 4C]


IFN-γ on day 5
IFN-γ Conc.(pg/mL)
2,500
2,000
1,500
1,000
500
OKT3
0
TAC2396
TAC2367
TY24859
TY24865
TY24866
TY24869
TY24876
TY24878
TY24879
TY24884
TY24890
hIgG4 (neg)
Commercial anti-CD28

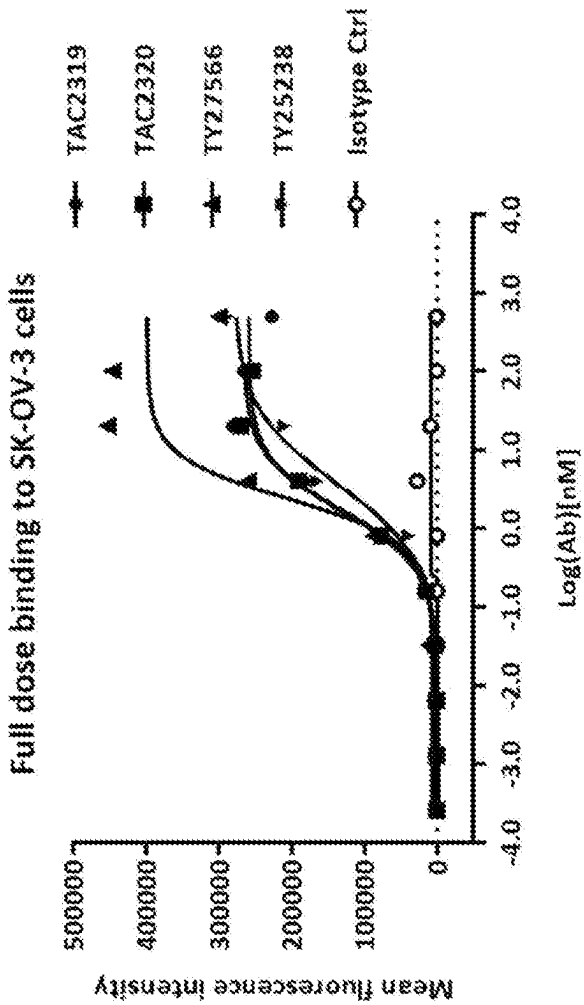
[Fig. 5A]


Commercial anti-CD28
TAC2387
TY24859
TY24865
TY24866
TY24890
IgG1 (mcg)
CTG Luminescence
1,800,000
1,500,000
1,200,000
900,000
600,000
300,000
0
OKT3
w/o OKT3
0.025nM
0.1nM
1nM
10nM

[Fig. 5B]

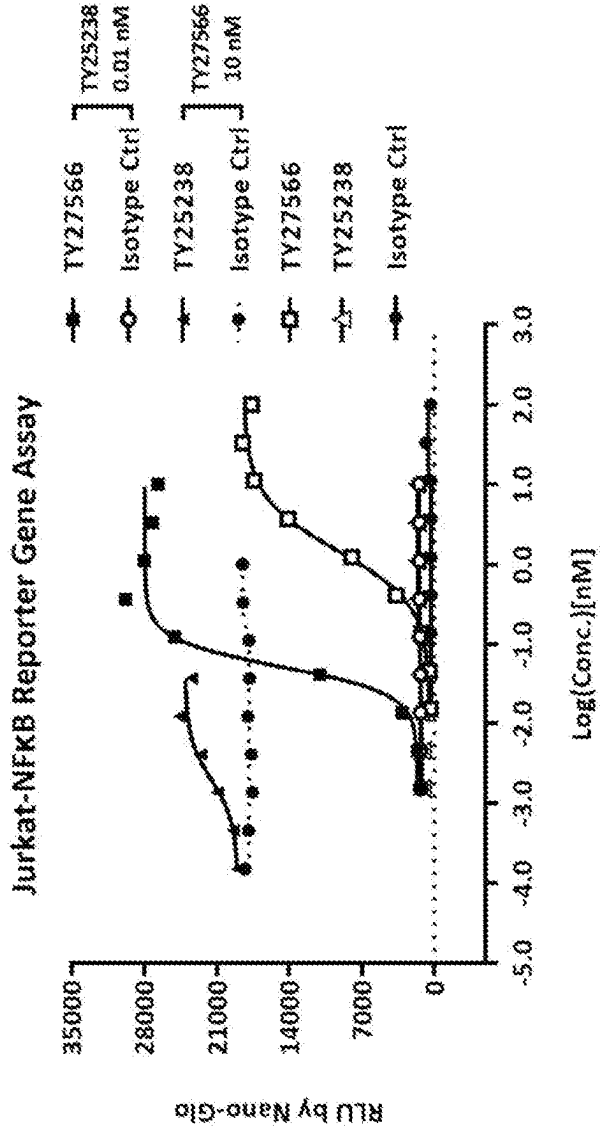

T cell activation by test antibodies with OKT3
IL-2 Conc.(pg/ml)
500
400
300
200
100
0
0.025nM
0.1nM
1nM
10nM
HIgG4 (neg)
Commercial anti-CD28
TAC2387
TY24859
TY24865
TY24866
TY24890

[Fig. 6]



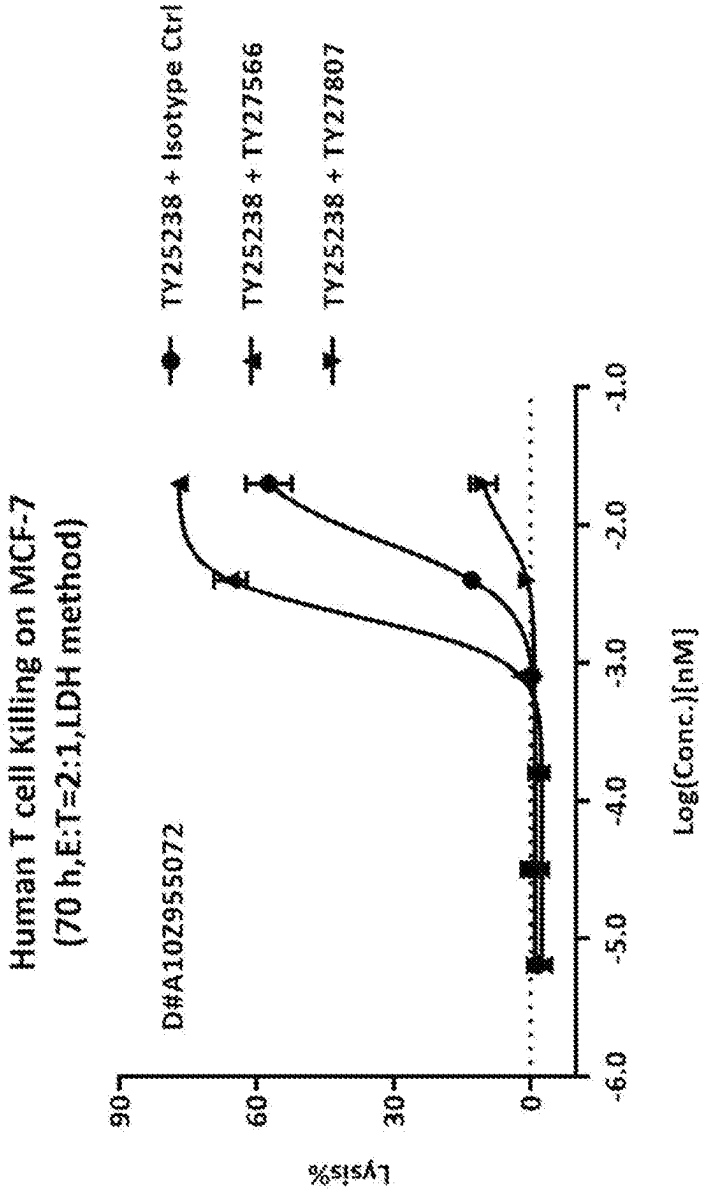
Abs	EC_{50}(nM)	Max
TAC2319	1.617	256422
TAC2320	1.75	265535
TY27566	2.318	391919
TY25238	3.739	281926

[Fig. 7]



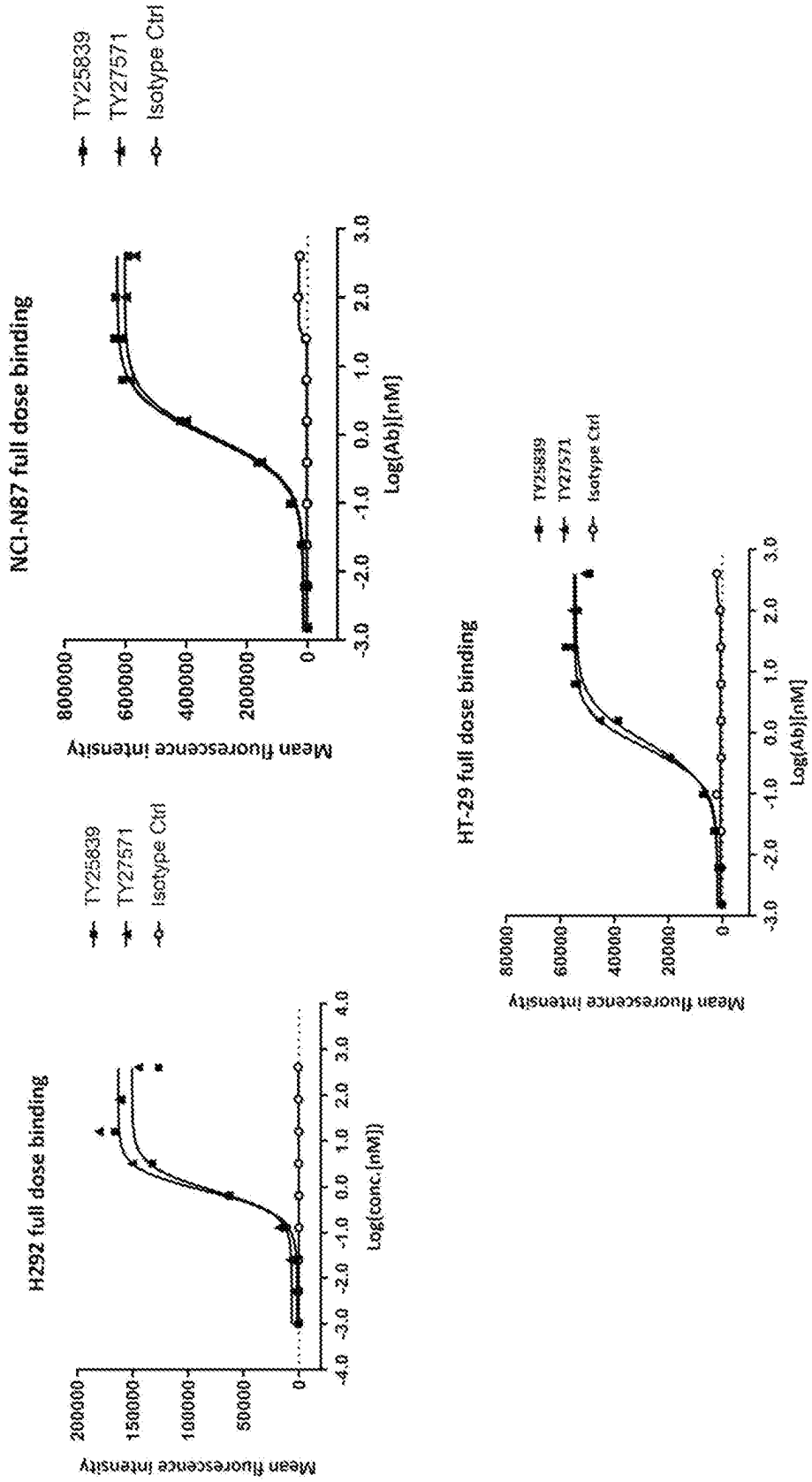
Ab ID	EC_{50} (nM)	Max RLU
TY27566	1.501	18864
TY25238	0.0827	1747
Isotype Ctrl	NA	869
TY27566+0.01 nM TY25238	0.0519	29940
Isotype Ctrl+0.01 nM TY25238	NA	1549
TY25238+10 nM TY27566	0.0019	24879
Isotype Ctrl+10 nM TY27566	NA	18657

[Fig. 8]

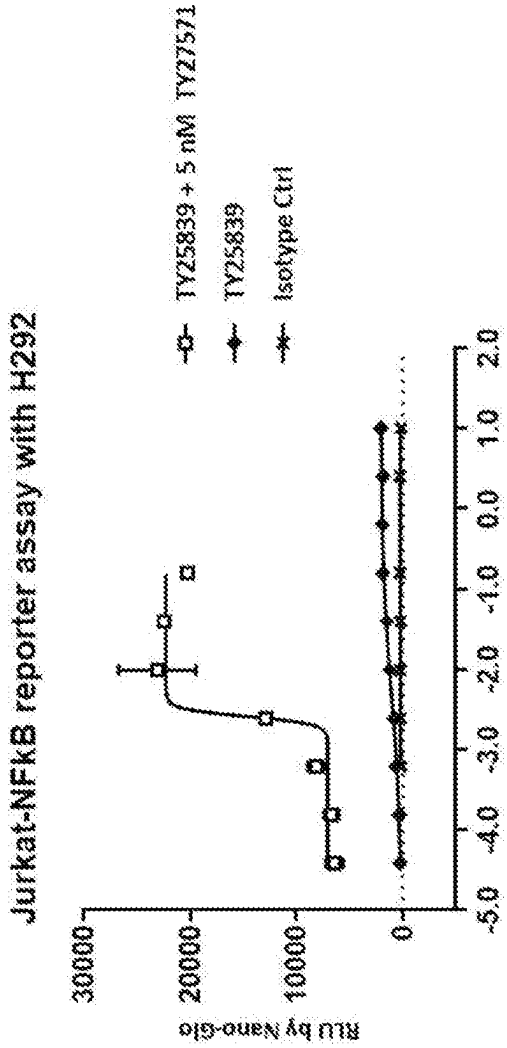


Ab ID	EC_{50} (pM)	Span	AUC
TY25238 + Isotype Ctrl	7.547	66.2	30.88
TY25238 + TY27566 (1 μg/mL)	2.13	79.68	77.78
TY25238 + TY27807 (1 μg/mL)	9.363	13.33	5.949

[Fig. 9]


H292 full dose binding
Mean fluorescence intensity
200000
150000
100000
50000
0
-4.0
-3.0
-2.0
-1.0
0.0
1.0
2.0
3.0
4.0
Log(conc.[nM])
TY25839
TY27571
Isotype Ctrl
MCI-N87 full dose binding
Mean fluorescence intensity
800000
600000
400000
200000
0
-3.0
-2.0
-1.0
0.0
1.0
2.0
3.0
Log(Ab)[nM]
TY25839
TY27571
Isotype Ctrl
HT-29 full dose binding
Mean fluorescence intensity
80000
60000
40000
20000
0
-3.0
-2.0
-1.0
0.0
1.0
2.0
3.0
Log(Ab)[nM]
TY25839
TY27571
Isotype Ctrl

[Fig. 10A]


Jurkat-NFkB reporter assay with H292
RLU by Nano-Glo
30000
20000
10000
0
-5.0
-4.0
-3.0
-2.0
-1.0
0.0
1.0
2.0
TY25839 + 5 nM TY27571
TY25839
Isotype Ctrl

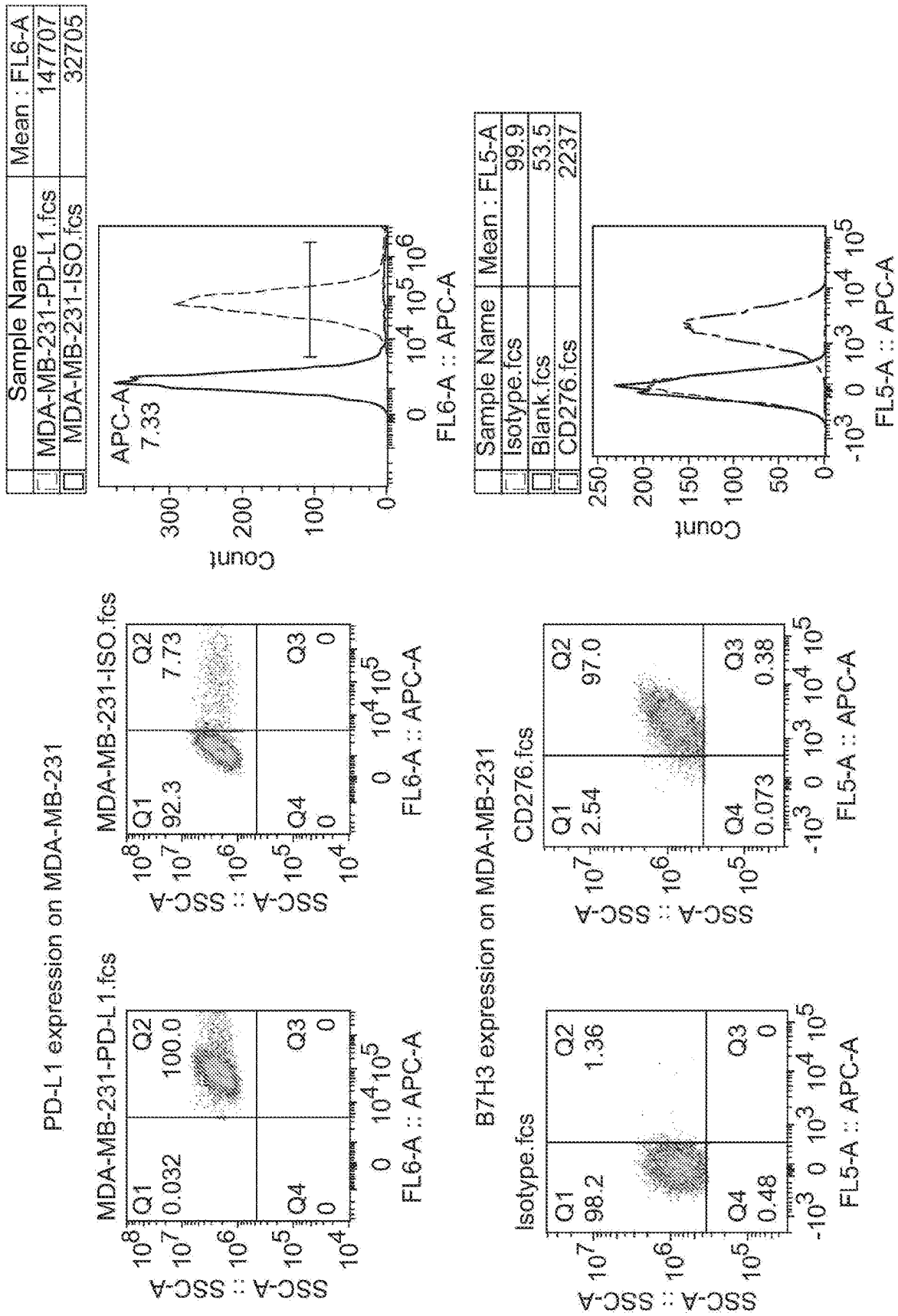
[Fig. 10B]

Log[Ab][nM]

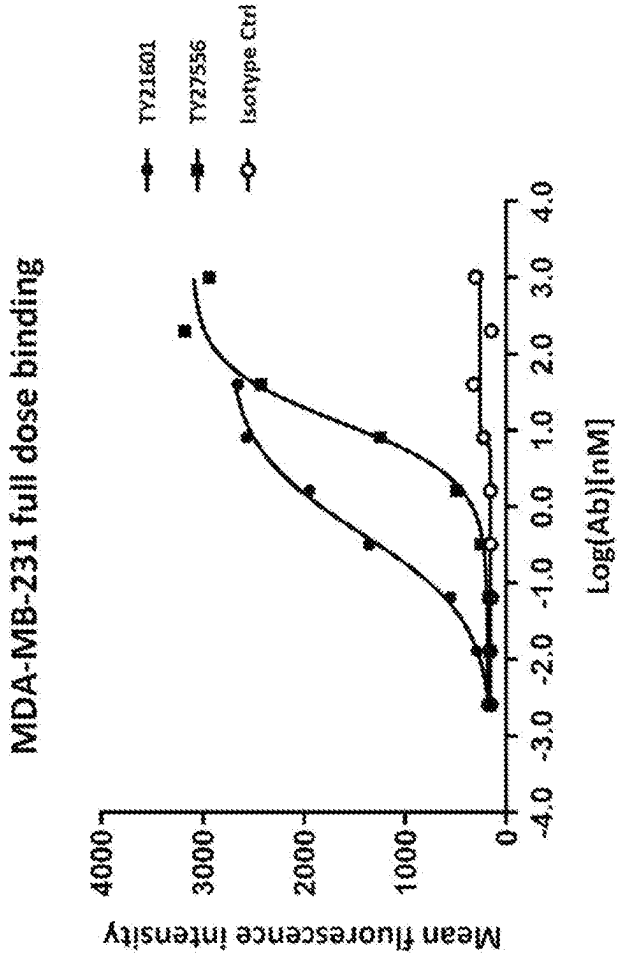
TAs		EC50 (nM)	Span
TROP2xCD3	TROP2xCD28		
TY25839	5 nM TY27571 CD28	0.00257	15186
TY25839	/	0.00585	1913

Jurkat-NFkB reporter assay with H292

[Fig. 11]

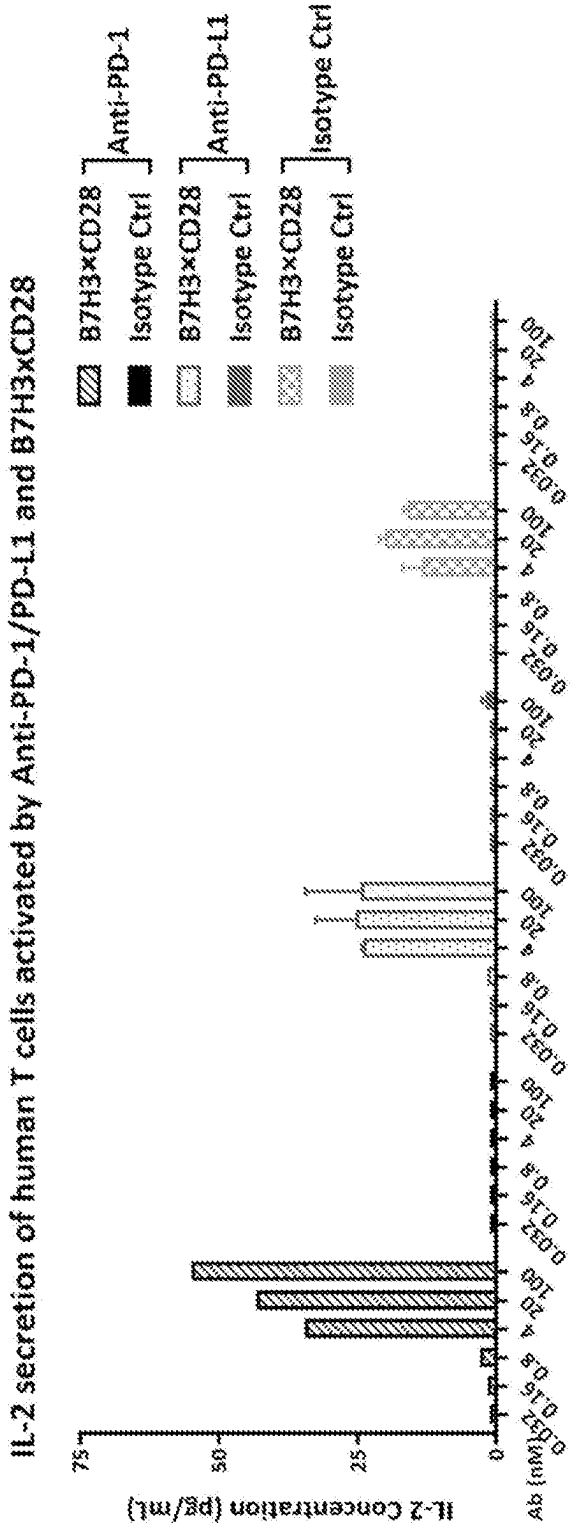

PD-L1 expression on MDA-MB-231
MDA-MB-231-PD-L1.fcs
Q1 0.032
Q2 100.0
Q4 0
Q3 0
MDA-MB-231-ISO.fcs
Q1 92.3
Q2 7.73
Q4 0
Q3 0
SSC-A :: SSC-A
FL6-A :: APC-A
Sample Name
Mean : FL6-A
MDA-MB-231-PD-L1.fcs 147707
MDA-MB-231-ISO.fcs 32705
APC-A 7.33
Count
B7H3 expression on MDA-MB-231
Isotype.fcs
Q1 98.2
Q2 1.36
Q4 0.48
Q3 0
CD276.fcs
Q1 2.54
Q2 97.0
Q4 0.073
Q3 0.38
FL5-A :: APC-A
Sample Name
Mean : FL5-A
Isotype.fcs 99.9
Blank.fcs 53.5
CD276.fcs 2237

[Fig. 12]

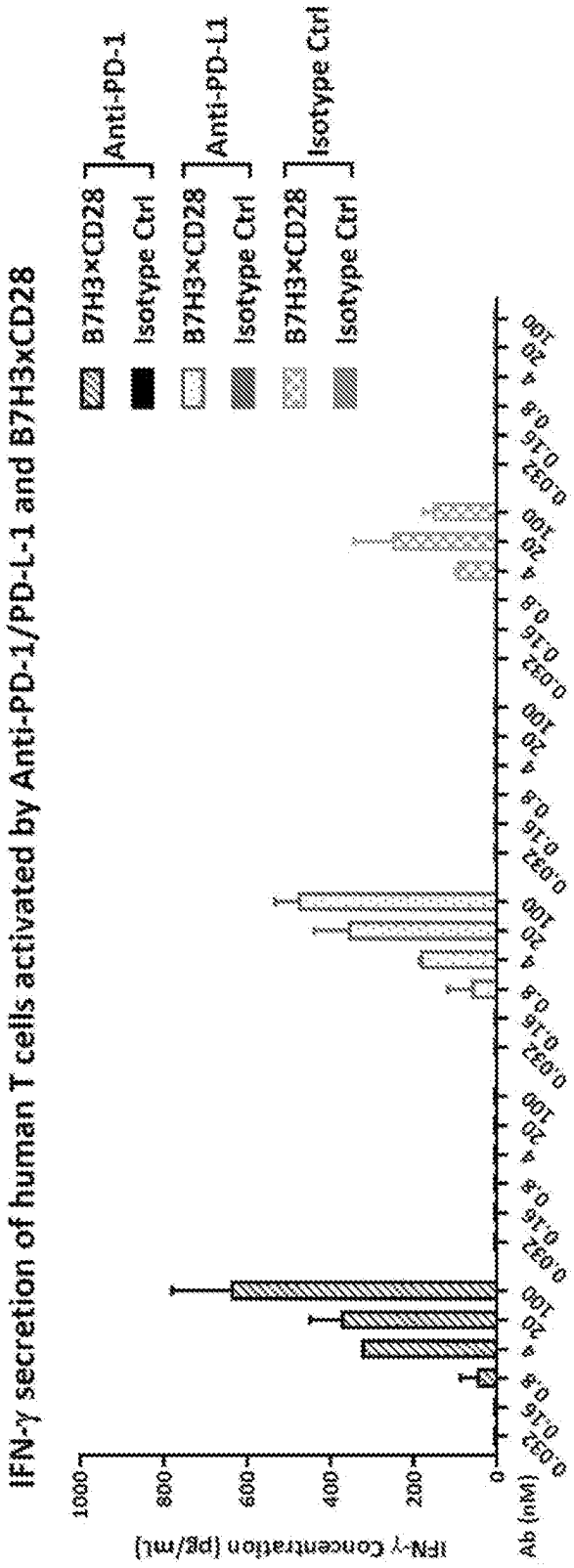


Abs	EC_{50}(nM)	Max
TY21601	0.4525	2658
TY27556	12.84	3177

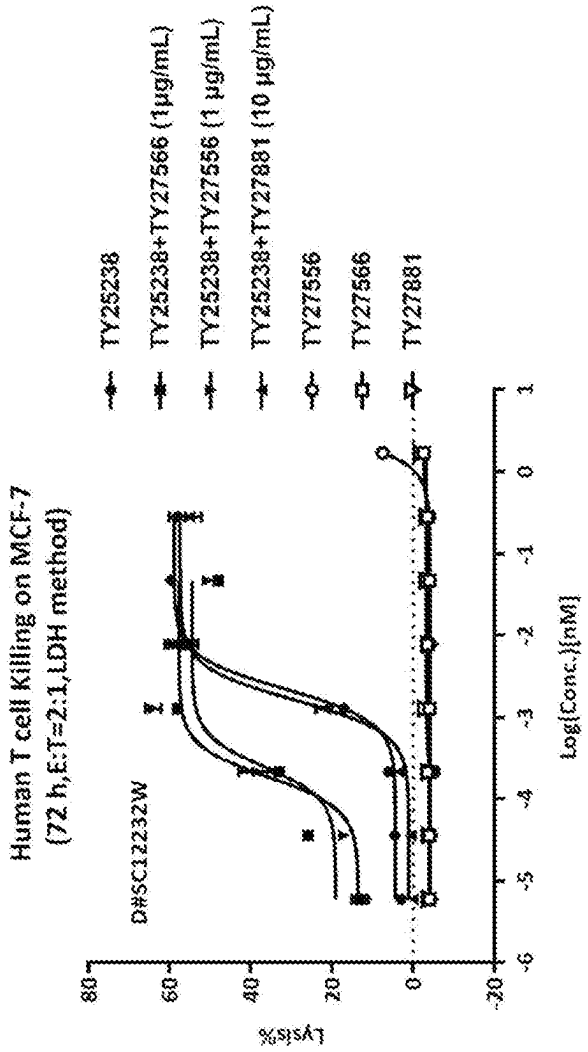
[Fig. 13A]


IL-2 secretion of human T cells activated by Anti-PD-1/PD-L1 and B7H3xCD28
B7H3×CD28
Isotype Ctrl
Anti-PD-1
B7H3×CD28
Isotype Ctrl
Anti-PD-L1
B7H3×CD28
Isotype Ctrl
Isotype Ctrl
IL-2 Concentration (pg/mL)
75
50
25
0
Ab (nM)
0
0.015
0.08
4
20
100
250
0.015
0.08
4
20
100
250
0.015
0.08
4
20
100
250
0.015
0.08
4
20
100
250

[Fig. 13B]

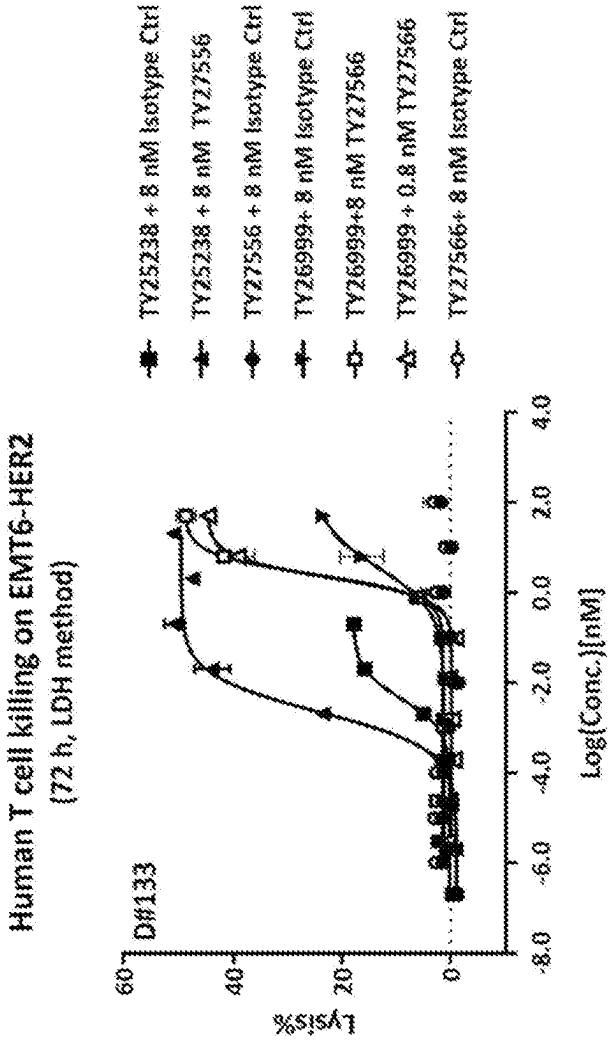

IFN-γ secretion of human T cells activated by Anti-PD-1/PD-L-1 and B7H3xCD28
B7H3×CD28
Isotype Ctrl
Anti-PD-1
B7H3×CD28
Isotype Ctrl
Anti-PD-L1
B7H3×CD28
Isotype Ctrl
Isotype Ctrl
IFN-γ Concentration [pg/mL]
1000
800
600
400
200
0
Ab (nM)
0.032
0.16
0.8
4
20
100

[Fig. 14]



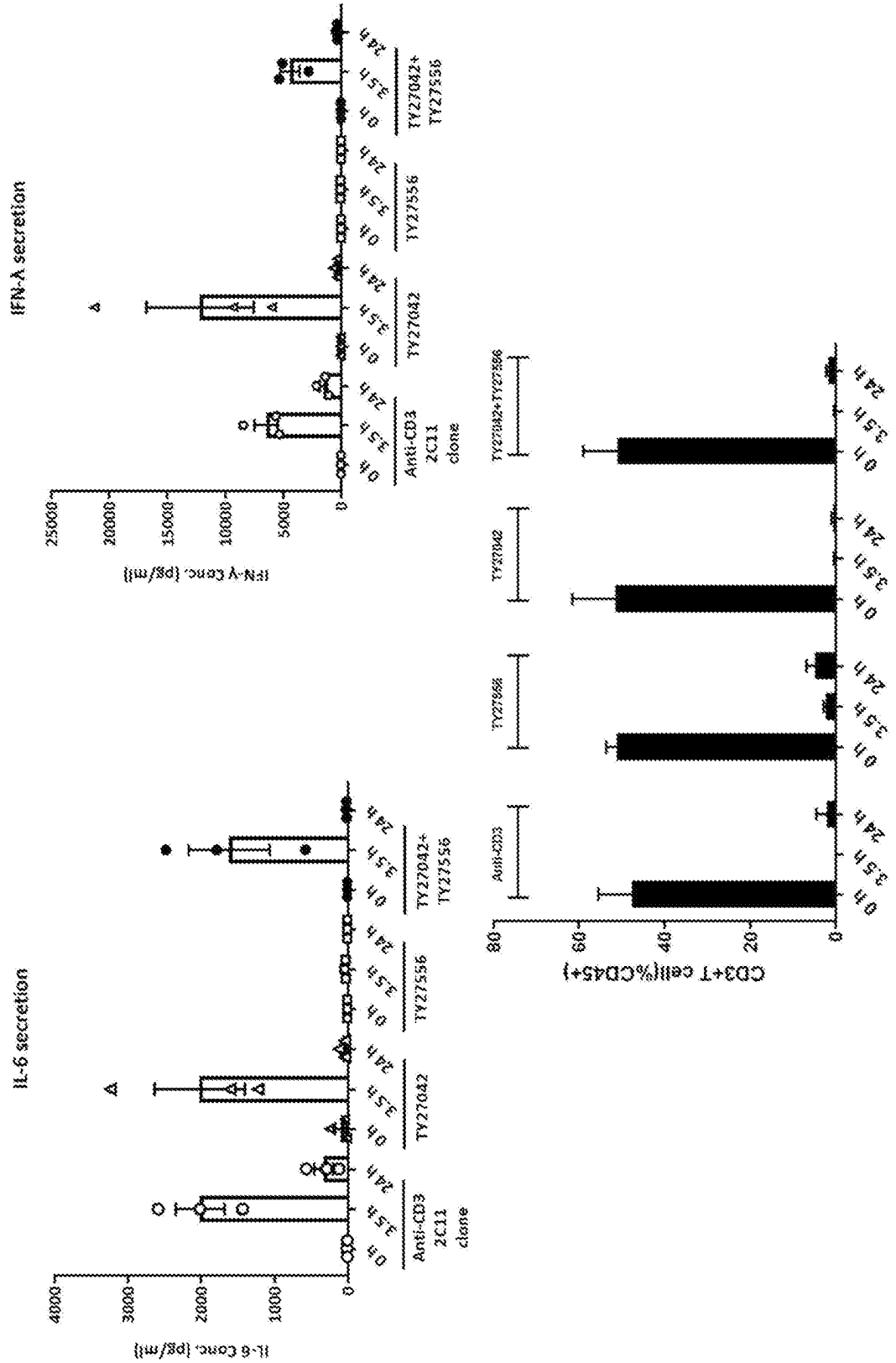
MCF-7 (72h)	EC_{50} (pM)	Span
TY25238	2.22	54.47
TY25238+ 1μg/mL TY27566	0.24	34.71
TY25238+ 1μg/mL TY27556	0.20	43.57
TY25238+ 10μg/mL TY27881	1.68	56.82

[Fig. 15]

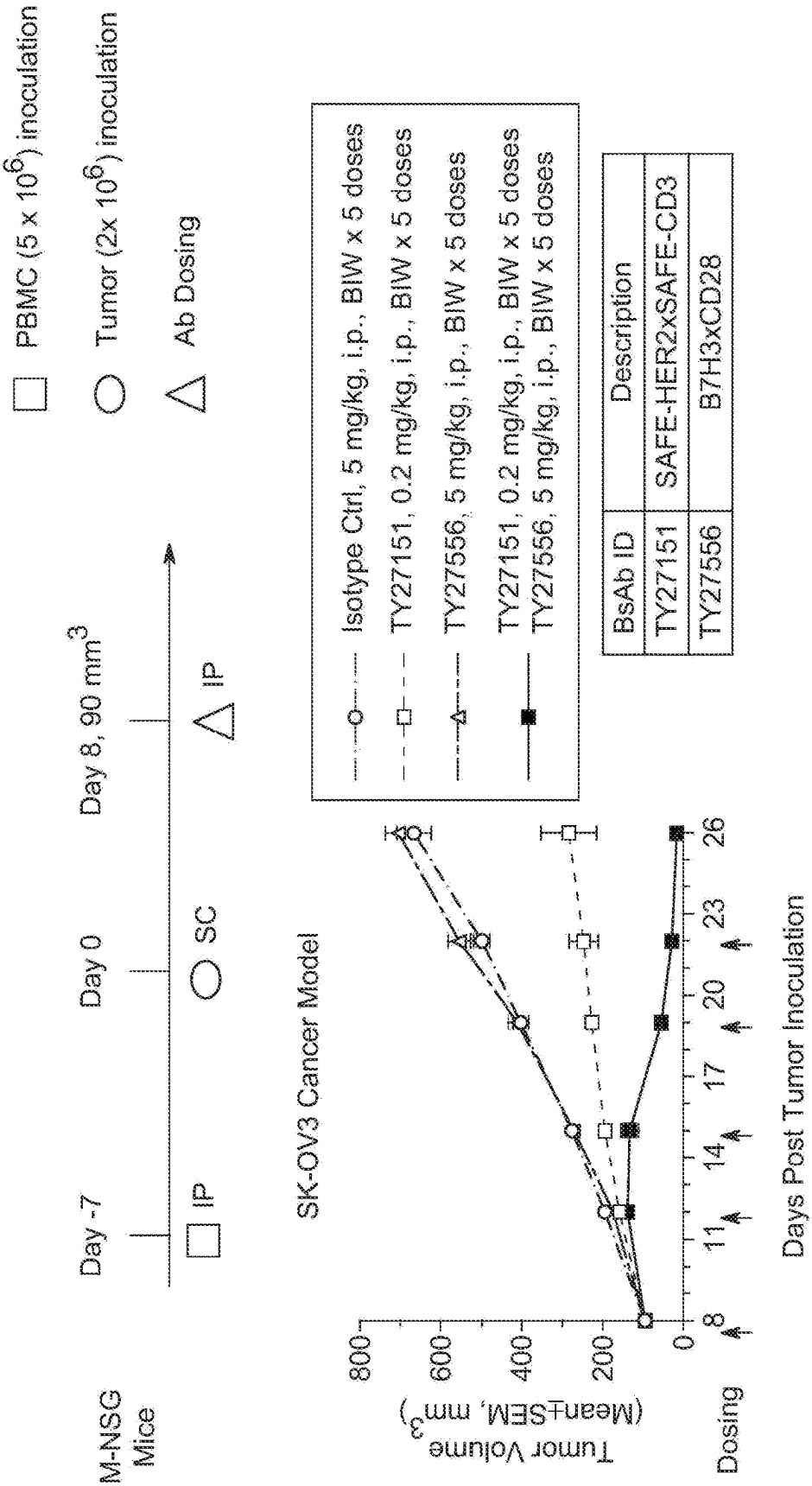


Ab ID	EC_{50}(nM)	Span
TY25238 + 8nM Isotype Ctrl	0.004355	17.70
TY25238 + 8nM TY27556	0.002221	50.72
Ab ID	**EC_{50}(nM)**	**Span**
TY26999 + 8nM Isotype Ctrl	3.428	23.71
TY26999 + 8nM TY27566	2.512	47.38
TY26999 + 0.8nM TY27566	2.132	44.92
Ab ID	**EC_{50}(nM)**	**Span**
TY27556 + 8nM Isotype Ctrl	NA	NA
TY27566 + 8nM Isotype Ctrl	NA	NA

[Fig. 16]

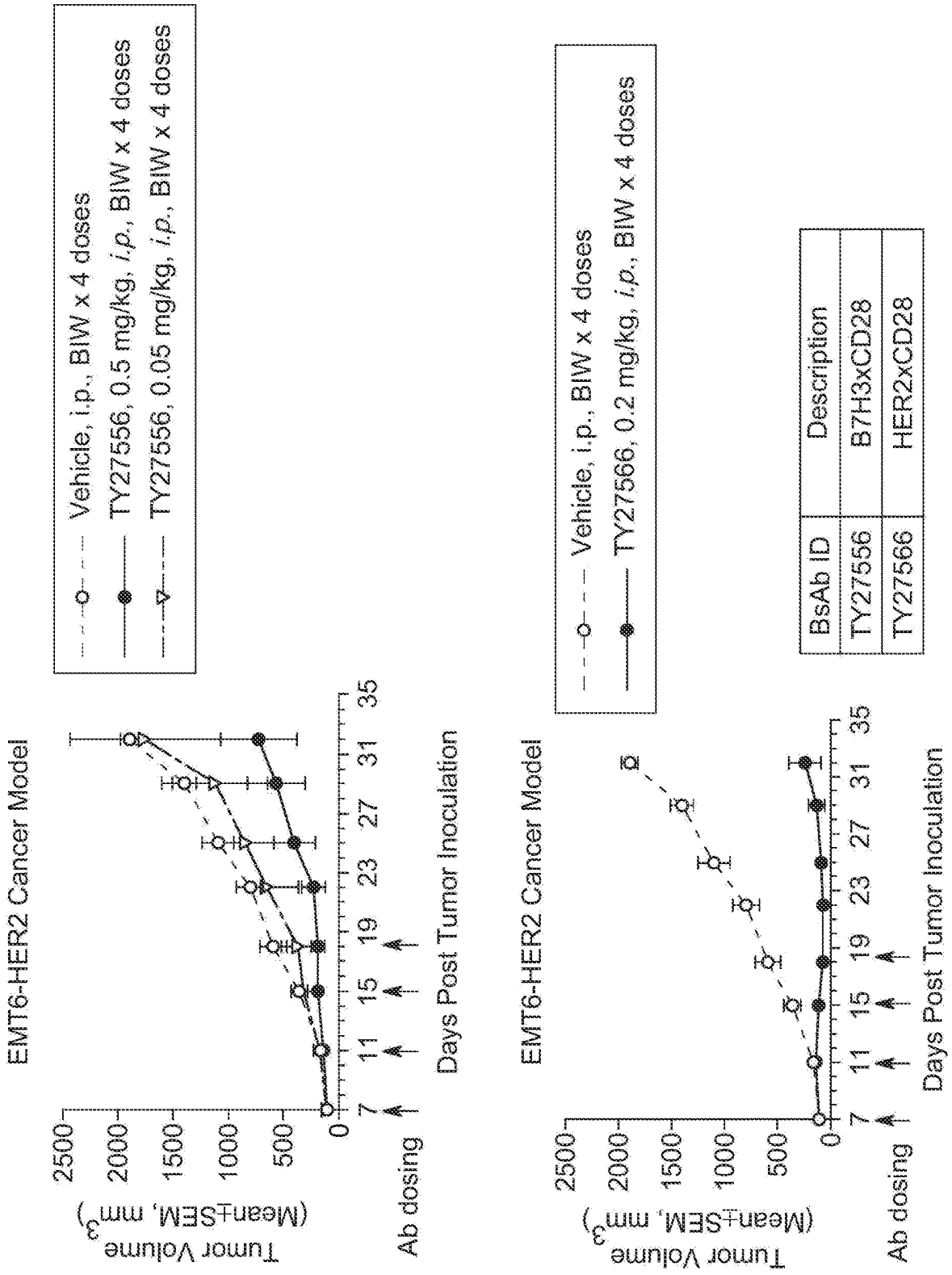

IFN-γ secretion
IFN-γ Conc. (pg/ml)
25000
20000
15000
10000
5000
0
Anti-CD3 2C11 clone
TY27042
TY27556
TY27042+ TY27556
0 h
3.5 h
24 h
IL-6 secretion
IL-6 Conc. (pg/ml)
4000
3000
2000
1000
0
Anti-CD3
TY27556
TY27042
TY27042+TY27556
CD3+T cell(%CD45+)
80
60
40
20
0

[Fig. 17]



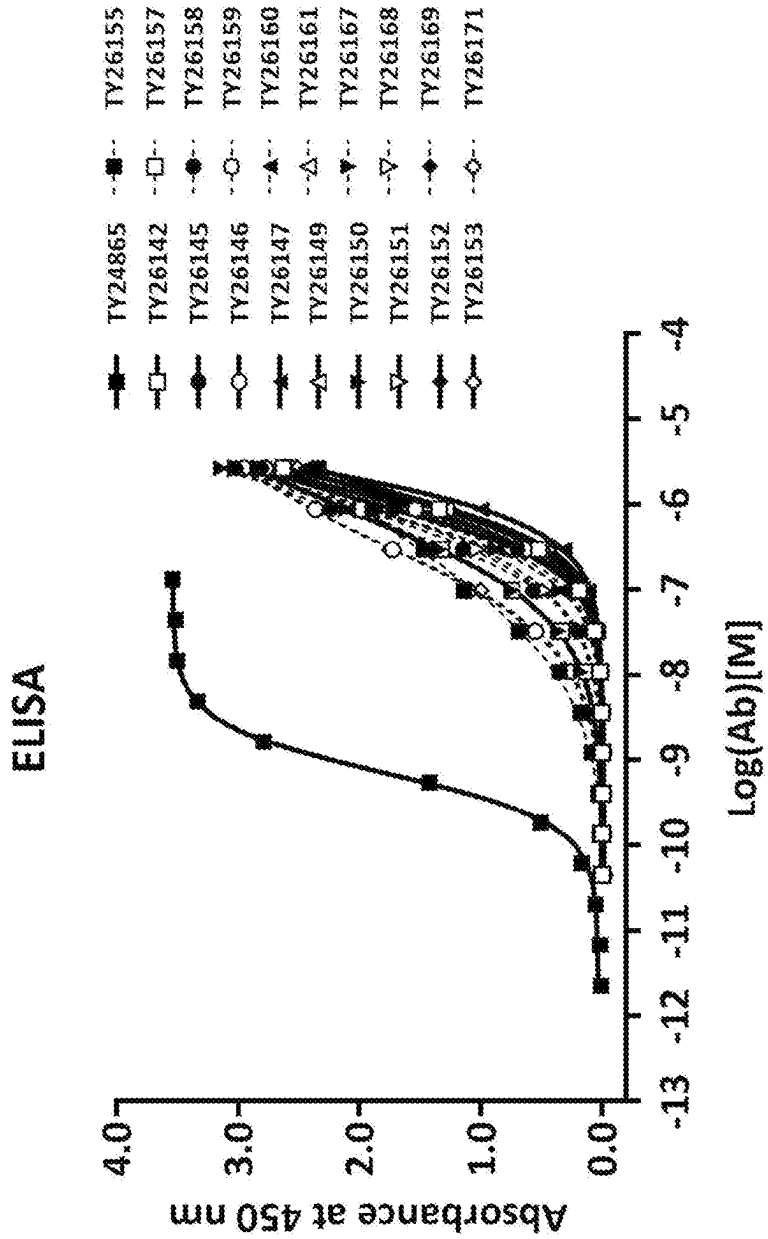
BsAb ID	Description
TY27151	SAFE-HER2xSAFE-CD3
TY27556	B7H3xCD28

[Fig. 18]

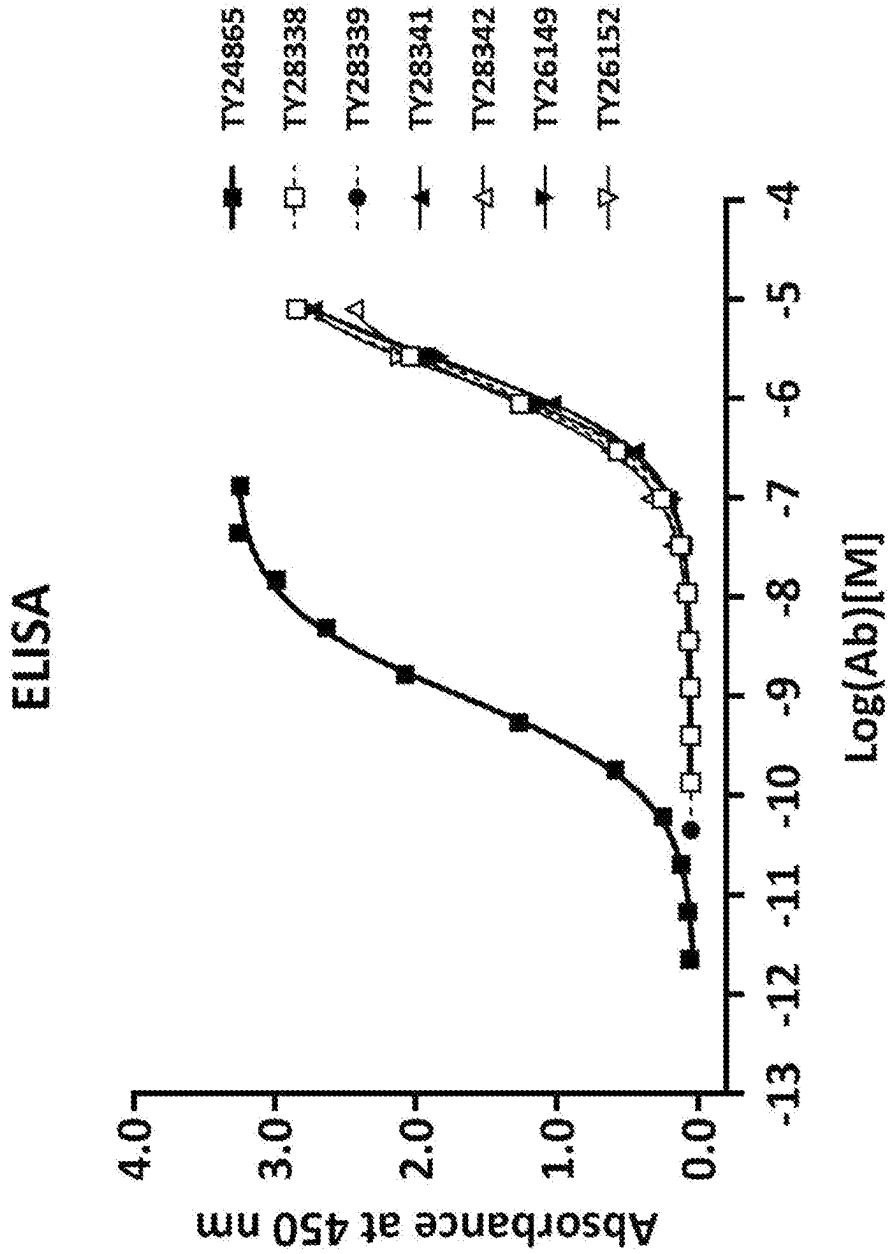


BsAb ID	Description
TY27556	B7H3xCD28
TY27566	HER2xCD28

[Fig. 19]


ELISA
Absorbance at 450 nm
4.0
3.0
2.0
1.0
0.0
-13
-12
-11
-10
-9
-8
-7
-6
-5
-4
Log(Ab)[M]
TY24865
TY26142
TY26145
TY26146
TY26147
TY26149
TY26150
TY26151
TY26152
TY26153
TY26155
TY26157
TY26158
TY26159
TY26160
TY26161
TY26167
TY26168
TY26169
TY26171

[Fig. 20]


ELISA
TY24865
TY28338
TY28339
TY28341
TY28342
TY26149
TY26152
Absorbance at 450 nm
4.0
3.0
2.0
1.0
0.0
-13
-12
-11
-10
-9
-8
-7
-6
-5
-4
Log(Ab)[M]

[Fig. 21]

Sequence number	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43
sp|P10747|CD28_HUMAN	N	K	I	L	V	K	Q	S	P	M	L	V	A	Y	D	N	A	V	N	L	S	C	K	Y	S
sp|P31041|CD28_MOUSE	N	K	I	L	V	K	Q	S	P	L	L	V	V	D	S	N	E	V	S	L	S	C	R	Y	S
TY24865	N	K	I	L	V	K	Q	S	P	M	L	V	A	Y	D	N	A	V	N	L	S	C	K	Y	S

Sequence number	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68
sp|P10747|CD28_HUMAN	Y	N	L	F	S	R	E	F	R	A	S	L	H	K	G	L	D	S	A	V	E	V	C	V	V
sp|P31041|CD28_MOUSE	Y	N	L	L	A	K	E	F	R	A	S	L	Y	K	G	V	N	S	D	V	E	V	C	V	G
TY24865	Y	N	L	F	S	R	E	F	R	A	S	L	H	K	G	L	D	S	A	V	E	V	C	V	V

Sequence number	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93
sp|P10747|CD28_HUMAN	Y	G	N	Y	S	Q	Q	L	Q	V	Y	S	K	T	G	F	N	C	D	G	K	L	G	N	E
sp|P31041|CD28_MOUSE	N	G	N	F	T	Y	Q	P	Q	F	R	S	N	A	E	F	N	C	D	G	D	F	D	N	E
TY24865	Y	G	N	Y	S	Q	Q	L	Q	V	Y	S	K	T	G	F	N	C	D	G	K	L	G	N	E

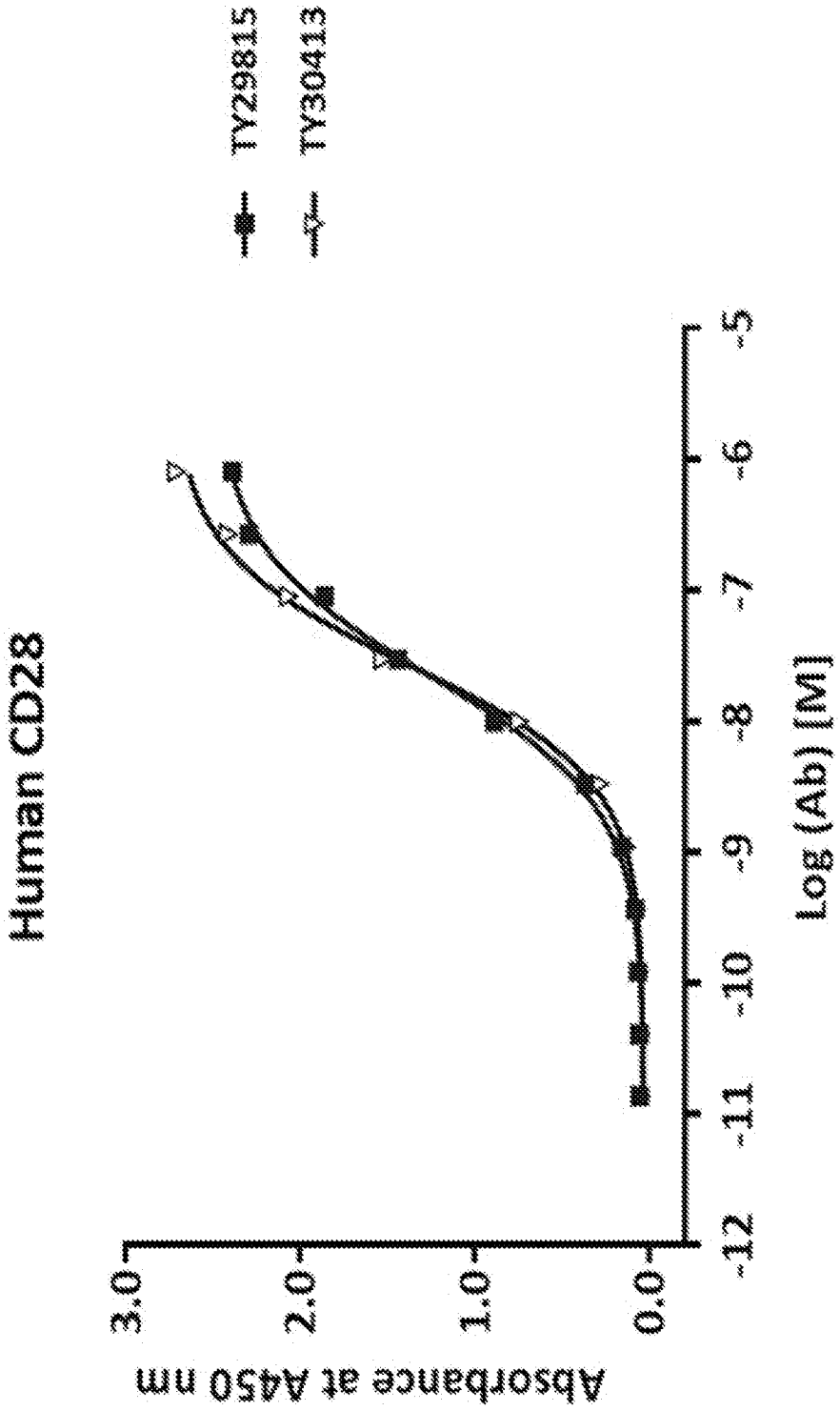
Sequence number	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118
sp|P10747|CD28_HUMAN	S	V	T	F	Y	L	Q	N	L	Y	V	N	Q	T	D	I	Y	F	C	K	I	E	V	M	Y
sp|P31041|CD28_MOUSE	T	V	T	F	R	L	W	N	L	H	V	N	H	T	D	I	Y	F	C	K	I	E	F	M	Y
TY24865	S	V	T	F	Y	L	Q	N	L	Y	V	N	Q	T	D	I	Y	F	C	K	I	E	V	M	Y

Sequence number	119	120	121	122	123	124	125	126
sp|P10747|CD28_HUMAN	P	P	P	Y	L	D	N	E
sp|P31041|CD28_MOUSE	P	P	P	Y	L	D	N	E
TY24865	P	P	P	Y	L	D	N	E

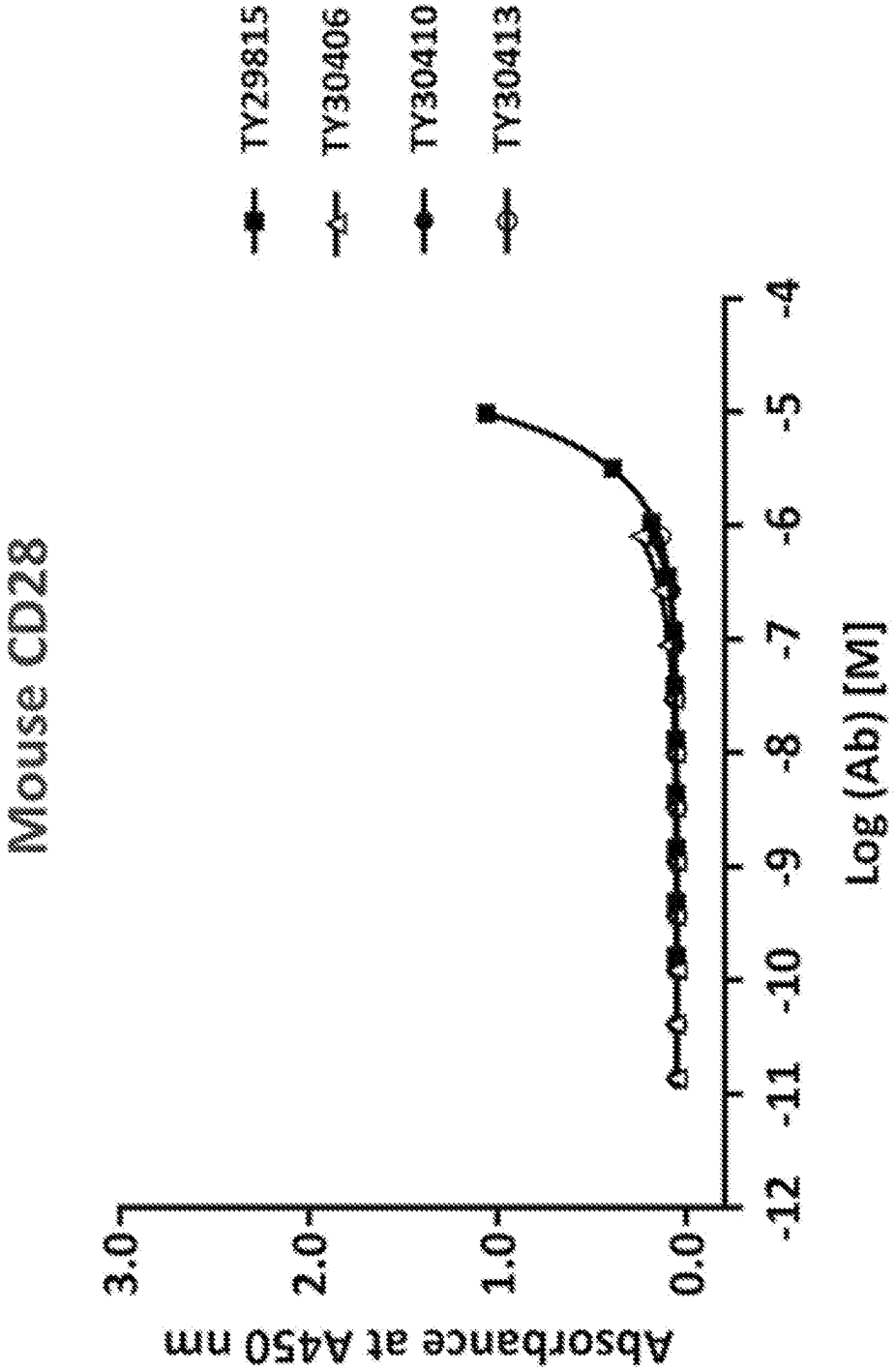
Binding Sites

Diffeerent Residues from human and mouse CD28

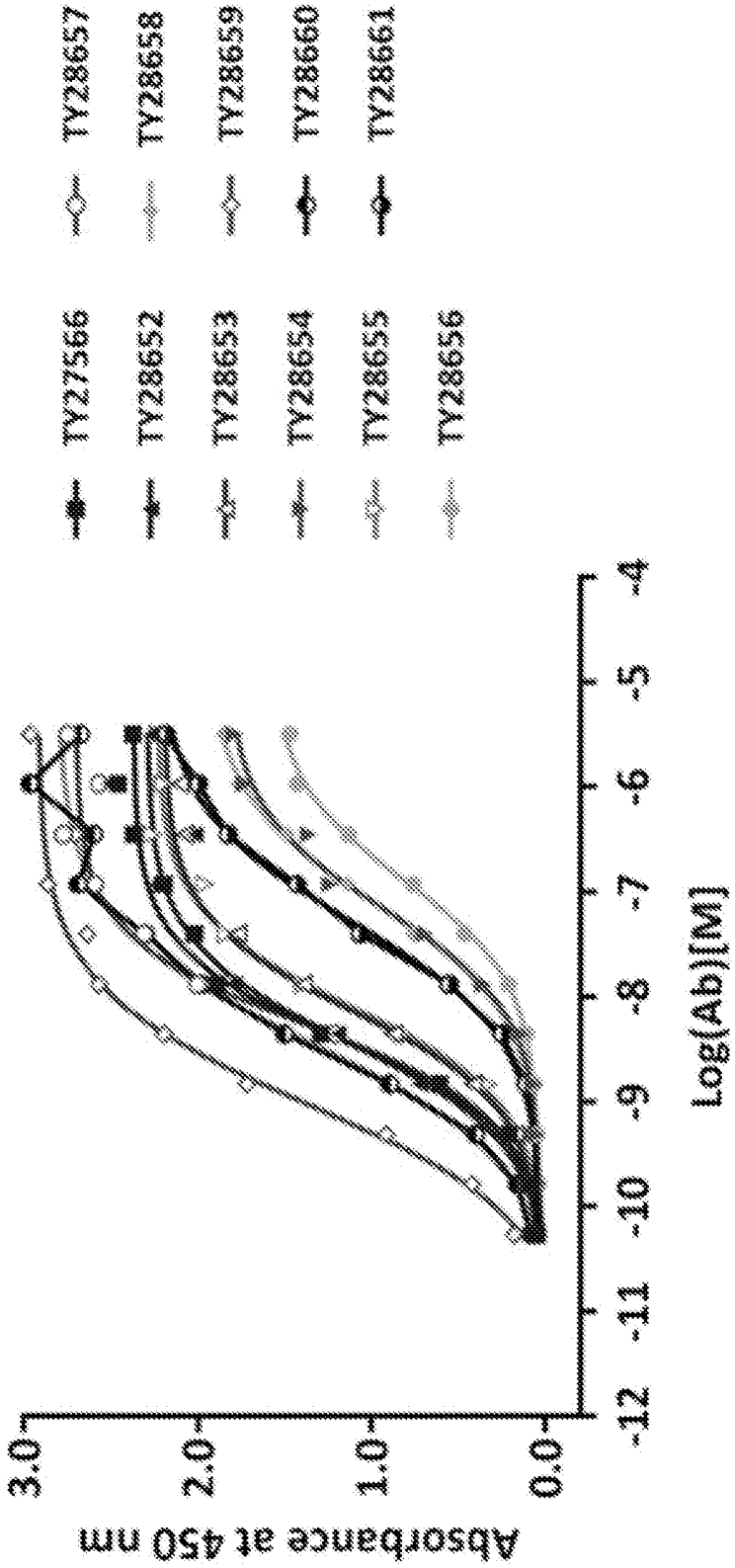
[Fig. 22A]


Human CD28
TY29815
TY30413
Absorbance at A450 nm
3.0
2.0
1.0
0.0
-12
-11
-10
-9
-8
-7
-6
-5
Log (Ab) [M]

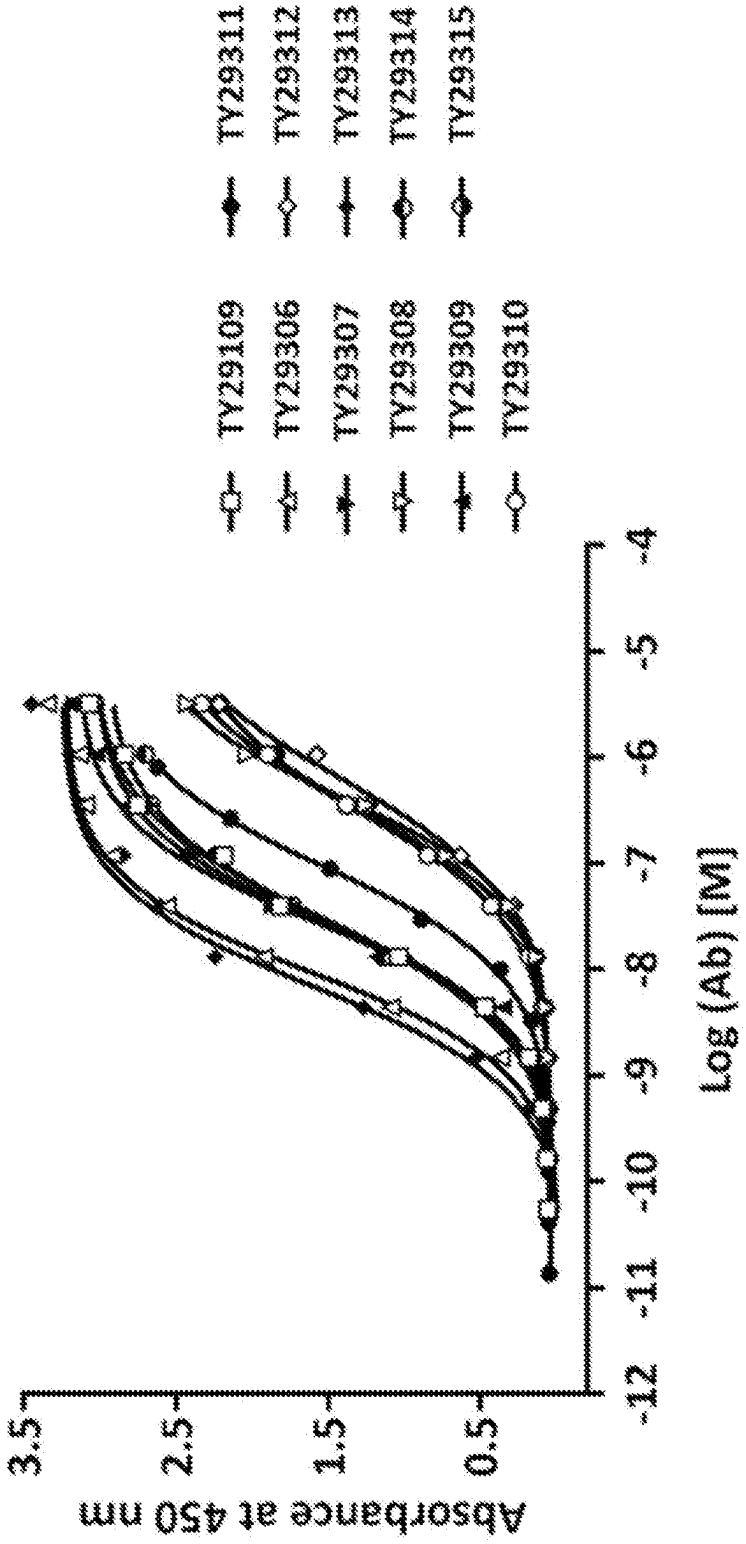
[Fig. 22B]


Mouse CD28
TY29815
TY30406
TY30410
TY30413
Absorbance at A450 nm
3.0
2.0
1.0
0.0
-12
-11
-10
-9
-8
-7
-6
-5
-4
Log (Ab) [M]

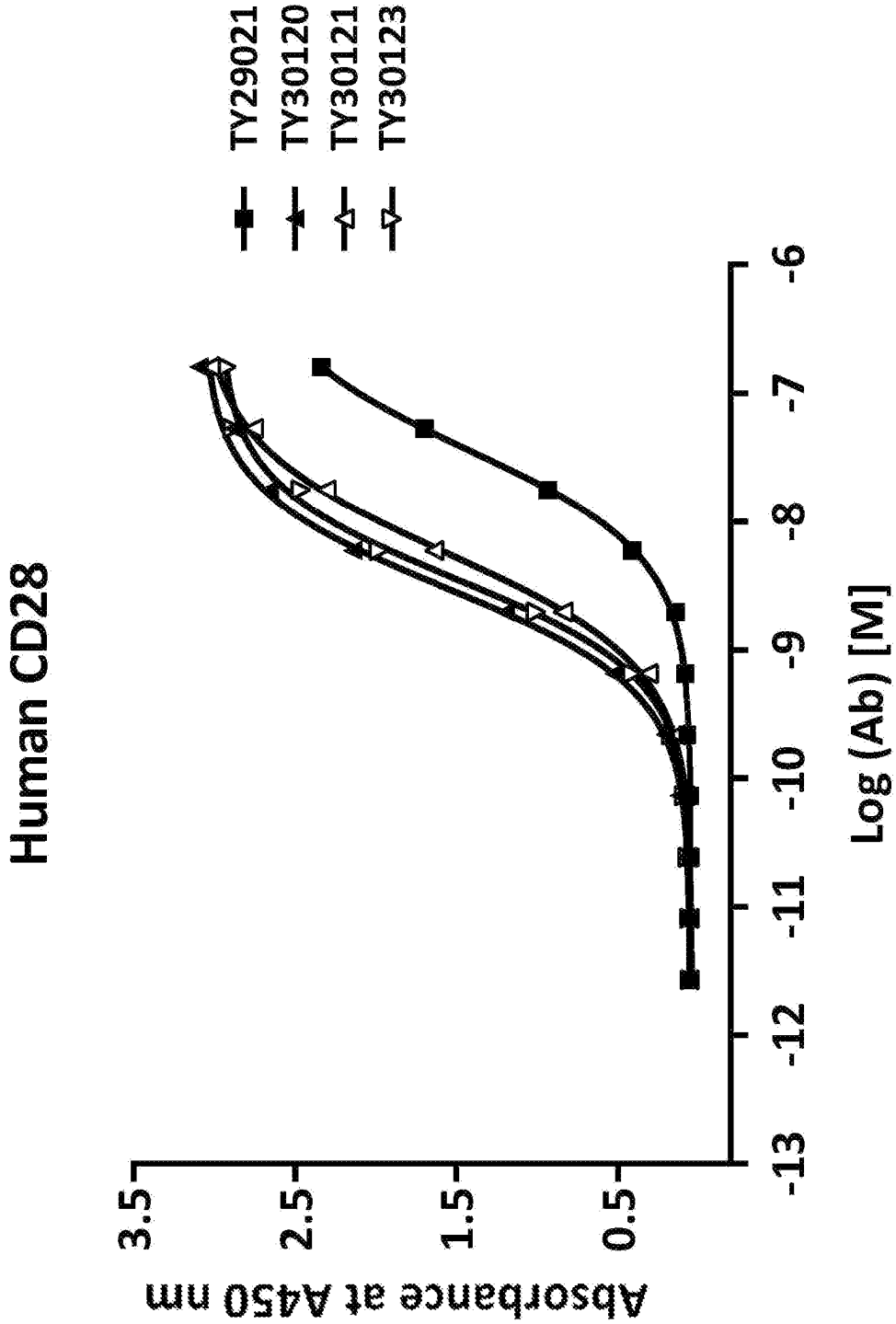
[Fig. 23A]


TY27566
TY28652
TY28653
TY28654
TY28655
TY28656
TY28657
TY28658
TY28659
TY28660
TY28661
Absorbance at 450 nm
3.0
2.0
1.0
0.0
-12
-11
-10
-9
-8
-7
-6
-5
-4
Log(Ab)[M]

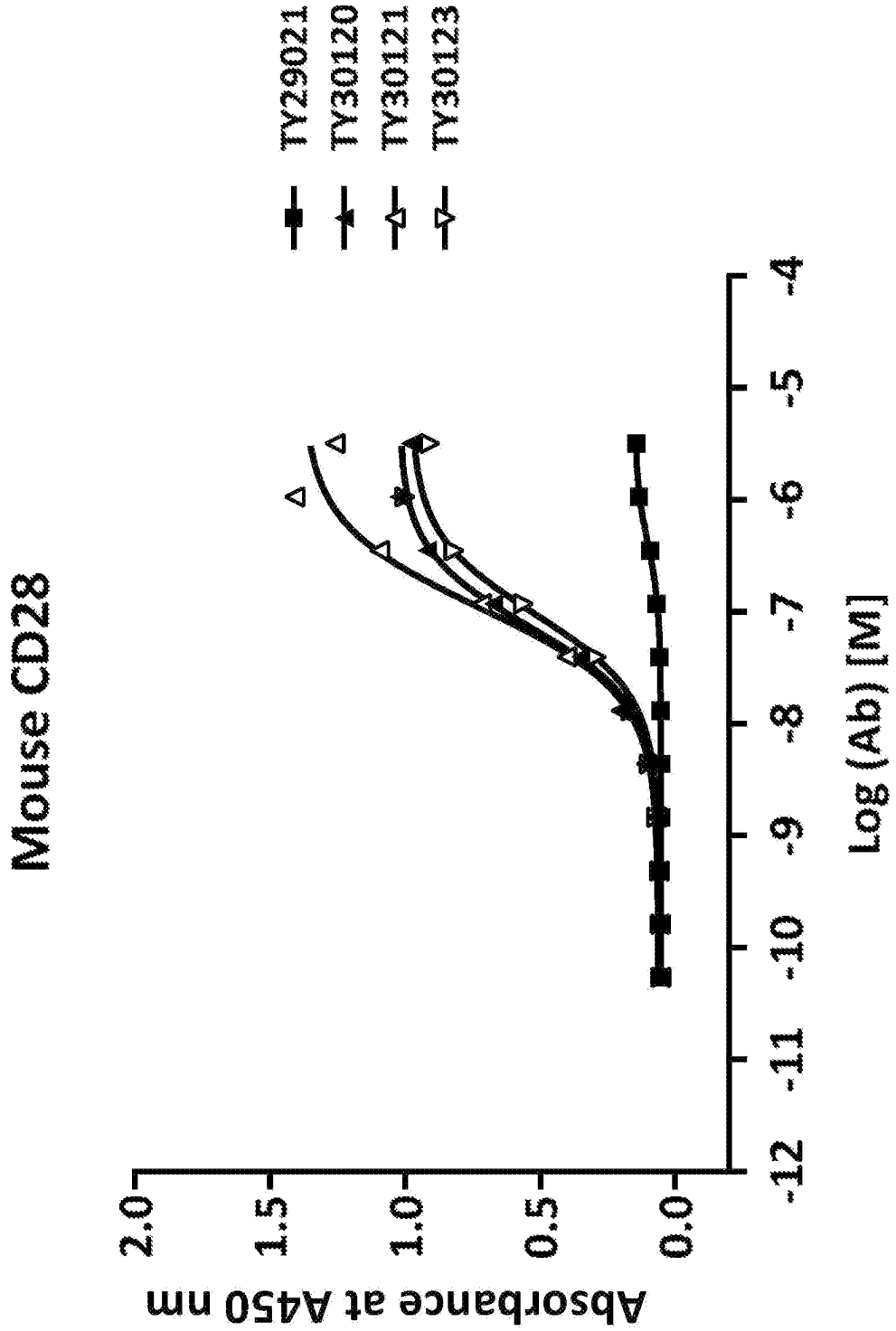
[Fig. 23B]


TY29311
TY29312
TY29313
TY29314
TY29315
TY29109
TY29306
TY29307
TY29308
TY29309
TY29310
Absorbance at 450 nm
3.5
2.5
1.5
0.5
-12
-11
-10
-9
-8
-7
-6
-5
-4
Log (Ab) [M]

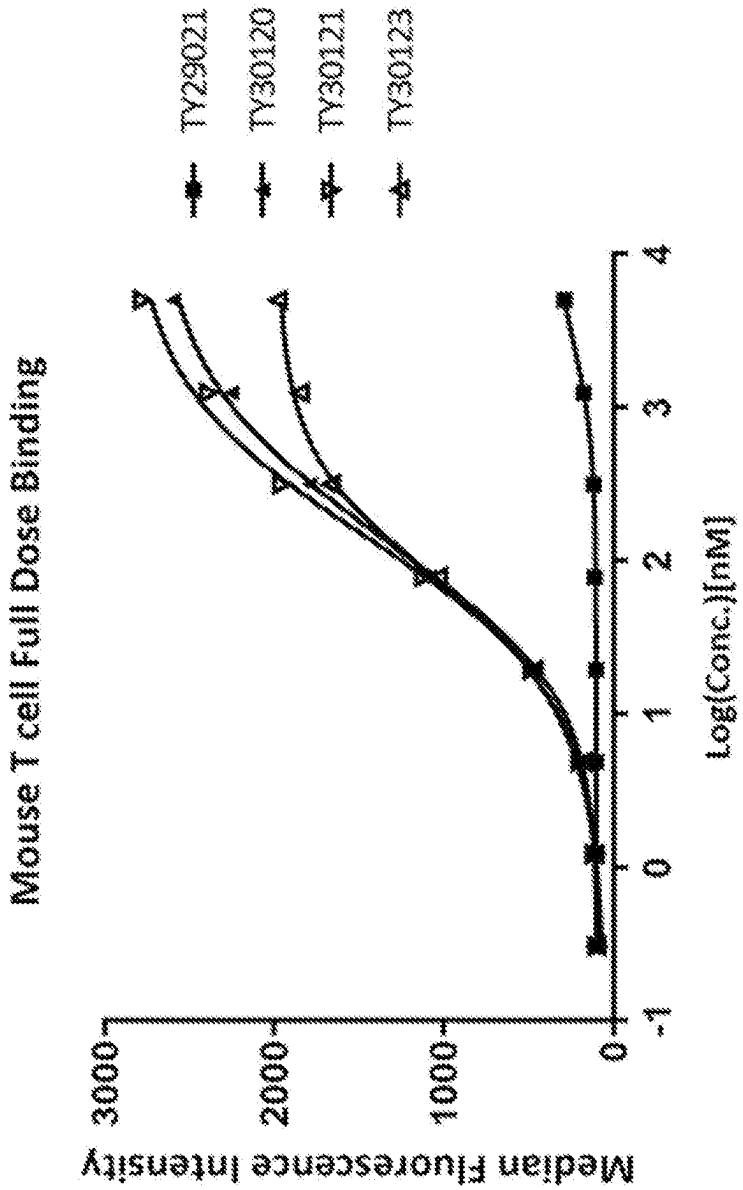
[Fig. 24A]


Human CD28
TY29021
TY30120
TY30121
TY30123
Absorbance at A450 nm
3.5
2.5
1.5
0.5
-13
-12
-11
-10
-9
-8
-7
-6
Log (Ab) [M]

[Fig. 24B]


Mouse CD28
TY29021
TY30120
TY30121
TY30123
Absorbance at A450 nm
2.0
1.5
1.0
0.5
0.0
-12
-11
-10
-9
-8
-7
-6
-5
-4
Log (Ab) [M]

[Fig. 25]



	EC_{50} (nM)	Max MFI	AUC
TY29021	NA	364.1	548.8
TY30120	144.8	2711	4375
TY30121	142.5	2857	4619
TY30123	76.18	1981	3822

ANTI-CD28 ANTIBODIES AND METHODS OF USE THEREOF

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application claims priority from PCT/CN2022/085838, filed Apr. 8, 2023, whose disclosure is incorporated by reference herein in its entirety.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing that has been submitted electronically in XML format and is hereby incorporated by reference in its entirety. The electronic copy of the Sequence Listing, created on Apr. 6, 2023 and named 123687_W0003_SL. xml, is 488, 908 bytes in size.

BACKGROUND OF THE INVENTION

[0003] CD28 is a costimulatory signaling molecule on T cells and plays a key role in their activation, proliferation, and survival. Activation of the CD28 costimulatory signal has the potential to enhance anti-tumor T cell immunity. However, therapies targeting CD28 for systemic T cell activation have caused deleterious cytokine storm and multiorgan failure (Suntharalingam et al., N Engl J Med. (2006) 355 (10): 1018-28). Thus, there is a need for improved CD28-targeting therapies that avoid serious autoimmune adverse events associated with systemic CD28 activation.

SUMMARY OF THE INVENTION

[0004] The present disclosure provides novel binding molecules (e.g., antibodies) targeting a tumor-associated antigen (e.g., B7-H3, HER2, TROP2, or PD-L1) and CD28, as well as pharmaceutical compositions comprising one or more of these binding molecules, and use of these binding molecules and pharmaceutical compositions for treating cancer. Compared to currently available cancer treatments, including antibody treatments, it is contemplated that the binding molecules of the present disclosure may provide a superior clinical response.

[0005] In some aspects, the present disclosure provides an antigen-binding protein such as an antibody or an antigen-binding fragment thereof, comprising an CD28-binding portion, wherein the CD28-binding portion binds human CD28 and is cross-reactive with cynomolgus monkey and mouse CD28. In some embodiments, the CD28-binding portion binds to a CD28 epitope comprising amino acid residues 51-122 of human CD28 (SEQ ID NO: 1). In particular embodiments, the CD28 epitope comprises amino acid residues 51, 52, 54, 55, 98-101, 110-111, 113-114, and 118-122 of SEQ ID NO: 1.

[0006] In some embodiments, the present disclosure provides an antigen-binding protein such as an antibody or an antigen-binding fragment thereof comprising a CD28-binding portion that binds human CD28, wherein the CD28-binding portion comprises an antibody heavy chain variable domain (V_H) and an antibody light chain variable domain (V_L), and wherein the V_H and V_L comprises heavy chain complementarity-determining regions (CDRs) 1-3 and light chain CDR1-3 set forth in SEQ ID NOs: 5-10, respectively, SEQ ID NOs: 15, 6, 16, 17-19, respectively, SEQ ID NOs: 24, 6, 25, 26-28, respectively, SEQ ID NOs: 33, 6, 35-38, respectively, SEQ ID NOs: 43, 6, 44, 45, 9, and 46, respectively, SEQ ID NOs: 33, 51-53, 300, and 10, respectively, SEQ ID NOs: 24, 58, 59, 60, 300, and 61, respectively, SEQ ID NOs: 66-69, 300 and 70, respectively, SEQ ID NOs: 24, 6, 75, 76, 18, and 28, respectively, SEQ ID NOs: 24, 58, 81, 82, 27, and 83, respectively, SEQ ID NOs: 88-91, 300, and 70, respectively, SEQ ID NOs: 24, 96-98, 9, and 70, respectively, SEQ ID NOs: 103-106, 18, and 83, respectively, SEQ ID NOs: 111, 6, 112, 113, 18, and 114, respectively, SEQ ID NOs: 15, 6, 119, 120, 9, and 121, respectively, SEQ ID NOs: 126, 67, 127, 128, 18, and 129, respectively, SEQ ID NOs: 134, 6, 135, 136, 27, and 83, respectively, SEQ ID NOs: 43, 58, 141, 142, 300, and 143, respectively, SEQ ID NOs: 148, 6, 149, 150, 300, and 83, respectively, SEQ ID NOs: 15, 155, 16, 156, 27, and 70, respectively, or SEQ ID NOs: 161, 6, 162, 163, 300, and 164.

[0007] In some embodiments, the CD28-binding portion comprises V_H and V_L set forth in SEQ ID NOs: 11 and 12, respectively, SEQ ID NOs: 20 and 21, respectively, SEQ ID NOs: 29 and 30, respectively, SEQ ID NOs: 39 and 40, respectively, SEQ ID NOs: 47 and 48, respectively, SEQ ID NOs: 54 and 55, respectively, SEQ ID NOs: 62 and 63, respectively, SEQ ID NOs: 71 and 72, respectively, SEQ ID NOs: 77 and 78, respectively, SEQ ID NOs: 84 and 85, respectively, SEQ ID NOs: 92 and 93, respectively, SEQ ID NOs: 99 and 100, respectively, SEQ ID NOs: 107 and 108, respectively, SEQ ID NOs: 115 and 116, respectively, SEQ ID NOs: 122 and 123, respectively, SEQ ID NOs: 130 and 131, respectively, SEQ ID NOs: 137 and 138 respectively, SEQ ID NOs: 144 and 145, respectively, SEQ ID NOs: 151 and 152, respectively, SEQ ID NOs: 157 and 158, respectively, SEQ ID NOs: 165 and 166, respectively, SEQ ID NOs: 362 and 363, respectively, SEQ ID NOs: 364 and 365, respectively, SEQ ID NOs: 366 and 367, respectively, SEQ ID NOs: 368 and 369, respectively, SEQ ID NOs: 370 and 371, respectively, SEQ ID NOs: 372 and 373, respectively, SEQ ID NOs: 374 and 375, respectively, SEQ ID NOs: 376 and 12, respectively, SEQ ID NOs: 377 and 378, respectively, SEQ ID NOs: 379 and 380, respectively, SEQ ID NOs: 381 and 12, respectively, SEQ ID NOs: 382 and 12, respectively, SEQ ID NOs: 383 and 12, respectively, SEQ ID NOs: 384 and 12, respectively, SEQ ID NOs: 385 and 12, respectively, or SEQ ID NOs: 386 and 12, respectively.

[0008] In some embodiments, the CD28-binding protein comprises a heavy chain (HC) and a light chain (LC) set forth in SEQ ID NOs: 13 and 14, respectively, SEQ ID NOs: 22 and 23, respectively, SEQ ID NOs: 31 and 32, respectively, SEQ ID NOs: 41 and 42, respectively, SEQ ID NOs: 49 and 50, respectively, SEQ ID NOs: 56 and 57, respectively, SEQ ID NOs: 64 and 65, respectively SEQ ID NOs: 73 and 74, respectively, SEQ ID NOs: 79 and 80, respectively, SEQ ID NOs: 86 and 87, respectively, SEQ ID NOs: 94 and 95, respectively, SEQ ID NOs: 101 and 102, respectively, SEQ ID NOs: 109 and 110, respectively, SEQ ID NOs: 117 and 118, respectively, SEQ ID NOs: 124 and 125, respectively, SEQ ID NOs: 141 and 142, respectively, SEQ ID NOs: 132 and 133, respectively, SEQ ID NOs: 139 and 140, respectively, SEQ ID NOs: 146 and 147, respectively, SEQ ID NOs: 153 and 154, respectively, SEQ ID NOs: 159 and 160, respectively, or SEQ ID NOs: 167 and 168, respectively.

[0009] In some aspects, the present disclosure also provides pharmaceutical compositions comprising an antigen-binding protein such as an antibody or an antigen-binding

fragment thereof herein and a pharmaceutically acceptable carrier; nucleic acid molecule (s) encoding the antigen-binding protein; expression vector (s) comprising the nucleic acid molecule (s); and a host cell comprising the vector (s), wherein the host cell may be a prokaryotic cell or an eukaryotic cell such as a mammalian cell.

[0010] In some aspects, the present disclosure also provides a method of producing the antigen-binding protein such as an antibody or an antigen-binding fragment thereof herein, comprising culturing the host cell under conditions that allow expression of the antigen-binding protein, and isolating the antigen-binding protein from the culture.

[0011] In some aspects, the present disclosure also provides a method of treating cancer in a patient in need thereof, comprising administering to the patient a therapeutically effective amount of the antigen-binding protein, such as an antibody or an antigen-binding fragment, herein. In some embodiments, the method further comprises administering to the patient another anti-cancer therapeutic. In further embodiments, the additional anti-cancer therapeutic is a bispecific antibody (bsAb) targeting CD3 and a tumor-associated antigen (TAA). In particular embodiments, the TAA is B7-H3, HER2, or TROP2. In some embodiments, the additional anti-cancer therapeutics is an immune checkpoint inhibitor, optionally an anti-PD-1, anti-CTLA-4, or anti-PD-L1 antibody.

[0012] Also provided herein are the present antigen-binding proteins such as antibodies or antigen-binding fragments thereof, or pharmaceutical compositions, for use in treating a cancer in a patient in need thereof; use of the present antigen-binding proteins such as antibodies or antigen-binding fragments thereof for the manufacture of a medicament for treating a cancer in a patient in need thereof; and articles of manufacture (e.g., kits) comprising one or more dosing units of the present antigen-binding proteins such as antibodies or or fragments thereof.

[0013] Other features, objects, and advantages of the invention are apparent in the detailed description that follows. It should be understood, however, that the detailed description, while indicating embodiments and aspects of the invention, is given by way of illustration only, not limitation. Various changes and modification within the scope of the invention will become apparent to those skilled in the art from the detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

[0014] FIG. **1** is a panel of graphs showing a binding affinity assay of anti-CD28 antibodies to recombinant CD28 (human and mouse) protein.

[0015] FIG. **2** is a graph showing binding of anti-CD28 IgGs to human CD3+ T cells.

[0016] FIG. **3** is a panel of graphs showing ligand blocking assays of IgGs for human CD28-CD80 (top right and top left graphs) and CTLA-4 CD80 pairs (bottom graph).

[0017] FIG. **4**A is a graph showing a T cell proliferation assay showing that IgGs does not induce systemic T cell activation in comparison to CD28 superagonist TAC2386 (TGN1412).

[0018] FIG. **4**B is a graph showing a T cell activation co-stimulation assay-proliferation by CellTiter-Glo® (CTG) readout.

[0019] FIG. **4**C is a graph showing a T cell activation co-stimulation assay for IFN-γ release.

[0020] FIG. **5**A is a graph showing a T cell activation and proliferation assay-proliferation by CTG readout using anti-CD28 test antibodies with OKT3.

[0021] FIG. **5**B is a graph that shows a T cell activation and proliferation assay for IL-2 release.

[0022] FIG. **6** is a graph showing binding of anti-HER2 antibodies and bispecific antibodies (BsAbs) to SK-OV3 cells. Also shown is a table containing plotted values.

[0023] FIG. **7** is a graph showing a Jurkat-NFκB Luciferase reporter gene assay measuring NFκB signaling stimulatory effects in terms of maximum signal and EC_{50} values of anti-HER2×CD28 BsAb (TY27566 or TY27807) in combination with a fixed concentration of anti-HER2×CD3 BsAb (TY25238), and anti-HER2×CD3 BsAb in combination with a fixed concentration of anti-HER2×CD28 BsAb. Also shown is a table containing plotted values.

[0024] FIG. **8** is a graph showing a killing assay to MCF-7 cells of CD28 BsAb and CD3 BsAb with the same or different HER2 epitope and a table containing plotted values.

[0025] FIG. **9** is a panel of graphs showing an assay to measure concentration-dependent binding activity of anti-TROP2 bispecific antibodies on tumor cell lines.

[0026] FIG. **10**A is a graph showing a Jurkat-NFκB Luciferase reporter assay measuring NFκB signaling stimulatory effects in terms of maximum signal and EC_{50} values of bispecific antibodies on H292 cells. Also shown is a table containing plotted values.

[0027] FIG. **10**B is a graph showing a Jurkat-NFκB Luciferase reporter assay measuring NFκB signaling stimulatory effects in terms of maximum signal and EC_{50} values of a bispecific antibodies on H292 cells. Also shown is a table containing plotted values.

[0028] FIG. **11** is a panel of flow cytometry plots showing the co-expression of PD-L1 and B7H3 on MDA-MB-231 cells.

[0029] FIG. **12** is a graph showing a binding assay of B7H3 IgG and B7H3×CD28 bsAb to MDA-MB-231 cells. Also shown is a table containing plotted values.

[0030] FIGS. **13**A and **13**B are graphs showing a one-way MLR assay to test the activity of B7H3×CD28 bsAb in combination with anti-PD-1 or anti-PD-L1 blocking mAbs on primary human T cell activation, as measured by IL-2 secretion (FIG. **13**A) and IFN-γ secretion (FIG. **13**B).

[0031] FIG. **14** is a graph showing an in vitro assay that measures tumor killing activity of anti-CD3-based, or anti-CD28-based HER2-targeted bsAbs or their combinations on the MCF-7 tumor cell line. Also shown is a table containing plotted values.

[0032] FIG. **15** is a graph showing an in vitro assay that measures tumor killing activity of anti-CD3-based, or anti-CD28-based HER2-targeted bsAbs or their combinations on the EMT6-HER2 tumor cell line. Also shown is a table containing plotted values.

[0033] FIG. **16** is panel of graphs showing an assay to measure systemic cytokine release of IL-6 and IFN-γ (top left and right graphs, respectively), and to measure CD3+ T cells percentage of total CD45+ T cells (bottom graph), in WT mice treated with TCEs.

[0034] FIG. **17** shows an in vivo efficacy study and graph of HER2×CD3 bsAb and B7H3×CD28 bsAb mono or in combination in SK-OV3+PBMC xenograft tumor model.

[0035] FIG. **18** is a panel of graphs showing an in vivo efficacy study of B7H3×CD28 or HER2×CD28 bsAb in EMT6-HER2 model.

[0036] FIG. **19** is a graph showing the ELISA measurement of masking efficiency of anti-CD28 activatable antibodies binding to recombinant human CD28.

[0037] FIG. **20** is a graph showing the ELISA measurement of masking efficiency of anti-CD28 activatable antibodies binding to recombinant human CD28.

[0038] FIG. **21** (SEQ ID NOs: 359-361) is table showing the different binding residues from human and mouse CD28.

[0039] FIG. **22**A is a graph showing binding of anti-PD-L1×CD28 bsAbs TY29815 and TY30413 to human CD28.

[0040] FIG. **22**B is a graph showing binding of anti-PD-L1×CD28 bsAbs TY29815, TY30406, TY30410, and TY30413 to mouse CD28.

[0041] FIG. **23**A is a graph showing binding of anti-HER2×CD28 bsAbs TY27566, TY28652, TY28653, TY28654, TY28655, TY28656, TY28657, TY28658, TY28659, TY28660, and TY28661 to human CD28.

[0042] FIG. **23**B is a graph showing binding of anti-HER2×CD28 bsAbs TY29109, TY29306, TY29307, TY29308, TY29309, TY29310, TY29311, TY29312, TY29313, TY29314, and TY29315 to human CD28.

[0043] FIG. **24**A is a graph showing binding of anti-B7H3×CD28 bsAbs TY29021, TY30120, TY30121, and TY30123 to human CD28.

[0044] FIG. **24**B is a graph showing binding of anti-B7H3×CD28 bsAbs TY29021, TY30120, TY30121, and TY30123 to mouse CD28.

[0045] FIG. **25** is a graph showing mouse T-cell binding assay measuring T-cell binding effects in terms of maximum signal, EC_{50}, and AUC values of anti-B7H3×CD28 bsAbs TY29021, TY30120, TY30121, and TY30123. Also shown is a table containing plotted values.

DETAILED DESCRIPTION

I. Definitions

[0046] Before describing the present disclosure in detail, it is to be understood that this present disclosure is not limited to particular compositions or biological systems, which can, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

[0047] The term "about" as used herein refers to the usual error range for the respective value readily known to the skilled person in this technical field. Reference to "about" a value or parameter herein includes (and describes) embodiments that are directed to that value or parameter per se.

[0048] It is understood that aspects and embodiments of the present disclosure described herein include "comprising," "consisting," and "consisting essentially of" aspects and embodiments.

[0049] The term "and/or" as used herein a phrase such as "A and/or B" is intended to include both A and B; A or B; A (alone); and B (alone). Likewise, the term "and/or" as used herein a phrase such as "A, B, and/or C" is intended to encompass each of the following embodiments: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0050] The term "antibody" encompasses various antibody structures, including but not limited to monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, masked antibodies (e.g., activatable or non-activatable antibodies), multi-specific antibodies (e.g., bispecific antibodies, including masked bispecific antibodies), and antibody fragments (e.g., a single-chain variable fragment or scFv) so long as they exhibit the desired biological activity (e.g., the ability to bind a target antigen with desired specificity and affinity).

[0051] The term "antibody" encompasses various antibody structures, including but not limited to monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, masked antibodies (e.g., activatable or non-activatable antibodies), and multi-specific antibodies (e.g., bispecific antibodies). The term "antibody" also includes, but is not limited to, chimeric antibodies, humanized antibodies, and fully human antibodies.

[0052] In some embodiments, the term "antibody" refers to an antigen-binding protein (i.e., immunoglobulin) having a basic four-polypeptide chain structure consisting of two identical heavy (H) chains and two identical light (L) chains. Each L chain is linked to an H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. Each heavy chain has, at the N-terminus, a variable region (also known as variable domain) (abbreviated herein as V_H) followed by a constant region. The heavy chain constant region is comprised of three domains, C_H1, C_H2 and C_H3. Each light chain has, at the N-terminus, a variable region (also known as variable domain) (abbreviated herein as V_L) followed by a constant region at its other end. The light chain constant region is comprised of one domain, C_L. The V_L is aligned with the V_H and the C_L is aligned with the first constant domain of the heavy chain (C_H1). The pairing of a V_H and V_L together forms a single antigen-binding site.

[0053] The V_H and V_L can be further subdivided into complementarity-determining regions (CDRs) and framework regions (FRs). CDRs are of highest sequence variability and/or involved in antigen recognition. CDRs and FRs intersperse in the order of FR1, CDR1, FR2, CDR2, FR3, CDR3, and FR4. CDRs also comprise "specificity determining residues," or "SDRs," which are residues that contact the antigen. SDRs are contained within regions of the CDRs called abbreviated-CDRs, or a-CDRs. Exemplary a-CDRs (a-LCDR1, a-LCDR2, a-LCDR3, a-HCDR1, a-HCDR2, and a-HCDR3) occur at amino acid residues 31-34, 50-55, 89-96 of the light chain, and 31-35, 50-58, and 95-102 of the heavy chain, respectively. See Almagro and Fransson, Front Biosci. (2008) 13: 1619-33). Unless otherwise indicated, residues in the variable domain are numbered herein according to Kabat et al., J Biol Chem. (1977) 252: 6609-16; Kabat et al., U.S. Dept. of Health and Human Services, "Sequences of proteins of immunological interest" (1991).

[0054] Table 1 below provides exemplary CDR definitions according to various algorithms known in the art.

TABLE 1

CDR Definitions					
	Kabat[1]	Chothia[2]	MacCallum[3]	IMGT[4]	AHo[5]
HCDR1	31-35	26-32	30-35	27-38	25-40
HCDR2	50-65	53-55	47-58	56-65	58-77
HCDR3	95-102	96-101	93-101	105-117	109-137

TABLE 1-continued

CDR Definitions					
	Kabat[1]	Chothia[2]	MacCallum[3]	IMGT[4]	AHo[5]
LCDR1	24-34	26-32	30-36	27-38	25-40
LCDR2	50-56	50-52	46-55	56-65	58-77
LCDR3	89-97	91-96	89-96	105-117	109-137

[1]Residue numbering follows the nomenclature of Kabat et al., supra.

[2]Residue numbering follows the nomenclature Chothia et al., J. Mol. Biol. (1987) 196: 901-917; Al-Lazikani B. et al., J. Mol. Biol. (1997) 273: 927-948.

[3]Residue numbering follows the nomenclature of MacCallum et al., J. Mol. Biol. (1996) 262: 732-745; Abhinandan amd Martin, Mol. Immunol. (2008) 45: 3832-3839.

[4]Residue numbering follows the nomenclature of Lefranc M. P. et al., Dev. Comp. Immunol. (2003) 27: 55-77; and Honegger and Plückthun, J. Mol. Biol. (2001) 309: 657-670.

[5]Residue numbering follows the nomenclature of Honegger and Plückthun, J. Mol. Biol. (2001) 309: 657-670.

[0055] The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains (C_H), antibodies can be assigned to different classes or isotypes. There are five classes of antibodies: IgA, IgD, IgE, IgG, and IgM, having heavy chains designated α (alpha), δ (delta), ε (epsilon), γ (gamma), and μ(mu), respectively. The IgG class of antibody can be further classified into four subclasses IgG_1, IgG_2, IgG_3, and IgG_4 by the gamma heavy chains, Y1-Y4, respectively.

[0056] The term "antigen-binding fragment" or "antigen-binding portion," used herein interchangeably, refers to parts of an antibody that retain the ability to bind to the antigen of the antibody. Examples of "antigen-binding fragments" of an antibody include, but are not limited to, (i) a Fab fragment, a monovalent fragment consisting of the V_L, V_H, C_L and C_{H1} domains, obtainable by papain digestion; (ii) a $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region, obtainable by pepsin digestion; (iii) a Fv fragment consisting of the V_L and V_H domains of a single arm of an antibody, (iv) a single chain Fv (scFv) fragment comprising the V_H and V_L domains of an antibody that are fused to each other; and (v) a single chain Fab (scFab) fragment comprising a single polypeptide comprising the V_L, V_H, C_L and C_{H1} domains.

[0057] The term "masked antibody" refers to an antibody (including a multi-specific antibody), or an antigen-binding fragment thereof, comprising a masking peptide that interferes with, obstructs, reduces the ability of, prevents, inhibits, or competes with the antigen binding domain of the antibody, for binding to its target. A masked antibody may be generated by linking a masking peptide to the antigen-binding domain of an antibody. In some embodiments, a masked antibody, or an antigen-binding fragment thereof, exhibits a first binding affinity to a target when in an inactivated state (e.g., inhibited or masked by a masking peptide), and exhibits a second binding affinity to the target in an activated state (e.g., uninhibited or unmasked by the masking peptide (e.g., the masking peptide is cleaved from the antibody)), where the second binding affinity is greater than the first binding affinity. A masked antibody may be generated by linking a masking peptide comprising an activatable component (e.g., a cleavable site within a linkage unit, or "LU") to the antigen binding domain of an antibody. In some embodiments, the masked antibody, or an masked antigen-binding fragment thereof, is a multi-specific antibody comprising a binding domain that is specific for a T-cell surface molecule (e.g., CD28, CD3) and a binding domain that is specific for tumor cell surface antigen (e.g., HER2, B7H3, TROP2, etc.). In some embodiments, the masked antibody is bivalent and has a single mask on one of the two binding domains. In some embodiments, the masked antibody is bivalent and has a mask on each of the two binding domains. For example, for a single-masked antibody, one of the binding domains of the antibody is masked by a fused or conjugated masking peptide. For a bispecific antibody, one or both binding domains may be masked by specific but different masking peptides. An unactivated bispecific antibody that targets both cancer cells and T cells may have the binding sites of both binding domains masked to inhibit (or minimize) binding to antigen-expressing cancer cells and T cells. However, in an activated state, the masks are cleaved off to allow binding of the antibody to both the tumor antigen and the T-cell surface molecule (e.g., CD28) in the tumor microenvironment (TME). In this instance, the activated bispecific antibody selectively engages T cells to kill target tumor antigen-expressing cancer cells.

[0058] A "masking peptide" refers to a peptide which inhibits binding of an antigen binding domain to its target antigen, and typically comprises, from N terminus to C terminus, a masking unit (MU) and a linkage unit (LU). The C terminus of the masking peptide is typically linked to the N terminus of the V_H or the V_L of the antigen-binding domain. In some embodiments, the masking peptide, or a portion thereof, interferes with or inhibits binding of the antigen binding domain to its target so efficiently that binding of the antigen-binding domain to its target is extremely low and/or below the limit of detection (e.g., binding cannot be detected in an ELISA or flow cytometry assay). The masked antibodies or polypeptides described herein may comprise one or more linkers, e.g., within the LU, disposed between MU and LU, LU and V_H or V_L, or V_H and hinge region of an Fc.

[0059] The LU of the masking peptide may comprise at least one cleavable site. A cleavage site generally includes an amino acid sequence that is cleavable, for example, serves as the substrate for an enzyme and/or a cysteine-cysteine pair capable of forming a reducible disulfide bond. As such, when the terms "cleavage," "cleavable," "cleaved" and the like are used in connection with a cleavage site, the terms encompass enzymatic cleavage, e.g., by a protease, as well as disruption of a disulfide bond between a cysteine-cysteine pair via reduction of the disulfide bond that can result from exposure to a reducing agent. The amino acid sequence of the cleavage site may overlap with or be included within the MU. Masked antibodies or masked polypeptides may comprise a cleavage site configured to mediate activation of the antibody or the polypeptide. For example, when the cleavage site of an activatable antibody is intact (e.g., uncleaved by a corresponding enzyme, and/or containing an unreduced cysteine-cysteine disulfide bond), the masking peptide, or a portion thereof, may interfere with or inhibit binding of the antigen binding domain to its target. In some embodiments, the LU of the masking peptide does not comprise a cleavable site.

[0060] The term "masking efficiency" refers to the efficiency with which the masking peptide inhibits binding of the antigen binding domain to the target antigen. Masking efficiency may be measured as the difference in or the ratio of the binding affinity of a masked antibody or masked

polypeptide comprising an antigen binding domain and the binding affinity of an unmasked antibody or unmasked polypeptide comprising an antigen binding domain (e.g., the masking peptide is cleaved from the antibody). For example, the masking efficiency may be measured by dividing the EC_{50} or K_D of a masked antibody for binding a target antigen in its inactivated (e.g., inhibited, masked, and/or uncleaved) state, relative to the EC_{50} or K_D of the unmasked antibody to bind to the target antigen in its activated (e.g., uninhibited, unmasked, and/or cleaved) state, or relative to EC_{50} or K_D of the parental antibody (e.g., not linked to a masking peptide) to bind to the target antigen. The EC_{50} values may be measured in an ELISA assay, or a Jurkat NFAT reporter assay, for example, as described in U.S. Pat. App. Pub. No. US2021/0207126 A1. The K_D values may be measured by, for example, using surface plasmon resonance.

[0061] The term "epitope" refers to a part of an antigen to which an antibody (or antigen-binding fragment thereof) binds. Epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed from contiguous amino acids are typically retained on exposure to denaturing solvents whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope can include various numbers of amino acids in a unique spatial conformation. Methods of determining spatial conformation of epitopes include, for example, x-ray crystallography, 2-dimensional nuclear magnetic resonance, deuterium and hydrogen exchange in combination with mass spectrometry, or site-directed mutagenesis, or all methods used in combination with computational modeling of antigen and its complex structure with its binding antibody and its variants (see e.g., Epitope Mapping Protocols in Methods in Molecular Biology, Vol. 66, G. E. Morris, Ed. (1996)). Once a desired epitope of an antigen is determined, antibodies to that epitope can be generated, e.g., using the techniques described herein. The generation and characterization of antibodies may also elucidate information about desirable epitopes. From this information, it is then possible to competitively screen antibodies for binding to the same epitope. An approach to achieve this is to conduct cross-competition studies to find antibodies that competitively bind with one another, i.e., the antibodies compete for binding to the antigen. A high throughput process for "binning" antibodies based upon their cross-competition is described in PCT Publication No. WO 03/48731.

[0062] The term "germline" refers to the nucleotide sequences of the antibody genes and gene segments as they are passed from parents to offspring via the germ cells. The germline sequence is distinguished from the nucleotide sequences encoding antibodies in mature B cells which have been altered by recombination and hypermutation events during the course of B cell maturation.

[0063] The term "glycosylation sites" refers to amino acid residues which are recognized by a eukaryotic cell as locations for the attachment of sugar residues. The amino acids where carbohydrate, such as oligosaccharide, is attached are typically asparagine (N-linkage), serine (O-linkage), and threonine (O-linkage) residues. The specific site of attachment is typically signaled by a sequence of amino acids, referred to herein as a "glycosylation site sequence". The glycosylation site sequence for N-linked glycosylation is: -Asn-X-Ser- or -Asn-X-Thr-, where X may be any of the conventional amino acids, other than proline. The terms "N-linked" and "O-linked" refer to the chemical group that serves as the attachment site between the sugar molecule and the amino acid residue. N-linked sugars are attached through an amino group; O-linked sugars are attached through a hydroxyl group. The term "glycan occupancy" refers to the existence of a carbohydrate moiety linked to a glycosylation site (i.e., the glycan site is occupied). Where there are at least two potential glycosylation sites on a polypeptide, either none (0-glycan site occupancy), one (1-glycan site occupancy) or both (2-glycan site occupancy) sites can be occupied by a carbohydrate moiety.

[0064] The term "host cell" refers to a cellular system which can be engineered to generate proteins, protein fragments, or peptides of interest. Host cells include, without limitation, cultured cells, e.g., mammalian cultured cells derived from rodents (rats, mice, guinea pigs, or hamsters) such as CHO, BHK, NSO, SP2/0, YB2/0; human cells (e.g., HEK293F cells, HEK293T cells; or human tissues or hybridoma cells, yeast cells, insect cells (e.g., S2 cells), bacterial cells (e.g., *E. coli* cells) and cells comprised within a transgenic animal or cultured tissue. The term encompasses not only the particular subject cell but also the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not be identical to the parent cell, but are still included within the scope of the term "host cell."

[0065] A "human antibody" is one which possesses an amino acid sequence which corresponds to that of an antibody produced by a human or a human cell or derived from a non-human source that utilizes human antibody repertoires or other human antibody-encoding sequences. This definition of a human antibody specifically excludes a humanized antibody comprising non-human antigen-binding residues.

[0066] The term "humanized antibody" refers to a chimeric antibody that contains amino acid residues derived from human antibody sequences. A humanized antibody may contain some or all of the CDRs from a non-human animal or synthetic antibody while the framework and constant regions of the antibody contain amino acid residues derived from human antibody sequences.

[0067] The term "exemplary antibody" refers to any one of the antibodies described herein. These antibodies may be in any class (e.g., IgA, IgD, IgE, IgG, and IgM). Thus, each antibody identified above encompasses antibodies in all five classes that have the same amino acid sequences for the V_L and V_H regions. Further, the antibodies in the IgG class may be in any subclass (e.g., IgG_1 IgG_2, IgG_3, and IgG_4). Thus, each antibody identified above in the IgG subclass encompasses antibodies in all four subclasses that have the same amino acid sequences for the V_L and V_H regions. The amino acid sequences of the heavy chain constant regions of human antibodies in the five classes, as well as in the four IgG subclasses, are known in the art.

[0068] An "isolated" antibody or binding molecule is one which has been separated from a component of its natural environment. In some embodiments, an antibody is purified to greater than 95% or 99% purity as determined by, for example, electrophoretic (e.g., SDS-PAGE, isoelectric focusing (IEF), capillary electrophoresis) or chromatographic (e.g., ion exchange or reverse phase HPLC). For review of methods for assessment of antibody purity, see e.g., Flatman et al., J. Chromatogr. B 848: 79-87 (2007). The term "k_d" refers to the association rate constant of a par-

ticular antibody-antigen interaction, whereas the term "k_d" refers to the dissociation rate constant of a particular antibody-antigen interaction.

[0069] The term "K_D" refers to the equilibrium dissociation constant of a particular antibody-antigen interaction. It is obtained from the ratio of k_d to k_d (i.e., k_d/k_d) and is expressed as a molar concentration (M). K_D is used as a measure for the affinity of an antibody's binding to its binding partner. The smaller the K_D, the more tightly bound the antibody is, or the higher the affinity between antibody and the antigen. For example, an antibody with a nanomolar (nM) dissociation constant binds more tightly to a particular antigen than an antibody with a micromolar (μM) dissociation constant. K_D values for antibodies can be determined using methods well established in the art. One method for determining the K_D of an antibody is by using an ELISA. For example, an assay procedure using an ELISA.

[0070] The term "mammal" refers to any animal species of the Mammalia class. Examples of mammals include: humans; laboratory animals such as rats, mice, hamsters, rabbits, non-human primates, and guinea pigs; domestic animals such as cats, dogs, cattle, sheep, goats, horses, and pigs; and captive wild animals such as lions, tigers, elephants, and the like.

[0071] The term "prevent" or "preventing," with reference to a certain disease condition in a mammal, refers to preventing or delaying the onset of the disease, or preventing the manifestation of clinical or subclinical symptoms thereof.

[0072] As used herein, "sequence identity" between two polypeptide sequences indicates the percentage of amino acids that are identical between the sequences. The amino acid sequence identity of polypeptides can be determined conventionally using known computer programs such as Bestfit, FASTA, or BLAST (see e.g., Pearson, Methods Enzymol. (1990) 183: 63-98; Pearson, Methods Mol. Biol. (2000) 132: 185-219; Altschul et al., J. Mol. Biol. (1990) 215: 403-10; Altschul et al., Nucleic Acids Res. (1997) 25: 3389-3402). When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference amino acid sequence, the parameters are set such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed. This aforementioned method in determining the percentage of identity between polypeptides is applicable to all proteins, fragments, or variants thereof disclosed herein.

[0073] As used herein, the term "binds," "binds to," "specifically binds" "specifically binds to" or is "specific for" refers to measurable and reproducible interactions such as binding between a target and an antibody, which is determinative of the presence of the target in the presence of a heterogeneous population of molecules including biological molecules. For example, an antibody that binds to or specifically binds to a target (which can be an epitope) is an antibody that binds this target with greater affinity, avidity, more readily, and/or with greater duration than it binds to other targets. In one embodiment, the extent of binding of an antibody to an unrelated target is less than about 10% of the binding of the antibody to the target as measured, e.g., by a radioimmunoassay (RIA). In certain embodiments, an antibody that specifically binds to a target has a dissociation constant (Kd) of ≤1 μM, ≤100 nM, ≤10 nM, ≤1 nM, or ≤0.1 nM. In certain embodiments, an antibody specifically binds to an epitope on a protein that is conserved among the protein from different species. In another embodiment, specific binding can include, but does not require exclusive binding. For example, a masked anti-CD28 antibody described herein is said to selectively bind to human CD28 if it binds to human CD28 at an EC_{50} that is below 10 percent of the EC_{50} at which it binds to different antigen in an in vitro assay.

[0074] The term "treat," "treating," or "treatment," with reference to a certain disease condition in a mammal, refers causing a desirable or beneficial effect in the mammal having the disease condition. The desirable or beneficial effect may include reduced frequency or severity of one or more symptoms of the disease (i.e., tumor growth and/or metastasis, or other effect mediated by the numbers and/or activity of immune cells, and the like), or arrest or inhibition of further development of the disease, condition, or disorder. In the context of treating cancer in a mammal, the desirable or beneficial effect may include inhibition of further growth or spread of cancer cells, death of cancer cells, inhibition of reoccurrence of cancer, reduction of pain associated with the cancer, or improved survival of the mammal. The effect can be either subjective or objective. For example, if the mammal is human, the human may note improved vigor or vitality or decreased pain as subjective symptoms of improvement or response to therapy. Alternatively, the clinician may notice a decrease in tumor size or tumor burden based on physical exam, laboratory parameters, tumor markers or radiographic findings. Some laboratory signs that the clinician may observe for response to treatment include normalization of tests, such as white blood cell count, red blood cell count, platelet count, erythrocyte sedimentation rate, and various enzyme levels. Additionally, the clinician may observe a decrease in a detectable tumor marker. Alternatively, other tests can be used to evaluate objective improvement, such as sonograms, nuclear magnetic resonance testing and positron emissions testing.

[0075] The term "vector" refers to a nucleic acid molecule capable of transporting a foreign nucleic acid molecule. The foreign nucleic acid molecule is linked to the vector nucleic acid molecule by a recombinant technique, such as ligation or recombination. This allows the foreign nucleic acid molecule to be multiplied, selected, further manipulated or expressed in a host cell or organism. A vector can be a plasmid, phage, transposon, cosmid, chromosome, virus, or virion. One type of vectors can be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome (e.g., non-episomal mammalian vectors). Another type of vector is capable of autonomous replication in a host cell into which it is introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Another specific type of vector capable of directing the expression of expressible foreign nucleic acids to which they are operatively linked is commonly referred to as "expression vectors." Expression vectors generally have control sequences that drive expression of the expressible foreign nucleic acids. Simpler vectors, known as "transcription vectors," are only capable of being transcribed but not translated: they can be replicated in a target cell but not expressed. The term "vector" encompasses all types of vectors regardless of their function. Vectors capable of

directing the expression of expressible nucleic acids to which they are operatively linked are commonly referred to "expression vectors." Other examples of "vectors" may include display vectors (e.g., vectors that direct expression and display of an encoded polypeptide on the surface of a virus or cell (such as a bacterial cell, yeast cell, insect cell, and/or mammalian cell).

[0076] As used herein, a "subject", "patient", or "individual" may refer to a human or a non-human animal. A "non-human animal" may refer to any animal not classified as a human, such as domestic, farm, or zoo animals, sports, pet animals (such as dogs, horses, cats, cows, etc.), as well as animals used in research. Research animals may refer without limitation to nematodes, arthropods, vertebrates, mammals, frogs, rodents (e.g., mice or rats), fish (e.g., zebrafish or pufferfish), birds (e.g., chickens), dogs, cats, and non-human primates (e.g., rhesus monkeys, cynomolgus monkeys, chimpanzees, etc.). In some embodiments, the subject, patient, or individual is a human.

[0077] An "effective amount" refers to at least an amount effective, at dosages and for periods of time necessary, to achieve one or more desired or indicated effects, including a therapeutic or prophylactic result. An effective amount can be provided in one or more administrations. For purposes of the present disclosure, an effective amount of antibody, drug, compound, or pharmaceutical composition is an amount sufficient to accomplish prophylactic or therapeutic treatment either directly or indirectly. As is understood in the clinical context, an effective amount of a drug, compound, or pharmaceutical composition may or may not be achieved in conjunction with another drug, compound, or pharmaceutical composition (e.g., an effective amount as administered as a monotherapy or combination therapy). Thus, an "effective amount" may be considered in the context of administering one or more therapeutic agents, and a single agent may be considered to be given in an effective amount if, in conjunction with one or more other agents, a desirable result may be or is achieved.

[0078] All references cited herein, including patent applications and publications, are hereby incorporated by reference in their entirety.

II. Antibodies

[0079] Certain aspects of the present disclosure relate to monospecific antibodies (e.g., traditional, non-masked monospecific antibodies), multi-specific antibodies (e.g., non-masked multi-specific antibodies), masked antibodies (e.g., activatable monospecific or multi-specific antibodies), antigen-binding fragments thereof, or derivatives of such antibodies.

A. Fc Regions and C_H3 Domains

[0080] In some embodiments, the antibody (e.g., multi-specific antibody) described herein comprises one or more antibody constant regions, such as human heavy chain constant regions and/or human light chain constant regions. In some embodiments, the human heavy chain constant region is of an isotype selected from IgA, IgG, and IgD. In some embodiments, the human light chain constant region is of an isotype selected from K and k. In some embodiments, the antibody comprises a human IgG constant region. In some embodiments, the antibody comprises a human IgG_4 heavy chain constant region. In some embodiments, the antibody comprises a human IgG_1 heavy chain constant region. In some such embodiments, the antibody comprises an S228P mutation in the human IgG_4 constant region.

[0081] Whether or not effector function is desirable may depend on the particular method of treatment intended for an antibody. In some embodiments, when effector function is desirable, an antibody comprising a human IgG_1 heavy chain constant region or a human IgG_3 heavy chain constant region is selected. In some embodiments, when effector function is not desirable, an antibody comprising a human IgG_4 or IgG_2 heavy chain constant region is selected. In some embodiments, the antibody comprises a human IgG_1 heavy chain constant region comprising one or more mutations that reduces effector function. In some embodiments, the antibody comprises an IgG_1 heavy chain constant region comprising an N297A substitution.

[0082] The multi-specific antibodies (including the activatable multi-specific antibodies) described herein may comprise C_H3 domains having one or more engineered disulfide bonds, one or more engineered (e.g., rearranged or inversed) salt bridges, or a combination thereof. Unless stated otherwise, all amino acid residue numbering herein is based on Eu numbering, and the amino acid substitutions are relative to the wildtype (or naturally occurring) sequence at the corresponding amino acid positions in a wild type (or naturally occurring) C_H3 domain sequence. It is appreciated that the mutations or substitutions described herein are applicable to all IgG subclasses and allotypes. IgG allotypes have been described, for example, in Jefferis and Lefranc, mAbs (2009) 1: 4, 1-7, which is incorporated herein by reference in its entirety. In some embodiments, the amino acid mutations or substitutions described herein are relative to a wildtype C_H3 domain sequence of an IgG1, such as IgG1 allotype G1m, 1 (a), 2 (x), 3 (f) or 17 (z). In some embodiments, the amino acid mutations or substitutions described herein are relative to a wildtype C_H3 domain sequence of an IgG_4. For example, a D356K substitution relative to a wildtype C_H3 domain of one human IgG_1 allotype (Uniprot ID P01857) is equivalent to an E356K substitution relative to a wildtype C_H3 domain of a second human IgG_1 allotype, or a wildtype C_H3 domain of a human IgG_4. Exemplary C_H3 domain mutations are shown in Tables 2 and 3. In some embodiments, the amino acid mutations or substitutions described herein are relative to a wildtype Fc region sequence, e.g., an IgG_1 Fc region or an IgG_4 Fc region. C_H3 sequences with the mutations are described in WO 2021/148006, the disclosure of which is incorporated herein by reference in its entirety. In the tables below and elsewhere in the specification, the apostrophes in the C_H3 mutation annotations denote residues in the second C_H3 domain. For example, in N390C-S400'C, the S400C mutation is in the second C_H3 domain.

TABLE 2

Fc mutations	
Designs	Mutations (first C_H3 domain-second C_H3 domain)
Disulfide bond	N390C-S400'C S400C-N390'C K392C-V397'C V397C-K392'C K392C-S400'C S400C-K392'C

TABLE 2-continued

Fc mutations	
Designs	Mutations (first C_H3 domain-second C_H3 domain)
Charge designs	E357K:T411K-L351'D:K370'D E357K:S364K-L351'D:K370'D D356K:E357K:S364K-L351'D:K370'D:K439'D
Charge + disulfide bond designs	E357K:S364K:N390C-L351'D:K370'D:S400'C E357K:S364K:S400C-L351'D:K370'D:N390'C D356K:E357K:S364K:N390C-L351'D:K370'D:S400'C:K439'D D356K:E357K:S364K:S400C-L351'D:K370'D:N390'C:K439'D

TABLE 3

Fc mutations ID	
Mutation ID	Mutations (first C_H3 domain-second C_H3 domain)
TRF01	T366S, L368A, Y407V, Y349C-T366'W, S354'C
TRF02	T350V, L351Y, F405A, Y407V-T350'V, T366'L, K392'L, T394'W
TRF03	K196Q, S228P, F296Y, E356K, R409K, H435R, L445P-K196'Q, S228'P; F296'Y, R409'K, K439'E, L445'P
TYM01	T366S, L368A, Y407V, N390C-T366'W, S400'C
TYM02	T366S, L368A, Y407V, S400C-T366'W, N390'C
TYM03	Y349C, L368V, Y407V-S354'C, T366'W
TYM04	L368V, Y407V-T366'W
TYM05	L368V, Y407V, N390C-T366'W, S400'C
TYM06	L368V, Y407V, S400C-T366'W, N390'C
TYM07	E357K:T411K-L351'D:K370'D
TYM08	E357K:S364K-L351'D:K370'D
TYM09	D or E356K:E357K:S364K-L351'D:K370'D:K439'D
TYM10	E357K:S364K:N390C-L351'D:K370'D:S400'C
TYM11	E357K:S364K:S400C-L351'D:K370'D:N390'C
TYM12	D or E356K:E357K:S364K:N390C-L351'D:K370'D:S400'C:K439'D
TYM13	D or E356K:E357K:S364K:S400C-L351'D:K370'D:N390'C:K439'D

[0083] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises an engineered disulfide bond between C390 in a first C_H3 domain and C400 in a second C_H3 domain, between C392 in a first C_H3 domain and C397 in a second C_H3 domain, or between C392 in a first C_H3 domain and C400 in a second C_H3 domain. In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises a rearranged salt-bridge network as compared to wildtype C_H3 domains, e.g., among positions 357 and 411 in a first C_H3 domain and positions 351 and 370 in a second C_H3 domain (e.g., E357K: T411K-L351'D: K370'D), or among positions 357 and 364 in a first C_H3 domain and positions 351 and 370 in a second C_H3 domain (e.g., E357K: S364K-L351'D: K370'D). In some embodiments, the multi-specific antibody comprises an inversed salt bridge as compared to wildtype C_H3 domains between position 356 in a first C_H3 domain and position 439 in a second C_H3 domain (e.g., D356-K439'). The antibodies having C_H3 mutations may have high yield, superior stability (e.g., resistance to aggregation and precipitation at high temperature or due to freeze-thaw cycles), and potent activity.

[0084] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises C_H3 domains having one or more engineered residues, which promote heterodimer formation as described herein. Heteromultimers comprising multiple heterodimers formed by a first polypeptide comprising a first engineered C_H3 domain and a second polypeptide comprising a second engineered C_H3 domain are also contemplated herein.

[0085] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises: i) a first C_H3 domain comprising a cysteine (C) residue at position 390 and a second C_H3 domain comprising a cysteine residue at position 400, or a first C_H3 domain comprising a cysteine residue at position 400 and a second C_H3 domain comprising a cysteine residue at position 390; or ii) a first C_H3 domain comprising a cysteine residue at position 392 and a second C_H3 domain comprising a cysteine residue at position 397, or a first C_H3 domain comprising a cysteine residue at position 397 and a second C_H3 domain comprising a cysteine residue at position 392; or iii) a first C_H3 domain comprising a cysteine residue at position 392 and a second C_H3 domain comprising a cysteine residue at position 400, or a first C_H3 domain comprising a cysteine residue at position 400 and a second C_H3 domain comprising a cysteine residue at position 392; and wherein the amino acid residue numbering is based on Eu numbering.

[0086] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises: a first polypeptide comprising a first C_H3 domain and a second polypeptide comprising a second C_H3 domain, wherein: i) the first C_H3 domain further comprises a positively charged residue at position 357 and the second C_H3 domain further comprises a negatively charged residue at position 351, or the first C_H3 domain further comprises a negatively charged residue at position 351 and the second C_H3 domain further comprises a positively charged residue at position 357; or ii) the first C_H3 domain further comprises a positively charged residue at position 411 and the second C_H3 domain further comprises a negatively charged residue at position 370, or the first C_H3 domain further comprises a negatively charged residue at position 370 and the second C_H3 domain further comprises a positively charged residue at position 411; or iii) the first C_H3 domain further comprises a positively charged residue at position 364 and the second C_H3 domain further comprises a negatively charged residue at position 370, or the first C_H3 domain further comprises a negatively charged residue at position 370 and the second C_H3 domain further comprises a positively charged residue at position 364; or a

combination of i) and ii), or a combination or i) and iii), wherein the amino acid residue numbering is based on Eu numbering.

[0087] In some embodiments, the first C_H3 domain further comprises a positively charged residue at position 356 and the second C_H3 domain further comprises a negatively charged residue at position 439, or the first C_H3 domain further comprises a negatively charged residue at position 439 and the second C_H3 domain further comprises a positively charged residue at position 356, and wherein the amino acid residue numbering is based on Eu numbering.

[0088] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises: a first polypeptide comprising a first C_H3 domain and a second polypeptide comprising a second C_H3 domain, wherein: i) the first C_H3 domain comprises a cysteine (C) residue at position 390 and the second C_H3 domain comprises a cysteine residue at position 400, or the first C_H3 domain comprises a cysteine residue at position 400 and the second C_H3 domain comprises a cysteine residue at position 390; or ii) the first C_H3 domain comprises a cysteine residue at position 392 and the second C_H3 domain comprises a cysteine residue at position 397, or the first C_H3 domain comprises a cysteine residue at position 397 and the second C_H3 domain comprises a cysteine residue at position 392; or iii) the first C_H3 domain comprises a cysteine residue at position 392 and the second C_H3 domain comprises a cysteine residue at position 400, or the first C_H3 domain comprises a cysteine residue at position 400 and the second C_H3 domain comprises a cysteine residue at position 392; and wherein: a) the first C_H3 domain further comprises a positively charged residue at position 357 and the second C_H3 domain further comprises a negatively charged residue at position 351, or the first C_H3 domain further comprises a negatively charged residue at position 351 and the second C_H3 domain further comprises a positively charged residue at position 357; or b) the first C_H3 domain further comprises a positively charged residue at position 411 and the second C_H3 domain further comprises a negatively charged residue at position 370, or the first C_H3 domain further comprises a negatively charged residue at position 370 and the second C_H3 domain further comprises a positively charged residue at position 411; or c) the first C_H3 domain further comprises a positively charged residue at position 364 and the second C_H3 domain further comprises a negatively charged residue at position 370, or the first C_H3 domain further comprises a negatively charged residue at position 370 and the second C_H3 domain further comprises a positively charged residue at position 364; or a combination of a) and b), or a combination of a) and c); wherein the amino acid residue numbering is based on Eu numbering.

[0089] In some embodiments, the first C_H3 domain further comprises a positively charged residue at position 356 and the second C_H3 domain further comprises a negatively charged residue at position 439, or first C_H3 domain further comprises a negatively charged residue at position 439 and the second C_H3 domain further comprises a positively charged residue at position 356, and wherein the amino acid residue numbering is based on Eu numbering.

[0090] The C_H3 domains may be derived from any naturally occurring immunoglobulin molecules. In some embodiments, the C_H3 domains are derived from an IgG1 molecule, an IgG_2 molecule, an IgG_3 molecule, or an IgG_4 molecule. In some embodiments, the C_H3 domains are human C_H3 domains. In some embodiments, the C_H3 domains are derived from human IgG_1 molecules.

[0091] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises: a first polypeptide comprising a first C_H3 domain and a second polypeptide comprising a second C_H3 domain, wherein: i) the first C_H3 domain comprises N390C substitution and the second C_H3 domain comprises S400C substitution, or the first C_H3 domain comprises S400C substitution and the second C_H3 domain comprises N390C substitution; or ii) the first C_H3 domain comprises K392C substitution and the second C_H3 domain comprises V397C substitution, or the first C_H3 domain comprises V397C substitution and the second C_H3 domain comprises K392C substitution; or iii) the first C_H3 domain comprises K392C substitution and the second C_H3 domain comprises S400C substitution, or the first C_H3 domain comprises S400C substitution and the second C_H3 domain comprises K392C substitution.

[0092] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises: a first polypeptide comprising a first C_H3 domain and a second polypeptide comprising a second C_H3 domain, wherein: i) the first C_H3 domain comprises E357K and T411K substitutions and the second C_H3 domain comprises L351D and K370D substitutions, or the first C_H3 domain comprises L351D and K370D substitutions and the second C_H3 domain comprises E357K and T411K substitutions; or ii) the first C_H3 domain comprises E357K and S364K substitutions and the second C_H3 domain comprises L351D and K370D substitutions, or the first C_H3 domain comprises L351D and K370D substitutions and the second C_H3 domain comprises E357K and S364K substitutions; or iii) the first C_H3 domain comprises D356K, E357K, and S364K substitutions and the second C_H3 domain comprises L351D, K370D, and K439D substitutions, or the first C_H3 domain comprises L351D, K370D, and K439D substitutions and the second C_H3 domain comprises D356K, E357K and S364K substitutions.

[0093] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises: a first polypeptide comprising a first C_H3 domain and a second polypeptide comprising a second C_H3 domain, wherein the first C_H3 domain comprises E357K, S364K, and N390C substitutions and the second C_H3 domain comprises L351D, K370D, and S400C substitutions, or the first C_H3 domain comprises L351D, K370D, and S400C substitutions and the second C_H3 domain comprises E357K, S364K, and N390C substitutions.

[0094] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises: a first polypeptide comprising a first C_H3 domain and a second polypeptide comprising a second C_H3 domain, wherein the first C_H3 domain comprises E357K, S364K, and S400C substitutions and the second C_H3 domain comprises L351D, K370D, and N390C substitutions, or the first C_H3 domain comprises L351D, K370D, and N390C substitutions and the second C_H3 domain comprises E357K, S364K, and S400C substitutions.

[0095] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises: a first polypeptide comprising a first C_H3 domain and a second polypeptide comprising a second C_H3 domain, wherein the first C_H3 domain comprises D356K, E357K, S364K, and S400C substitutions and the second C_H3 domain comprises L351D, K370D, N390C, and K439D substitutions, or the

first C_H3 domain comprises L351D, K370D, N390C, and K439D substitutions and the second C_H3 domain comprises D356K, E357K, S364K, and S400C substitutions.

[0096] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises: a first polypeptide comprising a first C_H3 domain and a second polypeptide comprising a second C_H3 domain, wherein the first C_H3 domain comprises D356K, E357K, S364K, and N390C substitutions and the second C_H3 domain comprises L351D, K370D, K439D, and S400C substitutions, or the first C_H3 domain comprises L351D, K370D, K439D, and S400C substitutions and the second C_H3 domain comprises D356K, E357K, S364K, and N390C substitutions.

[0097] In some embodiments, the multi-specific antibody (e.g., the activatable multi-specific antibody) comprises an IgG Fc region that comprises the engineered C_H3 domains. The Fc region may be derived from any suitable Fc subclasses, including, but not limited to, IgG_1, IgG_2, IgG_3, and IgG_4 subclasses.

B. Cysteine Mutations

[0098] In some embodiments, the multi-specific antibodies described herein (e.g., the activatable multi-specific antibodies described herein) comprise a first polypeptide comprising a first C_H3 domain and a second polypeptide comprising a second C_H3 domain, wherein the first C_H3 domain comprises a first engineered cysteine residue and the second C_H3 domain comprises a second engineered cysteine residue, wherein the first engineered cysteine residue and the second cysteine residue form a disulfide bond.

[0099] In some embodiments, the first C_H3 domain comprises a C at position 390 and the second C_H3 domain comprises a C at position 400, or the first C_H3 domain comprises a C at position 400 and the second C_H3 domain comprises a C at position 390. In some embodiments, the first C_H3 domain comprises N390C substitution and the second C_H3 domain comprises S400C substitution, or the first C_H3 domain comprises S400C substitution and the second C_H3 domain comprises N390C substitution.

[0100] In some embodiments, the first C_H3 domain comprises a C at position 392 and the second C_H3 domain comprises a C at position 397, or the first C_H3 domain comprises a C at position 397 and the second C_H3 domain comprises a C at position 392. In some embodiments, the first C_H3 domain comprises K392C substitution and the second C_H3 domain comprises V397C substitution, or the first C_H3 domain comprises V397C substitution and the second C_H3 domain comprises K392C substitution.

[0101] In some embodiments, the first C_H3 domain comprises a C at position 392 and the second C_H3 domain comprises a C at position 400, or the first C_H3 domain comprises a C at position 400 and the second C_H3 domain comprises a C at position 392. In some embodiments, the first C_H3 domain comprises K392C substitution and the second C_H3 domain comprises S400C substitution, or the first C_H3 domain comprises S400C substitution and the second C_H3 domain comprises K392C substitution.

C. Salt Bridge Mutations

[0102] In some embodiments, the multi-specific antibodies described herein (e.g., the activatable multi-specific antibodies described herein) comprise a first polypeptide comprising a first C_H3 domain and a second polypeptide comprising a second C_H3 domain, wherein the first C_H3 domain comprises an engineered positively charged residue and the second C_H3 domain comprises an engineered negatively charged residue, wherein the engineered positively charged residue and the engineered negatively charged residue form a salt bridge. The engineered salt bridge may introduce new salt bridges between the C_H3 domains, rearrange a salt-bridge network among two or more amino acid residues, or reverse the charges on the amino acid residues forming the salt bridge (i.e., "inverse" a salt bridge) with respect to wildtype C_H3 domains. In some embodiments, the engineered positively charged residue substitutes a negatively charged residue in a wildtype C_H3 domain with a positively charged residue. In some embodiments, the engineered negatively charged residue substitutes a positively charged residue in a wildtype C_H3 domain with a negatively charged residue. The rearranged and inversed salt bridges may result in changes in the isoelectric points (PI) of the heterodimer and the homodimer comprising the engineered C_H3 domains, thereby allowing better separation of the heterodimer from the homodimer in a purification process.

[0103] In some embodiments, the first C_H3 domain comprises a positively charged residue at position 357 and the second C_H3 domain comprises a negatively charged residue at position 351, or the first C_H3 domain comprises a negatively charged residue at position 351 and the second C_H3 domain comprises a positively charged residue at position 357. In some embodiments, the first C_H3 domain comprises a K at position 357 and the second C_H3 domain comprises a D at position 351, or the first C_H3 domain comprises a D at position 351 and the second C_H3 domain comprises a K at position 357. In some embodiments, the first C_H3 domain comprises a K at position 357 and the second C_H3 domain comprises an E at position 351, or the first C_H3 domain comprises an E at position 351 and the second C_H3 domain comprises a K at position 357. In some embodiments, the first C_H3 domain comprises an R at position 357 and the second C_H3 domain comprises a D at position 351, or the first C_H3 domain comprises a D at position 351 and the second C_H3 domain comprises an R at position 357. In some embodiments, the first C_H3 domain comprises an R at position 357 and the second C_H3 domain comprises an E at position 351, or the first C_H3 domain comprises an E at position 351 and the second C_H3 domain comprises an R at position 357. In some embodiments, the first C_H3 domain comprises E357K substitution and the second C_H3 domain comprises L351D substitution, or the first C_H3 domain comprises L351D substitution and the second C_H3 domain comprises E357K substitution.

[0104] In some embodiments, the first C_H3 domain comprises a positively charged residue at position 411 and the second C_H3 domain comprises a negatively charged residue at position 370, or the first C_H3 domain comprises a negatively charged residue at position 370 and the second C_H3 domain comprises a positively charged residue at position 411. In some embodiments, the first C_H3 domain comprises a K at position 411 and the second C_H3 domain comprises a D at position 370, or the first C_H3 domain comprises a D at position 370 and the second C_H3 domain comprises a K at position 411. In some embodiments, the first C_H3 domain comprises a K at position 411 and the second C_H3 domain comprises an E at position 370, or the first C_H3 domain comprises an E at position 370 and the second C_H3 domain comprises a K at position 411. In some embodiments, the

first C_H3 domain comprises an R at position 411 and the second C_H3 domain comprises a D at position 370, or the first C_H3 domain comprises a D at position 370 and the second C_H3 domain comprises an R at position 411. In some embodiments, the first C_H3 domain comprises an R at position 411 and the second C_H3 domain comprises an E at position 370, or the first C_H3 domain comprises an E at position 370 and the second C_H3 domain comprises an R at position 411. In some embodiments, the first C_H3 domain comprises T411K substitution and the second C_H3 domain comprises K370D substitution, or the first C_H3 domain comprises K370D substitution and the second C_H3 domain comprises T411K substitution.

[0105] In some embodiments, the first C_H3 domain comprises a positively charged residue at position 364 and the second C_H3 domain comprises a negatively charged residue at position 370, or the first C_H3 domain comprises a negatively charged residue at position 370 and the second C_H3 domain comprises a positively charged residue at position 364. In some embodiments, the first C_H3 domain comprises a K at position 364 and the second C_H3 domain comprises a D at position 370, or the first C_H3 domain comprises a D at position 370 and the second C_H3 domain comprises a K at position 364. In some embodiments, the first C_H3 domain comprises a K at position 364 and the second C_H3 domain comprises an E at position 370, or the first C_H3 domain comprises an E at position 370 and the second C_H3 domain comprises a K at position 364. In some embodiments, the first C_H3 domain comprises an R at position 364 and the second C_H3 domain comprises a D at position 370, or the first C_H3 domain comprises a D at position 370 and the second C_H3 domain comprises an R at position 364. In some embodiments, the first C_H3 domain comprises an R at position 364 and the second C_H3 domain comprises an E at position 370, or the first C_H3 domain comprises an E at position 370 and the second C_H3 domain comprises an R at position 364. In some embodiments, the first C_H3 domain comprises S364K substitution and the second C_H3 domain comprises K370D substitution, or the first C_H3 domain comprises K370D substitution and the second C_H3 domain comprises S364K substitution.

[0106] In some embodiments, the first C_H3 domain comprises a positively charged residue at position 356 and the second C_H3 domain comprises a negatively charged residue at position 439, or the first C_H3 domain comprises a negatively charged residue at position 439 and the second C_H3 domain comprises a positively charged residue at position 356. In some embodiments, the first C_H3 domain comprises a K at position 356 and the second C_H3 domain comprises a D at position 439, or the first C_H3 domain comprises a D at position 439 and the second C_H3 domain comprises a K at position 356. In some embodiments, the first C_H3 domain comprises a K at position 356 and the second C_H3 domain comprises an E at position 439, or the first C_H3 domain comprises an E at position 439 and the second C_H3 domain comprises a K at position 356. In some embodiments, the first C_H3 domain comprises an R at position 356 and the second C_H3 domain comprises a D at position 439, or the first C_H3 domain comprises a D at position 439 and the second C_H3 domain comprises an R at position 356. In some embodiments, the first C_H3 domain comprises an R at position 356 and the second C_H3 domain comprises an E at position 439, or the first C_H3 domain comprises an E at position 439 and the second C_H3 domain comprises an R at position 356. In some embodiments, the first C_H3 domain comprises D356K substitution and the second C_H3 domain comprises K439D substitution, or the first C_H3 domain comprises K439D substitution and the second C_H3 domain comprises D356K substitution.

[0107] Any of the engineered salt bridges described herein may be combined with each other. In some embodiments, the first C_H3 domain comprises a positively charged residue at position 357 and a positively charged residue at position 411, and the second C_H3 domain comprises a negatively charged residue at position 351 and a negatively charged residue at position 370, or the first C_H3 domain comprises a negatively charged residue at position 351 and a negatively charged residue at position 370, and the second C_H3 domain comprises a positively charged residue at position 357 and a positively charged residue at position 411. In some embodiments, the first C_H3 domain comprises E357K and T411K substitutions, and the second C_H3 domain comprises L351D and K370D substitutions, or the first C_H3 domain comprises L351D and K370D substitutions, and the second C_H3 domain comprises E357K and T411K substitutions.

[0108] In some embodiments, the first C_H3 domain comprises a positively charged residue at position 357 and a positively charged residue at position 364, and the second C_H3 domain comprises a negatively charged residue at position 351 and a negatively charged residue at position 370, or the first C_H3 domain comprises a negatively charged residue at position 351 and a negatively charged residue at position 370, and the second C_H3 domain comprises a positively charged residue at position 357 and a positively charged residue at position 364. In some embodiments, the first C_H3 domain comprises E357K and S364K substitutions, and the second C_H3 domain comprises L351D and K370D substitutions, or the first C_H3 domain comprises L351D and K370D substitutions, and the second C_H3 domain comprises E357K and S364K substitutions.

[0109] In some embodiments, the first C_H3 domain comprises a positively charged residue at position 356, a positively charged residue at position 357, and a positively charged residue at position 364 and the second C_H3 domain comprises a negatively charged residue at position 351, a negatively charged residue at position 370, and a negatively charged residue at position 439, or the first C_H3 domain comprises a negatively charged residue at position 351, a negatively charged residue at position 370, and a negatively charged residue at position 439 and the second C_H3 domain comprises a positively charged residue at position 356, a positively charged residue at position 357, and a positively charged residue at position 364. In some embodiments, the first C_H3 domain comprises D356K, E357K, and S364K substitutions and the second C_H3 domain comprises L351D, K370D, and K439D substitutions, or the first C_H3 domain comprises L351D, K370D, and K439D substitutions and the second C_H3 domain comprises D356K, E357K, and S364K substitutions.

D. Other Mutations

[0110] The C_H3 domains or the Fc regions described herein may further comprise engineered disulfide bonds and/or salt bridges listed in Table 4 below.

TABLE 4

Exemplary Fc Mutations	
Mutation(s) in first polypeptide chain	Mutation(s) in second polypeptide chain
F405L	K409R
S364H, F405A	Y349T, T394F
S364K, E357Q	L368D, K370S
T366W	T366S, L368A, Y407V
S354C, T366W	Y349C, T366S, L368A, Y407V
T350, L351, F405, Y407	T350, T366, K392, T394
T350 is T350V, T350I, T350L or T350M	T350 is T350V, T350I, T350L or T350M
	T366 is T366L, T366I, T366V or T366M
L351 is L351Y	K392 is K392F, K392L or K392M
F450 is F450A, F450V, F450T or F450S	T394 is T394W
Y407 is Y407V, Y407A or Y407I	
D399K, E356K	K409D, K392D
D221E, P228E, L368E	D221R, P228R, K409R
C223E, E225E, P228E, L368E	C223R, E225R, P228R, K409R
H435R	None
K196Q, S228P, F296Y, E356K, R409K, H435R, L445P	K196Q, S228P, F296Y, R409K, K439E, L445P
K409W	D399V/F40ST
K360E	Q347R
Y349C/K360E/K409W	Q347R/S354C/D399V/F405T
K360E/K409W	Q347R/D399V/F405T
Y349S/K409W	E357W/D399V/F405T
Y349S/S354C/K409W	Y349C/E357W/D399V/F405T
T366K	L351D
Y349E or D and L368E	L351D
Y349C/T366W	D356C/T366S/L368A/Y407V/F405K
Y349C/T366W/F405K	D356C/T366S/L368A/Y407V
Y349C/T366W/K409E	D356C/T366S/L368A/Y407V/F405K
Y349C/T366W/K409A	D356C/T366S/L368A/Y407V/F405K
S364K	L368D
S364K	K370S
F405K	K409F
F405R	K409F
S364K/K409F	L368D/F405R
S364K/K409F	K370S/F405R
S364K/K409W	K370S/F405R
K370E or E356K and K409R	E357K and K409R or K370E
S354I/S364L/Y407V	Q347V/Y349I/T350K/L351Q/T366W/L368I/Y407V
Y349I	S354I/E357Q/M/G/S364L/T366S/L368A/Y407V
P395K/P396K/V397K	T394D/P395D/P396D
F405E/Y407E/K409E	F405K/Y407K
M428S/N434S/Y436H	H435R

[0111] In some embodiments, the first C_H3 domain further comprises a C at position 392 and the second C_H3 domain comprises a C at position 399, or the first C_H3 domain comprises a C at position 399 and the second C_H3 domain comprises a C at position 392. In some embodiments, the first C_H3 domain further comprises K392C substitution and the second C_H3 domain further comprises D399C substitution, or the first C_H3 domain further comprises D399C substitution and the second C_H3 domain further comprises K392C substitution.

[0112] In some embodiments, the first C_H3 domain further comprises a C at position 394 and the second C_H3 domain comprises a C at position 354, or the first C_H3 domain comprises a C at position 354 and the second C_H3 domain comprises a C at position 394. In some embodiments, the first C_H3 domain further comprises Y394C substitution and the second C_H3 domain further comprises S354C substitution, or the first C_H3 domain further comprises S354C substitution and the second C_H3 domain further comprises Y394C substitution.

[0113] In some embodiments, the first C_H3 domain further comprises a C at position 356 and the second C_H3 domain comprises a C at position 349, or the first C_H3 domain comprises a C at position 349 and the second C_H3 domain comprises a C at position 356. In some embodiments, the first C_H3 domain further comprises D356C substitution and the second C_H3 domain further comprises Y349C substitution, or the first C_H3 domain further comprises Y349C substitution and the second C_H3 domain further comprises D356C substitution.

[0114] In some embodiments, the first C_H3 domain further comprises K392D and K409D substitutions and the second C_H3 domain further comprises D356K and D399K substitutions, or the first C_H3 domain further comprises D356K and D399K substitutions and the second C_H3 domain further comprises K392D and K409D substitutions.

[0115] In some embodiments, the first C_H3 domain further comprises L368D and K370S substitutions and the second C_H3 domain further comprises E357Q and S364K substitutions, or the first C_H3 domain further comprises E357Q and

S364K substitutions and the second C_H3 domain further comprises L368D and K370S substitutions.

[0116] In some embodiments, the first C_H3 domain further comprises L351K and T366K substitutions and the second C_H3 domain further comprises L351D and L368E substitutions, or the first C_H3 domain further comprises L351D and L368E substitutions and the second C_H3 domain further comprises L351K and T366K substitutions.

[0117] In some embodiments, the first C_H3 domain further comprises P395K, P396K, and V397K substitutions and the second C_H3 domain comprises T394D, P395D, and P396D substitutions, or the first C_H3 domain further comprises T394D, P395D, and P396D substitutions and the second C_H3 domain further comprises P395K, P396K, and V397K substitutions.

[0118] In some embodiments, the first C_H3 domain further comprises F405E, Y407E, and K409E substitutions and the second C_H3 domain comprises F405K and Y407K substitutions, or the first C_H3 domain further comprises F405K and Y407K substitutions and the second C_H3 domain further comprises F405E, Y407E and K409E substitutions.

[0119] In some embodiments, the first C_H3 domain further comprises T336S, L368A, and Y407V substitutions and the second C_H3 domain further comprises T366W substitution, or the first C_H3 domain further comprises T366W substitution and the second C_H3 domain further comprises T336S, L368A, and Y407V substitutions.

[0120] In some embodiments, the first C_H3 domain comprises L368V and Y407V substitutions and the second C_H3 domain comprises T366W substitution, or the first C_H3 domain comprises T366W substitution and the second C_H3 domain comprises L368V and Y407V substitutions.

III. CD28-Binding Molecules

[0121] The present disclosure provides isolated binding molecules that bind to human CD28, including anti-CD28 antibodies and anti-CD28 antigen-binding fragments thereof. In some embodiments, the binding molecules include antibodies described with reference to epitope binding and antibodies described with reference to specific amino acid sequences of complementarity determining regions (CDR), variable regions (V_L, V_H), and IgG (e.g., IgG_4) light and heavy chains.

[0122] In some embodiments, the antibodies or the antigen-binding fragments thereof bind to one or more amino acid residues within amino acid residues 34-108 of SEQ ID NO: 1. In some embodiments, the antibodies or antigen-binding fragments bind to one or more amino acid residues within amino acid residues 51-122 of SEQ ID NO: 1. In some embodiments, the antibodies or antigen-binding fragments bind to one or more amino acid residues selected from the group consisting of amino acid residues 51, 52, 54, 55, 98-101, 110-111, 113-114, and 118-122 of SEQ ID NO: 1. Methods of measuring an antibody or antigen-binding fragment's ability to bind a target antigen may be carried out using any method known in the art, including for example, by surface plasmon resonance, an ELISA, isothermal titration calorimetry, a filter binding assay, an EMSA, etc. In some embodiments, the ability of the antibody or antigen-binding fragment to bind a target antigen is measured by ELISA or Octet® RED96 (see, e.g., Example 3 below).

[0123] In some embodiments, the antibodies or antigen-binding fragments bind to human CD28 with a K_D of about 500 nM or less (e.g., about 500 nM or less, about 400 nM or less, about 300 nM or less, about 200 nM or less, about 150 nM or less, about 100 nM or less, about 90 nM or less, about 80 nM or less, about 75 nM or less, about 70 nM or less, about 60 nM or less, about 50 nM or less, about 40 nM or less, about 30 nM or less, about 25 nM or less, about 20 nM or less, about 10 nM or less, about 1 nM or less, about 0.1 nM or less, etc.) In some embodiments, the antibodies or antigen-binding fragments bind to human CD28 with a K_D of about 100 nM or less. In some embodiments, the antibodies or antigen-binding fragments bind to human CD28 with a K_D of about 50 nM or less. Methods of measuring the K_D of an antibody or antigen-binding fragment may be carried out using any method known in the art, including for example, by surface plasmon resonance, an ELISA, isothermal titration calorimetry, a filter binding assay, an EMSA, etc. In some embodiments, the K_D is measured by Octet® RED96 Systems (See, e.g., Example 3 below).

A. Anti-CD28 Antibodies

[0124] In some embodiments, the present disclosure provides an isolated monoclonal antibody that binds to human CD28 at an epitope within amino acid residues 33-37, 80-83, 92-96, and 100-104 of SEQ ID NO: 1. In particular embodiments, the present disclosure provides an isolated antibody that binds to human CD28 at an epitope represented by amino acid residues 33, 34, 36 and 37, 80-83, 92 and 93, 95 and 96, and 100-104 of SEQ ID NO: 1. The antibody, in some embodiments, binds human CD28 with a K_D of 10 nM or less as measured by Octet® RED96 Systems. In certain embodiments, in addition to binding human epitopes, the antibody disclosed herein is cross-reactive (exhibits cross-species binding features) with at least one non-human species selected from the list consisting of cynomolgus monkey, mouse, rat and dog. In certain embodiments, the antibody disclosed herein has the advantage of cross-species binding to mouse, humans and monkeys, whereas the benchmark controls TAC2386 and TAC2387 disclosed herein do not have this range of species cross-reactivity. In particular embodiments, the benchmark controls TAC2386 and TAC2387 bind human epitopes but not mouse epitopes (see Table 7 herein). The species cross reactivity of the antibody disclosed herein also provides the added advantage of being able to use a mouse to model the antibody's safety, activity, and function. Hence, compared to TAC2386 and TAC2387 disclosed herein, it is easier to do animal modeling with the antibody disclosed herein.

[0125] In particular embodiments, the isolated anti-CD28 monoclonal antibody comprises a HCDR1 of SEQ ID NO: 5, HCDR2 of SEQ ID NO: 6, and HCDR3 of SEQ ID NO:7, and a LCDR1 of SEQ ID NO: 8, a LCDR2 of SEQ ID NO: 9 and a LCDR3 of SEQ ID NO:10. In particular embodiments, the isolated monoclonal antibody comprises heavy chain variable region of a SEQ ID NO: 11 and light chain variable region of SEQ ID NO: 12. In particular embodiments, the isolated monoclonal antibody comprises a heavy chain of SEQ ID NO: 13 and light chain of SEQ ID NO: 14.

[0126] The CD28 antibodies described herein can be in any class, such as IgG, IgM, IgE, IgA, or IgD. It is preferred that the anti-CD28 antibodies are in the IgG class, such as IgG_1, IgG_2, IgG_3, or IgG_4 subclass. An anti-CD28 antibody can be converted from one class or subclass to another class or subclass using methods known in the art. An exemplary method for producing an antibody in a desired class or subclass comprises the steps of isolating a nucleic acid

encoding a heavy chain of an anti-CD28 antibody and a nucleic acid encoding a light chain of a CD28 antibody, isolating the sequence encoding the V_H region, ligating the V_H sequence to a sequence encoding a heavy chain constant region of the desired class or subclass, expressing the light chain gene and the heavy chain construct in a cell, and collecting the CD28 antibody.

[0127] The anti-CD28 antibodies described herein can be in any class, such as IgG, IgM, IgE, IgA, or IgD. It is preferred that the anti-CD28 antibodies are in the IgG class, such as IgG_1, IgG_2, IgG_3, or IgG_4 subclass. An anti-CD28 antibody can be converted from one class or subclass to another class or subclass using methods known in the art. An exemplary method for producing an antibody in a desired class or subclass comprises the steps of isolating a nucleic acid encoding a heavy chain of an anti-CD28 antibody and a nucleic acid encoding a light chain of an anti-CD28 antibody, isolating the sequence encoding the V_H region, ligating the V_H sequence to a sequence encoding a heavy chain constant region of the desired class or subclass, expressing the light chain gene and the heavy chain construct in a cell, and collecting the CD28 antibody.

[0128] Further, the antibodies provided by the present disclosure can be monoclonal or polyclonal, but preferably monoclonal.

[0129] Antibodies of the present disclosure can be produced by techniques known in the art, including conventional monoclonal antibody methodology e.g., the standard somatic cell hybridization technique (see e.g., Kohler and Milstein, Nature (1975) 256: 495), viral or oncogenic transformation of B lymphocytes, or recombinant antibody technologies as described in detail herein below.

[0130] Hybridoma production is a very well-established procedure. The common animal system for preparing hybridomas is the murine system. Immunization protocols and techniques for isolation of immunized splenocytes for fusion are known in the art. Fusion partners (e.g., murine myeloma cells) and fusion procedures are also known. One well-known method that may be used for making human CD28 antibodies provided by the present disclosure involves the use of a XenoMouse™ animal system. XenoMouse™ mice are engineered mouse strains that comprise large fragments of human immunoglobulin heavy chain and light chain loci and are deficient in mouse antibody production. See, e.g., Green et al., Nature Genetics (1994) 7: 13-21 and WO2003/040170. The animal is immunized with an CD28 antigen. The CD28 antigen is isolated and/or purified CD28, preferably CD28. It may be a fragment of CD28, such as the extracellular domain of CD28, particularly a CD28 extracellular domain fragment comprising amino acid resides 33, 34, 36 and 37, 80-83, 92 and 93, 95 and 96, and 100-104 of SEQ ID NO: 1. Immunization of animals can be carried out by any method known in the art. See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual, New York: Cold Spring Harbor Press, 1990. Methods for immunizing non-human animals such as mice, rats, sheep, goats, pigs, cattle and horses are well known in the art. See, e.g., Harlow and Lane, supra, and U.S. Pat. No. 5,994,619. The CD28 antigen may be administered with an adjuvant to stimulate the immune response. Exemplary adjuvants include complete or incomplete Freund's adjuvant, RIBI (muramyl dipeptides) or ISCOM (immune-stimulating complexes). After immunization of an animal with a CD28 antigen, antibody-producing immortalized cell lines are prepared from cells isolated from the immunized animal. After immunization, the animal is sacrificed and lymph node and/or splenic B cells are immortalized. Methods of immortalizing cells include, but are not limited to, transferring them with oncogenes, inflecting them with the oncogenic virus cultivating them under conditions that select for immortalized cells, subjecting them to carcinogenic or mutating compounds, fusing them with an immortalized cell, e.g., a myeloma cell, and inactivating a tumor suppressor gene. See, e.g., Harlow and Lane, supra. If fusion with myeloma cells is used, the myeloma cells preferably do not secrete immunoglobulin polypeptides (anon-secretory cell line). Immortalized cells are screened using CD28, a portion thereof, or a cell expressing CD28. CD28 antibody-producing cells, e.g., hybridomas, are selected, cloned and further screened for desirable characteristics, including robust growth, high antibody production and desirable antibody characteristics, as discussed further below. Hybridomas can be expanded in vivo in syngeneic animals, in animals that lack an immune system, e.g., nude mice, or in cell culture in vitro. Methods of selecting, cloning and expanding hybridomas are well known to those of ordinary skill in the art.

[0131] Antibodies of the disclosure can also be prepared using phage display or yeast display methods. Such display methods for isolating human antibodies are established in the art, such as Knappik, et al., "Fully Synthetic Human Combinatorial Antibody Libraries (HuCAL) Based on Modular Consensus Frameworks and CDRs Randomized with Trinucleotides. "J. Mol. Biol. (2000) 296, 57-86; and Feldhaus, et al, "Flow-cytometric isolation of human antibodies from a non-immune *Saccharomyces cerevisiae* surface display library" Nat Biotechnol (2003) 21: 163-170.

B. Antigen Binding Fragments

[0132] In some other aspects, the present disclosure provides antigen-binding fragments of any of the CD28 antibodies provided by the present disclosure.

[0133] The antigen-binding fragment may comprise any sequences of the antibody. In some embodiments, the antigen-binding fragment comprises the amino acid sequence of: (1) a light chain of an anti-CD28 antibody; (2) a heavy chain of a CD28 antibody; (3) a variable region from the light chain of an anti-CD28 antibody; (4) a variable region from the heavy chain of a CD28 antibody; (5) one or more CDRs (two, three, four, five, or six CDRs) of an anti-CD28 antibody; or (6) three CDRs from the light chain and three CDRs from the heavy chain of an anti-CD28 antibody.

[0134] In some other particular embodiments, the antigen-binding fragments of an anti-CD28 antibody include: (i) a Fab fragment, which is a monovalent fragment consisting of the V_L, V_H, C_L and C_H1 domains; (ii) a F (ab') 2 fragment, which is a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the V_H and C_H1 domains; (iv) a Fv fragment consisting of the V_L and V_H domains of a single arm of an antibody; (v) a dAb fragment (Ward et al., Nature (1989) 341: 544-546), which consists of a V_H domain; (vi) an isolated CDR, and (vii) single chain antibody (scFv), which is a polypeptide comprising a V_L region of an antibody linked to a V_H region of an antibody. Bird et al., Science (1988) 242: 423-426, and Huston et al., Proc. Natl. Acad. Sci. USA (1988) 85: 5879-5883.

[0135] In some embodiments, the anti-CD28 antibody or antibody fragment disclosed herein comprises a V_H region

that is at least 65%, at least 75%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOs: 11, 20, 29, 39, 47, 54, 62, 71, 77, 84, 92, 99, 107, 115, 122, 130, 137, 144, 151, 157, and 165. In some embodiments, the anti-CD28 antibody or antibody fragment disclosed herein comprises a V_L region that is at least 65%, at least 75%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOs: 12, 21, 30, 40, 48, 55, 63, 72, 78, 85, 93, 100, 108, 116, 123, 131, 138, 145, 152, 158 and 166. In some embodiments, the anti-CD28 antibody or antibody fragment disclosed herein comprises an HCDR1 amino acid sequence that is at least 65%, at least 75%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOs: 5, 15, 24, 33, 43, 66, 88, 103, 111, 126, 134, 148, and 161. In some embodiments, the anti-CD28 antibody or antibody fragment disclosed herein comprises an HCDR2 amino acid sequence that is at least 65%, at least 75%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOs: 6, 51, 58, 67, 89, 96, 104, and 155. In some embodiments, the anti-CD28 antibody or antibody fragment disclosed herein comprises an HCDR3 amino acid sequence that is at least 65%, at least 75%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOs: 7, 16, 25, 35, 44, 52, 59, 81, 90, 97, 105, 112, 119, 127, 135, 141, 149, and 162. In some embodiments, the anti-CD28 antibody or antibody fragment disclosed herein comprises an LCDR1 amino acid sequence that is at least 65%, at least 75%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOs: 8, 17, 26, 36, 45, 53, 60, 76, 82, 91, 98, 106, 113, 120, 128, 136, 142, 150, 156, and 163. In some embodiments, the anti-CD28 antibody or antibody fragment disclosed herein comprises an LCDR2 amino acid sequence that is at least 65%, at least 75%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOs: 9, 18, 27, 37, and 300. In some embodiments, the anti-CD28 antibody or antibody fragment disclosed herein comprises an LCDR3 amino acid sequence that is at least 65%, at least 75%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOs: 10, 19, 28, 38, 46, 61, 70, 83, 114, 121, 129, 143, and 164.

[0136] In some embodiments, the antibody disclosed herein comprises a heavy chain that is at least 65%, at least 75%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOs: 13, 22, 31, 41, 49, 56, 64, 73, 79, 86, 94, 101, 109, 117, 124, 141, 132, 139, 146, 153, 159, and 167.

[0137] In some embodiments, the antibody disclosed herein comprises a light chain that is at least 65%, at least 75%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOs: 14, 23, 32, 42, 50, 57, 65, 74, 80, 87, 95, 102, 110, 118, 125, 142, 133, 140, 147, 154, 160, and 168.

Iv. Multi-Specific Antibodies

[0138] Also provided are multi-specific antibodies that correspond to the activatable multi-specific antibodies or masked multi-specific antibodies described herein. One aspect of the present application provides multi-specific antibodies (including activatable bispecific T cell engager (TCE) molecules) that are capable of binding to both T cells and target cells such as tumor cells. Because of their on-target off-tumor effects, traditional TCE molecules are associated with high cytotoxicity, including toxicity to the central nervous system (CNS) and cytokine storms. Therefore, there is a need for antibodies capable of binding a T cell and a target cell such as a tumor cell with enhanced specificity and reduced side effects.

[0139] In some embodiments, the multi-specific antibody is bispecific (bsAb). In some embodiments, the multi-specific antibody is trispecific (tsAb).

[0140] In particular embodiments, a bispecific antibody of the present disclosure is specific for CD28 on the surface of T cells. In some embodiments, the multi-specific antibody is a tumor-associated antigen (TAA) ×CD28 bispecific antibody that specifically binds to the TAA and CD28. In some embodiments, the antibody of the present disclosure is an IgG antibody, e.g., comprises an IgG Fc region (e.g., a human IgG Fc region).

[0141] In some embodiments, the multi-specific antibody binds to CD28 on the surface of T cells. In some embodiments, the multi-specific antibody is a tumor-associated antigen (TAA) ×CD28 bispecific antibody that specifically binds to the TAA and CD28. In some embodiments, the multi-specific antibody does not comprise any masking moiety or cleavable moiety. In some embodiments, the multi-specific antibody is obtained upon cleavage of the cleavable moiety or cleavable moieties.

[0142] In some embodiments, the multi-specific antibody binds to CD3 on the surface of T cells. In some embodiments, the multi-specific antibody is a tumor-associated antigen (TAA) ×CD3 bispecific antibody that specifically binds to the TAA and CD3. In some embodiments, the multi-specific antibody specifically binds CD3 with a weak affinity, e.g., an EC_{50} of at least 10 nM (e.g., at least 100 nM) as determined by an ELISA assay, and/or a Kd of at least 50 nM. In some embodiments, the multi-specific antibody does not comprise any masking moiety or cleavable moiety. In some embodiments, the multi-specific antibody is obtained upon cleavage of the cleavable moiety or cleavable moieties.

[0143] In some embodiments, provided is a multi-specific antibody comprising: a) a first antigen-binding fragment comprising a VH1 and a V_L 1 of an antibody that specifically binds a target antigen (e.g., a tumor antigen, such as B7-H3, HER2, or TROP2); and b) a second antigen-binding fragment comprising a VH2 and a V_L 2 of an anti-CD3 antibody that specifically binds CD3, wherein the first and/or second antigen-binding fragment is fused to a first and/or second masking peptide (MP1/MP2). In some embodiments, provided is a multi-specific antibody comprising: a) a first antigen-binding fragment comprising a VH1 and a V_L 1 of an antibody that specifically binds a target antigen (e.g., a tumor antigen, such as B7-H3, HER2, or TROP2); and b) a second antigen-binding fragment comprising a VH2 and a V_L 2 of an anti-CD28 antibody that specifically binds CD28,

wherein the first and/or second antigen-binding fragment is fused to a first and/or second masking peptide (MP1/MP2).

[0144] In some embodiments, the first antigen-binding fragment is selected from the group consisting of a Fab, a Fv, a scFab and a scFv. In some embodiments, the first antigen-binding fragment is a Fab. In some embodiments, the second antigen-binding fragment is selected from the group consisting of a Fab, a Fv, a scFab and a scFv. In some embodiments, the second antigen-binding fragment is a scFv comprising, from N-terminus to C-terminus, V_L 2, an optional linker, and VH2. In some embodiments, the first antigen-binding fragment is a Fab and the second antigen-binding fragment is a Fab. In some embodiments, the first antigen-binding fragment is a Fab and the second antigen-binding fragment is a scFv.

[0145] The antibodies comprising engineered C_H3 domains with disulfide bonds and/or salt bridges described herein may further comprise one or more knob-into-hole residues. "Knob-into-hole" or "KIH" refers to an approach known in the art for making bispecific antibodies also known as the "protuberance-into-cavity" approach (see, e.g., U.S. Pat. No. 5,731,168). In this approach, two immunoglobulin polypeptides (e.g., heavy chain polypeptides) each comprise an interface. An interface of one immunoglobulin polypeptide interacts with a corresponding interface on the other immunoglobulin polypeptide, thereby allowing the two immunoglobulin polypeptides to associate. These interfaces may be engineered such that a "knob" or "protuberance" (these terms may be used interchangeably herein) located in the interface of one immunoglobulin polypeptide corresponds with a "hole" or "cavity" (these terms may be used interchangeably herein) located in the interface of the other immunoglobulin polypeptide. In some embodiments, the hole is of identical or similar size to the knob and suitably positioned such that when the two interfaces interact, the knob of one interface is positionable in the corresponding hole of the other interface. Without wishing to be bound to theory, this is thought to stabilize the heteromultimer and favor formation of the heteromultimer over other species, for example homomultimers. In some embodiments, the KIH approach is used in combination with the engineered disulfide bonds and/or salt bridges described herein to promote the heteromultimerization of two different immunoglobulin polypeptides, creating a bispecific antibody comprising two immunoglobulin polypeptides with binding specificities for different epitopes. In some embodiments, the C_H3 domains of the activatable multi-specific antibodies described herein do not comprise KIH residues.

[0146] In some embodiments, there is provided a bispecific antibody targeting CD28 and a tumor antigen (e.g., B7-H3, HER2, TROP2 or PD-L1), comprising a first polypeptide, a second polypeptide, and a third polypeptide, wherein:

[0147] (i) the first polypeptide comprises a structure represented by the formula: V_H1-C_H1-hinge-C_H2-first CH3;

[0148] (ii) the second polypeptide comprises a structure represented by the formula: scFv-hinge-C_H2-second CH3; and

[0149] (iii) the third polypeptide comprises a structure represented by the formula: V_L1-C_L;

[0150] wherein:

[0151] V_L1 is a first immunoglobulin light chain variable domain;

[0152] V_H1 is a first immunoglobulin heavy chain variable domain;

[0153] scFv is a single-chain variable fragment comprising a second immunoglobulin light chain variable domain (V_L2) and a second immunoglobulin heavy chain variable domain (V_H2);

[0154] C_L is an immunoglobulin light chain constant domain;

[0155] C_H1 is an immunoglobulin heavy chain constant domain 1;

[0156] C_H2 is an immunoglobulin heavy chain constant domain 2; and

[0157] hinge is an immunoglobulin hinge region connecting the C_H1 and C_H2 domains; wherein V_L1 and VH1 associate to form a first Fv that specifically binds the tumor antigen (e.g., B7-H3, HER2, TROP2 or PD-L1); and wherein the scFv specifically binds CD28. In some embodiments, the scFv binds CD28 with half-maximal binding at a concentration of antibody (EC_{50}) that ranges from 0.1 nM to 1000 nM as determined by ELISA (e.g., as described in Example 3). In some embodiments, the scFv binds CD28 with half-maximal binding at a concentration of antibody (EC_{50}) that is at less than 10 nM (e.g., between 1 nM and 0.1 μM) as determined by an Octet® RED96 assay (e.g., as described in Example 3). In particular embodiments, the scFv binds CD28 with a dissociation constant (Kd) of less than 10 nM.

[0158] In some embodiments, there is provided a bispecific antibody targeting CD28 and a tumor antigen (e.g., B7-H3, HER2, or TROP2), comprising a first polypeptide, a second polypeptide, a third polypeptide and a fourth polypeptide, wherein:

[0159] (i) the first polypeptide comprises a structure represented by the formula: V_H1-C_H1-hinge-C_H2-first CH3;

[0160] (ii) the second polypeptide comprises a structure represented by the formula: V_H2-C_H1-hinge-C_H2-second CH3;

[0161] (iii) the third polypeptide comprises a structure represented by the formula: V_L1-C_L; and

[0162] (iv) the fourth polypeptide comprises a structure represented by the formula: V_L2-C_L;

[0163] wherein:

[0164] V_L1 is a first immunoglobulin light chain variable domain;

[0165] V_H1 is a first immunoglobulin heavy chain variable domain;

[0166] V_L2 is a second immunoglobulin light chain variable domain;

[0167] V_H 2 is a second immunoglobulin heavy chain variable domain;

[0168] C_L is an immunoglobulin light chain constant domain;

[0169] C_H1 is an immunoglobulin heavy chain constant domain 1;

[0170] C_H2 is an immunoglobulin heavy chain constant domain 2; and

[0171] hinge is an immunoglobulin hinge region connecting the C_H1 and C_H2 domains; wherein V_L1 and V_H 1 associate to form a first Fv that specifically binds the tumor antigen (e.g., B7-H3, HER2, TROP2 or PD-L1); and wherein V_L2 and V_H 2 associate to form a second Fv that specifically binds CD28. In some

embodiments, the scFv binds CD28 with half-maximal binding at a concentration of antibody (EC_{50}) that is range from 0.1 nM to 1000 nM as determined by ELISA assay (e.g., as described in Example 3). In some embodiments, the second Fv binds CD28 with half-maximal binding at a concentration of antibody (EC_{50}) that is less than 10 nM (e.g., between 1 nM and 0.1 μM) as determined by an Octet® RED96 assay (e.g., as described in Example 3). In particular embodiments, the second Fv binds CD28 with a dissociation constant (Kd) of less than 10 nM.

[0172] In some embodiments, provided a multi-specific antibody comprising:

[0173] a) a first antigen-binding fragment comprising a V_H 1 and a V_L1 of an antibody that specifically binds a target antigen (e.g., a tumor antigen, such as B7-H3, HER2, or TROP2); and

[0174] b) a second antigen-binding fragment comprising a V_H 2 and a V_L2 of an anti-CD28 antibody that specifically binds CD28, wherein the second antigen-binding fragment is fused to a first masking peptide (MP1).

[0175] In some embodiments, there is provided a multi-specific antibody comprising:

[0176] a) a first antigen-binding fragment comprising a V_H 1 and a V_L1 of an antibody that specifically binds a target antigen (e.g., a tumor antigen, such as B7-H3, HER2, or TROP2), wherein the first antigen-binding fragment is fused to a first masking peptide (MP1); and

[0177] b) a second antigen-binding fragment comprising a V_H2 and a V_L2 of an anti-CD28 antibody that specifically binds CD28, wherein the second antigen-binding fragment is fused to a second masking peptide (MP2).

[0178] In some embodiments, the first antigen-binding fragment is selected from the group consisting of a Fab, a Fv, a scFab and a scFv. In some embodiments, the first antigen-binding fragment is a Fab. In some embodiments, the second antigen-binding fragment is selected from the group consisting of a Fab, a Fv, a scFab and a scFv. In some embodiments, the second antigen-binding fragment is a scFv comprising, from N-terminus to C-terminus, V_L2, an optional linker, and V_H2.

[0179] In some embodiments, provided a multi-specific antibody comprising a first polypeptide, a second polypeptide, and a third polypeptide, wherein:

[0180] (i) the first polypeptide comprises a structure represented by the formula: V_H1-C_H1-hinge-C_H2-first C_H3;

[0181] (ii) the second polypeptide comprises a structure represented by the formula: MP1-V_L2-V_H 2-hinge-C_H2-second C_H3; and

[0182] (iii) the third polypeptide comprises a structure represented by the formula: V_L1-C_L;

[0183] wherein:

[0184] V_L1 is a first immunoglobulin light chain variable domain;

[0185] V_H1 is a first immunoglobulin heavy chain variable domain;

[0186] V_L2 is a second immunoglobulin light chain variable domain;

[0187] V_H2 is a second immunoglobulin heavy chain variable domain;

[0188] C_L is an immunoglobulin light chain constant domain;

[0189] C_H1 is an immunoglobulin heavy chain constant domain 1;

[0190] C_H2 is an immunoglobulin heavy chain constant domain 2;

[0191] first C_H3 is a first immunoglobulin heavy chain constant domain 3;

[0192] second C_H3 is a second immunoglobulin heavy chain constant domain 3;

[0193] hinge is an immunoglobulin hinge region connecting the C_H1 and C_H2 domains;

[0194] MP1 is a first masking peptide; MP1 comprises, from N-terminus to C-terminus, an N-terminal unit (NU), a masking unit (MU), and a linkage unit (LU); the LU of the masking peptide may not comprise a cleavage site, or comprise at least one cleavage site.

[0195] In some embodiments, there is provided a multi-specific antibody comprising a first polypeptide, a second polypeptide, and a third polypeptide, wherein:

[0196] (i) the first polypeptide comprises a structure represented by the formula: V_H1-C_H1-hinge-C_H2-first C_H3);

[0197] (ii) the second polypeptide comprises a structure represented by the formula: MP2-V_L2-V_H2-hinge-C_H2-second C_H3; and

[0198] (iii) the third polypeptide comprises a structure represented by the formula: MP1-V_L1-C_L;

[0199] wherein:

[0200] V_L1 is a first immunoglobulin light chain variable domain;

[0201] V_H1 is a first immunoglobulin heavy chain variable domain;

[0202] V_L2 is a second immunoglobulin light chain variable domain;

[0203] V_H2 is a second immunoglobulin heavy chain variable domain;

[0204] C_L is an immunoglobulin light chain constant domain;

[0205] C_H1 is an immunoglobulin heavy chain constant domain 1;

[0206] C_H2 is an immunoglobulin heavy chain constant domain 2;

[0207] first C_H3 is a first immunoglobulin heavy chain constant domain 3;

[0208] second C_H3 is a second immunoglobulin heavy chain constant domain 3;

[0209] hinge is an immunoglobulin hinge region connecting the C_H1 and C_H2 domains;

[0210] MP1 is a masking peptide; MP1 comprises, from N-terminus to C-terminus, an N-terminal unit (NU), a masking unit (MU) and a linkage unit (LU); the LU of the masking peptide may comprise non, at least one or more cleavage site.

[0211] MP2 is a masking peptide; MP2 comprises, from N-terminus to C-terminus, an N-terminal unit (NU), a masking unit (MU) and a linkage unit (LU); the LU of the masking peptide may not comprise a cleavage site, or comprise at least one cleavage site.

[0212] In some embodiments, the bispecific antibody binds to a first and second target, where the first target is CD28, and the bispecific antibody comprises an HCDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 15, 24, 33, 43, 66, 88, 103,

111, 126, 134, 148, and 161; an HCDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 6, 51, 58, 67, 89, 96, 104, and 155; and an HCDR3 comprising an amino acid sequence selected from SEQ ID NOs: 7, 16, 25, 35, 44, 52, 59, 81, 90, 97, 105, 112, 119, 127, 135, 141, 149, and 162; and an LCDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 8, 17, 26, 36, 45, 53, 60, 76, 82, 91, 98, 106, 113, 120, 128, 136, 142, 150, 156, and 163; an LCDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 18, 27, 37, and 300; and an LCDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 19, 28, 38, 46, 61, 70, 83, 114, 121, 129, 143, and 164. In some embodiments, the bispecific antibody binds to a first and second target, where the first target is human CD28, and where the bispecific antibody comprises a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 11, 20, 29, 39, 47, 54, 62, 71, 77, 84, 92, 99, 107, 115, 122, 130, 137, 144, 151, 157, and 165, and a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 12, 21, 30, 40, 48, 55, 63, 72, 78, 85, 93, 100, 108, 116, 123, 131, 138, 145, 152, 158 and 166.

[0213] In some embodiments, the bispecific antibody binds to a first and second target, wherein the first target is CD28 and the second target is B7H3, wherein the bispecific antibody comprises a CD28-binding portion comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 11, 12, and 171, and where the bispecific antibody comprises a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 176, and a light chain comprising an amino acid sequence set forth in SEQ ID NO: 175. In particular embodiments, the bispecific antibody binds to a first and second target, wherein the first target is CD28 and the second target is B7H3, wherein the bispecific antibody comprises a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 171, a second heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 1176, and a light chain comprising an amino acid sequence set forth in SEQ ID NO: 175.

[0214] In some embodiments, the bispecific antibody binds to a first and second target, wherein the first target is CD28 and the second target is HER2, wherein the bispecific antibody comprises a CD28-binding portion comprising an amino acid sequence set forth in SEQ ID NO: 172, and where the bispecific antibody comprises a heavy chain comprising an amino acid set forth in SEQ ID NO: 170, and a light chain comprising an amino acid sequence set forth in SEQ ID NO: 169. In particular embodiments, the bispecific antibody binds to a first and second target, wherein the first target is CD28 and the second target is HER2, wherein the bispecific antibody comprises a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 172, a second heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 170, and a light chain comprising an amino acid sequence set forth in SEQ ID NO: 169.

[0215] In some embodiments, the bispecific antibody binds to a first and second target, wherein the first target is CD28 and the second target is HER2, wherein the bispecific antibody comprises a CD28-binding portion comprising an amino acid sequence set forth in SEQ ID NO: 11, 12, 171, a heavy chain comprising an amino acid set forth in SEQ ID NO: 170, and a light chain comprising an amino acid sequence set forth in SEQ ID NO: 169. In particular embodiments, the bispecific antibody binds to a first and second target, wherein the first target is CD28 and the second target is HER2, wherein the bispecific antibody comprises a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 171, a second heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 170, and a light chain comprising an amino acid sequence set forth in SEQ ID NO: 169.

[0216] In some embodiments, the bispecific antibody binds to a first and second target, wherein the first target is human CD28 and the second target is TROP2, wherein the bispecific antibody comprises a CD28-binding portion comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 13, 14, and 171, and where the bispecific antibody comprises a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 174, and a light chain comprising an amino acid sequence set forth in SEQ ID NO: 173. In particular embodiments, the bispecific antibody binds to a first and second target, wherein the first target is CD28 and the second target is TROP2, wherein the bispecific antibody comprises a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 171, a second heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 174, and a light chain comprising an amino acid sequence set forth in SEQ ID NO: 173.

[0217] In particular embodiments, the bispecific antibody binds to a first and second target, where the first target is CD3 and the second target is B7-H3, and where the bispecific antibody comprises a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 177 or an scFv fusion polypeptide set forth in SEQ ID NO: 299, a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 176, and a light chain comprising an amino acid sequence set forth in SEQ ID NO: 175.

[0218] In particular embodiments, the bispecific antibody binds to a first and second target, where the first target is CD3 and the second target is TROP2.

[0219] In some embodiments, the bispecific antibody binds to a first and second target, where the first target is human CD28, and where the bispecific antibody comprises a heavy chain amino acid sequence selected from the group consisting of SEQ ID NOs: 13, 22, 31, 41, 49, 56, 64, 73, 79, 86, 94, 101, 109, 117, 124, 141, 132, 139, 146, 153, 159, and 167, and a light chain amino acid sequence selected from the group consisting of SEQ ID NOs: 14, 23, 32, 42, 50, 57, 65, 74, 80, 87, 95, 102, 110, 118, 125, 142, 133, 140, 147, 154, 160, and 168.

V. Masked Antibodies

[0220] In some embodiments, the present disclosure provides a masked antibody which may be a masked monoclonal antibody to a specific target or a multi-specific (e.g., bispecific) antibody. In some embodiments, the masked antibody provided herein comprises a full-length antibody light chain, e.g., a kappa or lambda light chain. Additionally or alternatively, in some embodiments, the antibody comprises a full-length antibody heavy chain. The antibody heavy chain may be in any class, such as IgG, IgM, IgE, IgA, or IgD. In some embodiments, the antibody heavy chain is in the IgG class, such as IgG_1, IgG_2, IgG_3, or IgG_4 subclass. An antibody heavy chain described herein may be converted from one class or subclass to another class or subclass using methods known in the art. In some embodiments, the

masked antibody is or comprises a full-length antibody that comprises an Fc region, e.g., a human Fc region or a variant thereof. In some embodiments, the human Fc region is a human IgG_1 Fc region, a human IgG_2 Fc region, a human IgG_4 Fc region, or a variant of any one of the preceding. In some embodiments, the variant Fc region comprises one or more amino acid substitutions, insertions, or deletions relative to the wild type human Fc region from which the variant is derived. In some embodiments, the masked antibody comprises a variant of a human IgG_1 Fc region. In some embodiments, the IgG_1 Fc variant comprises one or more amino acid substitutions that increases the affinity of the Fc variant for FcγRIIb. In some embodiments, the variant of the human IgG_1 Fc region comprises substitution (s) selected from the group consisting of: G236D; L328F; S239D; S267E; G236D and S267E; S239D and S267E; S267E and L328S; and S267E and L328F, wherein amino acid numbering is according to the EU index (see, e.g., Edelman et al., Proc Natl Acad Sci USA (1969) 63: 78-85). The preceding substitutions are described in Chu et al. Mol Immunol. (2008) 45 (15): 3926-33. Additionally or alternatively, in some embodiments, the variant of the human IgG_1 Fc region comprises substitution (s) selected from the group consisting of: E233D and P238D; G237D and P238D; H268D and P238D; P271G and P238D; A330R and P238D; E233D, P238D, and A330R; E233D, P231G, P238D. and A330R; G237D, H268D, P238D, and P271G; G237D, P238D, P271G, and A330R; E233D, H268D, P238D, P271G, and A330R; G237D, H268D, P238D, P271G, and A330R; and E233D, G237D, P238D, H268D, P271G and A330R, wherein amino acid numbering is according to the EU index. The preceding substitutions are described in Mimoto et al. Protein Eng Des Sel. (2013) 26 (10): 589-98. Additionally or alternatively, in some embodiments, the variant of the human IgG_1 Fc region comprises an S2657A substitution (see Buschor et al. Int Arch Allergy Immunol. (2014) 163 (3): 206-14), wherein amino acid numbering is according to the EU index. Additionally or alternatively, in some embodiments, the variant of the human IgG_1 Fc region comprises a T437R and/or a K248E substitution (see Zhang et al. MAbs. (2017) 9 (7): 1129-1142), wherein amino acid numbering is according to the EU index. In some embodiments, the masked antibody comprises a variant of a human IgG_4 Fc region. In some embodiments, the IgG_4 Fc variant comprises one or more amino acid substitutions that increases the affinity of the Fc variant for FcγRIIb. In some embodiments, the variant of the human IgG_4 Fc region comprises substitution (s) selected from the group consisting of: G236D; L328F; S239D; S267E; G236D and S267E; S239D and S267E; S267E and L328S; and S267E and L328F, wherein amino acid numbering is according to the EU index. Additionally or alternatively, in some embodiments, the variant of the human IgG_4 Fc region comprises substitution (s) selected from the group consisting of: E233D and P238D; G237D and P238D; H268D and P238D; P271G and P238D; A330R and P238D; E233D, P238D, and A330R; E233D, P231G, P238D. and A330R; G237D, H268D, P238D, and P271G; G237D, P238D, P271G, and A330R; E233D, H268D, P238D, P271G, and A330R; G237D, H268D, P238D, P271G, and A330R; and E233D, G237D, P238D, H268D, P271G and A330R, wherein amino acid numbering is according to the EU index. Additionally or alternatively, in some embodiments, the variant of the human IgG_4 Fc region comprises an S2657A substitution, wherein amino acid numbering is according to the EU index. Additionally or alternatively, in some embodiments, the variant of the human IgG_1 Fc region comprises a T437R and/or a K248E substitution wherein amino acid numbering is according to the EU index.

[0221] In some embodiments, the masked antibodies disclosed herein further comprise a human IgG_1 domain or a variant thereof that comprises one or more substitution mutation (s). In some embodiments the IgG_1 variant comprises substitution (s) selected from the group consisting of: G236D; L328F; S239D; S267E; G236D and S267E; S239D and S267E; S267E and L328S; and S267E and L328F; E233D and P238D; G237D and P238D; H268D and P238D; P271G and P238D; A330R and P238D; E233D, P238D, and A330R; E233D, P231G, P238D. and A330R; G237D, H268D, P238D, and P271G; G237D, P238D, P271G, and A330R; E233D, H268D, P238D, P271G, and A330R; G237D, H268D, P238D, P271G, and A330R; and E233D, G237D, P238D, H268D, P271G and A330R; S2657A; T437R; K248E; and T437R and K248E, wherein amino acid numbering is according to the EU index. In some embodiments, the masked antibodies disclosed herein further comprise a human IgG_4 domain or a variant thereof that comprises one or more substitution mutation (s). In some embodiments the IgG_4 variant comprises substitution (s) selected from the group consisting of: G236D; L328F; S239D; S267E; G236D and S267E; S239D and S267E; S267E and L328S; and S267E and L328F; E233D and P238D; G237D and P238D; H268D and P238D; P271G and P238D; A330R and P238D; E233D, P238D, and A330R; E233D, P231G, P238D. and A330R; G237D, H268D, P238D, and P271G; G237D, P238D, P271G, and A330R; E233D, H268D, P238D, P271G, and A330R; G237D, H268D, P238D, P271G, and A330R; and E233D, G237D, P238D, H268D, P271G and A330R; S2657A; T437R; K248E; and T437R and K248E, wherein amino acid numbering is according to the EU index.

[0222] In some embodiments, the term "masked antibody" refers to an antibody fragment, e.g., a masked antigen-binding fragment of a masked anti-CD28 antibody. In some embodiments, the antibody fragment is or comprises a Fab, an Fab', a Fab'-SH, a F (ab') 2, an Fv, an scFv (see Bird et al. (1988) Science 242: 423-426 and Huston et al. (1988) Proc. Natl. Acad. Sci. USA 85: 5879-5883), an (scFv) 2, a linear antibody, a single-chain antibody, a minibody, or a diabody.

[0223] In some embodiments, a masked anti-CD28 antibody described herein cross-reacts with CD28 from different species, thus permitting the masked anti-CD28 antibody to be used in both preclinical and clinical studies. In some embodiments, a masked anti-CD28 antibody described herein binds to two or more of human CD28, cynomolgus CD28, murine (mouse) CD28, and/or rat CD28 following activation (i.e., after activation of the masked antibody via cleavage, e.g., protease cleavage). In some embodiments, a masked anti-CD28 antibody binds human CD28, cynomolgus CD28, murine (mouse) CD28, and a rat CD28 following activation (i.e., after activation of the masked antibody via cleavage, e.g., protease cleavage).

[0224] In some embodiments, masked anti-CD28 antibodies described herein are context-dependent (e.g., are activated (are only capable of binding their targets) in certain contexts (such as in the protease-rich tumor microenvironment)). In some embodiments, the masked anti-CD28 anti-

bodies described herein provide improved safety over more traditional, non-masked antibodies (e.g., show reduced toxicity, do not induce significant alterations to the weights of many organs, do not alter liver histopathology, hematology, and/or blood biochemistry, etc.). In some embodiments, masked anti-CD28 antibodies described herein exhibit pharmacokinetic properties that are similar to those of traditional, non-masked anti-CD28 antibodies (e.g., have similar in vivo half-lives). In some embodiments, masked anti-CD28 antibodies described herein exhibit improved pharmacokinetic properties as compared to more traditional, non-masked anti-CD28 antibodies (e.g., have longer in vivo half-lives).

[0225] In some embodiments, the antibody heavy chain variable region (V_H) and the antibody light chain variable region (V_L) of a masked anti-CD28 antibody described herein form an antigen binding domain (ABD) that binds hCD28. In some embodiments, the masking unit (MU) of a masked anti-CD28 antibody described herein binds to the ABD of the and reduces or inhibits binding of the masked anti-CD28 antibody to hCD28, as compared to the binding of a corresponding anti-CD28 antibody lacking the MU to hCD28 and/or as compared to the binding of the ABD to hCD28.

[0226] In some embodiments, the masking unit (MU) has a masking efficiency of at least about 2.0 (e.g., at least about 2.0, at least about 3.0, at least about 4.0, at least about 5.0, at least about 6.0, at least about 7.0, at least about 8.0, at least about 9.0, at least about 10, at least about 25, at least about 50, at least about 75, at least about 100, at least about 150, at least about 200, at least about 300, at least about 400, at least about 500, at least about 600, at least about 700, at least about 800, at least about 900, at least about 1,000, at least about 1,100, at least about 1, 200, at least about 1, 300, at least about 1, 400, at least about 1,500, etc., including any range in between these values) prior to removing the MU from a masked antibody provided herein. For example, and in some embodiments, the masking efficiency of a masked anti-CD28 antibody is measured as the difference in affinity of the masked anti-CD28 antibody comprising the masking unit (MU) for binding to hCD28 (i.e., before activation of the masked antibody) relative to the affinity of an anti-CD28 antibody lacking the MU for binding to hCD28. In a further example, masking efficiency is measured as the difference in affinity for hCD28 of a masked anti-CD28 antibody comprising a MU (i.e., before activation of the masked antibody via cleavage, e.g., protease cleavage) relative to the affinity for hCD28 of the unmasked anti-CD28 antibody (i.e., after activation of the masked antibody via cleavage, e.g., protease cleavage). In some embodiments, the masking efficiency is measured by dividing the EC_{50} for target-binding of a masked antibody comprising an MU (i.e., before activation) by the EC_{50} of a corresponding antibody specific for the same target that lacks the masking peptide or masking unit. In some embodiments, the EC_{50} is measured by ELISA. In some embodiments, the masking unit (MU) of the masked antibody binds to the ABD, and prevents the masked polypeptide from binding to its target. In particular embodiments, the target is CD28. In other embodiments, the target is CD3, B7-H3, HER2, or TROP2.

[0227] In some embodiments, the affinity of a masked antibody of the present disclosure increases by at least about 2-fold (e.g., at least about 2-fold, at least about 2.5-fold, at least about 3, at least about 3.5-fold, at least about 4-fold, at least about 4.5-fold, at least about 5-fold, at least about 5.5-fold, at least about 6-fold, at least about 6.5-fold, at least about 7-fold, at least about 7.5-fold, at least about 8-fold, at least about 8.5-fold, at least about 9-fold, at least about 9.5-fold, at least about 10-fold, at least about 25-fold, at least about 50-fold, at least about 75-fold, at least about 100-fold, at least about 250-fold, at least about 500-fold, at least about 750-fold, or at least about 1000-fold, or more, including any range in between the preceding values) when the masking unit is removed from the antibody (e.g., after activation by treatment with one or more proteases that cleave within the linkage unit) as compared to a corresponding antibody specific for the same target but without the masking peptide or masking unit. In some embodiments, the EC_{50} of a masked antibody described herein decreases by at least about 2-fold (e.g., at least about 2-fold, at least about 2.5-fold, at least about 3, at least about 3.5-fold, at least about 4-fold, at least about 4.5-fold, at least about 5-fold, at least about 5.5-fold, at least about 6-fold, at least about 6.5-fold, at least about 7-fold, at least about 7.5-fold, at least about 8-fold, at least about 8.5-fold, at least about 9-fold, at least about 9.5-fold, at least about 10-fold, at least about 25-fold, at least about 50-fold, at least about 75-fold, at least about 100-fold, at least about 250-fold, at least about 500-fold, at least about 750-fold, or at least about 1000-fold, or more, including any range in between the preceding values) after activation by treatment with one or more proteases that cleave within the linkage unit (e.g., as measured by an ELISA or FACS assay).

[0228] In some embodiments, when the masking unit is bound to the ABD of a masked antibody described herein, the K_D of the antibody for its target is about 2 (e.g., about 2, about 2.5, about 3, about 3.5 about 4, about 4.5, about 5, about 5.5, about 6, about 6.5, about 7, about 7.5, about 8, about 8.5, about 9, about 9.5, about 10, about 25, about 50, about 75, about 100, about 250, about 500, about 750, or about 1000 or more, including any range in between the preceding values) times greater than the K_D of the antibody when the masking unit of the masked anti-CD28 antibody is removed from the ABD (such as after protease treatment to cleave within the linkage unit). In some embodiments, when the masking unit is bound to the ABD of a masked antibody described herein, the K_D of the antibody for its target is about 2 (e.g., about 2, about 2.5, about 3, about 3.5 about 4, about 4.5, about 5, about 5.5, about 6, about 6.5, about 7, about 7.5, about 8, about 8.5, about 9, about 9.5, about 10, about 25, about 50, about 75, about 100, about 250, about 500, about 750, or about 1000 or more, including any range in between the preceding values) times greater than the K_D of a corresponding antibody that is specific to the same target but lacks a masking peptide or masking unit.

[0229] In some embodiments, the masking unit sterically hinders binding of the masked binding polypeptide to its target and/or allosterically hinders binding of the masked binding polypeptide to its target.

[0230] In some embodiments, the dissociation constant of the masking unit for the ABD of a masked antibody (e.g., anti-CD28) described herein is greater than the dissociation constant of the masked antibody for its target (e.g., hCD28; when the masked antibody is in active form, such as after protease treatment). In some embodiments, the dissociation constant of the masking unit for the ABD of a masked antibody (e.g., anti-CD28) described herein is about 2 (e.g., about 2, about 2.5, about 3, about 3.5 about 4, about 4.5,

about 5, about 5.5, about 6, about 6.5, about 7, about 7.5, about 8, about 8.5, about 9, about 9.5, about 10, about 25, about 50, about 75, about 100, about 250, about 500, about 750, or about 1000 or more, including any range in between the preceding values) times greater than the dissociation constant of the masked antibody for its target (e.g., hCD28; when the masked antibody is in active form, such as after protease treatment). In some embodiments, the dissociation constant of the masking unit for the ABD of a masked antibody (e.g., anti-CD28) described herein is about equal to the dissociation constant of the masked antibody for its target (e.g., hCD28; when the masked antibody is in active form, such as after protease treatment). In some embodiments, the masking unit (MU) binds to the ABD of a masked antibody (e.g., anti-CD28) described herein and prevents the antibody from binding to its target (e.g., hCD28) only when the masked antibody has not been activated (e.g., by treatment with one or more proteases that cleave within the linkage unit). In some embodiments, activation induces cleavage of the polypeptide within the cleavage site. In some embodiments, activation induces conformation changes in the polypeptide (e.g., displacement of the masking unit (MU)), leading to the masking peptide no longer preventing the polypeptide from binding to its target.

A. Single-Masked Antibodies

[0231] In some embodiments, provided is a masked monoclonal antibody comprising a masking peptide (MP) and an antibody that binds CD28, wherein the antibody comprises a heavy chain variable regions (V_H) and a light chain variable region (V_L), wherein the MP is linked to an N-terminus of the V_L, wherein the MP comprises, from N-terminus to C-terminus, a masking unit (MU), and a linkage unit (LU), wherein the MP comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 215-248, and wherein the antibody V_H region comprises a HCDR1 amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 15, 24, 33, 43, 66, 88, 103, 111, 126, 134, 148, and 161; a HCDR2 amino acid sequence selected from the group consisting of SEQ ID NOs: 6, 51, 58, 67, 89, 96, 104, and 155; and a HCDR3 amino acid sequence selected from the group consisting of SEQ ID NOs: 7, 16, 25, 35, 44, 52, 59, 81, 90, 97, 105, 112, 119, 127, 135, 141, 149, and 162; and the antibody V_L region comprises a LCDR1 amino acid sequence selected from the group consisting of SEQ ID NOs: 8, 17, 26, 36, 45, 53, 60, 76, 82, 91, 98, 106, 113, 120, 128, 136, 142, 150, 156, and 163; a LCDR2 amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 18, 27, 37, and 300; and a LCDR3 amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 19, 28, 38, 46, 61, 70, 83, 114, 121, 129, 143, and 164.

[0232] In some embodiments, provided is a masked monoclonal antibody comprising a masking peptide (MP) and an antibody that binds CD28, wherein the antibody comprises a heavy chain variable regions (V_H) and a light chain variable region (V_L), wherein the MP is linked to an N-terminus of the V_L, wherein the MP comprises, from N-terminus to C-terminus, a masking unit (MU), and a linkage unit (LU), wherein the MP comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 215-248, and wherein the antibody heavy chain variable region comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11, 20, 29, 39, 47, 54, 62, 71, 77, 84, 92, 99, 107, 115, 122, 130, 137, 144, 151, 157, and 165, and the light chain variable region comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 12, 21, 30, 40, 48, 55, 63, 72, 78, 85, 93, 100, 108, 116, 123, 131, 138, 145, 152, 158 and 166. In some embodiments, provided is a masked monoclonal antibody comprising a masking peptide (MP) and an antibody that binds human CD28, wherein the antibody comprises a heavy chain and a light chain, wherein the MP is linked to an N-terminus of the LC, wherein the MP comprises, from N-terminus to C-terminus, a masking unit (MU), and a linkage unit (LU), wherein the MP comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 215-248, wherein the antibody HC comprises an amino acid sequence selected from group consisting of SEQ ID NOs: 13, 22, 31, 41, 49, 56, 64, 73, 79, 86, 94, 101, 109, 117, 124, 141, 132, 139, 146, 153, 159, and 167, and wherein the antibody LC comprises the amino acid sequences selected from group consisting of SEQ ID NOs: 14, 23, 32, 42, 50, 57, 65, 74, 80, 87, 95, 102, 110, 118, 125, 142, 133, 140, 147, 154, 160, and 168.

B. Single-Masked Multi-Specific Antibodies

[0233] In some embodiments, also provided is a masked bispecific monoclonal antibody specific for a first and second target, where the first target is CD28, wherein the antibody comprises a masking peptide (MP) and a CD28-binding portion, wherein the antibody comprises a heavy chain variable region (V_H) and a light chain variable region (V_L), wherein the MP is linked to an N-terminus of the V_L, wherein the MP comprises, from N-terminus to C-terminus, a masking unit (MU), and a linkage unit (LU), wherein the MP comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 215-248, wherein the CD28-binding portion comprises a V_H region comprising a HCDR1 of SEQ ID NO: 5, HCDR2 of SEQ ID NO: 6, and HCDR3 of SEQ ID NO: 7, and a V_L region comprising a LCDR1 of SEQ ID NO: 8, a LCDR2 of SEQ ID NO: 9 and a LCDR3 of SEQ ID NO: 10, and wherein the second target is a B7-H3, HER2, or TROP2 protein.

[0234] In some embodiments, also provided is a masked bispecific monoclonal antibody specific for a first and second target, where the first target is CD28, wherein the antibody comprises a masking peptide (MP) and a CD28-binding portion, wherein the antibody comprises a heavy chain variable region (V_H) and a light chain variable region (V_L), wherein the MP is linked to an N-terminus of the V_L, wherein the MP comprises, from N-terminus to C-terminus, a masking unit (MU), and a linkage unit (LU), wherein the MP comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 215-248, and wherein the CD28-binding portion comprises a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 11, 20, 29, 39, 47, 54, 62, 71, 77, 84, 92, 99, 107, 115, 122, 130, 137, 144, 151, 157, and 165; and a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 12, 21, 30, 40, 48, 55, 63, 72, 78, 85, 93, 100, 108, 116, 123, 131, 138, 145, 152, 158 and 166, and wherein the second target is a B7-H3, HER2, or TROP2 protein.

C. Double-Masked Multi-Specific Antibodies

[0235] In particular embodiments, also provided is a masked bispecific monoclonal antibody specific for a first

and second target, where the first target is CD28 and the second target is a tumor associated antigen selected from HER2, B7-H3, and TROP2, wherein the antibody comprises two masking peptides (MP).

VI. Masking Peptides

[0236] In some embodiments, the MP further comprises a N-terminal unit. In some embodiments, the N-terminal unit is between about 1 and 10 amino acids in length. In some embodiments, the N-terminal unit comprises SEQ ID NO: 210. In some embodiments, the LU comprises at least a first cleavage site (CS_1) (e.g., a first protease cleavage site). In some embodiments, the LU further comprises a second cleavage site (CS_2). In some embodiments, the first and/or second cleavage site are a protease cleavage site. In some embodiments, the first and second cleavage sites are the same. In some embodiments, the first and second cleavage sites are different. Any suitable protease cleavage site recognized and/or cleaved by any protease (e.g., a protease that is known to be co-localized with a target of a polypeptide comprising the cleavage site) known in the art may be used, including, for example, a protease cleavage site recognized and/or cleaved by urokinase-type plasminogen activator (uPA); matrix metalloproteinases (e.g., MMP-1, MMP-2, MMP-3, MMP-7, MMP-8, MMP-9, MMP-10, MMP-11, MMP-12, MMP-13, MMP-14, MMP-15, MMP-16, MMP-17, MMP-19, MMP-20, MMP-23, MMP-24, MMP-26, and/or MMP-27); Tobacco Etch Virus (TEV) protease; plasmin; Thrombin; PSA; PSMA; ADAMS/ADAMTS (e.g., ADAM 8, ADAM 9, ADAM10, ADAM12, ADAM15, ADAM17/TACE, ADAMDEC1, ADAMTS1, ADAMTS4, and/or ADAMTS5); caspases (e.g., Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, and/or Caspase-14); aspartate proteases (e.g., RACE and/or Renin); aspartic cathepsins (e.g., Cathepsin D and/or Cathepsin E); cysteine cathepsins (e.g., Cathepsin B, Cathepsin C, Cathepsin K, Cathepsin L, Cathepsin S, Cathepsin V/L2, and/or Cathepsin X/Z/P); cysteine proteinases (e.g., Cruzipain, Legumain, and/or Otubain-2); KLKs (e.g., KLK4, KLK5, KLK6, KLK7, KLK8, KLK10, KLK11, KLK13, and/or KLK14); metalloproteinases (e.g., Meprin, Neprilysin, PSMA, and/or BMP-1); serine proteases (e.g., activated protein C, cathepsin A, cathepsin G, chymase, and/or coagulation factor proteases (such as FVIIa, FIXa, FXa, FXIa, FXIIa)); elastase; granzyme B; guanidinobenzoatase; HtrA1; human neutrophil elastase; lactoferrin; marapsin; NS3/4A; PACE4; tPA; tryptase; type II transmembrane serine proteases (TTSPs) (e.g., DESC1, DPP-4, FAP, hepsin, matriptase-2, MT-SP1/matriptase, TMPRSS2, TMPRSS3 and/or TMPRSS4); etc. In some embodiments, the first protease cleavage site is a cleavage site for a protease selected from uPA, MMP-1, MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, TEV protease, plasmin, thrombin, Factor X, PSA, PSMA, cathepsin D, cathepsin K, cathepsin S, ADAM10, ADAM12, ADAMTS, caspase-1, caspase-2, caspase-3, caspase-4, caspase-5, caspase-6, caspase-7, caspase-8, caspase-9, caspase-10, caspase-11, caspase-12, caspase-13, caspase-14, and TACE. In some embodiments, the first protease cleavage site is a cleavage site for a protease selected from uPA, MMP-2, MMP-9, and/or TEV protease.

[0237] In some embodiments, the LU further comprises a first linker (L_1). In some embodiments, the first linker (L_1) is C-terminal to the first cleavage site (CS_1) (e.g., a first protease cleavage site). In some embodiments, the LU comprises a structure, from N-terminus to C-terminus, of: (CS_1)-L_1. In some embodiments, the LU further comprises a second linker (L_2). In some embodiments, the L_2 is C-terminal to the second cleavage site. In some embodiments, the LU comprises a structure, from N-terminus to C-terminus, of: (CS_1)-L_1-(CS_2)-L_2. In some embodiments, L_1 and L_2 are any suitable linker (e.g., a flexible linker) known in the art, including, without limitation, e.g., glycine polymers (G) n, where n is an integer of at least 1 (e.g., at least one, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, etc.); glycine-serine polymers (GS) n, where n is an integer of at least 1 (e.g., at least one, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, etc.) such as SEQ ID NOs: 249-257; glycine-alanine polymers; alanine-serine polymers; and the like. Linker sequences may be of any length, such as from about 1 amino acid (e.g., glycine or serine) to about 20 amino acids (e.g., 20 amino acid glycine polymers or glycine-serine polymers), about 1 amino acid to about 15 amino acids, about 3 amino acids to about 12 amino acids, about 4 amino acids to about 10 amino acids, about 5 amino acids to about 9 amino acids, about 6 amino acids to about 8 amino acids, etc. In some embodiments, the linker is any of about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids in length.

[0238] In some embodiments, the LU comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 213 and 213. In some embodiments, the masking peptide (MP) comprises the structure, from N-terminus to C-terminus, of: (MU)-(LU), wherein LU comprises the structure (CS_1)-L, or (CS_1)-L_1-(CS_2)-L_2. In some embodiments, the masking peptide of the present disclosure comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 215-248.

[0239] In some embodiments, the masking peptide (MP) comprises an MU set forth in any one of SEQ ID NOs: 178-211 and an LU set forth in SEQ ID NO: 213 or 214. In some embodiments, the MP comprises a sequence set forth in any one of SEQ ID NOs: 215-248.

VII. Antibody Production

[0240] Another aspect of the disclosure provides one or more isolated nucleic acid molecule (s) that comprises nucleotide sequence (s) encoding an amino acid sequence (s) of an anti-CD28 antibody described herein, including a masked anti-CD28 antibody. In some embodiments, provided herein is one or more isolated nucleic acid molecule (s) that comprises nucleotide sequence (s) encoding an amino acid sequence (s) of a multi-specific antibody described herein, including a masked multi-specific antibody. The amino acid sequence encoded by the nucleotide sequence may be any portion of an antibody described herein, such as a CDR, a sequence comprising one, two, or three CDRs, a variable region of a heavy chain, variable region of a light chain, or may be a full-length heavy chain or full-length light chain. A nucleic acid of the disclosure can be, for example, DNA or RNA, and may or may not contain intronic sequences. Typically, the nucleic acid is a cDNA molecule.

[0241] In some embodiments, the disclosure provides an isolated nucleic acid molecule that comprises or consists of

a nucleotide sequence encoding an amino acid sequence of, e.g., a heavy chain variable region and/or a light chain variable region of an antibody described herein, or, e.g., a full-length heavy chain and/or full-length light chain of an antibody described herein.

[0242] Nucleic acids of the disclosure can be obtained using any suitable molecular biology techniques, e.g., PCR amplification or cDNA cloning techniques. For antibodies described herein obtained via library screening, the nucleic acid encoding the antibody can be recovered from the library.

[0243] The isolated DNA encoding the V_H region can be converted to a full-length heavy chain gene by operatively linking the V_H-encoding DNA to another DNA molecule encoding heavy chain constant regions (C_H1, C_H2 and C_H3). The sequences of human heavy chain constant region genes are known in the art (see e.g., Kabat et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and DNA fragments encompassing these regions can be obtained by standard PCR amplification. The heavy chain constant region can be an IgG_1, IgG_2, IgG_3, IgG_4, IgA, IgE, IgM or IgD constant region, but most preferably is an IgG_4 or IgG_2 constant region without ADCC effect. The IgG_4 constant region sequence can be any of the various alleles or allotypes known to occur among different individuals. These allotypes represent naturally occurring amino acid substitution in the IgG_4 constant regions. For a Fab fragment heavy chain gene, the V_H-encoding DNA can be operatively linked to another DNA molecule encoding only the heavy chain C_H1 constant region.

[0244] The isolated DNA encoding the V_L region can be converted to a full-length light chain gene (as well as a Fab light chain gene) by operatively linking the V_L-encoding DNA to another DNA molecule encoding the light chain constant region, C_L. The sequences of human light chain constant region genes are known in the art (see e.g., Kabat et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and DNA fragments encompassing these regions can be obtained by standard PCR amplification. The light chain constant region can be a kappa or lambda constant region.

[0245] To create a scFv gene, the V_H- and V_L-encoding DNA fragments are operatively linked to another fragment encoding a flexible linker, e.g., encoding the amino acid sequence $(Gly_4\text{-}Ser)_3$, such that the V_H and V_L sequences can be expressed as a contiguous single-chain protein, with the V_L and V_H regions joined by the flexible linker (see e.g., Bird et al., Science (1988) 242: 423-426; Huston et al., Proc. Natl. Acad. Sci. USA (1988) 85: 5879-83; and McCafferty et al., Nature (1990) 348: 552-554).

[0246] The present disclosure further provides a vector that comprises one or more nucleic acid molecule (s) provided by the present disclosure. In some embodiments, the vector is an expression vector useful for the expression of an antibody described herein or an antigen binding fragment of such an antibody. In some embodiments, provided herein are vectors, wherein a first vector comprises a polynucleotide sequence encoding a heavy chain variable region as described herein, and a second vector comprises a polynucleotide sequence encoding a light chain variable region as described herein. In some embodiments, a single vector comprises polynucleotides encoding a heavy chain variable region as described herein and a light chain variable region as described herein.

[0247] To express a binding molecule of the disclosure, DNAs encoding partial or full-length light and heavy chains are inserted into expression vectors such that the DNA molecules are operatively linked to transcriptional and translational control sequences. In this context, the term "operatively linked" means that an antibody gene is ligated into a vector such that transcriptional and translational control sequences within the vector serve their intended function of regulating the transcription and translation of the DNA molecule. The expression vector and expression control sequences are chosen to be compatible with the expression host cell used. The antibody light chain gene and the antibody heavy chain gene can be inserted into separate vector or, more typically, both genes are inserted into the same expression vector. The antibody genes are inserted into the expression vector by any suitable methods (e.g., ligation of complementary restriction sites on the antibody gene fragment and vector, or homologous recombination-based DNA ligation). The light and heavy chain variable regions of the antibodies described herein can be used to create full-length antibody genes of any antibody isotype and subclass by inserting them into expression vectors already encoding heavy chain constant and light chain constant regions of the desired isotype and subclass such that the V_H segment is operatively linked to the C_H segment (s) within the vector and the V_L segment is operatively linked to the C_L segment within the vector. Additionally or alternatively, the recombinant expression vector can encode a signal peptide that facilitates secretion of the antibody chain from a host cell. The antibody chain gene can be cloned into the vector such that the signal peptide is linked in-frame to the amino terminus of the antibody chain gene. The signal peptide can be an immunoglobulin signal peptide or a heterologous signal peptide (i.e., a signal peptide from a non-immunoglobulin protein).

[0248] In addition to the antibody chain genes, the expression vectors of the disclosure typically carry regulatory sequences that control the expression of the antibody chain genes in a host cell. The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals) that control the transcription or translation of the antibody chain genes. Such regulatory sequences are described, for example, in Goeddel (Gene Expression Technology. Methods in Enzymology 185, Academic Press, San Diego, Calif. (1990)). It will be appreciated by those skilled in the art that the design of the expression vector, including the selection of regulatory sequences, may depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. Examples of regulatory sequences for mammalian host cell expression include viral elements that direct high levels of protein expression in mammalian cells, such as promoters and/or enhancers derived from cytomegalovirus (CMV), Simian Virus 40 (SV40), adenovirus, (e.g., the adenovirus major late promoter (AdMLP) and polyoma. Alternatively, nonviral regulatory sequences may be used, such as the ubiquitin promoter or β-globin promoter. Still further, regulatory elements composed of sequences from different sources, such as the SR promoter system, which contains sequences from the SV40 early promoter and the long terminal repeat

of human T cell leukemia virus type 1 (Takebe, Y. et al. Mol. Cell. Biol. (1988) 8: 466-72).

[0249] In addition to the antibody chain genes and regulatory sequences, the expression vectors may carry additional sequences, such as enhancer element (s), a transcription termination sequence (s), sequence (s) that regulate replication of the vector in host cells (e.g., origins of replication) and selectable marker gene (s). The selectable marker gene facilitates selection of host cells into which the vector has been introduced (see, e.g., U.S. Pat. Nos. 4,399,216, 4,634,665 and 5,179,017, all by Axel et al.). For example, typically the selectable marker gene confers resistance to drugs, such as G418, hygromycin or methotrexate, on a host cell into which the vector has been introduced. Selectable marker genes include the dihydrofolate reductase (DHFR) gene (for use in dhfr-host cells with methotrexate selection/amplification) and the neo gene (for G418 selection).

[0250] For expression of the light and heavy chains, the expression vector (s) encoding the heavy and light chains is transfected into a host cell by any suitable techniques. The various forms of the term "transfection" are intended to encompass a wide variety of techniques commonly used for the introduction of exogenous DNA into a prokaryotic or eukaryotic host cell, e.g., electroporation, calcium-phosphate precipitation, DEAE-dextran transfection and the like. Although it is possible to express the antibodies described herein in either prokaryotic or eukaryotic host cells, expression of antibodies in eukaryotic cells, e.g., mammalian host cells, is most typical.

[0251] The present disclosure further provides a host cell containing nucleic acid molecule (s) or vector (s) provided by the present disclosure. The host cell can be virtually any cell for which expression vectors are available. It may be, for example, a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, and may be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant nucleic acid construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, electroporation or phage infection.

[0252] Suitable prokaryotic hosts for transformation include *E. coli, Bacillus subtilis, Salmonella typhimurium* and various species within the genera *Pseudomonas, Streptomyces*, and *Staphylococcus*.

[0253] Mammalian host cells for expressing a binding molecule of the disclosure include, for example, Chinese Hamster Ovary (CHO) cells (including dhfr-CHO cells, described in Urlaub and Chasin, Proc. Natl. Acad. Sci. USA (1980) 77: 4216-20, used with a DHFR selectable marker, e.g., as described in Kaufman and Sharp, J. Mol. Biol. (1982) 159: 601-21, NSO myeloma cells, COS cells and Sp2 cells. In particular, for use with NSO myeloma or CHO cells, another expression system is the GS (glutamine synthetase) gene expression system disclosed in WO 87/04462, WO 89/01036, and EP338841.

[0254] An antibody (or antigen binding fragment thereof) of the present disclosure may be produced by any means known in the art. Exemplary techniques for antibody production are in U.S. Pat. No. 4,816,567; however, these exemplary techniques are provided for illustrative purposes only and are not intended to be limiting. When nucleic acid (s) or expression vector (s) encoding an antibody described herein are introduced into a host cell, the antibody is produced by culturing the host cell for a period of time sufficient to allow for expression of the antibody in the host cells or secretion of the antibody into the culture medium in which the host cells are grown. Thus, in some embodiments, provided is a method of producing an antibody described herein, which method comprises culturing a host cell comprising one or more nucleic acid (s) or vector (s) that encode the antibody (e.g., as provided above) under conditions suitable for expression of the antibody. In some embodiments, the method further comprises recovering the antibody from the host cell (or host cell culture medium). The antibody can be recovered from the culture medium using any suitable protein purification methods.

VIII. Pharmaceutical Compositions

[0255] In some embodiments, the present disclosure provides a composition comprising one or more of the antibodies described herein. In some embodiments, the composition is a pharmaceutical composition comprising an antibody described herein and a pharmaceutically acceptable carrier. The compositions can be prepared by conventional methods known in the art.

[0256] The term "pharmaceutically acceptable carrier" refers to any inactive substance that is suitable for use in a formulation for the delivery of a polypeptide (e.g., an antibody described herein). A carrier may be an anti-adherent, binder, coating, disintegrant, filler or diluent, preservative (such as antioxidant, antibacterial, or antifungal agent), sweetener, absorption delaying agent, wetting agent, emulsifying agent, buffer, and the like. Examples of suitable pharmaceutically acceptable carriers include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like) dextrose, vegetable oils (such as olive oil), saline, buffer, buffered saline, and isotonic agents such as sugars, polyalcohols, sorbitol, and sodium chloride.

[0257] The compositions may be in any suitable forms, such as liquid, semi-solid, and solid dosage forms. Examples of liquid dosage forms include solution (e.g., injectable and infusible solutions), microemulsion, liposome, dispersion, or suspension. Examples of solid dosage forms include tablet, pill, capsule, microcapsule, and powder. A particular form of the composition suitable for delivering an antibody described herein is a sterile liquid, such as a solution, suspension, or dispersion, for injection or infusion. Sterile solutions can be prepared by incorporating the antibody in the required amount in an appropriate carrier, followed by sterilization microfiltration. Dispersions may be prepared by incorporating the antibody into a sterile vehicle that contains a basic dispersion medium and other carriers. In the case of sterile powders for the preparation of sterile liquid, methods of preparation include vacuum drying and freeze-drying (lyophilization) to yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof. The various dosage forms of the compositions can be prepared by conventional techniques known in the art.

[0258] The relative amount of an antibody included in the composition will vary depending upon a number of factors, such as the specific polypeptide and carriers used, dosage form, and desired release and pharmacodynamic characteristics. The amount of an antibody in a single dosage form will generally be that amount which produces a therapeutic effect, but may also be a lesser amount. Generally, this amount will range from about 0.01 percent to about 99

percent, from about 0.1 percent to about 70 percent, or from about 1 percent to about 30 percent relative to the total weight of the dosage form.

[0259] In addition to the antibody described herein, one or more additional therapeutic agents may be included in the composition. In some embodiments, the at least one additional therapeutic agent is selected from the group consisting of viral gene therapy, immune checkpoint inhibitors, target therapies, radiation therapies, and chemotherapies. In some embodiments, the at least one additional therapeutic agent is selected from the group consisting of pomalyst, revlimid, lenalidomide, pomalidomide, thalidomide, a DNA-alkylating platinum-containing derivative, cisplatin, 5-fluorouracil, cyclophosphamide, an anti-CTLA4 antibody, an anti-PD-1 antibody, an anti-PD-L1 antibody, an anti-CD20 antibody, an anti-CD40 antibody, an anti-DR5 antibody, an anti-CD1d antibody, an anti-TIM3 antibody, an anti-SLAMF7 antibody, an anti-KIR receptor antibody, an anti-OX40 antibody, an anti-HER2 antibody, an anti-ErbB-2 antibody, an anti-EGFR antibody, cetuximab, rituximab, trastuzumab, pembrolizumab, radiotherapy, single dose radiation, fractionated radiation, focal radiation, whole organ radiation, IL-12, IFNα, GM-CSF, a chimeric antigen receptor, adoptively transferred T cells, an anti-cancer vaccine, and an oncolytic virus. The suitable amount of the additional therapeutic agent to be included in the composition can be readily selected by a person skilled in the art, and will vary depending on a number of factors, such as the particular agent and carriers used, dosage form, and desired release and pharmacodynamic characteristics. The amount of the additional therapeutic agent included in a single dosage form will generally be that amount of the agent which produces a therapeutic effect, but may be a lesser amount as well.

[0260] The antibodies described herein may be further modified. In some embodiments, the antibodies are linked to an additional molecular entity. Examples of additional molecular entities include pharmaceutical agents, peptides or proteins, detection agent or labels, and antibodies.

[0261] In some embodiments, an antibody described herein is linked to a pharmaceutical agent. Examples of pharmaceutical agents include cytotoxic agents or other cancer therapeutic agents, and radioactive isotopes. Specific examples of cytotoxic agents include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents also include, for example, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine). Examples of radioactive isotopes that can be conjugated to antibodies for use diagnostically or therapeutically include, but are not limited to, iodine^{31}, indium^{111}, yttrium^{90} and lutetium^{177}. Methods for linking a polypeptide to a pharmaceutical agent are known in the art, such as using various linker technologies. Examples of linker types include hydrazones, thioethers, esters, disulfides and peptide-containing linkers. For further discussion of linkers and methods for linking therapeutic agents to antibodies see e.g., Saito et al., Adv. Drug Deliv. Rev. (2003) 55: 199-15; Trail, et al., Cancer Immunol. Immunother. (2003) 52: 328-37; Payne, Cancer Cell (2003) 3:207-12; Allen, Nat. Rev. Cancer (2002) 2: 750-63; Pastan and Kreitman, Curr. Opin. Investig. Drugs (2002) 3: 1089-91; Senter and Springer Adv. Drug Deliv. Rev. (2001) 53: 247-64.

[0262] Any of the antibodies and/or compositions (e.g., pharmaceutical compositions) described herein may be used in the preparation of a medicament (e.g., a medicament for use in treating or delaying progression of cancer in a subject in need thereof).

IX. Methods of Treatment

[0263] The antibodies and pharmaceutical compositions described herein are useful for therapeutic purposes, such as treating cancer or enhancing the efficacy of other cancer therap(ies). Thus, in some embodiments, the present disclosure provides methods of using the antibodies or pharmaceutical compositions described herein. In some embodiments, the present disclosure provides a method of treating cancer in a subject (e.g., a human subject), comprising administering to the subject an effective amount of an antibody described herein. In some embodiments, the cancer is breast cancer, liver cancer, or colorectal cancer, gastric cancer, ovarian cancer, lung cancer, pancreatic cancer, or kidney cancer.

[0264] In practicing the therapeutic methods, the masked anti-CD28 antibodies described herein may be administered alone, i.e., as monotherapy, or administered in combination with one or more additional therapeutic agents or therapies. Thus, in another aspect, the present disclosure provides a combination therapy, which comprises a binding molecule in combination with one or more additional therapies or therapeutic agents for separate, sequential or simultaneous administration. In some embodiments, the term "additional therapy" refers to a therapy which does not employ an antibody described herein as a therapeutic agent. In some embodiments, the term "additional therapeutic agent" refers to any therapeutic agent other than an antibody described herein. In some embodiments, the present disclosure provides a method of treating cancer in a subject (e.g., a human subject) that comprises administering to the subject an effective amount of an antibody described herein (e.g., an anti-CD28 antibody or multi-specific antibody that targets CD28 and one or more other targets) and an effective amount of an anti-PD-1 antibody. In some embodiments, the present disclosure provides a method of treating cancer in a subject (e.g., a human subject) that comprises administering to the subject an effective amount of an antibody described herein (e.g., an anti-CD28 antibody or multi-specific antibody that targets CD28 and one or more other targets) and an effective amount of an anti-CTLA4 antibody. In some embodiments, the anti-CTLA4 antibody is a masked anti-CTLA4 antibody.

X. Kits and Articles of Manufacture

[0265] In some embodiments, provided is a kit comprising one or more antibodies described herein (e.g., an anti-CD28

antibody or multi-specific antibody that targets CD28 and one or more other targets). In some embodiments, the kit further comprises a package insert comprising instructions for use of the antibodies described herein. In some embodiments, the article of manufacture or kit comprises a container containing one or more of the masked antibodies or compositions described herein. In certain embodiments, the article of manufacture or kit comprises a container containing nucleic acid (s) encoding one (or more) of the masked antibodies described herein. In some embodiments, the kit includes a cell of cell line that produces an antibody described herein. In some embodiments, the kit includes one or more positive controls, for CD28 (e.g., human CD28, cynomolgus CD28, mouse CD28, rat CD28 or fragments of any of the preceding) or $CD28^+$ cells. In some embodiments, the kit includes negative controls, for example a surface or solution that is substantially free of CD28, or a cell that does not express CD28.

[0266] In certain embodiments, the article of manufacture or kit comprises a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, IV solution bags, test tubes, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds an antibody described herein (or a composition comprising such an antibody), which is by itself or combined with another composition effective for treating, delaying progression of, and/or preventing cancer in a subject (e.g., a human subject). The container may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). In some embodiments, the label or package insert indicates that the composition is used for treating breast cancer, liver cancer, or colorectal cancer in a subject (e.g., a human subject).

[0267] Moreover, the article of manufacture or kit may comprise (a) a first container with a composition contained therein, wherein the composition comprises an antibody described herein (or immunologically active fragment thereof); and (b) a second container with a composition contained therein, wherein the composition comprises a further cytotoxic or otherwise therapeutic agent. In some embodiments, the second container contains a composition comprising an anti-PD-1 antibody, and the article of manufacture comprises a the label or package insert indicates that the antibody and the anti-PD-L1 are for use in the treatment of colon cancer in a subject (e.g., human subject) in need thereof, e.g., according to a method provided herein. In some embodiments, the second container contains a composition comprising an anti-CTLA4 antibody (e.g., a masked anti-CTLA4 antibody), and the article of manufacture comprises a label or package insert indicates that the antibody described herein and the anti-CTLA4 antibody (e.g., a masked anti-CTLA4 antibody) are for use in the treatment of colon cancer in a subject (e.g., human subject) in need thereof, e.g., according to a method provided herein.

[0268] Additionally, the article of manufacture may further comprise an additional container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

[0269] The foregoing written description is considered to be sufficient to enable one skilled in the art to practice the present disclosure. The following Examples are offered for illustrative purposes only, and are not intended to limit the scope of the present disclosure in any way. Indeed, various modifications of the present disclosure in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

[0270] Unless otherwise defined herein, scientific and technical terms used in connection with the present disclosure shall have the meanings that are commonly understood by those of ordinary skill in the art. Exemplary methods and materials are described below, although methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present disclosure. In case of conflict, the present specification, including definitions, will control. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. Throughout this specification and embodiments, the words "have" and "comprise," or variations such as "has," "having," "comprises," or "comprising," will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers. All references cited herein, including patent applications, patent and non-patent publications, and UniProtKB/Swiss-Prot Accession numbers, are herein incorporated by reference in their entirety, as if each individual reference were specifically and individually indicated to be incorporated by reference in its entirety. Although a number of documents are cited herein, this citation does not constitute an admission that any of these documents forms part of the common general knowledge in the art. As used herein, the term "approximately" or "about" as applied to one or more values of interest refers to a value that is similar to a stated reference value. In certain embodiments, the term refers to a range of values that fall within 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or less in either direction (greater than or less than) of the stated reference value unless otherwise stated or otherwise evident from the context.

[0271] According to the present disclosure, back-references in the dependent claims are meant as short-hand writing for a direct and unambiguous disclosure of each and every combination of claims that is indicated by the back-reference. Any compound disclosed herein can be used in any of the treatment method here, wherein the individual to be treated is as defined anywhere herein. Further, headers herein are created for ease of organization and are not intended to limit the scope of the claimed invention in any manner.

[0272] In order that this invention may be better understood, the following examples are set forth. These examples are for purposes of illustration only and are not to be construed as limiting the scope of the invention in any manner.

EXAMPLES

Example 1: Generation of Primary Fabs that Specifically Bind to Human CD28

[0273] Proprietary phagemid libraries were employed to pan against human CD28 antigens. A total of three or four rounds of panning were conducted. After the final round of

panning, the culture supernatants of individual clones were tested by ELISA to identify those that specifically recognized human CD28 (i.e., primary hits). Clones were defined as positive when ELISA signals were at least twice that of background. The positive clones were picked to confirm sequence and the Fabs corresponding to the unique hits were expressed in in *E. coli* and affinity purified. Their affinities against human CD28 were measured by the Octet® RED96 Systems (ForteBio). Briefly, Dip and Read Anti-Human IgG Fc Capture (AHC) biosensors (ForteBio) were used to capture human or mouse CD28-Fc fusion proteins, and dipped into wells containing purified Fabs that were diluted 5 to 10-fold with ForteBio kinetic buffer (10 mM HEPES, 150 mM NaCl, 3 mM EDTA, 0.005% v/v Surfactant P20, pH 7.4). The acquired data were processed with Octet Data Analysis Software Version 7.1 (ForteBio), and kinetic data were fitted to a 1:1 Langmuir binding model.

[0274] The primary Fabs hits were further characterized for human and mouse CD28 species cross-reactivity by ELISA and, from these primary hits, a panel of 46 unique sequence Fabs were then converted into IgG_4 isotype mAbs with the core hinge mutation S241P (Kabat numbering scheme) for detailed biophysical and functional characterization (Table 5).

Example 2: IgG_4 Conversion and Expression

[0275] The heavy chains and light chains of the engineered human anti-CD28 IgG_4 isotype mAbs listed in Table 5 were cloned into the mammalian expression vector pcDNA3.3 (ThermoFisher Scientific). Pairs of plasmids bearing one heavy and one light chain were transiently transfected into HEK293 cells following the manufacturer's instructions. After incubation, the supernatants were harvested, cleared by centrifugation and filtration, and the IgG_4 isotype mAbs were captured by MabSelect™ SuRe™ protein A affinity chromatography (GE Healthcare).

[0276] The mAbs were eluted and neutralized, and the eluate buffer exchanged into restore buffer (20 mM histidine, pH 5.5). Protein concentrations were determined by UV spectrophotometry, and IgG purity was analyzed under denaturing, reducing, and non-reducing conditions by SDS-PAGE or SEC-HPLC.

TABLE 5

List of Human Anti-CD28 IgG_4 Monoclonal Antibodies

No.	IgG ID	Isotype/mutation
1	TY24853	$hIgG_4$/S241P
2	TY24854	$hIgG_4$/S241P
3	TY24855	$hIgG_4$/S241P
4	TY24856	$hIgG_4$/S241P
5	TY24857	$hIgG_4$/S241P
6	TY24858	$hIgG_4$/S241P
7	TY24859	$hIgG_4$/S241P
8	TY24860	$hIgG_4$/S241P
9	TY24861	$hIgG_4$/S241P
10	TY24862	$hIgG_4$/S241P
11	TY24863	$hIgG_4$/S241P
12	TY24864	$hIgG_4$/S241P
13	TY24865	$hIgG_4$/S241P
14	TY24866	$hIgG_4$/S241P
15	TY24867	$hIgG_4$/S241P
16	TY24868	$hIgG_4$/S241P
17	TY24869	$hIgG_4$/S241P
18	TY24870	$hIgG_4$/S241P
19	TY24871	$hIgG_4$/S241P

TABLE 5-continued

List of Human Anti-CD28 IgG_4 Monoclonal Antibodies

No.	IgG ID	Isotype/mutation
20	TY24872	$hIgG_4$/S241P
21	TY24873	$hIgG_4$/S241P
22	TY24874	$hIgG_4$/S241P
23	TY24875	$hIgG_4$/S241P
24	TY24876	$hIgG_4$/S241P
25	TY24877	$hIgG_4$/S241P
26	TY24878	$hIgG_4$/S241P
27	TY24879	$hIgG_4$/S241P
28	TY24880	$hIgG_4$/S241P
29	TY24881	$hIgG_4$/S241P
30	TY24882	$hIgG_4$/S241P
31	TY24883	$hIgG_4$/S241P
32	TY24884	$hIgG_4$/S241P
33	TY24885	$hIgG_4$/S241P
34	TY24886	$hIgG_4$/S241P
35	TY24887	$hIgG_4$/S241P
36	TY24888	$hIgG_4$/S241P
37	TY24889	$hIgG_4$/S241P
38	TY24890	$hIgG_4$/S241P
39	TY24891	$hIgG_4$/S241P
40	TY24892	$hIgG_4$/S241P
41	TY24772	$hIgG_4$/S241P
42	TY24773	$hIgG_4$/S241P
43	TY24774	$hIgG_4$/S241P
44	TY24775	$hIgG_4$/S241P
45	TY24776	$hIgG_4$/S241P
46	TY24777	$hIgG_4$/S241P

Example 3: Binding Characterization of Anti-CD28 Antibodies

[0277] The binding affinities of the panel of anti-CD28 mAbs to human, cynomolgus monkey, and mouse CD28 and human CTLA4 were measured by the Octet® RED96 Systems (ForteBio), ELISA, and CytoFlex flow cytometry (Beckman). The anti-CD28 antibody TAC2386 (also known as TGN1412 as described in Patent WO2006/050949A2) and TAC2387 (as described in Patent WO2019/246514A2) were used as a benchmark control.

Binding Affinity to Human CD28 and CTLA4 by the Octet RED96 Systems

[0278] The Octet® RED96 Systems (ForteBio) was used to assess the binding kinetics of the panel of anti-CD28 mAbs to human CD28 and CTLA4. Briefly, the mAbs were diluted to 15 μg/mL in kinetic buffer (PBS supplemented with 0.02% Tween 20 and 0.1% BSA), and captured by Dip and Read AHC biosensors (ForteBio) in parallel. The sensors were then allowed to associate with His-tagged human CD28 and CTLA4 proteins (100 nM) for 300 seconds, and to dissociate in kinetic buffer for another 300 seconds. The association and dissociation curves were fitted to a 1:1 Langmuir binding model using the Octet® Data Analysis Software Version 7.1 (ForteBio).

[0279] As shown in Table 6, the panel of anti-CD28 test and benchmark mAbs exhibited high binding affinity (<10 nM) to human CD28, as measured by the Octet® RED96 Systems. In addition, the test mAbs TY24773, TY24853, TY24854, TY24860, TY24865, and TY24871 and the benchmark control mAbs exhibited no detectable affinity to human CTLA4.

TABLE 6

Binding Affinity to Human CD28 and CTLA4

	Human CD28			Human CTLA4		
mAb ID	KD (nM)	Kon (1/Ms)	Koff (1/s)	KD (nM)	Kon (1/Ms)	Koff (1/s)
TAC2386	<0.001	9.625E+04	<1.0E−07		ND	
TAC2387	4.873	7.071E+04	3.446E−04			
TY24773	8.285	3.848E+04	3.188E−04			
TY24853	3.955	4.159E+04	1.645E−04			
TY24854	5.434	6.488E+04	3.526E−04			
TY24855	7.927	7.918E+04	6.277E−04	4.022	7.596E+05	3.055E−03
TY24856	7.805	6.887E+04	5.376E−04	5.127	3.036E+05	1.557E−03
TY24857	8.639	7.294E+04	6.301E−04	5.442	6.515E+05	3.546E−03
TY24858	9.882	7.101E+04	7.017E−04	7.904	3.055E+05	2.415E−03
TY24859	2.684	7.081E+04	1.900E−04	6.631	4.687E+05	3.108E−03
TY24860	6.664	6.323E+04	4.213E−04		ND	
TY24864	4.413	9.418E+04	4.157E−04	5.501	5.168E+05	2.843E−03
TY24865	<0.001	5.958E+04	<1.0E−07		ND	
TY24866	<0.001	5.804E+04	<1.0E−07	7.645	5.238E+05	4.004E−03
TY24869	2.733	4.676E+04	1.278E−04	1.198	3.793B+05	4.544E−04
TY24871	4.993	7.011E+04	3.501E−04		ND	
TY24876	<0.001	3.251E+04	<1.0E−07	4.280	1.366E+05	5.848E−04
TY24877	7.191	2.686E+04	1.931E−04	13.20	2.353E+05	3.105E−03
TY24878	4.214	9.747E+04	4.108E−04	0.9686	4.233E+05	4.100E−04
TY24879	<0.001	5.939E+04	<1.0E−07	7.165	4.369E+05	3.130E−03
TY24881	5.246	1.262E+05	6.618E−04	2.353	1.114E+06	2,622E−03
TY24884	2.420	6.836E+04	1.655E−04	6.359	6.409E+05	4.076E−03
TY24890	4.440	9.846E+04	4.371E−04	3.133	1.099E+06	3.444E−03

ND: Not detected

Binding Affinity to Human and Mouse CD28 Using ELISA

[0280] Recombinant human and mouse CD28-Fc were diluted to 2 g/mL in PBS and coated on Nunc MaxiSorp™ high protein-binding capacity 96 well ELISA plates (ThermoFisher Scientific) at 4° C. overnight. Plates were blocked with PBS supplemented with 3% non-fat milk at 37° C. for 1 hour. After washing, 50 PL of 3-fold serial dilutions of a panel of anti-CD28 test mAbs were added to each well. After incubation at 37° C. for 1 hour, plates were washed four times, and 100 μL of a horseradish peroxidase (HRP)-conjugated anti-human IgG (Fab specific) (1:6000 dilution) secondary antibody was added to each well. Plates were incubated at 37° C. for 1 hour, washed four times, and then 50 μL of a TMB substrate (3, 3', 5, 5'-tetramethylbenzidine) solution was added to each well, and the plate was incubated at room temperature. Absorbance at 450 nm was measured after the reactions were stopped by adding 50 μL of a sulfuric acid stop solution to each well. The EC_{50} was evaluated by fitting the ELISA data using the asymmetrical sigmoidal (4-parameter logistic equation) model of GraphPad Prism version 7 for Windows, GraphPad Software, La Jolla California USA, www.graphpad.com.

[0281] As shown in Table 7 and FIG. **1**, the panel of anti-CD28 test mAbs exhibited similar affinities to human CD28 as the two benchmark controls. Moreover, the test mAbs except TY24890 bound to mouse CD28 while the two benchmark controls did not.

TABLE 7

Binding Affinity to Recombinant CD28 Measured by ELISA

	EC_{50} (nM)	
mAb ID	Human CD28	Mouse CD28
TAC2386	0.78	ND
TAC2387	>1.65	ND
TY24859	1.34	>44.44
TY24865	0.58	>4.94
TY24866	0.57	>1.65
TY24869	0.87	>14.81
TY24876	1.02	3.93
TY24878	1.06	>14.81
TY24879	0.9	>1.65
TY24884	1.02	>44.44
TY24890	1.55	ND

ND: Not detected

Binding Activities of Anti-CD28 Antibodies on Jurkat Cells

[0282] Jurkat (clone E6-1) cells were seeded in 96-well plates at 1.0×10^5 (50 μL/well) and incubated with serially diluted benchmark positive controls, an isotype negative control antibody, and a panel of anti-CD28 test mAbs (100, 20, 4, 0.8, 0.16, and 0.032 nM) for 30 minutes at 4° C. in 2% fetal bovine serum/Dulbecco's PBS (FBS/DPBS). Next, the cells were washed twice with DPBS and further incubated with a APC-anti-human IgG Fc secondary antibody (1 μg/mL, 100 μL/well, Biolegend) for 30 minutes at 4° C. Finally, the cells were washed twice with DPBS and suspended in FACS buffer for flow cytometry analysis. For analysis, the Mean Fluorescence Intensity (MFI) values versus concentrations were plotted using FlowJo 10 software (FlowJo LLC) and the data were further fitted with four-parameter non-linear regression to obtain EC_{50} values

by GraphPad Prism version 7 for Windows, GraphPad Software, La Jolla California USA, www.graphpad.com.

[0283] As shown in Table 8, except for TY24775 and TY24867, all other anti-CD28 test mAbs exhibited high binding activity (EC_{50} values ranging from 0.38 to 10.42 nM) to CD28 molecules on Jurkat cells. In addition, the measured binding activities were comparable to the two benchmark controls.

TABLE 8

Binding Affinity to CD28 expressed on Jurkat cells Measured by Flow Cytometry

Ab ID	EC_{50} (nM)	Ab ID	EC_{50} (nM)	Ab ID	EC_{50} (nM)
TAC2386	1.10	TY24863	2.60	TY24881	0.38
TAC2387	0.81	TY24864	0.54	TY24882	2.24
TY24772	0.74	TY24865	0.46	TY24883	5.92
TY24773	0.71	TY24866	0.70	TY24884	1.09
TY24774	3.35	TY24867	ND	TY24885	5.77
TY24775	ND	TY24868	2.08	TY24886	10.42
TY24776	1.83	TY24869	1.07	TY24887	3.17
TY24777	1.50	TY24870	3.95	TY24888	0.58
TY24853	0.43	TY24871	0.89	TY24889	2.32
TY24854	0.60	TY24872	1.07	TY24890	0.59
TY24855	0.61	TY24873	2.08	TY24891	0.62
TY24856	0.76	TY24874	1.65	TY24892	1.30
TY24857	0.75	TY24875	1.72	Isotype control	ND
TY24858	0.70	TY24876	0.38		
TY24859	0.97	TY24877	0.79		
TY24860	0.78	TY24878	0.39		
TY24861	2.25	TY24879	1.17		
TY24862	2.82	TY24880	1.62		

ND: Not detected

In Vitro Binding of Anti-CD28 Antibodies to Human T Cells by Flow Cytometry

[0284] Human $CD3^+$ T cells were isolated from cryopreserved peripheral blood mononuclear cells (PBMCs) using the EasySep™ Human Naïve Pan T Cell Isolation Kit (STEMCELL Technologies). The isolated human T cells were added in 96-well plate at 1.0×10^5 cells/well and incubated with 100 nM of benchmark controls, an isotype negative control antibody, and a panel of anti-CD28 test mAbs for 30 minutes on ice in FACS buffer. Next, the cells were washed three times with PBS and further incubated with PE-labeled secondary antibody for 30 minutes on ice. Finally, the cells were washed three times with PBS and resuspended in FACS buffer for flow cytometry analysis. For analysis, the MFI values were calculated using FlowJo 10 software (FlowJo LLC) and the geometric mean MFI values versus mAb were plotted using GraphPad Prism version 7 for Windows, GraphPad Software, La Jolla California USA, www.graphpad.com.

[0285] As shown in FIG. **2**, compared with the benchmark controls TAC2386 and TAC2387, all of the test mAbs except TY24772 exhibited comparable MFI values. TY24772 binding was approximately twice that of the benchmark controls.

Example 4: Ligand Competition Using Elisa

[0286] Antibodies were tested for their ability to block the binding of CD28 or CTLA4 to its natural ligand CD80 by ELISA.

[0287] As shown in FIG. **3** and Table 9, the benchmark controls TAC2386 and TAC2387 and all of the tested anti-CD28 test mAbs blocked the binding of CD28 to CD80, while none blocked the binding of CTLA4 to CD80, compared with an anti-CTLA4 antibody TY21580 included as a control.

TABLE 9

IC_{50} of Anti-CD28 or Anti-CTLA4 Antibodies for Human CD28-CD80 and CTLA4-CD80 Pairs

	IC_{50} (nM)	
Sample ID	CD28/CD80	CTLA4/CD80
TAC2386	0.48	—
TAC2387	0.12	—
TY24859	0.42	—
TY24865	0.68	—
TY24866	0.27	—
TY24890	0.21	—
TY24869	0.55	ND
TY24876	0.54	ND
TY24878	0.35	ND
TY24879	0.42	ND
TY24884	0.28	ND
TY21580	ND	37.24

Example 5: Assessment of Superagonism in Dry-Coated Human T Cell Proliferation Assays

[0288] The levels of lymphocyte proliferation induced by the benchmark controls TAC2386 and TAC2387, an isotype negative control antibody, and a panel of anti-CD28 test mAbs were measured by the CellTiter-Glo® Luminescent Cell Viability Assay (Promega). In this assay, 100 nM of test mAbs at 50 μL per well were added to 96-well microplate in triplicate and air-dried directly onto the walls of the wells. Next, the microplate were washed twice with PBS. Cryopreserved PBMCs were restored and the cell densities were adjusted to 5.0×10^5 cells/mL with 10% FBS/RPMI1640 and 1.0×10^5 PBMCs (200 μL per well) were added to the pre-coated microplates. The cells were incubated at 37° C., 5% CO_2 for 72 hours and then the lymphocyte proliferation was assessed using the CellTiter-Glo® assay.

[0289] As shown in FIG. **4**A, the level of lymphocyte proliferation induced by immobilized benchmark control TAC2386 (aknown CD28 superagonist) was significantly higher than that of all the test mAbs. Compared with TAC2386, the benchmark control TAC2387 and the anti-CD28 test mAbs including TAC2387, TY24865, TY24866, TY24876, TY24878, TY24879 and TY24884 exhibited weak super agonistic activity in vitro.

Example 6: Effects of Anti-CD28 Antibodies on Human T Cell Activation in Vitro T Cell Activation Co-Stimulation Assay: IFN-γ Release

[0290] The biological activity of the anti-CD28 mAbs, as agonistic T cell co-stimulatory agents in activating human T cells in vitro was measured by IFN-γ cytokine secretion using ELISA. Ultra-LEAF™ Purified anti-human CD28 Antibody (Biolegend) was included as a positive control.

[0291] Human $CD3^+$ T cells were isolated from cryopreserved PBMCs using the EasySep™ Human Naïve Pan T Cell Isolation Kit (STEMCELL Technologies). The isolated cells were cultured in 96-well tissue culture plates (1.0×10^5 per well) pre-coated with a suboptimal concentration (10 nM, 50 μL per well) of anti-human CD3 antibody (OKT3),

in the presence of serially diluted benchmark controls, an isotype negative control antibody, a commercial anti-human CD28 positive control antibody, and a panel of anti-CD28 test mAbs (0.1, 1, 10, and 100 nM). The cells were incubated at 37° C., 5% CO_2 for 120 hours and then cell supernatants were collected for IFN-γ cytokine analysis by ELISA, with T cell proliferation measured by CellTiter-Glo®.

[0292] As shown in FIGS. **4**B and **4**C, in comparison with the isotype control antibody, the anti-CD28 mAbs showed concentration-dependent biological activity including T cell proliferation and IFN-γ cytokine secretion. In general, the effects of anti-CD28 mAbs on human T cell activation were comparable to or more potent than the two benchmark control antibodies.

T Cell Activation Co-Stimulation Assay: IL-2 Release

[0293] The biological activity of the anti-CD28 mAbs as agonistic T cell co-stimulatory agents in activating human T cells in vitro was measured by T cell proliferation with the CellTiter-Glo® Luminescent Cell Viability Assay (Promega) and IL-2 cytokine secretion by ELISA. Ultra-LEAF™ Purified anti-human CD28 Antibody (Biolegend) was included as a positive control.

[0294] Human T cells were isolated from fresh PBMCs from Asian donor using the EasySep™ Human Naïve Pan T Cell Isolation Kit (STEMCELL Technologies). The cells were cultured in 96-well tissue culture plates (1.0×10^5 cells/well) pre-coated with a suboptimal concentration (5 nM) of anti-human CD3 antibody (OKT3), in the presence of serially diluted benchmark control TAC2387, an isotype negative control antibody, a commercial anti-human CD28 positive control antibody, and a panel of anti-CD28 test mAbs. The cells were incubated at 37° C., 5% CO, for 72 hours, and then the cell supernatants were collected for IL-2 cytokine analysis by ELISA and the level of T cell proliferation was measured using the CellTiter-Glo®ωassay.

[0295] As shown in FIGS. **5**A-B, in comparison with the isotype control antibody, the anti-CD28 antibodies showed concentration-dependent biological activity including T cell proliferation and IL-2 cytokine secretion. The effects of TY24859, TY24865, TY24866, and TY24890 on human T cell activation were comparable to the benchmark control TAC2387. The negative control groups without pre-coating anti-CD3 showed no detectable T cell proliferation and IL-2 cytokine secretion.

Example 7: Anti-HER2×CD28 Bispecific Antibody Construction and Functional Characterization

Generation of Anti-HER2×CD28 Bispecific Antibodies

[0296] A heterodimeric bispecific scaffold was engineered using the TYM13 Fc mutant (D or E356K: E357K: S364K: S400C L351'D: K370'D: N390'C: K439'D; according to Kabat numbering scheme for an IgG1 C_H3 domain). A light chain-heavy chain half antibody and a single-chain fragment variable (scFv)-Fc chain were combined to form a bispecific antibody (BsAb), with TYM13 mutations in the hetero-Fc domain.

[0297] Plasmids encoding the heavy chain, light chain, and scFv-Fc chain of BsAbs were transiently transfected into mammalian cells. Bispecific antibody-containing cell culture supernatants were harvested 7 days after transfection by centrifugation at 14000 g for 30 minutes and were filtered through a sterile filter (0.22 μm). Antibodies were purified by protein A affinity chromatography using MabSelect™ SuRe™ prepacked columns (GE Healthcare) and were subsequently buffer exchanged in 20 mM histidine (pH 5.5) buffer.

[0298] TY24865 (high affinity CD28) and TY24865 mutant (low affinity CD28) were selected for constructing CD28 BsAbs using this scaffold. The constructs are described in Table 10.

TABLE 10

Design of Anti-HER2xCD28 Bispecific Antibody

BsAb ID	Fab Arm (Anti-HER2)	scFv Arm (Anti-CD28)
TY27566	Perjeta ®	TY24865
TY27881	Perjeta ®	TY24865 mutant
TY27807	Herceptin ®	TY24865

Binding to SK-OV-3 Cells by FACS

[0299] The concentration-dependent binding activities of anti-HER2×CD28 BsAb (TY27566), anti-HER2×CD3 BsAb (TY25238, also described in PCT/CN2021/076626, which is incorporated by reference herein in its entirety) and anti-HER2 mAbs for Perjeta® (TAC2319) or Herceptin ((TAC2320) were measured using flow cytometry. Perjeta® (TAC2319) binds to a different epitope of the HER2 dimerization domain than Herceptin® (TAC2320).

[0300] SK-OV-3 cells were cultured and added to 96-well plates at 8.0×10^4 cells/well and incubated with serially diluted test BsAbs for 60 minutes at 4° C. in 2% FBS/RPMI1640 buffer. Next, the cells were washed twice with DPBS and further incubated with a secondary APC-anti-human IgG Fc antibody (1:400 dilution) for 30 minutes at 4° C. Finally, the cells were washed twice with DPBS and resuspended in FACS buffer for flow cytometry analysis. For analysis, the MFI values versus concentrations were plotted using FlowJo 10 software (FlowJo LLC) and the data were further fitted with four-parameter non-linear regression to obtain EC_{50} values by GraphPad Prism version 7 for Windows, GraphPad Software, La Jolla California USA, www.graphpad.com. An isotype antibody was included as a negative control.

[0301] As shown in FIG. **6**, anti-HER2×CD28 or anti-HER2×CD3 BsAbs showed very similar binding affinity to SK-OV-3 cells, compared with anti-HER2 mAbs for Perjeta® (TAC2319) or Herceptin® (TAC2320).

Stimulatory Activities on T Cell Receptor and CD28 Receptor Signaling

[0302] The stimulatory activities on T Cell Receptor (TCR) and CD28 receptor signaling by the anti-HER2×CD3 BsAb, the anti-HER2×CD28 BsAb, or their combination were evaluated. In this assay, the simultaneous TCR and CD28 activation leads to enhanced transcriptional activity of NFkB, which in turn induces the production of the reporter gene. Isotype antibodies were included as negative controls.

[0303] Jurkat-NFkB-Nluc effector (E) reporter cells (5×10^4 cells/well) were co-cultured with SK-OV-3 target (T) cells (1×10^4 cells/well for a E:T=5:1), that endogenously express HER2 antigen. Serially diluted anti-HER2×CD3 BsAb or isotype control antibody with a fixed concentration of anti-HER2×CD28 BsAb (10 nM), or conversely serially diluted anti-HER2×CD28 BsAb or isotype control antibody with a fixed concentration of anti-HER2×CD3 BsAb (0.01 nM), were added to the reporter cell system to evaluate their combined effect in stimulating downstream luciferase activity. The co-cultured cells were incubated at 37° C., 5% CO_2 for 6 hours. Then, 100 μL of Nano-Glo Luciferase Assay System (Promega) reagent was added to the cells, and the cells were lysed for 10 minutes. Supernatants (100 L) were collected for luminescence measurements using a SpectraMax® i3× Multi-Mode Microplate Reader (Molecular Devices).

[0304] As shown in FIG. **7**, anti-HER2×CD28 BsAb (TY27566) in combination with a fixed concentration of anti-HER2×CD3 BsAb (TY25238), and anti-HER2×CD3 BsAb in combination with a fixed concentration of anti-HER2×CD28 BsAb, exhibited synergistic or enhanced stimulatory effects in terms of maximum signal and EC_{50} values.

Cytotoxicity of Anti-HER2×CD28 BsAb and Anti-HER2×CD3 BsAb with the Same or Different TAA Epitopes

[0305] The in vitro cytotoxicity activity of anti-HER2×CD3 BsAb (TY25238) alone or combined with anti-HER2×CD28 BsAbs (TY27566 or TY27807) on the MCF-7 tumor cell line was measured using a lactate dehydrogenase (LDH) release assay. TY25238 binds to a different tumor-associated antigen (TAA) epitope of the HER2 dimerization domain than TY27566 but to the same TAA epitope as TY27807.

[0306] Human T cells were isolated from cryopreserved PBMCs. Cultured MCF-7 tumor target cells (1×10^4 cells/well) were incubated with serially diluted anti-CD3 BsAb FG14127 alone or combined with a fixed concentration (1 μg/mL) of two anti-CD28 BsAbs against different TAA epitopes, TY27566 or TY27807, for 30 minutes at 37° C. Then, isolated human T effector cells (2×10^4 cells/well) were added and incubated at 37° C., 5% CO_2 for 72 hours (E:T=2:1). Cellular cytotoxicity based on LDH release into supernatants by killed MCF-7 target cells was quantified using the CytoTox 96® Non-Radioactive Cytotoxicity Assay (Promega).

[0307] As shown in FIG. **8**, as a single agent, anti-HER2×CD3 BsAb (TY25238) elicited potent concentration-dependent cytotoxicity on MCF-7 target cells. The combination of the anti-HER2×CD28 BsAb (TY27566) and anti-HER2×CD3 BsAb (TY25238) against different TAA epitopes further enhanced the in vitro tumor killing activity in terms of EC_{50}. However, compared to treatment with anti-HER2×CD3 BsAb (TY25238) alone, the addition of anti-HER2×CD28 BsAb (TY27807) with the same TAA epitope significantly decreased the MCF-7 tumor cell lysis in terms of EC_{50} and maximum lysis. An isotype antibody was included as a negative control for the single agent assay.

Example 8: Anti-TROP2×CD28 or Anti-TROP2×CD3 BsAb Construction and Functional Characterization

[0308] An anti-tumor-associated calcium signal transducer 2 (TROP2) ×CD28 or anti-TROP2×CD3 heterodimeric bispecific scaffold was designed using the TYM13 Fc mutant as described in Example 7. The constructs of anti-TROP2×CD28 BsAb are described in Table 11.

[0309] The constructs of anti-TROP2×CD3 BsAb are described in Table 12.

TABLE 11

Design of Anti-TROP2xCD28 Bispecific Antibody

BsAb ID	Fab Arm (Anti-TROP2)	scFv Arm (Anti-CD28)
TY27571	TY25616	TY24865

TABLE 12

Design of Anti-TROP2xCD3 Bispecific Antibody

BsAb ID	Fab Arm (Anti-TROP2)	scFv Arm (Anti-CD3)
TY25839	TY25616	TY24742

CD3- or CD28-Based Bispecific Binding to Tumor Cell Lines with High, Medium, or Low TROP2 Expression

[0310] The concentration-dependent binding activity of anti-TROP2 BsAbs on different tumor cell lines with high, medium, or low TROP2 expression, was measured using flow cytometry. Isotype antibodies were included as negative controls.

[0311] H292, NCI-N87, or HT29 cells were cultured and seeded in 96-well plates at 1.0×10^5 cells/well and incubated with serially diluted test anti-TROP2 BsAbs for 30 minutes at 4° C. in 2% FBS/RPMI1640 buffer. Next, the cells were washed twice with DPBS and further incubated with secondary anti-human IgG antibodies (APC-anti-human IgG Fc antibody, 1:300 dilution for H292 cell; APC-F (ab') 2 fragment goat anti-human IgG (H+L), 1:500 dilution for NCI-N87 and HT29 cells) for 30 minutes at 4° C. Finally, the cells were washed twice with DPBS and resuspended in FACS buffer for flow cytometry analysis. For analysis, the MFI values versus concentrations were plotted using FlowJo 10 software (FlowJo LLC) and the data were further fitted with four-parameter non-linear regression to obtain EC_{50} values by GraphPad Prism version 7 for Windows.

[0312] As shown in FIG. **9** and Table 13, the TROP2 arm binding activities were similar between TY25839 and TY27571 on three different tumor cell lines with high, medium, or low TROP2 expression.

TABLE 13

EC_{50} Values of Anti-TROP2 Bispecific Antibodies on Tumor Cell Lines									
	H292			NCI-N87			HT-29		
BsAb ID	EC_{50} (nM)	Span	AUC	EC_{50} (BM)	Span	AUC	EC_{50} (BM)	Span	AUC
TY25839	0.813	149008	418398	0.901	612873	1715321	0.693	52548	156975
TY27571	0.822	156304	465058	0.911	589022	1644423	0.559	52992	162739

Stimulatory Activities on TCR and CD28 Receptor Signaling

[0313] The stimulatory activities on TCR and CD28 receptor signaling by anti-TROP2×CD3 BsAbs, anti-TROP2×CD28 BsAbs or the combination were evaluated. The simultaneous TCR and CD28 activation leads to enhanced transcriptional activity of NFkB, which in turn induces the production of the reporter gene.

[0314] The Jurkat-NFkB-Nluc effector reporter cells (5×10^4 cells/well) were co-cultured with H292 target cells (E:T=5:1). Serially diluted anti-TROP2×CD3 BsAbs with fixed concentration of anti-TROP2×CD28 BsAb (5 nM), or conversely serially diluted anti-TROP2×CD28 BsAbs with fixed concentration of anti-TROP2×CD3 BsAb (0.01 nM), were added to the reporter cell system to evaluate their combined activity in stimulating downstream luciferase activity. The co-cultured cells were incubated at 37° C., 5% CO_2 for 6 hours. Then, 100 μL of Nano-Glo Luciferase Assay System (Promega) reagent was added to the cells, and the cells were lysed for 10 minutes. Supernatants (100 μL) were collected for luminescence measurements using a SpectraMax i3x Multi-Mode Microplate Reader (Molecular Devices).

[0315] As shown in FIG. **10**, single agent CD28-based BsAbs exhibited very weak reporter gene activity. However, the combination of anti-TROP2×CD3 and anti-TROP2×CD28 BsAbs exhibited synergistic or enhanced stimulatory effects in terms of maximal signals or EC_{50} values.

Example 9: B7H3×CD28 Bispecific Antibody Construction and Functional Characterization

[0316] A B7H3×CD28 BsAb was constructed. The constructs are described in Table 14.

[0317] The constructs of B7H3×CD3 BsAbs are described in Table 15.

TABLE 14

Design of B7H3xCD28 Bispecific Antibody		
BsAb ID	Fab Arm (Anti-B7H3)	scFv Arm (Anti-CD28)
TY27556	TY21601	TY24865

TABLE 15

Design of B7H3xCD3 Bispecific Antibody		
BsAb ID	Fab Arm (Anti-B7H3)	scFv Arm (Anti-CD3)
TY26999	TY21601	Medium affinity CD3

Binding to MDA-MB-231 Cells by FACS

[0318] The concentration-dependent binding activity of anti-B7H3×CD28 BsAb TY27556 and its parental anti-B7H3 mAb TY21601 on MDA-MB-231 cells, was measured using flow cytometry (FIG. **11**). An isotype antibody was included as a negative control.

[0319] MDA-MB-231 cells were cultured and seeded in 96-well plates at 1.0×10^5 cells/well and incubated with serially diluted test BsAbs for 60 minutes at 4° C. in 2% FBS/RPMI1640 buffer. Next, the cells were washed twice with DPBS and further incubated with secondary APC-anti-human IgG Fe antibody (1:400 dilution) for 30 minutes at 4° C. Finally, the cells were washed twice with DPBS and resuspended in FACS buffer for flow cytometry analysis. For analysis, the MFI values versus concentrations were plotted using FlowJo 10 software (FlowJo LLC) and the data were further fitted with four-parameter non-linear regression to obtain EC_{50} values by GraphPad Prism version 7 for Windows.

[0320] As shown in FIG. **12**, the anti-B7H3 mAb TY21601 showed sub-nM (0.4525 nM) binding affinity for MDA-MB-231 target cells and the binding activity of the BsAb TY27556 to target cells was reduced by about 28-fold (12.84 nM).

B7H3×CD28 Bispecific Antibody Enhanced the Ability of PD-1 or PD-L1 Blockade to Induce T Cell Activation in Vitro

[0321] The effect of combining anti-PD-1 blocking mAbs with the B7H3×CD28 bispecific Abs on primary human T cell activation in vitro, was measured with IFN-γ and IL-2 secretion by ELISA. A modified mixed lymphocyte reaction (MLR) to simulate physiological PD-L1 expression and TCR/CD3 stimulation was used here. To generate a one-way MLR assay, human T cells (1×10^5 cells per well) from one healthy donor (D #XC11147W) were incubated with allogenic MDA-MB-231 cells (E:T=5:1) in the presence of different test antibodies (B7H3×CD28 or isotype control) alone or in combinations with anti-PD-1 (pembrolizumab, Keytruda®) or anti-PD-L1 (atezolizumab, Tecentriq®). The cells were then co-cultured at 37° C., 5% CO_2 in the incubator for 120 h. IL-2 (72 h) and IFN-γ (120 h) cytokine secretion into supernatants by activated T cells was quantified with Elisa kit.

[0322] As shown in FIGS. **13A-13B**, in this MLR assay, addition of 100 nM PD-1/PD-L1 mAbs or titrated B7H3×CD28 resulted in no or only slight cytokine release. However, B7H3×CD28 combination with 100 nM PD-1/PD-L1 mAbs markedly increased T cell activation, compared with monotherapy. These results demonstrate that the B7H3×CD28 bispecific can synergistically combine with PD-1/PD-

L1 blockade to promote T cell activation in the presence of tumor cells, that endogenously express PD-L1 and B7H3.

Co-Stimulatory Bispecific Antibodies Enhance in Vitro T Cell Cytotoxicity Against MCF-7 Cells Upon Bidirectional Binding

[0323] In vitro tumor cell killing activity of anti-CD3-based, or anti-CD28-based BsAbs or their combination on MCF-7 tumor cell line was measured using a LDH release cytotoxicity assay.

[0324] Human T cells were isolated from cryopreserved PBMCs. MCF-7 cells (1×10^4 cells/well) were incubated with serially diluted anti-HER2×CD3 BsAb TY25238 or combined with fixed concentrations of the high affinity CD28 arm anti-HER2×CD28 BsAb TY27566, anti-CD28×B7H3 TY27556, or the low affinity CD28 arm anti-HER2×CD28 BsAb TY27881 (1 ug/mL or 10 μg/mL) for 30 minutes at 37° C., and the human T cells (2×10^4 cells/well) were added and incubated at 37° C., 5% CO_2 for 72 hours (E:T=2:1). Cellular cytotoxicity based on LDH release into supernatants by killed MCF-7 target cells was quantified using the CytoTox 96® Non-Radioactive Cytotoxicity Assay (Promega).

[0325] As shown in FIG. **14**, as single agents, CD28-based BsAbs elicited no cytotoxicity on MCF-7 target cells. In contrast, as a single agent, the anti-CD3 BsAb TY25238 showed concentration-dependent effects and the highest cytotoxicity was elicited with BsAb directed against HER2 with 54.47% of MCF-7 cells lysed. The combination of anti-CD3 and anti-CD28 BsAbs further enhanced the in vitro tumor cell killing activity as manifested by EC_{50} reduction. Compared to treatment with anti-CD3 BsAb TY25238 alone, the addition of anti-CD28 BsAb TY27566 with a high affinity CD28 arm considerably enhanced tumor cell lysis by about 10-fold (EC_{50}). However, when combined with anti-CD28 BsAb TY27881 with a low affinity CD28 arm, no enhanced cytotoxicity was observed.

Co-Stimulatory Bispecific Antibodies Enhance in Vitro T Cell Cytotoxicity Against EMT-6-HER2 Cells Upon Bidirectional Binding

[0326] In vitro tumor cell killing activity of anti-CD3-based or anti-CD28-based BsAbs or their combination on EMT-6-HER2 tumor cell line was measured using a LDH release cytotoxicity assay.

[0327] The human T cells were isolated from fresh PBMCs using EasySep™ Human Naïve Pan T Cell Isolation Kit (STEMCELL Technologies). EMT-6-HER2 (5×10^3 cells/well) target cells were incubated with serially diluted anti-HER2×CD3 BsAb (TY25238) or in combination with fixed concentrations of anti-B7H3×CD28 BsAb TY27556 (8 nM) for 30 minutes at 37° C., or conversely EMT-6-HER2 (5×10^3 cells/well) cells were incubated with serially diluted anti-B7H3×CD3 BsAbs TY26999 or combination with fixed concentrations of anti-HER2×CD28 BsAb TY27566 (8 or 0.8 nM) for 30 minutes at 37° C. Next, isolated human T effector cells (2×10^4 cells/well) were added and incubated at 37° C., 5% CO_2 for 72 hours (E:T=2:1). Cellular cytotoxicity based on LDH release into supernatants by killed EMT-6-HER2 target cells was quantified using the CytoTox 96® Non-Radioactive Cytotoxicity Assay (Promega). An isotype antibody was included as a negative control for the single agent assays.

[0328] As shown in FIG. **15**, as a single agent, TY27556 (anti-B7H3×CD28) or TY27566 (anti-HER2×CD28) exhibited no killing potency on EMT-6-HER2 cells. TY25238 in combination with TY27556 resulted in about 2-fold decrease of EC_{50}, and about 3-fold increase of maximal killing (from 17% to 50%), compared with TY25238.

[0329] TY26999 combined with TY27566 resulted in about 1.3-fold decrease of EC_{50} and about 2-fold increase of maximal killing (from 23% to 47%), compared with TY26999.

In Vivo Systemic Cytokine Release Risk of Anti-CD3- or Anti-CD28-Based Bispecific Antibodies or their Combination

[0330] In vivo systemic cytokine release risk (IL-6 and IFN-γ) of anti-mouse CD3- or anti-CD28-based BsAbs alone or combined in BALB/c mouse model was measured using ELISA.

[0331] The BALB/c mice were randomly divided into four groups (3 mice per group), and were injected with an anti-mouse CD3 mAb (145-2C11 clone, 1 mg/kg), anti-B7H3×CD28 (TY27556, 2 mg/kg), anti-B7H3×CD3 (TY27042, in which CD3 arm was derived from mouse specific 145-2C11 clone, 2 mg/kg) or the combination (TY27556, 2 mg/kg with TY27042, 2 mg/kg), respectively. The mouse serum and whole blood were collected at various time points before and post injection (pre-dose, 3.5, and 24 hours). The systemic cytokine release risk was assessed with IL-6 and IFN-γ by ELISA. The percentage of total peripheral T cells that were $CD3^+$ T cells was determined by flow cytometry at each time point.

[0332] As shown in FIG. **16**, mice administered anti-mCD3 or anti-B7H3×CD3 (TY27042) lead to a significant induction of cytokine release (IL-6 and IFN-γ) at 3.5 h after test antibody treatment. Mice treated with anti-B7H3×CD28 (TY27556) showed no detectable cytokine release after test antibody treatment. In addition, anti-B7H3×CD3 (TY27042) combined with anti-B7H3×CD28 (TY27556) showed no increased cytokine release risk above that found with the single agent anti-B7H3×CD3 (TY27042). The peripheral $CD3^+$ T cells were sharply reduced to almost zero in the single agent anti-mouse CD3, anti-B7H3×CD3 (TY27042), and anti-B7H3×CD28 (TY27556) groups and in the anti-B7H3×CD3 (TY27042) combined with anti-B7H3×CD28 (TY27556) group. Only about 2% to 3% of $CD3^+$ T cells remained in the peripheral blood at 3.5 hours post injection.

Example 10: In Vivo Efficacy Studies

In Vivo Efficacy Study of B7H3×CD28 BsAb Monotherapy or Combination Therapy with HER2×CD3 BsAb in SK-OV3 Model

[0333] Immunodeficient M-NSG mice (n=8 per group, female, 7-8 weeks old) were transplanted with 5×10^6 PBMC through i. p. injection. Seven days later, the mice were inoculated subcutaneously with 2×10^6 SK-OV3 cells. Treatment began at Day 8 post tumor inoculation when the average tumor volume reached about 90 mm^3. The mice were administered with $hIgG_1$ isotype control at 5 mg/kg, anti-HER2×CD3 bispecific double masked antibody at 0.2 mg/kg, anti-B7H3×CD28 bispecific antibody TY27556 at 5 mg/kg, or TY27151 at 0.2 mg/kg in combination with TY27556 at 5 mg/kg by i. p. injection. TY27151 was previously described in PCT/CN2021/076626. The mice were administered these Abs twice per week for a total of

five doses. Tumor growth was monitored twice a week and reported as the mean tumor volume±s. e. m. over time.

[0334] As shown in FIG. **17**, the double masked anti-HER2×CD3 bispecific antibody TY27151 showed strong synergistic anti-tumor effect with the anti-B7H3×CD28 bispecific antibody TY27556 in this model.

In Vivo Efficacy Study of CD28 BsAbs in EMT6-HER2 Murine Breast Cancer Syngeneic Model

[0335] BALB/c mice (n=5 per group, female, 8-9 weeks old) were inoculated subcutaneously with 5×10^5 EMT-HER2 cells. Treatment began at Day 7 post tumor inoculation when the average tumor volume reached about 110 mm^3. The mice were administered Vehicle, anti-B7H3×CD28 BsAb TY27556 at 0.5 mg/kg and 0.05 mg/kg, or anti-HER2×CD28 bispecific antibody TY27566 at 0.2 mg/kg by i. p. injection. The mice were administered these Abs twice per week for a total of four doses. Tumor growth was monitored twice a week and reported as the mean tumor volume±s. e. m. over time.

[0336] As shown in FIG. **18**, anti-B7H3×CD28 bispecific antibody TY27556 showed dose dependent anti-tumor effect in this model. As shown in FIG. **18**, anti-HER2×CD28 bispecific antibody TY27566 showed strong anti-tumor effect.

Example 11: Methods of Identifying Self-Blocking Peptides for Masked Anti-CD28 Antibodies

Generation of Masked Anti-CD28 Antibodies

[0337] A screening system has been designed and executed for efficient discovery of masking moieties that can effectively mask a non-masked parental anti-CD28 antibody with good developability. In this system, the target anti-CD28 scFv was first displayed on the surface of yeast and confirmed to be functional in binding to its CD28 antigen. Then masking peptides (MP) from an improved MP peptide library were directly fused to the N-terminus of the light chain of the target anti-CD28 scFv, and a yeast library was constructed that displayed the fusion protein on the yeast surface. The yeast library then underwent several rounds of FACS-based screening: 1) the yeast clones that had low binding to antigen were enriched, 2) the enriched yeast clones were treated with a protease to remove the N-terminal MP, and 3) the resulting clones that exhibited high binding to antigen were selected. After 5 to 6 rounds of sorting, the plasmids were extracted from these clones and the MP sequences were confirmed through DNA sequencing. The selected masked anti-CD28 antibody clones in scFv format, exhibited little binding to antigen in the presence of MP. However, binding to antigen was dramatically increased when the yeast cells were treated with Tobacco Etch Virus nuclear-inclusion-a endopeptidase (TEV) to remove the MP. The incorporation of the TEV recognition site as a cleavage site in the MP, combined with the application of TEV protease to verify the selected clones, significantly increased the success rate of MP selection.

[0338] To identify the MP sequences, the shuttle plasmids were extracted from the selected yeast clones using a plasmid extraction kit (Generay), and transformed into competent *E. coli* cells. The plasmids were prepared, and the regions encoding the MPs were sequenced and aligned. As anticipated, these sequences could be separated into several groups, indicating clear enrichment through rounds of sorting. The masking efficiency selected MPs are shown in the Table 16 below and the sequences of each MP is shown in the Sequences section below.

[0339] The masked anti-CD28 scFv proteins were converted into IgG_4 isotype mAbs. The masked IgG_4 mAbs were engineered to include a MP with a single invariant matrix metalloproteinase (MMP) cleavage site fused to the N-terminus of the light chain in the same manner as displayed on the yeast surface. The heavy and light chains were cloned into the mammalian expression vector pCDNA3.3 (Thermo Fisher Scientific) separately. The V_H and V_L sequences for the parental anti-CD28 antibody (TY24865) are listed in the Sequences section below.

[0340] Pairs of plasmids were transiently transfected into HEK293F cells. After six days, the supernatants were harvested, cleared by centrifugation and filtration, and IgGs were purified with standard protein A affinity chromatography (MabSelect SuRe, GE Healthcare). The IgGs were eluted and neutralized, and buffer exchanged into 20 mM histidine, pH 5.5 buffer. Protein concentrations were determined by UV-spectrophotometry, and IgG purity was analyzed under denaturing, reducing and non-reducing conditions by SDS-PAGE or SEC-HPLC. Importantly, the expression levels of the masked antibodies in HEK293 cells were similar to or lower than their parental antibody, and their purification yields after protein A resin were also similar, suggesting that the presence of the masking and cleavage peptides do not have a significantly negative impact on antibody expression in mammalian cells.

TABLE 16

Masking Peptides					
IgG ID	ELISA Masking Efficiency	IgG ID	ELISA Masking Efficiency	IgG ID	ELISA Masking Efficiency
TY26142	3062	TY26152	1867	TY26162	ND
TY26143	ND	TY26153	1825	TY26163	ND
TY26144	ND	TY26154	ND	TY26164	ND
TY26145	1430	TY26155	368	TY26165	ND
TY26146	2179	TY26156	670	TY26166	ND
TY26147	4882	TY26157	ND	TY26167	1427
TY26148	ND	TY26158	887	TY26168	2567
TY26149	3841	TY26159	468	TY26169	1818
TY26150	1027	TY26160	1461	TY26170	ND
TY26151	2476	TY26161	1484	TY26171	406

Measurement of Masking Efficiency

[0341] When measuring the masking efficiency through ELISA, recombinant human CD28-Fc was diluted to 2 g/mL in PBS and coated onto a MaxiSorp™ high protein-binding capacity 96 well ELISA plate (ThermoFisher Scientific) at 4° C. overnight. Plates were blocked with PBS supplemented with 3% non-fat milk at 37° C. for 1 hour. After washing, 100 μL of 3-fold serial dilutions of anti-CD28 test mAbs were added to each well. After incubation at 37° C. for 1 hour, plates were washed four times, and 100 μL horseradish peroxidase (HRP)-conjugated anti-human IgG (Fab specific) (1:6000 dilution) secondary antibody was added to each well. Plates were incubated at 37° C. for 1 hour, washed four times, and then 50 μL a TMB substrate (3, 3', 5, 5'-tetramethylbenzidine) solution was added to each well, and the plate was incubated at room temperature. Absorbance at 450 nm was measured after the reactions were stopped with 50 μL sulfuric acid stop solution per well. The EC_{50} was evaluated by fitting the ELISA data using the sigmoidal (four-parameter logistic equation) model of GraphPad Prism version 6 for Windows, GraphPad Software, La Jolla California USA, www.graphpad.com.

[0342] Masking efficiencies for selected masked anti-CD28 test mAbs were calculated by dividing the EC_{50} for binding of the masked mAb by the EC_{50} of the non-masked parental mAb (TY24865), and are listed in Table 17. As shown in FIG. **19**, compared with the parental mAb, all of the activatable mAbs showed dramatically reduced binding to its antigen, and the calculated masking efficiency ranged from 368 to more than 4000. These results indicated that multiple MPs identified from an improved MP peptide library maintained their masking efficiency when expressed in mammalian cells, and as part of a full IgG molecule.

TABLE 17

SEC Purity and Masking Efficiencies of Masked Anti-CD28 Antibodies

IgG ID	SEC Purity HMW (%)	SEC Purity LMW (%)	Masking Efficiency
TY26142	2	0	3062
TY26143	>2.0	0	ND
TY26144	24.6	0	ND
TY26145	4.5	0	1430
TY26146	3.6	0.2	2179
TY26147	1.9	0	4882
TY26148	1.9	0.1	ND
TY26149	1.4	0.1	3841
TY26150	1.9	0	1027
TY26151	1.7	0	2476
TY26152	2.1	0	1867
TY26153	1.7	0	1825
TY26154	14.2	0	ND
TY26155	1.8	0	368
TY26156	2.7	0	670
TY26157	No main peak		ND
TY26158	Low peak		887
TY26159	36.6	0	468
TY26160	1.4	0	1461
TY26161	1.8	0	1484
TY26162	0.9	0	ND
TY26163	1.1	0	ND
TY26164	2.5	0	ND
TY26165	2.8	0	ND
TY26166	58.5	0	ND
TY26167	2.2	0.3	1427
TY26168	20.8	0	2567

TABLE 17-continued

SEC Purity and Masking Efficiencies of Masked Anti-CD28 Antibodies

IgG ID	SEC Purity HMW (%)	SEC Purity LMW (%)	Masking Efficiency
TY26169	Asymmetric main peak		1818
TY26170	3.9	0.8	ND
TY26171	5.9	0	406

Optimization of Selected Anti-CD28 Activatable Antibodies

[0343] For the two lead masked anti-CD28 mAbs, TY26149 and TY26152 were modified on their MPs, including removing some N-terminal residues, and adding an "S" amino acid residue between residues "D" and "G" of the TY26149 sequence (bolded and underlined residues of TY26149 in Table 18). As shown in FIG. **20**, the expression and masking efficiency of the new masked antibodies were not significantly influenced.

TABLE 18

Modification of Masking Peptide Sequences

IgG ID	Masking + cleavage peptide sequences:	SEQ ID NO:
TY26149	EVGSYAATYSDCYSDPYACH**DG**GGPLGLAGSGGS	301
TY28338	EAATYSDCYSDPYACHDSGGGPLGLAGSGGS	302
TY28339	EYSDCYSDPYACHDSGGGPLGLAGSGGS	303
TY26152	EVGSYAAFSPACYTDPYSCHAGGGPLGLAGSGGS	304
TY28341	EAAFSPACYTDPYSCHAGGGPLGLAGSGGS	305
TY28342	ESPACYTDPYSCHAGGGPLGLAGSGGS	306

Example 12: Epitope Mapping

[0344] To determine the binding regions of the tested antibodies at amino acid residue level, a series of mutations (Table 19) were made at the extracellular domain of human CD28. These CD28 mutation plasmids were used to transfect HEK293F cells. The binding of antibodies to the human CD28 mutants were assessed by flow cytometry analysis. The results are summarized in Table 19, together with the cross-reactivity of these antibodies with human, monkey, and mouse CD28 in interesting differentiation. TY24865 is cross-reactive to human, monkey, and mouse CD28, while TAC2386 and TAC2387 do not bind to mouse CD28. The mutant constructs were meant to differentiate the epitopes by TY24865 from the reference antibodies by TAC2386 and TAC2387. It is clearly that TY24865 kept the binding ability to RE49AA, VY68AA, YS79AA and KT81AA, which indicated TY24865 does not bind to residues RE49, VY68, YS79 and KT81, and these residues are in un-conserved region of human and mouse CD28. While TY24865 lost the binding ability to FR51AA, SL54AA, YL98AA, QN100AA, YF110AA, KI113AA, YP118AA, PPP119AAA, PP120AA, PY121AA, and Y122A mutations, indicating that their bind-

ing epitopes are within these regions, e.g., amino acid residues 51, 52, 54, 55, 98-101, 110-111, 113-114, 118-122 of SEQ ID NO.: 1.

TABLE 19

Epitope Mapping			
Mutations	TY24865	TAC2386	TAC2387
Hu_WT	+	+	+
Cyno_WT	+	+	+
Mouse_WT	+	−	−
Hu_RE49AA	+	+	−
Hu_FR51AA	−	−	−
Hu_SL54AA	−	−	−
Hu_VY68AA	+	+	−
Hu_Y69A	+	+	−
Hu_YS79AA	+	−	+
Hu_KT81AA	+	−	+
Hu_YL98AA	−	−	−
Hu_QN100AA	−	−	−
Hu_YF110AA	−	−	−
Hu_KI113AA	−	−	−
Hu_M117A	+	+	−
Hu_YP118AA	−	+	−
Hu_PPP119AAA	−	+	−
Hu_PP120AA	−	+	−
Hu_PY121AA	−	+	−
Hu Y122A	−	+	+

Example 13: TY24865 Variants

[0345] Two approaches were employed for generating variants of TY24865. Different point mutations were introduced into the YYYY sequences of TY24865 scFv and a new batch of TY24865 scFv variants were discovered through yeast-based maturation library screening. Anti-TAA×CD28 bispecific antibodies were constructed in Fab-scFv-Fc format and the CD28 affinities of these bsAbs were measured using ELISA.

[0346] Anti-PD-L1×CD28 bispecific antibodies were constructed in Fab-scFv-Fc format with anti-PD-L1 TY21421 Fab (see WO 2019/185035) and TY24865 scFv (in VH-VL format) or its variants. The affinities of some of these bsAbs to CD28 are summarized in the Table 20 and FIGS. **22**A and **22**B; TY29815 is the wild type bsAb and TY30413 has similar affinity as TY29815, while the other bsAbs have higher or reduced affinity.

TABLE 20

Construction and Characterization of Anti-PD-L1 × CD28 BsAbs with TY24865 Variants						
		Titer	SEC purity		Single point	ELISA
BsAb	CD28 scFv	(mg/L)	HMW(%)	LMW (%)	ELISA	EC_{50} (nM)
TY29815	VH-VL (YYYY)	54.1	6.4	0.6		22.26
TY30406	VH-VL (YDYY	37.5	7.2	1.6	Higher	
TY30410	VH-VL (YYEY)	23.2	9.5	1.7	Reduced	
TY30413	VH-VL (YYHY)	60.2	2.8	0.5	No change	26.81

[0347] Anti-HER2×CD28 bsAbs or anti-B7-H3×CD28 bsAbs were constructed using TY24865 scFv variants in VH-VL or VL-VH formats. As shown in Table 21, these bsAbs show normal titers and SEC-purity. The CD28 affinities of these bsAbs were measured through ELISA and shown in FIGS. **23**A and **23**B. These scFv variants shows various affinities, ranging from 0.954 to 417 nM, and scFvs in VL-VH formats have higher affinity than those in VH-VL formats. Some variants in Table 22 and FIGS. **24**A and **24**B show high affinity to human and mouse, and these affinities were further confirmed in a mouse T-cell binding assay (FIG. **25**).

TABLE 21

Construction and Characterization of Anti-HER2xCD28 BsAbs with TY24865 Variants					
	CD28 scFv	Titer	SEC purity		
BsAb ID	(VL-VH)	(mg/L)	HMW(%)	LMW (%)	EC_{50} (nM)
TY27566	WT	61.7	4.4	0.0	3.89
TY28652	BC8227	60.5	NA	NAA	3.68
TY28653	BC8228	42.2	6.8	0.1	7.30
TY28654	BC8230	59.6	3	0	68.41
TY28655	BC8233	55.2	3.4	0.2	8.14
TY28656	BC8235	70.6	2.7	0	127.7
TY28657	BC8237	67.1	3.3	0	5.29
TY28658	BC8240	67.3	4.9	0	78.02
TY28659	BC8242	64	3.4	0.3	0.954
TY28660	BC8257	67.5	4.9	0.4	3.77
TY28661	BC8263	62.8	4.9	0	52.57
	CD28 scFv	Titer	SEC purity		
BsAb ID	(VH-VL)	(mg/L)	HMW(%)	LMW (%)	EC_{50} (nM)
TY29109	WT	73.4	5.1	0.0	30.33
TY29306	BC8227	63.7	1.4	0.6	9.27
TY29307	BC8228	69.3	1.4	0	27.79
TY29308	BC8230	34.1	2.4	0	417.3
TY29309	BC8233	38.6	2	0	27.7
TY29310	BC8235	50.4	2.7	0	348.9
TY29311	BC8237	25.4	3	2.1	91.28
TY29312	BC8240	43.0	2.6	0	624.1
TY29313	BC8242	36.0	2.4	1.8	6.97
TY29314	BC8257	96.5	4	0.9	27.51
TY29315	BC8263	60.5	1.3	0	291.2

TABLE 22

Construction and Characterization of Anti-B7-H3xCD28 BsAbs with TY24865 Variants

BsAb ID	CD28 scFv (VH-VL)	Human CD28 EC_{50} (nM)	Mouse CD28 EC_{50} (nM)
TY29021	WT	36.39	NM
TY30120	BC10599	3.026	74.18
TY30121	BC10601	5.731	108.3
TY30123	BC10621	3.588	96.41

[0348] The above non-limiting examples are provided for illustrative purposes only in order to facilitate a more complete understanding of the disclosed subject matter. These examples should not be construed to limit any of the embodiments described in the present specification, including those pertaining to the antibodies, pharmaceutical compositions, or methods and uses for treating cancer, a neurodegenerative or an infectious disease.

SEQUENCES

[0349] The tables below list sequences disclosed herein and SEQ ID NOs (SEQ) are shown in the left columns.

SEQ	Description	Sequence
1	Human CD28	MLRLLLALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLF SREFRASLHKGLDSAVEVCVVYGNYSQQLQVYSKTGFNCDGKLGNES VTFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLC PSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLH SDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS
2	*Macaca mulatta* CD28	MLRLLLALNLLPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLF SREFRASLHKGLDSAVEVCVVYGNYSQQLQVYSKTGFNCDGKLGNES VTFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLC PSPLFPGPSKPFWALVVVGGVLACYSLLVTVAFCIFWMRSKRSRLLH SDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS
3	*Macaca fascicularis* CD28	MLRLLLALNLLPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLF SREFRASLHKGLDSAVEVCVVYGNYSQQLQVYSKTGFNCDGKLGNFS VTFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLC PSPLFPGPSKPFWALVVVGGVLACYSLLVTVAFCIFWMRSKRSRLLH SDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS
4	Mouse CD28	MTLRLLFLALNFFSVQVTENKILVKQSPLLVVDSNEVSLSCRYSYNL LAKEFRASLYKGVNSDVEVCVGNGNFTYQPQFRSNAEQNCDGDQDNE TVTFRLWNLHVNHTDIYFCKIEFMYPPPYLDNERSNGTIIHIKEKHL CHTQSSPKLFWALVVVAGVLFCYGLLVTVALCVIWTNSRRNRLLQSD YMNMTPRRPGLTRKPYQPYAPARDFAAYRP
		Non-masked Anti-CD28 Antibodies Anti-CD28 mAb (TY24865)
5	HCDR1	TGGVGVS
6	HCDR2	EIYHSGSTYYSPSLKS
7	HCDR3	YEYYYYDFDY
8	LCDR1	RASQSVDFHGISFLH
9	LCDR2	AASSLQS
10	LCDR3	QQSYRSPRT
11	VH	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVSWIRQAPGKGL EWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV YYCARYEYYYYDFDYWGQGTLVTVSS
12	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISFLHWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPRTFGQGTKVEIK
13	HC	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVSWIRQAPGKGL EWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV YYCARYEYYYYDFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVMHEALHNHYTQKSLSLSLGK

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SEQ	Description	Sequence
14		DIQLIQSPSSLSASVGDRVTITCRASQSVDFHGISFLHWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24853)
15	HCDR1	SGHHWS
6	HCDR2	EIYHSGSTYYSPSLKS
16	HCDR3	KDDYYAFDY
17	LCDR1	RASESVDFYGISFLH
18	LCDR2	AASTLQS
19	LCDR3	QQSYRTPIT
20	VH	EVQLVESGGGLVQPGGSLRLSCAASGYSITSGHHWSWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQINSIRAEDTAVY YCARKDDYYAFDYWGQGTLVTVSS
21	VL	DIQLTQSPSSLSASVGDRVTITCRASESVDFYGISFLHWYQQKPGKA PKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRTPITFGQGTKVEIK
22	HC	EVQLVESGGGLVQPGGSLRLSCAASGYSITSGHHWSWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQINSLRAEDTAVY YCARKDDYYAFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGEYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSC SVMHEALHNHYTQKSLSLSLGK
23	LC	DIQLTQSPSSLSASVGDRVTITCRASESVDFYGISFLHWYQQKPGKA PKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRTPITFGQGIKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24854)
24	HCDR1	SGYHWG
6	HCDR2	EIYHSGSTYYSPSLKS
25	HCDR3	RRGDGYFDF
26	LCDR1	RASQSVDFLGISFLH
27	LCDR2	DASNRAT
28	LCDR3	QQSYRTPLT
29	VH	EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYHWGWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARRRGDGYFDFWGQGTLVTVSS
30	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFLGISFLHWYQQKPGKA PKLLIYDASNRATGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRTPLTEGQGTKVEIK
31	HC	EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYHWGWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARARGDGYFDFWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHIFPAVLQSSGLYSLSSVVT VPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGG PSVFLFPPKPKDSLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV

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SEQ	Description	Sequence
		HNAKTKPREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSC SVMHEALHNHYTQKSLSLSLGK
32	LC	DIQLTQSPSSLSASVGDRVTITCRASQSVDFLGISFLHWYQQKPGKA PKLLIYDASNRATGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRTPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NEYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVCHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24859)
33	HCDR1	TGGVGVG
6	HCDR2	EIYHSGSTYYSPSLLKS
35	HCDR3	YGYSYYALDY
36	LCDR1	SASSSVGYVQ
37	LCDR2	DASNLET
38	LCDR3	QQSYTSPRT
39	VH	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVGWIRQAPGKGL EWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV YYCARYGYSYYALDYWGQGTLVTVSS
40	VL	DIQLTQSPSSLSASVGDRVTITCSASSSVGYVQWYQQKPGKAPKLLI YDASNLETGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYTSP RTFGQGTKVEIK
41	HC	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVGWIRQAPGKGL EWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV YYCARYGYSYYALDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSES TAALGQLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTTPPSQEEMTKNQVSLTCLVKGEYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVMHEALHNHYTQKSLSLSLGK
42	LC	DIQLTQSPSSLSASVSDRVTITCSASSSVGYVQWYQQKPGKAPKLLI YDASNLETGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYTSP RTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLILSKADYEKH KVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24860)
43	HCDR1	TSGVGVS
5	HCDR2	EIYHSGSTYYSPSLKS
44	HCDR3	KGYYYYAFDY
45	LCDR1	RASQDIGSFLA
9	LCDR2	AASSLQS
46	LCDR3	QQSYRSPPT
47	VH	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTSGVGVSWIRQAPGKGL EWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV YYCARKGYYYYAFDYWGPGTLVTVSS
48	VL	DIQLTQSPSSLSASVGDRVTITCRASQDIGSFLAWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRS PPTFGQGTKVEIK
49	HC	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTSGVGVSWIRQAPGKGL EWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV

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SEQ	Description	Sequence
		YYCARKGYYYYAFDYWGPGTLVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVMHEALHNHYTQKSLSLSLGK
50	LC	DIQLTQSPSSLSASVGDRVTITCRASQDIGSFLAWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRS PPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVIKSFNRGEC
		Anti-CD28 mAb (TY24866)
33	HCDR1	TGGVGVG
51	HCDR2	EIYHSGSTYYPPSLKS
52	HCDR3	YEYSSYGLDY
53	LCDR1	RASQDIRKFLA
300	LCDR2	DASSLES
10	LCDR3	QQSYRSPRT
54	VH	EVQLVESGGGLVQPGSSLRLSCAASGFSLSTGGVGVGWIRQAPGKGL EWIGETYHSGSTYYPPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV YYCARYEYSSYGLDYWGQGTLVTVSS
55	VL	DIQLTQSPSSLSASVGDRVTITCRASQDIRKFLAWYQQKEGKAPKLL IYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRS PRTEGQGTKVEIK
56	HC	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVGWIRQAPGKGL EWIGEIYISGSTYYPPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV YYCARYEYSSYGLDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV EVANAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGEYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVMHEALHNHYTQKSLSLSLGK
57	LC	DIQLTQSPSSLSASVGDRVTITCRASQDIRKFLAWYQQKPGKAPKLL TYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDEATYYCQQSYRS PRFFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSSNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVIKSFNRGEC
		Anti-CD28 mAb (TY24869)
24	HCDR1	SGYHWG
58	HCDR2	AIYHSGSTYYSPSLKS
59	HCDR3	SGLVYYAFDY
60	LCDR1	RASQGIGSYLA
300	LCDR2	DASSLES
61	LCDR3	QQYSTSPLT
62	VH	QVQLVQSGAEVKKPGSSVKVSCKASGYSISSGYHWGWIRQAPGQGLE WIGAIYHSGSTYYSPSLKSRVTITADKSTSTAYMELSSLRSEDTAVY YCARSGLVYYAFDYWGQGTLVTVSS

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SEQ	Description	Sequence
63	VL	DIQLTQSPSSLSASVGDRVTITCRASQGIGSYLAWYQQKPGKAPKLL IYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTS PLTFGQGTKVEIK
64	HC	QVQLVQSGAEVKKPGSSVKVSCKASGYSISSGYHWGWIRQAPGQGLE WIGAIYHSGSTYYSPSLKSRVTITADKSISTAYMELSSLRSEDIAVY YCARSGLVYYAFDYWSQGTLVTVSSASTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTKTYCCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYCQKSLSLSLGK
65	LC	DIQLTQSPSSLSASVGDRVTITCRASQGIGSYLAWYQQKPGKAPKLL IYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTS PLTFGQGTKVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24871)
66	HCDR1	SYAIH
67	HCDR2	SIYHSGSTYYSPSLKS
68	HCDR3	DVYGSYALDV
69	LCDR1	RASQSVDFDGISFLH
300	LCDR2	DASSLES
70	LCDR3	QQSYRSPIT
71	VH	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSSYAIHWVRQAPGQGLEW IGSIYHSGSTYYSPSLKSRVTITADKSTSTAYMELSSLRSEDTAVYY CARDVYGSYALDVWGQGTLVTVSS
72	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFDGISFLHWYQQKPGKA PKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPITFGQGTKVEIK
73	HC	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSSYAIHWVRQAPGQGLEW IGSIYHSGSTYYSPSLKSRVTITADKSTSTAYMELSSLRSEDTAVYY CARDVYGSYALDVWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGG PSVFLFPPKPKDTLMISRIPEVTCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSC SVMHEALHNHYTQKSLSLSLGK
74	LC	DIQLTQSPSSLSASVGDRVTITCRASQSVDFDGISFLHWYQQKPGKA PKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NEYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24773)
24	HCDR1	SGYHWG
6	HCDR2	EIYHSGSTYYSPSLKS
75	HCDR3	KDYYYALDY
76	LCDR1	RASQSVDFYGKSFLII
18	LCDR2	AASTLQS
28	LCDR3	QQSYRIPLT

-continued

SEQ	Description	Sequence
77	VH	EVQLVESGGGLVQPGGSLRLSCAASGYSISSGYHWGWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARKDYYYALDYWGQGTLVTVSS
78	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGKSFLHWYQQKPGKA PKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRTPLTFGQGTKVEIK
79	HC	EVQLVESGGGLVQPGGSLRLSCAASGYSISSGYHWGWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARKDYYYALDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSC SVMHEALHNHYTQKSLSLSLGK
80	LC	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGKSFLHWYQQKPGKA PKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRTPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NEYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24876)
24	HCDR1	SGYHWG
58	HCDR2	AIYHSGSTYYSPSLKS
81	HCDR3	GPLSYYAFDY
82	LCDR1	RASQSVSRYLA
27	LCDR2	DASNRAT
83	LCDRS	QQYYRSPIT
84	VH	QVQLVQSGAEVKKPGSSVKVSCKASGYSITSGYHWGWIRQAPGQGLE WIGAIYHSGSTYYSPSLKSRVTITADKSTSTAYMELSSLRSEDTAVY YCARGPLSYYAFDYWGQGTLVTVSS
85	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVSRYLAWYQQKPGKAPKLL IYDASNRATGIPSRFSGSGSGTDFTLTISSLQPEDEATYYCQQYYRS PITFGQGTKVEIK
86	HC	QVQLVQSGAEVKKPGSSVKVSCKASGYSITSGYHWGWIRQAPGQGLE WIGAIYHSGSTYYSPSLKSRVTITADKSTSTAYMELSSLRSEDTAVY YCARGPLSYYAFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVV TVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK
87	LC	DIQLTQSPSSLSASVGDRVTITCRASQSVSRYLAWYQQKPGKAPKLL IYDASNRATGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYRS PITFGQGTKVEIKRIVAAPSVFIFPPSDEQLKSGTASVVQLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24878)
88	HCDR1	TGGVAVA
89	HCDR2	QIYYSGSTYYNPSLKS
90	HCDR3	SSAHYYFDV
91	LCDR1	RASESVDFQGISFLD

-continued

SEQ	Description	Sequence
300	LCDR2	DASSLES
70	LCDR3	QQSYRSPIT
92	VH	QVQLVQSGAEVKKPGSSVKVSCKASGFSLSTGGVAVAWIRQAPGQGL EWIGQIYYSGSTYYNPSLKSRVTITADKSTSTAYMELSSLRSEDTAV YYCARSSAHYYEDVWGQGTLVTVSS
93	VL	DIQLTQSPSSLSASVGDRVTITCRASESVDFQGISFLDWYQQKPGKA PKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPITFGQGTKVEIK
94	HC	QVQLVQSGAEVKKPGSSVKVSCKASGFSLSIGGVAVAWIRQAPGQGL EWIGQIYYSGSTYYNPSLKSRVTITADKSTSTAYMELSSLRSEDTAV YYCARSSAHYYFDVWGQGTLVTVSSASTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTKIYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTTPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK
95	LC	DIQLTQSPSSLSASVGDRVTITCRASESVDFQGISFLDWYQQKPGKA PKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NEYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24879)
24	HCDR1	SGYHWG
96	HCDR2	SIYHSGSTYYNPSLKS
97	HCDR3	SGLRYYAFDV
98	LCDR1	AASQDVSTAVA
9	LCDR2	AASSLQS
70	LCDR3	QQSYRSPIT
99	VH	QVQLVQSGAEVKKPGSSVKVSCKASGYSISSGYHWGWIRQAPGQGLE WIGSIYHSGSTYYNPSLKSRVTITADKSTSTAYMELSSLRSEDTAVY YCARSGLRYYAFDVWGQGTLVTVSS
100	VL	DIQLTQSPSSLSASVGDRVTITCAASQDVSTAVAWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRS PITFGQGTKVEIK
101	HC	QVQLVQSGAEVKKPGSSVKVSCKASGYSISSGYHWGWIRQAPGQGLE WIGSIYHSGSTYYNPSLKSRVTITADKSTSTAYMELSSLRSEDTAVY YCARSGLRYYAFDVWGQGTLVTVSSASTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTKTYCCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK
102	LC	DIQLTQSPSSLSASVSDRVTITCAASQDVSTAVAWYQQKPGKAPKLL TYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDEATYYCQQSYRS PITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24884)
103	HCDR1	GYAIH
104	HCDR2	QIYHSGSTYYNPSLKS

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SEQ	Description	Sequence
105	HCDR3	SGYGGYDFDY
106	LCDRI	RASQSVPRRYLA
18	LCDR2	AASTLQS
83	LCDR3	QQYYRSPIT
107	VH	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSGYAIHWVRQAPGQGLEW IGQIYHSGSTYYNPSLKSRVTITADKSTSTAYMELSSLRSEDTAVYY CARSGYGGYDFDYWGQGTLVTVSS
108	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVPRRYLAWYQQKPGKAPKL LIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYR SPITFGQGTKVEIK
109	HC	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSGYAIHWVRQAPSQGLEW IGQIYHSGSTYYNPSLKSRVTITADKSTSTAYMELSSLRSEDTAVYY CARSGYGGYDFDYNGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYTCNVDHKPSNTKVFKRVESKYGPPCPPCPAPEFLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS IEKTISKAKGOPREPQVYTTPPSQEEMTKNQVSLTCLVKGEYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSC SVMHEALHNHYTQKSLSLSLGK
110	LC	DIQLTQSPSSLSASVGDRVTITCRASQSVPRRYLAWYQQKPGKAPKL LIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYR SPITFGQGTKVEIKRQVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEG
		Anti-CD28 mAb (TY24890)
111	HCDR1	SGHHWG
6	HCDR2	EIYHSGSTYYSPSLKS
112	HCDR3	RELGYAYFDY
113	LCDR1	RASQDIRKYLA
18	LCDR2	AASTLQS
114	LCDR3	QQYYRTPLT
115	VH	EVQLVESGGGLVQPGGSLRLSCAASGYSISSGHHWGWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARRELGYAYFDYWGQGTLVTVSS
116	VL	EIVLTQSPATLSLSPGERATLSCRASQDIRKYLAWYQQKPGQAPRLL IYAASTLQSGVPARFSGSGSGTDFTLTISSLEPEDEAVYYCQQYYRT PLTFGQGTKVEIK
117	HC	EVQLVESGGGLVQPGGSLRLSCAASGYSISSGHHWGWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARRELGYAYFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSEST AALGQLVKDYFPEPVCVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK
118	LC	EIVLTQSPATLSLSPGERATLSCRASQDIRKYLAWYQQKPGQAPRLL IYAASTLQSGVPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQYYRT PLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC

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SEQ	Description	Sequence
		Anti-CD28 mAb (TY24856)
15	HCDR1	SGHHWS
6	HCDR2	EIYHSGSTYYSPSLKS
119	HCDR3	RDFGASYFDY
120	LCDR1	RASQGVGPWLA
9	LCDR2	AASSLQS
121	LCDR3	QQYYSYST
122	VH	EVQLVESGGGLVQPGGSLRLSCAASGYSISSGHHWSWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARRDEGASYFDYWGQGTLVTVSS
123	VL	DIQLTQSPSSLSASVGDRVTITCRASQGVGPWLAWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSY STFGQGTKVEIK
124	HC	EVQLVESGGGLVQPGGSLRLSCAASGYSISSGHHWSWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARRDFGASYEDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVV TVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK
125	LC	DIQLTQSPSSLSASVGDRVTITCRASQGVGPWLAWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSY STFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKH KVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24881)
126	HCDR1	TGGVGVT
67	HCDR2	SIYHSGSTYYSPSLKS
127	HCDR3	YDYGYYSFDV
128	LCDR1	RASQSVDFDAFSELA
18	LCDR2	AASTLQS
129	LCDR3	QQSYSAST
130	VH	QVQLVQSGAEVKKPGSSVKVSCKASGFSLSTGGVGVTWIRQAPGQGL EWIGSIYHSGSTYYSPSLKSRVTITADKSTSTAYMELSSLRSEDTAV YYCARYDYGYYSFDVWGQGTLVTVSS
131	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFDAFSELAWYQQKPGKA PKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYSASTFGQGTKVEIK
132	HC	QVQLVQSGAEVKKPGSSVKVSCKASGFSLSTGGVGVTWIRQAPGQGL EWIGSIYHSGSTYYSPSLKSRVTITADKSTSTAYMELSSLRSEDTAV YYCARYDYGYYSFDVWGQGTLVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTTPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVMHEALHNHYTQKSLSLSLGK

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SEQ	Description	Sequence
133	LC	DIQLTQSPSSLSASVGDRVTITCRASQSVDFDAFSFLAWYQQKPGKA PKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYSASTEGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24858)
134	HCDR1	SGHHWT
6	HCDR2	EIYHSGSTYYSPSLKS
135	HCDR3	RDYGSSYFDY
136	LCDR1	RASQSVSRSFLA
27	LCDR2	DASNRAT
83	LCDR3	QQYYRSPIT
137	VH	EVQLVESGGGLVQPGGSLRLSCAASGYSISSGHHWTWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARRDYGSSYFDYWGQGTLVTVSS
138	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVSRSFLAWYQQKPGKAPKL LIYDASNRATGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYR SPITFGQGTKVEIK
139	HC	EVQLVESGGGLVQPGGSLRLSCAASGYSISSGHHWTWIRQAPGKGLE WIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARRDYGSSYEDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTKTYICNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK
140	LC	DIQLTQSPSSLSASVGDRVTITCRASQSVSRSFLAWYQQKPGKAPKL LIYDASNRATGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYR SPITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24864)
43	HCDR1	TSGVGVS
58	HCDR2	AIYHSGSTYYSPSLKS
141	HCDR3	YGYSYYAFDY
142	LCDR1	RASQTIGSFLN
300	LCDR2	DASSLES
143	LCDR3	QQSYSYQT
144	VH	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTSGVGVSWIRQAPGKGL EWIGAIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV YYCARYGYSYYAFDYWGQGTLVTVSS
145	VL	DIQLTQSPSSLSASVGDRVTITCRASQTIGSFLNWYQQKPGKAPKLL IYDASSLESGVESRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSY QTFGQGTKVEIK
146	HC	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTSGVGVSWIRQAPGKGL EWIGAIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV YYCARYGYSYYAFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV

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SEQ	Description	Sequence
		EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVMHEALHNHYTQKSLSLSLGK
147	LC	DIQLTQSPSSLSASVGDRVTITCRASQTIGSFLNWYQQKPGKAPKLL IYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSY QTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKH KVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24877)
148	HCDR1	NYGIH
6	HCDR2	EIYHSGSTYYSPSLKS
149	HCDR3	GPLSYYALDY
150	LCDR1	PASQSIRRFLN
300	LCDR2	DASSLES
83	LCDR3	QQYYRSPIT
151	VH	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYGIHWVRQAPGQGLEW IGEIYHSGSTYYSPSLKSRVTITADKSTSTAYMELSSLRSEDTAVYY CARGPLSYYALDYWGQGTLVTVSS
152	VL	DIQLTQSPSSLSASVGDRVTITCRASQSIRRFLNWYQQKPGKAPKLL IYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYRS PITFGQGTKVEIK
153	HC	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYGIHWVRQAPGQGLEW IGEIYHSGSTYYSPSLKSRVTITADKSTSTAYMELSSLRSEDTAVYY CARGPLSYYALDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSC SVMHEALHNHYTQKSLSLSLGK
154	LC	DIQLTQSPSSLSASVGDRVTITCRASQSIRRFLNWYQQKPGKAPKLL IYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYRS PITFGQGTKVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSSNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24855)
15	HCDR1	SGHHWS
155	HCDR2	DIYHSGSTYYNPSLKS
16	HCDR3	KDDYYAFDY
156	LCDR1	RAPQSVDFHGKSFLH
27	LCDR2	DASNRAT
70	LCDR3	QQSYRSPIT
157	VH	EVQLVESGGGLVQPGGSLRLSCAASGYSITSGHHWSWIRQAPGKGLE WIGDIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARKDDYYAFDYWGQGTLVTVSS
158	VL	DIQLTQSPSSLSASVSDRVTITCRAPQSVDFHGKSFLHWYQQKPGKA PKLLIYDASNRATGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPITFGQGTKVEIK
159	HC	EVQLVESGGGLVQPGGSLRLSCAASGYSITSGHHWSWIRQAPGKGLE WIGDIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVY

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SEQ	Description	Sequence
		YCARKDDYYAFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSC SVMHEALHNHYTQKSLSLSLGK
160	LC	DIQLTQSPSSLSASVGDRVTITCRAPQSVDFHGKSFLHWYQQKPGKA PKLLIYDASNRATGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVHQGLSSPVTKSFNRGEC
		Anti-CD28 mAb (TY24857)
161	HCDR1	TSGVAVG
6	HCDR2	EIYHSGSTYYSPSLKS
162	HCDR3	HGYHYYALDY
163	LCDR1	PASQDVGTAVA
300	LCDR2	DASSLES
164	LCDR3	QQYYSSPPT
165	VH	EVQLVESGGGLVQPGSSLRLSCAASGFSLSTSGVAVGWIRQAPGKGL EWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV YYCARHGYHYYALDYWGQGTLVTVSS
166	VL	DIQLTQSPSSLSASVGDRVTITCPASQDVGTAVAWYQQKPGKAPKLL IYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSS PPTFGQGTKVEIK
167	HC	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTSGVAVGWIRQAPGKGL EWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAV YYCARHGYHYYALDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTTPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVMHEALHNHYTQKSLSLSLGK
168	LC	DIQLTQSPSSLSASVGDRVTITCPASQDVGTAVAWYQQKPGKAPKLL IYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSS PPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSSNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC
		Non-masked Bispecific Antibodies HER2xCD28 Bispecific Antibodies-(Parent-TY24865) TY27566
169	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLL IYSASYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYIY PYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC
170	HC-A	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEW VADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVY YCARNLGPSFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRKKLTKNQVKLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDCDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK

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SEQ	Description	Sequence
171	HG-B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISFLHWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPRTFGQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGG LVQPGGSLRLSCAASGFSLSTGGVGVSWIRQAPGKGLEWIGEIYHSG STYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYEYYY YDFDYWGQGTLVSVSSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTDPPSRDELTKNQVSLTCLVDGFYPSDIAVEWESNGQP ENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQDSLSLSPGK
		TY27881
169	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLL IYSASYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYIY PYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC
170	HC-A	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEW VADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVY YCARNLGPSFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRKKLTKNQVKLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDCDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK
172	HC-B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGKSFLHWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPLTFGQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGG LVQPGGSLRLSCAASGFSLSTSGVGVSWIRQAPGKGLEWIGEIYHSG STYYSPSLKSRVTISRDNSKNTLYLQLNSLRVEDTAVYYCARDEYDY YAFDYWGQGTLVTVSSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTDPPSRDELTKNQVSLTCLVDGFYPSDIAVENESNGQP ENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQDSLSLSPGK
		TROP2xCD28 Bispecific Antibodies TY27571
173	LC	DIQLTQSPSSLSASVGDRVTITCRASQDVSIAVAWYQQKPGKAPKLL IYSASYRYTGVPARFSGSGSGTDFTLTISSLQPEDFATYYCQQHYIT PLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC
174	HC-A	QVQLLQSGSELKKPGASVKVSCKASGYTFTNYGINWVRQAPGQGLEW LGWIHTYTGEPTYTDDFKGRFVFSLDTSVSTAYLQISSLKADDTAVY YCARGGFGSSYWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSIGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSRKKLTKNQVKLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK
171	HC-B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISFLHWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPRTFGQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGG LVQPGGSLRLSCAASGFSLSTGGVGVSWIRQAPGKGLEWIGEIYHSG STYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYEYYY YDFDYWGQGTLVTVSSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTDPPSRDELTKNQVSLTCLVDGFYPSDIAVEWESNGQP ENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQDSLSLSPGK

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SEQ	Description	Sequence
		B7H3xCD28 Bispecific Antibody TY27556
175	LC	DIQLTQSPSSLSASVGDRVTITCRASQSIRKYLNWYQQKPGKAPKLL IYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCSQGTHV PFTEGQGTKVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC
176	HC-A	EVQLVESGGGLVQPGGSLRLSCAASGFTFSGYGIHWVRQAPGKGLEW IGWISPSGGDTKYAQKFQGRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARGGTVVYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRKKLTKNQVKLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDCDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK
171	HC-B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISFLHWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYRSPRTFGQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGG LVQPGGSLRLSCAASGFSLSTGGVGVSWIRQAPGKGLEWIGEIYHSG STYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYEYYY YDFDYWGQGTLVTVSSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTDPPSRDELTKNQVSLTCLVDGFYPSDIAVEWESNGQP ENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQDSLSLSPGK
		TY26999
175	LC	DIQLTQSPSSLSASVGDRVTITCRASQSIRKYLNWYQQKPGKAPKLL IYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCSQGTHV PFTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC
176	HC-A	EVQLVESGGGLVQPGGSLRLSCAASGFTFSGYGIHWVRQAPGKGLEW IGWISPSGGDTKYAQKFQGRVTISRDNSKNTLYLQLNSLRAEDTAVY YCARGGTVVYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRKKLTKNQVKLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDCDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK
177	HC-B	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYPNWVQQKPGQAPR GLIGGTNKRAPGVPARFSGSLLGGKAALTLSGAQPEDEAEYYCALWY SNLWVFGGGTKLTVLGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLV QPGGSLRLSCAASGFTFNTYAINWVRQAPGKGLEWVGRIRSKYNNYA TYYAESVKGRFTISRDDSKNTLYLQINSLRAEDTAVYYCVRHGNFGT SYVSWEAYWGQGTLVTVSSEPKSSDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGEYPSDIAVEWESN GQPENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQDSLSLSPGK

Masking Unit (MU)	
SEQ ID NO:	Sequence
178	ASDLYVCAHDPYFCHS
179	PNVEDTCYVDPYSCTI
180	YAAAPSCPPANYYCAD
181	HHADPLCFAQHSACNT
182	YDTHDYCLIHYHSCDT
183	ADFAPYCYADPYYCHD
184	DIASDSCYYAPNHCDT
185	AATYSDCYSDPYACHD
186	PTYDHDCAVYNNFCNA
187	HNHALTCYTDPYACHS
188	AAFSPACYTDPYSCHA
189	TPHPDACEVDPYHCHT
190	APSDAYCYADPYACHT
191	AVDDDPCYTDPYQCTA
192	THSDAVCAPDHAYCLY
193	PYIYVDCYAPPFFCAY
194	YECAEGVPIVLCIG
195	DYCEGPPAFFYCAK
196	FPCEPLADPFLCRO
197	LVCEDVPEPAACRA
198	ALCEFYAFPYFCAR
199	IVCKYFDDPELCRR
200	YECPVRVPLAVCLR
201	PSCPDYVPFPVCAQ
202	VACAKAFAYVYCLV
203	VLCGDSVPFLLCEP
204	ILCPEGVPVVFCVL
205	SDCGLGVPLLVCLK
206	TDCGIPFPVDDCLS
207	HIPDAYCAADHHYCYY
208	AATYSDCYSDPYACHD
209	YSDCYSDPYACHD
210	AAFSPACYTDPYSCHA
211	SPACYTDPYSCHA

Masking peptide components		
SEQ ID NO:	Description	Sequence
212	N-terminal Unit	EVGSY
213	Linkage Unit (LU)	GGGPLGLAGSGGS
214	Linkage Unit (LU)	SGGGPLGLAGSGGS

SEQ ID NO:	Sample ID Name	Masking + Cleavage Peptide Sequences:	SEQ ID NO LC	HC	MU	LU
215	TY26142	*EVGSY***ASDLYVCAHDPYFCHS**GGGPLGLAGSGGS	14	13	171	213

SEQ ID NQ:	Sample ID Name	Masking + Cleavage Peptide Sequences:	SEQ ID NQ			
216	TY26143	*EVGSY***PNVEDTCYVDPYSCTI**GGGPLGLAGSGGS	14	13	172	213
227	TY26144	*EVGSY***YAAAPSCPPANYYCAD**GGGPLGLAGSGGS	14	13	173	213
218	TY26145	*EVGSY***HHADPLCFAQHSACNT**GGGPLGLAGSGGS	14	13	174	213
219	TY26146	*EVGSY***YDTHDYCLIHYHSCDT**GGGPLGLAGSGGS	14	13	175	213
220	TY26147	*EVGSY***ADFAPYCYADPYYCHD**GGGPLGLAGSGGS	14	13	176	213
221	TY26148	*EVGSY***DIASDSCYYHPNECDT**GGGPLGLAGSGGS	14	13	177	213
222	TY26149	*EVGSY***AATYSDCYSDPYACHD**GGGPLGLAGSGGS	14	13	178	213
223	TY26150	*EVGSY***PTYDHDCAVYNNFCNA**GGGPLGLAGSGGS	14	13	179	213
224	TY26151	*EVGSY***HNHALTCYTDPYACHS**GGGPLGLAGSGGS	14	13	180	213
225	TY26152	*EVGSY***AAFSPACYTDPYSCHA**GGGPLGLAGSGGS	14	13	181	213
226	TY26153	*EVGSY***TPHPDACFVDPYHCHT**GGGPLGLAGSGGS	14	13	182	213
227	TY26154	*EVGSY***APSDAYCYADPYACHT**GGGPLGLAGSGGS	14	13	183	213
228	TY26155	*EVGSY***AVDDDPCYTDPYQCTA**GGGPLGLAGSGGS	14	13	184	213
229	TY26156	*EVGSY***THSDAVCAPDHAYCLY**GGGPLGLAGSGGS	14	13	185	213
230	TY26157	*EVGSY***PYIYVDCYAPPFFCAY**GGGPLGLAGSGGS	14	13	186	213
231	TY26158	*EVGSY***YFCAEGVPIVLCIG**GGGPLGLAGSGGS	14	13	187	213

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SEQ ID NO:	Sample ID Name	Masking + Cleavage Peptide Sequences:	SEQ ID NO			
232	TY26159	*EVGSY***DYCEGPPAFFYCAK**GG GPLGLAGSGGS	14	13	188	213
233	TY26160	*EVGSY***FPCEPLADPFLCRQ**GG GPLGLAGSGGS	14	13	189	213
234	TY26161	*EVGSY***LVCEDVPFPAACRA**GG GPLGLAGSGGS	14	13	190	213
235	TY26162	*EVGSY***ALCEFYAFPYFCAR**GG GPLGLAGSGGS	14	13	191	213
236	TY26163	*EVGSY***IVCKYFDDPFLCRR**GG GPLGLAGSGGS	14	13	192	213
237	TY26164	*EVGSY***YFCPVRVPLAVCLR**GG GPLGLAGSGGS	14	13	193	213
238	TY26165	*EVGSY***PSCPDYVPEPVCAQ**GG GPLGLAGSGGS	14	13	194	213

SEQ ID NO:	Sample ID Name	Masking + Cleavage Peptide Sequences;	SEQ ID NO			
239	TY26166	*EVGSY***VACAKAFAYVYCLV** GGGPLGLAGSGGS	14	13	195	213
240	TY26167	*EVGSY***VLCGDSVPFLLCEP** GGGPLGLAGSGGS	14	13	196	213
241	TY26168	*EVGSY***ILCPEGVPVVFCVL** GGGPLGLAGSGGS	14	13	197	213
242	TY26169	*EVGSY***SDCGLGVPLLVCLK** GGGPLGLAGSGGS	14	13	198	213
243	TY26170	*EVGSY***TDCGIPFPVDDCLS** GGGPLGLAGSGGS	14	13	199	213

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SEQ ID NO:	Sample ID Name	Masking + Cleavage Peptide Sequences;	SEQ ID NO			
244	TY26171	*EVGSY***HIPDHYCAADHHYC** YYGGGPLGLAGSGGS	14	13	200	213
245	TY28338	***E*AATYSDCYSDPYACHD**SG GGPLGLAGSGGS	14	13	201	214
246	TY28339	***E*YSDCYSDPYACHD**SGGGP LGLAGSGGS	14	13	202	214
247	TY28341	***E*AAFSPACYTDPYSCHA**GG GPLGLAGSGGS	14	13	203	213
248	TY28342	***E*SPACYTDPYSCHA**GGGPL GLAGSGGS	14	13	204	213

SEQ	Flexible Linkers
249	GGGGS
250	GGGGT
251	SGGS
252	GGSG
253	GGSGG
254	GSGSG
255	GSGGG
256	GGGSG
257	GSSSG

masked Bispecific Antibodies	
HER2 × CD28 Bispecific Antibodies - (Parent - TY24865) TY27566	
258 LCDR1	KASQDVSIGVA
259 LCDR2	SASYRYT
260 LCDR3	QQYYIYPYT
261 VL	DIQMTQSPSSLSASVGDRVIITCKASQDVSIGVAWYQQKEGKAPKLLIYSA SYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYTYPYTFGQGT KVEIK
262 HCDR1-A	DYTMD
263 HCDR2-A	DVNPNSGGSIYNQREKG
264 HCDR3-A	NLGPSFYFDY
265 VH-A	EVQLVESGGGLVQPGGSLRLSCAASGETFEDYIMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYFDYWGQGTLVTVSS

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masked Bispecific Antibodies	
5HCDR1-B	TGGVGVS
6HCDR2-B	EIYHSGSTYYSPSLKS
7HCDR3-B	YEYYYYDEDY
8LCDR1-B	RASQSVDFHGISELH
9LCDR2-33	AASSLQS
10LCDR3-B	QQSYRSPRT
266SCFV-B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFEGISFLHWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGEDEILTISSLQPEDFATYYCQQSYRSPRTF GQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSLSTGGVGVSWIRQAPGKGLEWIGEIYHSGSTYYSPSLKSRVTISR DNSKNILYLQLNSLRAEDTAVYYCARYEYYYYDEDYWGQGTEVTVSS
TY27807	
267LCDR1	RASQDVNTAVA
268LCDR2	SASFLYS
269LCDR3	QQHYTTPPT
270VL	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSA SFLYSGVPSRESGSRSGIDFQLTISSLQPEDFATYYCQQHYTTPPTFGQGT KVEIK
271LC	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSA SFLYSGVPSRESGSRSGIDEELTISSLQPEDFATYYCQQHYTTPPTFGQGT KVEIKRIVAAPSVEIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSENRGEC
272HCDR1-A	DTYIH
273HCDR2-A	RIYPINGYTRYADSVKG
274HCDR3-A	WGGDGFYAMDY
275VH-A	EVQLVESGGGLVQPGGSLRLSCAASGENIKDTYIHWVRQAPGKGLEWVARI YPTNGYTRYADSVKGRETISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGD GFYAMDYWGQGTLVTVSS
276HC-A	EVQLVESGGGLVQPGGSLRLSCAASGENIKDTYIHWVRQAPGKGLEWVARI YPINGYTRYADSVKGRETISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGD GTYAMDYWGQGTLVTVSSASTKGPSVIPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVIVESSSIGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVIGVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS RKKLIKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDCDGSEE LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
5HCDR1-B	TGGVGVS
6HCDR2-B	EIYHSGSTYYSPSLKS
7HCDR3-B	YEYYYYDEDY
8LCDR1-B.	PASQSVDEHGISFLH
9LCDR2-B	AASSLQS
10LCDR3-B	QQSYRSPRT
266SCFv-B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISELHWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGEDFTLTISSLQPEDEATYYCQQSYRSPRTE GQGIKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSLSTGGVGVSWIRQAPGKGLEWIGETYHSGSTYYSPSLKSRVTISR DNSKNTLYLQLNSLRAEDTAVYYCARYEYYYYDFDYWGQGTLVTVSS

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masked Bispecific Antibodies

171HC-B DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISELHWYQQKPGKAPKLL
IYAASSLQSGVPSRESGSGSGEDFTLTISSLQPEDEATYYCQQSYRSPRTE
GQGIKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC
AASGESLSTGGVGVSWIRQAPGKGLEWIGEIYHSGSTYYSPSLKSRVTISR
DNSKNTLYLQLNSLRAEDTAVYYCARYEYYYYDFDYWGQGTLVTVSSEPKS
SDKIHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
PEVKFNWYVDGVEVHNAKIKPREEQYASTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGF
YPSDIAVEWESNGQPENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVE
SCSVMHEALHNHYTQDSLSLSPGK

TROP2 × CD28 Bispecific Antibodies
TY27571

277LCDR1-A RASQDVSIAVA

259LCDR2-A SASYRYT

278LCDR3-A QQHYITPLT

279VL-A DIQLTQSPSSLSASVGDRVTITCRASQDVSIAVAWYQQKPGKAPKLLIYSA
SYRYTGVPARFSGSGSGIDFTLTISSLQPEDFATYYCQQHYITPLQFGQGT
KVEIK

280HCDR1-A NYGIN

281HCDR2-A WIHTYTGEPTYTDDEKG

282HCDR3-A GGFGSSYWYFDV

283VH-A QVQLLQSGSELKKPGASVKVSCKASGYTFENYGINWVRQAPGQGLEWLGWI
HTYTGEPTYTDDFKGREVESLDTSVSTAYLQISSLKADDEAVYYCARGGEG
SSYWYFDVWGQGTLVTVSS

5HCDR1-B TGGVGVS

6HCDR2-B EIYHSGSTYYSPSLKS

7HCDR3-B YEYYYYDEDY

8LCDR1-B RASQSVDFHGISFLH

9LCDR2-B AASSLQS

10LCDR3-B QQSYRSPRT

266SCEV-B DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISELHWYQQKPGKAPKLL
IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRSPRTE
GQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC
AASGFSLSTGGVGVSWIRQAPGKGLEWIGEIYHSGSTYYSPSLKSRVTLSR
DNSKNTLYLQLNSLRAEDTAVYYCARYEYYYYDEDYWGQGELVQVSS

B7H3 × CD28 Bispecific Antibody
TY27556

287LCDR1-A RASQSIRKYLN

18LCDR2-A AASTLQS

288LCDR3-A QGTHVPET

289VL-A DIQLTQSPSSLSASVGDRVTITCRASQSIRKYLNWYQQKPGKAPKLLIYAA
STLQSGVPSRESGSGSGTDETLTISSLQPEDFATYECSQGTHVPFCFGQGT
KVEIK

290HCDR1-A GYGIH

291HCDR2-A WISPSGGDTKYAQKFQG

292HCDR3-A GGTVVYFDY

293VH-A EVQLVESGGGLVQPGGSLRLSCAASGFTFSGYGIHWVRQAPGKGLEWIGWI
SPSGGDTKYAQKFQGRVTISRDNSKNILYLQINSIRAEDTAVYYCARGGTV
VYFDYWGQGTLVTVSS

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masked Bispecific Antibodies	
5HCDR1-B	TGGVGVS
6HCDR2-B	EIYHSGSTYYSPSLKS
7HCDR3-B	YEYYYYDEDY
8LCDR1-B	RASQSVDEHGISELI
9LCDR2-B.	AASSLQS
10LCDR3-B	QQSYRSPRT
266SCEV-B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISFLHWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRSPRTF GQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSLSTGGVGVSWIRQAPGKGLEWIGEIYHSGSTYYSPSLKSRVTISR DNSKNTLYLQLNSLRAEDTAVYYCARYEYYYYDFDYWGQGELVTVSS
B7H3 × CD3 Bispecific Antibody TY26999	
287LCDR1-A	RASQSIRKYLN
18LCDR2-A	AASTLQS
288LCDR3-A	QGTHVPFT
289VL-A	DIQLTQSPSSLSASVGDRVTITCRASQSIRKYLNWYQQKPGKAPKLLIYAA STLQSGVPSRFSGSGSGTCFTLTISSLQPEDFATYFCSQGTHVPETFGQGT KVEIK
290HCDR1-A	GYGIH
291HCDR2-A	WISPSGGDTKYAQKFQG
292HCDR3-A	GGTVVYFDY
293VH-A	EVQLVESGGGLVQPGGSLRLSCAASGFTFSGYGIHWVRQAPGKGLEWIGWI SPSGGDTKYAQKFQGRVTISRDNSKNTLYLQINSLRAEDTAVYYCARGGTV VYFDYWGQGTLVTVSS
5HCDR1-B	TYAIN
294HCDR2-B	RIRSKYNNYATYYAESVKG
295HCDR3-B	HGNFGTSYVSWFAY
296LCDR1-B	GSSTGAVITSNYPN
297LCDR2-B	GINKRAP
298LCDR3-B	ALWYSNLWV
299SCFV-B	QAVVTQEPSLIVSPGGTVILTCGSSTGAVTTSNYPNWVQQKPGQAPRGLIG GINKRAPGVPARFSGSLLGGKAALTLSGAQPEDEAEYYCALWYSNLWVEGG GTKLTVLGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAA SGFTENTYAINWVRQAPGKGLEWVGRIRSKYNNYATYYAESVKGRFTISRD DSKNILYLQINSLRAEDTAVYYCVRHGNEGTSYVSWFAYWGQGELVTVSS

SEQ ID NO:	IgG ID	Masking + cleavage peptide sequences:
301	TY26149	EVGSYAATYSDCYSDPYACH**DG**GGPLGLAGSGGS
302	TY28338	EAATYSDCYSDPYACHDSGGGPLGLAGSGGS
303	TY28339	EYSDCYSDPYACHDSGGGPLGLAGSGGS
304	TY26152	EVGSYAAFSPACYTDPYSCHAGGGPLGLAGSGGS

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SEQ ID NO:	IgG ID	Masking + cleavage peptide sequences:
305	TY28341	EAAFSPACYTDPYSCHAGGGPLGLAGSGGS
306	TY28342	ESPACYTDPYSCHAGGGPLGLAGSGGS

TY24865 Variants		
SEQ ID NO:	Description	Sequence
		TY28652
5	HCDR1	TGGVGVS
96	HCDR2	SIYHSGSTYYNPSLKS
307	UICDR3	YEYDYYAFDY
76	LCDR1	RASQSVDFYGKSFLH
308	LCDR2	AASSLES
46	LCDR3	QQSYRSPPT
362	VH	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVSWIRQAPGK GLEWIGSIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSERAE DTAVYYCARYEYDYYAFDYWGQGTLVTVSS
363		DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGKSFLHWYQQKPG KAPKLLIYAASSLESGVPSRESGSGSGIDETLTISSLQPEDFATY YCQQSYRSPPTEGQGTKVEIK
		TY28653
5	HCDR1	TGGVGVS
96	HCDR2	SIYHSGSTYYNPSLKS
309	HCDR3	YEYGYYALDY
310	LCDR1	RASQSVDFYGISFLH
9	LCDR2	AASSLQS
311	LCDR3	QQSYRTPPT
364	VH	EVQLVESGGGLVQPGGSLRLSCAASGESLSTGGVGVSWIRQAPGK GLEWIGSIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSLRAE DTAVYYCARYEYGYYALDYWGQGTLVTVSS
365	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGISFLHWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQSYRIPPTFGQGTKVEIK
		TY28654
43	HCDR1	TSGVGVS
96	HCDR2	SIYHSGSTYYNPSLKS
312	HCDR3	YEYGYYAFDY
76	LCDR1	RASQSVDFYGKSFLH
9	LCDR2	AASSLQS
28	LCDR3	QQSYRTPLT
366	VH	EVQLVESGGGLVQPGGSLRLSCAASGFSISTSGVGVSWIRQAPGK GLEWIGSIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSLRAE DTAVYYCARYEYGYYAFDYWGQGTLVTVSS
367	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGKSFLHWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQSYRTPLTFGQGTKVEIK
		TY28655
43	HCDR1	TSGVGVS
96	HCDR2	SIYHSGSTYYNPSLKS
307	HCDR3	YEYDYYAFDY

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SEQ ID NO:	Description	Sequence
		TY24865 Variants
310	LCDR1	RASQSVDFYGISFLH
9	LCDR2	AASSLQS
313	LCDR3	QQSYRTPRT
368	VH	EVQLVESGGGLVQPGGSLRLSCAASGESLSTSGVGVSWIRQAPGK GLEWIGSIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQINSLRAE DTAVYYCARYEYDYYAEDYWGQGTLVTVSS
369	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGISFLHWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDETLTISSLQPEDFATY YCQQSYRIPRTFGQGTKVEIK
		TY28656
314	HCDR1	TSGVGVG
315	HCDR2	EIYHSGSTNYNPSLKS
309	HCDR3	YEYGYYALDY
76	LCDR1	RASQSVDFYGKSFLH
9	LCDR2	AASSLQS
313	LCDR3	QQSYRTPRT
370	VH	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTSGVGVGWIRQAPGK GLEWIGEIYHSGSTNYNPSLKSRVTISRDNSKNTLYLQINSLRAE DTAVYYCARYEYGYYALDYWGQGTLVTVSS
371	VL	DIQLTQSPSSLSASVGDRVTIT- CRASQSVDFYGKSFLHWYQQKPG. KAPKLLIYAASSLQSGVPSRESGSGSGTDETLTISSLQPEDFATY YCQQSYRTPRTFGQGTKVEIK
		TY28657
33	HCDR1	TGGVGVG
316	HCDR2	EIYHSGSTYYNPSLKS
312	HCDR3	YEYGYYAFDY
8	LCDR1	RASQSVDFHGISFLH
308	LCDR2	AASSLES
313	LCDR3	QQSYRIPRT
372	VH	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVGWIRQAPGK GLEWIGEIYUSGSTYYNPSLKSRVTISRDNSKNILYLQINSLRAE DTAVYYCARYEYGYYAFDYWGQGTLVTVSS
373	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISFLHWYQQKPG KAPKLLIYAASSLESGVPSRFSGSGSGIDETLTISSLQPEDFATY YCQQSYRTPRIFGQGTKVEIK
		TY28658
314	HCDR1	TSGVGVG
96	HICDR2	SIYHSGSTYYNPSLKS
317	HCDR3	YEYDYYDEDY
76	LCDR1	RASQSVDFYGKSFLH
308	LCDR2	AASSLES

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SEQ ID NO:	Description	Sequence
		TY24865 Variants
318	LCDR3	QQSYRSPLT
374	VH	EVQLVESGGGLVQPGGSLRLSCAASGESLSTSGVGVGWIRQAPGK GLEWIGSIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSLRAE DTAVYYCARYEYDYYDEDYWGQGTLVTVSS
375	VI	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGKSELHWYQQKPG KAPKLLIYAASSLESGVPSRFSGSGSGTDETLTISSLQPEDFATY YCQQSYRSPLTFGQGTKVEIK
		TY28659
43	HCDR1	TSGVGVS
316	HCDR2	EIYHSGSTYYNPSLKS
312	HCDR3	YEYGYYAFDY
8	LCDR1	RASQSVDFHGISFELH
9	LCDR2	AASSLQS
10	LCDR3	QQSYRSPRT
376	VH	EVQLVESGGGLVQPGGSLRLSCAASGESLSTSGVGVSWIRQAPGK GLEWIGEIYHSGSTYYNPSLKSRVTISRDNSKNILYLQLNSIRAE DTAVYYCARYEYGYYAFDYWGQGTLVTVSS
12	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDEHGISFLHWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDETLTISSLQPEDFATY YCQQSYRSPRIFGQGTKVEIK
		TY28660
43	HCDR1	TSGVGVS
6	HCDR2	EIYHSGSTYYSPSLKS
319	HCDR3	YEYYSYAFDY
320	LCDR1	RASQSVDEHGKSFLH
9	LCDR2	AASSLQS
10	LCDR3	QQSYRSPRT
377	VH	EVQLVESGGGLVQPGGSLRLSCAASGESLSTSGVGVSWIRQAPGK GLEWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAE DTAVYYCARYEYYSYAFDYWGQGTLVTVSS
378	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGKSFLHWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDETLTISSLQPEDFATY YCQQSYRSPRTEGQGTKVEIK
		TY28661
5	HCDR1	TGGVGVS
67	HCDR2	SIYHSGSTYYSPSLKS
307	HCDR3	YEYDYYAFDY
310	LCDR1	RASQSVDFYGISFLH
308	LCDR2	AASSLES
28	LGDR3	QQSYRIPLT
379	VH	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVSWIRQAPGK GLEWIGSIYHSGSTYYSPSLKSRVTISRDNSKNILYLQINSLRAE DTAVYYCARYEYDYYAFDYWGQGTLVTVSS

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SEQ ID NO:	Description	Sequence
		TY24865 Variants
380	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGISFLHWYQQKPG KAPKLLIYAASSLESGVPSRFSGSGSGIDETLTISSLQPEDFATY YCQQSYRTPLTFGQGTKVEIK
		TY30120
43	HCDR1	TSGVGVS
6	HCDR2	EIYHSGSTYYSPSLKS
321	HCDR3	YGYYYYDEDY
8	LCDR1	RASQSVDEHGISFLH
9	LCDR2	AASSLQS
10	LCDR3	QQSYRSPRT
381	VH	EVQLVESGGGLVQPGGSLRLSCAASGESLSTSGVGVSWIRQAPGK GLEWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAE DTAVYYCARYGYYYYDEDYWGQGTLVTVSS
12	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDEHGISFLHWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGIDFTLTISSLQPEDFATY YCQQSYRSPRTFGQGTKVEIK
		TY30121
314	HCDR1	TSGVGVG
316	HCDR2	EIYHSGSTYYNPSLKS
322	HCDR3	YKYDYYDEDY
8	LCDR1	RASQSVDFHGISELH
9	LCDR2	AASSLQS
10	LCDR3	QQSYRSPRT
382	VH	EVQLVESGGGLVQPGGSLRLSCAASGESLSTSGVGVGWIRQAPGK GLEWIGEIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSIRAE DTAVYYCARYKYDYYDEDYWGQGTLVTVSS
12	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDEHGISFLHWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGIDETLTISSLQPEDFATY YCQQSYRSPRIFGQGTKVEIK
		TY30123
33	HCDR1	TGGVGVG
6	HCDR2	EIYHSGSTYYSPSLKS
321	HCDR3	YGYYYYDEDY
8	LCDR1	RASQSVDERGISFLH
9	LCDR2	AASSLQS
10	LCDR3	QQSYRSPRT
383	VH	EVQLVESGGGLVQPGGSLRLSCAASGESLSIGGVGVGWIRQAPGK GLEWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAE DTAVYYCARYGYYYYDEDYWGQGTLVTVSS
12	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISFLHWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDETLTISSLQPEDFATY YCQQSYRSPRIEGQGTKVEIK

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TY24865 Variants		
SEQ ID NO:	Description	Sequence
		TY30406
5	HCDR1	TGGVGVS
6	HCDR2	EIYHSGSTYYSPSLKS
317	HCDR3	YEYDYYDEDY
8	LCDR1	RASQSVDFHGISFLH
9	LCDR2	AASSLQS
10	LCDR3	QQSYRSPRT
384	VH	EVQLVESGGGLVQPGGSLRISCAASGFSLSIGGVGVSWIRQAPGK GLEWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQINSLRAE DTAVYYCARYEYDYYDEDYWGQGTLVTVSS
12	VI	DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISELHWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQSYRSPRIFGQGTKVEIK
		TY30410
5	HCDR1	TGGVGVS
6	HCDR2	EIYHSGSTYYSPSLKS
323	HCDR3	YEYYEYDEDY
8	LCDR1	RASQSVDFHGISFLH
9	LCDR2	AASSLQS
10	LCDR3	QQSYRSPRT
385	VH	EVQLVESGGGLVQPGGSLRLSCAASGESLSTGGVGVSWIRQAPGK GLEWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAE DIAVYYCARYEYYEYDEDYWGQGTLVTVSS
12	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDEHGISFLHWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQSYRSPRTEGQGTKVEIK
		TY30413
5	HCDR1	TGGVGVS
6	HCDR2	EIYHSGSTYYSPSLKS
324	HCDR3	YEYYHYDEDY
8	LCDR1	RASQSVDFHGISFLH
9	LCDR2	AASSLQS
10	LCDR3	QQSYRSPRT
386	VH	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVSWIRQAPGK GLEWIGEIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAE DTAVYYCARYEYYHYDEDYWGQGTLVTVSS
12	VL	DIQLTQSPSSLSASVGDRVTITCRASQSVDFHGISFLHWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQSYRSPRTFGQGTKVEIK

SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
325	LC	DIQLTQSPSSLSASVGDRVTITCRASQSIPSFLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGSGIDFTLTISSLQPEDFATYYCQHYISWPRQFTEGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVIKSENRGEC*
326	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGYSISSGYYWGWIRQAPGKGLEWIGI IYPSGGGINYAQKFQGRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARGGG LGFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFRE PVTVSWNSGALTSGVHTFPAVLQSSGLYSISSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKINWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRK KLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDQDGSEFLY SKLTVDKSRWQQGNVESCSVMHEALHNHYTQKSLSLSPGK*
327	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVSWIRQAPGKGLEWIG EIYHSGSTYYSPSLKSRVJISRDNSKNTLYLQLNSLRAEDTAVYYCARYEY YYYDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDEHGISELHWYQQKPGKAPKLLIYAASSLQSGVPS RESGSGSGTDFTLQISSLQPEDFATYYCQQSYRSPRTFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKQKPREEQYASTYRVVSVLTVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGF YPSDIAVEWESNGQPENCYKTTPPVLDSDGSEFLYSKLEVDKSRWQQGNVT SCSVMHEALHNHYQQDSLSLSPGK*
		TY30406
325	LC	DIQLTQSPSSLSASVGDRVTITCRASQSIPSELNWYQQKPGKAPKLLIYAA SSLQSGVPSRESGSGSGTDETLT-SSLQPEDEATYYCQHYISWPRQFTEGQ GIKVEIKRTVAAPSVFIEPPSDEQLKSGTASVVCLINNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSSTLELSKADYEKHKVYACEVTHQGLS SPVTKSENRGEC*
326	HC_A	EVQLVESGGGLVQPGGSURLSCAASGYSISSGYYWGWIRQAPGKGLEWIGI IYPSGGGTNYAQKFQGRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARGGG LGFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGQLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCEKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRK KLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALIINHYTQKSLSLSPGK*
328	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVSWIRQAPGKGLEWIG EIYHSGSTYYSPSLKSRVJISRDNSKNILYLQLNSLRAEDTAVYYCARYEY DYYDFDYWGQGTLVIVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDEHGISELHWYQQKPGKAPKLLIYAASSLQSGVPS RESGSGSGIDFTLCISSLQPEDFATYYCQQSYRSPRTFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKIKPREEQYASTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYQDPPSRDELTKNQVSLTCLVDGF YPSDIAVEWESNGQPENCYKTTPPVLDSDGSEFLYSKLEVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY30410
325	LC	DIQLTQSPSSLSASVGDRVTITCRASQS-PSELNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGSGTDETLTISSLQPEDFATYYCQHYISWPRQFTEGQ GTKVEIKRTVAAPSVFIEPPSDEQLKSGTASVVCLINNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSSTLQLSKADYEKHKVYACEVTHQGLS SPVTKSENRGEC*
326	HC_A	EVQLVESGGGLVQPGGSLRISCAASGYSISSGYYWGWIRQAPGKGLEWIGI IYPSGGGTNYAQKFQGRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARGGG LGEDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGQLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRK KLTKNQVKLTCLVKGEYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*

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SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
329	HC_B	EVQLVESGGGLVQPGGSIRLSCAASGESLSIGGVGVSWIRQAPGKGLEWIG EIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYEY YEYDEDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDEHGISFLHWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRSPRTFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLEPPKPKDTIMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKIKPREEQYASTYRVVSVLIVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLICLVDGE YPSDIAVEWESNGQPENCYKTTPPVLDSDGSFFLYSKLTVEKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY30413
325	LC	DIQLTQSPSSLSASVGDRVTITCRASQSIPSFLNWYQQKPGKAPKLLIYAA SSLQSGVPSRESGSGSGTDFTLTISSLQPEDFATYYCQHYISWPRQFTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVIKSENRGEC*
326	HC_A	EVQLVESGGGLVQPGGSIRLSCAASGYSISSGYYWGWIRQAPGKGLEWIGI IYPSGGGINYAQKTQGRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARGGG LGFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRK KLIKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
330	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVSWIRQAPGKGLEWIG EIYHSGSTYYSPSLKSRVTISRQNSKNTLYLQLNSERAEDTAVYYCARYEY YHYDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDFHGISFLHWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTITISSLQPEDFATYYCQQSYRSPRIEGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTIMISRIPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLIVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLICLVDGF YPSDIAVEWESNGQPENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVE SCSVMHEALUNHYTQDSLSLSPGK*
		HER2xCD28 Bispecific Antibodies (VL-VH) TY27566 (WT)
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRFSGSGSGTDETLTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRTVAAPSVEIFPPSDEQLKSGIASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLILSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYFDYWGQGILVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
333	HC_B	DIQLTQSPSSLSASVGDRVTITCRASQSVDERGISFLHWYQQKPGKAPKLL IYAASSLQSGVPSRESGSGSGIDFILTISSLQPEDFATYYCQQSYRSPRTE GQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGESLSIGGVGVSWIRQAPGKGLEWIGEIYHSGSTYYSPSLKSRVTISR DNSKNTLYLQLNSLRAEDTAVYYCARYEYYYYDFDYWGQGTLVTVSSEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYIDPPSRDELTKNQVSLICLVDGF YPSDIAVEWESNGQPENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*

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SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
		TY28652
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRFSGSGSGTDFILTISSLQPEDFATYYCQQYYIYPYTEGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGFIFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNIGP SFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVVIVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHICPPCPAPELLGGPSVELFPPKPKDTIMI SRTPEVTCVVVDVSHEDPEVKENNYVDGVEVHNAKTKPREEQYASTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLIKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDCDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
334	HC_B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGKSFLHWYQQKPGKAPKLL IYAASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRSPPTE GQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSLSTGGVGVSWIRQAPGKGLEWIGSIYHSGSTYYNPSLKSRVTISR DNSKNTLYLQLNSLRAEDTAVYYCARYEYDYYAFDYWGQGTLVTVSSEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLICLVDGF YPSDIAVEWESNGQPENCYKTIPPVLDSDGSEFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQDSLSLSPGK*
		TY28653
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYTYPYTFGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSFNRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYEP EPVTVSWNSGALTSGVHTTPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKIKPREEQYASTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
335	HC_B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGISELAWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRIPPTF GQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSLSTGGVGVSWIRQAPGKGLEWIGSIYHSGSTYYNPSLKSRVTISR DNSKNTLYLQLNSLRAEDTAVYYCARYEYGYYALDYWGQGTLVTVSSEPKS SDKTHTCPPCPAPELLGGPSVFLEPPKPKDTLMISRIPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSVLIVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELIKNQVSLTCLVDGF YPSDIAVEWESNGQPENCYKTIPPVLDSDGSFFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY28654
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRFSGSGSGTDFILTISSLQPEDFATYYCQQYYTYPYTFGQGT KVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNIGP SFYEDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGIAALGCLVKDYFP EPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTLMI SRTPEVICVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTIPPSR

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SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
		KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDCDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
336	HC_B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGKSFLHWYQQKPGKAPKLL IYAASSLQSGVESRESGSGSGIDFTLTISSLQPEDEATYYCQQSYRTPITE GQGTKVEIKGGGSGGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSLSTSGVGVSWIRQAPGKGLEWIGSIYHSGSTYYNPSLKSRVTISR DNSKNTLYLQLNSLRAEDTAVYYCARYEYGYYAFDYWGQGTLVTVSSEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTIMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSVLIVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYIDPPSRDELTKNQVSLTCLVDGE YPSDIAVEWESNGQPENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQDSLSLSPGK*
		TY28655
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRESGSGSGTDFTLTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRIVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVIHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYFDYWGQGTLVTVSSASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHIFPAVLQSSGLYSLSSVVTVPSSSLGIQTYICNV NHKPSNIKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVICVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSEFL YSKLTVDKSRWQQGNVESCSVMHEALHNHYTQKSLSLSPGK*
337	HC_B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGISELHWYQQKPGKAPKIL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRTPRTE GQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSLSTSGVGVSWIRQAPGKGLEWIGSIYHSGSTYYNPSLKSRVTISR DNSKNTLYLQLNSLRAEDTAVYYCARYEYDYYAFDYWGQGTLVTVSSEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGF YPSDIAVEWESNGQPENCYKITPPVLDSDGSFFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY28656
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRESGSGSGIDFTLTISSLQPEDFATYYCQQYYTYPYTFGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLILSKADYEKHKVYACEVTHQGLSSP VTKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGETFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRETLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYEDYWGQGTLVTVSSASTKGPSVIPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVIVESSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELEPPKPKDTLMI SRIPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKIKPREEQYASTYRVVS VLIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLTCLVKGEYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFEL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
338	HC_B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGKSFLHWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRTPRTF GQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGESLSTSGVGVGWIRQAPGKGLEWIGEIYHSGSTNYNPSLKSRVTISR DNSKNTLYLQLNSLRAEDTAVYYCARYEYGYYALDYWGQGTLVTVSSEPKS SDKTHTCPPCPAPELLGGPSVFLEPPKPKDTLMISRIPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKIKPREEQYASTYRVVSVLIVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELIKNQVSLTCLVDGF YPSDIAVEWESNGQPENCYKTTPPVLDSDGSTELYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*

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SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
		TY28657
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRFSGSGSGIDFTLTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSISSTLILSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSERLSCAASGETFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRETLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYEDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALISGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHICPPCPAPELLGGPSVFLFPPKPKDTLMI SRIPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKIKPREEQYASTYRVVS VLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTIPPSR KKLIKNQVKLTCLVKGEYPSDIAVEWESNGQPENNYKITPPVLDCDGSFEL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
339	HC_B	DIQLTQSPSSLSASVGDRVTITCRASQSVDEHGISFLHWYQQKPGKAPKLL IYAASSLESGVPSRFSGSGSGIDFTLTISSLQPEDFATYYCQQSYRTPRTF GQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSLSTGGVGVGWIRQAPGKGLEWIGEIYHSGSTYYNPSLKSRVTISR DNSKNTLYLQLNSLRAEDTAVYYCARYEYGYYAFDYWGQGTLVTVSSEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTIMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLIVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGE YPSDIAVEWESNGQPENCYKTIPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQDSLSLSPGK*
		TY28658
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRESGSGSGTDFTLTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRIVAAPSVFIFPPSDEQLKSGIASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGSSLRISCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLPPPKPKDTLMI SRIPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKIKPREEQYASTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFL YSKLIVDKSRWQQGNVESCSVMHEALHNHYTQKSLSLSPGK*
340	HC_B	DIQLIQSPSSLSASVGDRVTITCRASQSVDFYGKSFLHWYQQKPGKAPKLL IYAASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRSPLTF GQGIKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSLSTSGVGVGWIRQAPGKGLEWIGSIYHSGSTYYNPSLKSRVTISR DNSKNTLYLQINSLRAEDTAVYYCARYEYDYYDFDYWGQGTLVTVSSEPKS SDKTHTCPPCPAPELLGGPSVELFPPKPKDILMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELIKNQVSLTCLVDGE
		TY28659
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRESGSGSGTDETLIISSLQPEDFATYYCQQYYIYPYTEGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSISSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGETETDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNIGP SFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NIKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKIKPREEQYASTYRVVS

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SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
		VLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTIPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDCDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
341	HC_B	DIQLIQSPSSLSASVGDRVTITCRASQSVDFHGISFLHWYQQKPGKAPKLL IYAASSLQSGVPSRESGSGSGTDFILTISSLQPEDFATYYCQQSYRSPRTF GQGIKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSLSTSGVGVSWIRQAPGKGLEWIGEIYHSGSTYYNPSLKSRVTISR DNSKNTLYLQLNSLRAEDTAVYYCARYEYGYYAFDYWGQGTLVTVSSEPKS SDKTHTCPPCPAPELLGGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELIKNQVSITCLVDGF YPSDIAVEWESNGQPENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY28660
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYGARNLGP SFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTTPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLEPPKPKDILMI SRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKIKPREEQYASTYRVVS VLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLIKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFEL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSESLSPGK*
342	HC_B	DIQLTQSPSSLSASVGDRVTITCRASQSVDEHGKSFLHWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRSPRTF GQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSISTSGVGVSWIRQAPGKGLEWIGEIYHSGSTYYSPSLKSRVTISR DNSKNTLYLQINSLRAEDTAVYYCARYEYYSYAFDYWGQGTLVTVSSEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGE YPSDIAVEWESNGQPENCYKTTPPVLDSDGSIFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQDSLSLSPGK*
		TY28661
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRESGSGSGTDETLTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGETETDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNIGP SFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTTPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREBQYASTYRVVS VLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTIPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDCDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
343	HC. B	DIQLTQSPSSLSASVGDRVTITCRASQSVDFYGISFLHWYQQKPGKAPKLL IYAASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRTPLTF GQGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSC AASGFSLSTGGVGVSWIRQAPGKGLEWIGSIYHSGSTYYSPSLKSRVTISR DNSKNTLYLQLNSLRAEDTAVYYCARYEYDYYAFDYWGQGTLVTVSSEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTIMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLIVLHQDNINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLICLVDGE YPSDIAVEWESNGQPENCYKITPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQDSLSLSPGK*

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SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
		HER2XCD28 Bispecific Antibodies (VH-VL) TY29109 (WT)
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRFSGSGSGTDETLTISSLQPEDEATYYCQQYYTYPYTEGQGT KVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTISKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYEP EPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLEPPKPKDTIMI SRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKIKPREEQYASTYRVVS VLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSEFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
327	HC_B	EVQLVESGGGLVQPGSSLRLSCAASGFSLSTGGVGVSWIRQAPGKGLEWIG EIYHSGSTYYSPSLKSRVTISRDNSKNILYLQLNSLRAEDTAVYYCARYEY YYYDEDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDFHGISELHWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFILTISSLQPEDFATYYCQQSYRSPRTFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKIKPREEQYASTYRVVSVLTVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELIKNQVSLTCLVDGF YPSDIAVEWESNGQPENCYKTIPPVLDSDGSFFLYSKLIVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY29306
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRESGSGSGIDFTLTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLINNEYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYEDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLEPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYASTYRVVS VLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTIPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
344	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGESLSTGGVGVSWIRQAPGKGLEWIG SIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYEY DYYAFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDEYGKSFLHWYQQKPGKAPKLLIYAASSLESGVPS RFSGSGSGIDFTLTISSLQPEDFATYYCQQSYRSPPTFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKIKPREEQYASTYRVVSVLIVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGF YPSDIAVEWESNGQPENCYKITPPVLDSDGSFFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY29307
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRFSGSGSGIDFILTISSLQPEDFATYYCQQYYIYPYTFGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGSSLRISCAASGFIFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYEDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTTPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKIKPREEQYASTYRVVS

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SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
		VITVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDCDGSFEL YSKLTVDKSRWQQGNVESCSVMHEALHNHYTQKSLSLSPGK*
345	HC_B	EVQLVESGGGLVQPGGSLRISCAASGFSLSIGGVGVSWIRQAPGKGLEWIG SIYHSGSTYYNPSLKSRVTISRDNSKNILYLQLNSLRAEDTAVYYCARYEY GYYALDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITGRASQSVDFYGISELHWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRTPPTFGQGIKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTIMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKIKPREEQYASTYRVVSVLIVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGF YPSDIAVEWESNGQPENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY29308
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRESGSGSGTDFTLTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLINNEYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLILSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALISGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLEPPKPKDTLMI SRTREVTCVVVDVSHEDPEVKENWYVDGVEVHNAKIKPREEQYASTYRVVS VLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDCDGSFEL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
346	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTSGVGVSWIRQAPGKGLEWIG SIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYEY GYYAFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDFYGKSELHWYQQKPGKAPKLLIYAASSLQSGVPS RESGSGSGIDETLTISSLQPEDFATYYCQQSYRTPLIEGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKIKPREEQYASTYRVVSVLIVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGE YPSDIAVEWESNGQPENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQDSLSLSPGK*
		TY29309
331	LC	DIQMTQSPSSLSASVGDRVTITCKAS@DVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRESGSGSGTDFILTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLILSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSIRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRETLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SEYEDYWGQGILVTVSSASTKGPSVIPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNIKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTIMI SRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVS VLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLIKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDCDGSFFL YSKLTVDKSRWQQGNVESCSVMHEALHNHYTQKSLSLSPGK*
347	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGESLSTSGVGVSWIRQAPGKGLEWIG SIYHSGSTYYNPSLKSRVTISRDNSKNILYLQLNSLRAEDTAVYYCARYEY DYYAFDYWGQGTLVIVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDFYGISELHWYQQKPGKAPKLLIYAASSLQSGVPS RESGSGSGTDFTLTISSLQPEDFATYYCQQSYRTPRIFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLEPPKPKDTIMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLIVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELIKNQVSLTCLVDGE YPSDIAVEWESNGQPENCYKTTPPVLDSDGSEFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*

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SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
		TY29310
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRFSGSGSGIDFILTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC.	AEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYEP EPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRIPEVICVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVS VLIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
348	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGESLSTSGVGVGWIRQAPGKGLEWIG EIYHSGSTNYNPSLKSRVTISRDNSKNTLYLQINSLRAEDTAVYYCARYEY GYYALDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDFYGKSFLHWYQQKPGKAPKLLIYAASSLQSGVPS RESGSGSGTDFTLTISSLQPEDFATYYCQQSYRTPRTFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTIMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELIKNQVSLTCLVDGE YPSDIAVEWESNGQPENCYKTIPPVLDSDGSEFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY29311
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYIGVPSRESGSGSGIDFILTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRIVAAPSVEIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGETFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRETLSVDRSKNTLYLQMNSLRAEDTAVYYCARNIGP STYFDYWGQGTLVIVSSASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHIFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSEFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
349	HC_B	EVQLVESGGGLVQPGGSIRLSCAASGESLSTGGVGVGWIRQAPGKGLEWIG EIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYEY GYYAFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDFHGISFLHWYQQKPGKAPKLLI- YAASSLESGVPS. RESGSGSGTDFTLTISSLQPEDFATYYCQQSYRIPRTFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKIKPREEQYASTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGF YPSDIAVEWESNGQPENCYKTIPPVLDSDGSFFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY29312
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRESGSGSGIDETLTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLUNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC*
332	HC_A	EVQLVESGGGLVQPGGSIRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SEYEDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALISGVHTEPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLEPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVS VLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR

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SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
		KKLTKNQVKLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFL YSKLTVDKSRWQQGNVESCSVMHEALHINHYTQKSLSLSPGK*
350	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTSGVGVGWIRQAPGKGLEWIG SIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYEY DYYDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDFYGKSFLHWYQQKPGKAPKLLIYAASSLESGVPS RESGSGSGTDETLTISSLQPEDFATYYCQQSYRSPLIEGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKIKPREEQYASTYRVVSVLIVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYIDEPSRDELIKNQVSLTCLVDGE YPSDIAVEWESNGQPENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY29313
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRESGSGSGIDFTLTISSLQPEDFATYYCQQYYTYPYTEGQGT KVEIKRTVAAPSVFIEPPSDEQLKSGIASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLILSKADYEKHKVYACEVTHQGLSSP VIKSFNRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGETFTDYTMDWVRQAPGKGLEWVADV NPNSGGSTYNQRFKGRETLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYFDYWGQGTLVTVSSASTKGPSVTPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVIVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVS VLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
351	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGFSISTSGVGVSWIRQAPGKGLEWIG EIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYEY GYYAEDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITGRASQSVDFHGISFLHWYQQKPGKAPKLLIYAASSLQSGVPS RESGSGSGIDETLTISSLQPEDFATYYCQQSYRSPRIEGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKIKPREEQYASTYRVVSVLIVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGE YPSDIAVEWESNGQPENCYKTIPPVLDSDGSFFLYSKLTVEKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY29314
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRFSGSGSGIDETLTISSLQPEDFATYYCQQYYTYPYTFGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSISSTLILSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGFTETDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRETLSVDRSKNILYLQMNSLRAEDTAVYYCARNLGP SFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTYPAVLQSSGLYSLSSVVTVPSSSLGIQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKENNYVDGVEVHNAKIKPREEQYASTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTIPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDCDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
352	HC_B	EVQLVESGGGEVQPGGSLRISCAASGFSLSTSGVGVSWIRQAPGKGLEWIG ETYHSGSTYYSPSLKSRVTISRDNSKNILYLQLNSLRAEDTAVYYCARYEY YSYAFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDEHGKSELHWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRSPRTFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKINWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGE YPSDIAVEWESNGQPENCYKTTPPVLDSDGSEFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQDSLSLSPGK*

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SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
		TY29315
331	LC	DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIYSA SYRYTGVPSRESGSGSGTDETLTISSLQPEDFATYYCQQYYIYPYTEGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
332	HC_A	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADV NPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGP SFYEDYWGQGILVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTTPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLEPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR KKLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDCDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
353	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGESLSTGGVGVSWIRQAPGKGLEWIS SIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQINSLRAEDTAVYYCARYEY DYYAFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITGRASQSVDFYGISFLHWYQQKPGKAPKLLIYAASSLESGVPS RESGSGSGTDETLTISSLQPEDFATYYCQQSYRTPLTFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKIKPREEQYASTYRVVSVLTVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYIDPPSRDELTKNQVSLTCLVDGE YPSDIAVEWESNGQPENCYKITPPVLDSDGSFFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		B7H3XCD28 Bispecific Antibodies (VH-VL) TY29021 (WT)
354	LC	DIQLTQSPSSLSASVGDRVTITCRASQSIRKYLNWYQQKPGKAPKLLIYAA STLQSGVPSRESGSGSGIDETLTISSLQPEDFATYFCSQGTHVPFTFGQGT KVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
355	HC_A	EVQLVESGGGLVQPGGSLRISCAASGFTESGYGIHWVRQAPGKGLEWIGWI SPSGGDTKYAQKFQGRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARGGTV VYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALISGVHTEPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSV ITVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRK KLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
327	HC_B	EVQLVESGGGLVQPGGSIRLSCAASGESLSIGGVGVSWIRQAPGKGLEWIG EIYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYEY YYYDEDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDFHGISELHWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRSPRIFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLEPPKPKDTIMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKIKPREEQYASTYRVVSVLIVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLICLVDGF YPSDIAVEWESNGQPENCYKTTPPVLDSDGSFFLYSKLTVEKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*
		TY30120
354	LC	DIQLTQSPSSLSASVGDRVTITCRASQSIRKYLNWYQQKPGKAPKLLIYAA STLQSGVPSRESGSGSGTDFTLTISSLQPEDFATYFCSQGTHVPFTFGQGT KVEIKRIVAAPSVEIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
355	HC_A	EVQLVESGGGLVQPGGSIRLSCAASGFTESGYGIHWVRQAPGKGLEWIGWI SPSGGDTKYAQKTQGRVTISRDNSKNTLYLQINSLRAEDTAVYYCARGGTV VYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTIMIS

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SEQ ID NO:		PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
		RTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSV LIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRK KLIKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDCDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
356	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTSGVGVSWIRQAPGKGLEWIG ETYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSERAEDTAVYYCARYGY YYYDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDFHGISFLHWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRSPRIEGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTIMISRIPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSVLIVLHQDWINGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLICLVDGE YPSDIAVEWESNGQPENCYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVE SCSVMHEALUNHYTQDSLSLSPGK*
		TY30121
354	LC	DIQLTQSPSSLSASVGDRVTITCRASQSIRKYLNWYQQKPGKAPKLLIYAA STLQSGVPSRESGSGSGTDFTLTISSLQPEDFATYFCSQGTHVPFTFGQGT KVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLINNEYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VIKSENRGEC*
355	HC	EVQLVESGGGLVQPGGSLRLSCAASGFTESGYGIHWVRQAPGKGLEWIGWI SPSGGDTKYAQKFQGRVTISRDNSKNTLYLQINSLRAEDTAVYYCARGGTV VYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFRE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLEPPKPKDTLMIS RIPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRK KLTKNQVKLTCLVKGEYPSDIAVEWESNGQPENNYKTIPPVLDCDGSEFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*
357	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTSGVGVGWIRQAPGKGLEWIG EIYHSGSTYYNPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYKY DYYDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITGRASQSVDFHGISFLHWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDETLTISSLQPEDFATYYCQQSYRSPRTFGQGTKVEIKEPKS SDKTHTCPPCPAPELLGGPSVELFPPKPKDTIMISRTPEVTCVVVDVSHED PEVKENWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGF YPSDIAVEWESNGQPENCYKTTPPVEDSDGSEFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQDSLSLSPGK*
		TY30123
354	LC	DIQLTQSPSSLSASVGDRVTITCRASQSIRKYLNWYQQKPGKAPKLLIYAA STLQSGVPSRFSGSGSGTDFLTISSLQPEDEATYFCSQGTHIVPFTFGQGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLILSKADYEKHKVYACEVTHQGLSSP VTKSENRGEC*
355	HC_A	EVQLVESGGGLVQPGGSLRISCAASGFTFSGYGIHWVRQAPGKGLEWIGWI SPSGGDIKYAQKFQGRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARGGTV VYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELEPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRK KLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDCDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHINHYTQKSLSLSPGK*
358	HC_B	EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVGWIRQAPGKGLEWIG ETYHSGSTYYSPSLKSRVTISRDNSKNTLYLQLNSLRAEDTAVYYCARYGY YYYDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSVDFHGISELHWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFILTISSLQPEDFATYYCQQSYRSPRTFGQGIKVEIKEPKS SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

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SEQ ID NO:	PD-L1xCD28 Bispecific Antibodies (VH-VL) TY29815 (WT)
	PEVKFNWYVDGVEVHNAKIKPREEQYASTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTDPPSRDELTKNQVSLTCLVDGF YPSDIAVEWESNGQPENCYKTTPPVLDSDGSEFLYSKLTVDKSRWQQGNVE SCSVMHEALHNHYTQDSLSLSPGK*

SEQUENCE LISTING

```
Sequence total quantity: 361
SEQ ID NO: 1            moltype = AA  length = 220
FEATURE                 Location/Qualifiers
REGION                  1..220
                        note = misc_feature - Human CD28
source                  1..220
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1
MLRLLLALNL FPSIQVTGNK ILVKQSPMLV AYDNAVNLSC KYSYNLFSRE FRASLHKGLD  60
SAVEVCVVYG NYSQQLQVYS KTGFNCDGKL GNESVTFYLQ NLYVNQTDIY FCKIEVMYPP  120
PYLDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR  180
SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS                        220

SEQ ID NO: 2            moltype = AA  length = 220
FEATURE                 Location/Qualifiers
REGION                  1..220
                        note = misc_feature - Macaca mulatta CD28
source                  1..220
                        mol_type = protein
                        organism = Macaca mulatta
SEQUENCE: 2
MLRLLLALNL LPSIQVTGNK ILVKQSPMLV AYDNAVNLSC KYSYNLFSRE FRASLHKGLD  60
SAVEVCVVYG NYSQQLQVYS KTGFNCDGKL GNESVTFYLQ NLYVNQTDIY FCKIEVMYPP  120
PYLDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWALVVVG GVLACYSLLV TVAFCIFWMR  180
SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS                        220

SEQ ID NO: 3            moltype = AA  length = 220
FEATURE                 Location/Qualifiers
REGION                  1..220
                        note = misc_feature - Macaca fascicularis CD28
source                  1..220
                        mol_type = protein
                        organism = Macaca fascicularis
SEQUENCE: 3
MLRLLLALNL LPSIQVTGNK ILVKQSPMLV AYDNAVNLSC KYSYNLFSRE FRASLHKGLD  60
SAVEVCVVYG NYSQQLQVYS KTGFNCDGKL GNESVTFYLQ NLYVNQTDIY FCKIEVMYPP  120
PYLDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWALVVVG GVLACYSLLV TVAFCIFWMR  180
SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS                        220

SEQ ID NO: 4            moltype = AA  length = 218
FEATURE                 Location/Qualifiers
REGION                  1..218
                        note = misc_feature - Mouse CD28
source                  1..218
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 4
MTLRLLFLAL NFFSVQVTEN KILVKQSPLL VVDSNEVSLS CRYSYNLLAK EFRASLYKGV  60
NSDVEVCVGN GNFTYQPQFR SNAEFNCDGD FDNETVTFRL WNLHVNHTDI YFCKIEFMYP  120
PPYLDNERSN GTIIHIKEKH LCHTQSSPKL FWALVVVAGV LFCYGLLVTV ALCVIWTNSR  180
RNRLLQSDYM NMTPRRPGLT RKPYQPYAPA RDFAAYRP                          218

SEQ ID NO: 5            moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: HCDR1/HCDR1-B
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 5
TGGVGVS                                                            7
```

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```
SEQ ID NO: 6            moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: HCDR2/HCDR2-B
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 6
EIYHSGSTYY SPSLKS                                                   16

SEQ ID NO: 7            moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3/HCDR3-B
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 7
YEYYYYDFDY                                                          10

SEQ ID NO: 8            moltype = AA  length = 15
FEATURE                 Location/Qualifiers
REGION                  1..15
                        note = Synthetic: LCDR1/LCDR1-B
source                  1..15
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 8
RASQSVDFHG ISFLH                                                    15

SEQ ID NO: 9            moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: LCDR2 / LCDR2-B
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 9
AASSLQS                                                             7

SEQ ID NO: 10           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3 / LCDR3-B
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 10
QQSYRSPRT                                                           9

SEQ ID NO: 11           moltype = AA  length = 120
FEATURE                 Location/Qualifiers
REGION                  1..120
                        note = Synthetic: VH
source                  1..120
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 11
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVSWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYYYYDFDYW GQGTLVTVSS  120

SEQ ID NO: 12           moltype = AA  length = 111
FEATURE                 Location/Qualifiers
REGION                  1..111
                        note = Synthetic: VL
source                  1..111
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 12
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR TFGQGTKVEI K          111

SEQ ID NO: 13           moltype = AA  length = 447
FEATURE                 Location/Qualifiers
REGION                  1..447
```

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```
                        note = Synthetic: HC
source                  1..447
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 13
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVSWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYYYYDFDYW GQGTLVTVSS  120
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  180
GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG  420
NVFSCSVMHE ALHNHYTQKS LSLSLGK                                      447

SEQ ID NO: 14           moltype = AA  length = 218
FEATURE                 Location/Qualifiers
REGION                  1..218
                        note = Synthetic: LC
source                  1..218
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 14
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR TFGQGTKVEI KRTVAAPSVF  120
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS  180
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC                          218

SEQ ID NO: 15           moltype = AA  length = 6
FEATURE                 Location/Qualifiers
REGION                  1..6
                        note = Synthetic: HCDR1
source                  1..6
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 15
SGHHWS                                                             6

SEQ ID NO: 16           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: HCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 16
KDDYYAFDY                                                          9

SEQ ID NO: 17           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
REGION                  1..15
                        note = Synthetic: LCDR1
source                  1..15
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 17
RASESVDFYG ISFLH                                                   15

SEQ ID NO: 18           moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: LCDR2 / LCDR2-A
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 18
AASTLQS                                                            7

SEQ ID NO: 19           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 19
QQSYRTPIT                                                          9
```

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```
SEQ ID NO: 20          moltype = AA  length = 118
FEATURE                Location/Qualifiers
REGION                 1..118
                       note = Synthetic: VH
source                 1..118
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 20
EVQLVESGGG LVQPGGSLRL SCAASGYSIT SGHHWSWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARKD DYYAFDYWGQ GTLVTVSS    118

SEQ ID NO: 21          moltype = AA  length = 111
FEATURE                Location/Qualifiers
REGION                 1..111
                       note = Synthetic: VL
source                 1..111
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 21
DIQLTQSPSS LSASVGDRVT ITCRASESVD FYGISFLHWY QQKPGKAPKL LIYAASTLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPI TFGQGTKVEI K           111

SEQ ID NO: 22          moltype = AA  length = 445
FEATURE                Location/Qualifiers
REGION                 1..445
                       note = Synthetic: HC
source                 1..445
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 22
EVQLVESGGG LVQPGGSLRL SCAASGYSIT SGHHWSWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARKD DYYAFDYWGQ GTLVTVSSAS  120
TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL  180
YSLSSVVTVP SSSLGTKTYT CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL  240
FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV  300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP PSQEEMTKNQ  360
VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSRLTV DKSRWQEGNV  420
FSCSVMHEAL HNHYTQKSLS LSLGK                                        445

SEQ ID NO: 23          moltype = AA  length = 218
FEATURE                Location/Qualifiers
REGION                 1..218
                       note = Synthetic: LC
source                 1..218
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 23
DIQLTQSPSS LSASVGDRVT ITCRASESVD FYGISFLHWY QQKPGKAPKL LIYAASTLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPI TFGQGTKVEI KRTVAAPSVF  120
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS  180
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC                          218

SEQ ID NO: 24          moltype = AA  length = 6
FEATURE                Location/Qualifiers
REGION                 1..6
                       note = Synthetic: HCDR1
source                 1..6
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 24
SGYHWG                                                             6

SEQ ID NO: 25          moltype = AA  length = 9
FEATURE                Location/Qualifiers
REGION                 1..9
                       note = Synthetic: HCDR3
source                 1..9
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 25
RRGDGYFDF                                                          9

SEQ ID NO: 26          moltype = AA  length = 15
FEATURE                Location/Qualifiers
REGION                 1..15
```

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```
                        note = Synthetic: LCDR1
source                  1..15
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 26
RASQSVDFLG ISFLH                                                15

SEQ ID NO: 27           moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: LCDR2
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 27
DASNRAT                                                         7

SEQ ID NO: 28           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 28
QQSYRTPLT                                                       9

SEQ ID NO: 29           moltype = AA  length = 118
FEATURE                 Location/Qualifiers
REGION                  1..118
                        note = Synthetic: VH
source                  1..118
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 29
EVQLVESGGG LVQPGGSLRL SCAASGYSIT SGYHWGWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARRR GDGYFDFWGQ GTLVTVSS    118

SEQ ID NO: 30           moltype = AA  length = 111
FEATURE                 Location/Qualifiers
REGION                  1..111
                        note = Synthetic: VL
source                  1..111
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 30
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FLGISFLHWY QQKPGKAPKL LIYDASNRAT  60
GIPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPL TFGQGTKVEI K           111

SEQ ID NO: 31           moltype = AA  length = 445
FEATURE                 Location/Qualifiers
REGION                  1..445
                        note = Synthetic: HC
source                  1..445
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 31
EVQLVESGGG LVQPGGSLRL SCAASGYSIT SGYHWGWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARRR GDGYFDFWGQ GTLVTVSSAS  120
TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL  180
YSLSSVVTVP SSSLGTKTYT CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL  240
FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV  300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP PSQEEMTKNQ  360
VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSRLTV DKSRWQEGNV  420
FSCSVMHEAL HNHYTQKSLS LSLGK                                        445

SEQ ID NO: 32           moltype = AA  length = 218
FEATURE                 Location/Qualifiers
REGION                  1..218
                        note = Synthetic: LC
source                  1..218
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 32
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FLGISFLHWY QQKPGKAPKL LIYDASNRAT  60
GIPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPL TFGQGTKVEI KRTVAAPSVF  120
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```
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS  180
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC                          218

SEQ ID NO: 33          moltype = AA  length = 7
FEATURE                Location/Qualifiers
REGION                 1..7
                       note = Synthetic: HCDR1
source                 1..7
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 33
TGGVGVG                                                            7

SEQ ID NO: 34          moltype = AA  length = 5
FEATURE                Location/Qualifiers
REGION                 1..5
                       note = Synthetic: HCDR1-B
source                 1..5
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 34
TYAIN                                                              5

SEQ ID NO: 35          moltype = AA  length = 10
FEATURE                Location/Qualifiers
REGION                 1..10
                       note = Synthetic: HCDR3
source                 1..10
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 35
YGYSYYALDY                                                         10

SEQ ID NO: 36          moltype = AA  length = 10
FEATURE                Location/Qualifiers
REGION                 1..10
                       note = Synthetic: LCDR1
source                 1..10
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 36
SASSSVGYVQ                                                         10

SEQ ID NO: 37          moltype = AA  length = 7
FEATURE                Location/Qualifiers
REGION                 1..7
                       note = Synthetic: LCDR2
source                 1..7
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 37
DASNLET                                                            7

SEQ ID NO: 38          moltype = AA  length = 9
FEATURE                Location/Qualifiers
REGION                 1..9
                       note = Synthetic: LCDR3
source                 1..9
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 38
QQSYTSPRT                                                          9

SEQ ID NO: 39          moltype = AA  length = 120
FEATURE                Location/Qualifiers
REGION                 1..120
                       note = Synthetic: VH
source                 1..120
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 39
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVGWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY GYSYYALDYW GQGTLVTVSS  120

SEQ ID NO: 40          moltype = AA  length = 106
FEATURE                Location/Qualifiers
```

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```
REGION                  1..106
                        note = Synthetic: VL
source                  1..106
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 40
DIQLTQSPSS LSASVGDRVT ITCSASSSVG YVQWYQQKPG KAPKLLIYDA SNLETGVPSR  60
FSGSGSGTDF TLTISSLQPE DFATYYCQQS YTSPRTFGQG TKVEIK                 106

SEQ ID NO: 41           moltype = AA  length = 447
FEATURE                 Location/Qualifiers
REGION                  1..447
                        note = Synthetic: HC
source                  1..447
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 41
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVGWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY GYSYYALDYW GQGTLVTVSS  120
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  180
GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG  420
NVFSCSVMHE ALHNHYTQKS LSLSLGK                                      447

SEQ ID NO: 42           moltype = AA  length = 213
FEATURE                 Location/Qualifiers
REGION                  1..213
                        note = Synthetic: LC
source                  1..213
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 42
DIQLTQSPSS LSASVGDRVT ITCSASSSVG YVQWYQQKPG KAPKLLIYDA SNLETGVPSR  60
FSGSGSGTDF TLTISSLQPE DFATYYCQQS YTSPRTFGQG TKVEIKRTVA APSVFIFPPS  120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL  180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC                               213

SEQ ID NO: 43           moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: HCDR1
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 43
TSGVGVS                                                            7

SEQ ID NO: 44           moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 44
KGYYYYAFDY                                                         10

SEQ ID NO: 45           moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 45
RASQDIGSFL A                                                       11

SEQ ID NO: 46           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
```

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```
SEQUENCE: 46
QQSYRSPPT                                                          9

SEQ ID NO: 47          moltype = AA  length = 120
FEATURE                Location/Qualifiers
REGION                 1..120
                       note = Synthetic: VH
source                 1..120
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 47
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVSWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARK GYYYYAFDYW GPGTLVTVSS  120

SEQ ID NO: 48          moltype = AA  length = 107
FEATURE                Location/Qualifiers
REGION                 1..107
                       note = Synthetic: VL
source                 1..107
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 48
DIQLTQSPSS LSASVGDRVT ITCRASQDIG SFLAWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYRSPPTFGQ GTKVEIK                107

SEQ ID NO: 49          moltype = AA  length = 447
FEATURE                Location/Qualifiers
REGION                 1..447
                       note = Synthetic: HC
source                 1..447
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 49
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVSWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARK GYYYYAFDYW GPGTLVTVSS  120
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  180
GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG  420
NVFSCSVMHE ALHNHYTQKS LSLSLGK                                      447

SEQ ID NO: 50          moltype = AA  length = 214
FEATURE                Location/Qualifiers
REGION                 1..214
                       note = Synthetic: LC
source                 1..214
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 50
DIQLTQSPSS LSASVGDRVT ITCRASQDIG SFLAWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYRSPPTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 51          moltype = AA  length = 16
FEATURE                Location/Qualifiers
REGION                 1..16
                       note = Synthetic: HCDR2
source                 1..16
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 51
EIYHSGSTYY PPSLKS                                                  16

SEQ ID NO: 52          moltype = AA  length = 10
FEATURE                Location/Qualifiers
REGION                 1..10
                       note = Synthetic: HCDR3
source                 1..10
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 52
YEYSSYGLDY                                                         10

SEQ ID NO: 53          moltype = AA  length = 11
```

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```
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 53
RASQDIRKFL A                                                        11

SEQ ID NO: 54           moltype = AA  length = 120
FEATURE                 Location/Qualifiers
REGION                  1..120
                        note = Synthetic: VH
source                  1..120
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 54
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVGWIR QAPGKGLEWI GEIYHSGSTY  60
YPPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYSSYGLDYW GQGTLVTVSS  120

SEQ ID NO: 55           moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic: VL
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 55
DIQLTQSPSS LSASVGDRVT ITCRASQDIR KFLAWYQQKP GKAPKLLIYD ASSLESGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYRSPRTFGQ GTKVEIK               107

SEQ ID NO: 56           moltype = AA  length = 447
FEATURE                 Location/Qualifiers
REGION                  1..447
                        note = Synthetic: HC
source                  1..447
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 56
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVGWIR QAPGKGLEWI GEIYHSGSTY  60
YPPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYSSYGLDYW GQGTLVTVSS  120
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  180
GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG  420
NVFSCSVMHE ALHNHYTQKS LSLSLGK                                      447

SEQ ID NO: 57           moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 57
DIQLTQSPSS LSASVGDRVT ITCRASQDIR KFLAWYQQKP GKAPKLLIYD ASSLESGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYRSPRTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 58           moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: HCDR2
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 58
AIYHSGSTYY SPSLKS                                                   16

SEQ ID NO: 59           moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
```

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```
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 59
SGLVYYAFDY                                                          10

SEQ ID NO: 60           moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 60
RASQGIGSYL A                                                        11

SEQ ID NO: 61           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 61
QQYSTSPLT                                                           9

SEQ ID NO: 62           moltype = AA  length = 119
FEATURE                 Location/Qualifiers
REGION                  1..119
                        note = Synthetic: VH
source                  1..119
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 62
QVQLVQSGAE VKKPGSSVKV SCKASGYSIS SGYHWGWIRQ APGQGLEWIG AIYHSGSTYY  60
SPSLKSRVTI TADKSTSTAY MELSSLRSED TAVYYCARSG LVYYAFDYWG QGTLVTVSS   119

SEQ ID NO: 63           moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic: VL
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 63
DIQLTQSPSS LSASVGDRVT ITCRASQGIG SYLAWYQQKP GKAPKLLIYD ASSLESGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTSPLTFGQ GTKVEIK               107

SEQ ID NO: 64           moltype = AA  length = 446
FEATURE                 Location/Qualifiers
REGION                  1..446
                        note = Synthetic: HC
source                  1..446
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 64
QVQLVQSGAE VKKPGSSVKV SCKASGYSIS SGYHWGWIRQ APGQGLEWIG AIYHSGSTYY  60
SPSLKSRVTI TADKSTSTAY MELSSLRSED TAVYYCARSG LVYYAFDYWG QGTLVTVSSA  120
STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTKTY TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF  240
LFPPKPKDTL MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR  300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL PPSQEEMTKN  360
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT VDKSRWQEGN  420
VFSCSVMHEA LHNHYTQKSL SLSLGK                                       446

SEQ ID NO: 65           moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 65
DIQLTQSPSS LSASVGDRVT ITCRASQGIG SYLAWYQQKP GKAPKLLIYD ASSLESGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTSPLTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214
```

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```
SEQ ID NO: 66           moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: HCDR1
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 66
SYAIH                                                           5

SEQ ID NO: 67           moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: HCDR2
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 67
SIYHSGSTYY SPSLKS                                               16

SEQ ID NO: 68           moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 68
DVYGSYALDV                                                      10

SEQ ID NO: 69           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
REGION                  1..15
                        note = Synthetic: LCDR1
source                  1..15
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 69
RASQSVDFDG ISFLH                                                15

SEQ ID NO: 70           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 70
QQSYRSPIT                                                       9

SEQ ID NO: 71           moltype = AA  length = 118
FEATURE                 Location/Qualifiers
REGION                  1..118
                        note = Synthetic: VH
source                  1..118
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 71
QVQLVQSGAE VKKPGSSVKV SCKASGFTFS SYAIHWVRQA PGQGLEWIGS IYHSGSTYYS  60
PSLKSRVTIT ADKSTSTAYM ELSSLRSEDT AVYYCARDVY GSYALDVWGQ GTLVTVSS    118

SEQ ID NO: 72           moltype = AA  length = 111
FEATURE                 Location/Qualifiers
REGION                  1..111
                        note = Synthetic: VL
source                  1..111
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 72
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FDGISFLHWY QQKPGKAPKL LIYDASSLES  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPI TFGQGTKVEI K           111

SEQ ID NO: 73           moltype = AA  length = 445
FEATURE                 Location/Qualifiers
REGION                  1..445
```

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```
                        note = Synthetic: HC
source                  1..445
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 73
QVQLVQSGAE VKKPGSSVKV SCKASGFTFS SYAIHWVRQA PGQGLEWIGS IYHSGSTYYS  60
PSLKSRVTIT ADKSTSTAYM ELSSLRSEDT AVYYCARDVY GSYALDVWGQ GTLVTVSSAS  120
TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL  180
YSLSSVVTVP SSSLGTKTYT CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL  240
FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV  300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP PSQEEMTKNQ  360
VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSRLTV DKSRWQEGNV  420
FSCSVMHEAL HNHYTQKSLS LSLGK                                        445

SEQ ID NO: 74           moltype = AA  length = 218
FEATURE                 Location/Qualifiers
REGION                  1..218
                        note = Synthetic: LC
source                  1..218
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 74
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FDGISFLHWY QQKPGKAPKL LIYDASSLES  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPI TFGQGTKVEI KRTVAAPSVF  120
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS  180
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC                          218

SEQ ID NO: 75           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: HCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 75
KDYYYALDY                                                          9

SEQ ID NO: 76           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
REGION                  1..15
                        note = Synthetic: LCDR1
source                  1..15
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 76
RASQSVDFYG KSFLH                                                   15

SEQ ID NO: 77           moltype = AA  length = 118
FEATURE                 Location/Qualifiers
REGION                  1..118
                        note = Synthetic: VH
source                  1..118
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 77
EVQLVESGGG LVQPGGSLRL SCAASGYSIS SGYHWGWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARKD YYYALDYWGQ GTLVTVSS    118

SEQ ID NO: 78           moltype = AA  length = 111
FEATURE                 Location/Qualifiers
REGION                  1..111
                        note = Synthetic: VL
source                  1..111
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 78
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGKSFLHWY QQKPGKAPKL LIYAASTLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPL TFGQGTKVEI K           111

SEQ ID NO: 79           moltype = AA  length = 445
FEATURE                 Location/Qualifiers
REGION                  1..445
                        note = Synthetic: HC
source                  1..445
                        mol_type = protein
                        organism = synthetic construct
```

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```
SEQUENCE: 79
EVQLVESGGG LVQPGGSLRL SCAASGYSIS SGYHWGWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARKD YYYALDYWGQ GTLVTVSSAS  120
TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL  180
YSLSSVVTVP SSSLGTKTYT CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL  240
FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV  300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP PSQEEMTKNQ  360
VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSRLTV DKSRWQEGNV  420
FSCSVMHEAL HNHYTQKSLS LSLGK                                        445

SEQ ID NO: 80          moltype = AA  length = 218
FEATURE                Location/Qualifiers
REGION                 1..218
                       note = Synthetic: LC
source                 1..218
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 80
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGKSFLHWY QQKPGKAPKL LIYAASTLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPL TFGQGTKVEI KRTVAAPSVF  120
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS  180
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC                          218

SEQ ID NO: 81          moltype = AA  length = 10
FEATURE                Location/Qualifiers
REGION                 1..10
                       note = Synthetic: HCDR3
source                 1..10
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 81
GPLSYYAFDY                                                         10

SEQ ID NO: 82          moltype = AA  length = 11
FEATURE                Location/Qualifiers
REGION                 1..11
                       note = Synthetic: LCDR1
source                 1..11
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 82
RASQSVSRYL A                                                       11

SEQ ID NO: 83          moltype = AA  length = 9
FEATURE                Location/Qualifiers
REGION                 1..9
                       note = Synthetic: LCDR3
source                 1..9
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 83
QQYYRSPIT                                                          9

SEQ ID NO: 84          moltype = AA  length = 119
FEATURE                Location/Qualifiers
REGION                 1..119
                       note = Synthetic: VH
source                 1..119
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 84
QVQLVQSGAE VKKPGSSVKV SCKASGYSIT SGYHWGWIRQ APGQGLEWIG AIYHSGSTYY  60
SPSLKSRVTI TADKSTSTAY MELSSLRSED TAVYYCARGP LSYYAFDYWG QGTLVTVSS   119

SEQ ID NO: 85          moltype = AA  length = 107
FEATURE                Location/Qualifiers
REGION                 1..107
                       note = Synthetic: VL
source                 1..107
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 85
DIQLTQSPSS LSASVGDRVT ITCRASQSVS RYLAWYQQKP GKAPKLLIYD ASNRATGIPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYRSPITFGQ GTKVEIK                107

SEQ ID NO: 86          moltype = AA  length = 446
```

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```
FEATURE                 Location/Qualifiers
REGION                  1..446
                        note = Synthetic: HC
source                  1..446
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 86
QVQLVQSGAE VKKPGSSVKV SCKASGYSIT SGYHWGWIRQ APGQGLEWIG AIYHSGSTYY  60
SPSLKSRVTI TADKSTSTAY MELSSLRSED TAVYYCARGP LSYYAFDYWG QGTLVTVSSA  120
STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTKTY TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF  240
LFPPKPKDTL MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR  300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL PPSQEEMTKN  360
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT VDKSRWQEGN  420
VFSCSVMHEA LHNHYTQKSL SLSLGK                                       446

SEQ ID NO: 87           moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 87
DIQLTQSPSS LSASVGDRVT ITCRASQSVS RYLAWYQQKP GKAPKLLIYD ASNRATGIPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYRSPITFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 88           moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: HCDR1
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 88
TGGVAVA                                                            7

SEQ ID NO: 89           moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: HCDR2
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 89
QIYYSGSTYY NPSLKS                                                  16

SEQ ID NO: 90           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: HCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 90
SSAHYYFDV                                                          9

SEQ ID NO: 91           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
REGION                  1..15
                        note = Synthetic: LCDR1
source                  1..15
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 91
RASESVDFQG ISFLD                                                   15

SEQ ID NO: 92           moltype = AA  length = 119
FEATURE                 Location/Qualifiers
REGION                  1..119
                        note = Synthetic: VH
source                  1..119
                        mol_type = protein
                        organism = synthetic construct
```

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```
SEQUENCE: 92
QVQLVQSGAE VKKPGSSVKV SCKASGFSLS TGGVAVAWIR QAPGQGLEWI GQIYYSGSTY  60
YNPSLKSRVT ITADKSTSTA YMELSSLRSE DTAVYYCARS SAHYYFDVWG QGTLVTVSS   119

SEQ ID NO: 93          moltype = AA  length = 111
FEATURE                Location/Qualifiers
REGION                 1..111
                       note = Synthetic: VL
source                 1..111
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 93
DIQLTQSPSS LSASVGDRVT ITCRASESVD FQGISFLDWY QQKPGKAPKL LIYDASSLES  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPI TFGQGTKVEI K           111

SEQ ID NO: 94          moltype = AA  length = 446
FEATURE                Location/Qualifiers
REGION                 1..446
                       note = Synthetic: HC
source                 1..446
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 94
QVQLVQSGAE VKKPGSSVKV SCKASGFSLS TGGVAVAWIR QAPGQGLEWI GQIYYSGSTY  60
YNPSLKSRVT ITADKSTSTA YMELSSLRSE DTAVYYCARS SAHYYFDVWG QGTLVTVSSA  120
STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTKTY TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF  240
LFPPKPKDTL MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR  300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL PPSQEEMTKN  360
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT VDKSRWQEGN  420
VFSCSVMHEA LHNHYTQKSL SLSLGK                                       446

SEQ ID NO: 95          moltype = AA  length = 218
FEATURE                Location/Qualifiers
REGION                 1..218
                       note = Synthetic: LC
source                 1..218
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 95
DIQLTQSPSS LSASVGDRVT ITCRASESVD FQGISFLDWY QQKPGKAPKL LIYDASSLES  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPI TFGQGTKVEI KRTVAAPSVF  120
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS  180
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC                          218

SEQ ID NO: 96          moltype = AA  length = 16
FEATURE                Location/Qualifiers
REGION                 1..16
                       note = Synthetic: HCDR2
source                 1..16
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 96
SIYHSGSTYY NPSLKS                                                  16

SEQ ID NO: 97          moltype = AA  length = 10
FEATURE                Location/Qualifiers
REGION                 1..10
                       note = Synthetic: HCDR3
source                 1..10
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 97
SGLRYYAFDV                                                         10

SEQ ID NO: 98          moltype = AA  length = 11
FEATURE                Location/Qualifiers
REGION                 1..11
                       note = Synthetic: LCDR1
source                 1..11
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 98
AASQDVSTAV A                                                       11

SEQ ID NO: 99          moltype = AA  length = 119
```

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```
FEATURE                 Location/Qualifiers
REGION                  1..119
                        note = Synthetic: VH
source                  1..119
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 99
QVQLVQSGAE VKKPGSSVKV SCKASGYSIS SGYHWGWIRQ APGQGLEWIG SIYHSGSTYY  60
NPSLKSRVTI TADKSTSTAY MELSSLRSED TAVYYCARSG LRYYAFDVWG QGTLVTVSS   119

SEQ ID NO: 100          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic: VL
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 100
DIQLTQSPSS LSASVGDRVT ITCAASQDVS TAVAWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYRSPITFGQ GTKVEIK               107

SEQ ID NO: 101          moltype = AA  length = 446
FEATURE                 Location/Qualifiers
REGION                  1..446
                        note = Synthetic: HC
source                  1..446
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 101
QVQLVQSGAE VKKPGSSVKV SCKASGYSIS SGYHWGWIRQ APGQGLEWIG SIYHSGSTYY  60
NPSLKSRVTI TADKSTSTAY MELSSLRSED TAVYYCARSG LRYYAFDVWG QGTLVTVSSA  120
STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTKTY TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF  240
LFPPKPKDTL MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR  300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL PPSQEEMTKN  360
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT VDKSRWQEGN  420
VFSCSVMHEA LHNHYTQKSL SLSLGK                                       446

SEQ ID NO: 102          moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 102
DIQLTQSPSS LSASVGDRVT ITCAASQDVS TAVAWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYRSPITFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 103          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: HCDR1
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 103
GYAIH                                                              5

SEQ ID NO: 104          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: HCDR2
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 104
QIYHSGSTYY NPSLKS                                                  16

SEQ ID NO: 105          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
```

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```
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 105
SGYGGYDFDY                                                          10

SEQ ID NO: 106          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
REGION                  1..12
                        note = Synthetic: LCDR1
source                  1..12
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 106
RASQSVPRRY LA                                                       12

SEQ ID NO: 107          moltype = AA  length = 118
FEATURE                 Location/Qualifiers
REGION                  1..118
                        note = Synthetic: VH
source                  1..118
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 107
QVQLVQSGAE VKKPGSSVKV SCKASGFTFS GYAIHWVRQA PGQGLEWIGQ IYHSGSTYYN  60
PSLKSRVTIT ADKSTSTAYM ELSSLRSEDT AVYYCARSGY GGYDFDYWGQ GTLVTVSS    118

SEQ ID NO: 108          moltype = AA  length = 108
FEATURE                 Location/Qualifiers
REGION                  1..108
                        note = Synthetic: VL
source                  1..108
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 108
DIQLTQSPSS LSASVGDRVT ITCRASQSVP RRYLAWYQQK PGKAPKLLIY AASTLQSGVP  60
SRFSGSGSGT DFTLTISSLQ PEDFATYYCQ QYYRSPITFG QGTKVEIK               108

SEQ ID NO: 109          moltype = AA  length = 445
FEATURE                 Location/Qualifiers
REGION                  1..445
                        note = Synthetic: HC
source                  1..445
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 109
QVQLVQSGAE VKKPGSSVKV SCKASGFTFS GYAIHWVRQA PGQGLEWIGQ IYHSGSTYYN  60
PSLKSRVTIT ADKSTSTAYM ELSSLRSEDT AVYYCARSGY GGYDFDYWGQ GTLVTVSSAS  120
TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL  180
YSLSSVVTVP SSSLGTKTYT CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL  240
FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV  300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP PSQEEMTKNQ  360
VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSRLTV DKSRWQEGNV  420
FSCSVMHEAL HNHYTQKSLS LSLGK                                        445

SEQ ID NO: 110          moltype = AA  length = 215
FEATURE                 Location/Qualifiers
REGION                  1..215
                        note = Synthetic: LC
source                  1..215
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 110
DIQLTQSPSS LSASVGDRVT ITCRASQSVP RRYLAWYQQK PGKAPKLLIY AASTLQSGVP  60
SRFSGSGSGT DFTLTISSLQ PEDFATYYCQ QYYRSPITFG QGTKVEIKRT VAAPSVFIFP  120
PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL  180
TLSKADYEKH KVYACEVTHQ GLSSPVTKSF NRGEC                             215

SEQ ID NO: 111          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
REGION                  1..6
                        note = Synthetic: HCDR1
source                  1..6
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 111
SGHHWG                                                              6
```

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```
SEQ ID NO: 112          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 112
RELGYAYFDY                                                          10

SEQ ID NO: 113          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 113
RASQDIRKYL A                                                        11

SEQ ID NO: 114          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 114
QQYYRTPLT                                                           9

SEQ ID NO: 115          moltype = AA  length = 119
FEATURE                 Location/Qualifiers
REGION                  1..119
                        note = Synthetic: VH
source                  1..119
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 115
EVQLVESGGG LVQPGGSLRL SCAASGYSIS SGHHWGWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARRE LGYAYFDYWG QGTLVTVSS   119

SEQ ID NO: 116          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic: VL
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 116
EIVLTQSPAT LSLSPGERAT LSCRASQDIR KYLAWYQQKP GQAPRLLIYA ASTLQSGVPA  60
RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ YYRTPLTFGQ GTKVEIK                107

SEQ ID NO: 117          moltype = AA  length = 446
FEATURE                 Location/Qualifiers
REGION                  1..446
                        note = Synthetic: HC
source                  1..446
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 117
EVQLVESGGG LVQPGGSLRL SCAASGYSIS SGHHWGWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARRE LGYAYFDYWG QGTLVTVSSA  120
STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTKTY TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF  240
LFPPKPKDTL MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR  300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL PPSQEEMTKN  360
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT VDKSRWQEGN  420
VFSCSVMHEA LHNHYTQKSL SLSLGK                                       446

SEQ ID NO: 118          moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
```

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                        organism = synthetic construct
SEQUENCE: 118
EIVLTQSPAT LSLSPGERAT LSCRASQDIR KYLAWYQQKP GQAPRLLIYA ASTLQSGVPA  60
RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ YYRTPLTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 119          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 119
RDFGASYFDY                                                         10

SEQ ID NO: 120          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 120
RASQGVGPWL A                                                       11

SEQ ID NO: 121          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
REGION                  1..8
                        note = Synthetic: LCDR3
source                  1..8
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 121
QQYYSYST                                                           8

SEQ ID NO: 122          moltype = AA  length = 119
FEATURE                 Location/Qualifiers
REGION                  1..119
                        note = Synthetic: VH
source                  1..119
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 122
EVQLVESGGG LVQPGGSLRL SCAASGYSIS SGHHWSWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARRD FGASYFDYWG QGTLVTVSS   119

SEQ ID NO: 123          moltype = AA  length = 106
FEATURE                 Location/Qualifiers
REGION                  1..106
                        note = Synthetic: VL
source                  1..106
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 123
DIQLTQSPSS LSASVGDRVT ITCRASQGVG PWLAWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYSYSTFGQG TKVEIK                 106

SEQ ID NO: 124          moltype = AA  length = 446
FEATURE                 Location/Qualifiers
REGION                  1..446
                        note = Synthetic: HC
source                  1..446
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 124
EVQLVESGGG LVQPGGSLRL SCAASGYSIS SGHHWSWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARRD FGASYFDYWG QGTLVTVSSA  120
STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTKTY TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF  240
LFPPKPKDTL MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR  300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL PPSQEEMTKN  360
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT VDKSRWQEGN  420
VFSCSVMHEA LHNHYTQKSL SLSLGK                                       446
```

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SEQ ID NO: 125          moltype = AA  length = 213
FEATURE                 Location/Qualifiers
REGION                  1..213
                        note = Synthetic: LC
source                  1..213
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 125
DIQLTQSPSS LSASVGDRVT ITCRASQGVG PWLAWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYSYSTFGQG TKVEIKRTVA APSVFIFPPS  120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL  180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC                               213

SEQ ID NO: 126          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: HCDR1
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 126
TGGVGVT                                                            7

SEQ ID NO: 127          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 127
YDYGYYSFDV                                                         10

SEQ ID NO: 128          moltype = AA  length = 15
FEATURE                 Location/Qualifiers
REGION                  1..15
                        note = Synthetic: LCDR1
source                  1..15
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 128
RASQSVDFDA FSFLA                                                   15

SEQ ID NO: 129          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
REGION                  1..8
                        note = Synthetic: LCDR3
source                  1..8
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 129
QQSYSAST                                                           8

SEQ ID NO: 130          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
REGION                  1..120
                        note = Synthetic: VH
source                  1..120
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 130
QVQLVQSGAE VKKPGSSVKV SCKASGFSLS TGGVGVTWIR QAPGQGLEWI GSIYHSGSTY  60
YSPSLKSRVT ITADKSTSTA YMELSSLRSE DTAVYYCARY DYGYYSFDVW GQGTLVTVSS  120

SEQ ID NO: 131          moltype = AA  length = 110
FEATURE                 Location/Qualifiers
REGION                  1..110
                        note = Synthetic: VL
source                  1..110
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 131
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FDAFSFLAWY QQKPGKAPKL LIYAASTLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYSAST FGQGTKVEIK             110

SEQ ID NO: 132          moltype = AA  length = 447
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```
FEATURE                 Location/Qualifiers
REGION                  1..447
                        note = Synthetic: HC
source                  1..447
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 132
QVQLVQSGAE VKKPGSSVKV SCKASGFSLS TGGVGVTWIR QAPGQGLEWI GSIYHSGSTY  60
YSPSLKSRVT ITADKSTSTA YMELSSLRSE DTAVYYCARY DYGYYSFDVW GQGTLVTVSS  120
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  180
GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG  420
NVFSCSVMHE ALHNHYTQKS LSLSLGK                                      447

SEQ ID NO: 133          moltype = AA  length = 217
FEATURE                 Location/Qualifiers
REGION                  1..217
                        note = Synthetic: LC
source                  1..217
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 133
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FDAFSFLAWY QQKPGKAPKL LIYAASTLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYSAST FGQGTKVEIK RTVAAPSVFI  120
FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD SKDSTYSLSS  180
TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                           217

SEQ ID NO: 134          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
REGION                  1..6
                        note = Synthetic: HCDR1
source                  1..6
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 134
SGHHWT                                                             6

SEQ ID NO: 135          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 135
RDYGSSYFDY                                                         10

SEQ ID NO: 136          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
REGION                  1..12
                        note = Synthetic: LCDR1
source                  1..12
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 136
RASQSVSRSF LA                                                      12

SEQ ID NO: 137          moltype = AA  length = 119
FEATURE                 Location/Qualifiers
REGION                  1..119
                        note = Synthetic: VH
source                  1..119
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 137
EVQLVESGGG LVQPGGSLRL SCAASGYSIS SGHHWTWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARRD YGSSYFDYWG QGTLVTVSS   119

SEQ ID NO: 138          moltype = AA  length = 108
FEATURE                 Location/Qualifiers
REGION                  1..108
                        note = Synthetic: VL
source                  1..108
                        mol_type = protein
```

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```
                        organism = synthetic construct
SEQUENCE: 138
DIQLTQSPSS LSASVGDRVT ITCRASQSVS RSFLAWYQQK PGKAPKLLIY DASNRATGIP  60
SRFSGSGSGT DFTLTISSLQ PEDFATYYCQ QYYRSPITFG QGTKVEIK               108

SEQ ID NO: 139          moltype = AA  length = 446
FEATURE                 Location/Qualifiers
REGION                  1..446
                        note = Synthetic: HC
source                  1..446
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 139
EVQLVESGGG LVQPGGSLRL SCAASGYSIS SGHHWTWIRQ APGKGLEWIG EIYHSGSTYY  60
SPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARRD YGSSYFDYWG QGTLVTVSSA  120
STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTKTY TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF  240
LFPPKPKDTL MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR  300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL PPSQEEMTKN  360
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT VDKSRWQEGN  420
VFSCSVMHEA LHNHYTQKSL SLSLGK                                       446

SEQ ID NO: 140          moltype = AA  length = 215
FEATURE                 Location/Qualifiers
REGION                  1..215
                        note = Synthetic: LC
source                  1..215
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 140
DIQLTQSPSS LSASVGDRVT ITCRASQSVS RSFLAWYQQK PGKAPKLLIY DASNRATGIP  60
SRFSGSGSGT DFTLTISSLQ PEDFATYYCQ QYYRSPITFG QGTKVEIKRT VAAPSVFIFP  120
PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL  180
TLSKADYEKH KVYACEVTHQ GLSSPVTKSF NRGEC                             215

SEQ ID NO: 141          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 141
YGYSYYAFDY                                                         10

SEQ ID NO: 142          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 142
RASQTIGSFL N                                                       11

SEQ ID NO: 143          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
REGION                  1..8
                        note = Synthetic: LCDR3
source                  1..8
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 143
QQSYSYQT                                                           8

SEQ ID NO: 144          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
REGION                  1..120
                        note = Synthetic: VH
source                  1..120
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 144
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVSWIR QAPGKGLEWI GAIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY GYSYYAFDYW GQGTLVTVSS  120
```

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```
SEQ ID NO: 145          moltype = AA  length = 106
FEATURE                 Location/Qualifiers
REGION                  1..106
                        note = Synthetic: VL
source                  1..106
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 145
DIQLTQSPSS LSASVGDRVT ITCRASQTIG SFLNWYQQKP GKAPKLLIYD ASSLESGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSYQTFGQG TKVEIK                106

SEQ ID NO: 146          moltype = AA  length = 447
FEATURE                 Location/Qualifiers
REGION                  1..447
                        note = Synthetic: HC
source                  1..447
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 146
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVSWIR QAPGKGLEWI GAIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY GYSYYAFDYW GQGTLVTVSS  120
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  180
GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG  420
NVFSCSVMHE ALHNHYTQKS LSLSLGK                                     447

SEQ ID NO: 147          moltype = AA  length = 213
FEATURE                 Location/Qualifiers
REGION                  1..213
                        note = Synthetic: LC
source                  1..213
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 147
DIQLTQSPSS LSASVGDRVT ITCRASQTIG SFLNWYQQKP GKAPKLLIYD ASSLESGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSYQTFGQG TKVEIKRTVA APSVFIFPPS  120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL  180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC                              213

SEQ ID NO: 148          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: HCDR1
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 148
NYGIH                                                             5

SEQ ID NO: 149          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 149
GPLSYYALDY                                                        10

SEQ ID NO: 150          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 150
RASQSIRRFL N                                                      11

SEQ ID NO: 151          moltype = AA  length = 118
FEATURE                 Location/Qualifiers
REGION                  1..118
                        note = Synthetic: VH
source                  1..118
```

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```
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 151
QVQLVQSGAE VKKPGSSVKV SCKASGYTFT NYGIHWVRQA PGQGLEWIGE IYHSGSTYYS  60
PSLKSRVTIT ADKSTSTAYM ELSSLRSEDT AVYYCARGPL SYYALDYWGQ GTLVTVSS    118

SEQ ID NO: 152          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic: VL
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 152
DIQLTQSPSS LSASVGDRVT ITCRASQSIR RFLNWYQQKP GKAPKLLIYD ASSLESGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYRSPITFGQ GTKVEIK               107

SEQ ID NO: 153          moltype = AA  length = 445
FEATURE                 Location/Qualifiers
REGION                  1..445
                        note = Synthetic: HC
source                  1..445
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 153
QVQLVQSGAE VKKPGSSVKV SCKASGYTFT NYGIHWVRQA PGQGLEWIGE IYHSGSTYYS  60
PSLKSRVTIT ADKSTSTAYM ELSSLRSEDT AVYYCARGPL SYYALDYWGQ GTLVTVSSAS  120
TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL  180
YSLSSVVTVP SSSLGTKTYT CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL  240
FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV  300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP PSQEEMTKNQ  360
VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSRLTV DKSRWQEGNV  420
FSCSVMHEAL HNHYTQKSLS LSLGK                                       445

SEQ ID NO: 154          moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 154
DIQLTQSPSS LSASVGDRVT ITCRASQSIR RFLNWYQQKP GKAPKLLIYD ASSLESGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYRSPITFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                             214

SEQ ID NO: 155          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: HCDR2
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 155
DIYHSGSTYY NPSLKS                                                 16

SEQ ID NO: 156          moltype = AA  length = 15
FEATURE                 Location/Qualifiers
REGION                  1..15
                        note = Synthetic: LCDR1
source                  1..15
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 156
RAPQSVDFHG KSFLH                                                  15

SEQ ID NO: 157          moltype = AA  length = 118
FEATURE                 Location/Qualifiers
REGION                  1..118
                        note = Synthetic: VH
source                  1..118
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 157
EVQLVESGGG LVQPGGSLRL SCAASGYSIT SGHHWSWIRQ APGKGLEWIG DIYHSGSTYY  60
```

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NPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARKD DYYAFDYWGQ GTLVTVSS    118

SEQ ID NO: 158          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
REGION                  1..111
                        note = Synthetic: VL
source                  1..111
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 158
DIQLTQSPSS LSASVGDRVT ITCRAPQSVD FHGKSFLHWY QQKPGKAPKL LIYDASNRAT  60
GIPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPI TFGQGTKVEI K           111

SEQ ID NO: 159          moltype = AA  length = 445
FEATURE                 Location/Qualifiers
REGION                  1..445
                        note = Synthetic: HC
source                  1..445
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 159
EVQLVESGGG LVQPGGSLRL SCAASGYSIT SGHHWSWIRQ APGKGLEWIG DIYHSGSTYY  60
NPSLKSRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARKD DYYAFDYWGQ GTLVTVSSAS  120
TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL  180
YSLSSVVTVP SSSLGTKTYT CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL  240
FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV  300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP PSQEEMTKNQ  360
VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSRLTV DKSRWQEGNV  420
FSCSVMHEAL HNHYTQKSLS LSLGK                                        445

SEQ ID NO: 160          moltype = AA  length = 218
FEATURE                 Location/Qualifiers
REGION                  1..218
                        note = Synthetic: LC
source                  1..218
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 160
DIQLTQSPSS LSASVGDRVT ITCRAPQSVD FHGKSFLHWY QQKPGKAPKL LIYDASNRAT  60
GIPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPI TFGQGTKVEI KRTVAAPSVF  120
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS  180
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC                          218

SEQ ID NO: 161          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: HCDR1
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 161
TSGVAVG                                                            7

SEQ ID NO: 162          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 162
HGYHYYALDY                                                         10

SEQ ID NO: 163          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 163
PASQDVGTAV A                                                       11

SEQ ID NO: 164          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
```

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```
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 164
QQYYSSPPT                                                          9

SEQ ID NO: 165          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
REGION                  1..120
                        note = Synthetic: VH
source                  1..120
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 165
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVAVGWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARH GYHYYALDYW GQGTLVTVSS  120

SEQ ID NO: 166          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic: VL
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 166
DIQLTQSPSS LSASVGDRVT ITCPASQDVG TAVAWYQQKP GKAPKLLIYD ASSLESGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYSSPPTFGQ GTKVEIK               107

SEQ ID NO: 167          moltype = AA  length = 447
FEATURE                 Location/Qualifiers
REGION                  1..447
                        note = Synthetic: HC
source                  1..447
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 167
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVAVGWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARH GYHYYALDYW GQGTLVTVSS  120
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  180
GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG  420
NVFSCSVMHE ALHNHYTQKS LSLSLGK                                      447

SEQ ID NO: 168          moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 168
DIQLTQSPSS LSASVGDRVT ITCPASQDVG TAVAWYQQKP GKAPKLLIYD ASSLESGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYSSPPTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 169          moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 169
DIQMTQSPSS LSASVGDRVT ITCKASQDVS IGVAWYQQKP GKAPKLLIYS ASYRYTGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYIYPYTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 170          moltype = AA  length = 449
FEATURE                 Location/Qualifiers
REGION                  1..449
                        note = Synthetic: HC-A
```

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source                  1..449
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 170
EVQLVESGGG LVQPGGSLRL SCAASGFTFT DYTMDWVRQA PGKGLEWVAD VNPNSGGSIY  60
NQRFKGRFTL SVDRSKNTLY LQMNSLRAED TAVYYCARNL GPSFYFDYWG QGTLVTVSSA  120
STKGPSVFPL APSSKSTSGG TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYAS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSRKKL  360
TKNQVKLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DCDGSFFLYS KLTVDKSRWQ  420
QGNVFSCSVM HEALHNHYTQ KSLSLSPGK                                    449

SEQ ID NO: 171          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC-B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 171
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STGGVGVSWI RQAPGKGLEW  180
IGEIYHSGST YYSPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYYYYDFDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 172          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC-B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 172
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGKSFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPL TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STSGVGVSWI RQAPGKGLEW  180
IGEIYHSGST YYSPSLKSRV TISRDNSKNT LYLQLNSLRV EDTAVYYCAR DEYDYYAFDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 173          moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 173
DIQLTQSPSS LSASVGDRVT ITCRASQDVS IAVAWYQQKP GKAPKLLIYS ASYRYTGVPA  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ HYITPLTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 174          moltype = AA  length = 451
FEATURE                 Location/Qualifiers
REGION                  1..451
                        note = Synthetic: HC-A
source                  1..451
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 174
QVQLLQSGSE LKKPGASVKV SCKASGYTFT NYGINWVRQA PGQGLEWLGW IHTYTGEPTY  60
TDDFKGRFVF SLDTSVSTAY LQISSLKADD TAVYYCARGG FGSSYWYFDV WGQGTLVTVS  120
SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG  240
GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY  300
ASTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP QVYTLPPSRK  360
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KLTKNQVKLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDCDGSFFL YSKLTVDKSR  420
WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K                                 451

SEQ ID NO: 175         moltype = AA  length = 214
FEATURE                Location/Qualifiers
REGION                 1..214
                       note = Synthetic: LC
source                 1..214
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 175
DIQLTQSPSS LSASVGDRVT ITCRASQSIR KYLNWYQQKP GKAPKLLIYA ASTLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYFCSQ GTHVPFTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 176         moltype = AA  length = 448
FEATURE                Location/Qualifiers
REGION                 1..448
                       note = Synthetic: HC-A
source                 1..448
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 176
EVQLVESGGG LVQPGGSLRL SCAASGFTFS GYGIHWVRQA PGKGLEWIGW ISPSGGDTKY  60
AQKFQGRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARGG TVVYFDYWGQ GTLVTVSSAS  120
TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL  180
YSLSSVVTVP SSSLGTQTYI CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYAST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSRKKLT  360
KNQVKLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD CDGSFFLYSK LTVDKSRWQQ  420
GNVFSCSVMH EALHNHYTQK SLSLSPGK                                     448

SEQ ID NO: 177         moltype = AA  length = 486
FEATURE                Location/Qualifiers
REGION                 1..486
                       note = Synthetic: HC-B
source                 1..486
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 177
QAVVTQEPSL TVSPGGTVTL TCGSSTGAVT TSNYPNWVQQ KPGQAPRGLI GGTNKRAPGV  60
PARFSGSLLG GKAALTLSGA QPEDEAEYYC ALWYSNLWVF GGGTKLTVLG GGGSGGGGSG  120
GGGSGGGGSE VQLVESGGGL VQPGGSLRLS CAASGFTFNT YAINWVRQAP GKGLEWVGRI  180
RSKYNNYATY YAESVKGRFT ISRDDSKNTL YLQINSLRAE DTAVYYCVRH GNFGTSYVSW  240
FAYWGQGTLV TVSSEPKSSD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL MISRTPEVTC  300
VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYASTYR VVSVLTVLHQ DWLNGKEYKC  360
KVSNKALPAP IEKTISKAKG QPREPQVYTD PPSRDELTKN QVSLTCLVDG FYPSDIAVEW  420
ESNGQPENCY KTTPPVLDSD GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQDSL  480
SLSPGK                                                             486

SEQ ID NO: 178         moltype = AA  length = 16
FEATURE                Location/Qualifiers
REGION                 1..16
                       note = Synthetic: Masking Unit (MU)
source                 1..16
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 178
ASDLYVCAHD PYFCHS                                                  16

SEQ ID NO: 179         moltype = AA  length = 16
FEATURE                Location/Qualifiers
REGION                 1..16
                       note = Synthetic: Masking Unit (MU)
source                 1..16
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 179
PNVFDTCYVD PYSCTI                                                  16

SEQ ID NO: 180         moltype = AA  length = 16
FEATURE                Location/Qualifiers
REGION                 1..16
                       note = Synthetic: Masking Unit (MU)
source                 1..16
```

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```
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 180
YAAAPSCPPA NYYCAD                                                   16

SEQ ID NO: 181          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 181
HHADPLCFAQ HSACNT                                                   16

SEQ ID NO: 182          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 182
YDTHDYCLIH YHSCDT                                                   16

SEQ ID NO: 183          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 183
ADFAPYCYAD PYYCHD                                                   16

SEQ ID NO: 184          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 184
DIASDSCYYH PNHCDT                                                   16

SEQ ID NO: 185          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 185
AATYSDCYSD PYACHD                                                   16

SEQ ID NO: 186          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 186
PTYDHDCAVY NNFCNA                                                   16

SEQ ID NO: 187          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 187
HNHALTCYTD PYACHS                                                   16

SEQ ID NO: 188          moltype = AA  length = 16
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```
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 188
AAFSPACYTD PYSCHA                                                   16

SEQ ID NO: 189          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 189
TPHPDACFVD PYHCHT                                                   16

SEQ ID NO: 190          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 190
APSDAYCYAD PYACHT                                                   16

SEQ ID NO: 191          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 191
AVDDDPCYTD PYQCTA                                                   16

SEQ ID NO: 192          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 192
THSDAVCAPD HAYCLY                                                   16

SEQ ID NO: 193          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 193
PYIYVDCYAP PFFCAY                                                   16

SEQ ID NO: 194          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 194
YFCAEGVPIV LCIG                                                     14

SEQ ID NO: 195          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
```

-continued

```
SEQUENCE: 195
DYCEGPPAFF YCAK                                                14

SEQ ID NO: 196          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 196
FPCEPLADPF LCRQ                                                14

SEQ ID NO: 197          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 197
LVCEDVPFPA ACRA                                                14

SEQ ID NO: 198          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 198
ALCEFYAFPY FCAR                                                14

SEQ ID NO: 199          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 199
IVCKYFDDPF LCRR                                                14

SEQ ID NO: 200          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 200
YFCPVRVPLA VCLR                                                14

SEQ ID NO: 201          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 201
PSCPDYVPFP VCAQ                                                14

SEQ ID NO: 202          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 202
VACAKAFAYV YCLV                                                14

SEQ ID NO: 203          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
```

-continued

```
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 203
VLCGDSVPFL LCEP                                                    14

SEQ ID NO: 204          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 204
ILCPEGVPVV FCVL                                                    14

SEQ ID NO: 205          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 205
SDCGLGVPLL VCLK                                                    14

SEQ ID NO: 206          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Masking Unit (MU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 206
TDCGIPFPVD DCLS                                                    14

SEQ ID NO: 207          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 207
HIPDHYCAAD HHYCYY                                                  16

SEQ ID NO: 208          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 208
AATYSDCYSD PYACHD                                                  16

SEQ ID NO: 209          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
REGION                  1..13
                        note = Synthetic: Masking Unit (MU)
source                  1..13
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 209
YSDCYSDPYA CHD                                                     13

SEQ ID NO: 210          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: Masking Unit (MU)
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 210
AAFSPACYTD PYSCHA                                                  16
```

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```
SEQ ID NO: 211          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
REGION                  1..13
                        note = Synthetic: Masking Unit (MU)
source                  1..13
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 211
SPACYTDPYS CHA                                                  13

SEQ ID NO: 212          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: N-terminal Unit
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 212
EVGSY                                                           5

SEQ ID NO: 213          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
REGION                  1..13
                        note = Synthetic: Linkage Unit (LU)
source                  1..13
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 213
GGGPLGLAGS GGS                                                  13

SEQ ID NO: 214          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: Linkage Unit (LU)
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 214
SGGGPLGLAG SGGS                                                 14

SEQ ID NO: 215          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 215
EVGSYASDLY VCAHDPYFCH SGGGPLGLAG SGGS                           34

SEQ ID NO: 216          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 216
EVGSYPNVFD TCYVDPYSCT IGGGPLGLAG SGGS                           34

SEQ ID NO: 217          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 217
EVGSYYAAAP SCPPANYYCA DGGGPLGLAG SGGS                           34

SEQ ID NO: 218          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
```

-continued

```
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 218
EVGSYHHADP LCFAQHSACN TGGGPLGLAG SGGS                                34

SEQ ID NO: 219          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 219
EVGSYYDTHD YCLIHYHSCD TGGGPLGLAG SGGS                                34

SEQ ID NO: 220          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 220
EVGSYADFAP YCYADPYYCH DGGGPLGLAG SGGS                                34

SEQ ID NO: 221          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 221
EVGSYDIASD SCYYHPNHCD TGGGPLGLAG SGGS                                34

SEQ ID NO: 222          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 222
EVGSYAATYS DCYSDPYACH DGGGPLGLAG SGGS                                34

SEQ ID NO: 223          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 223
EVGSYPTYDH DCAVYNNFCN AGGGPLGLAG SGGS                                34

SEQ ID NO: 224          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 224
EVGSYHNHAL TCYTDPYACH SGGGPLGLAG SGGS                                34

SEQ ID NO: 225          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 225
EVGSYAAFSP ACYTDPYSCH AGGGPLGLAG SGGS                                34

SEQ ID NO: 226          moltype = AA  length = 34
```

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```
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 226
EVGSYTPHPD ACFVDPYHCH TGGGPLGLAG SGGS                                34

SEQ ID NO: 227          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 227
EVGSYAPSDA YCYADPYACH TGGGPLGLAG SGGS                                34

SEQ ID NO: 228          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 228
EVGSYAVDDD PCYTDPYQCT AGGGPLGLAG SGGS                                34

SEQ ID NO: 229          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 229
EVGSYTHSDA VCAPDHAYCL YGGGPLGLAG SGGS                                34

SEQ ID NO: 230          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 230
EVGSYPYIYV DCYAPPFFCA YGGGPLGLAG SGGS                                34

SEQ ID NO: 231          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 231
EVGSYYFCAE GVPIVLCIGG GGPLGLAGSG GS                                  32

SEQ ID NO: 232          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 232
EVGSYDYCEG PPAFFYCAKG GGPLGLAGSG GS                                  32

SEQ ID NO: 233          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
```

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```
SEQUENCE: 233
EVGSYFPCEP LADPFLCRQG GGPLGLAGSG GS                                32

SEQ ID NO: 234          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 234
EVGSYLVCED VPFPAACRAG GGPLGLAGSG GS                                32

SEQ ID NO: 235          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 235
EVGSYALCEF YAFPYFCARG GGPLGLAGSG GS                                32

SEQ ID NO: 236          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 236
EVGSYIVCKY FDDPFLCRRG GGPLGLAGSG GS                                32

SEQ ID NO: 237          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 237
EVGSYYFCPV RVPLAVCLRG GGPLGLAGSG GS                                32

SEQ ID NO: 238          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 238
EVGSYPSCPD YVPFPVCAQG GGPLGLAGSG GS                                32

SEQ ID NO: 239          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 239
EVGSYVACAK AFAYVYCLVG GGPLGLAGSG GS                                32

SEQ ID NO: 240          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 240
EVGSYVLCGD SVPFLLCEPG GGPLGLAGSG GS                                32

SEQ ID NO: 241          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
```

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```
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 241
EVGSYILCPE GVPVVFCVLG GGPLGLAGSG GS                                32

SEQ ID NO: 242          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 242
EVGSYSDCGL GVPLLVCLKG GGPLGLAGSG GS                                32

SEQ ID NO: 243          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
REGION                  1..32
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 243
EVGSYTDCGI PFPVDDCLSG GGPLGLAGSG GS                                32

SEQ ID NO: 244          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 244
EVGSYHIPDH YCAADHHYCY YGGGPLGLAG SGGS                              34

SEQ ID NO: 245          moltype = AA  length = 31
FEATURE                 Location/Qualifiers
REGION                  1..31
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..31
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 245
EAATYSDCYS DPYACHDSGG GPLGLAGSGG S                                 31

SEQ ID NO: 246          moltype = AA  length = 28
FEATURE                 Location/Qualifiers
REGION                  1..28
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..28
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 246
EYSDCYSDPY ACHDSGGGPL GLAGSGGS                                     28

SEQ ID NO: 247          moltype = AA  length = 30
FEATURE                 Location/Qualifiers
REGION                  1..30
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..30
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 247
EAAFSPACYT DPYSCHAGGG PLGLAGSGGS                                   30

SEQ ID NO: 248          moltype = AA  length = 27
FEATURE                 Location/Qualifiers
REGION                  1..27
                        note = Synthetic: Masking+Cleavage Peptide Sequence
source                  1..27
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 248
ESPACYTDPY SCHAGGGPLG LAGSGGS                                      27
```

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```
SEQ ID NO: 249          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: Flexible Linker
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 249
GGGGS                                                           5

SEQ ID NO: 250          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: Flexible Linker
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 250
GGGGT                                                           5

SEQ ID NO: 251          moltype = AA  length = 4
FEATURE                 Location/Qualifiers
REGION                  1..4
                        note = Synthetic: Flexible Linker
source                  1..4
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 251
SGGS                                                            4

SEQ ID NO: 252          moltype = AA  length = 4
FEATURE                 Location/Qualifiers
REGION                  1..4
                        note = Synthetic: Flexible Linker
source                  1..4
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 252
GGSG                                                            4

SEQ ID NO: 253          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: Flexible Linker
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 253
GGSGG                                                           5

SEQ ID NO: 254          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: Flexible Linker
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 254
GSGSG                                                           5

SEQ ID NO: 255          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: Flexible Linker
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 255
GSGGG                                                           5

SEQ ID NO: 256          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: Flexible Linker
source                  1..5
```

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```
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 256
GGGSG                                                           5

SEQ ID NO: 257          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: Flexible Linker
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 257
GSSSG                                                           5

SEQ ID NO: 258          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 258
KASQDVSIGV A                                                    11

SEQ ID NO: 259          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: LCDR2 / LCDR2-A
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 259
SASYRYT                                                         7

SEQ ID NO: 260          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 260
QQYYIYPYT                                                       9

SEQ ID NO: 261          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic: VL
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 261
DIQMTQSPSS LSASVGDRVT ITCKASQDVS IGVAWYQQKP GKAPKLLIYS ASYRYTGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYIYPYTFGQ GTKVEIK               107

SEQ ID NO: 262          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: HCDR1-A
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 262
DYTMD                                                           5

SEQ ID NO: 263          moltype = AA  length = 17
FEATURE                 Location/Qualifiers
REGION                  1..17
                        note = Synthetic: HCDR2-A
source                  1..17
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 263
DVNPNSGGSI YNQRFKG                                              17
```

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```
SEQ ID NO: 264          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3-A
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 264
NLGPSFYFDY                                                          10

SEQ ID NO: 265          moltype = AA  length = 119
FEATURE                 Location/Qualifiers
REGION                  1..119
                        note = Synthetic: VH-A
source                  1..119
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 265
EVQLVESGGG LVQPGGSLRL SCAASGFTFT DYTMDWVRQA PGKGLEWVAD VNPNSGGSIY  60
NQRFKGRFTL SVDRSKNTLY LQMNSLRAED TAVYYCARNL GPSFYFDYWG QGTLVTVSS   119

SEQ ID NO: 266          moltype = AA  length = 251
FEATURE                 Location/Qualifiers
REGION                  1..251
                        note = Synthetic: scFv-B
source                  1..251
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 266
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STGGVGVSWI RQAPGKGLEW  180
IGEIYHSGST YYSPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYYYYDFDY  240
WGQGTLVTVS S                                                       251

SEQ ID NO: 267          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 267
RASQDVNTAV A                                                        11

SEQ ID NO: 268          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: LCDR2
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 268
SASFLYS                                                             7

SEQ ID NO: 269          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 269
QQHYTTPPT                                                           9

SEQ ID NO: 270          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic: VL
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 270
DIQMTQSPSS LSASVGDRVT ITCRASQDVN TAVAWYQQKP GKAPKLLIYS ASFLYSGVPS  60
RFSGSRSGTD FTLTISSLQP EDFATYYCQQ HYTTPPTFGQ GTKVEIK                107
```

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SEQ ID NO: 271          moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 271
DIQMTQSPSS LSASVGDRVT ITCRASQDVN TAVAWYQQKP GKAPKLLIYS ASFLYSGVPS  60
RFSGSRSGTD FTLTISSLQP EDFATYYCQQ HYTTPPTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 272          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: HCDR1-A
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 272
DTYIH                                                              5

SEQ ID NO: 273          moltype = AA  length = 17
FEATURE                 Location/Qualifiers
REGION                  1..17
                        note = Synthetic: HCDR2-A
source                  1..17
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 273
RIYPTNGYTR YADSVKG                                                 17

SEQ ID NO: 274          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: HCDR3-A
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 274
WGGDGFYAMD Y                                                       11

SEQ ID NO: 275          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
REGION                  1..120
                        note = Synthetic: VH-A
source                  1..120
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 275
EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR IYPTNGYTRY  60
ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCSRWG GDGFYAMDYW GQGTLVTVSS  120

SEQ ID NO: 276          moltype = AA  length = 450
FEATURE                 Location/Qualifiers
REGION                  1..450
                        note = Synthetic: HC-A
source                  1..450
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 276
EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR IYPTNGYTRY  60
ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCSRWG GDGFYAMDYW GQGTLVTVSS  120
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  180
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  240
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYA  300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRKK  360
LTKNQVKLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDCDGSFFLY SKLTVDKSRW  420
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   450

SEQ ID NO: 277          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1-A
source                  1..11
```

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```
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 277
RASQDVSIAV A                                                        11

SEQ ID NO: 278          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3-A
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 278
QQHYITPLT                                                           9

SEQ ID NO: 279          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic: VL-A
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 279
DIQLTQSPSS LSASVGDRVT ITCRASQDVS IAVAWYQQKP GKAPKLLIYS ASYRYTGVPA  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ HYITPLTFGQ GTKVEIK                107

SEQ ID NO: 280          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: HCDR1-A
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 280
NYGIN                                                               5

SEQ ID NO: 281          moltype = AA  length = 17
FEATURE                 Location/Qualifiers
REGION                  1..17
                        note = Synthetic: HCDR2-A
source                  1..17
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 281
WIHTYTGEPT YTDDFKG                                                  17

SEQ ID NO: 282          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
REGION                  1..12
                        note = Synthetic: HCDR3-A
source                  1..12
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 282
GGFGSSYWYF DV                                                       12

SEQ ID NO: 283          moltype = AA  length = 121
FEATURE                 Location/Qualifiers
REGION                  1..121
                        note = Synthetic: VH-A
source                  1..121
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 283
QVQLLQSGSE LKKPGASVKV SCKASGYTFT NYGINWVRQA PGQGLEWLGW IHTYTGEPTY  60
TDDFKGRFVF SLDTSVSTAY LQISSLKADD TAVYYCARGG FGSSYWYFDV WGQGTLVTVS  120
S                                                                   121

SEQ ID NO: 284          moltype =   length =
SEQUENCE: 284
000

SEQ ID NO: 285          moltype =   length =
SEQUENCE: 285
000
```

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```
SEQ ID NO: 286          moltype =   length =
SEQUENCE: 286
000

SEQ ID NO: 287          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
REGION                  1..11
                        note = Synthetic: LCDR1-A
source                  1..11
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 287
RASQSIRKYL N                                                        11

SEQ ID NO: 288          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
REGION                  1..8
                        note = Synthetic: LCDR3-A
source                  1..8
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 288
QGTHVPFT                                                            8

SEQ ID NO: 289          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic: VL-A
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 289
DIQLTQSPSS LSASVGDRVT ITCRASQSIR KYLNWYQQKP GKAPKLLIYA ASTLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYFCSQ GTHVPFTFGQ GTKVEIK                107

SEQ ID NO: 290          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
REGION                  1..5
                        note = Synthetic: HCDR1-A
source                  1..5
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 290
GYGIH                                                               5

SEQ ID NO: 291          moltype = AA  length = 17
FEATURE                 Location/Qualifiers
REGION                  1..17
                        note = Synthetic: HCDR2-A
source                  1..17
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 291
WISPSGGDTK YAQKFQG                                                  17

SEQ ID NO: 292          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: HCDR3-A
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 292
GGTVVYFDY                                                           9

SEQ ID NO: 293          moltype = AA  length = 118
FEATURE                 Location/Qualifiers
REGION                  1..118
                        note = Synthetic: VH-A
source                  1..118
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 293
EVQLVESGGG LVQPGGSLRL SCAASGFTFS GYGIHWVRQA PGKGLEWIGW ISPSGGDTKY  60
AQKFQGRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARGG TVVYFDYWGQ GTLVTVSS    118
```

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```
SEQ ID NO: 294          moltype = AA  length = 19
FEATURE                 Location/Qualifiers
REGION                  1..19
                        note = Synthetic: HCDR2-B
source                  1..19
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 294
RIRSKYNNYA TYYAESVKG                                                19

SEQ ID NO: 295          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: HCDR3-B
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 295
HGNFGTSYVS WFAY                                                     14

SEQ ID NO: 296          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
REGION                  1..14
                        note = Synthetic: LCDR1-B
source                  1..14
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 296
GSSTGAVTTS NYPN                                                     14

SEQ ID NO: 297          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: LCDR2-B
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 297
GTNKRAP                                                             7

SEQ ID NO: 298          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3-B
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 298
ALWYSNLWV                                                           9

SEQ ID NO: 299          moltype = AA  length = 254
FEATURE                 Location/Qualifiers
REGION                  1..254
                        note = Synthetic: scFv-B
source                  1..254
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 299
QAVVTQEPSL TVSPGGTVTL TCGSSTGAVT TSNYPNWVQQ KPGQAPRGLI GGTNKRAPGV  60
PARFSGSLLG GKAALTLSGA QPEDEAEYYC ALWYSNLWVF GGGTKLTVLG GGGSGGGGSG  120
GGGSGGGGSE VQLVESGGGL VQPGGSLRLS CAASGFTFNT YAINWVRQAP GKGLEWVGRI  180
RSKYNNYATY YAESVKGRFT ISRDDSKNTL YLQINSLRAE DTAVYYCVRH GNFGTSYVSW  240
FAYWGQGTLV TVSS                                                    254

SEQ ID NO: 300          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: LCDR2
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 300
DASSLES                                                             7

SEQ ID NO: 301          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
```

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```
REGION                  1..34
                        note = Synthetic: Masking+cleavage peptide sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 301
EVGSYAATYS DCYSDPYACH DGGGPLGLAG SGGS                                34

SEQ ID NO: 302          moltype = AA  length = 31
FEATURE                 Location/Qualifiers
REGION                  1..31
                        note = Synthetic: Masking+cleavage peptide sequence
source                  1..31
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 302
EAATYSDCYS DPYACHDSGG GPLGLAGSGG S                                   31

SEQ ID NO: 303          moltype = AA  length = 28
FEATURE                 Location/Qualifiers
REGION                  1..28
                        note = Synthetic: Masking+cleavage peptide sequence
source                  1..28
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 303
EYSDCYSDPY ACHDSGGGPL GLAGSGGS                                       28

SEQ ID NO: 304          moltype = AA  length = 34
FEATURE                 Location/Qualifiers
REGION                  1..34
                        note = Synthetic: Masking+cleavage peptide sequence
source                  1..34
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 304
EVGSYAAFSP ACYTDPYSCH AGGGPLGLAG SGGS                                34

SEQ ID NO: 305          moltype = AA  length = 30
FEATURE                 Location/Qualifiers
REGION                  1..30
                        note = Synthetic: Masking+cleavage peptide sequence
source                  1..30
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 305
EAAFSPACYT DPYSCHAGGG PLGLAGSGGS                                     30

SEQ ID NO: 306          moltype = AA  length = 27
FEATURE                 Location/Qualifiers
REGION                  1..27
                        note = Synthetic: Masking+cleavage peptide sequence
source                  1..27
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 306
ESPACYTDPY SCHAGGGPLG LAGSGGS                                        27

SEQ ID NO: 307          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 307
YEYDYYAFDY                                                           10

SEQ ID NO: 308          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: LCDR2
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 308
```

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```
AASSLES                                                          7

SEQ ID NO: 309          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 309
YEYGYYALDY                                                       10

SEQ ID NO: 310          moltype = AA  length = 15
FEATURE                 Location/Qualifiers
REGION                  1..15
                        note = Synthetic: LCDR1
source                  1..15
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 310
RASQSVDFYG ISFLH                                                 15

SEQ ID NO: 311          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 311
QQSYRTPPT                                                        9

SEQ ID NO: 312          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 312
YEYGYYAFDY                                                       10

SEQ ID NO: 313          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 313
QQSYRTPRT                                                        9

SEQ ID NO: 314          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
REGION                  1..7
                        note = Synthetic: HCDR1
source                  1..7
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 314
TSGVGVG                                                          7

SEQ ID NO: 315          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: HCDR2
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 315
EIYHSGSTNY NPSLKS                                                16

SEQ ID NO: 316          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
REGION                  1..16
                        note = Synthetic: HCDR2
```

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```
source                  1..16
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 316
EIYHSGSTYY NPSLKS                                                  16

SEQ ID NO: 317          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 317
YEYDYYDFDY                                                         10

SEQ ID NO: 318          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
REGION                  1..9
                        note = Synthetic: LCDR3
source                  1..9
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 318
QQSYRSPLT                                                          9

SEQ ID NO: 319          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 319
YEYYSYAFDY                                                         10

SEQ ID NO: 320          moltype = AA  length = 15
FEATURE                 Location/Qualifiers
REGION                  1..15
                        note = Synthetic: LCDR1
source                  1..15
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 320
RASQSVDFHG KSFLH                                                   15

SEQ ID NO: 321          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 321
YGYYYYDFDY                                                         10

SEQ ID NO: 322          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 322
YKYDYYDFDY                                                         10

SEQ ID NO: 323          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 323
YEYYEYDFDY                                                         10
```

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```
SEQ ID NO: 324          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Synthetic: HCDR3
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 324
YEYYHYDFDY                                                          10

SEQ ID NO: 325          moltype = AA  length = 216
FEATURE                 Location/Qualifiers
REGION                  1..216
                        note = Synthetic: LC
source                  1..216
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 325
DIQLTQSPSS LSASVGDRVT ITCRASQSIP SFLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQH YISWPRQFTF GQGTKVEIKR TVAAPSVFIF  120
PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST  180
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC                            216

SEQ ID NO: 326          moltype = AA  length = 448
FEATURE                 Location/Qualifiers
REGION                  1..448
                        note = Synthetic: HC_A
source                  1..448
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 326
EVQLVESGGG LVQPGGSLRL SCAASGYSIS SGYYWGWIRQ APGKGLEWIG IIYPSGGGTN  60
YAQKFQGRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARG GGLGFDYWGQ GTLVTVSSAS  120
TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL  180
YSLSSVVTVP SSSLGTQTYI CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYAST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSRKKLT  360
KNQVKLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD CDGSFFLYSK LTVDKSRWQQ  420
GNVFSCSVMH EALHNHYTQK SLSLSPGK                                     448

SEQ ID NO: 327          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 327
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVSWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYYYYDFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 328          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 328
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVSWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYDYYDFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483
```

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```
SEQ ID NO: 329          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 329
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVSWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYYEYDFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 330          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 330
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVSWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYYHYDFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 331          moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 331
DIQMTQSPSS LSASVGDRVT ITCKASQDVS IGVAWYQQKP GKAPKLLIYS ASYRYTGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYIYPYTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 332          moltype = AA  length = 449
FEATURE                 Location/Qualifiers
REGION                  1..449
                        note = Synthetic: HC_A
source                  1..449
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 332
EVQLVESGGG LVQPGGSLRL SCAASGFTFT DYTMDWVRQA PGKGLEWVAD VNPNSGGSIY  60
NQRFKGRFTL SVDRSKNTLY LQMNSLRAED TAVYYCARNL GPSFYFDYWG QGTLVTVSSA  120
STKGPSVFPL APSSKSTSGG TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYAS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSRKKL  360
TKNQVKLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DCDGSFFLYS KLTVDKSRWQ  420
QGNVFSCSVM HEALHNHYTQ KSLSLSPGK                                    449

SEQ ID NO: 333          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 333
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR TFGQGTKVEI KGGGGSGGGG  120
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SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STGGVGVSWI RQAPGKGLEW  180
IGEIYHSGST YYSPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYYYYDFDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 334          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 334
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGKSFLHWY QQKPGKAPKL LIYAASSLES  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPP TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STGGVGVSWI RQAPGKGLEW  180
IGSIYHSGST YYNPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYDYYAFDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 335          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 335
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGISFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPP TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STGGVGVSWI RQAPGKGLEW  180
IGSIYHSGST YYNPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYGYYALDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 336          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 336
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGKSFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPL TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STSGVGVSWI RQAPGKGLEW  180
IGSIYHSGST YYNPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYGYYAFDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 337          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 337
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGISFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPR TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STSGVGVSWI RQAPGKGLEW  180
IGSIYHSGST YYNPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYDYYAFDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
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NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 338          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 338
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGKSFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPR TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STSGVGVGWI RQAPGKGLEW  180
IGEIYHSGST NYNPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYGYYALDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 339          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 339
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY QQKPGKAPKL LIYAASSLES  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPR TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STGGVGVGWI RQAPGKGLEW  180
IGEIYHSGST YYNPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYGYYAFDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 340          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 340
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGKSFLHWY QQKPGKAPKL LIYAASSLES  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPL TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STSGVGVGWI RQAPGKGLEW  180
IGSIYHSGST YYNPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYDYYDFDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 341          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 341
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STSGVGVSWI RQAPGKGLEW  180
IGEIYHSGST YYNPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYGYYAFDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483
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SEQ ID NO: 342          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 342
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGKSFLHWY QQKPGKAPKL LIYAASSLQS  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STSGVGVSWI RQAPGKGLEW  180
IGEIYHSGST YYSPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYYSYAFDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 343          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 343
DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGISFLHWY QQKPGKAPKL LIYAASSLES  60
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPL TFGQGTKVEI KGGGGSGGGG  120
SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFSL STGGVGVSWI RQAPGKGLEW  180
IGSIYHSGST YYSPSLKSRV TISRDNSKNT LYLQLNSLRA EDTAVYYCAR YEYDYYAFDY  240
WGQGTLVTVS SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 344          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 344
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVSWIR QAPGKGLEWI GSIYHSGSTY  60
YNPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYDYYAFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGKSFLHWY  180
QQKPGKAPKL LIYAASSLES GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPP  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 345          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 345
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVSWIR QAPGKGLEWI GSIYHSGSTY  60
YNPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYGYYALDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGISFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPP  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 346          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
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source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 346
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVSWIR QAPGKGLEWI GSIYHSGSTY  60
YNPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYGYYAFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGKSFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPL  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 347          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 347
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVSWIR QAPGKGLEWI GSIYHSGSTY  60
YNPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYDYYAFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGISFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 348          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 348
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVGWIR QAPGKGLEWI GEIYHSGSTN  60
YNPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYGYYALDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGKSFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 349          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 349
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVGWIR QAPGKGLEWI GEIYHSGSTY  60
YNPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYGYYAFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY  180
QQKPGKAPKL LIYAASSLES GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 350          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 350
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EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVGWIR QAPGKGLEWI GSIYHSGSTY  60
YNPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYDYYDFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGKSFLHWY  180
QQKPGKAPKL LIYAASSLES GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPL  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 351          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 351
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVSWIR QAPGKGLEWI GEIYHSGSTY  60
YNPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYGYYAFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 352          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 352
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVSWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYYSYAFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGKSFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 353          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 353
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVSWIR QAPGKGLEWI GSIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY EYDYYAFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FYGISFLHWY  180
QQKPGKAPKL LIYAASSLES GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRTPL  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                                483

SEQ ID NO: 354          moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic: LC
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 354
DIQLTQSPSS LSASVGDRVT ITCRASQSIR KYLNWYQQKP GKAPKLLIYA ASTLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYFCSQ GTHVPFTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214
```

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SEQ ID NO: 355          moltype = AA  length = 448
FEATURE                 Location/Qualifiers
REGION                  1..448
                        note = Synthetic: HC_A
source                  1..448
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 355
EVQLVESGGG LVQPGGSLRL SCAASGFTFS GYGIHWVRQA PGKGLEWIGW ISPSGGDTKY  60
AQKFQGRVTI SRDNSKNTLY LQLNSLRAED TAVYYCARGG TVVYFDYWGQ GTLVTVSSAS  120
TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL  180
YSLSSVVTVP SSSLGTQTYI CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYAST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSRKKLT  360
KNQVKLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD CDGSFFLYSK LTVDKSRWQQ  420
GNVFSCSVMH EALHNHYTQK SLSLSPGK                                    448

SEQ ID NO: 356          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 356
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVSWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY GYYYYDFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                               483

SEQ ID NO: 357          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 357
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TSGVGVGWIR QAPGKGLEWI GEIYHSGSTY  60
YNPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY KYDYYDFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                               483

SEQ ID NO: 358          moltype = AA  length = 483
FEATURE                 Location/Qualifiers
REGION                  1..483
                        note = Synthetic: HC_B
source                  1..483
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 358
EVQLVESGGG LVQPGGSLRL SCAASGFSLS TGGVGVGWIR QAPGKGLEWI GEIYHSGSTY  60
YSPSLKSRVT ISRDNSKNTL YLQLNSLRAE DTAVYYCARY GYYYYDFDYW GQGTLVTVSS  120
GGGGSGGGGS GGGGSGGGGS DIQLTQSPSS LSASVGDRVT ITCRASQSVD FHGISFLHWY  180
QQKPGKAPKL LIYAASSLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSYRSPR  240
TFGQGTKVEI KEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV  300
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYASTYRVVS VLTVLHQDWL NGKEYKCKVS  360
NKALPAPIEK TISKAKGQPR EPQVYTDPPS RDELTKNQVS LTCLVDGFYP SDIAVEWESN  420
GQPENCYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQDSLSLS  480
PGK                                                               483
```

-continued

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SEQ ID NO: 359          moltype = AA  length = 108
FEATURE                 Location/Qualifiers
REGION                  1..108
                        note = misc_feature - sp10747:28_HUMAN
source                  1..108
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 359
NKILVKQSPM LVAYDNAVNL SCKYSYNLFS REFRASLHKG LDSAVEVCVV YGNYSQQLQV  60
YSKTGFNCDG KLGNESVTFY LQNLYVNQTD IYFCKIEVMY PPPYLDNE               108

SEQ ID NO: 360          moltype = AA  length = 108
FEATURE                 Location/Qualifiers
REGION                  1..108
                        note = misc_feature - sp[P3]1041:28_MOUSE
source                  1..108
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 360
NKILVKQSPL LVVDSNEVSL SCRYSYNLLA KEFRASLYKG VNSDVEVCVG NGNFTYQPQF  60
RSNAEFNCDG DFDNETVTFR LWNLHVNHTD IYFCKIEFMY PPPYLDNE               108

SEQ ID NO: 361          moltype = AA  length = 108
FEATURE                 Location/Qualifiers
REGION                  1..108
                        note = Synthetic: TY24865
source                  1..108
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 361
NKILVKQSPM LVAYDNAVNL SCKYSYNLFS REFRASLHKG LDSAVEVCVV YGNYSQQLQV  60
YSKTGFNCDG KLGNESVTFY LQNLYVNQTD IYFCKIEVMY PPPYLDNE               108
```

1. An antigen-binding protein, or an antigen-binding fragment thereof, comprising an CD28-binding portion, wherein the CD28-binding portion binds human CD28 and is cross-reactive with cynomolgus monkey and mouse CD28.

2. The antigen-binding protein or fragment thereof of claim **1**, wherein the CD28-binding portion binds to a CD28 epitope comprising amino acid residues 51-122 of human CD28 (SEQ ID NO: 1).

3. The antigen-binding protein or fragment thereof of claim **2**, wherein the CD28 epitope comprises amino acid residues 51, 52, 54, 55, 98-101, 110-111, 113-114, and 118-122 of SEQ ID NO: 1.

4. The antigen-binding protein or fragment thereof of any one of claims **1-3**, wherein the CD28-binding portion comprises an antibody heavy chain variable domain (V_H) and an antibody light chain variable domain (V_L), and wherein the V_H and V_L comprise heavy chain complementarity-determining regions (CDRs) 1-3 and light chain CDR1-3 set forth in

SEQ ID NOs: 5-10, respectively,
SEQ ID NOs: 15, 6, 16, 17-19, respectively,
SEQ ID NOs: 24, 6, 25, 26-28, respectively,
SEQ ID NOs: 33, 6, 35-38, respectively,
SEQ ID NOs: 43, 6, 44, 45, 9, and 46, respectively,
SEQ ID NOs: 33, 51-53, 300, and 10, respectively,
SEQ ID NOs: 24, 58, 59, 60, 300, and 61, respectively,
SEQ ID NOs: 66-69, 300 and 70, respectively,
SEQ ID NOs: 24, 6, 75, 76, 18, and 28, respectively,
SEQ ID NOs: 24, 58, 81, 82, 27, and 83, respectively,
SEQ ID NOs: 88-91, 300, and 70, respectively,
SEQ ID NOs: 24, 96-98, 9, and 70, respectively,
SEQ ID NOs: 103-106, 18, and 83, respectively,
SEQ ID NOs: 111, 6, 112, 113, 18, and 114, respectively,
SEQ ID NOs: 15, 6, 119, 120, 9, and 121, respectively,
SEQ ID NOs: 126, 67, 127, 128, 18, and 129, respectively,
SEQ ID NOs: 134, 6, 135, 136, 27, and 83, respectively,
SEQ ID NOs: 43, 58, 141, 142, 300, and 143, respectively,
SEQ ID NOs: 148, 6, 149, 150, 300, and 83, respectively,
SEQ ID NOs: 15, 155, 16, 156, 27, and 70, respectively,
SEQ ID NOs: 161, 6, 162, 163, 300, and 164, respectively,
SEQ ID NOs: 5, 96, 307, 76, 308, and 46, respectively,
SEQ ID NOs: 5, 96, 309, 310, 9, and 311, respectively,
SEQ ID NOs: 43, 96, 312, 76, 9, and 28, respectively,
SEQ ID NOs: 43, 96, 307, 310, 9, and 313, respectively,
SEQ ID NOs: 314, 315, 309, 76, 9, and 313, respectively,
SEQ ID NOs: 33, 316, 312, 8, 308, and 313, respectively,
SEQ ID NOs: 314, 96, 317, 76, 308, and 318, respectively,
SEQ ID NOs: 43, 316, 312, 8, 9, and 10, respectively,
SEQ ID NOs: 43, 6, 319, 320, 9, and 10, respectively,
SEQ ID NOs: 5, 67, 307, 310, 308, and 28, respectively,
SEQ ID NOs: 43, 6, 321, 8, 9, and 10, respectively,
SEQ ID NOs: 314, 316, 322, 8, 9, and 10, respectively,
SEQ ID NOs: 33, 6, 321, 8, 9, and 10, respectively,
SEQ ID NOs: 5, 6, 317, 8, 9, and 10, respectively,
SEQ ID NOs: 5, 6, 323, 8, 9, and 10, respectively, or
SEQ ID NOs: 5, 6, 324, 8, 9, and 10, respectively.

5. An antigen-binding protein or antigen-binding fragment thereof, comprising a CD28-binding portion that binds human CD28, wherein the CD28-binding portion comprises an antibody heavy chain variable domain (V_H) and an antibody light chain variable domain (V_L), and wherein the

V_H and V_L comprise heavy chain complementarity-determining regions (CDRs) 1-3 and light chain CDR1-3 set forth in

SEQ ID NOs: 5-10, respectively,
SEQ ID NOs: 15, 6, 16, 17-19, respectively,
SEQ ID NOs: 24, 6, 25, 26-28, respectively,
SEQ ID NOs: 33, 6, 35-38, respectively,
SEQ ID NOs: 43, 6, 44, 45, 9, and 46, respectively,
SEQ ID NOs: 33, 51-53, 300, and 10, respectively,
SEQ ID NOs: 24, 58, 59, 60, 300, and 61, respectively,
SEQ ID NOs: 66-69, 300 and 70, respectively,
SEQ ID NOs: 24, 6, 75, 76, 18, and 28, respectively,
SEQ ID NOs: 24, 58, 81, 82, 27, and 83, respectively,
SEQ ID NOs: 88-91, 300, and 70, respectively,
SEQ ID NOs: 24, 96-98, 9, and 70, respectively,
SEQ ID NOs: 103-106, 18, and 83, respectively,
SEQ ID NOs: 111, 6, 112, 113, 18, and 114, respectively,
SEQ ID NOs: 15, 6, 119, 120, 9, and 121, respectively,
SEQ ID NOs: 126, 67, 127, 128, 18, and 129, respectively,
SEQ ID NOs: 134, 6, 135, 136, 27, and 83, respectively,
SEQ ID NOs: 43, 58, 141, 142, 300, and 143, respectively,
SEQ ID NOs: 148, 6, 149, 150, 300, and 83, respectively,
SEQ ID NOs: 15, 155, 16, 156, 27, and 70, respectively, or
SEQ ID NOs: 161, 6, 162, 163, 300, and 164, respectively
SEQ ID NOs: 5, 96, 307, 76, 308, and 46, respectively,
SEQ ID NOs: 5, 96, 309, 310, 9, and 311, respectively,
SEQ ID NOs: 43, 96, 312, 76, 9, and 28, respectively,
SEQ ID NOs: 43, 96, 307, 310, 9, and 313, respectively,
SEQ ID NOs: 314, 315, 309, 76, 9, and 313, respectively,
SEQ ID NOs: 33, 316, 312, 8, 308, and 313, respectively,
SEQ ID NOs: 314, 96, 317, 76, 308, and 318, respectively,
SEQ ID NOs: 43, 316, 312, 8, 9, and 10, respectively,
SEQ ID NOs: 43, 6, 319, 320, 9, and 10, respectively,
SEQ ID NOs: 5, 67, 307, 310, 308, and 28, respectively,
SEQ ID NOs: 43, 6, 321, 8, 9, and 10, respectively,
SEQ ID NOs: 314, 316, 322, 8, 9, and 10, respectively,
SEQ ID NOs: 33, 6, 321, 8, 9, and 10, respectively,
SEQ ID NOs: 5, 6, 317, 8, 9, and 10, respectively,
SEQ ID NOs: 5, 6, 323, 8, 9, and 10, respectively, or
SEQ ID NOs: 5, 6, 324, 8, 9, and 10, respectively.

6. The antigen-binding protein or fragment thereof of claim **4** or **5**, wherein the CD28-binding portion comprises V_H and V_L set forth in

SEQ ID NOs: 11 and 12, respectively,
SEQ ID NOs: 20 and 21, respectively,
SEQ ID NOs: 29 and 30, respectively,
SEQ ID NOs: 39 and 40, respectively,
SEQ ID NOs: 47 and 48, respectively,
SEQ ID NOs: 54 and 55, respectively,
SEQ ID NOs: 62 and 63, respectively,
SEQ ID NOs: 71 and 72, respectively,
SEQ ID NOs: 77 and 78, respectively,
SEQ ID NOs: 84 and 85, respectively,
SEQ ID NOs: 92 and 93, respectively,
SEQ ID NOs: 99 and 100, respectively,
SEQ ID NOs: 107 and 108, respectively,
SEQ ID NOs: 115 and 116, respectively,
SEQ ID NOs: 122 and 123, respectively,
SEQ ID NOs: 130 and 131, respectively,
SEQ ID NOs: 137 and 138 respectively,
SEQ ID NOs: 144 and 145, respectively,
SEQ ID NOs: 151 and 152, respectively,
SEQ ID NOs: 157 and 158, respectively,
SEQ ID NOs: 165 and 166, respectively,
SEQ ID NOs: 362 and 363, respectively,
SEQ ID NOs: 364 and 365, respectively,
SEQ ID NOs: 366 and 367, respectively,
SEQ ID NOs: 368 and 369, respectively,
SEQ ID NOs: 370 and 371, respectively,
SEQ ID NOs: 372 and 373, respectively,
SEQ ID NOs: 374 and 375, respectively,
SEQ ID NOs: 376 and 12, respectively,
SEQ ID NOs: 377 and 378, respectively,
SEQ ID NOs: 379 and 380, respectively,
SEQ ID NOs: 381 and 12, respectively,
SEQ ID NOs: 382 and 12, respectively,
SEQ ID NOs: 383 and 12, respectively,
SEQ ID NOs: 384 and 12, respectively,
SEQ ID NOs: 385 and 12, respectively, or
SEQ ID NOs: 386 and 12, respectively.

7. The antigen-binding protein of claim **4** or **5**, comprising an antibody heavy chain and antibody light chain set forth in

SEQ ID NOs: 13 and 14, respectively,
SEQ ID NOs: 22 and 23, respectively,
SEQ ID NOs: 31 and 32, respectively,
SEQ ID NOs: 41 and 42, respectively,
SEQ ID NOs: 49 and 50, respectively,
SEQ ID NOs: 56 and 57, respectively,
SEQ ID NOs: 64 and 65, respectively
SEQ ID NOs: 73 and 74, respectively,
SEQ ID NOs: 79 and 80, respectively,
SEQ ID NOs: 86 and 87, respectively,
SEQ ID NOs: 94 and 95, respectively,
SEQ ID NOs: 101 and 102, respectively,
SEQ ID NOs: 109 and 110, respectively,
SEQ ID NOs: 117 and 118, respectively,
SEQ ID NOs: 124 and 125, respectively,
SEQ ID NOs: 141 and 142, respectively,
SEQ ID NOs: 132 and 133, respectively,
SEQ ID NOs: 139 and 140, respectively,
SEQ ID NOs: 146 and 147, respectively,
SEQ ID NOs: 153 and 154, respectively,
SEQ ID NOs: 159 and 160, respectively, or
SEQ ID NOs: 167 and 168, respectively.

8. The antigen-binding protein or fragment thereof of any one of claims **1-7**, wherein the antigen-binding protein or fragment thereof does not have superagonist activity.

9. The antigen-binding protein or fragment thereof of any one of claims **1-8**, further comprising a second antigen-binding portion targeting a tumor-associated antigen (TAA).

10. The antigen-binding protein or fragment thereof of claim **9**, wherein the TAA is HER2, B7-H3, or TROP-2.

11. The antigen-binding protein or fragment thereof of claim **10**, comprising a HER2-binding portion comprising

HCDR1-3 and LCDR1-3 set forth in SEQ ID NOs: 262-264 and 258-260, respectively, or
V_H and V_L set forth in SEQ ID NOs: 265 and 261, respectively.

12. The antigen-binding protein or fragment thereof of claim **10**, comprising a B7-H3-binding portion comprising

HCDR1-3 and LCDR1-3 set forth in SEQ ID NOs: 290-292 and 287, 18, and 288, respectively, or
V_H and V_L set forth in SEQ ID NOs: 293 and 289, respectively.

13. The antigen-binding protein or fragment thereof of claim **10**, comprising a TROP-2-binding portion comprising

HCDR1-3 and LCDR1-3 set forth in SEQ ID NOs: 280-282 and 277, 259, and 278, respectively, or

V_H and V_L set forth in SEQ ID NOs: 283 and 279, respectively.

14. The antigen-binding protein or fragment thereof of any one of claims **1-13**, wherein either or both of the CD28-binding portion and the TAA-binding portion are a single chain Fv (scFv), Fv, scFab, or Fab.

15. The antigen-binding protein or fragment thereof of claim **11**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 169 and 170, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 171 or a scFv fusion polypeptide comprising SEQ ID NO: 266.

16. The antigen-binding protein or fragment thereof of claim **11**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 169 and 170, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 172 or a scFv fusion polypeptide comprising SEQ ID NO: 266.

17. The antigen-binding protein or fragment thereof of claim **11**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 271 and 276, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 171 or a scFv fusion polypeptide comprising SEQ ID NO: 266.

18. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 327.

19. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 333.

20. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 334.

21. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 335.

22. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 336.

23. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 337.

24. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 338.

25. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 339.

26. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 340.

27. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 341.

28. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 342.

29. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 343.

30. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 344.

31. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 345.

32. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 346.

33. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 347.

34. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 348.

35. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 349.

36. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 350.

37. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 351.

38. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 352.

39. The antigen-binding protein or fragment thereof of claim **10**, wherein the HER2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 331 and 332, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 353.

40. The antigen-binding protein or fragment thereof of claim **12**, wherein the B7-H3-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 175 and 176, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 171 or a scFv fusion polypeptide comprising SEQ ID NO: 266.

41. The antigen-binding protein or fragment thereof of claim **10**, wherein the B7-H3-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 354 and 355, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 327.

42. The antigen-binding protein or fragment thereof of claim **10**, wherein the B7-H3-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 354 and 355, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 356.

43. The antigen-binding protein or fragment thereof of claim **10**, wherein the B7-H3-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 354 and 355, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 357.

44. The antigen-binding protein or fragment thereof of claim **10**, wherein the B7-H3-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 354 and 355, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 358.

45. The antigen-binding protein or fragment thereof of claim **13**, wherein the TROP2-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 173 and 174, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 171 or a scFv fusion polypeptide comprising SEQ ID NO: 266.

46. The antigen-binding protein or fragment thereof of any one of claims **1-45**, further comprising another antigen-binding portion targeting an immune checkpoint inhibitor.

47. The antigen-binding protein of claim **46**, wherein the immune checkpoint inhibitor is PD-L1.

48. The antigen-binding protein or fragment thereof of claim **47**, wherein the PD-L1-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 325 and 326, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 327.

49. The antigen-binding protein or fragment thereof of claim **47**, wherein the PD-L1-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 325 and 326, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 328.

50. The antigen-binding protein or fragment thereof of claim **47**, wherein the PD-L1-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 325 and 326, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 329.

51. The antigen-binding protein or fragment thereof of claim **47**, wherein the PD-L1-binding portion comprises an antibody light chain and an antibody heavy chain comprising SEQ ID NOs: 325 and 326, respectively, and wherein the CD28-binding portion comprises a heavy chain comprising SEQ ID NO: 330.

52. The antigen-binding protein or fragment thereof of any one of claims **1-51**, further comprising an Fc region.

53. The antigen-binding protein or fragment thereof of claim **52**, wherein the Fc region is of the human IgG1 subclass.

54. The antigen-binding protein or fragment thereof of claim **52**, wherein the Fc region is of the human IgG4 subclass.

55. The antigen-binding protein or fragment thereof of any one of claims **52-54**, wherein the Fc region has reduced or no effector function, reduced or no antibody-dependent cell cytotoxicity (ADCC) effect, and/or reduced or no cross-linking effects.

56. The antigen-binding protein or fragment thereof of any one of claims **1-55**, comprising a first CH3 domain and a second CH3 domain, wherein:

i) the first CH3 domain comprises a cysteine (C) residue at position 390 and the second CH3 domain comprises a cysteine residue at position 400, or the first CH3 domain comprises a cysteine residue at position 400 and the second CH3 domain comprises a cysteine residue at position 390; or

ii) the first CH3 domain comprises a cysteine residue at position 392 and the second CH3 domain comprises a cysteine residue at position 397, or the first CH3

domain comprises a cysteine residue at position 397 and the second CH3 domain comprises a cysteine residue at position 392; or

iii) the first CH3 domain comprises a cysteine residue at position 392 and the second CH3 domain comprises a cysteine residue at position 400, or the first CH3 domain comprises a cysteine residue at position 400 and the second CH3 domain comprises a cysteine residue at position 392; and wherein the amino acid residue numbering is based on Eu numbering.

57. The antigen-binding protein or fragment thereof of claim **56**, wherein:

i) the first CH3 domain further comprises a positively charged residue at position 357 and the second CH3 domain further comprises a negatively charged residue at position 351, or the first CH3 domain further comprises a negatively charged residue at position 351 and the second CH3 domain further comprises a positively charged residue at position 357; or

ii) the first CH3 domain further comprises a positively charged residue at position 411 and the second CH3 domain further comprises a negatively charged residue at position 370, or the first CH3 domain further comprises a negatively charged residue at position 370 and the second CH3 domain further comprises a positively charged residue at position 411; or

iii) the first CH3 domain further comprises a positively charged residue at position 364 and the second CH3 domain further comprises a negatively charged residue at position 370, or the first CH3 domain further comprises a negatively charged residue at position 370 and the second CH3 domain further comprises a positively charged residue at position 364; or a combination of i) and ii), or a combination of i) and iii); and wherein the amino acid residue numbering is based on Eu numbering.

58. The antigen-binding protein or fragment thereof of claim **57**, wherein the first CH3 domain comprises D/E356K, E357K, S364K and S400C substitutions and the second CH3 domain comprises L351D, K370D, N390C and K439D substitutions, or the first CH3 domain comprises L351D, K370D, N390C and K439D substitutions and the second CH3 domain comprises D/E356K, E357K, S364K and S400C substitutions (Eu numbering).

59. The antigen-binding protein or fragment thereof of claim **58**, wherein the CH3 domain further comprises an N297A substitution (Eu numbering).

60. The antigen-binding protein or fragment thereof of any one of claims **1-60**, further comprising at least one masking peptide, wherein the masking peptide (MP) is linked to an N-terminus of the V_L, wherein the MP comprises, from N-terminus to C-terminus, a masking unit (MU) and a linkage unit (LU) with or without cleavage sites.

61. The antigen-binding protein or fragment thereof of claim **60**, and wherein the MU comprises a sequence selected from the group consisting of SEQ ID NOs: 173-206.

62. The antigen-binding protein or fragment thereof of claim **61**, wherein the MP further comprises an N-terminal unit (NU) linked to the N-terminus of the MU.

63. The antigen-binding protein or fragment thereof of claim **62**, wherein the N-terminal unit is about 1-10 amino acid residues long.

64. The antigen-binding protein or fragment thereof of claim **63**, wherein the N-terminal unit comprises E or EVGSY.

65. The antigen-binding protein or fragment thereof of any one of claims **60-64**, wherein the LU comprises a cleavage site.

66. The antigen-binding protein or fragment thereof of claim **65**, wherein the first cleavage site is a protease cleavage site for a protease selected from the group consisting of urokinase-type plasminogen activator/uPA, matrix metalloproteinase-1/MMP-1, MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, Tobacco Etch Virus protease/TEV protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE.

67. The antigen-binding protein or fragment thereof of any one of claims **60-66**, wherein at least one masking peptide is linked to the B7-H3-, HER2-, or TROP2-binding portion or CD28-binding portion, optionally wherein the antigen-binding protein or fragment thereof comprises two masking peptides that bind respectively the B7-H3-, HER2-, or TROP2-binding portion and the CD28-binding portion.

68. The antigen-binding protein or fragment thereof of any one of claims **1-67**, further comprising a conjugated therapeutic moiety, optionally wherein the therapeutic moiety is a radioactive moiety or a cytotoxic moiety.

69. A pharmaceutical composition comprising the antigen-binding protein or fragment thereof of any one of claims **1-68** and a pharmaceutically acceptable carrier.

70. A nucleic acid molecule or nucleic acid molecule (s) encoding the antigen-binding protein or fragment thereof of any one of claims **1-68**.

71. A host cell comprising nucleotide sequence (s) claim **70**.

72. A method of producing an antigen-binding protein or antigen-binding fragment thereof, comprising:

culturing the host cell of claim **71** under conditions that allow expression of the antigen-binding protein or fragment thereof, and isolating the antigen-binding protein or fragment thereof from the culture.

73. A method of treating cancer in a patient in need thereof, comprising administering to the patient a therapeutically effective amount of the antigen-binding protein or fragment thereof of any one of claims **1-68** or the pharmaceutical composition of claim **69**.

74. The method of claim **73**, further comprising administering to the patient another anti-cancer therapeutic.

75. The method of claim **74**, wherein the additional anti-cancer therapeutic is a bispecific antibody targeting CD3 and a tumor antigen, optionally wherein the tumor antigen is the same as or different from the TAA.

76. The antigen-binding protein or fragment thereof of claim **75**, wherein the TAA is B7-H3, HER2, or TROP2.

77. The method of claim **74**, wherein the additional anti-cancer therapeutics is an immune checkpoint inhibitor, optionally an anti-PD-1, anti-CTLA-4, or anti-PD-L1 antibody.

78. The method of any one of claims **73-77**, wherein the patient has a solid tumor or a hematological malignancy,

optionally selected from breast cancer, gastric cancer, lung cancer, ovarian cancer, kidney cancer, pancreatic cancer, and colon cancer.

79. Use of the antigen-binding protein or fragment thereof of any one of claims **1-68** for the manufacture of a medicament in treating cancer, optionally in a method of any one of claims **73-78**.

80. The antigen-binding protein or fragment thereof of any one of claims **1-68**, or the pharmaceutical composition of claim **69**, for use in treating cancer, optionally in a method of any one of claims **73-78**.

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