

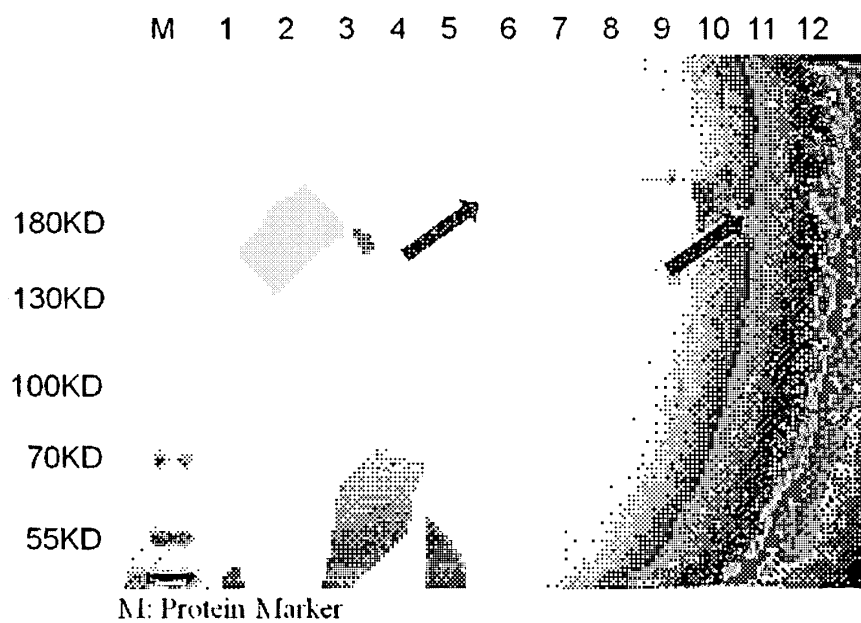


FIG. 1

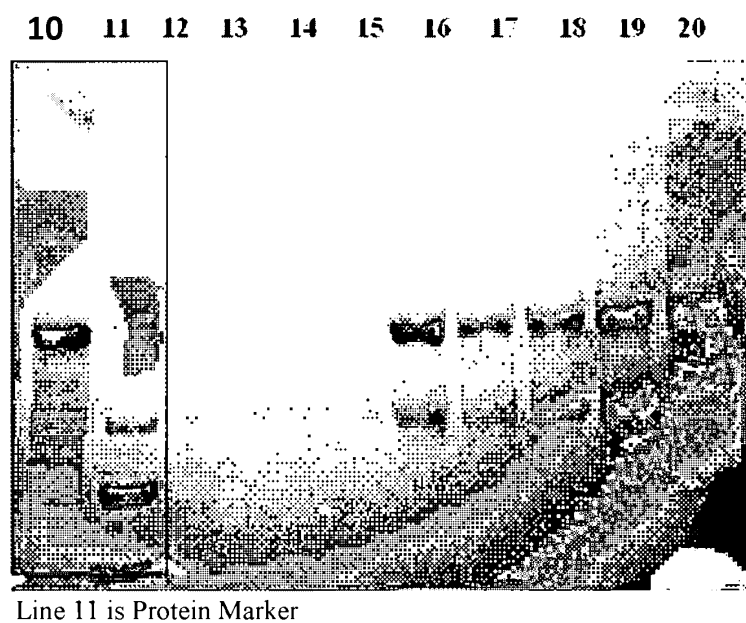


FIG. 2

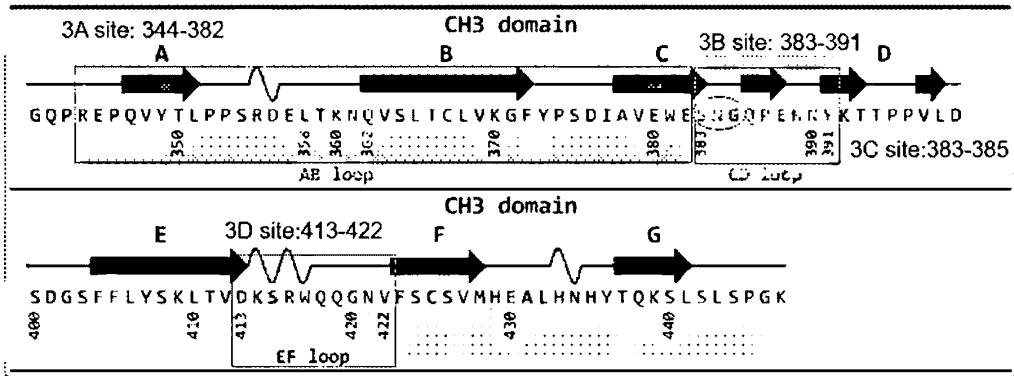


FIG. 3

EU numbering	119	128	138	148	158	168	178
hIgG1-CH	-TKGPSVFPLAFLSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG						
hIgG2-CH	STKGPSVFPLAFCRSTSESTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG						
hIgG4-CH	STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG						
hIgG1-CH	LYSLSSVTVFPSSSLGTQTYICNVNHRKPSNFKVDKKEPKSCDKTHCTCPPEFAPELLGGP						
hIgG2-CH	LYSLSSVTVFPSSNFGTQTYICNVNHRKPSNFKVDKKEPKSCDKTHCTCPPEFAPELLGGP						
hIgG4-CH	LYSLSSVTVFPSSSLGTQTYICNVNHRKPSNFKVDKKEPKSCDKTHCTCPPEFAPELLGGP						
	231 -- -- --						
hIgG1-CH	SVFLFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN						
hIgG2-CH	SVFLFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN						
hIgG4-CH	SVFLFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN						
	----- CH2 -----						
hIgG1-CH	TIRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPAPIEKTIISKAKGQPREPQVYITLPPSR						
hIgG2-CH	TIRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPAPIEKTIISKAKGQPREPQVYITLPPSR						
hIgG4-CH	TIRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYITLPPSR						
	----- CH2 ----- 341 340 CH3 -----						
hIgG1-CH	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSEFLYSLKLTVDKSR						
hIgG2-CH	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSEFLYSLKLTVDKSR						
hIgG4-CH	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSEFLYSLKLTVDKSR						
	----- CH3 -----						
hIgG1-CH	QGNVFSCSVMHEALHNHYTQKSLSLSPGK						
hIgG2-CH	QGNVFSCSVMHEALHNHYTQKSLSLSPGK						
hIgG4-CH	EGNVFSCSVMHEALHNHYTQKSLSLSPGK						
	----- CH3 ----- 447						

FIG. 4

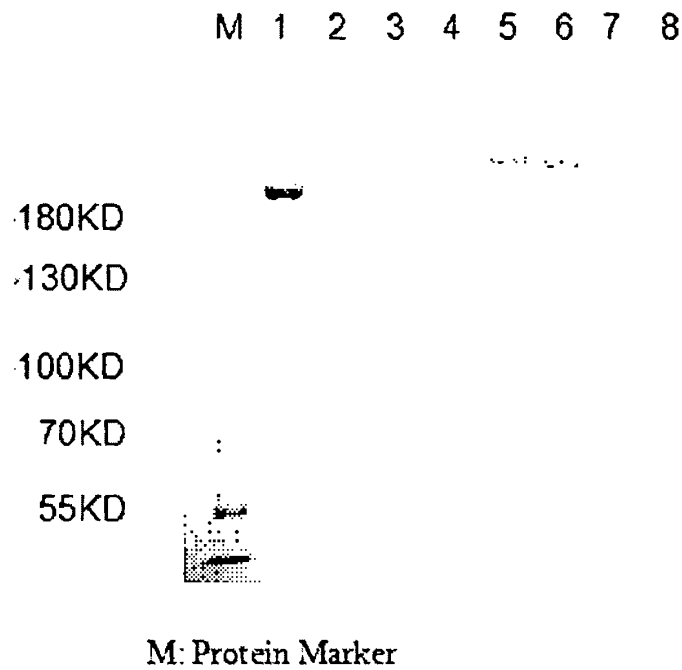


FIG. 5A

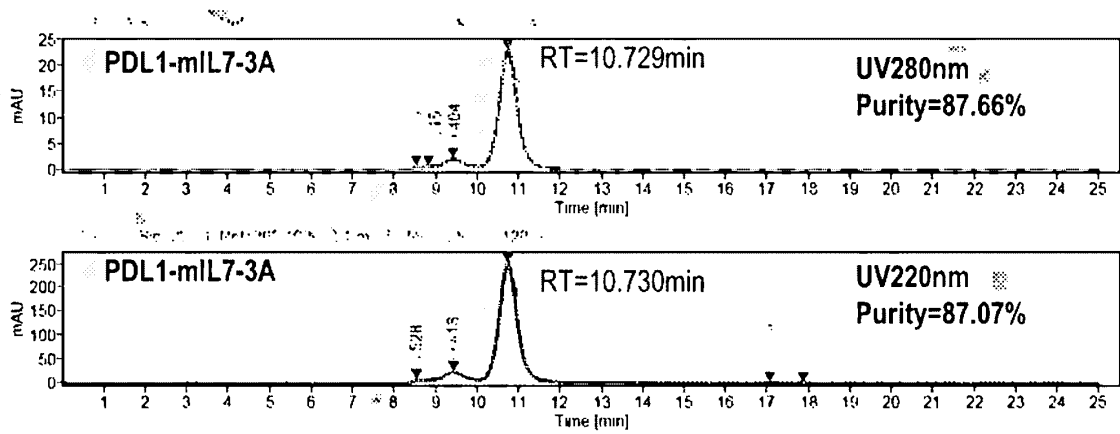


FIG. 5B

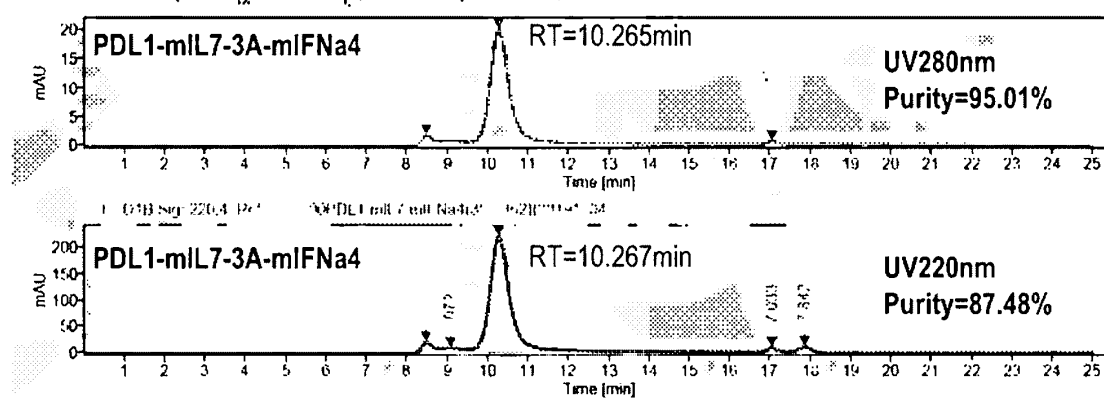


FIG. 5C

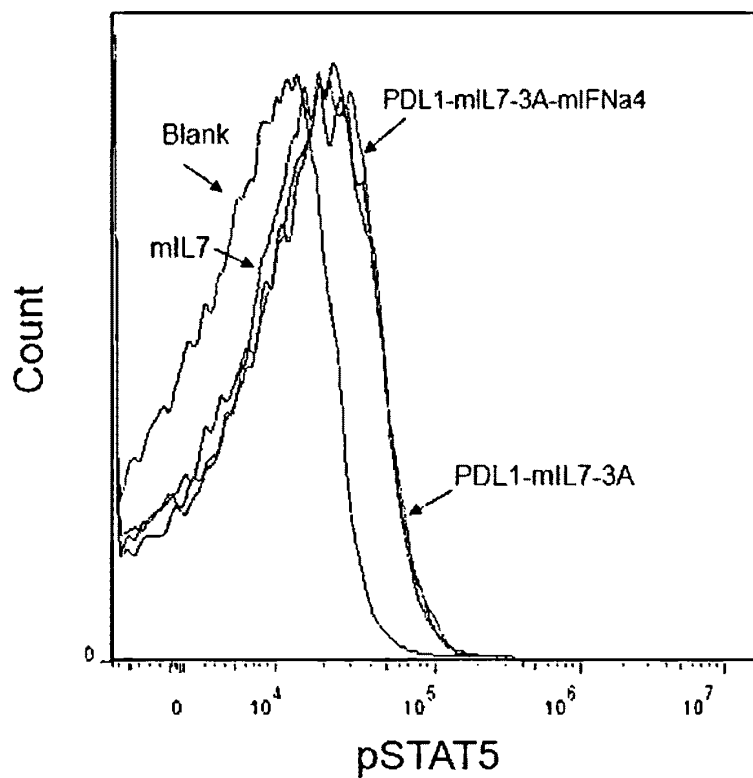


FIG. 6

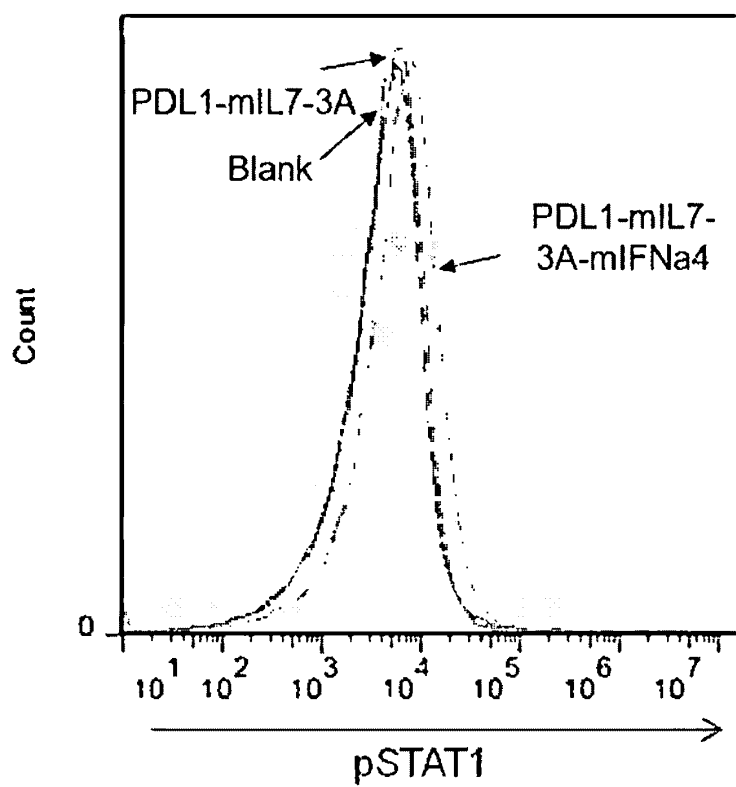


FIG. 7

Fc Receptor	Antibody	Analyte Range	KD (M)	Rmax	Legend level
FcγRIIB-Acro	PDL1-avelumab	3200nm-25nm	3.33E-06	109.5	52.0
FcγRIIB-Acro	PDL1-mIL7-3A-mIFNa4	3200nm-50nm	1.26E-06	309.0	51.9
FcγRIIB-Acro	PDL1-mIL7-3A	3200nm-25nm	2.47E-06	150.3	54.5
FcγRIIA-H167-Acro	PDL1-avelumab	800nm-6.25nm	1.05E-06	181.5	63.5
FcγRIIA-H167-Acro	PDL1-mIL7-3A-mIFNa4	800nm-6.25nm	1.15E-07	287.3	63.8
FcγRIIA-H167-Acro	PDL1-mIL7-3A	800nm-6.25nm	4.26E-07	146.0	65.7
FcγRIIIA-V176-Acro	PDL1-avelumab	400nm-3.125nm	2.63E-07	130.9	42.3
FcγRIIIA-V176-Acro	PDL1-mIL7-3A-mIFNa4	400nm-3.125nm	1.73E-08	267.9	42.3
FcγRIIIA-V176-Acro	PDL1-mIL7-3A	400nm-3.125nm	7.55E-08	190.6	41.9
FcγRIIB-NA1-Acro	PDL1-avelumab	800nm-6.25nm	3.31E-05	734.5	51.4
FcγRIIB-NA1-Acro	PDL1-mIL7-3A-mIFNa4	800nm-6.25nm	5.01E-07	280.0	52.3
FcγRIIB-NA1-Acro	PDL1-mIL7-3A	800nm-6.25nm	4.79E-07	173.9	52.6
FcγRI-Sino	PDL1-avelumab	400nm-6.25nm	1.01E-07	77.6	56.5
FcγRI-Sino	PDL1-mIL7-3A	400nm-6.25nm	1.94E-07	97.1	56.9
FcγRI-Sino	PDL1-mIL7-3A-mIFNa4	400nm-6.25nm	2.71E-08	93.2	57.0
FcRn-Acro	PDL1-avelumab	1000nm-15.625nm	1.25E-06	1011.8	217.0
FcRn-Acro	PDL1-mIL7-3A	1000nm-15.625nm	5.27E-07	1022.4	218.0
FcRn-Acro	PDL1-mIL7-3A-mIFNa4	1000nm-15.625nm	1.60E-07	1028.3	220.6

FIG. 8A

Fc Receptor	PD1-PL1-3F2- FV3A-IgG1	AB-IgG1	PDL1-C40-6A7- FV3A-IgG4	AB-IgG4
	KD (M)	KD (M)	KD (M)	KD (M)
FcyRI-Sino	2.94E-09	2.31E-10	1.22E-09	7.56E-10
FcyRIIA-H167-Acro	6.33E-07	4.75E-07	1.13E-06	1.63E-06
FcyRIIA-R167	3.26E-07	5.93E-07	7.06E-07	7.19E-07
FcyRIIB	2.35E-06	2.39E-06	7.66E-07	1.26E-06
FcyRIIIA-F176	8.46E-08	3.01E-07	negative	negative
FcyRIIIA-V176-Acro	1.30E-07	1.77E-07	7.53E-08	6.75E-07
FcyRIIIB-NA1-Acro	1.18E-06	4.42E-07	negative	negative

FIG. 8B

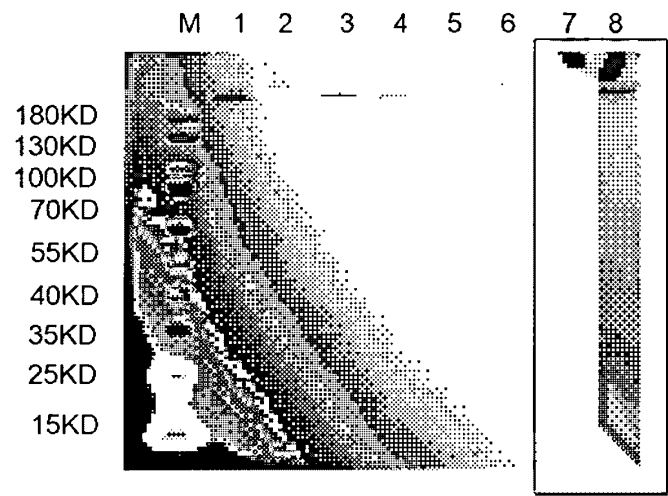


FIG. 9A

Lane	Name (storage temperature)	Theoretical MW	Apparent MW
7	PDL1-mIL7-3A (40°C)	183KD	≥180KD
8	PDL1-mIL7-3A (-20°C)	183KD	≥180KD

FIG. 9B

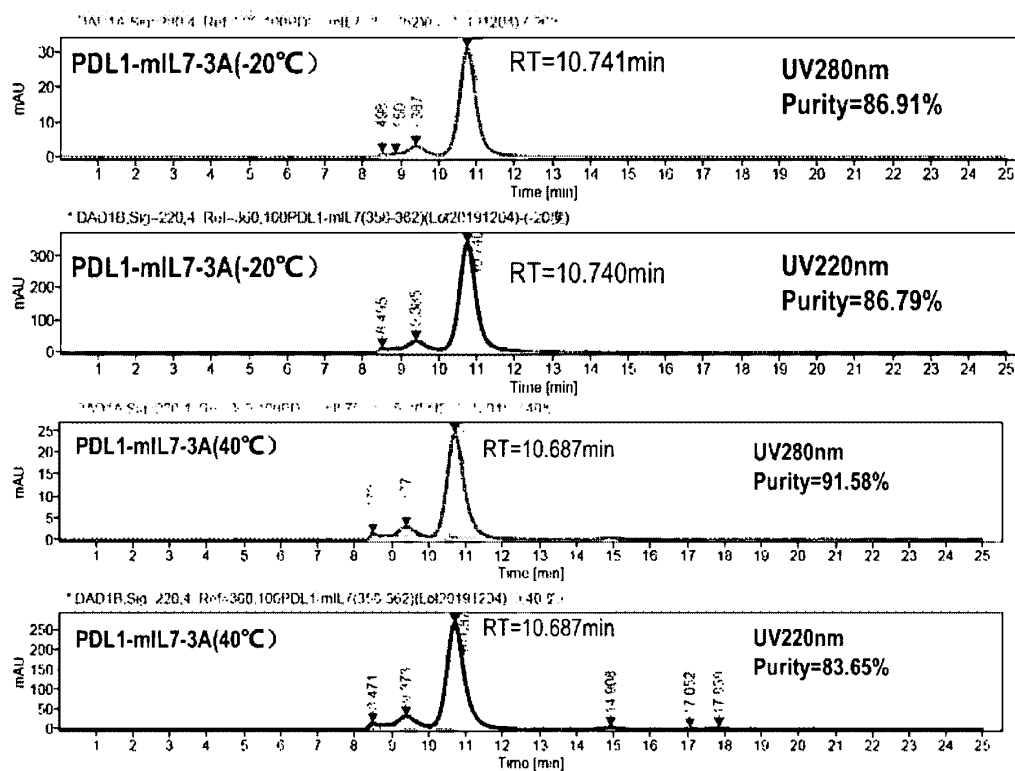
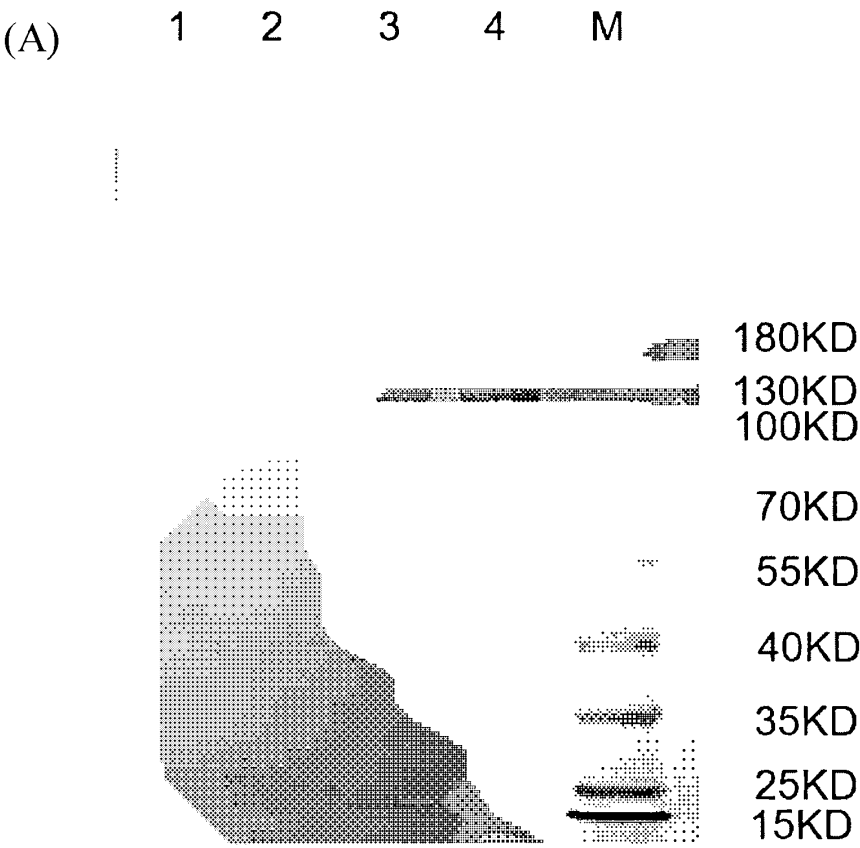


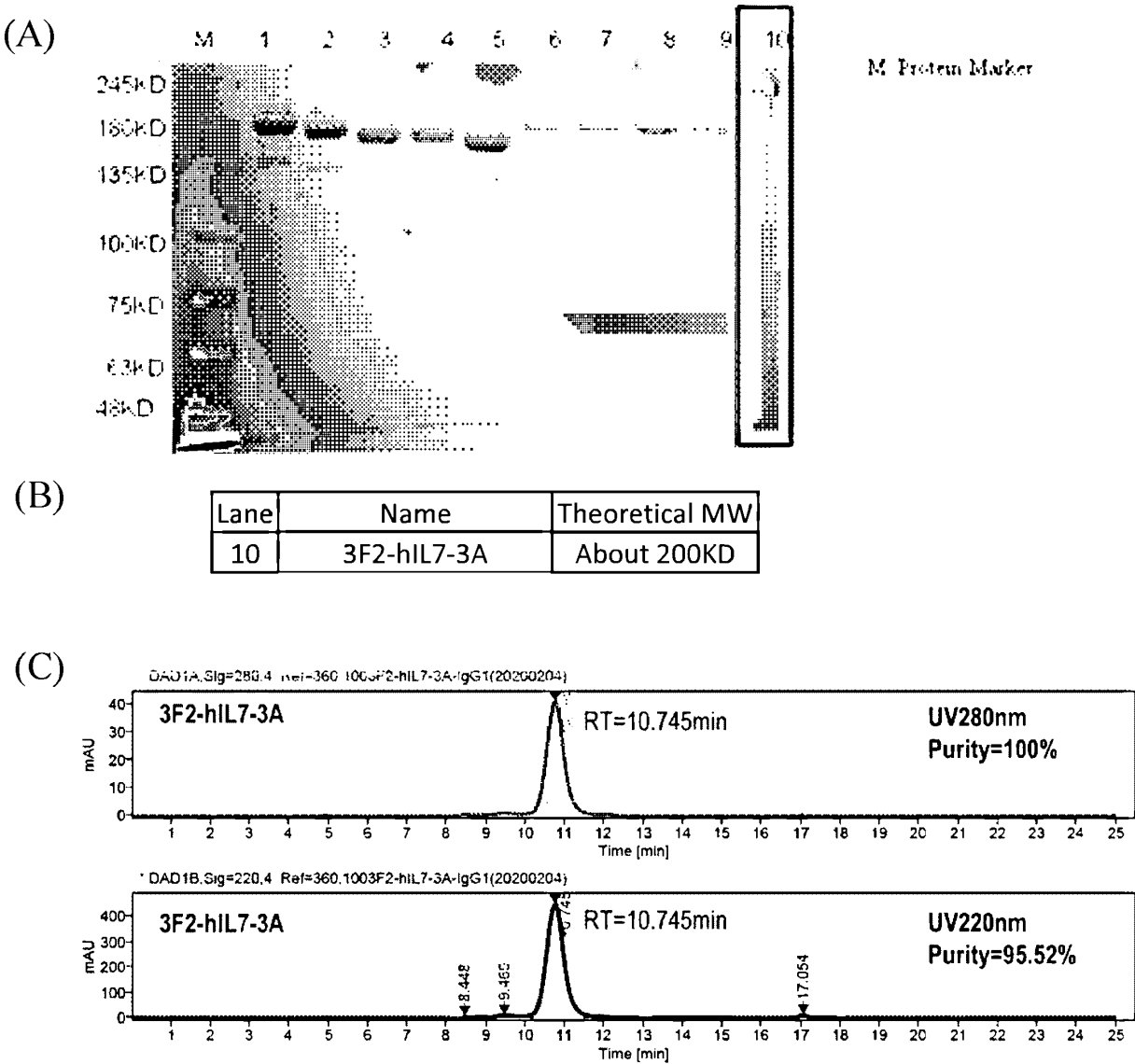
FIG. 9C



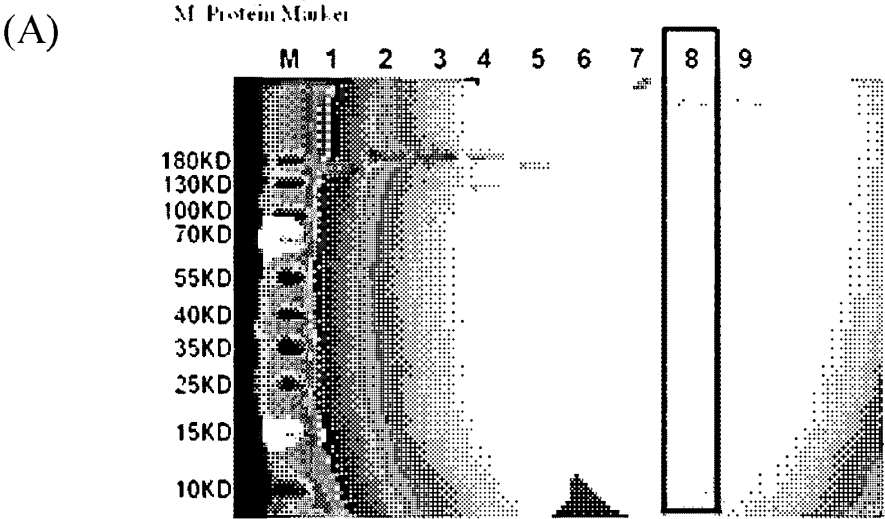
(B)

Lane	Name
1	PDL1-mIL7-3A
2	PDL1-mIL7-Fab-half-3A-KIH
3	PDL1-mIL7-3A-hole
4	PDL1-mIL7-3A-knob

FIGS. 10A-10B

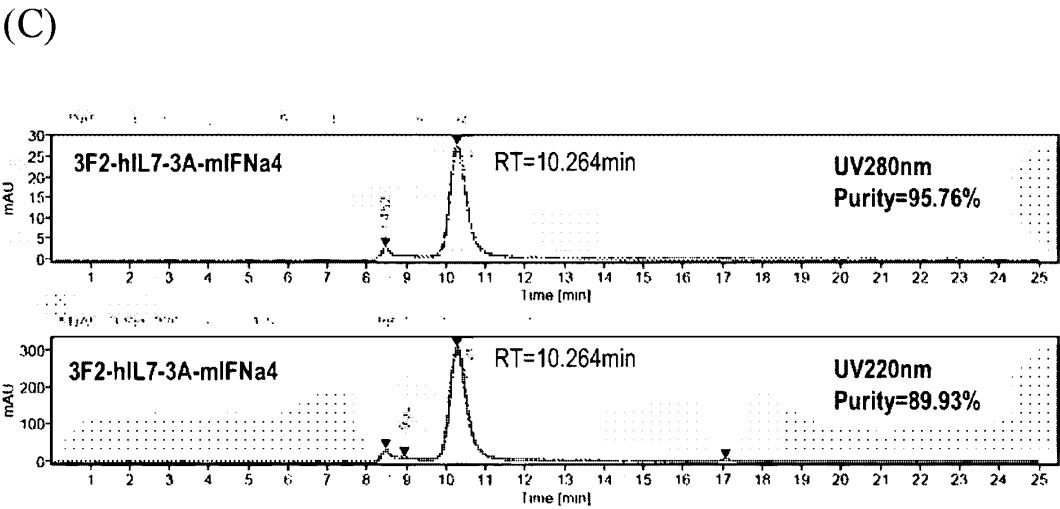


FIGS. 11A-11C



(B)

Lane	Name	Theoretical MW	Apparent MW
8	3F2-hIL7-3A-mIFNa4	231KD	≥180KD



FIGS. 12A-12C

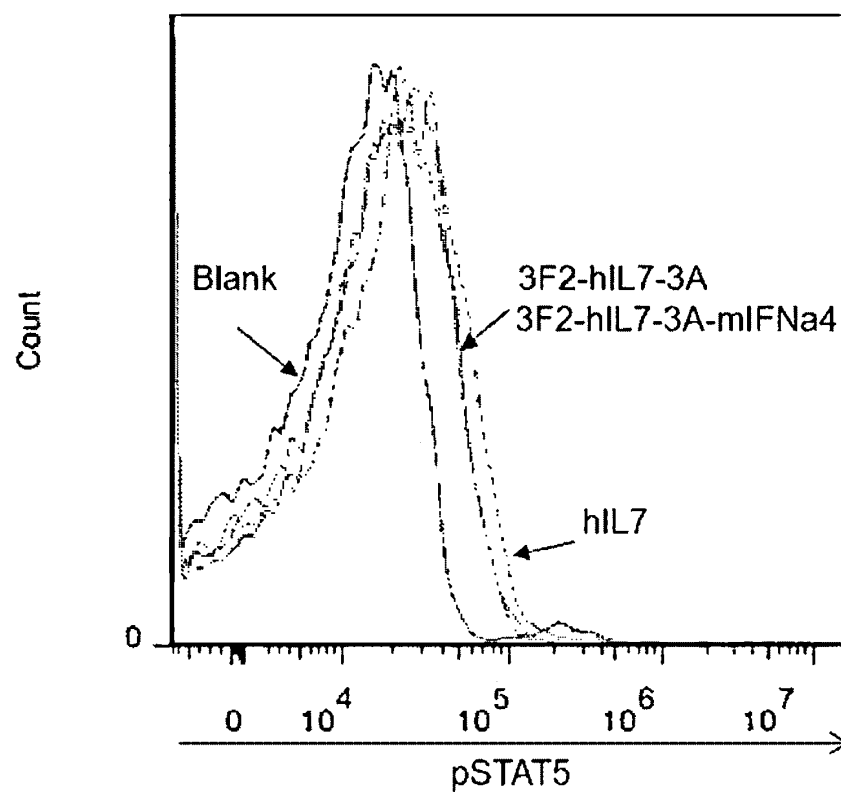
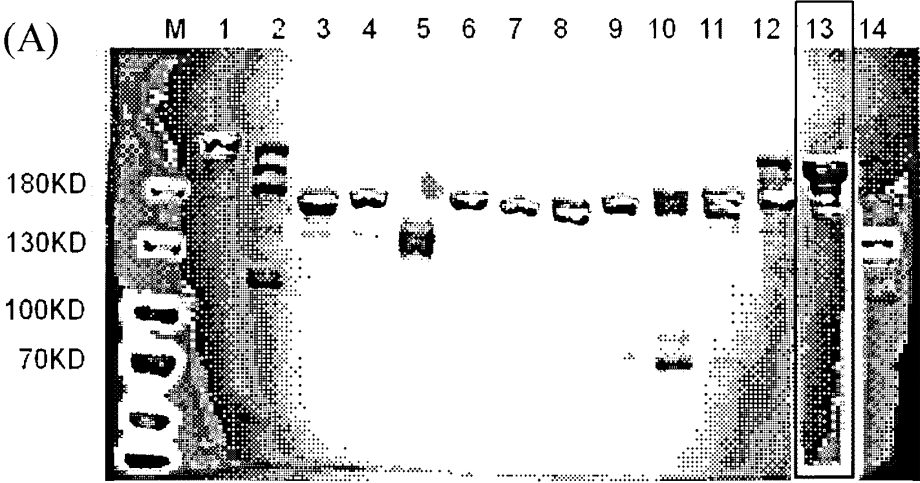


FIG. 13

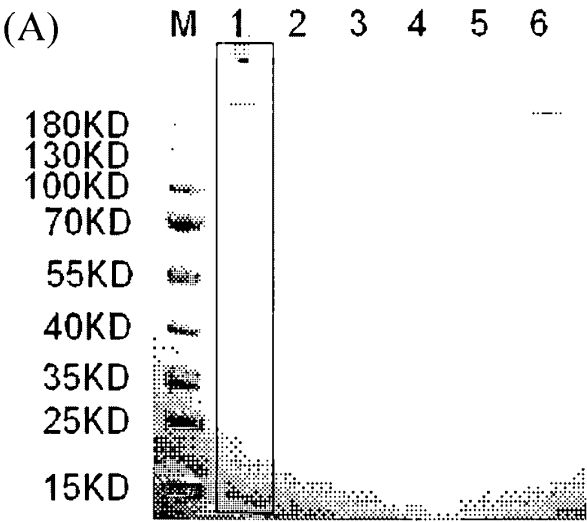


M: Protein Marker

(B)

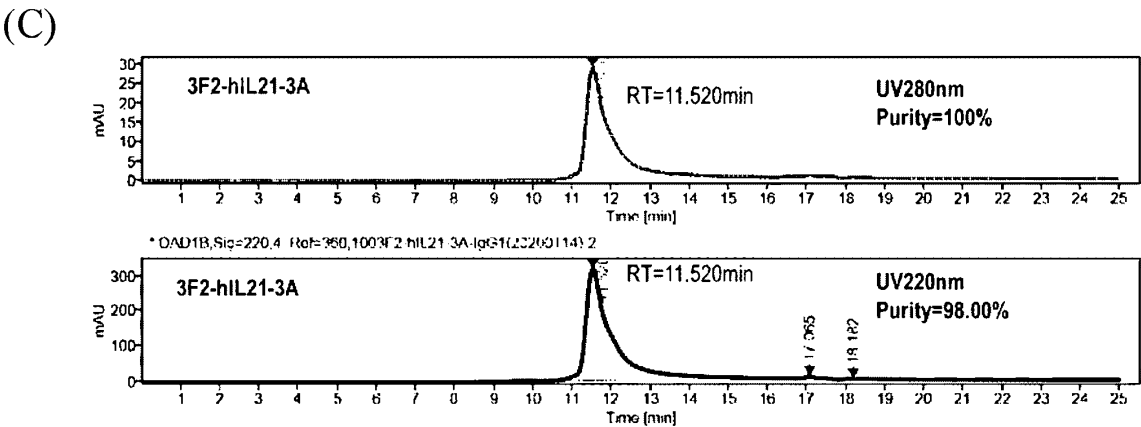
Lane	Name
13	PDL1-hIL21-HC

FIGS. 14A-14B

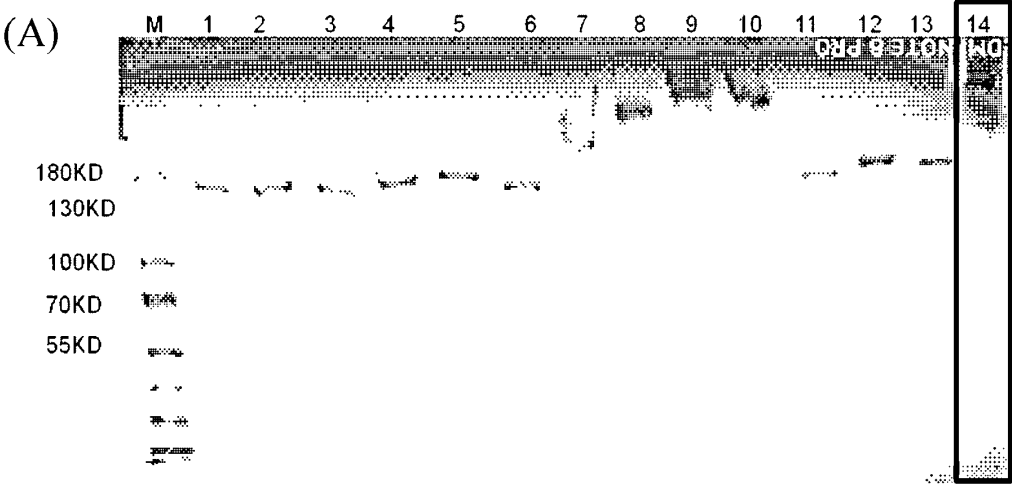


(B)

Lane	Name
1	3F2-hIL21-3A

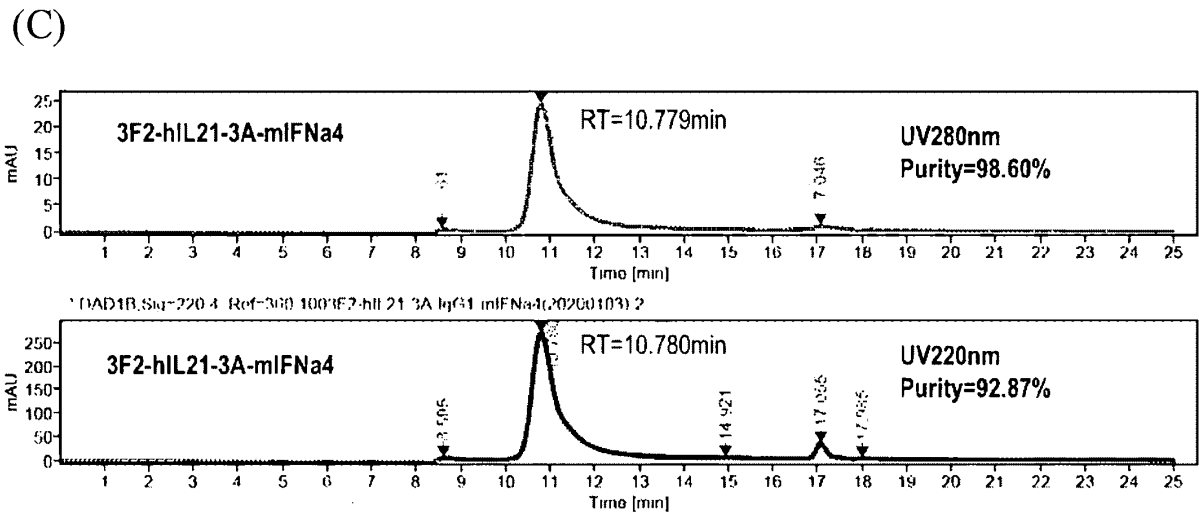


FIGS. 15A-15C



(B)

Lane	Name
14	3F2-hIL21-3A-mIFNa4



FIGS. 16A-16C

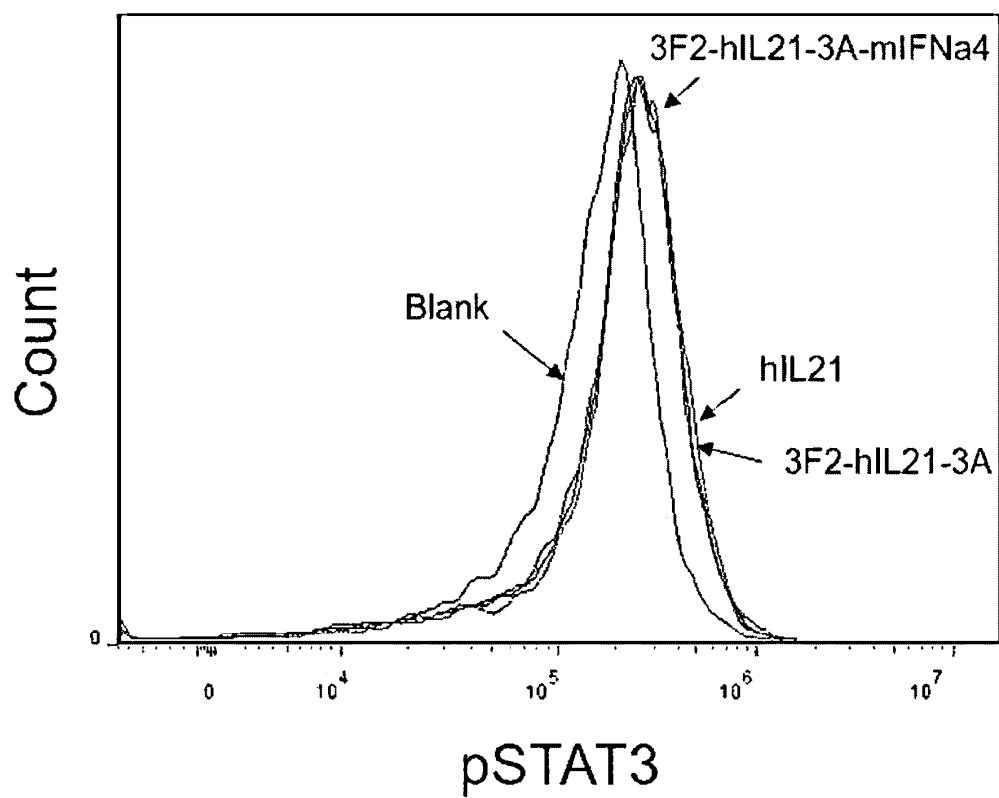
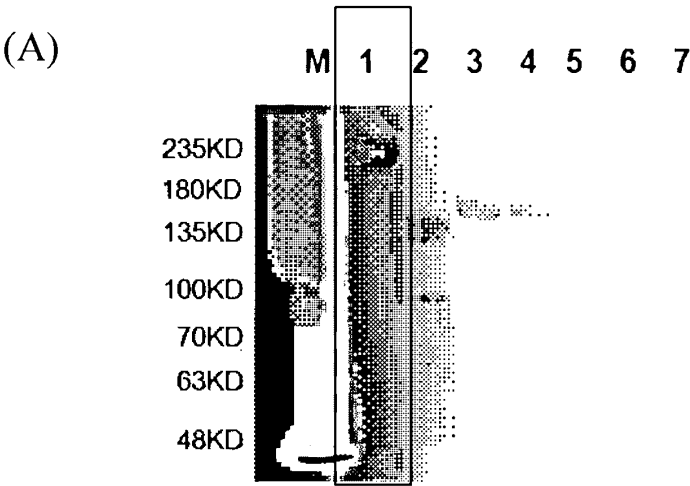
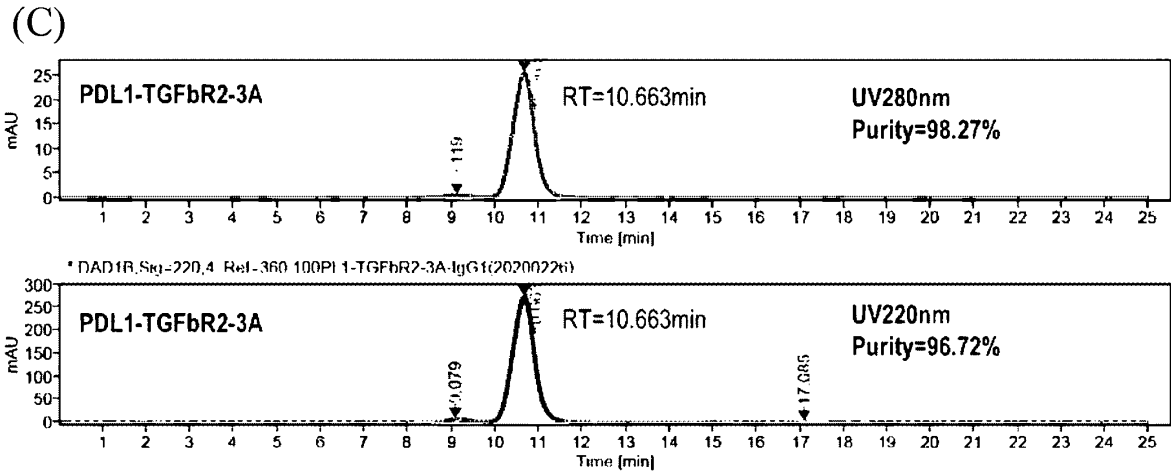


FIG. 17



(B)

Lane	Name	Theoretical MW	Apparent MW
1	PDL1-TGFbR2-3A	About 230KD	About 235KD



FIGS. 18A-18C

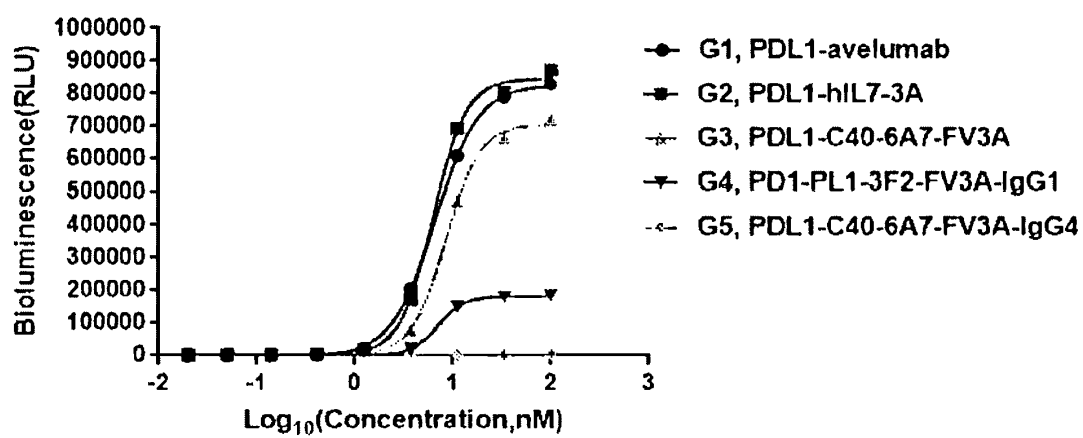


FIG. 19

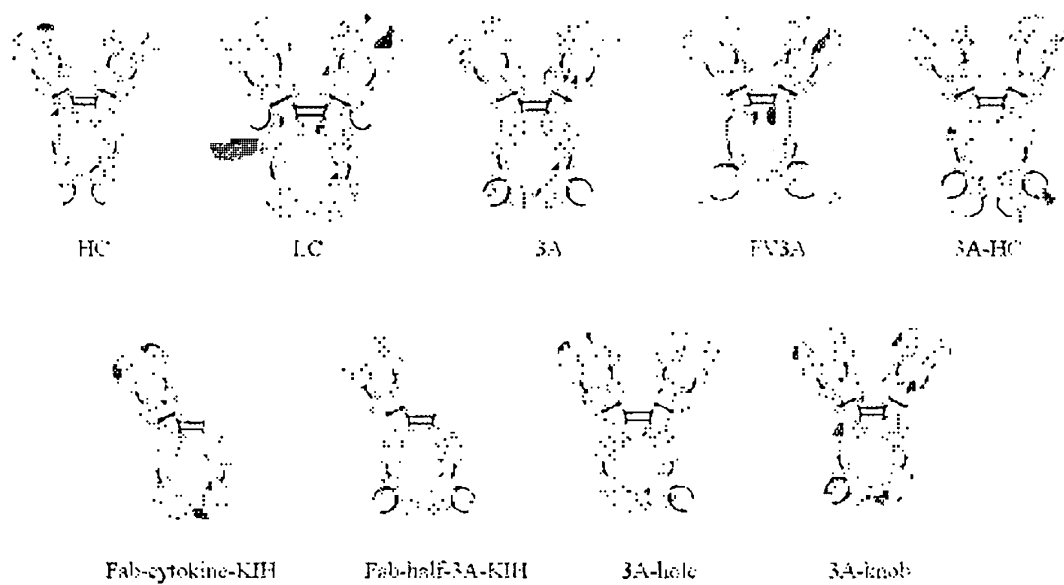


FIG. 20A

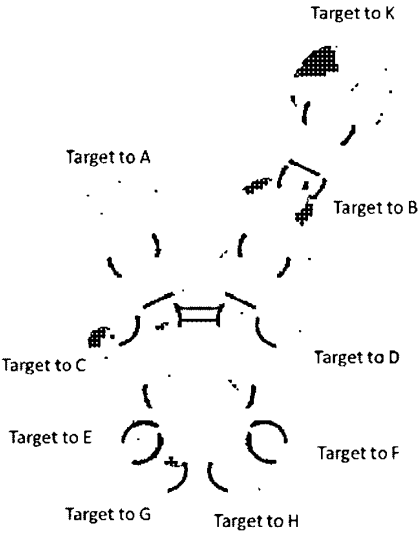


FIG. 20B

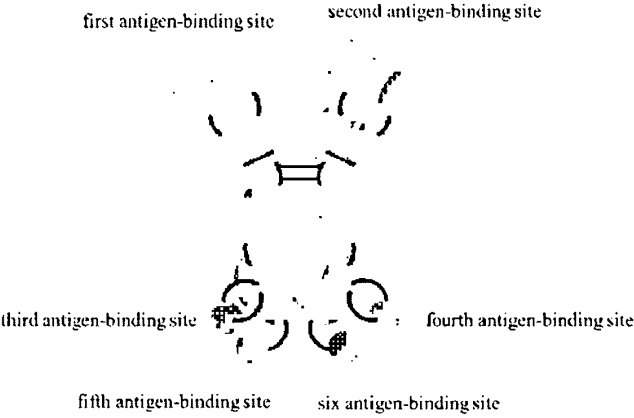


FIG. 20C

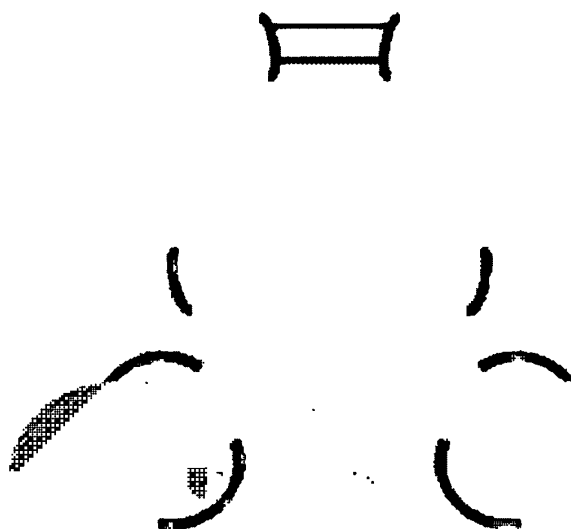


FIG. 20D

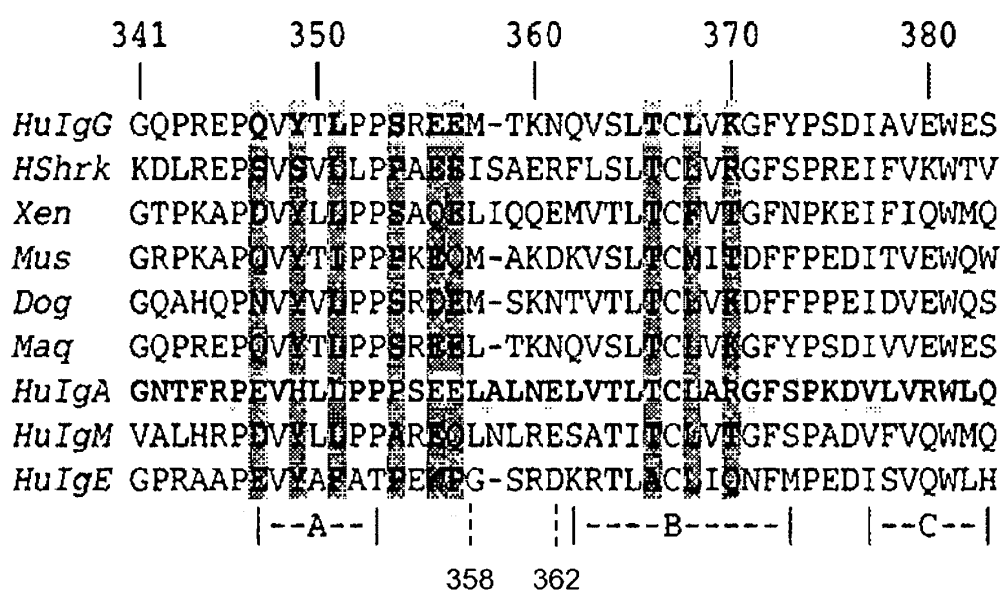


FIG. 21

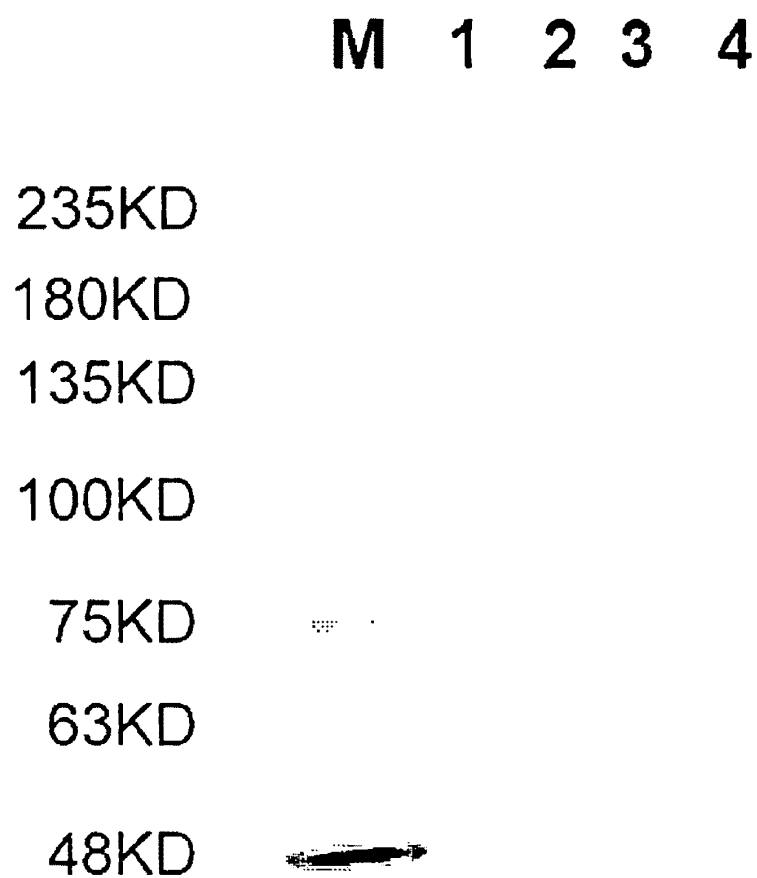


FIG. 22

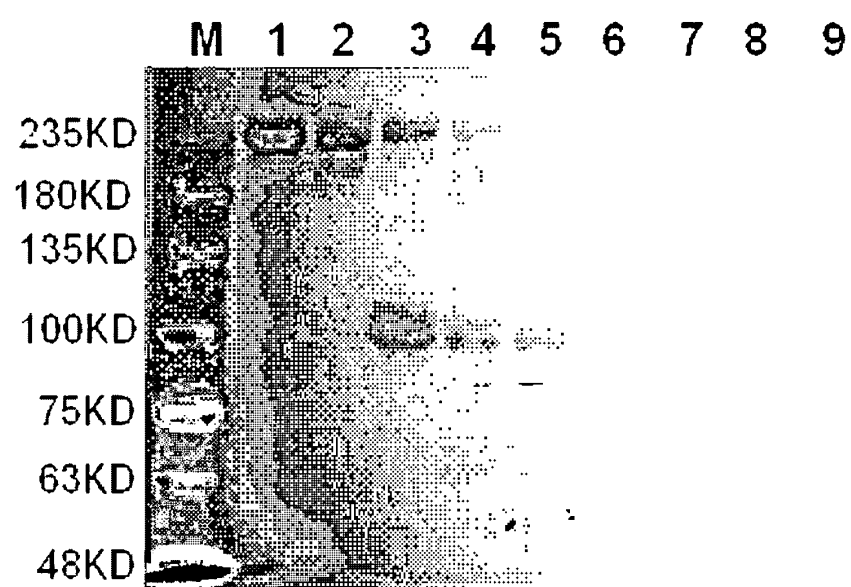


FIG. 23

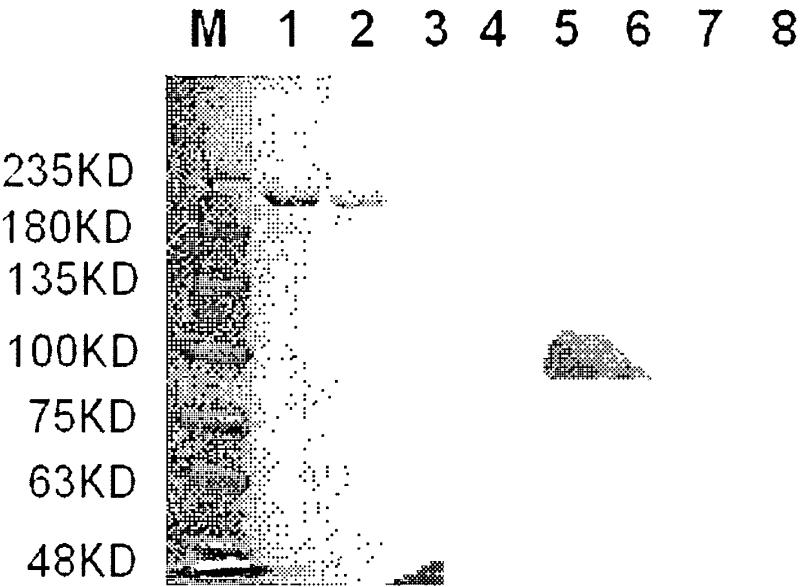


FIG. 24

M: Protein Marker

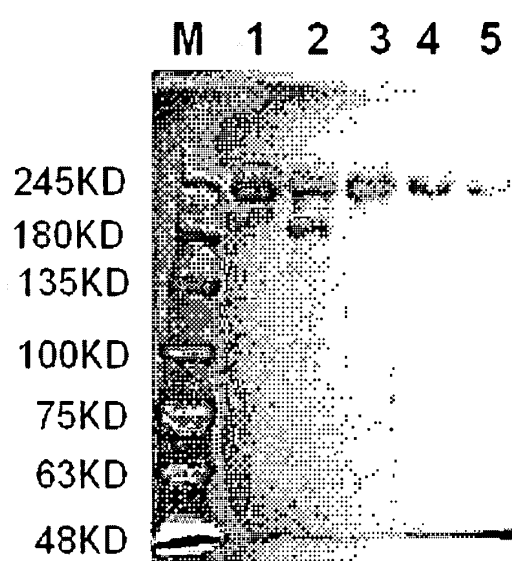


FIG. 25A

M: Protein Marker

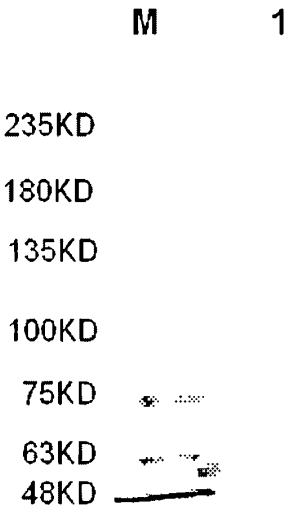


FIG. 25B

M: Protein Marker

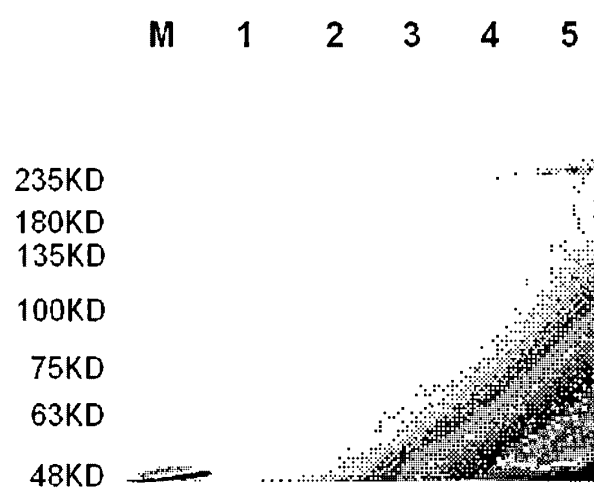


FIG. 26

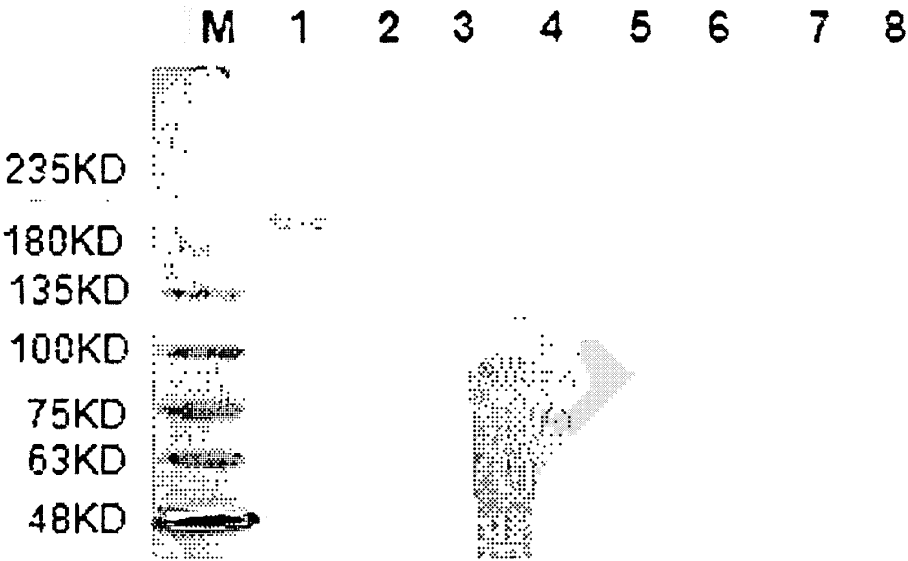


FIG. 27

M: Protein Marker

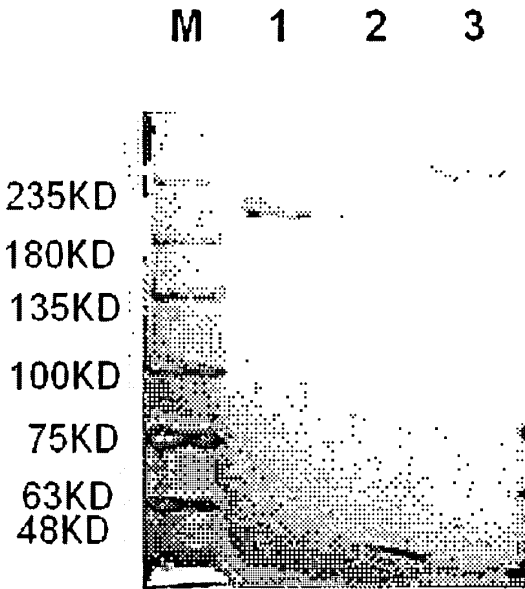


FIG. 28

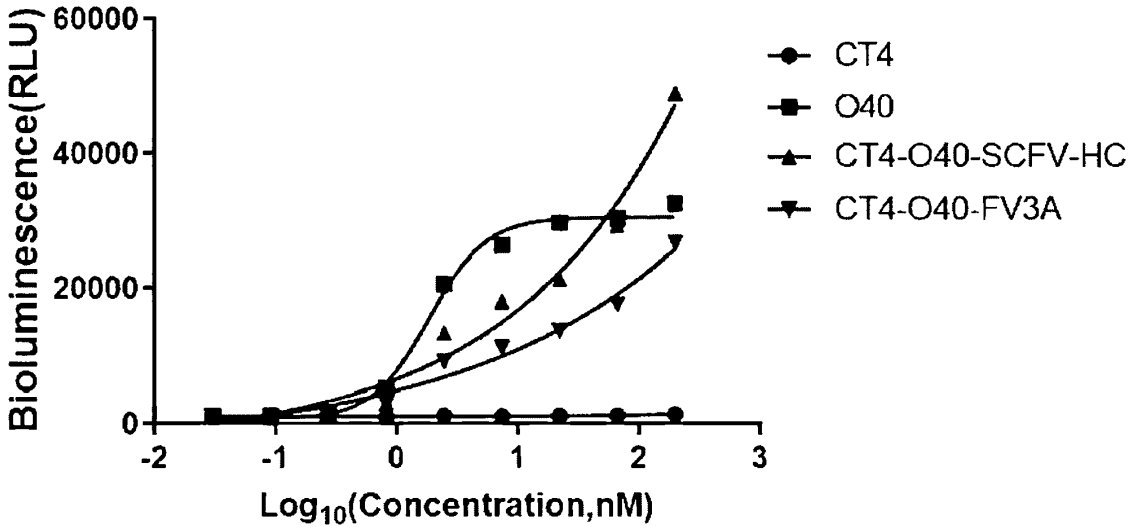


FIG. 29

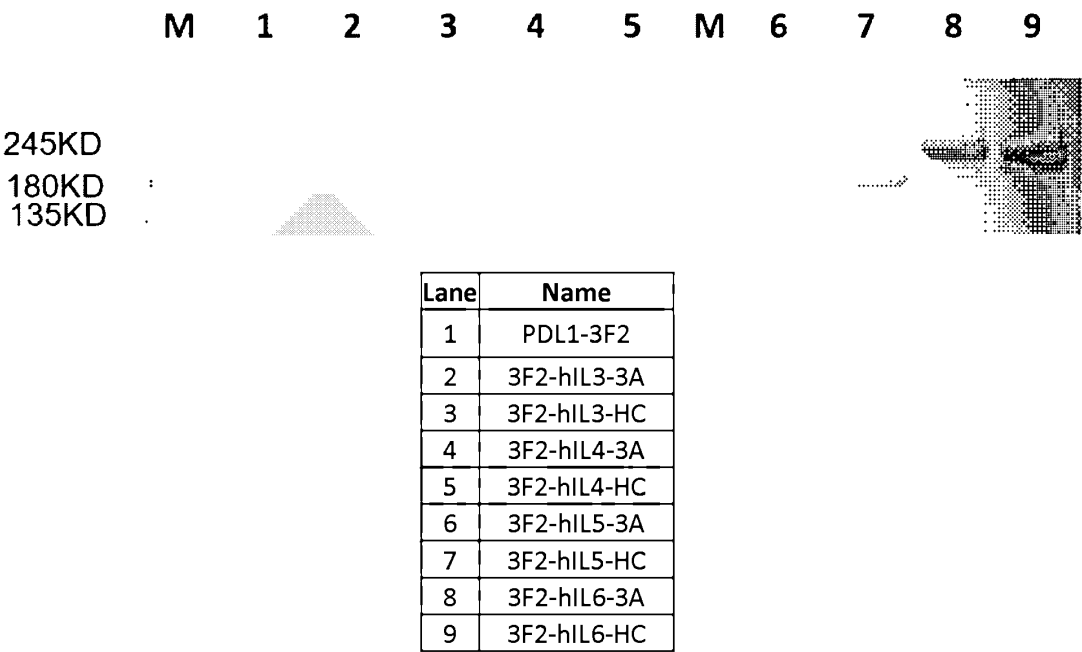


FIG. 30A

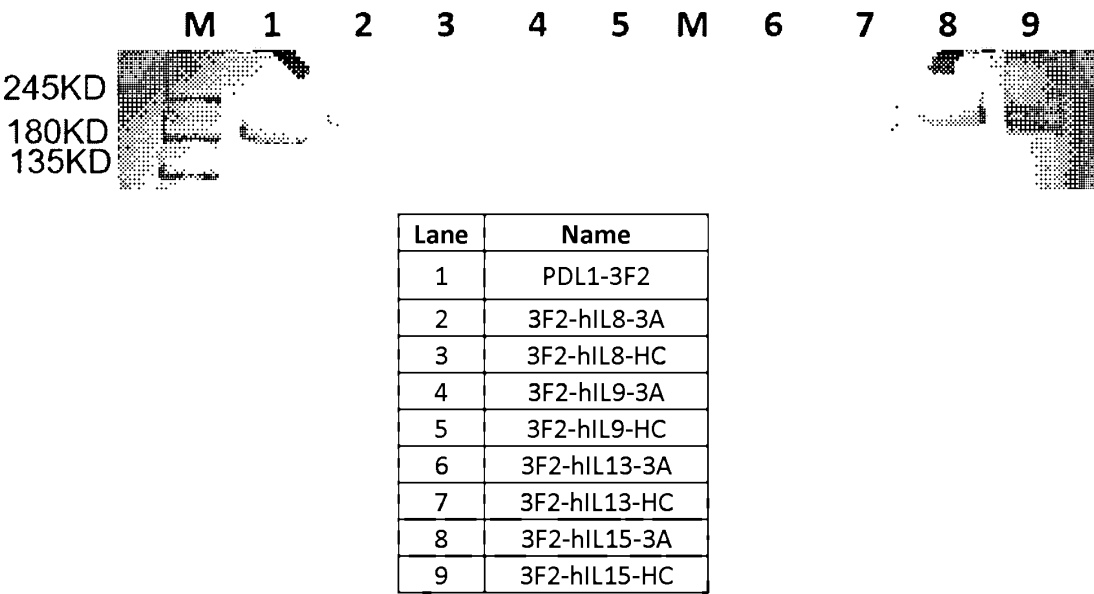


FIG. 30B

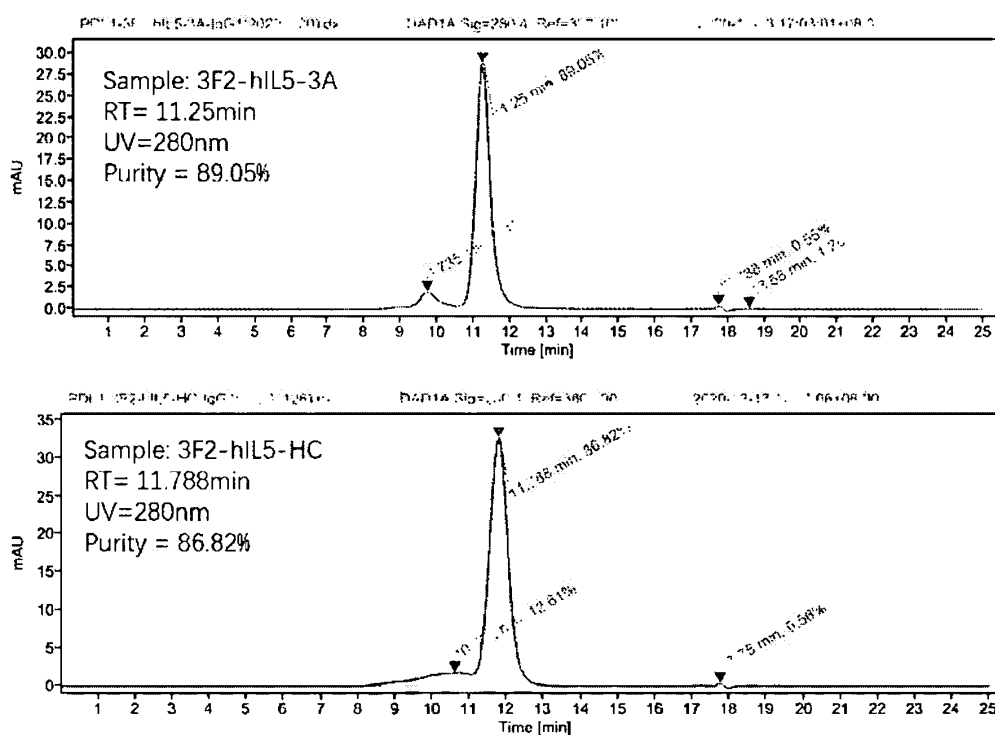


FIG. 31A

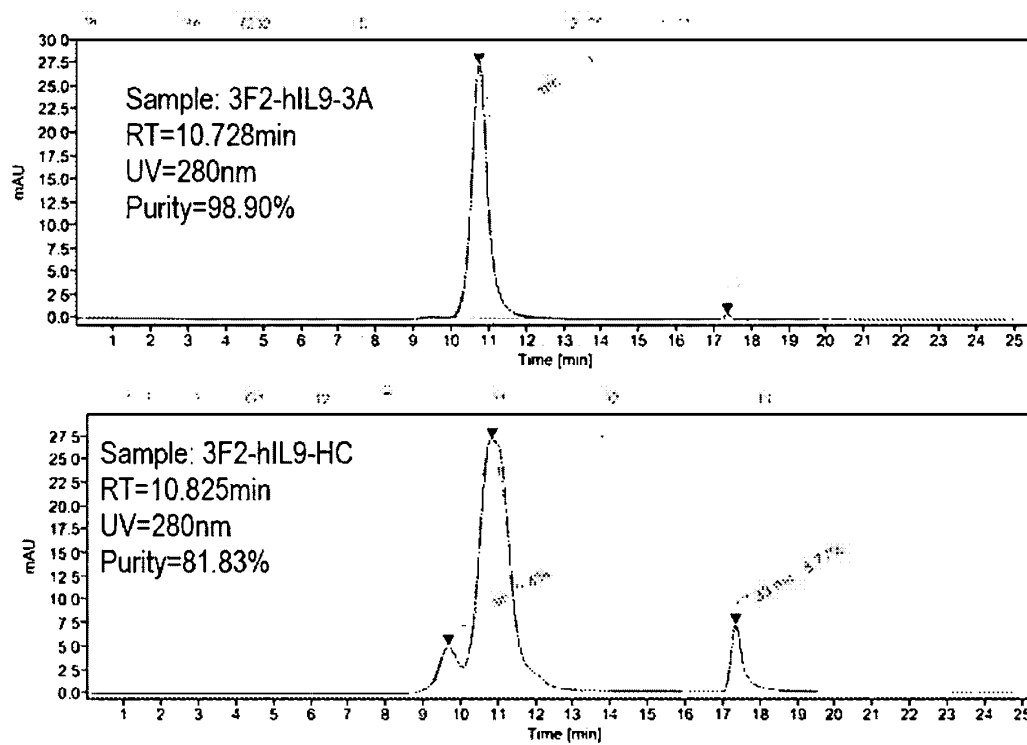


FIG. 31B

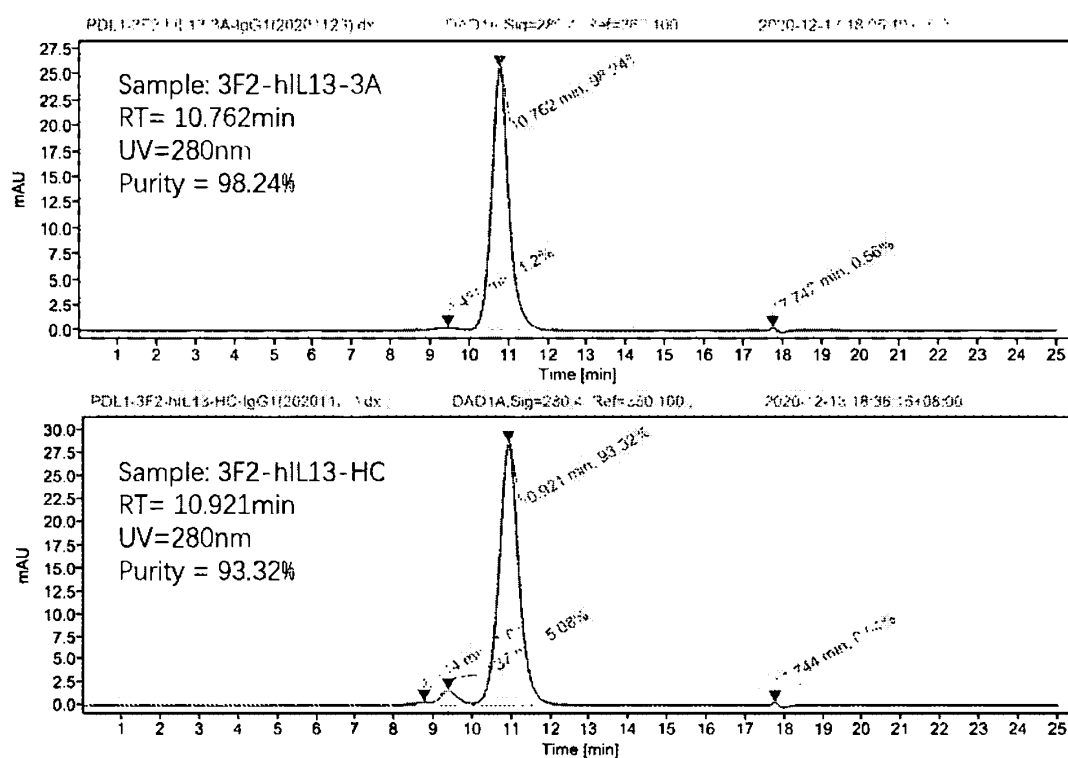


FIG. 31C

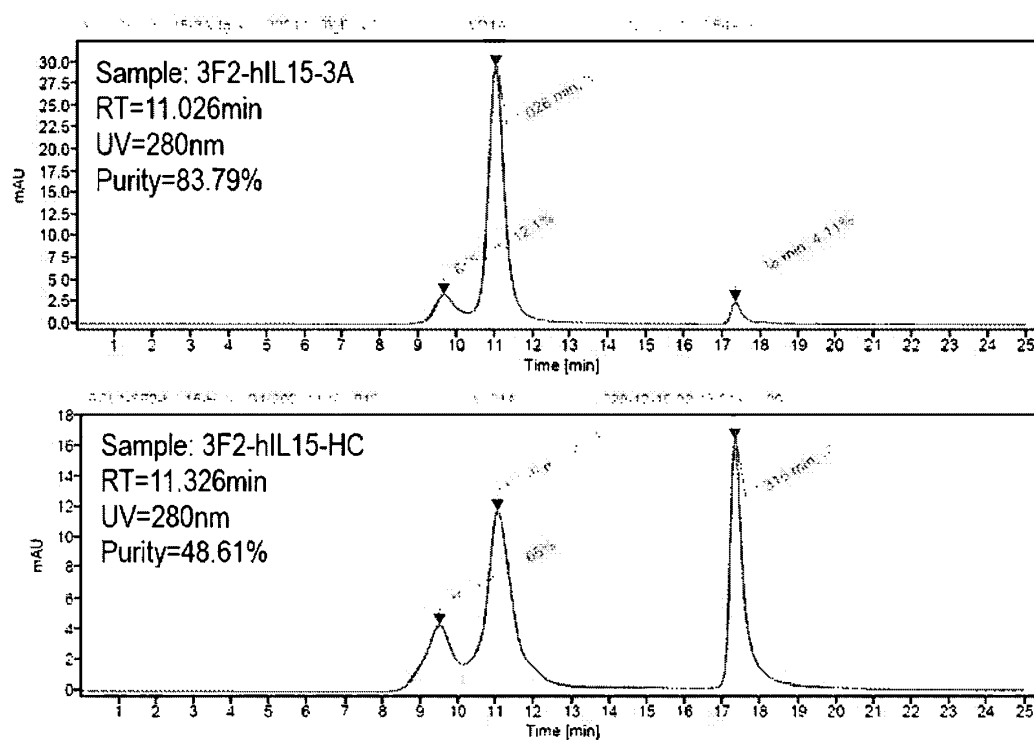


FIG. 31D

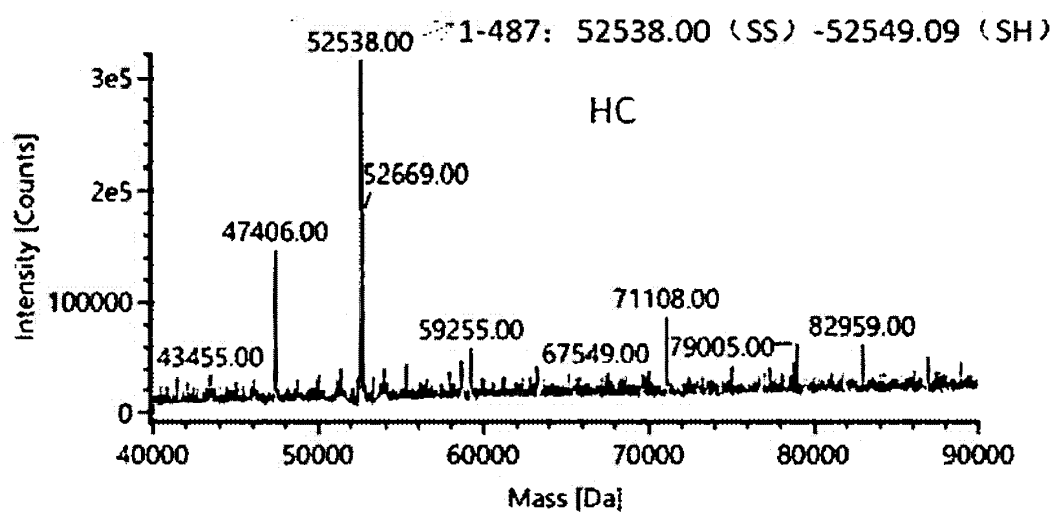


FIG. 32A

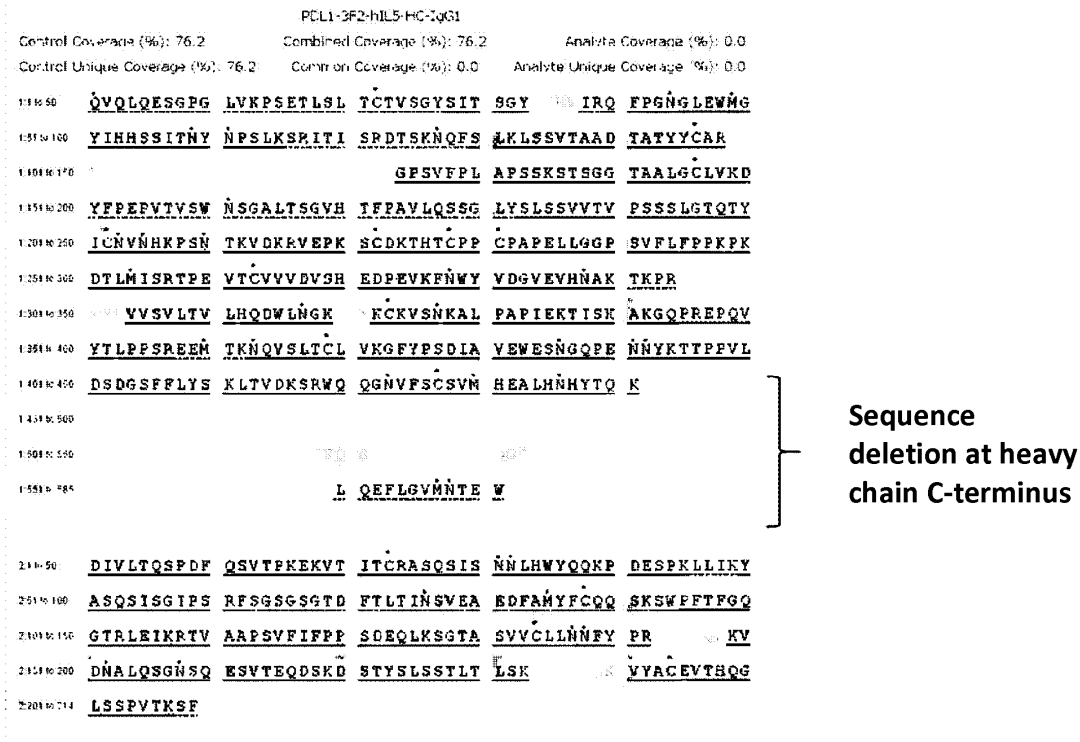


FIG. 32B

IgD	AQAPVKLSLNLLASS---DPPEAASWLLCEVSGFSPPNILLMWLEDQREVNTSGFAPA--	55
IgG4	--QPREPQVYTLPPSREEMTKN-QVSLTCLVKGFYPSDIAVEWESNGQPENN--YKTPP	55
IgG3	--QPREPQVYTLPPSREEMTKN-QVSLTCLVKGFYPSDIAVEWESSGQPENN--YNTTP	55
IgG1	--QPREPQVYTLPPSRDELTKN-QVSLTCLVKGFYPSDIAVEWESNGQPENN--YKTPP	55
IgG2	--QPREPQVYTLPPSREEMTKN-QVSLTCLVKGFYPSDIAVEWESNGQPENN--YKTPP	55
IgA	--NTFRPEVHLLPPPSEELALNELVTLTCLARGFSFKDVLVRWLQGSQELPREKYLTWAS	58
IgM	-VALHRPDVYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAP	59
	... * ... : * . ** * : : * . : :	
IgD	RPPFPQRSTTFWAWSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSLEVS---	107
IgG4	V---LDSQGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNNHYT-QKSLSLSL--	104
IgG3	M---LDSQGSFFLYSKLTVDKSRWQQGNIFSCSVMHREALHNNRFT-QKSLSLSLSP--	104
IgG1	V---LDSQGSFFLYSKLTVDKSRWQQGNVFSCSVMHREALHNNHYT-QKSLSLSLSPGK	106
IgG2	M---LDSQGSFFLYSKLTVDKSRWQQGNVFSCSVMHREALHNNHYT-QKSLSLSLSP--	104
IgA	RQEPSQGTITTFVAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFT-QKTIDRLA--	110
IgM	MPEPQAPG-RYFAHSILTVSEEEWNTGETYTCV-AHEALPNRVT-ERTVDKST--	109
	: * * * : : * *	

FIG. 33

358 362

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RECTIFIED SHEET (RULE 91)

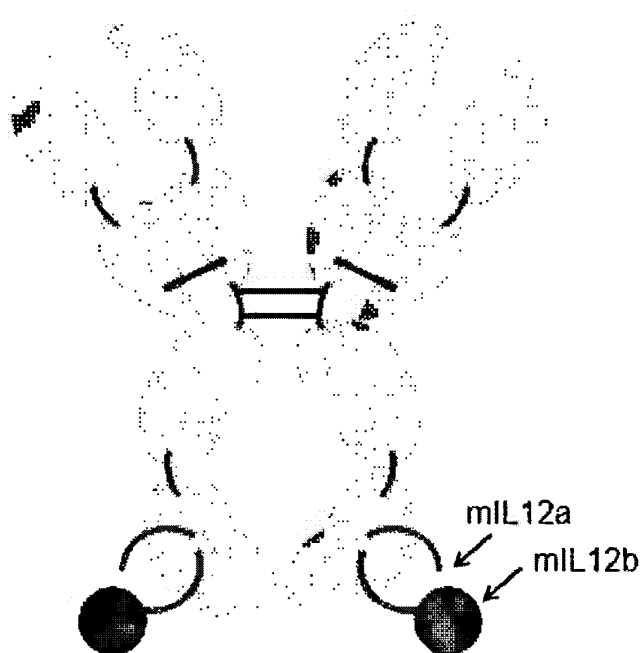
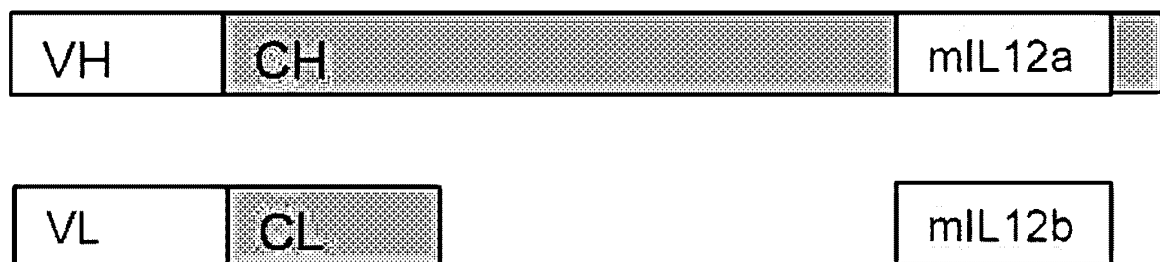
	358 362
RatNor_6_chr6 IGHG2C*01 Rattus	GKARTPQVYTIPPPREQMSKKVSLTCMVTSFYFASISVEWERNCELEQDYKNTLPVLDS
X00915 IGHG3*01 Mus	GRAQTPQVYTIPPPREQMSKKVSLTCLVTNFFSEAI SVEWERNCELEQDYKNTPPILDS
J00228 IGHG1*01 Homo	GQPREPQVYTLPPSRDELTKNQVSLTCLVKCFYPSDIAVEWESNCGQPENNYKTTTPVLDS
RatNor_6_chr6 IGHG1*01 Rattus	GRTQVPHVYTN SPTKEENTQNEVSITCMVKCFYPPDIYVEWQMNCGQPENNYKNTPTMDT
RatNor_6_chr6 IGHG2A*01 Rattus	GTPRGQVYTMAPPKEENTQSQVSITCMVKCFYPPDIYTEWKMNCQPENNYKNTPTMDT
J00453 IGHG1*01 Mus	CRPEAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNCQPAENYKNTQPIMNT
V00763 IGHG2E*01 Mus	GLVRAPQVYTLPPFAEQLSRKDVSLTCLVVGCFNPGDISVEWTSNCHTEENYKDTAPVLDS
RatNor_6_chr6 IGHG2E*01 Rattus	GLVRKPQVYVMCPPEQLTEQTVSLTCLTSCFLPNDIGVEWTSNCHIEKNYKNTPEVMDS
V00825 IGHG2A*01 Mus	GSVRAPQVYVLFPPPEENTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTPEVLDS
J00479 IGHG2C*01 Mus	GPVRAPQVYVLPFAEENTKKEFSLTCMITCFLPAEIAVDWTSNCRTEQNYKNTATVLDS
	* : * : * : . : * : : : : . . : * : : . * : * : . : * : * : : : :

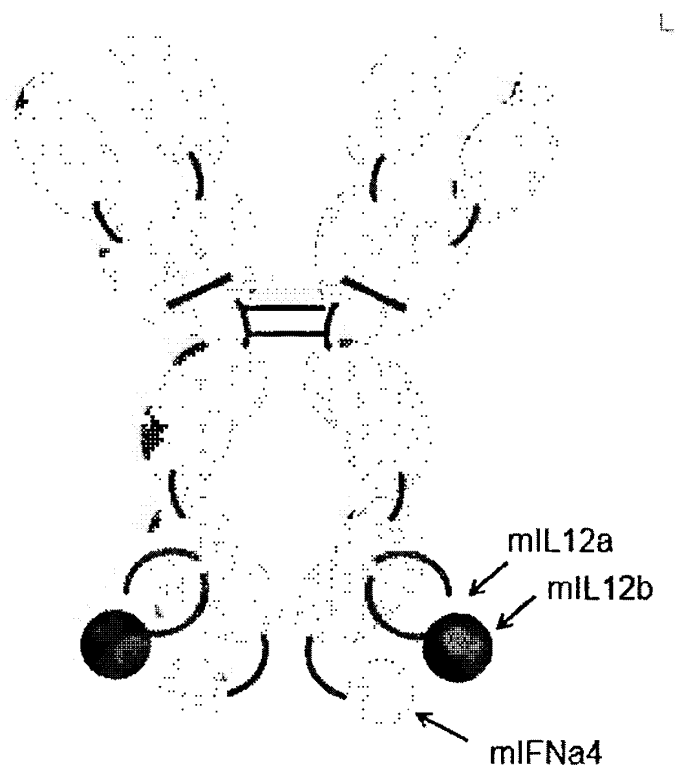
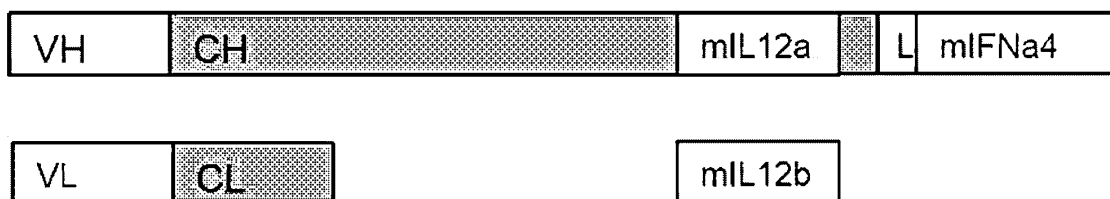
FIG. 35

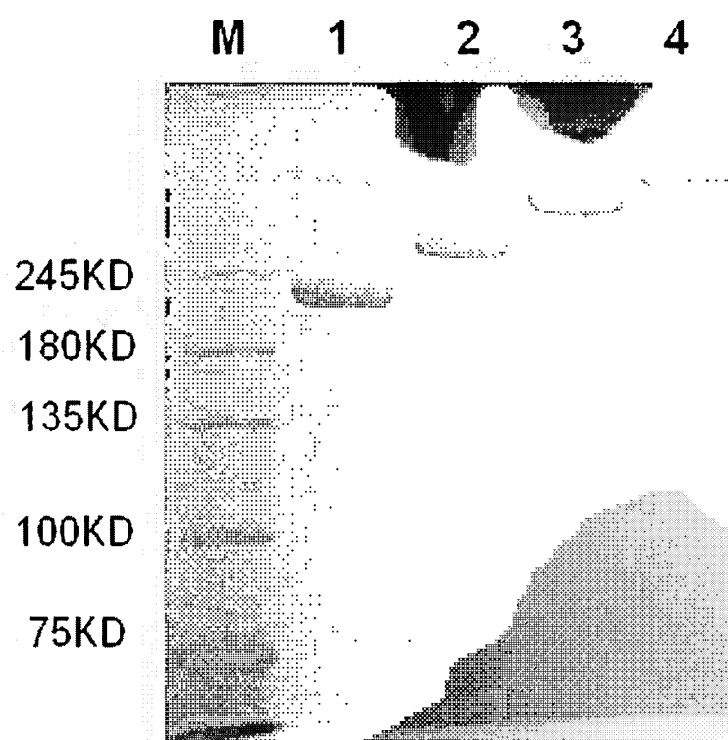
FIG. 36

	358 ...362	
J00228 IGHC1*01 Homo	GQFREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPV	57
IMGT000001 IGHG2*01 Canis	GQAHQPSVYVLPFSREELS-KNTVSLTCLIKDFFPPDIDVEWQSNQQQEPESKYRTTPPQ	59
AF354266 IGHG3*01 Canis	GQAHQPNVYVLPFSRDEMS-KNTVTLTCLVKDFFPPDIDVEWQSNQQQEPESKYRNTTPPQ	59
AF354264 IGHG1*01 Canis	GRAHEPSVYVLPFSPELSSSDTVSITCLIKDFYPPDIDVEWQSNQQQEPEKHKRNTTPPQ	60
AF354267 IGHG4*01 Canis	GQAHQPSVYVLPFSPELSSSDTVTLTCLIKDFFPPDIDVEWQSNQQQEPEPESKYHTAPQ	60
	: :: **.* ** .*: : .: *:***:*.*: * **:* ** * :*: *	
J00228 IGHC1*01 Homo	LDSDGSFFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQKSLSLSPGK	107
IMGT000001 IGHG2*01 Canis	LDSDGSYFLYSKLSVDKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK	109
AF354266 IGHG3*01 Canis	LDSDGSYFLYSKLSVDKSRWQRGDTFICAVMHEALHNHYTQISLSHSPGK	109
AF354264 IGHG1*01 Canis	LDSDGSYFLYSKLSVDKSRWQQGDFFTCAVMHETLQNHYTDLSLSHSPGK	110
AF354267 IGHG4*01 Canis	LDSDGSYFLYSKLSVDKSRWQQGDTFTCAVMHEALQNHYTDLSLSHSPGK	110
	.* **:* **:* **:* *: * *:*:* **:* ** *	

FIG. 37

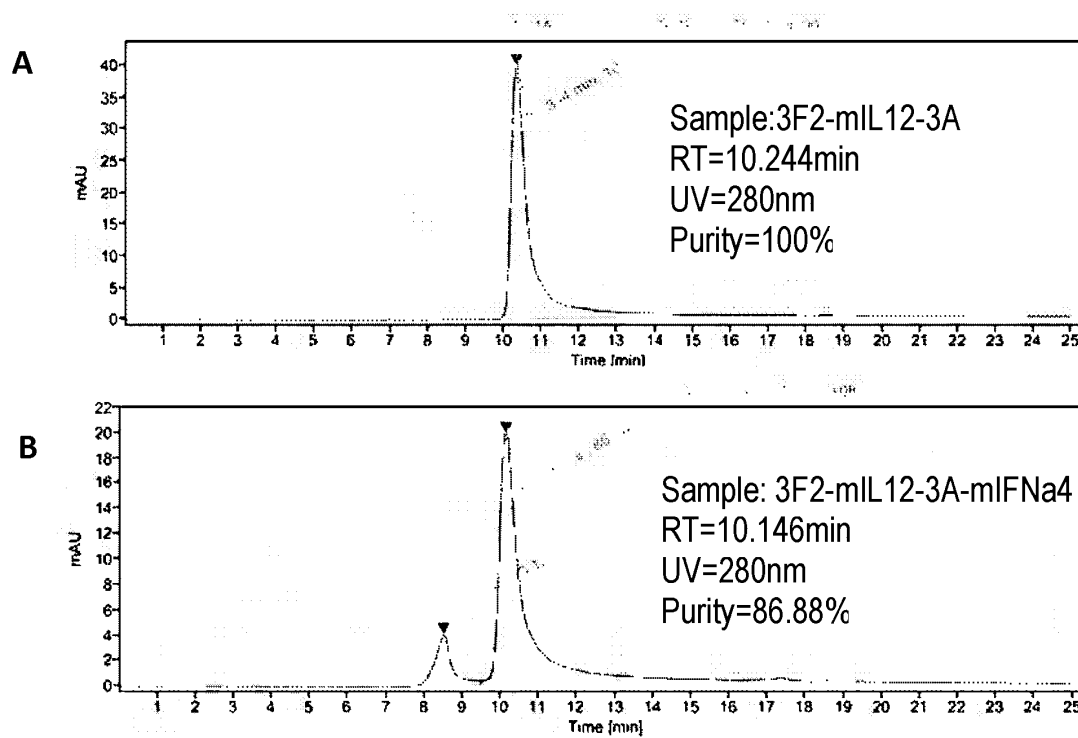
**3F2-mIL12-3A****FIG. 38A****FIG. 38B**

**3F2-mIL12-3A-mIFNa4****FIG. 39A****FIG. 39B**



ID	Fusion protein
3	3F2-mIL12-3A
4	3F2-mIL12-3A-mIFNa4

FIG. 40



FIGS. 41A-41B

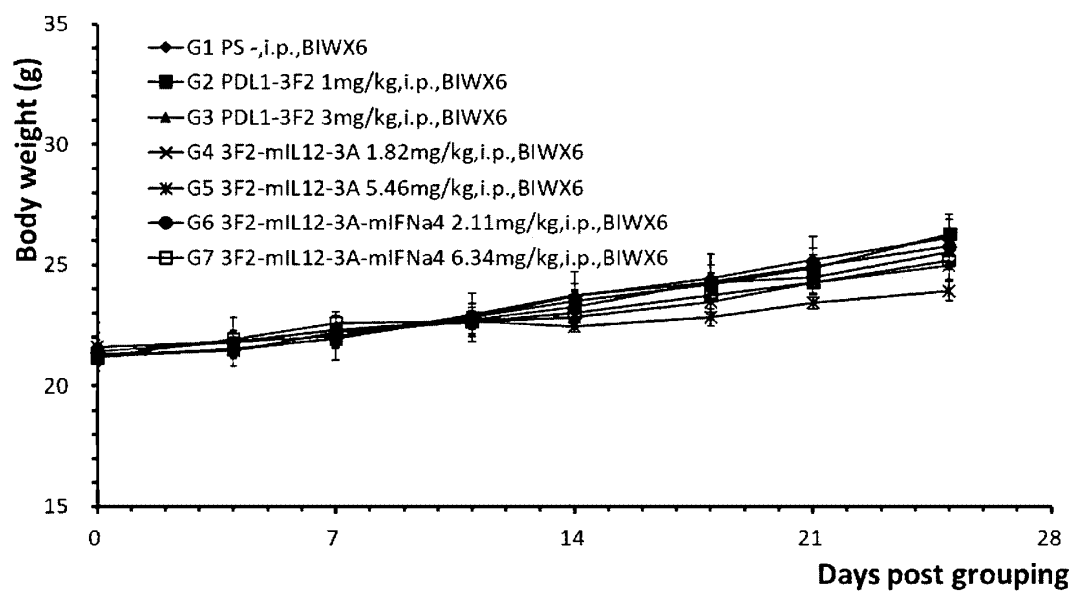


FIG. 42

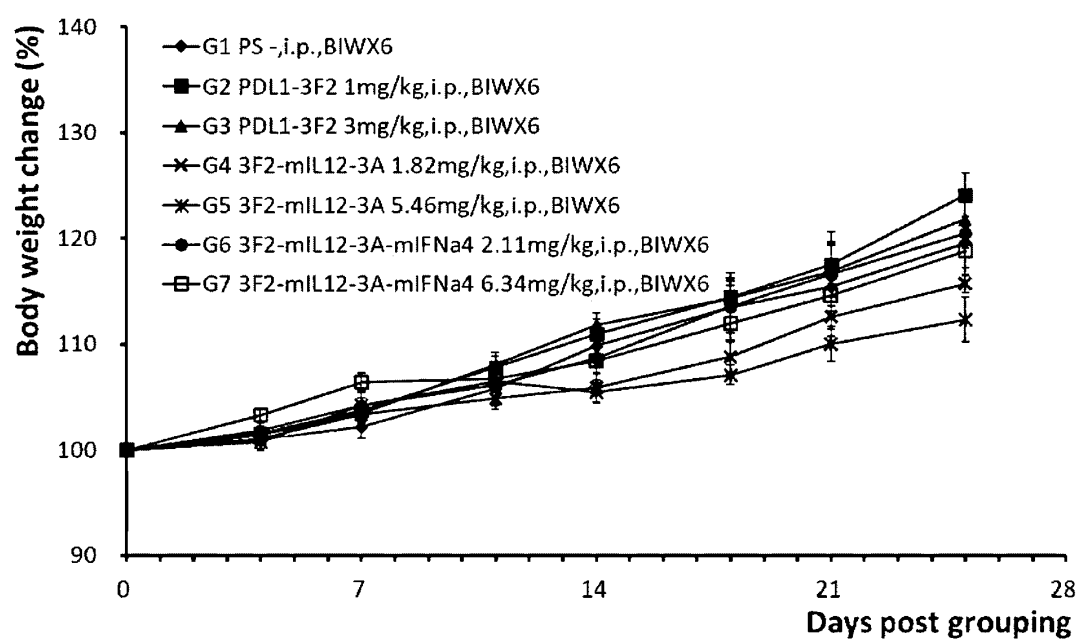


FIG. 43

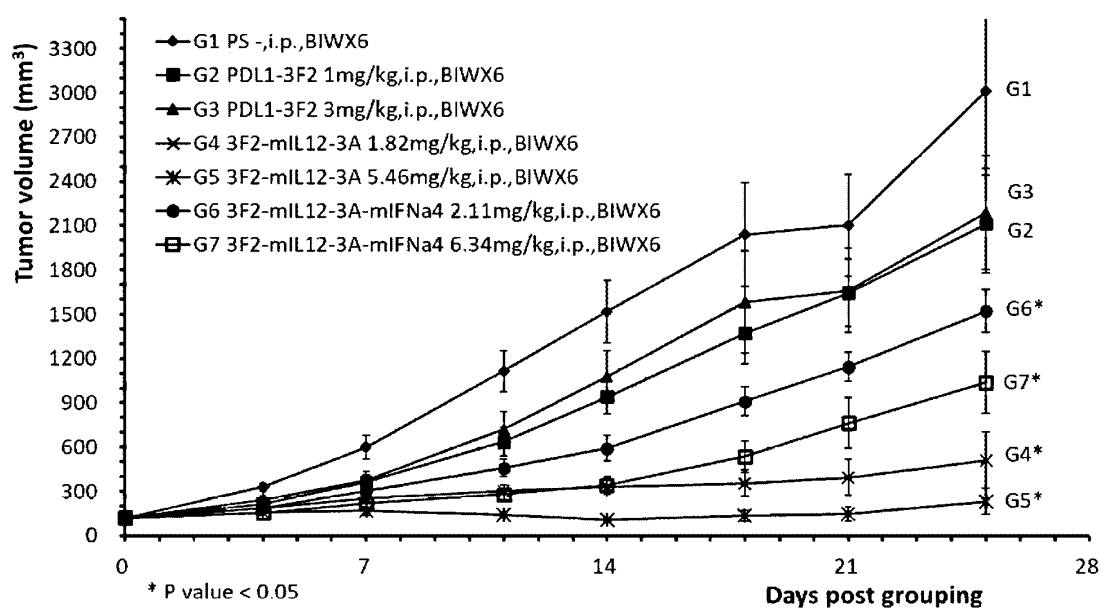


FIG. 44

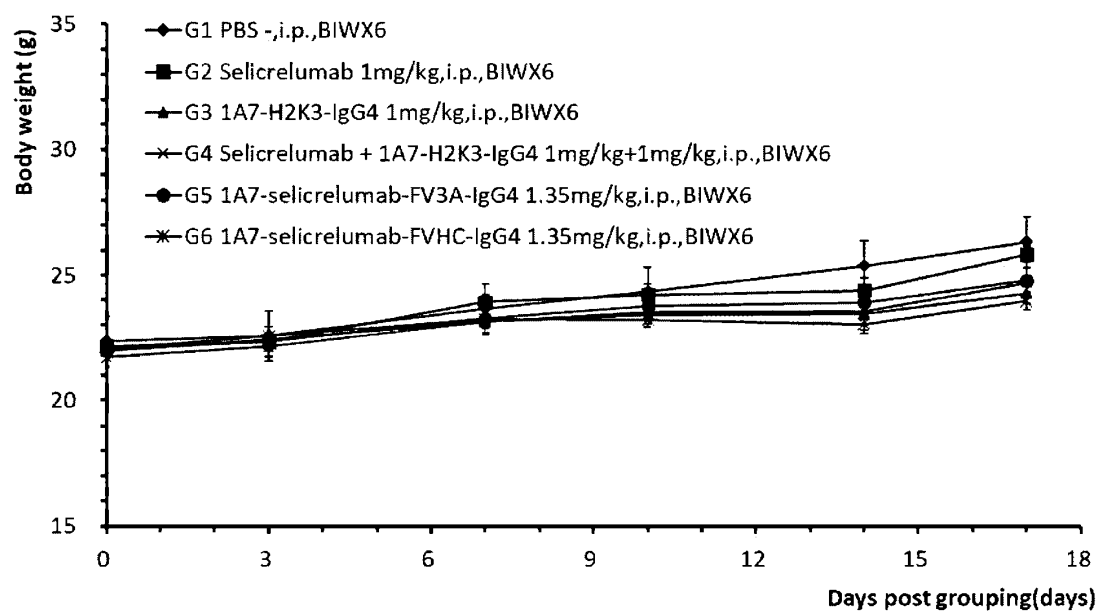


FIG. 45A

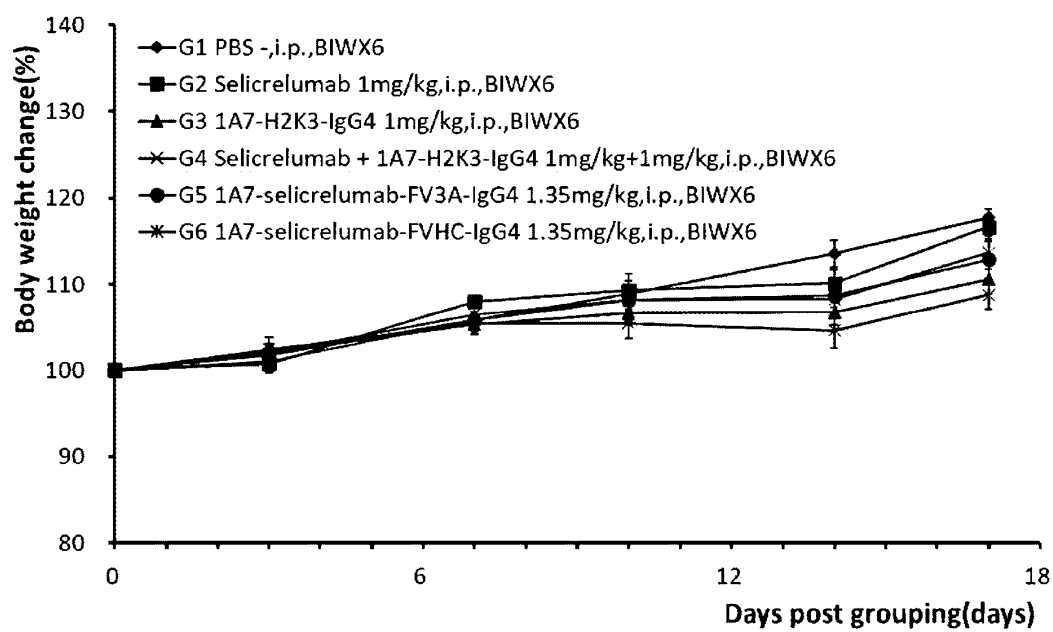


FIG. 45B

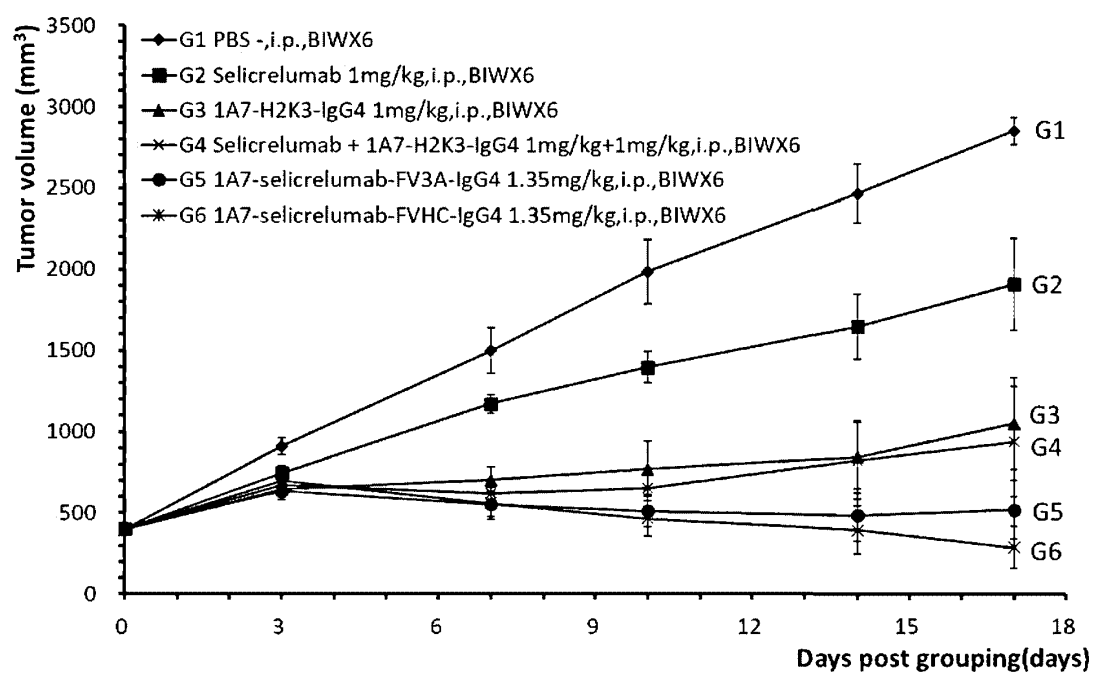


FIG. 45C

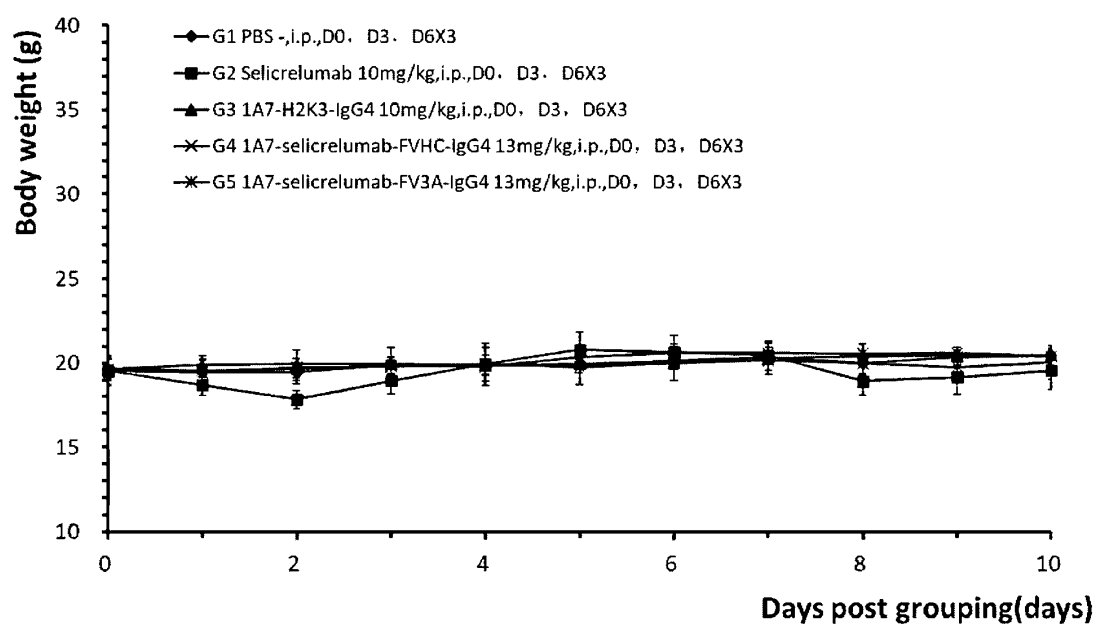


FIG. 46A

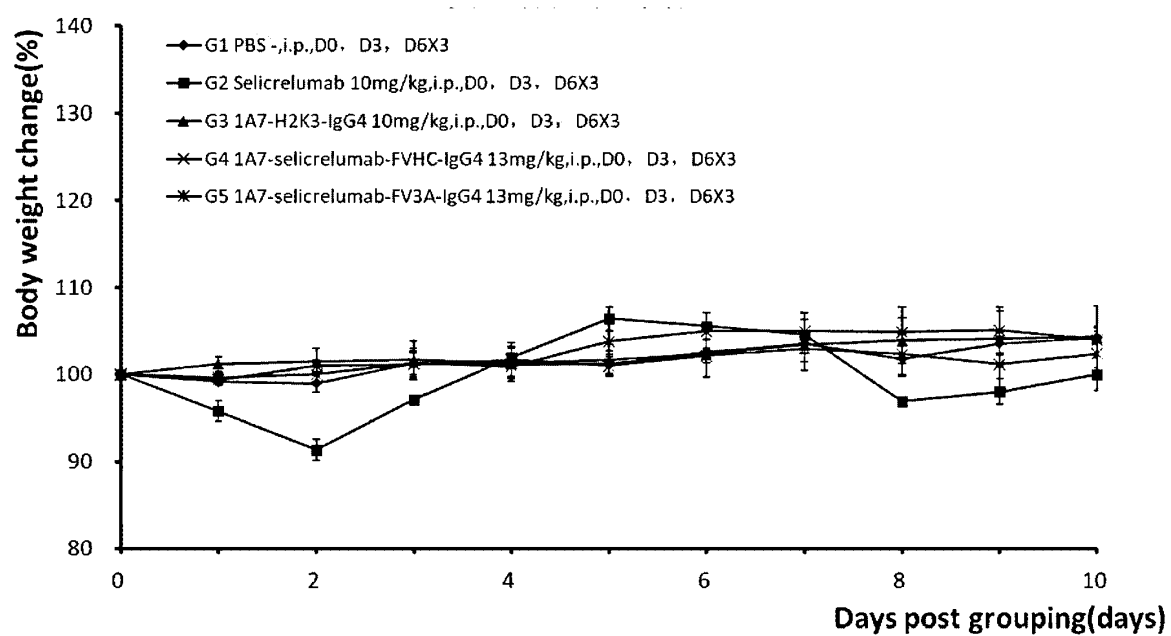


FIG. 46B

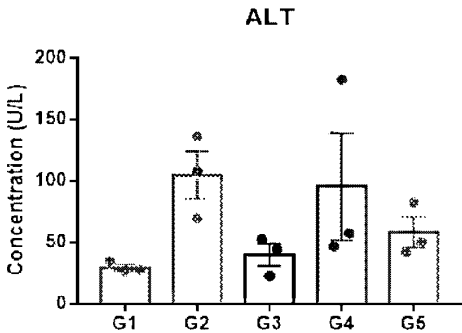


FIG. 47A

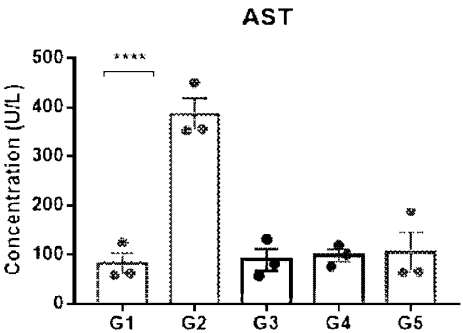


FIG. 47B

FIG. 48**IgG1-heavy chain constant region(CH) (SEQ ID NO: 1)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

IgG2-CH (SEQ ID NO: 2)

STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSN
FGTQTYTCNVDHKPSNTKVDKVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED
PEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

IgG4-CH (SEQ ID NO: 3)

STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
LGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSQE
DPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP
REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRW
QEGNVFSCSVMHEALHNHYTQKSLSLSPGK

PDL1-avelumab antibody light chain (SEQ ID NO: 4)

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTAS
LTISGLQAEDEADYYCSSYTSSTRVFGTGTQVTVLGGPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAV
TVAWKADGSPVKAGVETTKPSKQSNKNYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

PDL1-mIL7-3A heavy chain (SEQ ID NO: 5)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADTVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEGGGGSGGGGS
ECHIKDKEGKAYESVLMISIDELDKMTGTDSNCPNNEPNFRKHVCDDTKEAAFLNRAARKLKQFLKMNISEEF
NVHLLTVSOGTQTLVNCTSKKEKNVKEOKKNDACFLKRLRLREIKTCWNKILKGSIGGGGSGGGGSVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GA*

*The underlined sequence is mIL7 (26-154aa of NP_032397.1). It replaces 358-362 (EU numbering) of the heavy chain.

PDL1-mIL7-3B heavy chain (SEQ ID NO: 6)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADTVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
LVKGFYPSDIAVEWEGGGGSGGGGSECHIKDKEGKAYESVLMISIDELDKMTGTDSNCPNNEPNFRKHVCDDT
KEAAFLNRAARKLKQFLKMNISEEFNVHLLTVSOGTQTLVNCTSKKEKNVKEOKKNDACFLKRLRLREIKTCWNK
ILKGSIGGGGSGGGGSKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGA*

*The underlined sequence is mIL7 (26-154aa of NP_032397.1). It replaces 383-391 (EU numbering) of the heavy chain.

PDL1-mIL7-3C heavy chain (SEQ ID NO: 7)

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADTVKGRFTISRDN
 SKNTLYLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
 LVKGFPYPSDIAVEWESNGGGSGGGGSECHIKDKEGKAYESVLMISIDELDKMTGTDSCNCPNNEPNFFRKHVCD
DTKEAFLNRAARKLKQFLKMNISEEFNVHLLTVSOGTQTLVNCTSKKEKNVKEQKNDACFLKRLLEIKTCW
NKILKSGISGGGSGGGSGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSFSVMHEALHNHYTQKS
 LSLSPGA*

*The underlined sequence is mIL7 (26-154aa of NP_032397.1). It is inserted between amino acids 384 and 385 (EU numbering) of the heavy chain.

PDL1-mIL7-3D heavy chain (SEQ ID NO: 8)

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADTVKGRFTISRDN
 SKNTLYLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
 LVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVGGGSGGGGSECHIKDKEGKAYESVLMIS
IDELDKMTGTDSCNCPNNEPNFFRKHVCDDTKEAFLNRAARKLKQFLKMNISEEFNVHLLTVSOGTQTLVNCTSK
KEKNVKEQKNDACFLKRLLEIKTCWNKILKSGISGGGSGGGGFSFSVMHEALHNHYTQKSLSLSPGA*

*The underlined sequence is mIL7 (26-154aa of NP_032397.1). It replaces 413-422 (EU numbering) of the heavy chain.

HC linker sequence (SEQ ID NO: 9):

GGGGSGGGSGGGSGGGG

mIFN α 4 (SEQ ID NO: 10)

CDLPHTYNLGNKRALTVLEEMRRLPPLSCLKDRKDFGFPLEKVDNQIQKAQAILVLRDLTQQILNLFSTKDL
 ATWNTLLDLSFCNDLHQLNDLKACVMQEPPLTQEDSLLAVRTYFHRITVYLRKKKHSCLCAWEVIRAEVWRALS
 SSTNLLARLSEEKE*

hIL7 NP_000871.1 26 to 177aa (SEQ ID NO: 11)

DCDIEGKDGKQYESVLMVSIDQLDSMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGD
 FDLHLLKVSEGTITLLNCTGQVKGRKPAALGEAQPTKSLEENKSLKEQKLLNDLCFLKRLLEIKTCWNKILMG
 TKEH

hIL21 NP_068575.1 25 to 162aa (SEQ ID NO: 12)

HKSSSQGQDRHMIRMRLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIIN
 SIKKLKRKPPSTNAGRQKHRLTSPSCDSYEKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS

hTGFB β 2 NP_003233.4 24 to 159 (SEQ ID NO: 13)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCAVWRKNDENITL
 ETVCHDPKLPYHDFILEAASPKCIMKEKKKPGETFFMCSSSDECNDNIIIFSEYNTSNPD

ATOR1015-CD86 (SEQ ID NO: 14)

APLKIQAYFNETADLPCQFANSQNLSELVVFWDQENLVLENYLGKERFDSVDSKYMGRSFDSDSWTLRL
 HNLQIKDKGRYQCIHHKKPTGMINIHQMNSLSVLA

KN035 VHH (SEQ ID NO: 15)

QVQLVESGGGLVQPGGSLRLSCAASGFTFSRRCAWFRQAPGKERERVAKLLTTSGSTYLADSVKGRFTISRDN
SKNTVYLQMNSLRAEDTAVYYCAADSFEDPTCTLTSSGAFQYWGQGLTVTVSS

C40-6A7 scFv (SEQ ID NO: 16)

DVVMQTQSPLSLPVTLGQPASISCRSSQSLLSHNGNTYLHWYQQRPQSPNHLYQVSNRFSGVDPDRFSGSGSGT
DFTLKISRVEAEDVGVYFCSQTTHVPWTFGCGTKVEIKGGGSGGGGSGGGGSGGGGSGVQLVQSGAEVKKPGA
SVKLSCKASGYTFISYYIYVVKQAPGQCLEWIGGINPRNGGTNENEKFKSRATLTVDTSISTAYMELSLRSED
TAVYYCTRHGNGVYWGQGLTVTVSS

PDL1-3F2 scFv (SEQ ID NO: 17)

QVQLQESGPGLVKPSSETLSLTCTVSGYSITSGYNWHWIRQFPGNCLEWMGYIHHSSITNYPNPSLKSRTISRDT
SKNQFSLKLSVTAADTATYYCAREGYDYDFAYWGQGLTVTVSSASTGGGSGGGGSGGGGSGGGGSDIVLTQ
SPDFQSVTPKEKVTLSRASQSIENNHLHWYQQKPDSPKLLIKYASQSIGIPSRFSGSGSGTDFTLTINSVEA
EDFAMFYCQSKSWPFTFGCGTRLEIK

Linker sequence (SEQ ID NO: 30)

GGGSGGGGS

Linker sequence (SEQ ID NO: 31)

GGGGS

IGHG1 isoform NCBI Reference No: J00228 (SEQ ID NO: 32)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSS
SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

IGHG2 isoform NCBI Reference No: J00230 (SEQ ID NO: 33)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSS
NFGTQTYTCNVNHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
DPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQP
REPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

IGHG4 isoform NCBI Reference No: K01316 (SEQ ID NO: 34)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSS
SLGKTQTYTCNVNHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
EDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQ
PREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSR
WQEGNVFSCSVMHEALHNHYTQKSLSLSPGK

PDL1-avelumab antibody heavy chain (SEQ ID NO: 35)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADTVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
CDKHTCTPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT
CLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
LSLSPGK

PDL1-3F2-IgG1 heavy chain (SEQ ID NO: 36)

QVQLQESGPGLVKPSSETLSLTCTVSGYSITSGYNWHWIRQFPGNGLEWMGYIHHSSITNYPNPSLKSRTISRDT
SKNQFSLKLSSVTAADTATYYCAREGYDYDFAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKSLS
LSPGK

PDL1-3F2-IgG1 light chain (SEQ ID NO: 37)

DIVLTQSPDFQSVTPKEKVTITCRASQSISSNNLHWYQQKPDSEPKLLIKYASQSISSGIPSRFSGSGSGTDFTLT
INSVEAEDFAMYFCQQSKSWPFTFGQGRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDYSLSSITLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

M7824 heavy chain (SEQ ID NO: 38)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADTVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC
LVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKSLS
LSPGAGGGGSGGGGSGGGGSGGGGSGIPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDFRFSCTDNQKSCMSN
CSITSICEKPKQEVCAVWRKNDENITLETVCHDPKLPYHDFILEDAAAPKIMKEKKKPGETTFMCSGSSSDECN
DNIIFSEYNTSNPD

M7824 light chain (SEQ ID NO: 39)

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFGSGSKSGNTAS
LTISGLQAEDADYYCSSYTSSSTRVFGTGTQVTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAV
TVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

PD1-1A7 VH (SEQ ID NO: 40)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKRLEWVAHISGGSSSTIYPDTPVKGRFTISRDN
SKNTLYLQMNSLRAEDTAMYYCTRQFYFGSSFWYFDVWGAGTTVTVSS

PD1-1A7 VL (SEQ ID NO: 41)

DNVLTQSPATLSVSPGERATLSCASQSVDFDGDSYMNWYQQKPGQPPRLLIYAASNLESGIPARFSGSGSGTD
FTLTISSEVEDFATYYCQQSNEDPPTFGGGTKVEIK

CT4-4G12-IgG1 heavy chain (SEQ ID NO: 42)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMSWVRQAPGKLEWVATISRGGGYTSYPDSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAREDYGSSYVHWFAYWGQGLTVTVSAASTKGPSVFPLAPSSKSTSGGTAALG
CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP
KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL
TCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK
SLSLSPGK

CT4-4G12-IgG1 light chain (SEQ ID NO: 43)

DIQMTQSPFSLASVGDRTITCRAGENIYSYLAWYQQKPGKAPKLLIYNARTLAEGVPSRFSGSGSGTEFTLT
ISSLPEDFATYYCQHHYGSPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDYSLSSITLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

CT4-4G12 VH (SEQ ID NO: 44)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMSWVRQAPGKLEWVATISRGGGYTSYPDSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAREDYGSSYVHWFAYWGQGLTVTVSA

CT4-4G12 VL (SEQ ID NO: 45)

DIQMTQSPSFLSASVGDRVTITCRAGENIYSYLAHYQQKPGKAPKLLIYNARTLAEGVPSRFSGSGSGTEFTLT
ISSLPEDFATYYCQHHYGSPTFGGGTKLEIKR

CT4-O40-SCFV-HC heavy chain (SEQ ID NO: 46)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMSWVRQAPGKGLEWVATISRGGGYTSYPDSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAREDYGSSYVHWFAYWGQGLTVTVSAASTKGPSVFPLAPSSKSTSGGTAALG
CLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP
KSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL
TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQK
SLSLSPGGGGGGGGGGGGGGGGGGDIQMTQSPSSLSASVGDRVTITCRASQDINNYLNWYQQKPGGAVKLLIYYTS
RLHTGVPSPRFSGSGSGTDFTLTITSSLPEDIATYYCQQTNTLPWTFGCGTKLEVKGSGGGGGGGGGGGGGGGGG
SQVQLVESGGGVVQPGSRSLRISCAVSGFSLTSYGVWVRQAPGKCLEWLGVIWGGSTDYNAAFISRLTISRDN
SKSTVYFQMNSLRAEDTAVYYCAREEFGYWGQGLTVTVSS

CT4-O40-FV3A heavy chain (SEQ ID NO: 47)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMSWVRQAPGKGLEWVATISRGGGYTSYPDSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAREDYGSSYVHWFAYWGQGLTVTVSAASTKGPSVFPLAPSSKSTSGGTAALG
CLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP
KSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTGGGGSG
GGGSDIQMTQSPSSLSASVGDRVTITCRASQDINNYLNWYQQKPGGAVKLLIYYTSRLHTGVPSPRFSGSGSGTD
FTLTITSSLPEDIATYYCQQTNTLPWTFGCGTKLEVKGSGGGGGGGGGGGGGGGGGSQVQLVESGGGVVQPGSR
LRISCAVSGFSLTSYGVWVRQAPGKCLEWLGVIWGGSTDYNAAFISRLTISRDNKSTVYFQMNSLRAEDTA
VYYCAREEFGYWGQGLTVTVSSGGGGGGGGGGGGGGGGGGKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD
GSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

O40-9H3 VH (SEQ ID NO: 48)

QVQLVESGGGVVQPGSRSLRISCAVSGFSLTSYGVWVRQAPGKGLEWLGVIWGGSTDYNAAFISRLTISRDN
KSTVYFQMNSLRAEDTAVYYCAREEFGYWGQGLTVTVSS

O40-9H3 VL (SEQ ID NO: 49)

DIQMTQSPSSLSASVGDRVTITCRASQDINNYLNWYQQKPGGAVKLLIYYTSRLHTGVPSPRFSGSGSGTDFTLT
ISSLPEDIATYYCQQTNTLPWTFGGGKLEVKR

Mouse CT4-4G12 VH (SEQ ID NO: 50)

DVKLVESGGGLVKPGGSLKLSCTASGFTFSSYTMSWVRQTPEKRLEWVATISRGGGYTSYPDSVKGRFTISRDN
AKNTLYLQMSSLQSEDTAMYYCARDYGYSSYVHWFAYWGQGLTVTVSA

Mouse CT4-4G12 VL (SEQ ID NO: 51)

DIQMTQSPASLSASVGETVTITCRAGENIYSYLAHYQQKQKSPQLLVYNARTLAEGVPSRFSGSGSGTQFSLK
INSLQPEDFGSYCQHHYGSPTFGGGTKLEIK

Mouse OX40 antibody 9H3 VH (SEQ ID NO: 52)

QVQLKQSGPGLVQPSQSLSTICTVSGFSLTSYGVWVRQPPGKLEWLGVIWGGSTDYNAAFISRLSISKDNS
KQVFFKMNSLQADDTAIYYCAREEFGYWGQGLTVTVSA

Mouse OX40 antibody 9H3 VL (SEQ ID NO: 53)

DIQMTQTTSSLSASLGRVTISCRASQDINNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLT
ISNLEQEDIATYFCQQTNTLPWTFGGGKLEIK

HC Linker sequence (SEQ ID NO: 90)

GGGGSGGGSGGGSGGGSG

C40-6A7 VH (SEQ ID NO: 91)

QVQLVQSGAEVKKPGASVKLSCKASGYTFISYYIYVWKQAPGQGLEWIGGINPRNGGTNFNEKFKSRATLTVDTSISTAYMELSRLRSED TAVYYCTRHGNGVYWGQGTTLTVSS

C40-6A7 VL (SEQ ID NO: 92)

DVVMTQSPSLPVTLGQPASISCRSSQSLLHSNGNTYLHWYQQRPGQSPNHLYQVSNRFSGVPDRFSGSGSGTDTFLKISRVEAEDVG VYFCSQTTHVPWTFGGGTKVEIK

hIL3 (SEQ ID NO: 93)

NCSNMIDEIITHLKQPPLPLLD FNNLNGEDQDILMENNLRPNLEAFNRAVKSLQNASAIESILKNLLPCLPLATAAPTRHPIHIKGDWNEFRRKLT FYLKTLENAQAQQTTL SLAIF

hIL4 (SEQ ID NO: 94)

HKCDITLQEIIKTLNSLTEQKTLCTELTVTDIFAASKNTEKETFCRAATVLRQFYSHHEKDTRCLGATAQQFHRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQSTLENFLERLKTIMREKYSKCSS

hIL5 (SEQ ID NO: 95)

IPTEIPTSALVKETLALLSTHRTL LIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVN QFLDYLQEFLGVMNTEWIIES

hIL6 (SEQ ID NO: 96)

VPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGC FQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQLQDMTTHLILRSFKEFLQSSLRALRQM

hIL8 (SEQ ID NO: 97)

PKFIKELRVIESGPHCANTEIIVKLS DGRELCCLDPKENWVQRVVEKFLKRAENS

hIL9 (SEQ ID NO: 98)

QGCPTLAGILDINFLINKMQEDPASKCHCSANVTSCLC LGIPSDNCTRPCFSERLSQMTNTTMQTRYPLIFSRVKKSVEVLKNNKCPYFSCEQPCNQTTAGNAL TFLKSLEIFQKEKMRGMRGKI

hIL13 (SEQ ID NO: 99)

STALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALES LINVSGCSAIEKTQRM LSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLK KLFREG

hIL15 (SEQ ID NO: 100)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLELQVISLES GDASIHDTVENLIILANNSLSSNGNVTESGCKECEEEKNIKEFLQSFVHIVQMFIN TS

Amino acids 224-333 of human IgA (SEQ ID NO: 101)

NTFRPEVHLLPPPSEELALNELVTLTCLARGFS PKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTFATVTSILRVA AEDWKKGDTFSCMVGHEALPLAFTQKTIDRLA

Amino acids 269-375 of human IgD (SEQ ID NO: 102)

AQAPVKLSLNLLASSDPPEAASWLLCEVSGFSPPNILLMWLEDQREVNTSGFAPARPPPQPRSTTFWAWSVLRVPAPPSPQPATYTCVSHEDSRTLLNASRSLEVS

Amino acids 324-433 of human IgM (SEQ ID NO: 103)

VALHRPDVYLLPPAREQLNLRESATITCLVTGFS PADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEWNTGETYTCVAHEALPNRV TERTVDKST

CH3-CHS region of human IgG1 (J00228|IGHG1*01|Homo sapiens) (SEQ ID NO: 104)

GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDK
SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

CH3-CHS region of human IgG2 (J00230|IGHG2*01|Homo sapiens) (SEQ ID NO: 105)

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDGSFFLYSKLTVDK
SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

CH3-CHS region of human IgG3 (X03604|IGHG3*01|Homo sapiens) (SEQ ID NO: 106)

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPMLDSDGSFFLYSKLTVDK
SRWQQGNIFSCSCVMHEALHNRYTQKSLSLSPGK

CH3-CHS region of human IgG4 (K01316|IGHG4*01|Homo sapiens) (SEQ ID NO: 107)

GQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSRLTVDK
SRWQEGNVFCSCVMHEALHNHYTQKSLSLSPGK

CH3-CHS region of rat IgG1 (RatNor_6_chr6|IGHG1*01|Rattus norvegicus) (SEQ ID NO: 108)

GRTQVPVHYTMSPTKEEMTQNEVSITCMVKGFYPDDIYVEWQMNQGPQENYKNTPTMTDGSYFLYSKLNKK
EKWQQGNTFTCSVLHEGLHNHHTKSLSHSPGK

CH3-CHS region of rat IgG2A (RatNor_6_chr6|IGHG2A*01|Rattus norvegicus) (SEQ ID NO: 109)

GTPRGPPQVYTMAPPKEEMTQSQVSITCMVKGFYPDDIYTEWKMNQGPQENYKNTPTMTDGSYFLYSKLNKK
ETWQQGNTFTCSVLHEGLHNHHTKSLSHSPGK

CH3-CHS region of rat IgG2B (RatNor_6_chr6|IGHG2B*01|Rattus norvegicus) (SEQ ID NO: 110)

GLVRKPQVYVMGPPTEQLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTPEVMDSDGSFFMYSKLNVER
SRWDSRAPFVCSVVHEGLHNHHTKSLSHSPGK

CH3-CHS region of rat IgG2C (RatNor_6_chr6|IGHG2C*01|Rattus norvegicus) (SEQ ID NO: 111)

GKARTPQVYTIPPPREQMSKNKVSITCMVTSFYFASISVEWERNGELEQDYKNTLPVLDSDGSYFLYSKLSVDT
DSWMRGDIYTCVVHEALHNHHTQKNLSRSPGK

CH3-CHS region of mouse IgG1 (J00453|IGHG1*01|Mus musculus) (SEQ ID NO: 112)

GRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNNGSYFVYSKLNQK
SNWEAGNTFTCSVLHEGLHNHHTKSLSHSPGK

CH3-CHS region of mouse IgG2A (V00825|IGHG2A*01|Mus musculus) (SEQ ID NO: 113)

GSVRAPQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTPEVLDSDGSYFMYSKLRVEK
KNWVERNSYSCSVVHEGLHNHHTKSFRTSGK

CH3-CHS region of mouse IgG2B (V00763|IGHG2B*01|Mus musculus) (SEQ ID NO: 114)

GLVRAPQVYTLPPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNMT
SKWEKTDSCNVRHEGLKNYYLKKTISRSPGK

CH3-CHS region of mouse IgG2C (J00479|IGHG2C*01|Mus musculus) (SEQ ID NO: 115)

GPVRAPQVYVLPPEAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSYFMYSKLRVQK
STWERGSLFACSVVHEVLHNHLTTKTISRSLGK

CH3-CHS region of mouse IgG3 (X00915|IGHG3*01|Mus musculus) (SEQ ID NO: 116)

GRAQTPQVYTIPPPREQMSKKKVSILTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVD
DSWLQGEIFTCSVVHEALHNHHTQKNLSRSPGK

CH3-CHS region of monkey IgG1 (NW_001121238|IGHG1*01|Macaca mulatta) (SEQ ID NO: 117)

GQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVVEWESSGQPENTYKTPPVLDSDGSYFLYSKLTVDK
SRWQQGNVFCSCVMHEALHNHYTQKSLSVSPGK

CH3-CHS region of monkey IgG2 (AY292519|IGHG2*01|Macaca mulatta) (SEQ ID NO: 118)

GQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVVEWASNGQPENTYKTPPVLDSDGSYFLYSKLTVDK
SRWQQGNTFCSCVMHEA

CH3 region of monkey IgG3 (AY292512|IGHG3*01|Macaca mulatta) (SEQ ID NO: 119)

GQPREPQVYILPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQPENTYKTPPVLDSDGSYFLYSKLTVDK
SRWQQGNTFCSCVMHEA

CH3-CHS region of dog IgG1 (AF354264|IGHG1*01|Canis lupus familiaris) (SEQ ID NO: 120)

GRAHKPSVYVLPSPKELSSSDTVSITCLIKDFYPPDIDVEWQSNQQEPERKHRMTPPQLDEDGSYFLYSKLS
VDKSRWQQGDPFTCAVMHETLQNHYTDLSSLHSPGK

CH3-CHS region of dog IgG2 (IMGT000001|IGHG2*01|Canis lupus familiaris) (SEQ ID NO: 121)

GQAHQPSVYVLPSPREELSKNTVSLTCLIKDFFPDIDVEWQSNQQEPESKYRTTPPQLDEDGSYFLYSKLSV
DKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK

CH3-CHS region of dog IgG3 (AF354266|IGHG3*01|Canis lupus familiaris) (SEQ ID NO: 122)

GQAHQPNVYVLPSPRDEMSKNTVTLTCLVKDFFPEIDVEWQSNQQEPESKYRTTPPQLDEDGSYFLYSKLSV
DKSRWQRGDTFICAVMHEALHNHYTQISLSHSPGK

CH3-CHS region of dog IgG4 (AF354267|IGHG4*01|Canis lupus familiaris) (SEQ ID NO: 123)

GQAHQPSVYVLPSPKELSSSDTVTLTCLIKDFFPPEIDVEWQSNQQEPESKYHTTAPQLDEDGSYFLYSKLS
VDKSRWQQGDTFTCAVMHEALQNHYTDLSSLHSPGK

Linker sequence3 (SEQ ID NO: 124)

GGGGSGGGSGGGGS

mIL12a (SEQ ID NO: 125)

VIPVSGPARCLSQSRNLLKTDDMVKTAREKLKHYSCAEDIDHEDITRDQSTLKTCLPLELHKNESCLATRE
TSSTTRGSLPPQKTSMLMTLCLGSIYEDLKMYQTEFQAINAALQNNHQQIILDKGMLVAIDELMQSLNHNGE
TLRQKPPVGEADPYRVKMKLCILLHAFSTRVVTINRVMGYLSSA

mIL12b (SEQ ID NO: 126)

MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSQDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGET
LSHSHLLLHKKENGWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVRNMDLKFNKSSSSSPDSRAVTCGMA
SLSAEKVTLQDQDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDI IKPDPPKNLQMKPL
KNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQCKGGNVCVQAQDRY
YNSSCSKWACVPCRVR

hIL12a (SEQ ID NO: 127)

ARNLPVATPDPGMFPCLLHHSQNLRLRAVSNNMLQKARQTLFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNES
CLNSRETSFITNGSCLASRKTSFMALCLSSIIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNLAVIDELMQA
LNFNSETVPQKSSLEEDFYTKIKLCILLHAFRIRAVTIDRVMSYLNAS

hIL12b (SEQ ID NO: 128)

IWELKKDVYVVELDWYDAPGEMVVLTCDTPEEDGITWTLQDSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEV
LSHSHLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWLLTTISTDLTFSVKSSRGSSDPQGVTC
GAATLSAERVGRDNKEYEYSEVCQEDSACPAEESLPIEVMDAVHKLKYENYSTSFFIRDI IKPDPPKNLQMLK
PLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKDRVFTDKTSATVICRKNASISVRAQDRYSSS
WSEWASVPCS

hIFNa4 (SEQ ID NO: 129)

CDLPQTHSLGNRRALILLAQMGRISHFSCLKDRHDFGFPEEEFDGHQFQKAQISVLHEMIQQTFLNLFSTEDSS
AAWEQSLLEKFSTELYQQLNDLEACVIEVGEETPLMNEDSILAVRKYFQRITLYLTEKKYSPCAWEVVRAEI
MRSLSFSTNLQKRLRRKD

selicrelumab VH (SEQ ID NO: 130)

QVQLVQSGAEVKKPGASVKVCSKASGYTFTGYMHVVRQAPGQGLEWMGWINPDSGGTNYAQKFQGRVTMTTRDT
SISTAYMELNRLRSDDTAVYYCARDQPLGYCTNGVCSYFDYWQGTLLVTVSS

selicrelumab VL (SEQ ID NO: 131)

DIQMTQSPSSVSASVGDRTITCRASQGIYSWLAWYQQKPGKAPNLLIYTASTLQSGVPSRFSGSGSGTDFTLT
ISSLPEDFATYYCQANIFPLTFGGGTKEIK

selicrelumab scFV (SEQ ID NO: 132)

DIQMTQSPSSVSASVGDRTITCRASQGIYSWLAWYQQKPGKAPNLLIYTASTLQSGVPSRFSGSGSGTDFTLT
ISSLPEDFATYYCQANIFPLTFGGGTKEIKGGGSGGGSGGGSGGGSGGGSGVQLVQSGAEVKKPGASVKVSC
KASGYTFTGYMHVVRQAPGQGLEWMGWINPDSGGTNYAQKFQGRVTMTTRDTSISTAYMELNRLRSDDTAVYY
CARDQPLGYCTNGVCSYFDYWQGTLLVTVSS

1A7-selicrelumab-FV3A-IgG4 (heavy chain) (SEQ ID NO: 133)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMSVVRQAPGKRLEWVAHISGGGSTYYPDTPVKGRFTISRDN
SKNTLYLQMNLSRAEDTAMYYCTRQFYFGSSFWYFDVWGAGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALG
CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTCNVDPKPKNTKVDKRVES
KYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVHLQDNLNKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEGGGSGGGGSD
IQMTQSPSSVSASVGDRTITCRASQGIYSWLAWYQQKPGKAPNLLIYTASTLQSGVPSRFSGSGSGTDFTLT
SSLPEDFATYYCQANIFPLTFGGGTKEIKGGGSGGGSGGGSGGGSGGGSGVQLVQSGAEVKKPGASVKVSC
KASGYTFTGYMHVVRQAPGQGLEWMGWINPDSGGTNYAQKFQGRVTMTTRDTSISTAYMELNRLRSDDTAVYYC
ARDQPLGYCTNGVCSYFDYWQGTLLVTVSSGGGSGGGGSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPP
VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK

1A7-selicrelumab-FV3A-IgG4 (light chain) (SEQ ID NO: 134)

DNVLTQSPATLSVSPGERATLSCASQSVDFDGSYMNWYQQKPGQPPRLIYAASNLESIGIPARFSGSGSGTD
FTLTISSVEPEDFATYYCQQSNEDPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREA
KVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

1A7-selicrelumab-FVHC-IgG4 heavy chain (SEQ ID NO: 135)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKRLEWVAHISSGGSSTYYPD TVKGRFTISRDN
SKNTLYLQMNSLRAEDTAMYYCTRQFYFGSSFWYFDVWGAGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALG
CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTCNV DHKPSNTKVDKRVES
KYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLS
LSPGGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQGIYSWLAWYQQKPGKAPNLLIYTASTLQ
SGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQANIFPLTFGGGKVEIKGGGSGGGGSGGGGSGGGGSQV
QLVQSGAEVKKPGASVKVSCKASGYTF TGYMHWVRQAPGQGLEWMGW INPDSGGTNYAQKFQGRVTMTRDTSI
STAYMELNRLRSDDTAVYYCARDQPLGYCTNGVCSYFDYWGQGLTVTVSS

1A7-selicrelumab-FVHC-IgG4 light chain (SEQ ID NO: 136)

DNVLTQSPATLSVSPGERATLSCKASQSVDFDGD SYMNWYQQKPGQPPRLLIYAASNLESGIPARFSGSGSGTD
FTLTIS SVPEPEDFATYYCQQSNEDPPTFGGGTKVEIKGGGSGGGGQVQLVQSGAEVKKPGASVKVSCKASGYTF
TGYMHWVRQAPGQGLEWMGW INPDSGGTNYAQKFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCARDQPLG
YCTNGVCSYFDYWGQGLTVTVSSRTVAAPS VFI FPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGN
SQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIG. 49
Kabat CDR

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
4G12 or humanized 4G12 (CTLA4)	SYTMS	54	TISRGGGYTSYPD SVKG	55	EDYGSSYVH WFAY	56	RAGENIYSYLA	57	NARTLAE	58	QHHYGSP RT	59
9H3 or humanized 9H3 (OX40)	SYGVL	60	VIWSGGSTDYNA AFIS	61	EEFGY	62	RASQDINNYLN	63	YTSRLHS	64	QQTNTLP WT	65
3F2 or humanized 3F2 (PD-L1)	SGYN WH	18	YIHHSSITNYN PSLKS	19	EGYDYDW FAY	20	RASQSSNNL H	21	YASQSSIS	22	QQSKS WPFT	23
1A7 or humanized 1A7 (PD-1)	SYSMS	24	HISGGSSYYPD TVKG	25	QFYGGSSFW YFDV	26	KASQSVDFDG DSYMN	27	AASNLES	28	QQSNED PPT	29

FIG. 50
Chothia CDR

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
4G12 or humanized 4G12 (CTLA4)	GFTFS SYTMS	66	SRGGGY	67	EDYGSSYVH WFAY	68	RAGENIYSYLA	69	NARTLAE	70	QHHYGSP RT	71
9H3 or humanized 9H3 (OX40)	GFSLT SYGVL	72	WSGGS	73	EEFGY	74	RASQDINNYLN	75	YTSRLHS	76	QQTNTLP WT	77
3F2 or humanized 3F2 (PD-L1)	GYSIT SGYN WH	78	HHSSI	79	EGYDYDW FAY	80	RASQSISNNL H	81	YASQSIG	82	QQSKS WPFT	83
1A7 or humanized 1A7 (PD-1)	GFTFS SYSMS	84	SSGGSS	85	QFYGGSSFW YFDV	86	KASQSVDFDG DSYMN	87	AASNLES	88	QQSNED PPT	89