

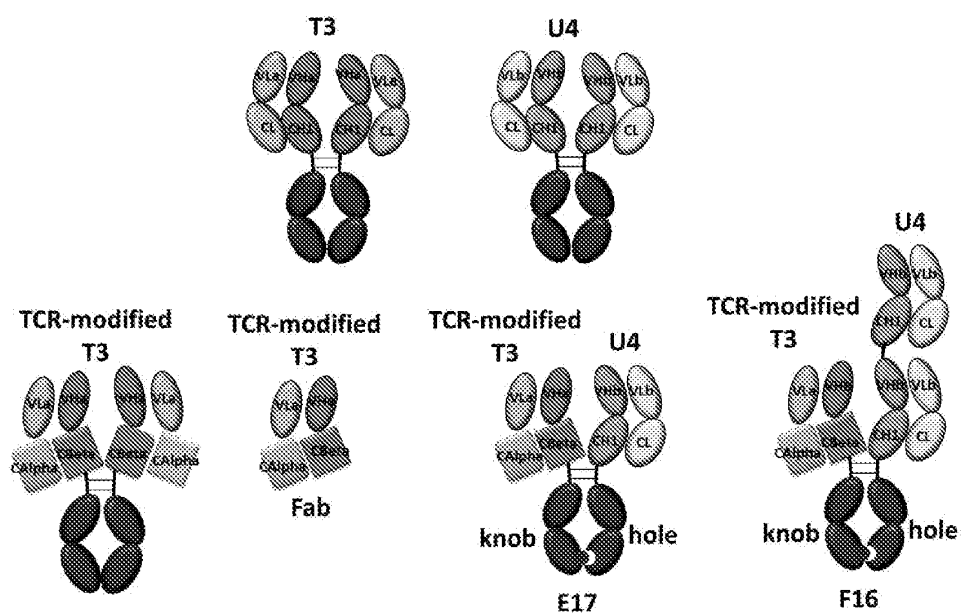


Figure 1

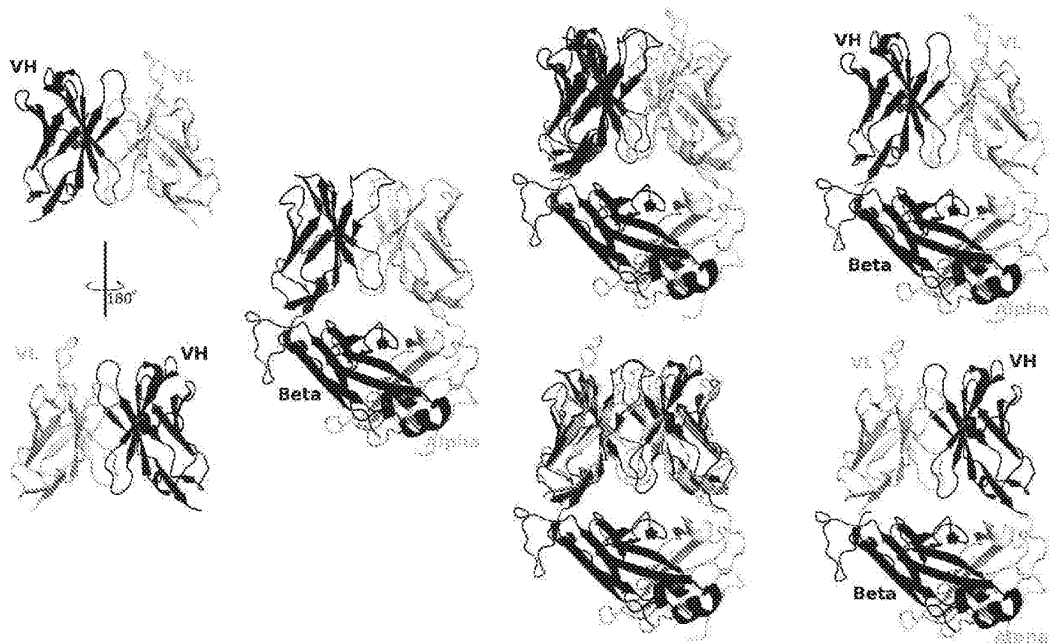


Figure 2A

Figure 2B

Figure 2C

Figure 2D

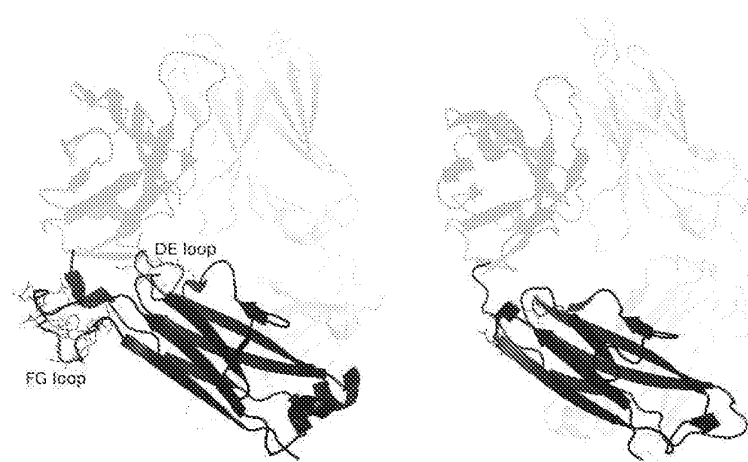


Figure 3A

Figure 3B

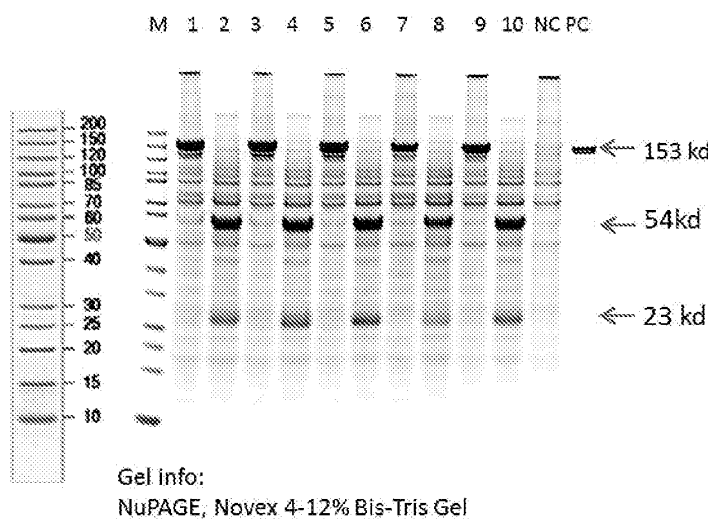


Figure 4

Cell Based CD3 Binding on Jurkat

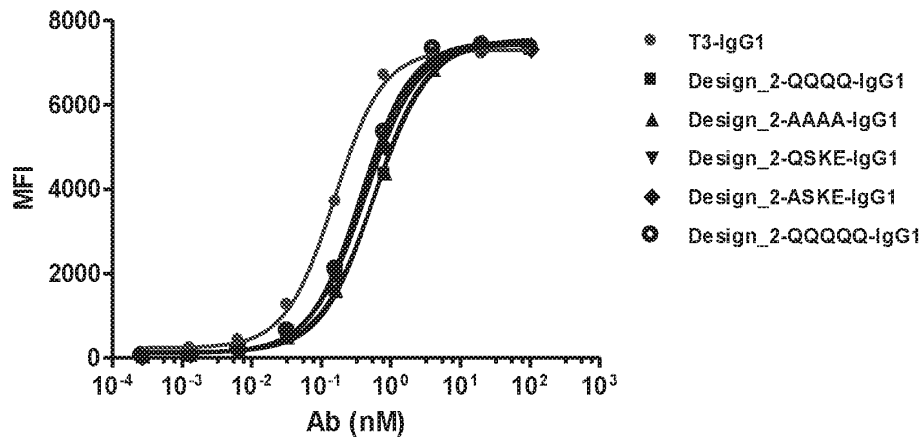


Figure 5

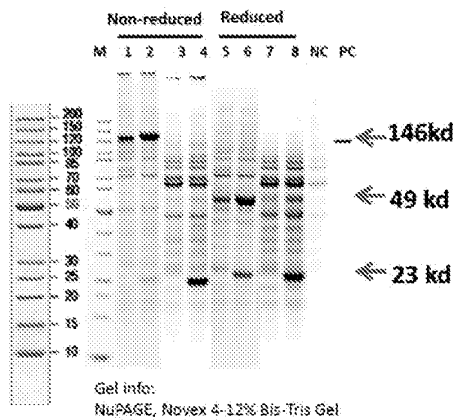


Figure 6A

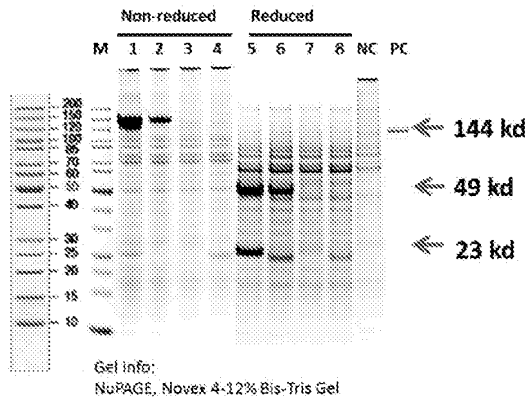


Figure 6B

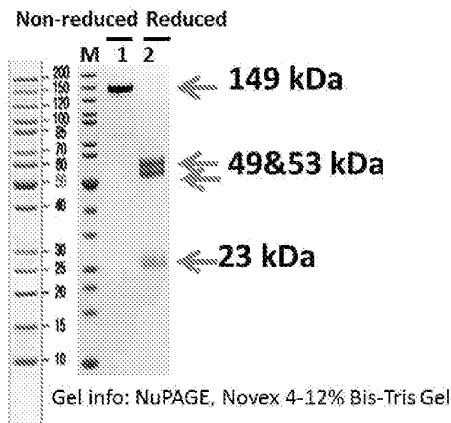


Figure 7A

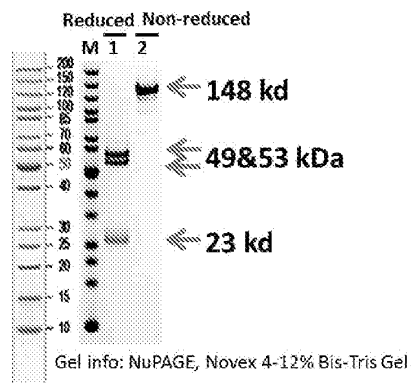


Figure 7B

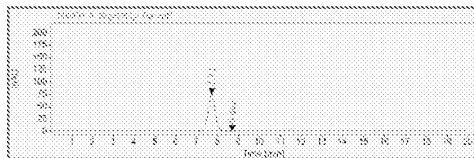


Figure 7C

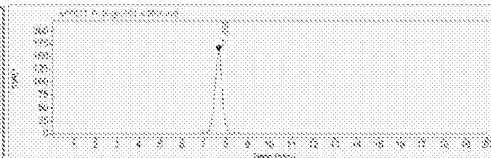


Figure 7D

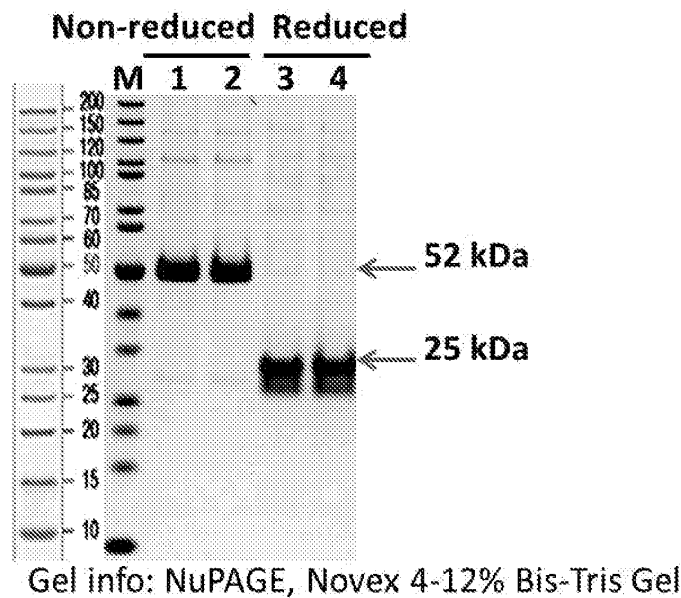


Figure 8

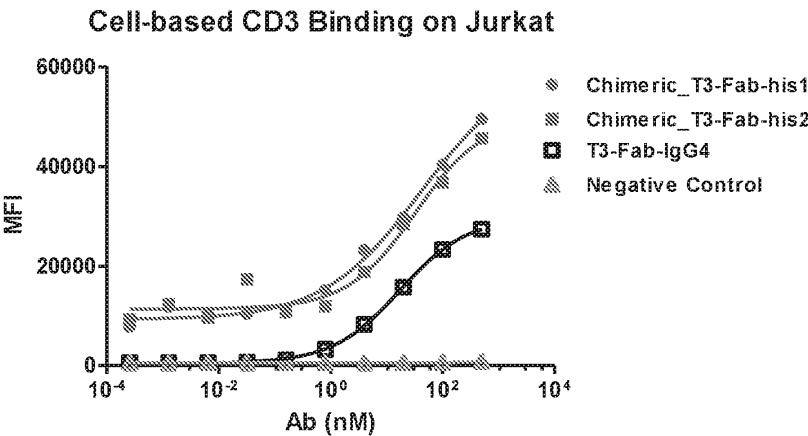


Figure 9

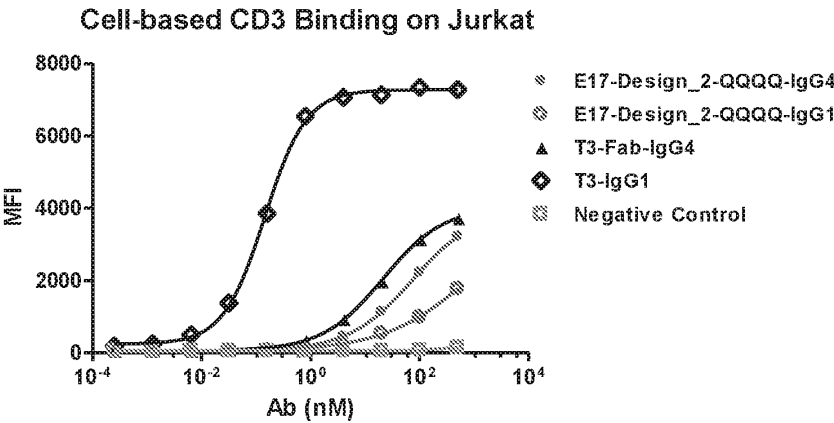


Figure 10A

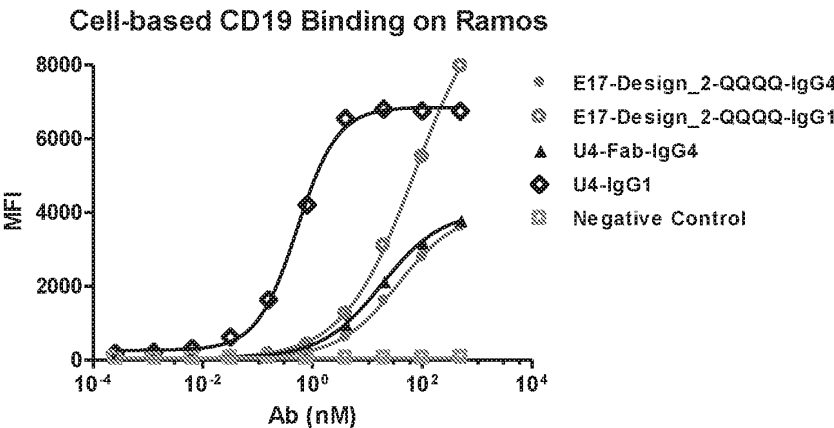


Figure 10B

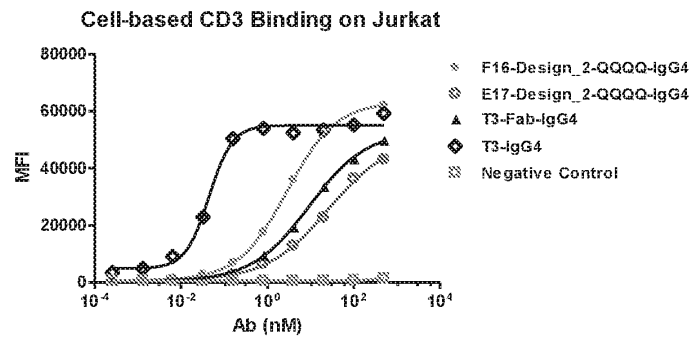


Figure 11A

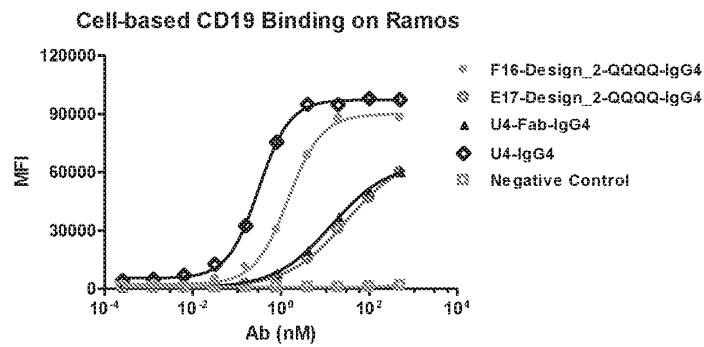


Figure 11B

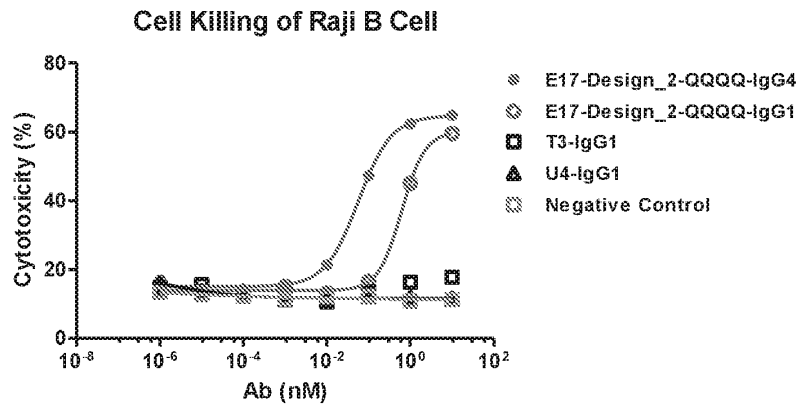


Figure 12

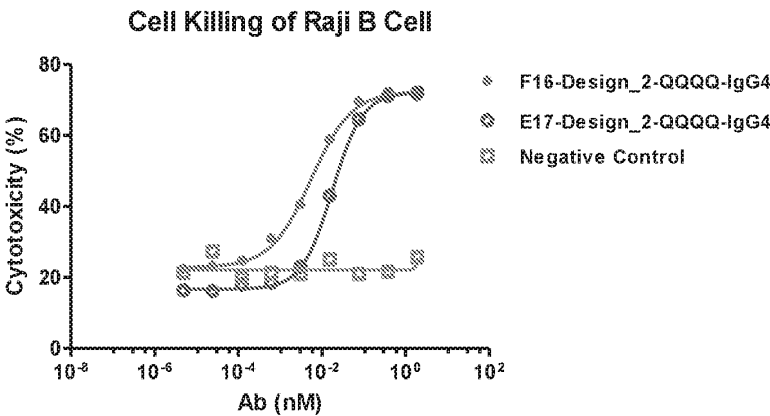


Figure 13

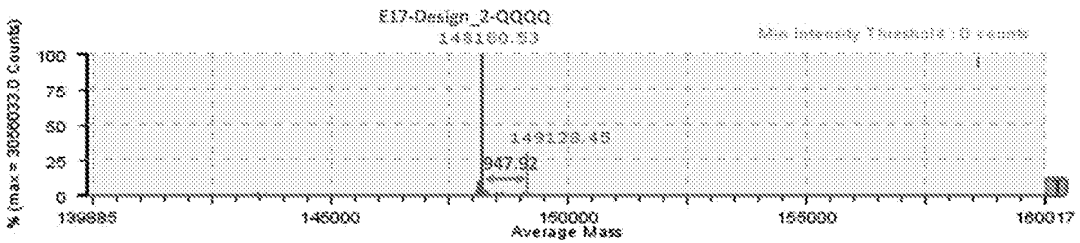


Figure 14A

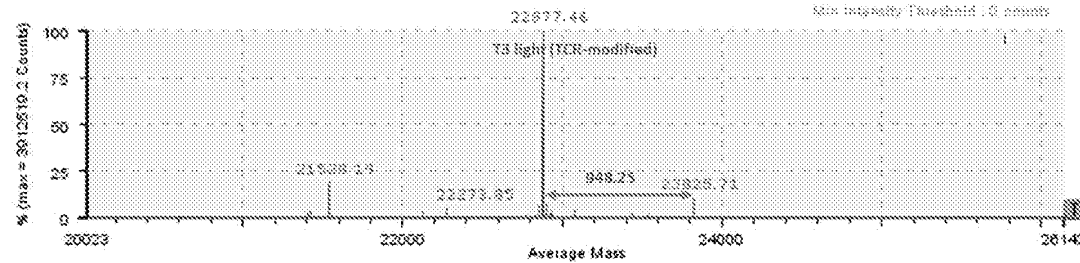


Figure 14B

With Disulphide Bond

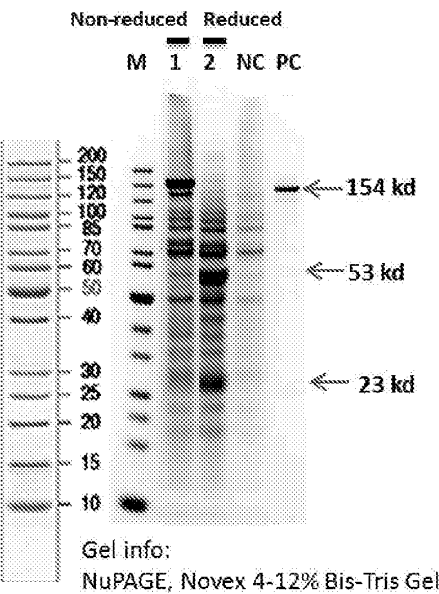


Figure 15A

Without Disulphide Bond

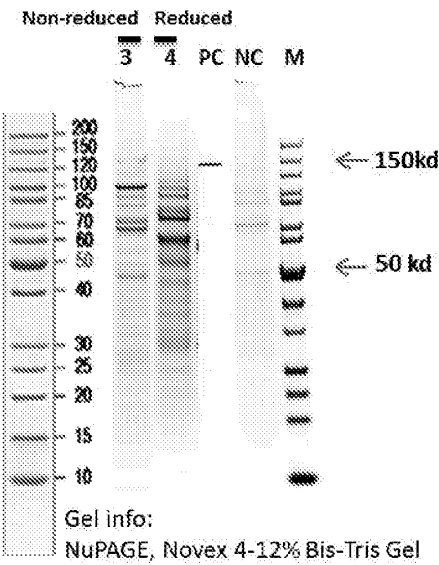


Figure 15B

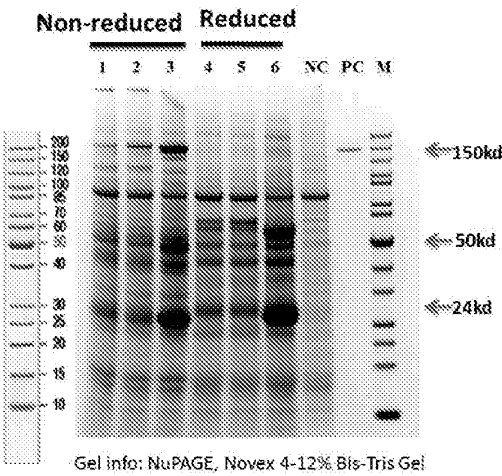


Figure 16

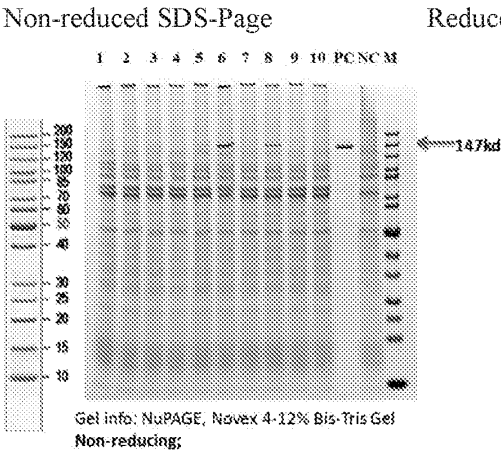


Figure 17A

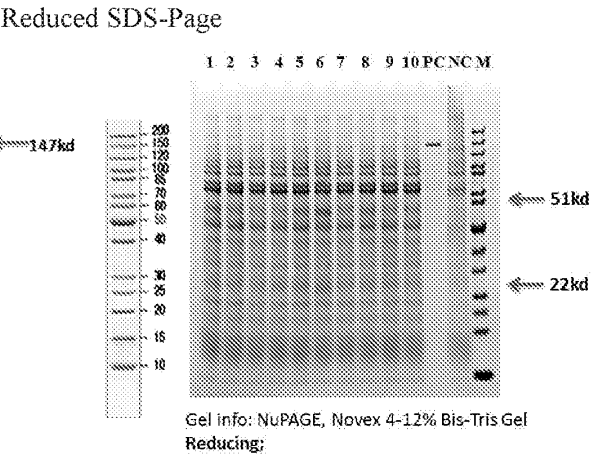


Figure 17B

Constant region sequence of TCR alpha chain:

TRAC_Human	PNTQNPDPAY YQLRDSKSSD KSVCLFTDFD SQTNVSQSKD SDVYITDKTV
4L4T_Alpha_Crystal	PDIQNPDPAY YQLRDSKSSD KSVCLFTDFD SQTNVSQSKD SDVYITDKCV
TRAC_Human	LDMSMDERS NSAVAVSNKS DFACANAFNN SIIPEDTTFP SPSSCDVKL
4L4T_Alpha_Crystal	LDMSMDERS NSAVAVSNKS DFACANAFNN SIIPEDTTFP SPSS-----
TRAC_Human	VEKSFETDTN LNFQNLVIG FRILLKVGAG FNLMTLRLW SS SEQ ID NO:254
4L4T_Alpha_Crystal	----- SEQ ID NO:255

Figure 18A

Constant region sequence of TCR beta chain:

TRBC1_Human	EDLNKVFPE VAVFEPSEAE ISHTQKATLY CLATGFYPDH VELSWVNGK
TRBC2_Human	-DLKNVFPE VAVFEPSEAE ISHTQKATLY CLATGFYPDH VELSWVNGK
4L4T_Beta_Crystal	EDLNKVFPE VAVFEPSEAE ISHTQKATLY CLATGFYPDH VELSWVNGK
TRBC1_Human	EVHSGVSTDP QPLKEQPALN DSRVCLSSRL RVSATFWQNP RNIFRCQVQF
TRBC2_Human	EVHSGVSTDP QPLKEQPALN DSRVCLSSRL RVSATFWQNP RNIFRCQVQF
4L4T_Beta_Crystal	EVHSGVSTDP QPLKEQPALN DSRVCLSSRL RVSATFWQNP RNIFRCQVQF
TRBC1_Human	YGLSENDEWT QDRAPVTQI VSAEAWGRAD CGFTSVSYQQ GVLSATILYE
TRBC2_Human	YGLSENDEWT QDRAPVTQI VSAEAWGRAD CGFTSVSYQQ GVLSATILYE
4L4T_Beta_Crystal	YGLSENDEWT QDRAPVTQI VSAEAWGRAD -----
TRBC1_Human	ILLGKATLYA VLVSAVLMA MVRKDF--- SEQ ID NO:256
TRBC2_Human	ILLGKATLYA VLVSAVLMA MVRKDSRG SEQ ID NO:257
4L4T_Beta_Crystal	----- SEQ ID NO:258

Figure 18B

Constant region sequence of pre-alpha:

PTCRA_HUMAN	MAGTWLLLL ALGCPALFTG VGGTFPFLA PPIMLLVDGK QQMVVVCLVL
30F6_PreAlpha_Crystal	----- -GAHMLPTG VGGTFPFLA PPIMLLVDGK QQMVVVCLVL
PTCRA_HUMAN	DVAPPGLDSP DWFSAENGSA LDAFTYGPSP ATDGTWNL A HSLPSEELA
30F6_PreAlpha_Crystal	DVAPPGLDSP DWFSAENGSA LDAFTYGPSP ATDGTWNL A HSLPSEELA
PTCRA_HUMAN	SWEPLVCHTC PGAEGHSRST QPMHLSCEAS TARTCPQEPL RGTGPGALWL
30F6_PreAlpha_Crystal	SWEPLVCHTC PGAEGHSRST QPMHLSCEAS TARTC-SCDD DDK-----
PTCRA_HUMAN	GVLRLLLFKL LFDLLLTCS CLCDPAGPLP SPATTTTLRA LGSHRLHPAT
30F6_PreAlpha_Crystal	-----
PTCRA_HUMAN	ETGCREATSS PRPQPRDRRW GDTPPGRKPG SPVWEGCSYL SSYPTCPAQA
30F6_PreAlpha_Crystal	-----
PTCRA_HUMAN	WCSRSALRAP SSSLGAFFAG DLPPPLQAGA A SEQ ID NO:259
30F6_PreAlpha_Crystal	----- - SEQ ID NO:260

Figure 18C

Constant region sequence of **delta**:

TRA@_Human	MLFSSLLCVF VAFSYSGSSV AQKVTQAQSS VMPVRKAVT LNCLYETS#W
4LFH_Delta_Crystal	-----ETG AQKVTQAQSS VMPVRKAVT LNCLYETS#W
TRA@_Human	SYIIFWYKQL PSKEMIFLIR QGSDEQNAKS GRYSVNFKA AKSVALTISA
4LFH_Delta_Crystal	SYIIFWYKQL PSKEMIFLIR QGSDEQNAKS GRYSVNFKA AKSVALTISA
TRA@_Human	LQLEDSAKYF CALGESFLPF RGNFHYTDKL IFGKGTRVTV EPRSQPHIKP
4LFH_Delta_Crystal	LQLEDSAKYF CALGD-----PGQLNTDKL IFGKGTRVTV EPRSQPHIKP
TRA@_Human	SVFVMKNGTN VACLVRKFYP KDIRINLYSS KKITEFDPAL VISPSCKYNA
4LFH_Delta_Crystal	SVFVMKNGTN VACLVRKFYP KDIRINLYSS KKITEFDPAL VISPSCKYNA
TRA@_Human	YKLCKYEDSN SVTCSVQHON KTVHSTDFEV KTDSTDHVKP KETENTKQPS
4LFH_Delta_Crystal	YKLCKYEDSN SVTCSVQHON KTVHSTDFEV KTDSTDHVKP KETENTKQPS
TRA@_Human	K--SCHKPKA IVHTEKVNMM SLTVLGLRML FAKTVAVNFI LTAKLFFL SEQ ID NO:261
4LFH_Delta_Crystal	KSASGLVPR-- ----- SEQ ID NO:262

Figure 18D

Constant region sequence of **gamma**:

TRGC1_Human	DKQLDADYSP KPTIFLPSIA ETKLQKAGTY LCLLEKFFPD VIKIH#QKK
4LFH_Gamma_Crystal	DKQLDADYSP KPTIFLPSIA ETKLQKAGTY LCLLEKFFPD VIKIH#QKK
TRGC2_Human	DKQLDADYSP KPTIFLPSIA ETKLQKAGTY LCLLEKFFPD IIKIH#QKK
TRGC1_Human	SNILGSQEG NTMKTNDTYM KPSWLTVPKE SLDEKHEHCIV RHENNKNCVD
4LFH_Gamma_Crystal	SNILGSQEG NTMKTNDTYM KPSWLTVPKE SLDEKHEHCIV RHENNKNCVD
TRGC2_Human	SNILGSQEG NTMKTNDTYM KPSWLTVPKE SLDEKHEHCIV RHENNKNCID
TRGC1_Human	QEIIFFPIKT DVTIMDPKD- -----NCSKD ANDTLLQLT
4LFH_Gamma_Crystal	QEIIFFPIKT DVTIMDPKD- -----N-----
TRGC2_Human	QEIIFFPIKT DVTIVDPKDS YSKDANDVIT MDPEDNWSKD ANDTLLQLT
TRGC1_Human	NTSAYMYLL LLLKSVVYFA IITCCLLRRT AFCNGEKS SEQ ID NO:263
4LFH_Gamma_Crystal	-ASG-----LVPR----- SEQ ID NO:264
TRGC2_Human	NTSAYMYLL LLLKSVVYFA IITCCLLGRT AFCNGEKS SEQ ID NO:265

Figure 18E

Numbering Defined for Alpha Constant Region:

	1	11	21	31	50	
TRAC_Human	PNIQNPDPAV	YQLRDSKSSD	KSVCLFTDFD	SQTINVSQSKD	SDVYITDKTV	
4L4T_Alpha_Crystal	PDIQNPDPAV	YQLRDSKSSD	KSVCLFTDFD	SQTINVSQSKD	SDVYITDKCV	
E17_Design_2_QQQQ_IgG4	PDIQNPDPAV	YQLRDSKSSD	KSVCLFTDFD	SQTQVSQSKD	SDVYITDKCV	
	51	61	71	81	95	SEQ ID NO:
TRAC_Human	LDMRSMDFKS	NSAVAWSNKS	DFACANAFNN	SIIPEDITFFP	SPESS	239
4L4T_Alpha_Crystal	LDMRSMDFKS	NSAVAWSNKS	DFACANAFNN	SIIPEDITFFP	SPESS	240
E17_Design_2_QQQQ_IgG4	LDMRSMDFKS	NSAVAWSQKS	DFACANAFQN	SIIPEDITFFP	SPESS	241

Figure 19A

Numbering Defined for Beta Constant Region:

	0	1	11	21	31	50	
TRBC1_Human	E	DLN	KVFPPEV	AVFEPSEAEI	SHTQKATLVC	LATGFPDPHV	ELSWVNGKE
4L4T_Beta_Crystal	LE	DLN	KVFPPEV	AVFEPSEAEI	SHTQKATLVC	LATGFTDPHV	ELSWVNGKE
E17_Design_2_QQQQ_IgG4	LE	DLN	KVFPPEV	AVFEPSEAEI	SHTQKATLVC	LATGFTDPHV	ELSWVNGKE
	51	61	71	81	100		
TRBC1_Human	VHSGVSTDPQ	PLKEQPALND	SRVCLSSRLR	VSATFWQNPR	NHFRQVQFY		
4L4T_Beta_Crystal	VHSGVCTDPQ	PLKEQPALND	SRVCLSSRLR	VSATFWQNPR	NHFRQVQFY		
E17_Design_2_QQQQ_IgG4	VHSGVCTDPQ	PLKEQPALQD	SRVCLSSRLR	VSATFWQNPR	NHFRQVQFY		
	101	111	124	128	SEQ ID NO:		
TRBC1_Human	GLSENDEWTQ	DRAKPVTQIV	SAEA	WGRA	242		
4L4T_Beta_Crystal	GLSENDEWTQ	DRAKPVTQIV	SAEA	WGRA	243		
E17_Design_2_QQQQ_IgG4	GLSENDEWTQ	DRAKPVTQIV	SAEA	WGRA	244		

Figure 19B

Numbering Defined for Pre-Alpha Constant Region:

	1	11	21	31	50	
PTCRA_Human	PTGVGGTFFP	SLAPPIMLLV	DGKQQMVVVC	LVLDVAPPGL	DSPIWFSAGN	
30F6_PreAlpha_Crystal	PTGVGGTFFP	SLAPPIMLLV	DGKQQMVVVC	LVLDVAPPGL	DSPIWFSAGN	
Design_6_Pre_TCR_Construction' 1_Cys14	PTGVGGTFFP	CLAPPIMLLV	DGKQQMVVVC	LVLDVAPPGL	DSPIWFSAGQ	
	51	61	71	81	100	
PTCRA_Human	GSALDAFTYG	PSPATDGTWT	NLAHLSLPSE	ELASWEPLVC	HTGPGAEGHS	
30F6_PreAlpha_Crystal	GSALDAFTYG	PSPATDGTWT	NLAHLSLPSE	ELASWEPLVC	HTGPGAEGHS	
Design_6_Pre_TCR_Construction' 1_Cys14	GSALDAFTYG	PSPATDGTWT	NLAHLSLPSE	ELASWEPLVC	HTGPGAEGHS	
	101	117	SEQ ID NO:			
PTCRA_Human	RSTQPMHLSG	EASTART	245			
30F6_PreAlpha_Crystal	RSTQPMHLSG	EASTART	246			
Design_6_Pre_TCR_Construction' 1_Cys14	RSTQPMHLSG	EASTART	247			

Figure 19C

Numbering Defined for Delta Constant Region:

	0	1	11	21	31	50
TRA@ Human	E	PRSQPHTKPS	VFVMMKNGTNV	ACLVKEFYK	DIRINLVSSK	KITEFDPAIV
4LFH_Delta_Crystal	E	PRSQPHTKPS	VFVMMKNGTNV	ACLVKEFYK	DIRINLVSSK	KITEFDPAIV
Design_2_Cys5_no_Glyco	E	PRSQPHTKPS	VFVMMKNGTNV	ACLVKEFYK	DIRINLVSSK	KITEFDPAIV
	51	61	71	88	SEQ ID NO:	
TRA_Human	ISPSGKYNAV	KLGGYEDSNS	VTCSVQHDNK	TVHSTDFE	248	
4LFH_Delta_Crystal	ISPSGKYNAV	KLGGYEDSNS	VTCSVQHDNK	TVHSTDFE	249	
Design_2_Cys5_no_Glyco	ISPSGKYNAV	KLGGYEDSNS	VTCSVQHDNK	TVHSTDFC	250	

Figure 19D

Numbering Defined for Gamma Constant Region:

	0	1	11	21	31	50
TRGC1_Human	TD	KQLDADVSPK	PTIFLPSIAE	TKLQKAGTYL	CLEKFFPDV	IKIHWQEKKS
4LFH_Gamma_Crystal	TD	KQLDADVSPK	PTIFLPSIAE	TKLQKAGTYL	CLEKFFPDV	IKIHWQEKKS
Design_2_Cys5_no_Glyco	TD	KQLDADVSPK	PTIFLPSICE	TKLQKAGTYL	CLEKFFPDV	IKIHWQEKKS
	51	61	71	81	100	
TRGC1_Human	NTILGSQEGN	TMKTNDTYMK	FSWLTVPES	LDKEHRCIVR	HENNKNGVDQ	
4LFH_Gamma_Crystal	NTILGSQEGN	TMKTNDTYMK	FSWLTVPES	LDKEHRCIVR	HENNKNGVDQ	
Design_2_Cys5_no_Glyco	NTILGSQEGN	TMKTNDTYMK	FSWLTVPES	LDKEHRCIVR	HENNKNGVDQ	
	101	SEQ ID NO:				
TRGC1_Human	EIIF	251				
4LFH_Gamma_Crystal	EIIF	252				
Design_2_Cys5_no_Glyco	EIIF	253				

Figure 19E

Positions of IgG1 “knob” mutations

	1		50
IgG1_wild	EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD		
IgG1_knob	EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD		
	51		100
IgG1_wild	VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN		
IgG1_knob	VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN		
	101		150
IgG1_wild	GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR EEMTKNQVSL		
IgG1_knob	GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR EEMTKNQVSL		
	151		200
IgG1_wild	TCLVKGFYPS DIAVEWESNG QPENNYKTP PVLDSGCSFF LYSKLTVDKS		
IgG1_knob	WCLVKGFYPS DIAVEWESNG QPENNYKTP PVLDSGCSFF LYSKLTVDKS		
	201	232	SEQ ID NO:
IgG1_wild	RWQQGNVFSC SVMHEALHNIH YTKSLSLSP GK	294	
IgG1_knob	RWQQGNVFSC SVMHEALHNIH YTKSLSLSP GK	295	

Figure 20A

Positions of IgG4 “knob” mutations

	1		50
IgG4_wild	ESKYGPPCPP CPAPEFLGCP SVFLFPPKPK DTLISRTPPE VTCVVVDVSQ		
IgG4_knob	ESKYGPPCPP CPAPEFLGCP SVFLFPPKPK DTLISRTPPE VTCVVVDVSQ		
	51		100
IgG4_wild	EDPEVQFNWY VDGVEVHNAK TKPREEQFNS TYRVVSVLTV LHQDWLNGKE		
IgG4_knob	EDPEVQFNWY VDGVEVHNAK TKPREEQFNS TYRVVSVLTV LHQDWLNGKE		
	101		150
IgG4_wild	YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM TKNQVSLTCL		
IgG4_knob	YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM TKNQVSLWCL		
	151		200
IgG4_wild	VKGFYPSDIA VEWESNGQPE NNYKTTTPVL DSDGSFFLYS RLTVDKSRWQ		
IgG4_knob	VKGFYPSDIA VEWESNGQPE NNYKTTTPVL DSDGSFFLYS RLTVDKSRWQ		
	201	229	SEQ ID NO:
IgG4_wild	EGNVFSCSVM HEALHNHYTQ KLSLSLGLK	297	
IgG4_knob	EGNVFSCSVM HEALHNHYTQ KLSLSLGLK	298	

Figure 20B

Positions of IgG1 “hole” mutations

	1		50
IgG1_wild	EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD		
IgG1_Hole	EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD		
	51		100
IgG1_wild	VSIEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN		
IgG1_Hole	VSIEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN		
	101		150
IgG1_wild	GKEYKCKVSN KALPAPIETK ISKAKGQPRE PQVYTLPPSR EEMTKNQVSL		
IgG1_Hole	GKEYKCKVSN KALPAPIETK ISKAKGQPRE PQVCTLPPSR EEMTKNQVSL		
	151		200
IgG1_wild	TCLVKGFYPS DIAVEWESNG QPENNYKTP PVLDSDGSFF LYSKLTVDKS		
IgG1_Hole	SCAVKGFYPS DIAVEWESNG QPENNYKTP PVLDSDGSFF LVSKLTVDKS		
	201	232	SEQ ID NO:
IgG1_wild	RWQQGNVFSC SVMHEALHNH YTKSLSLSP GK	294	
IgG1_Hole	RWQQGNVFSC SVMHEALHNH YTKSLSLSP GK	296	

Figure 20C

Positions of IgG4 “hole” mutations

	1		50
IgG4_wild	ESKYGPPCPP CPAPEFLGCP SVFLFPPKPK DTLISRTPV VTCVVVDVSQ		
IgG4_Hole	ESKYGPPCPP CPAPEFLGCP SVFLFPPKPK DTLISRTPV VTCVVVDVSQ		
	51		100
IgG4_wild	EDPEVQFNWY VDGVEVHNAK TKPREEQFNS TYRVVSVLTV LHQDWLNGKE		
IgG4_Hole	EDPEVQFNWY VDGVEVHNAK TKPREEQFNS TYRVVSVLTV LHQDWLNGKE		
	101		150
IgG4_wild	YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM TKNQVSLTCL		
IgG4_Hole	YKCKVSNKGL PSSIEKTISK AKGQPREPQV CTLPPSQEEM TKNQVSLSCA		
	151		200
IgG4_wild	VKGFYPSDIA VEWESNGQPE NNYKTTPPV L DSDGSFFLYS RLTVDKSRWQ		
IgG4_Hole	VKGFYPSDIA VEWESNGQPE NNYKTTPPV L DSDGSFFLYS RLTVDKSRWQ		
	201	229	SEQ ID NO:
IgG4_wild	EGNVFSCSVM HEALHNHYTQ KSLSLSLGK	297	
IgG4_Hole	EGNVFSCSVM HEALHNHYTQ KSLSLSLGK	299	

Figure 20D

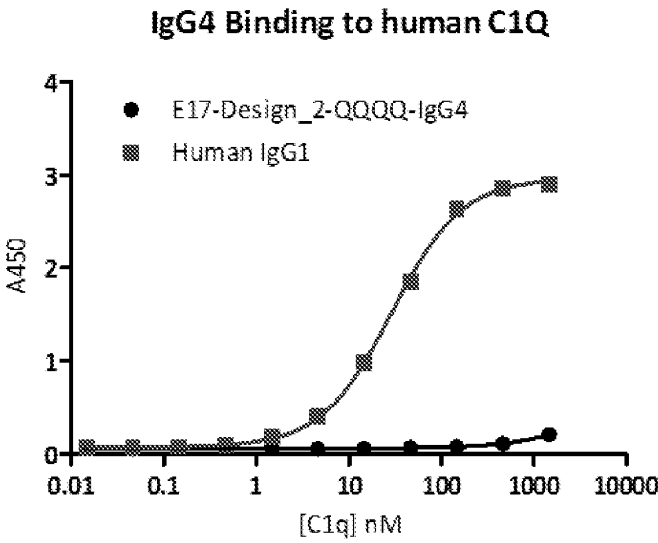


Figure 21A

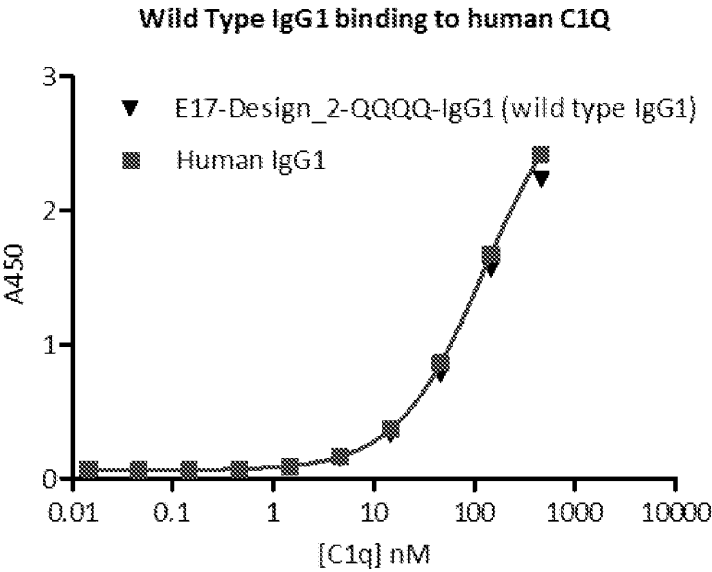


Figure 21B

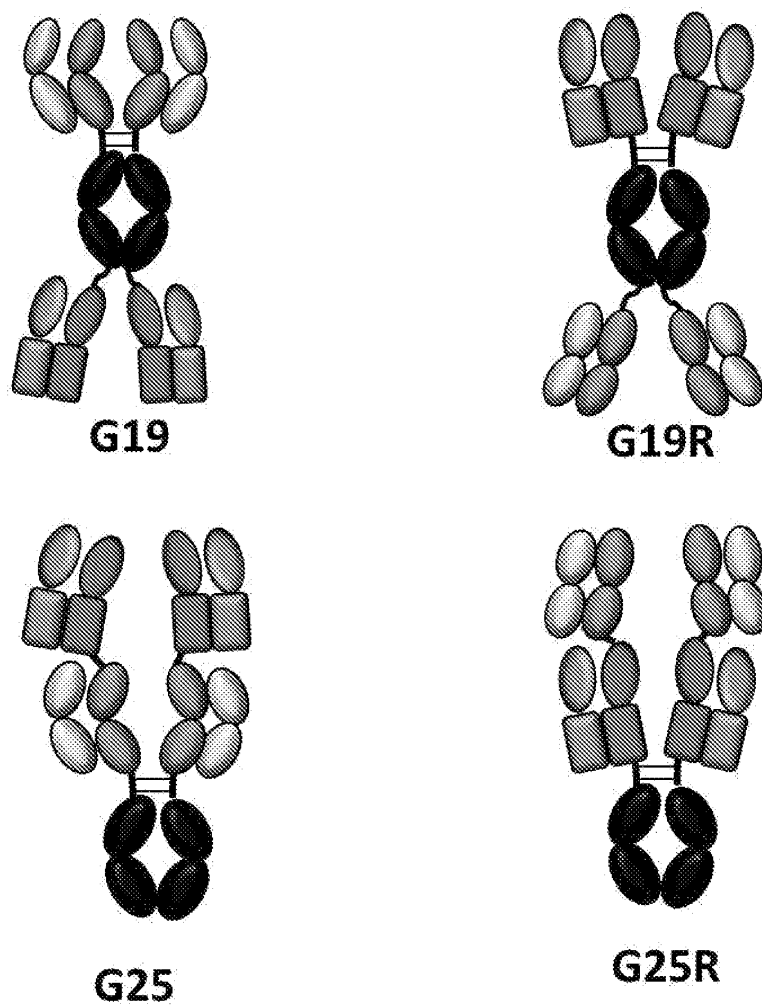


Figure 22

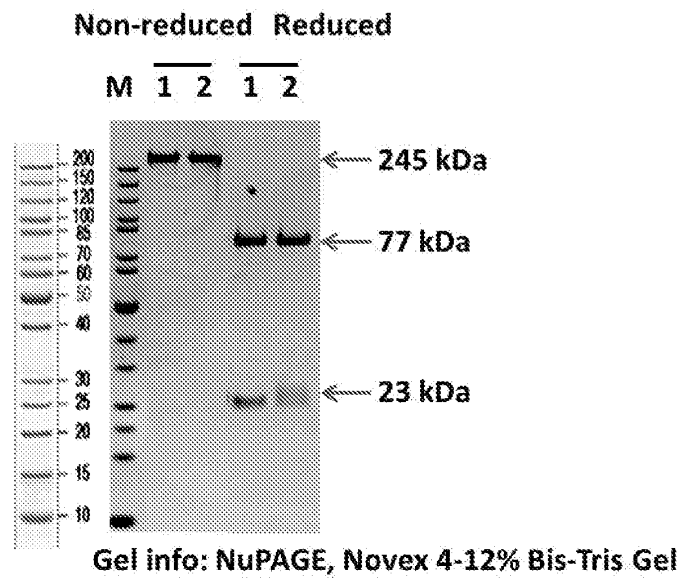


Figure 23A

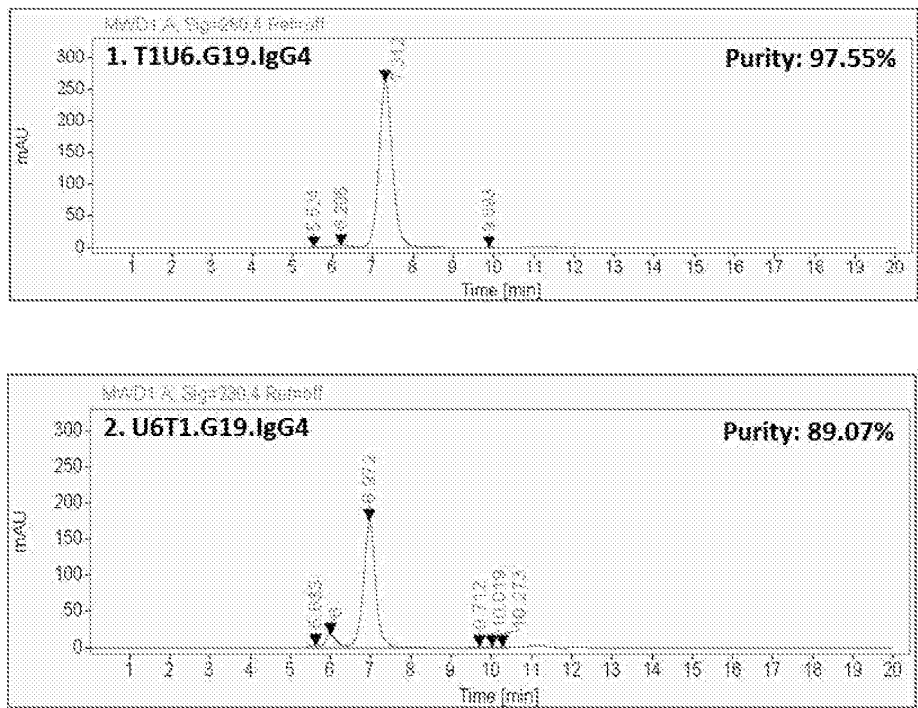


Figure 23B

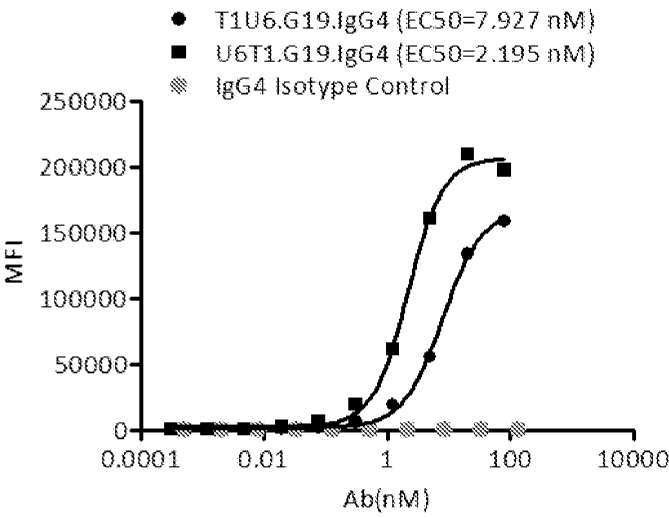


Figure 24A

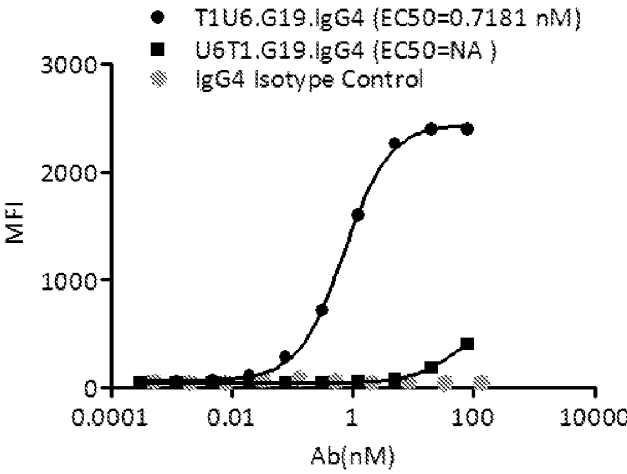


Figure 24B

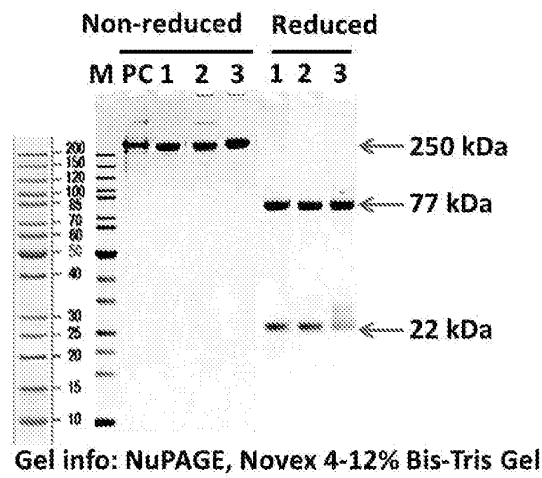


Figure 25A

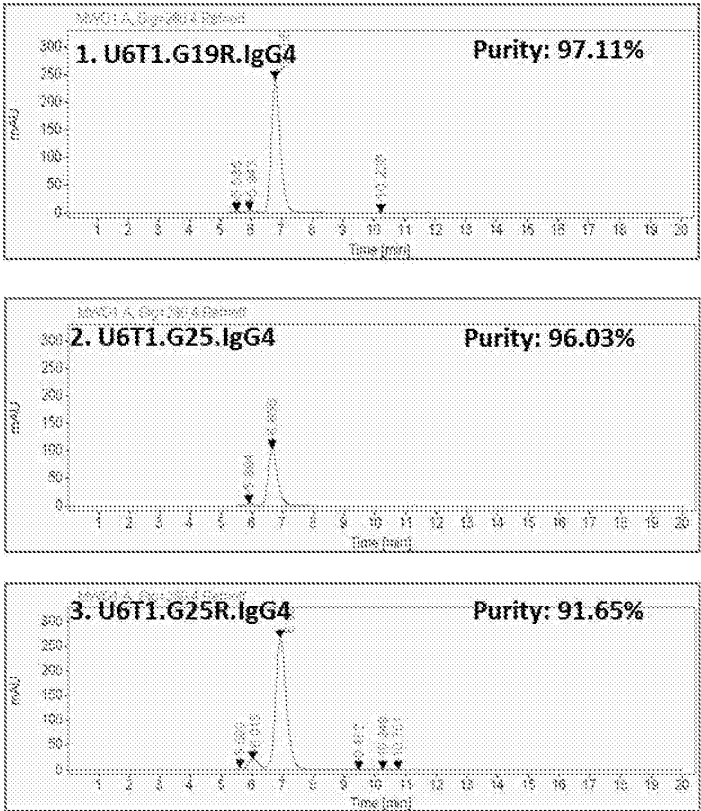


Figure 25B

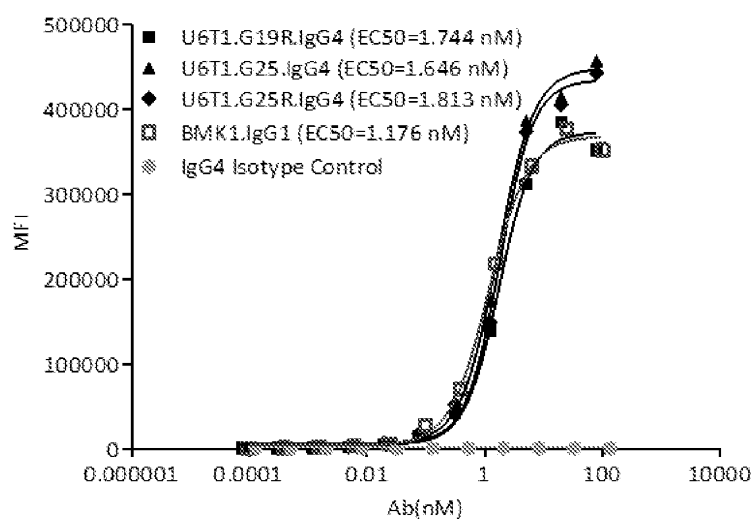


Figure 26A

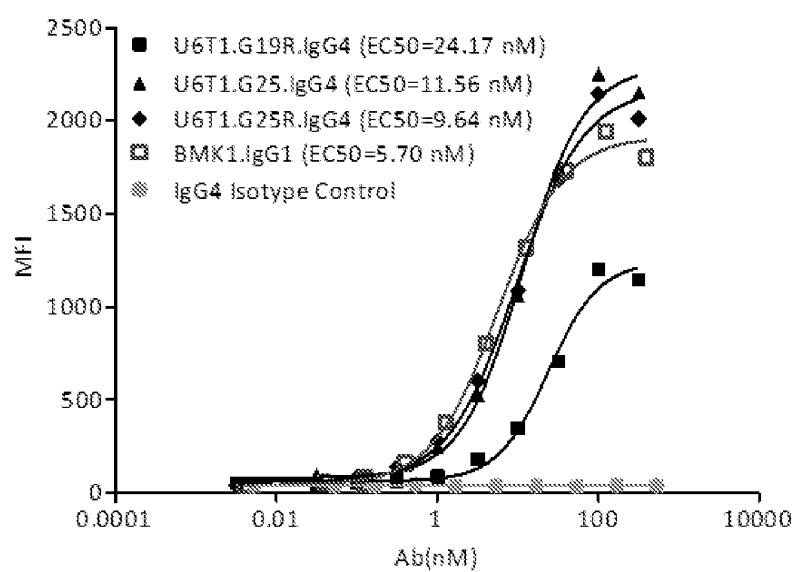


Figure 26B

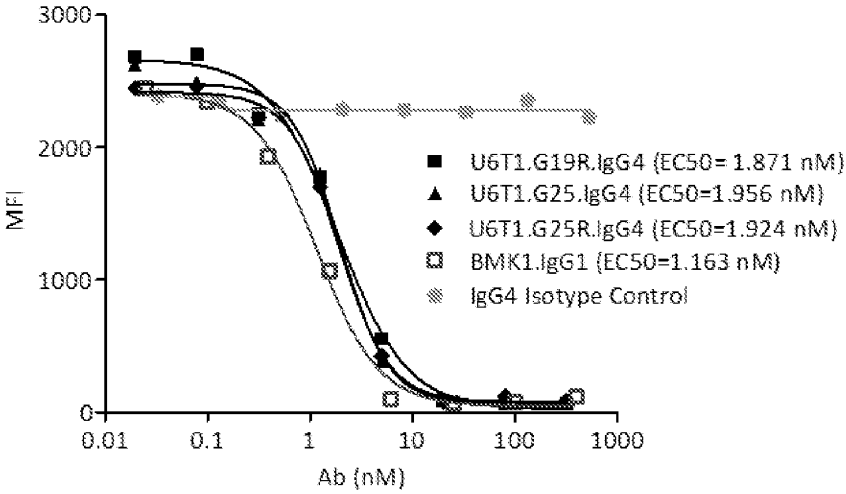


Figure 27A

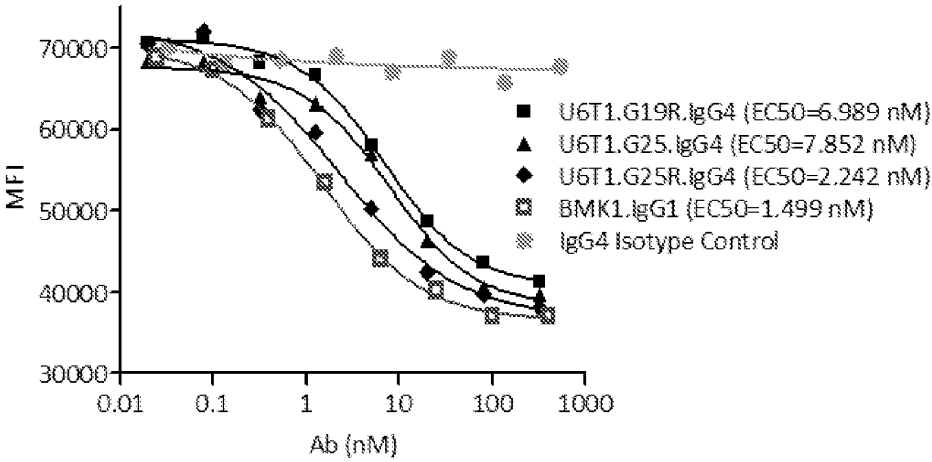


Figure 27B

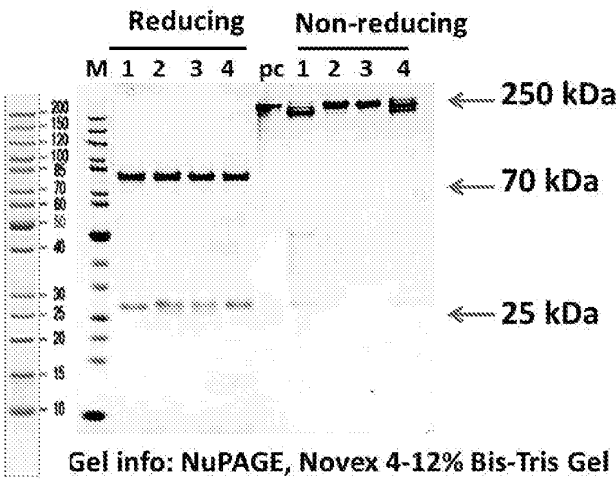


Figure 28A

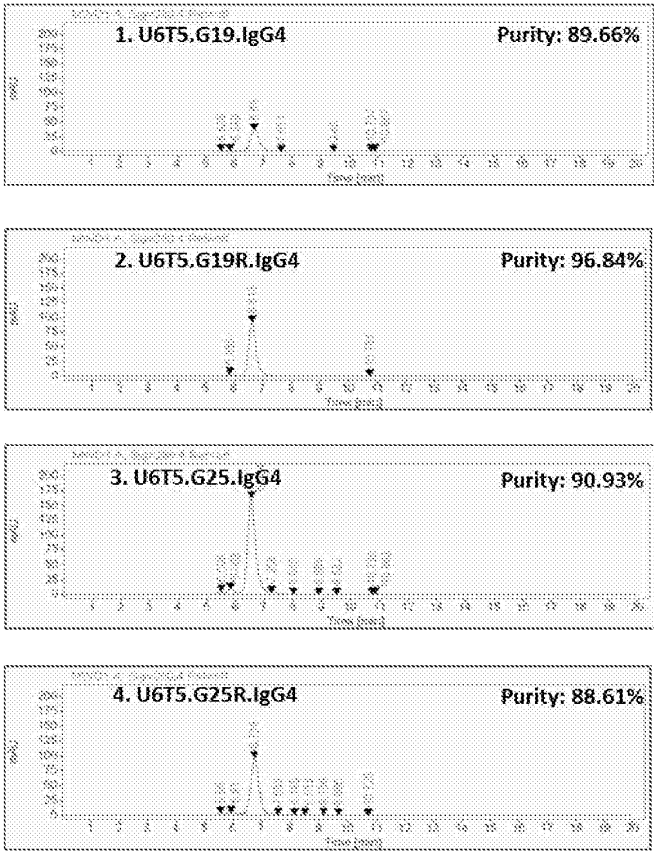


Figure 28B

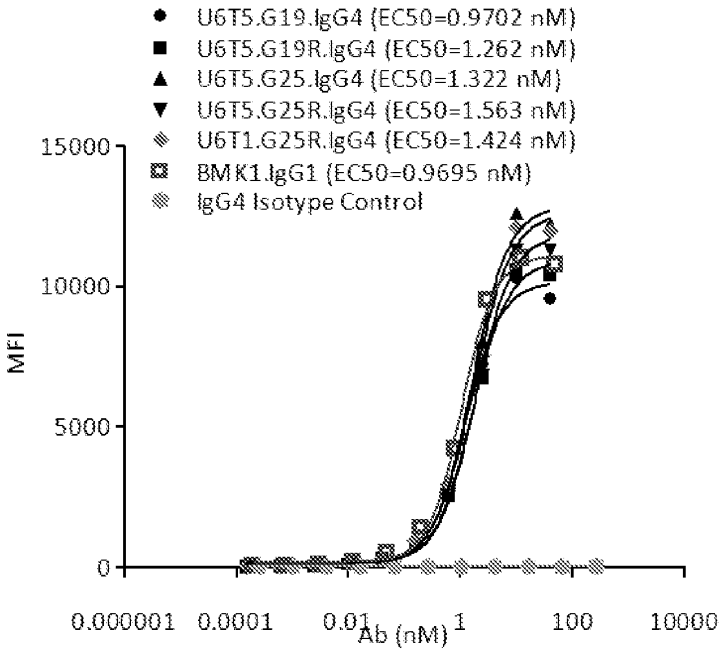


Figure 29A

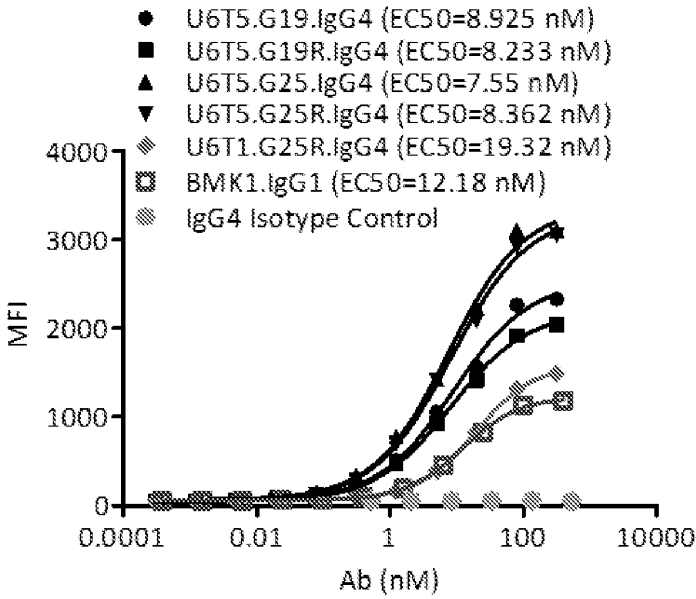


Figure 29B

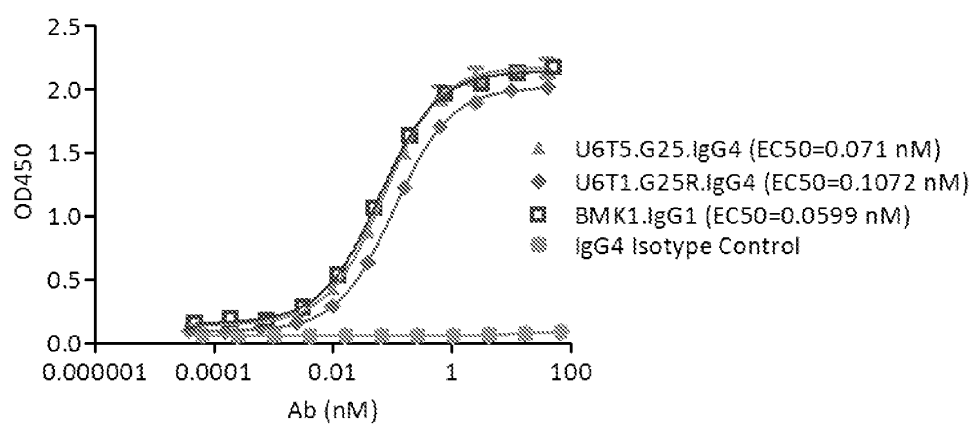


Figure 30

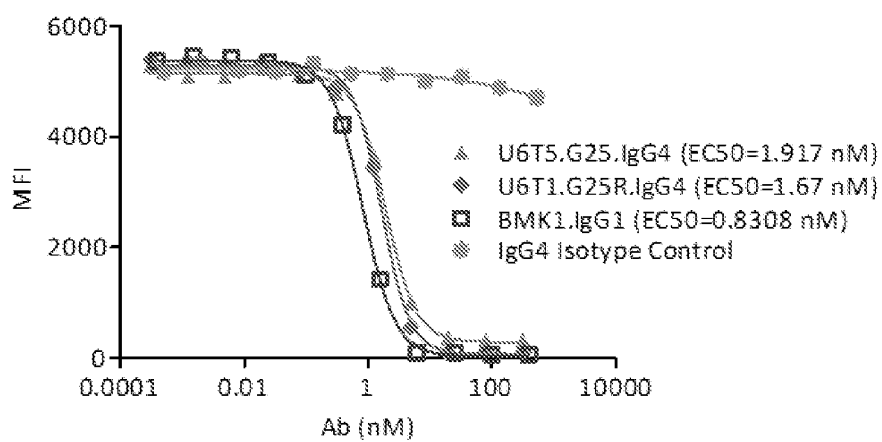


Figure 31A

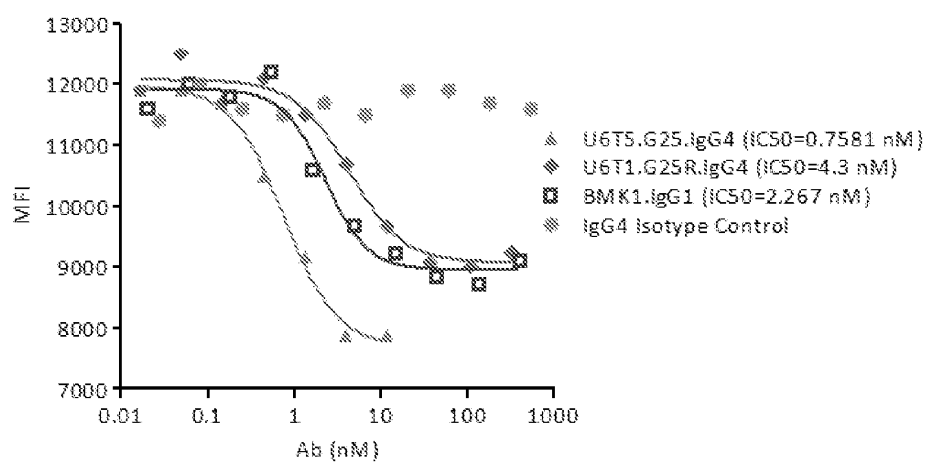


Figure 31B

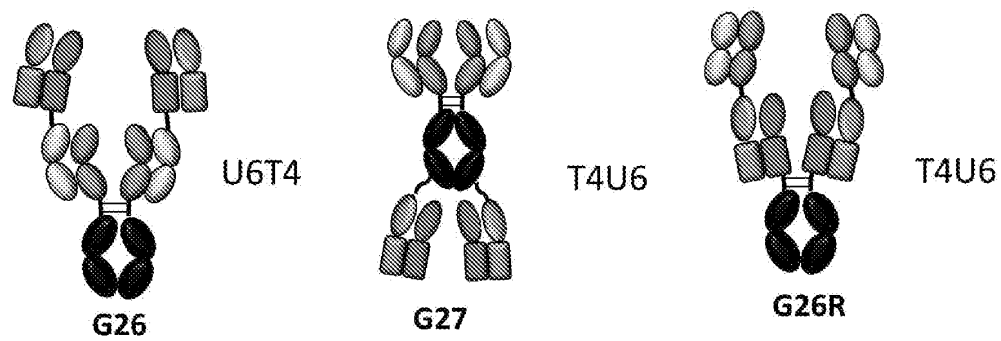
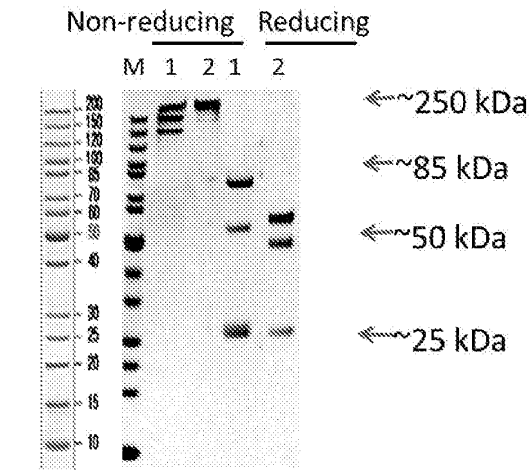


Figure 32



Gel info: NuPAGE, Novex 4-12% Bis-Tris Gel

Figure 33A

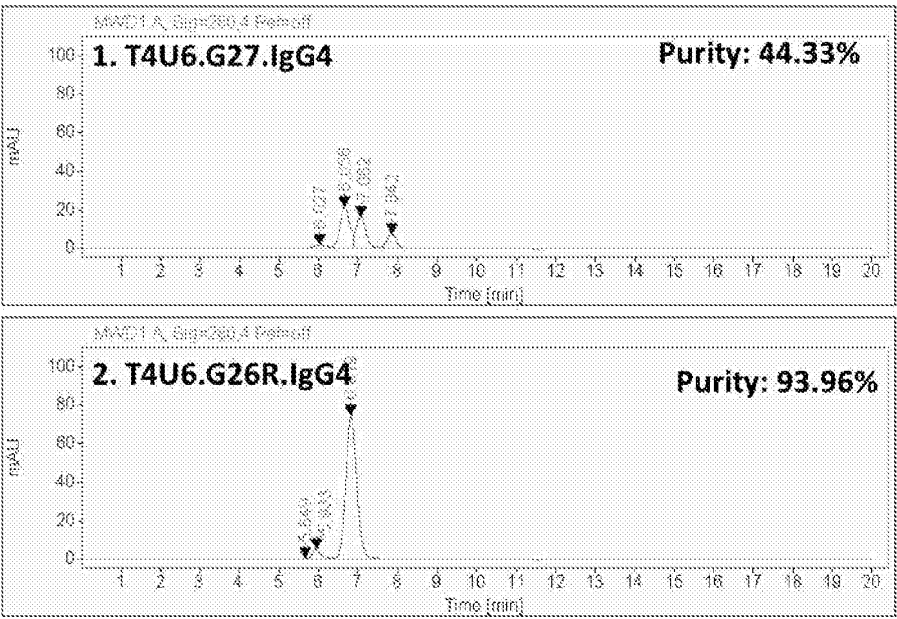


Figure 33B

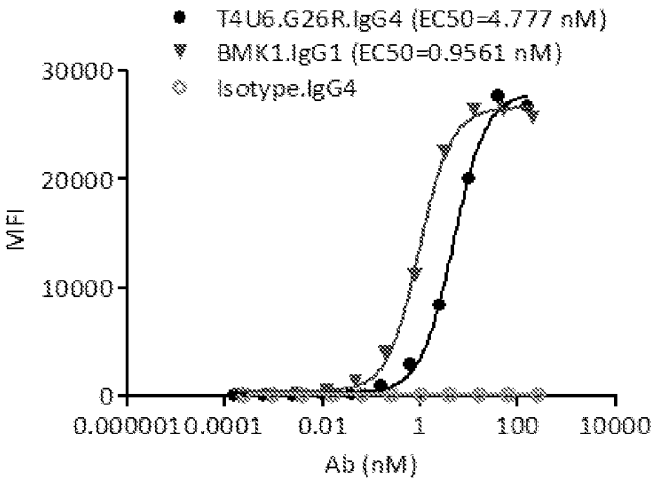


Figure 34A

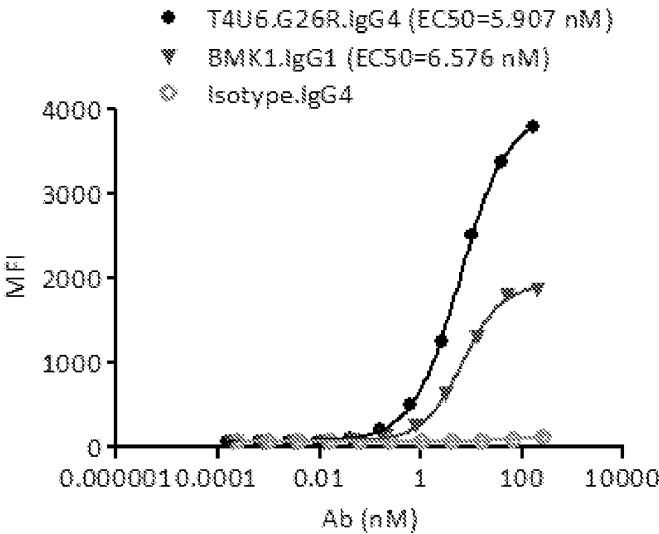


Figure 34B

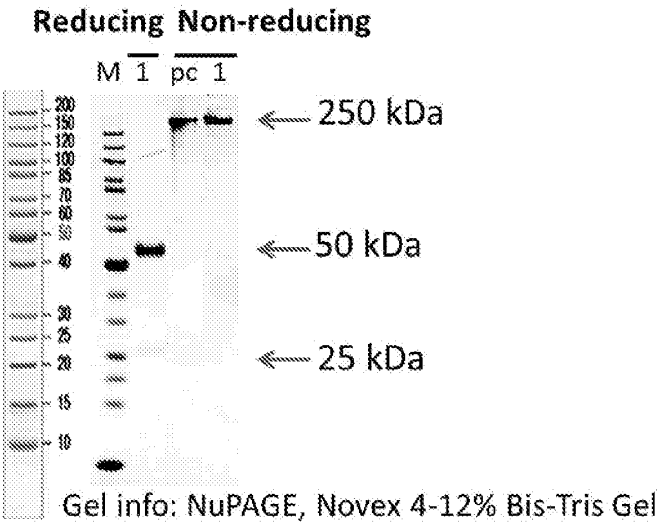


Figure 35A

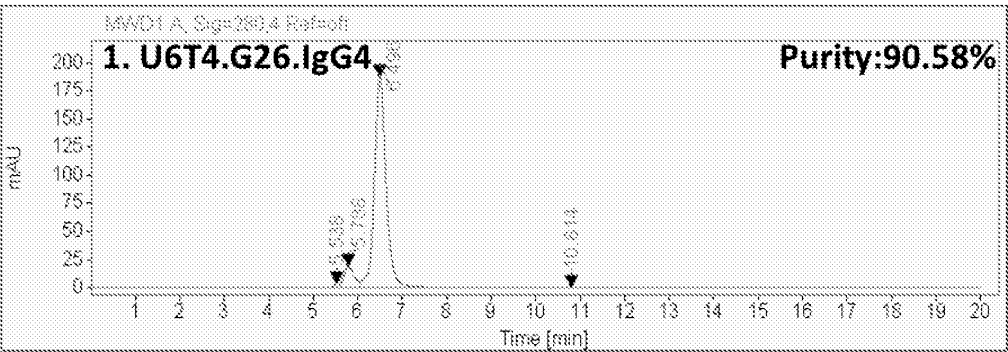


Figure 35B

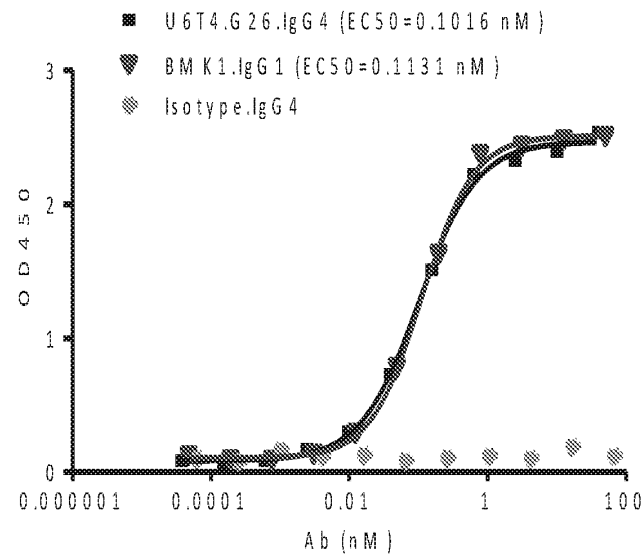


Figure 36A

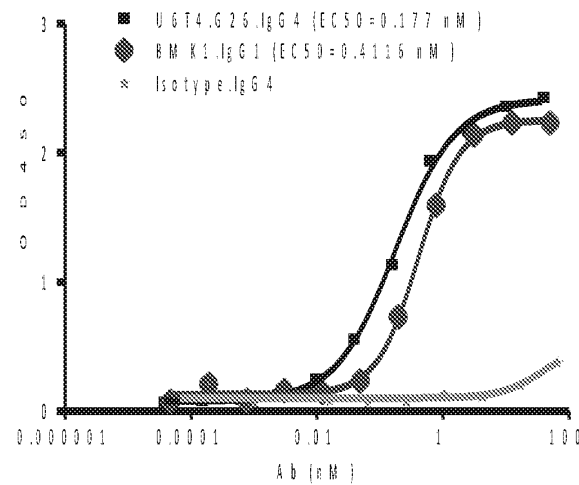


Figure 36B

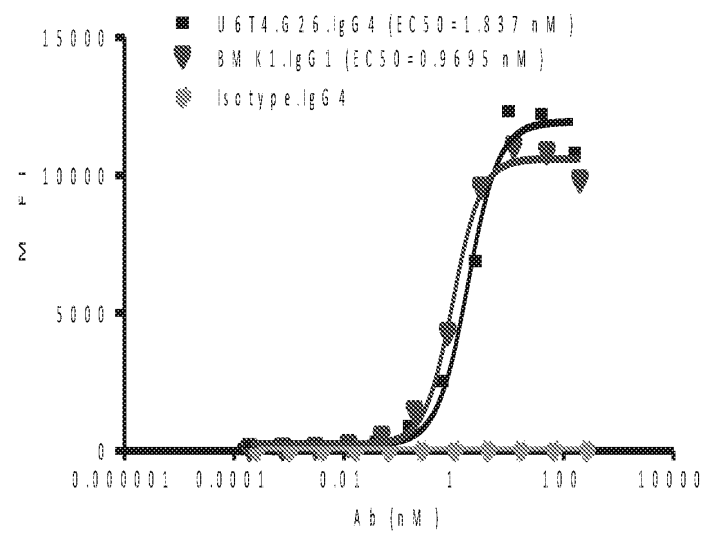


Figure 36C

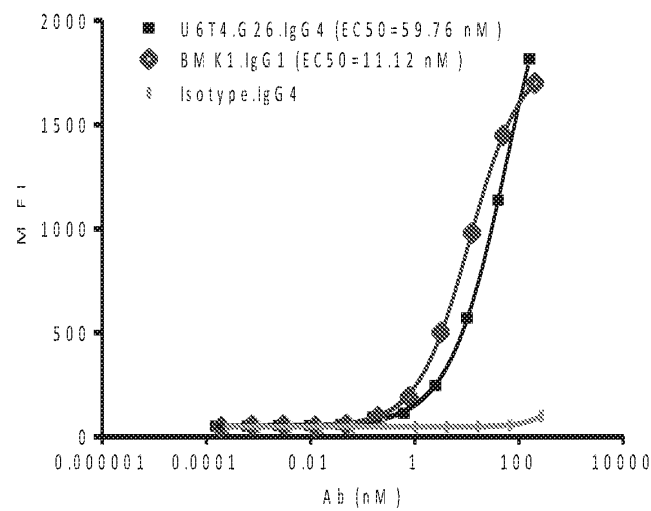


Figure 36D

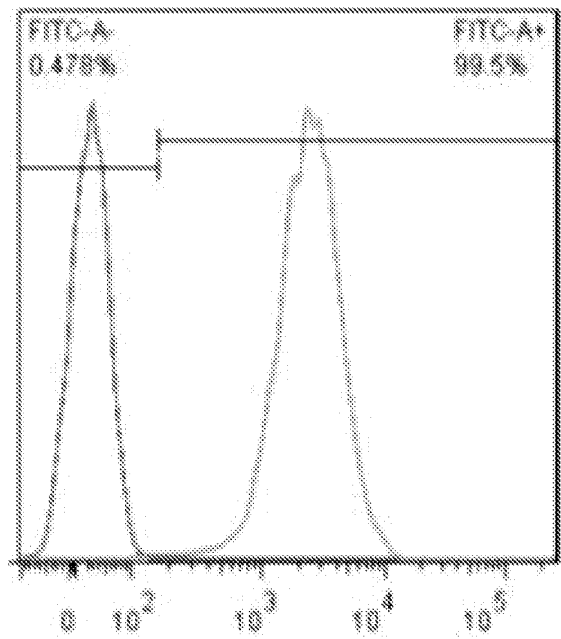


Figure 37

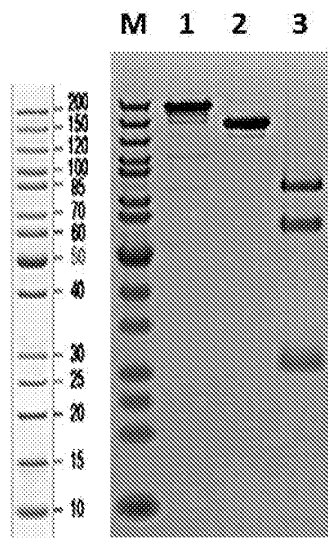


Figure 38

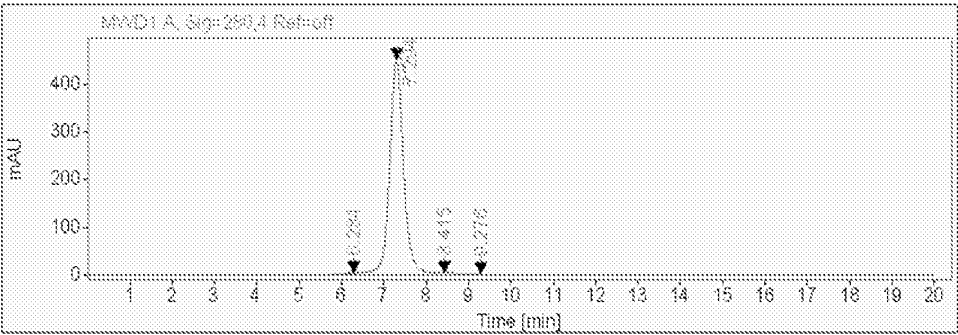


Figure 39

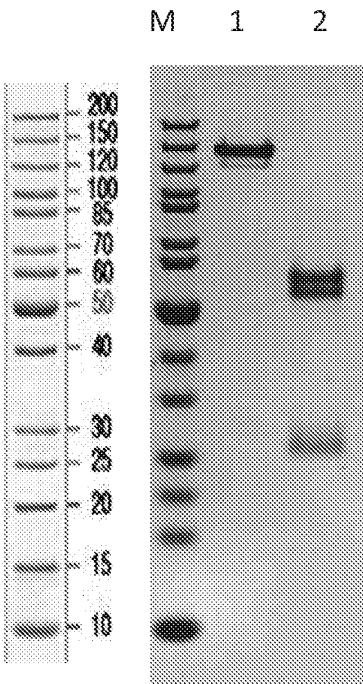


Figure 40

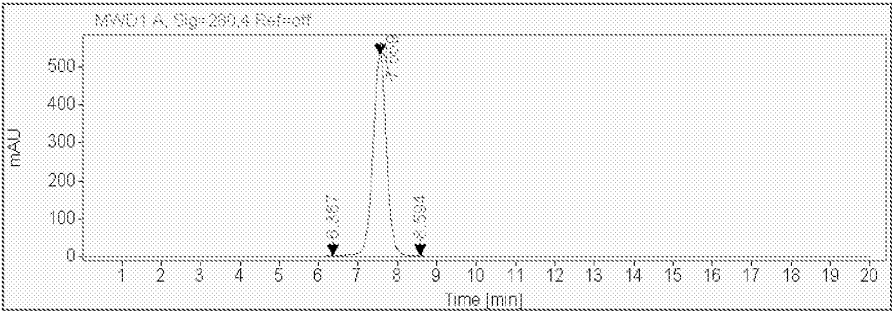


Figure 41

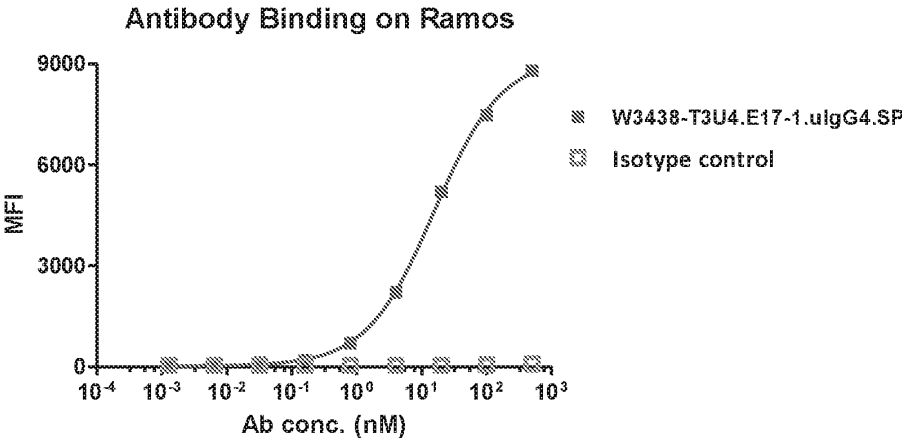


Figure 42A

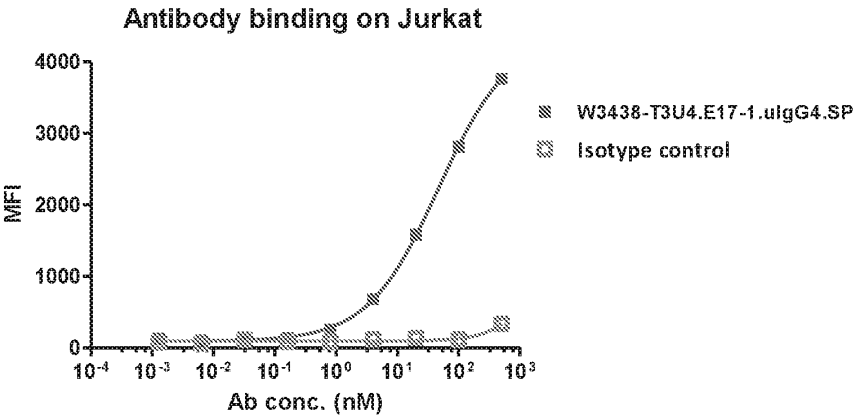


Figure 42B

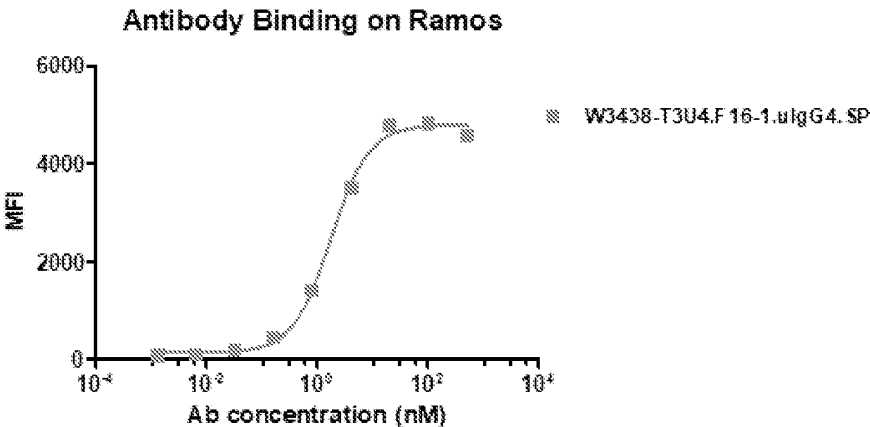


Figure 43A

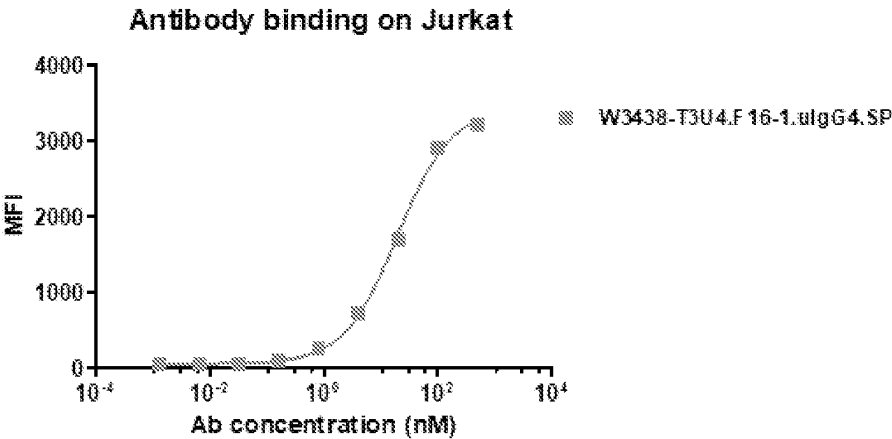


Figure 43B

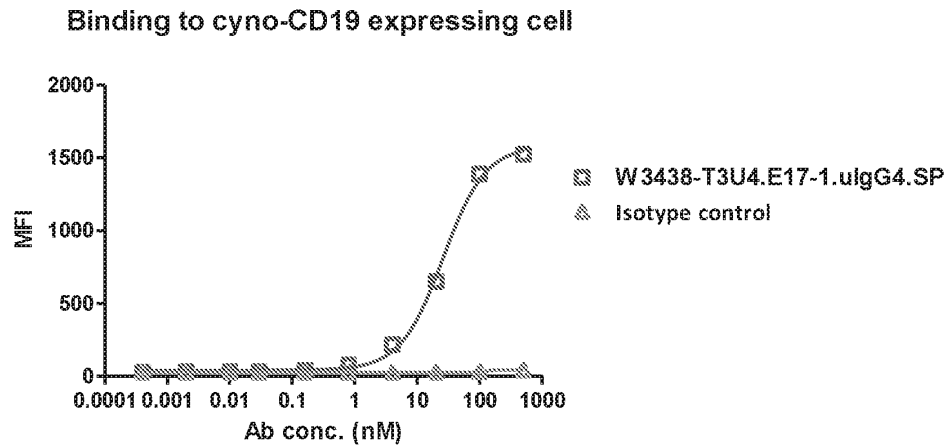


Figure 44

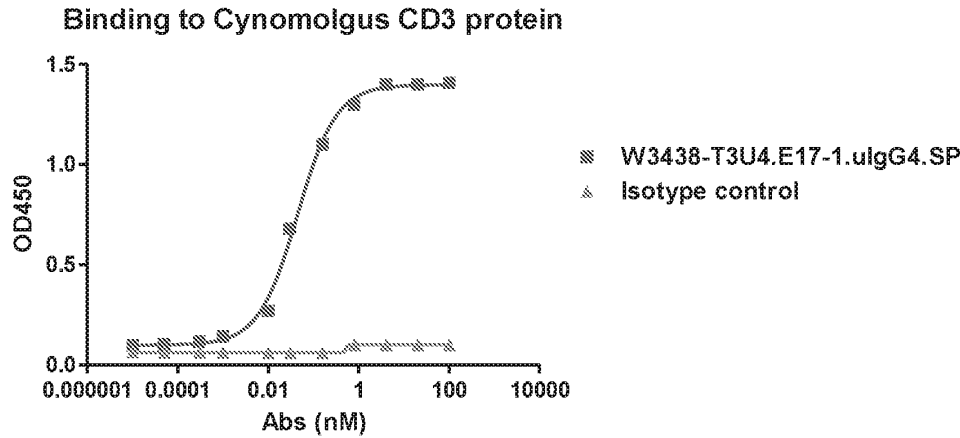


Figure 45

W3438-T3U4.E17-1.ulgG4.SP affinity test on Ramos

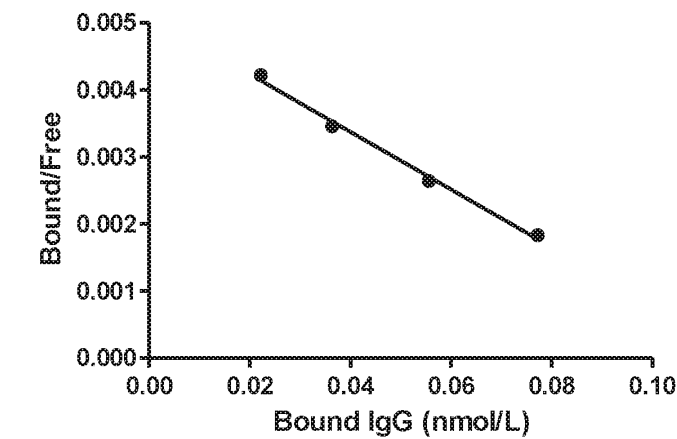


Figure 46A

W3438-T3U4.E17-1.ulgG4.SP affinity test on Jurkat

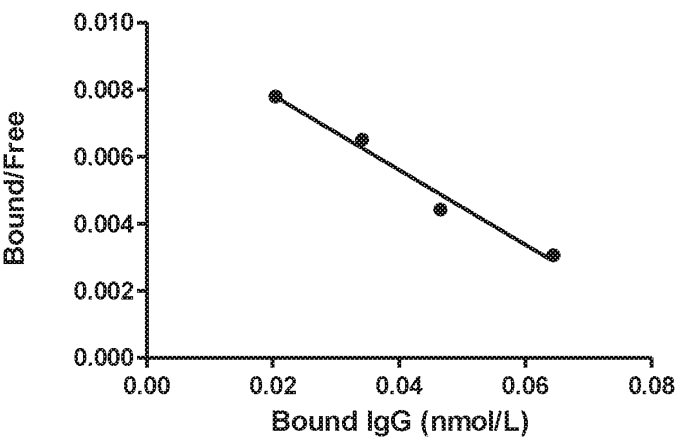


Figure 46B

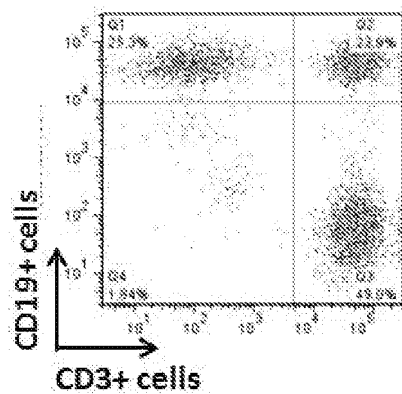


Figure 47A

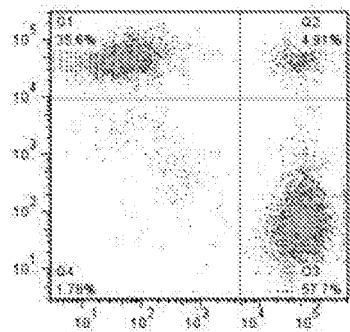


Figure 47B

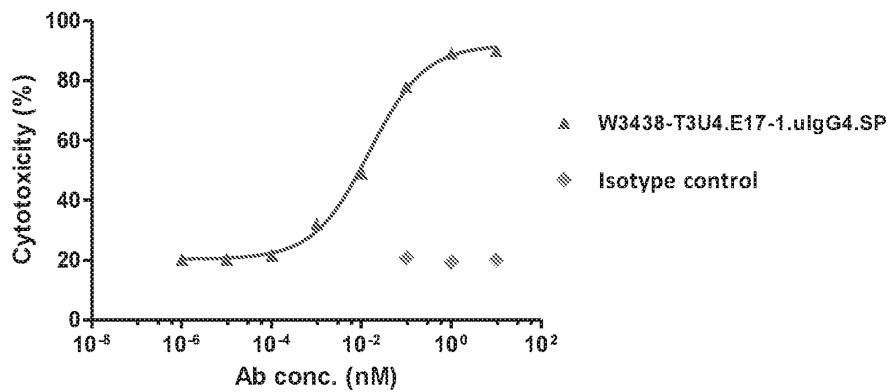


Figure 48A

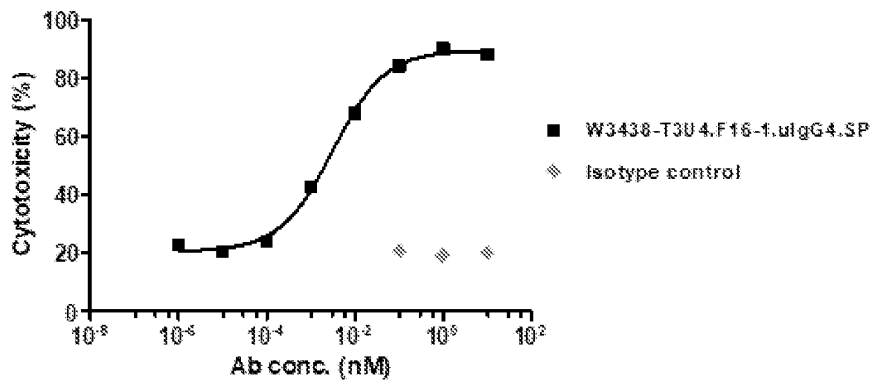


Figure 48B

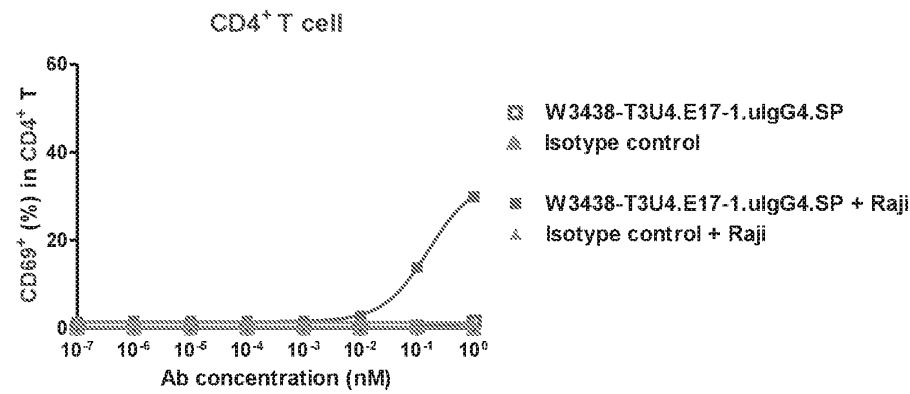


Figure 49A

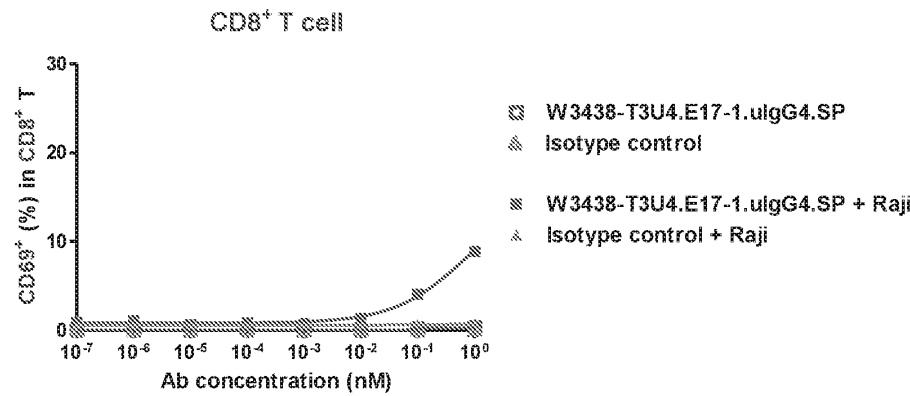


Figure 49B

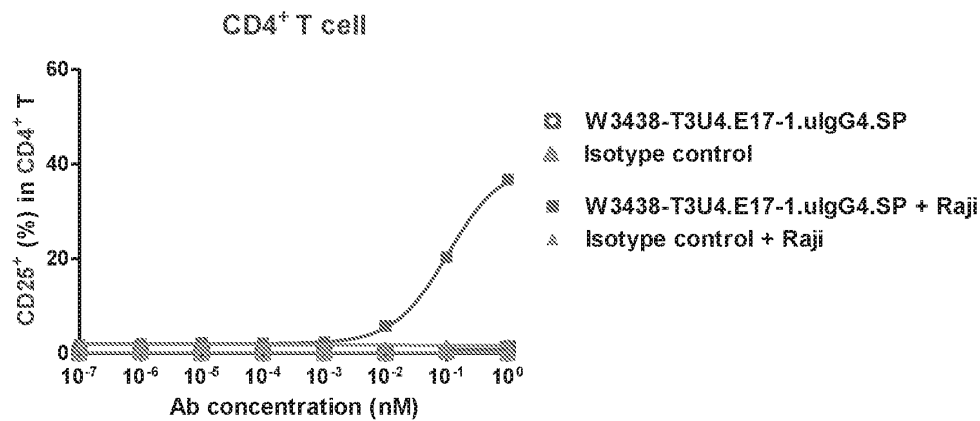


Figure 49C

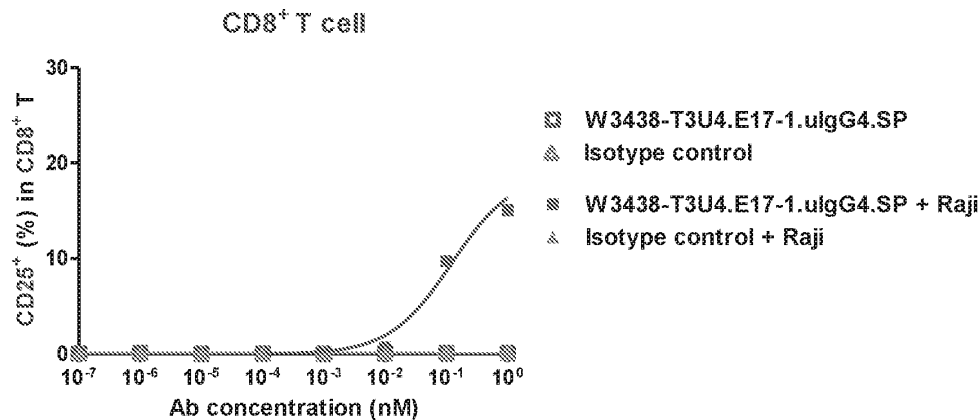


Figure 49D

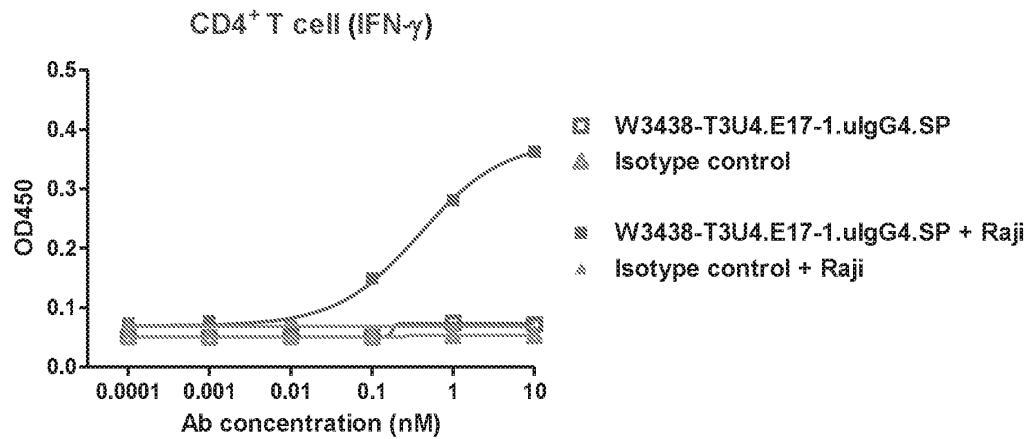


Figure 50A

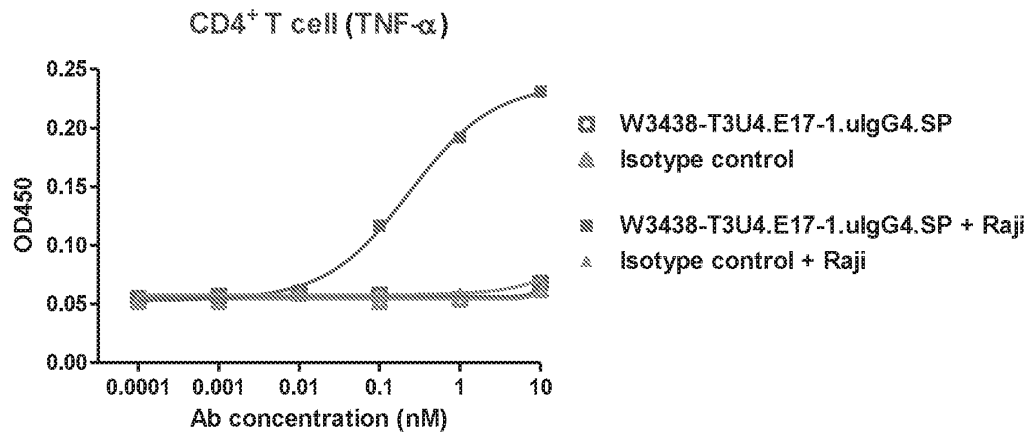


Figure 50B

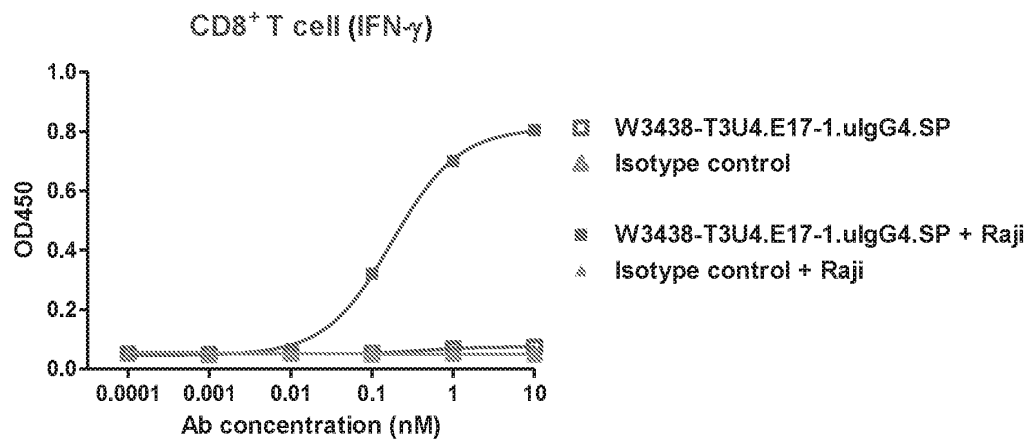


Figure 50C

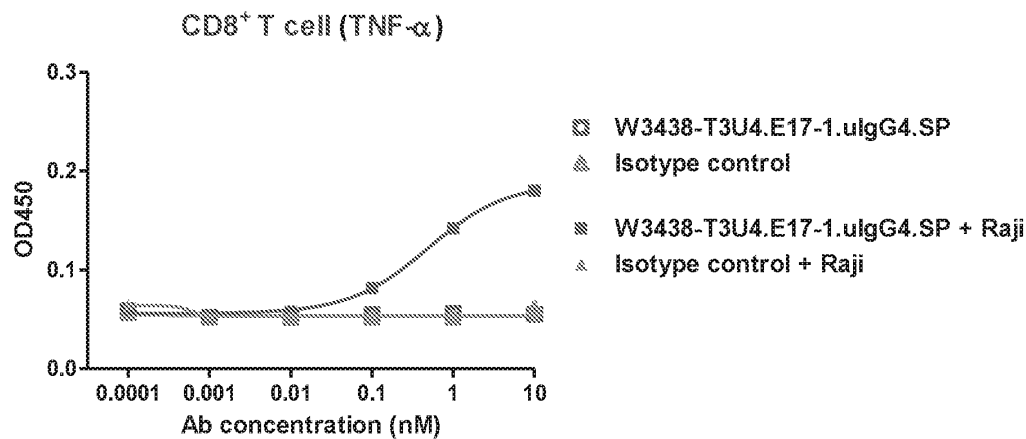


Figure 50D

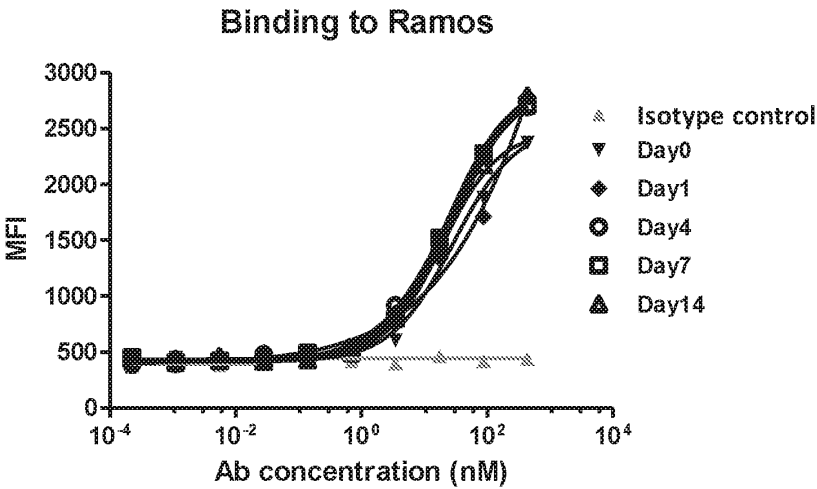


Figure 51A

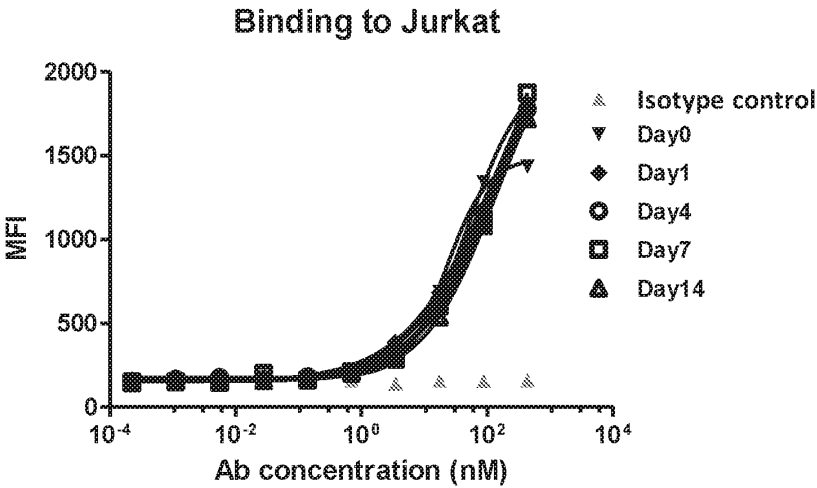


Figure 51B

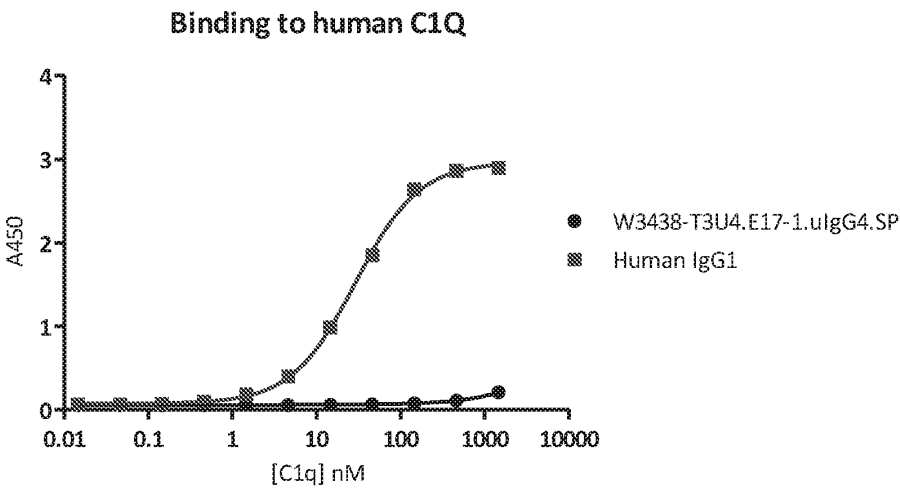


Figure 52

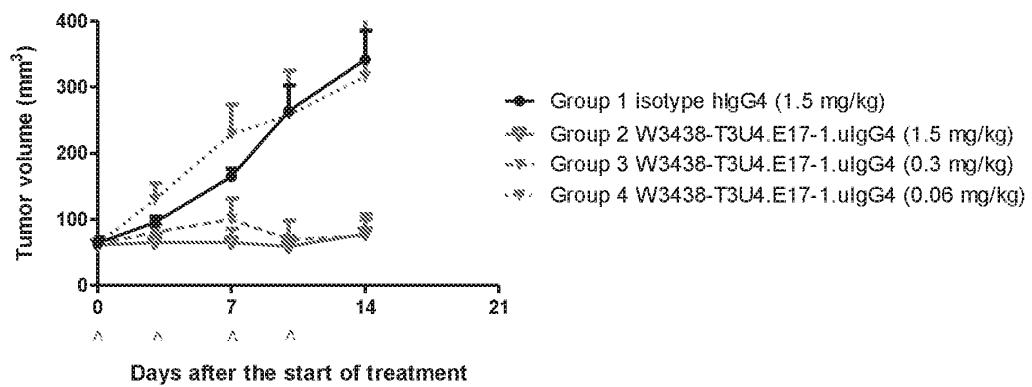


Figure 53

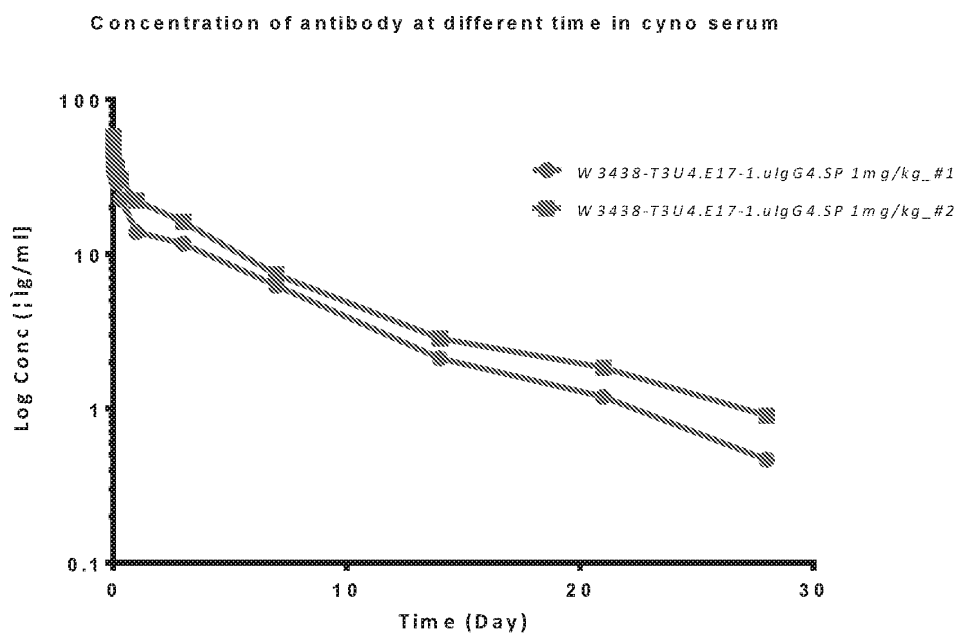


Figure 54

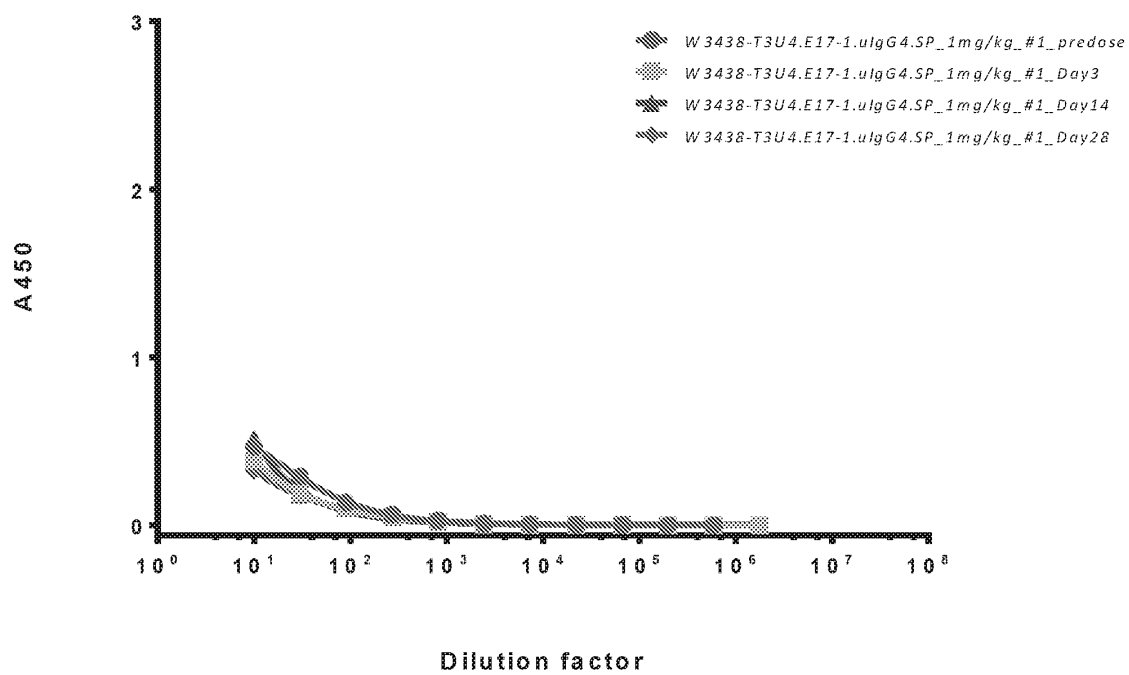


Figure 55A

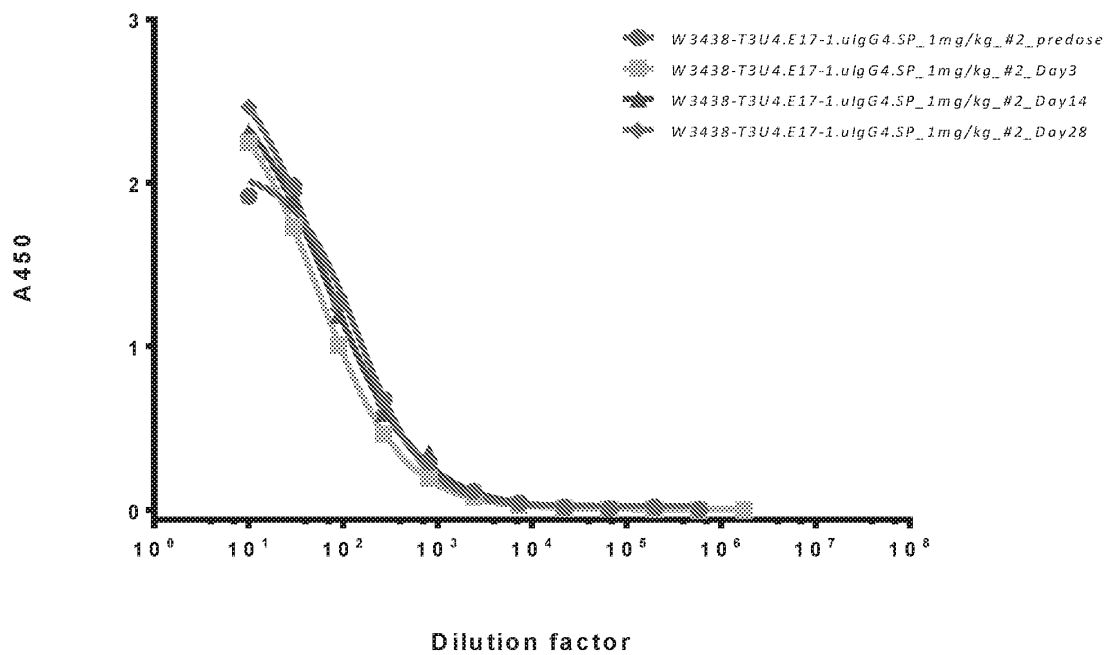
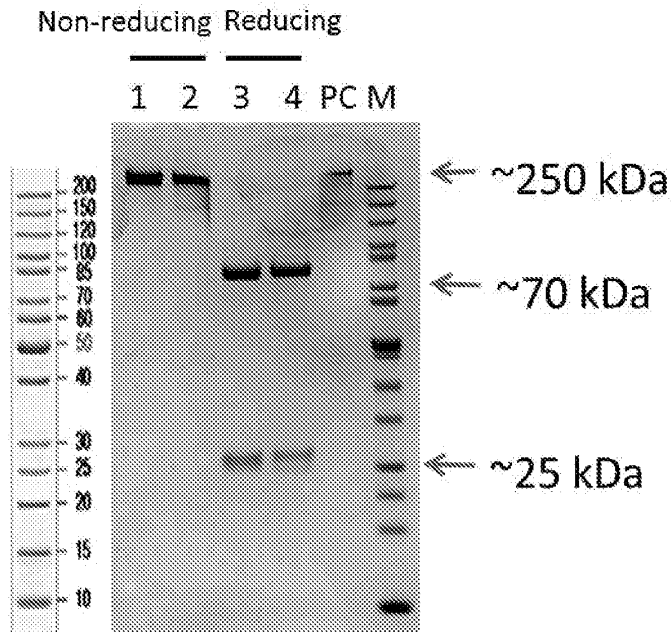


Figure 55B



Lane	Protein name	MW(kDa)
1	W3248-U6T1.G25R-1.ulgG4.SP	242.7
2	W3248-U6T5.G25-1.ulgG4.SP	244.7
3	W3248-U6T1.G25R-1.ulgG4.SP	22.5+76.6+22.2
4	W3248-U6T5.G25-1.ulgG4.SP	21.8+77.1+23.4
PC	BMK	250
M	PageRuler™ Unstained Protein Ladder	

Figure 56A

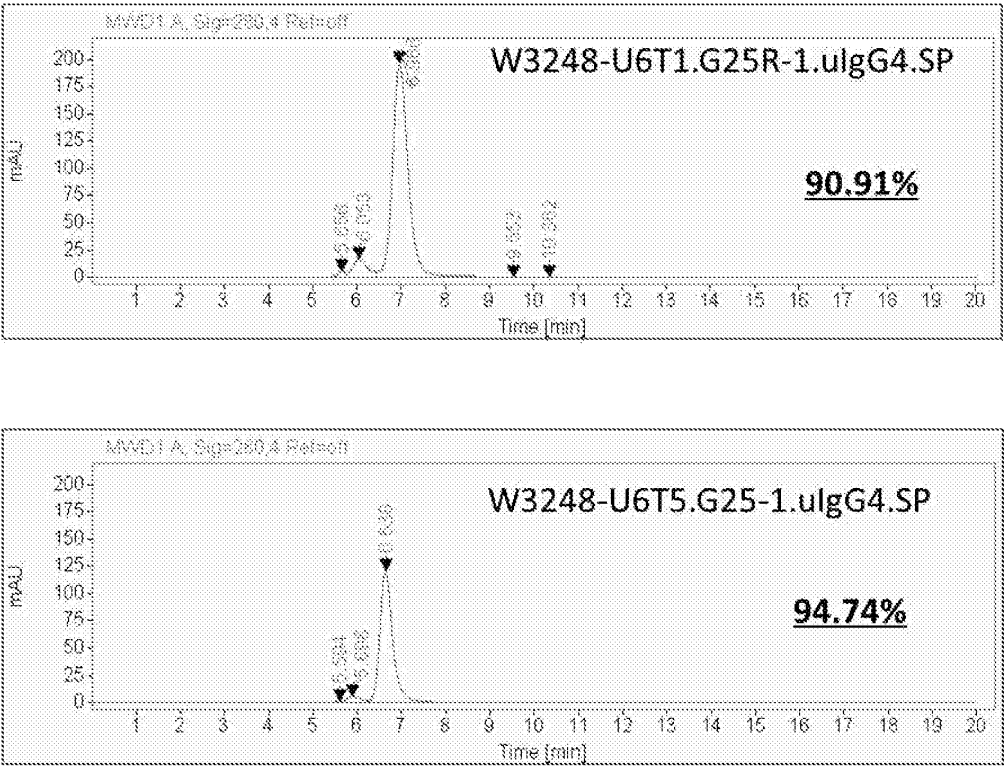
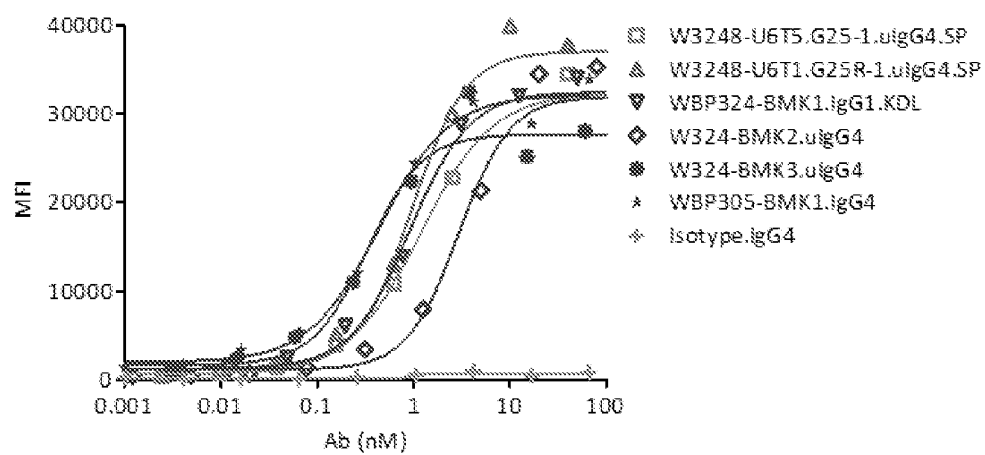


Figure 56B

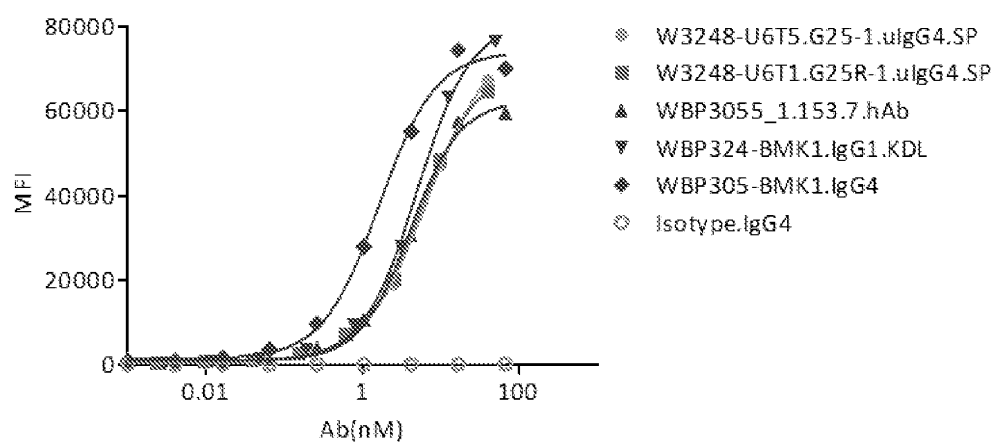
Antibody	Isotype	T _m 1(°C)	T _m 2(°C)
W3248-U6T1.G25R-1.ulgG4.SP	hlgG4, kappa	60.8	73.9
W3248-U6T5.G25-1.ulgG4.SP	hlgG4, kappa	63.4	-
W324-BMK1.ulgG1.KDL	hlgG1, kappa	57.4	79.6

Figure 57



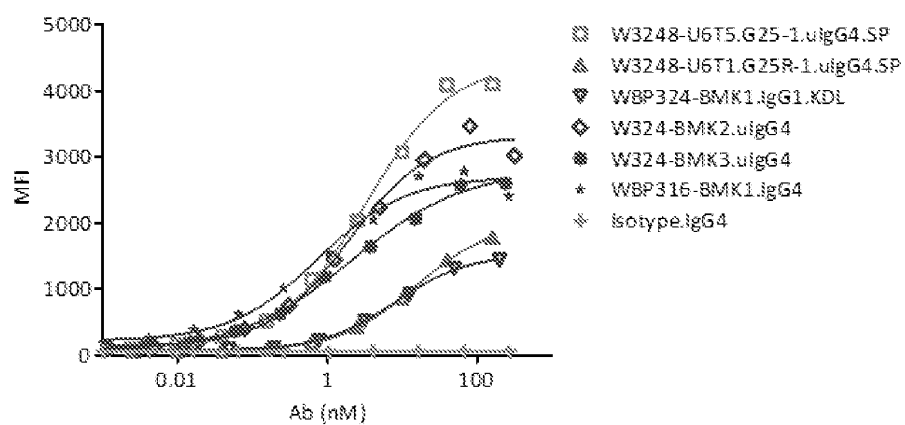
Antibody	EC ₅₀ (nM)	MFI
W3248-U6T5.G25-1.ulgG4.SP	1.176	32427
W3248-U6T1.G25R-1.ulgG4.SP	0.948	37076
WBP324-BMK1.lgG1.KDL	0.9131	32468
W324-BMK2.ulgG4	2.943	31973
W324-BMK3.ulgG4	0.3317	27715
WBP305-BMK1.lgG4	0.3528	28771

Figure 58



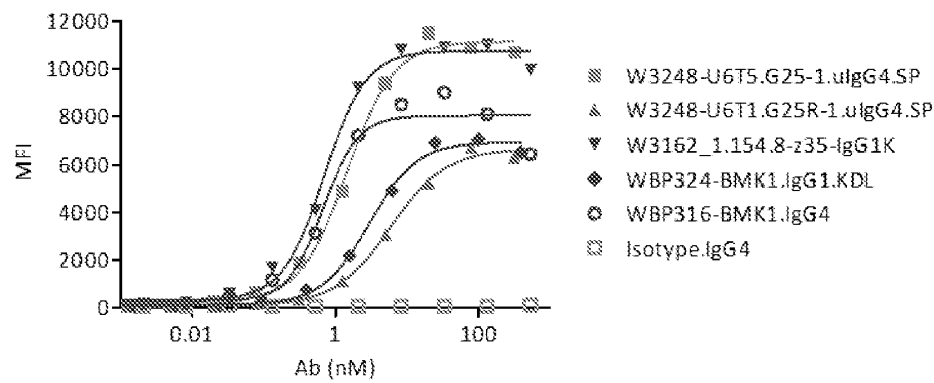
Antibody	EC ₅₀ (nM)	Top(MFI)
W3248-U6T5.G25-1.ulgG4.SP	5.131	68107
W3248-U6T1.G25R-1.ulgG4.SP	4.709	66813
WBP3055_1.153.7.hAb	3.482	56664
WBP324-BMK1.IgG1.KDL	4.661	78382
WBP305-BMK1.IgG4	1.435	69649

Figure 59



Antibody	EC ₅₀ (nM)	MFI
W3248-U6T5.G25-1.ulgG4.SP	3.173	4442
W3248-U6T1.G25R-1.ulgG4.SP	14.99	2021
WBP324-BMK1.IgG1.KDL	7.977	1535
W324-BMK2.ulgG4	1.91	3322
W324-BMK3.ulgG4	2.114	2811
WBP316-BMK1.IgG4	0.7471	2699

Figure 60

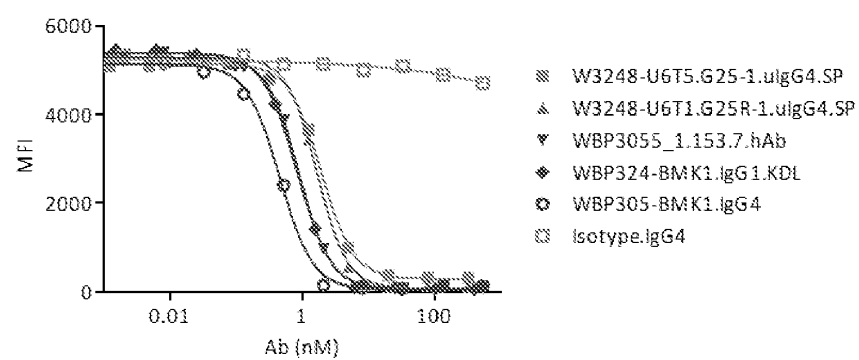


Antibody	EC ₅₀ (nM)	Top(MFI)
W3248-U6T5.G25-1.ulgG4.SP	1.45	11156
W3248-U6T1.G25R-1.ulgG4.SP	5.872	6653
W3162_1.154.8-z35-IgG1K	0.6994	10757
WBP324-BMK1.IgG1.KDL	2.98	6951
WBP316-BMK1.IgG4	0.6737	8052

Figure 61

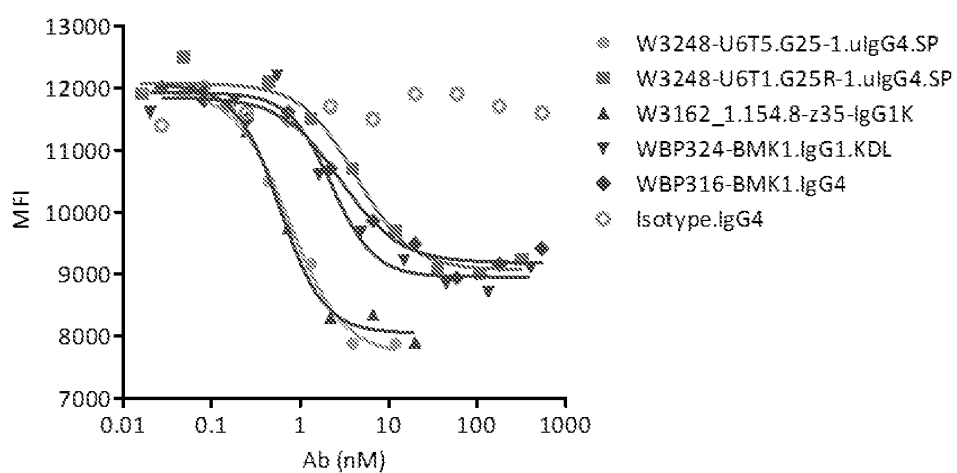
Analyte	Ligand	k _{on} (1/Ms)	k _{off} (1/s)	K _D (M)
CTLA4	W3248-U6T5.G25-1.ulgG4.SP	8.08E+05	2.88E-05	3.56E-11
	W3248-U6T1.G25R-1.ulgG4.SP	1.83E+05	6.54E-05	3.57E-10
	WBP316-BMK1.ulgG4.SP	3.83E+05	4.97E-05	1.30E-10
PD-1	W3248-U6T1.G25R-1.ulgG4.SP	5.42E+05	6.75E-04	1.24E-09
	W3248-U6T5.G25-1.ulgG4.SP	6.42E+05	8.44E-04	1.32E-09
	Parental Ab	3.27E+05	6.14E-04	1.88E-09

Figure 62



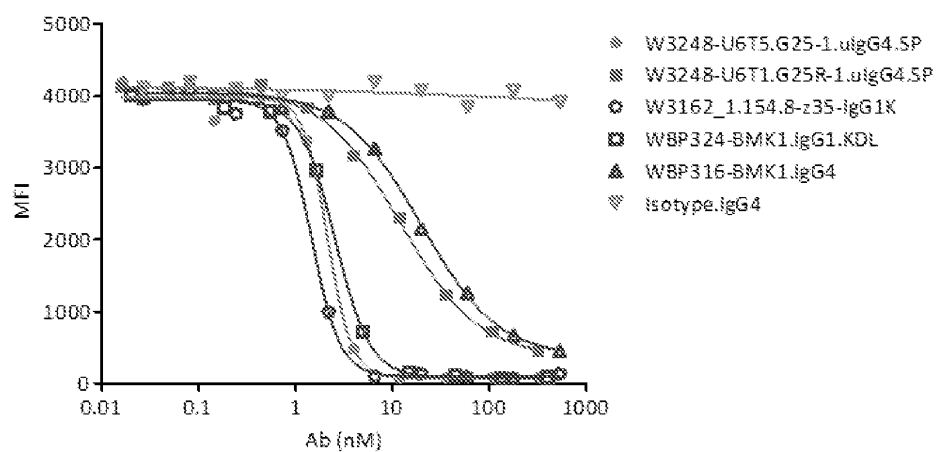
Antibody	IC ₅₀ (nM)	Inhibition %
W3248-U6T5.G25-1.ulgG4.SP	1.917	94.4
W3248-U6T1.G25R-1.ulgG4.SP	1.670	98.6
WBP3055_1.153.7.hAb	0.888	98.6
WBP324-BMK1.IgG1.KDL	0.8308	99.4
WBP305-BMK1.IgG4	0.4536	99.1

Figure 63



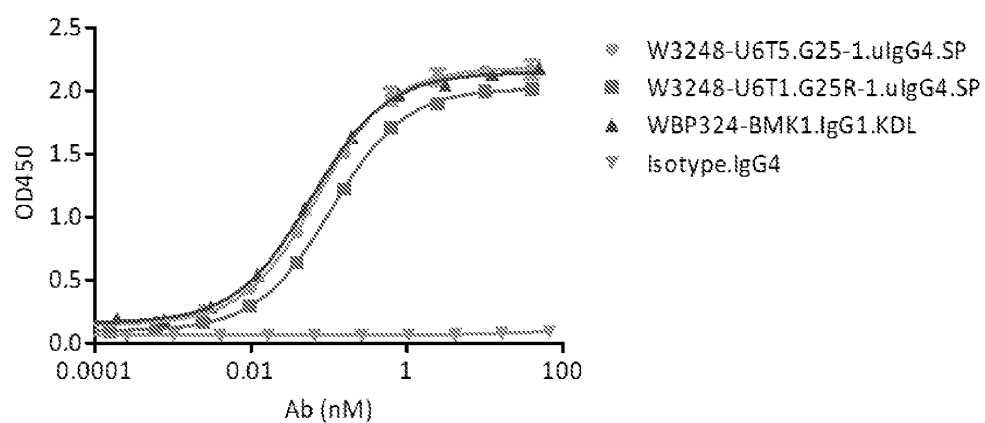
Antibody	IC ₅₀ (nM)	Inhibition %
W3248-U6T5.G25-1.ulgG4.SP	0.7581	35.9
W3248-U6T1.G25R-1.ulgG4.SP	4.300	24.4
W3162_1.154.8-z35-IgG1K	0.5935	32.9
WBP324-BMK1.IgG1.KDL	2.267	25.3
WBP316-BMK1.IgG4	2.862	23.4

Figure 64



Antibody	IC ₅₀ (nM)	Inhibition %
W3248-U6T5.G25-1.ulgG4.SP	2.138	98.2
W3248-U6T1.G25R-1.ulgG4.SP	11.98	91.0
W3162_1.154.8-z35-IgG1K	1.468	97.6
WBP324-BMK1.IgG1.KDL	2.553	97.9
WBP316-BMK1.IgG4	19.82	90.9

Figure 65



Antibody	EC ₅₀ (nM)	Top(OD450)
W3248-U6T5.G25-1.uIgG4.SP	0.0710	2.178
W3248-U6T1.G25R-1.uIgG4.SP	0.1072	2.016
WBP324-BMK1.IgG1.KDL	0.0599	2.145

Figure 66

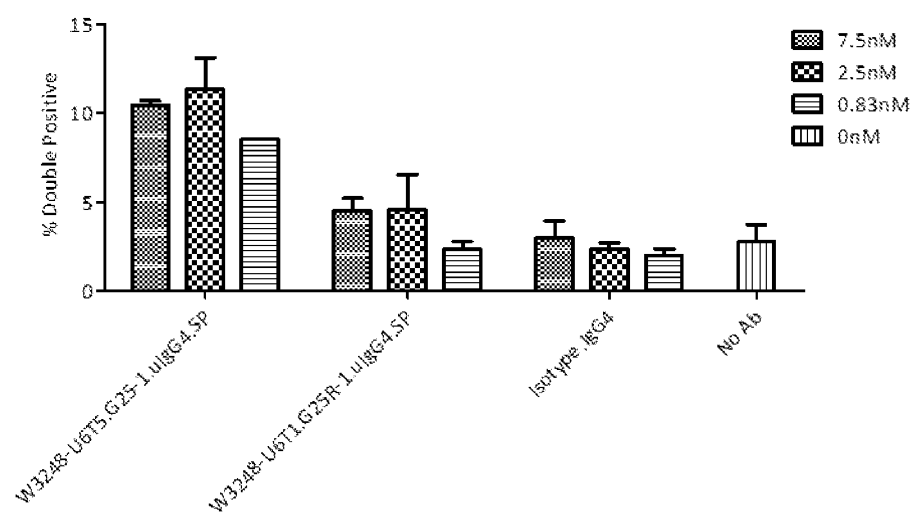


Figure 67

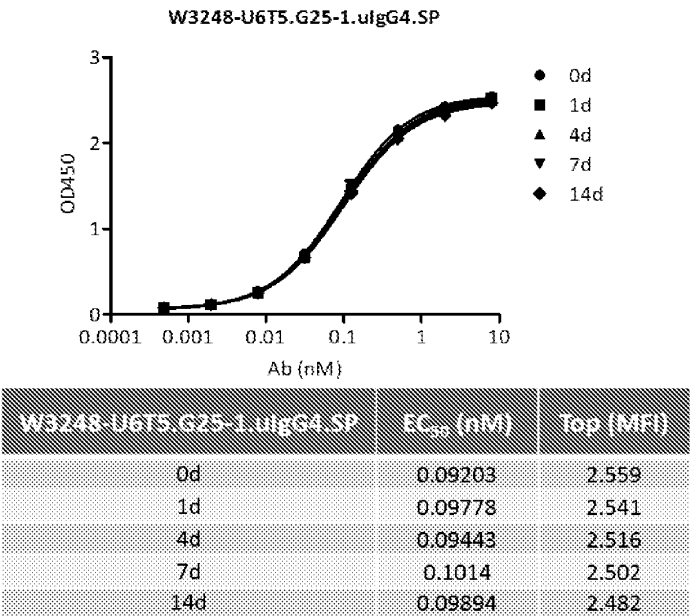


Figure 68A

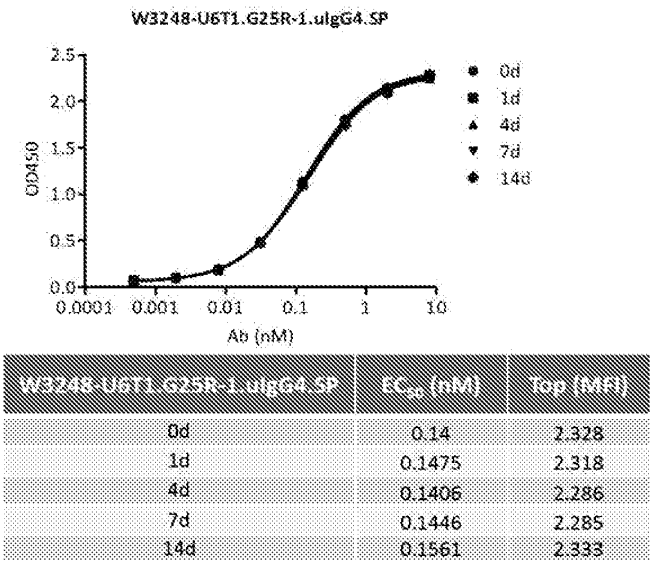


Figure 68B