

FIG. 1

Panel A:

Clone ID	CDR1	CDR2	CDR3	V-Gene	J-Gene
309157 (CD38-F11A)	GFTFSSYG (SEQ ID NO: 1)	ISDDGSNK (SEQ ID NO: 6)	AKDRGTMRVVVD TLDI (SEQ ID NO: 13)	IGHV3- 30*18	IGHJ1*01
Consensus Sequence (nt FR1- FR4)	CAGGTGCAGCTGGTGGAGTCGGGGGAGGCGTGGT CCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGC CTCTGGATTACCTTCAGTAGCTATGGCATGCACTGG GTCCGCCAGGCTCCAGGCAAGGAGCGGGAGTGGGTG GCAGTTATATCAGATGATGGAAGTAATAAATATTATG CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGA CAATCCAAGAACACGCTGTATCTCAAATGAACAGC CTGAGAGTTGAGGACACGGCTGTGTATTACTGTGCGA AAGATCGGGTACTATGAGAGTAGTGGTTTATGATAC TTTGGATATCTGGGGCCAGGGCACCTGGTCACCGTC TCCTCA (SEQ ID NO: 32)			Percent CD38 Hydrolase Inhibition	24
Consensus Sequence (aa FR1- FR4)	QVQLVESGGGVVQPGRLRLSCAAS GFTFSSYGMHWVRQAPGKEREWVA VISDDGSNKYYADSVKGRFTISRDN KNTLYLQMNSLRVEDTAVYYCAKD RGTMRVVVDTLDIWGQGLTVSS (SEQ ID NO: 18)			Cell Binding MFI	5201

Panel B:

Clone ID	CDR1	CDR2	CDR3	V-Gene	J-Gene
309159 (CD38-F11B)	GFTFSSYG (SEQ ID NO: 1)	ISDDGSNK (SEQ ID NO: 6)	AKDRGTMRVAVVD AFDL (SEQ ID NO: 14)	IGHV3- 30*18	IGHJ1*01
Consensus Sequence (nt FR1-FR4)	GAGGTGCAGCTGTGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGGAGGTCCCTGAGACTCTCTTGTGCAG CCTCTGGATTACCTTCAGTAGCTATGGCATGCACT GGGTCCGCCAGGCTCCAGGCAAGGAGCGGGAGTGG GTGGCAGTTATATCAGATGATGGAAGTAATAAATA CTATGCAGACTCCGTGAAGGGCCGATTACCATCTC CAGAGACAATTCCAAGAACACGCTGTATCTGCAAAT GAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTA CTGTGCGAAAGATCGGGGTACTATGAGAGTAGCGGT TTATGATGCTTTTGATCTCTGGGGCCAGGGCACCTG GTCACCGTCTCCTCA (SEQ ID NO: 33)			Percent CD38 Hydrolase Inhibition	ND
Consensus Sequence (aa FR1-FR4)	EVQLLESGGGVVQPGRLRLSCAASG FTFSSYGMHWVRQAPGKEREWVAVIS DDGSNKYYADSVKGRFTISRDNKNTL YLQMNSLRAEDTAVYYCAKDRGTMRV AVYDAFDLWGQGLTVSS (SEQ ID NO: 19)			Cell Binding MFI	ND

FIG. 1, Cont.

Panel C:

Clone ID	CDR1	CDR2	CDR3	V-Gene	J-Gene
350191 (CD38-F11C)	GFTFSSYG (SEQ ID NO: 1)	ISDDGSNK (SEQ ID NO: 6)	AKDRGTMRVAVYD TLDI (SEQ ID NO: 15)	IGHV3- 30*18	IGHJ1*01
Consensus Sequence (nt FR1- FR4)	CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGACACTCTCCTGTG CAGCCTCTGGATTACCTTCAGTAGCTATGGCAT GCACTGGGTCCGCCAGGCTCCAGGCAAGGAGCG GGAGTGGGTGGCAGTTATATCAGATGATGGAAG TAATAAATATTATGCAGACTCCGTGAAGGGCCG ATTACCATCTCCAGAGACAATTCCAAGAACAC GCTGTATCTGCAAATGAACAGCCTGAGAGTTGA GGACACGGCTGTGTATTACTGTGCGAAAGATCG GGGTACTATGAGAGTAGCGGTTTATGATACTTTG GATATCTGGGGCCAGGGCACCTGGTCACCGTCT CCTCA (SEQ ID NO: 34)			Percent CD38 Hydrolase Inhibition	25
Consensus Sequence (aa FR1- FR4)	QVQLVESGGGVVQPGRSLTSCAASGFTFSS YGMHWVRQAPGKEREWVAVISDDGSNKYY ADSVKGRFTISRDN SKNTLYLQMNSLRVEDT AVYYCAKDRGTMRVAVYDTLDIWGQGLV TVSS (SEQ ID NO: 20)			Cell Binding MFI	5480

Panel D:

Clone ID	CDR1	CDR2	CDR3	V-Gene	J-Gene
350210 (CD38-F11D)	GFTFSSYG (SEQ ID NO: 1)	ISYDGSKK (SEQ ID NO: 7)	AKDRGTMRVVYDT LDI (SEQ ID NO: 13)	IGHV3- 30*18	IGHJ1*01
Consensus Sequence (nt FR1- FR4)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTC CAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCT CTGGATTACCTTCAGTAGCTATGGCATGCACTGGGT CCGCCAGGCTCCAGGCAAGGAGCGGGAGTGGGTGGC AGTTATATCATATGATGGAAGTAAGAAATACTATGC AGACTCCGTGAAGGGCCGATTACCATCTCCAGAGA CAATTCCAAGAACACGCTGTATCTCCAAATGAACAG CCTGAGAGTTGAGGACACGGCTGTGTATTACTGTGC GAAAGATCGGGTACTATGAGAGTAGTGGTTTATGA TACTTTGGATATCTGGGGCCAGGGCACCTGGTCACC GTCTCCTCA (SEQ ID NO: 35)			Percent CD38 Hydrolase Inhibition	35
Consensus Sequence (aa FR1- FR4)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYG MHWVRQAPGKEREWVAVISYDGSKKYYADSV KGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCA KDRGTMRVVYDTLDIWGQGLVTVSS (SEQ ID NO: 21)			Cell Binding MFI	4089

FIG. 1, Cont.

Panel E:

Clone ID	CDR1	CDR2	CDR3	V-Gene	J-Gene
350250 (CD38-F11E)	GFTFSGYG (SEQ ID NO: 2)	ISYDGSNK (SEQ ID NO: 8)	AKDRGTMRVVVD TLDI (SEQ ID NO: 13)	IGHV3- 30*18	IGHJ1*0 1
Consensus Sequence (nt FR1- FR4)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTT GGTACAGCCTGGGGGGTCCCTGAGACTCTCCTG TGCAGCCTCTGGATTACCTTCAGTGGCTATGG CATGCACTGGCTCCGCCAGGCTCCAGGCAAGGA GCGGGAGTGGGTGGCAGTTATATCATATGATGG AAGTAATAAATACTATGCAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTCCAAATGAACAGCCTGAGAGTTG AGGACACGGCTGTGTATTACTGTGCGAAAGATCG GGGTACTATGAGAGTAGTGGTTTATGATACTTTGG ATATCTGGGGCCAGGGCACCTGGTCACCGTCTC CTCA (SEQ ID NO: 36)			Percent CD38 Hydrolase Inhibition	32
Consensus Sequence (aa FR1- FR4)	QVQLVESGGGLVQPGGSLRLSCAASGFTFSGY GMHWLRQAPGKEREWVAVISYDGSNKYYAD SVKGRFTISRDN SKNTLYLQMNSLRVEDTAVY YCAKDRGTMRVVVDTLDIWGQGTILVTVSS (SEQ ID NO: 22)			Cell Binding MFI	5240

FIG. 2

Panel A:

Clone ID	CDR1	CDR2	CDR3	V-Gene	J-Gene
330304 (CD38-F12A)	GFTFSSSW (SEQ ID NO: 3)	IKQDGSEK (SEQ ID NO: 9)	ARDRRGPFHHI (SEQ ID NO: 16)	IGHV3-7*01	IGHJ1*01
Consensus Sequence (nt FR1-FR4)	GGGGTGCAGCTGGTGGAGTCTGGGGGAGGC TTGGTCCAGCCTGGGGGGTCCCTGAGACTCT CCTGTACAGCCTCTGGATTACCTTTAGTAGC TCTTGGATGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAATGGGTGGCCAACATAAAG CAAGATGGAAGTGAGAAAGACTATGTGGACT CTGCGAAGGGCCGATTACCATCTCCAGAGAC AACGCCAAGAACTCACTGTATCTGCAAATGAA CAACCTGAGAGCCGAGGACACGGCTGTGTATT ACTGTGCGAGAGATAGGAGGGGGCCCTTTTTC ATATCTGGGGCCAGGGCACCTGGTCACCGTCT CCTCA (SEQ ID NO: 37)			Percent CD38 Hydrolase Inhibition	40
Consensus Sequence (aa FR1-FR4)	GVQLVESGGGLVQPGGSLRLSCTASGFTFSSS WMSWVRQAPGKGLEWVANIKQDGSEKDYV DSAKGRFTISRDNKNSLYLQMNNLRAEDTA VYYCARDRRGPFHHIWGQGLVTVSS (SEQ ID NO: 23)			Cell Binding MFI	5554

Panel B:

Clone ID	CDR1	CDR2	CDR3	V-Gene	J-Gene
330484 (CD38-F12B)	GFTFSSSW (SEQ ID NO: 3)	IKQDGSEK (SEQ ID NO: 9)	ARDRRGPFHHI (SEQ ID NO: 16)	IGHV3-7*01	IGHJ1*01
Consensus Sequence (nt FR1-FR4)	GGGGTGCAGCTGGTGGAGTCTGGGGGAGGCT TGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC TGTGCAGCCTCTGGATTACCTTTAGTAGCTC TTGGATGAGCTGGGTCCGCCAGGCTCCAGGG AAGGGGCTGGAATGGGTGGCCAACATAAAGC AAGATGGAAGTGAGAAAGACTATGTGGACTC TGCGAAGGGCCGATTACCATCTCCAGAGACA ACGCCAAGAACTCACTGTATCTGCAAATGAACA ACCTGAGAGCCGAGGACACGGCTGTGTATTACT GTGCGAGAGATAGGAGGGGGCCCTTTTTCATA TCTGGGGCCAGGGCACCTGGTCACCGTCTC CTCA (SEQ ID NO: 38)			Percent CD38 Hydrolase Inhibition	50
Consensus Sequence (aa FR1-FR4)	GVQLVESGGGLVQPGGSLRLSCAASGFTFSSS WMSWVRQAPGKGLEWVANIKQDGSEKDYVD SAKGRFTISRDNKNSLYLQMNNLRAEDTAVY YCARDRRGPFHHIWGQGLVTVSS (SEQ ID NO: 24)			Cell Binding MFI	ND

FIG. 2, Cont.

Panel C:

Clone ID	CDR1	CDR2	CDR3	V-Gene	J-Gene
350313 (CD38-F12C)	GFTFSSSW (SEQ ID NO: 3)	INQDGSEK (SEQ ID NO: 10)	ARDRRGPFHHI (SEQ ID NO: 16)	IGHV3-7*01	IGHJ1*01
Consensus Sequence (nt FR1-FR4)	GGGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGCTCTTGGATGAGCTGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATGGGTGCCAACATAAAACCAAGATGGAAGTGAGAAAGACTATGTGGACTCTGCGAAGGGCCGATTACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGTCGAGGACACGGCTGTGTATTACTGTGCGAGAGATAGGAGGGGGCCCTTTTTCATATCTGGGGCCAGGGCACCCCTGGTCACCGTCTCCTCA (SEQ ID NO: 39)			Percent CD38 Hydrolase Inhibition	45
Consensus Sequence (aa FR1-FR4)	GVQLVESGGGLVQPGGSLRLSCAASGFTFSSSWMSWVRQAPGKGLEWVANINQDGSEKDYVDSAKGRFTISRDNKNSLYLQMNSLRVEDTAVYYCARDRRGPFFHIWGQGTILTVSS (SEQ ID NO: 25)			Cell Binding MFI	5984

Panel D:

Clone ID	CDR1	CDR2	CDR3	V-Gene	J-Gene
350337 (CD38-F12D)	GFTFSSSW (SEQ ID NO: 3)	IKQDGSEK (SEQ ID NO: 9)	ARDRRGPFHHI (SEQ ID NO: 16)	IGHV3-7*03	IGHJ1*01
Consensus Sequence (nt FR1-FR4)	GGGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGCTCTTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATGGGTGCCAACATAAAGCAAGATGGAAGTGAGAAAGACTATGTGGACTCTGCGAAGGGCCGATTACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGACAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGATAGGAGGGGGCCCTTTTTCATATCTGGGGCCAGGGCACCCCTGGTCACCGTCTCCTCA (SEQ ID NO: 40)			Percent CD38 Hydrolase Inhibition	46
Consensus Sequence (aa FR1-FR4)	GVQLVESGGGLVQPGGSLRLSCAASGFTFSSSWMSWVRQAPGKGLEWVANIKQDGSEKDYVDSAKGRFTISRDNKNSLYLQMNSLTAEDTAVYYCARDRRGPFFHIWGQGTILTVSS (SEQ ID NO: 26)			Cell Binding MFI	5785

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FIG. 3

Panel A:

Clone ID	CDR1	CDR2	CDR3	V-Gene	J-Gene
330505 (CD38-F13A)	GGSISSSLFY (SEQ ID NO: 4)	IHDSGST (SEQ ID NO: 11)	ARGPRGFYSSGPDDFDI (SEQ ID NO: 17)	IGHV4-39*01	IGHJ1*01
Consensus Sequence (nt FR1-FR4)	CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGACT GGTGAAGCCTTCGGAGACCCTGTCCCTCACCTG CACTGTCTCTGGTGGCTCCATCAGTAGTAGTCT TTTCTACTGGGGGTGGATCCGCCAGCCCCGGG GAAGGGGCTGGAGTGGATTGGGAGTATCCATG ATAGTGGGAGCACCTACTACAACCCGTCCCTCA AGAGTCGAGTCACCATATCCGCAGACACGTCCA AGAACCAGTTCTCCCTGAAGCTGAAGTCTGTGA CCGCCACAGACACGGCTGAGTATTACTGTGCGA GAGGGCCGCGCGGTTTCTATAGCAGTGGCCCTG ATGATTTTGATATCTGGGGCCAGGGCACCTGG TCACCGTCTCCTCA (SEQ ID NO: 41)			Percent CD38 Hydrolase Inhibition	38
Consensus Sequence (aa FR1-FR4)	QLQLQESGPGLVKPSETLSLTCTVSGSISSSLFY WGWIRQPPGKGLEWIGSIHDSGSTYYNPSLKSRV TISADTSKNQFSLKLNSVTATDTAEYYCARGPRG FYSSGPDDFDIWGQGTTLVTVSS (SEQ ID NO: 27)			Cell Binding MFI	1296

Panel B:

Clone ID	CDR1	CDR2	CDR3	V-Gene	J-Gene
339296 (CD38-F13B)	GGSISSSNYH (SEQ ID NO: 5)	IYYSGST (SEQ ID NO: 12)	ARGPRGFYSSGPDDFDI (SEQ ID NO: 17)	IGHV4-39*01	IGHJ1*01
Consensus Sequence (nt FR1-FR4)	CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAC TGGTGAAGTCTTCGGAGACCCTGTCCCTCACC TGCATTGTCTCTGGTGGCTCCATCAGCAGTAG TAATTACCACTGGGGCTGGAGCCGCCAGCCCC CAGGGAAGGGGCAGGAGTGGATCGGGAGTAT CTATTACAGTGGAAGTACCTACTACAACCCGT CCCTCAAGAGTCGAGTCACCATTTCCGGAGAC ACGTCCAAGAACCAGTTCTCCCTGAAGCTGAG CTCTGTGACCGCCGACACACGGCTGTGTATTA CTGTGCGAGAGGGCCGCGCGGTTTCTATAGCAG TGGCCCTGATGATTTTGATATCTGGGGCCAGGG CACCTTGGTCACCGTCTCCTCA (SEQ ID NO: 42)			Percent CD38 Hydrolase Inhibition	0
Consensus Sequence (aa FR1-FR4)	QLQLQESGPGLVKSSETLSLTCTVSGSISSSNYH WGWSRQPPGKGQEWIGSIYYSYSTYYNPSLKSR VTISGDTSKNQFSLKLSSVTAADTAVYYCARGPR GFYSSGPDDFDIWGQGTTLVTVSS (SEQ ID NO: 28)			Cell Binding MFI	2974

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FIG. 4

Additional Sequences:

Name	Amino Acid Sequence	SEQ ID NO:
G4S linker (n=1)	GGGGS	SEQ ID NO: 29
G4S linker (n=2)	GGGSGGGGS	SEQ ID NO: 45
Isatuximab heavy chain	QVQLVQSGAEVAKPGTSVKLSCKASGYTFTDYWMQ WVKQRPGQGLEWIGTTPGDGDTGYAQKFQGKATL TADKSSKTVYMHLSLASEDSAVYYCARGDYYSN SLDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVM HEALHNHYTQKSLSLSPGK	SEQ ID NO: 30
Isatuximab light chain	DIVMTQSHLSMSTSLGDPVSITCKASQDVSTVVAWY QQKPGQSPRRLIYSASYRYIGVPDRFTGSGAGTDFTF TISSVQAEDLAVYYCQQHYSPPYTFGGGKLEIKRTV AAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSSTYSSTLTLSK ADYEKHKVYACEVTHQGLSPVTKSFNRGEC	SEQ ID NO: 31
Human IgG1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSL SPGK	SEQ ID NO: 43
Human IgG4	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS SLGKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCP APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFCFSVMHEALHNHYTQKSLSLS LGK	SEQ ID NO: 44

FIG. 5

Additional Sequences:

Name	Amino Acid Sequence
HC1 polypeptide sequence (F11A VH, IgG4 Fc CH3 knob)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVR QAPGKEREWVAVISDDGSNKYYADSVKGRFTISRDNK NTLYLQMNSLRVEDTAVYYCAKDRGTMRVVVYDTLDI WGQGTLLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPP CPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK GQPREPQVYTLPPSQEEMTKNQVSLWCLVKGFYPSDIA VEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSR WQEGNVFSCSVMEALHNHYTQKSLSLGLGK (SEQ ID NO: 46)
HC2 polypeptide sequence (F12A HCO VH, IgG4 Fc CH3 hole)	GVQLVESGGGLVQPGGSLRLSCTASGFTFSSSWMSWVR QAPGKGLEWVANIKQDGSEKDYVDSAAGRFTISRDNK NSLYLQMNLRRAEDTAVYYCARDRRGPFHFWGQGTLL VTVSSESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLSCA VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLV SRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGL GK (SEQ ID NO: 47)
LC1 (VL, Kappa light chain)	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQK PGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISLQS EDFAVYYCQQYNNWPWTFGQGTKVEIKRTVAAPSVEFIF PPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQS GNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACE VTHQGLSPVTKSFNRGEC (SEQ ID NO: 48)
LC1 CDR1	QSVSSN (SEQ ID NO: 49)
LC1 CDR2	GAS (SEQ ID NO: 50)
LC1 CDR3	QQYNNWPWT (SEQ ID NO: 51)
LC1 VL	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQK PGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISLQS EDFAVYYCQQYNNWPWTFGQGTKVEIK (SEQ ID NO: 52)

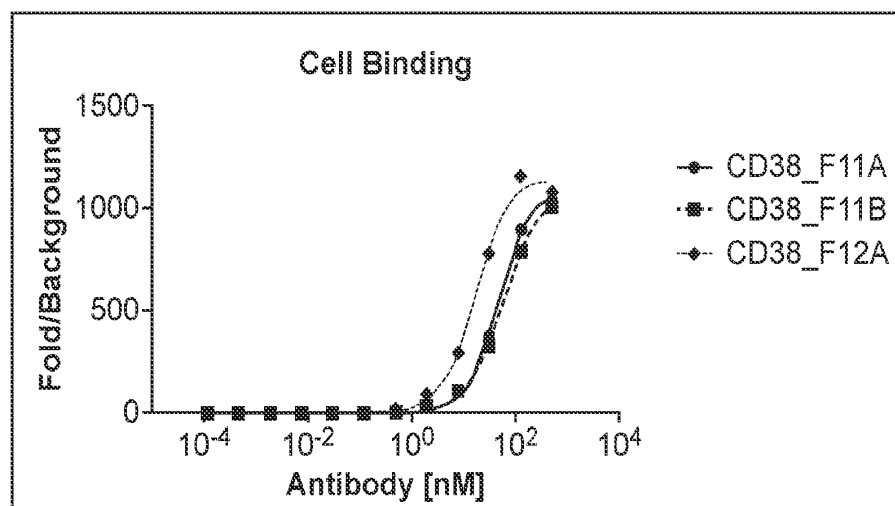
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FIG. 5, cont.

Name	Amino Acid Sequence
Silenced IgG4 (CH1 - hinge - CH2 - CH3; knob (S228P, F234A, L235A; T366W))	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTCNVDPHKPSNTKVDK RVESKYGPPCP <u>P</u> CPAPE <u>AA</u> GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE MTKNQVSL <u>W</u> CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGS FFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSLGK (SEQ ID NO: 53)
Silenced IgG4 (hinge - CH2 - CH3; hole (S228P, F234A, L235A; T366S, L368A, Y407V))	ESKYGPPCP <u>P</u> CPAPE <u>AA</u> GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMT KNQVSL <u>S</u> CAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFL <u>V</u> SRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSLGK (SEQ ID NO: 54)
HC1 polypeptide sequence (F11A VH, IgG4 Fc silenced PAA; CH3 knob)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKERE WVAVISDDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTA VYYCAKDRGTMRVVVDYLDIWGQGT LVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVTVPSSSLGKTYTCNVDPHKPSNTKVDKRVESKYGPPCP <u>P</u> CPA PE <u>AA</u> GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWY VDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSL <u>W</u> CLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSRLTVDKSRWQE GNVFSCSVMEALHNHYTQKSLSLSLGK (SEQ ID NO: 55)
HC2 polypeptide sequence (F12A HCO VH, IgG4 Fc silenced PAA; CH3 hole)	GVQLVESGGGLVQPGGSLRLSCTASGFTFSSSWMSWVRQAPGKGLE WVANIKQDGSEKDYVDSAKGRFTISRDN AKNSLYLQMNNLRAEDTA VYYCARDRRGPFPHIWGQGT LVTVSSSESKYGPPCP <u>P</u> CPAPE <u>AA</u> GGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSI EKTISKAKGQPREPQVYTLPPSQEEMTKNQVSL <u>S</u> CAVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSGGSFFL <u>V</u> SRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSLGK (SEQ ID NO: 56)

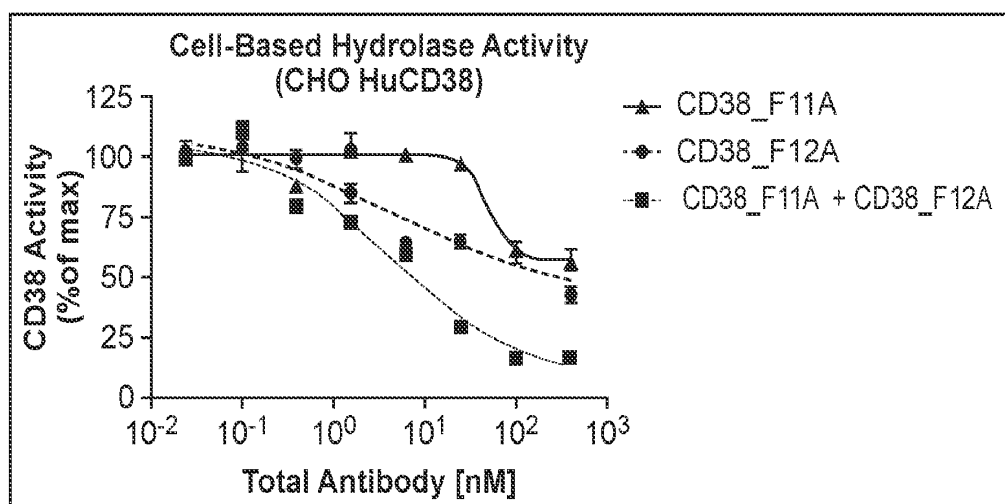
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FIG. 6



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FIG. 7



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FIG. 8

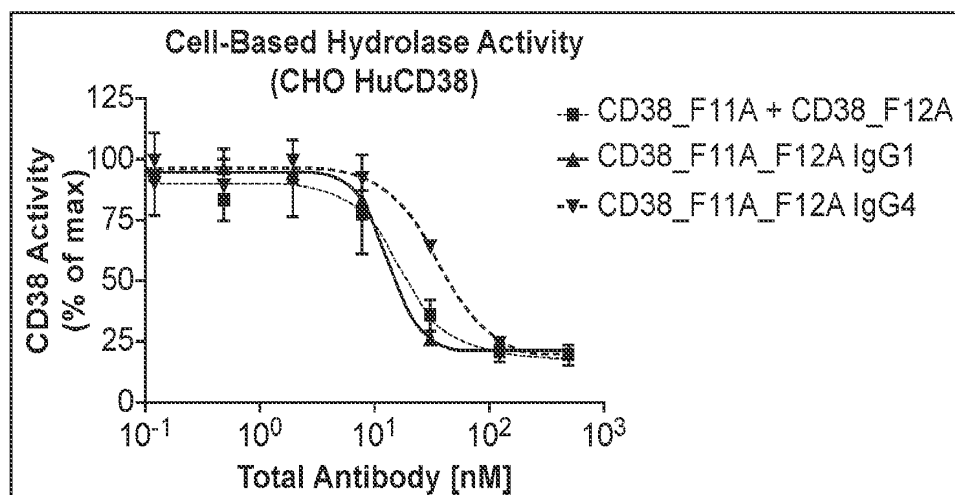
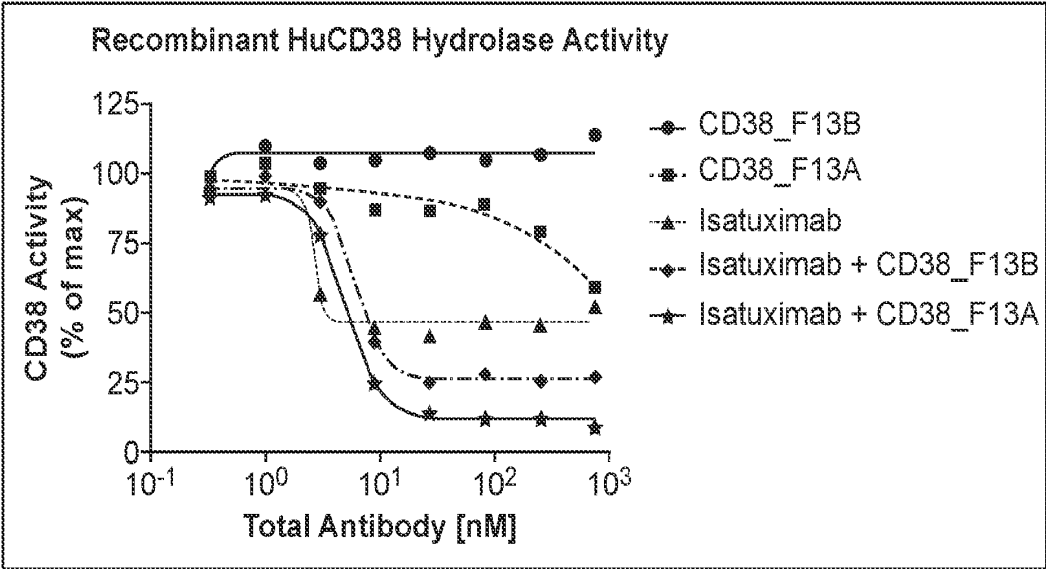
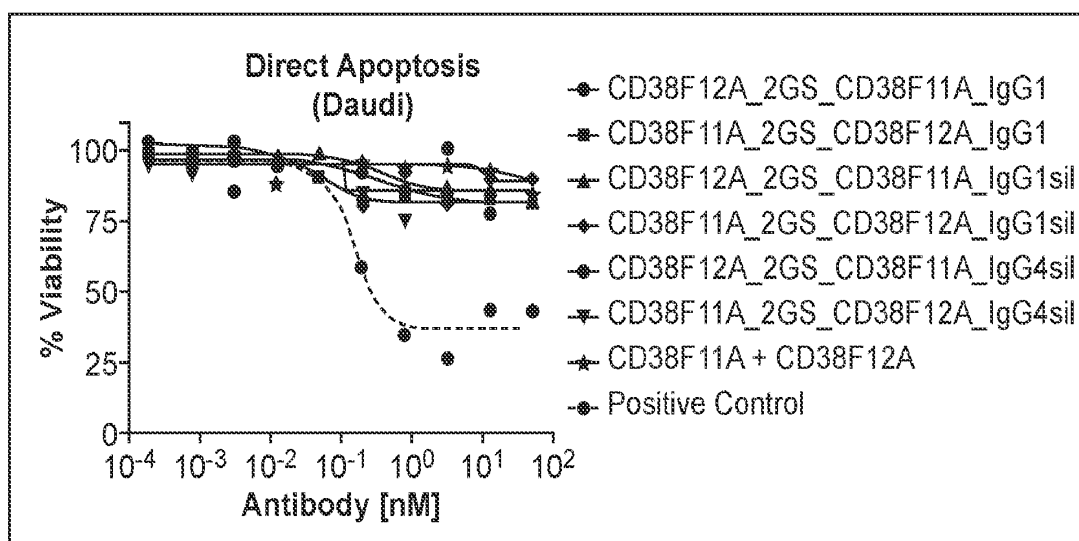


FIG. 9



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FIG. 10



	EC50 [nM]	% Max Cell Death
CD38F12A_2GS_CD38F11A_IgG1	0.03	18.63
CD38F11A_2GS_CD38F12A_IgG1	0.29	18.46
CD38F12A_2GS_CD38F11A_IgG1sil	0.31	14.01
CD38F11A_2GS_CD38F12A_IgG1sil	0.11	14.55
CD38F12A_2GS_CD38F11A_IgG4sil	10.05	10.22
CD38F11A_2GS_CD38F12A_IgG4sil	0.08	18.87
CD38F11A + CD38F12A	736.60	4.48
Positive Control	0.15	63.25

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FIG. 11

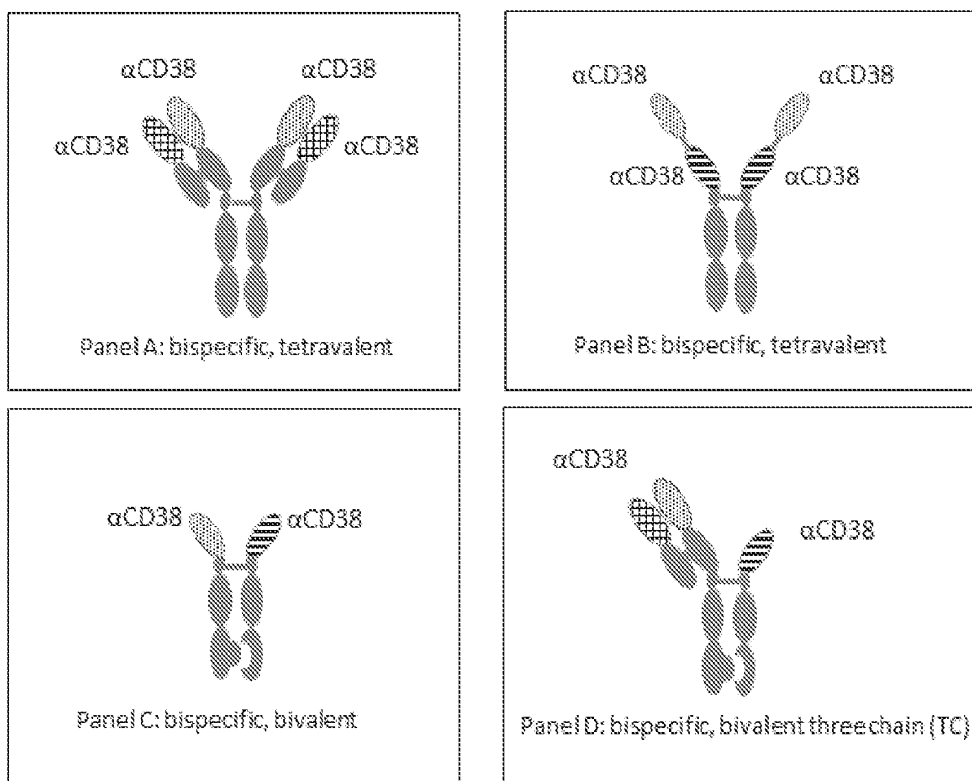
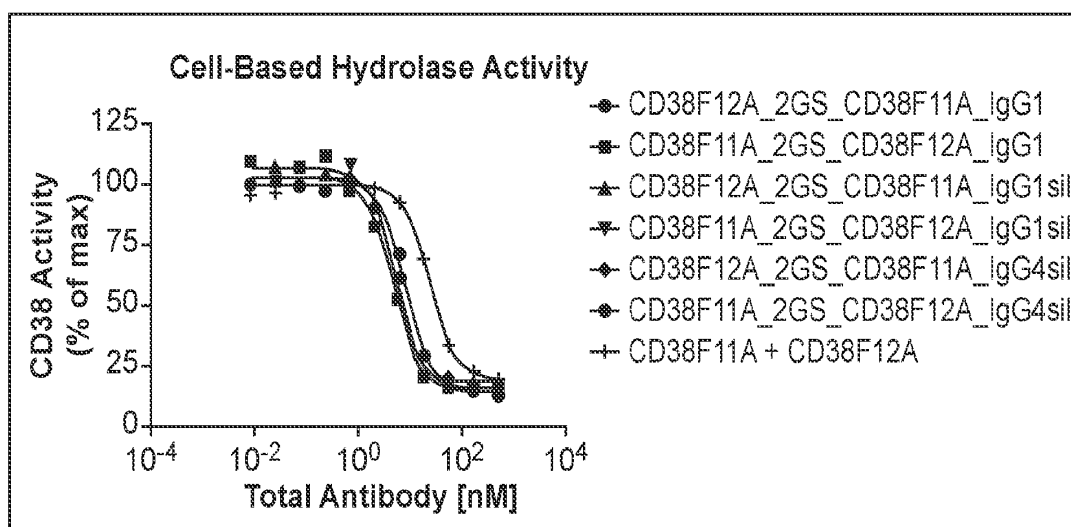


FIG. 12



	EC50 [nM]	% Max Inhibition
CD38F12A_2GS_CD38F11A_IgG1	6.3	83.6
CD38F11A_2GS_CD38F12A_IgG1	4.5	86.0
CD38F12A_2GS_CD38F11A_IgG1sil	5.0	83.3
CD38F11A_2GS_CD38F12A_IgG1sil	5.7	85.5
CD38F12A_2GS_CD38F11A_IgG4sil	6.0	81.4
CD38F11A_2GS_CD38F12A_IgG4sil	8.7	86.1
CD38F11A + CD38F12A	24.2	79.9

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FIG. 13

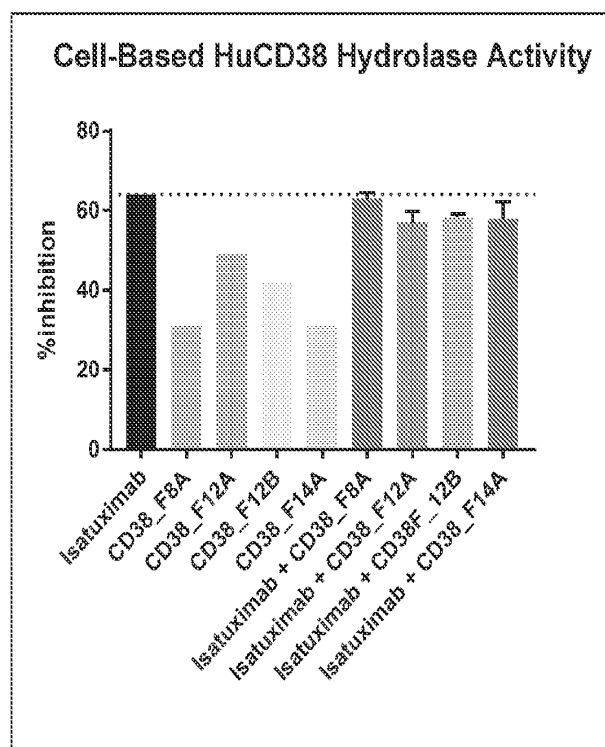
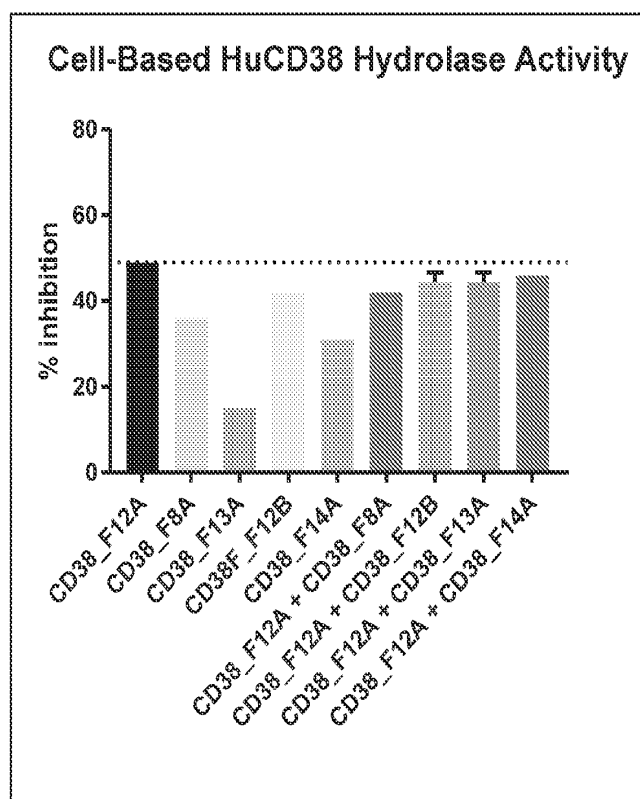


FIG. 14



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FIG. 15

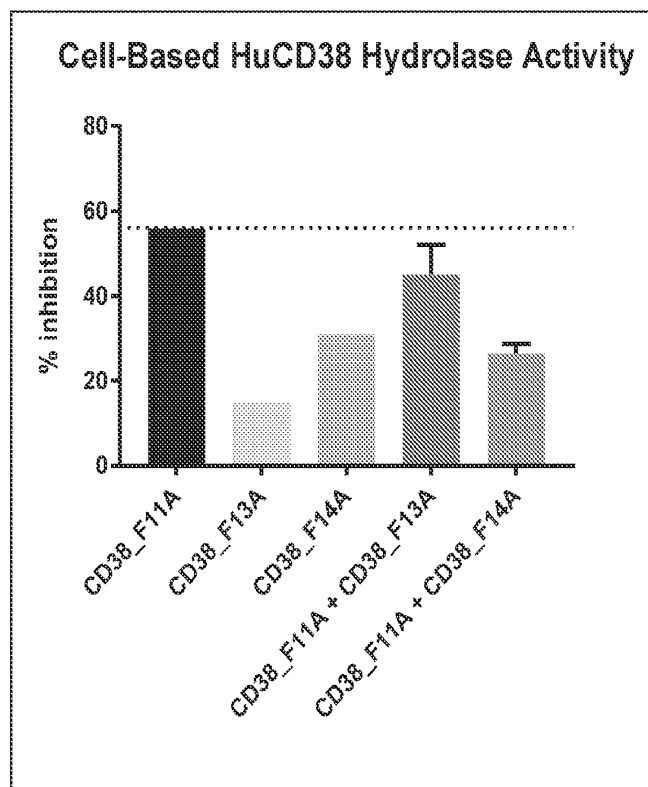
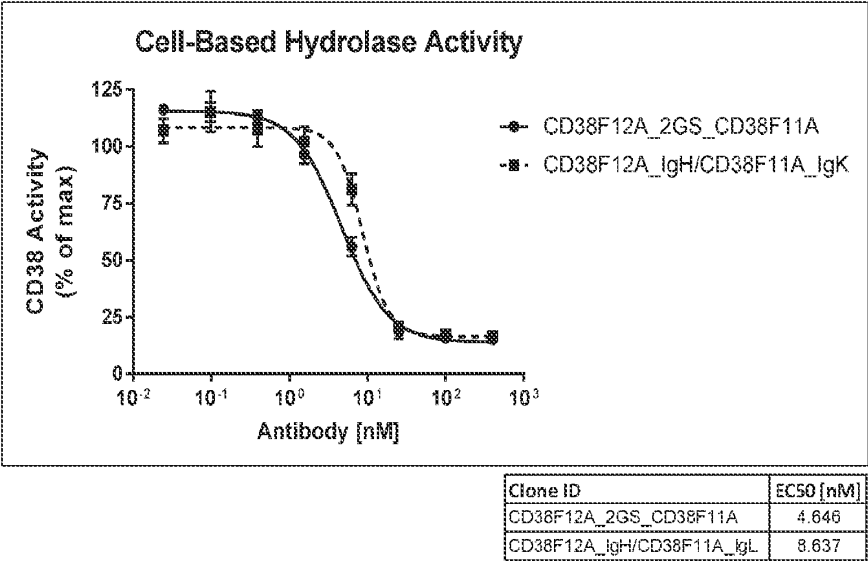


FIG. 16



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FIG. 17

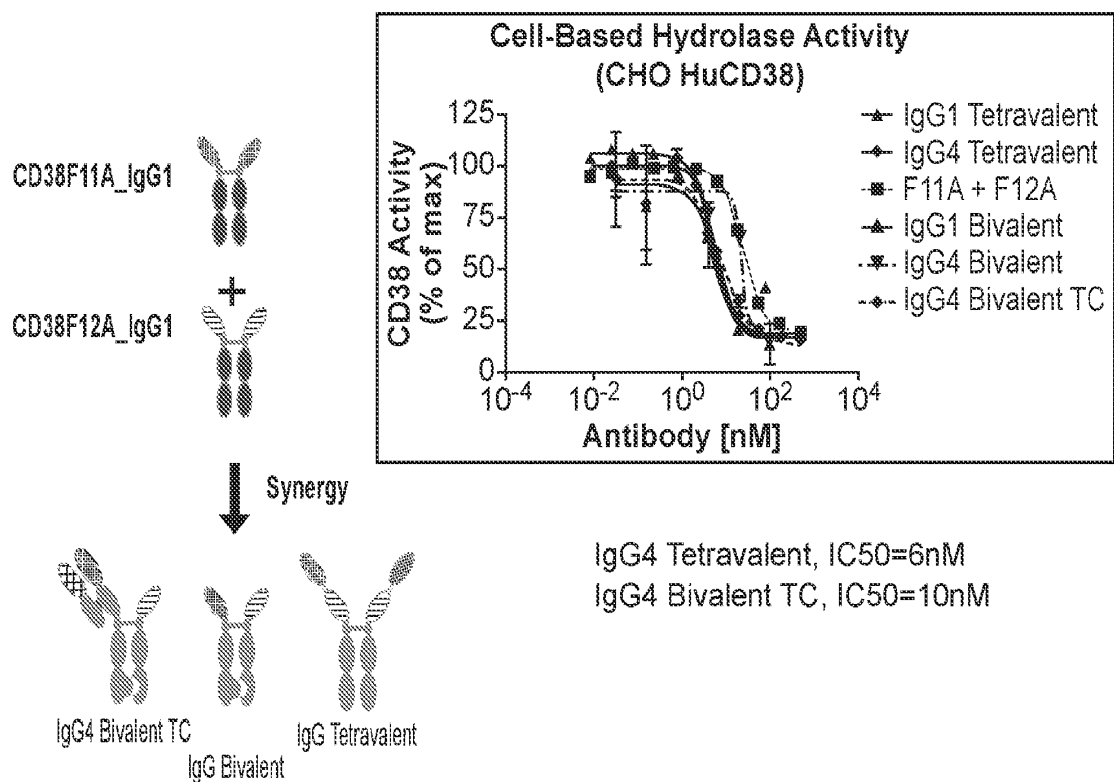


FIG. 18

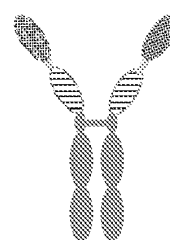
	Enzyme inhibition	Cell Binding	Apoptosis
Bivalent IgG1	++++++	++++++	ND
Tetravalent IgG1	++++++	ND	-
Sil-IgG4 Tetravalent	++++++	ND	-
Sil-IgG4 Bivalent	++++++	++++++	-
Sil-IgG4 Bivalent Triple Chain	++++++	++++++	-
Sil-IgG1 Tetravalent	++++++	++++	-
Sil-IgG1 Bivalent	++++++	++++++	-
Isatuximab	++++	++++++	+++++
Daratumumab	-	++++++	+++++



IgG4 Bivalent TC



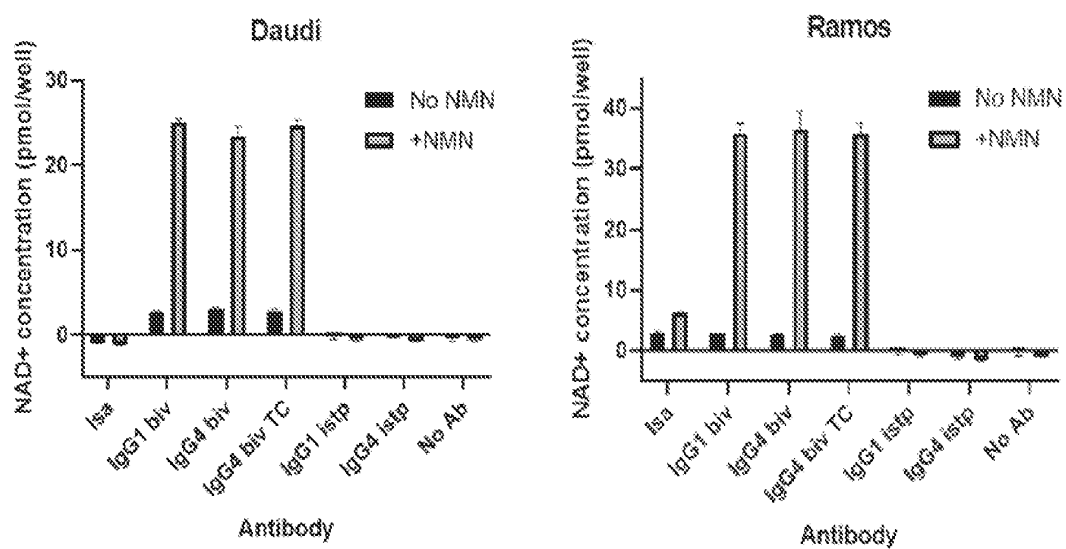
IgG Bivalent



IgG Tetravalent

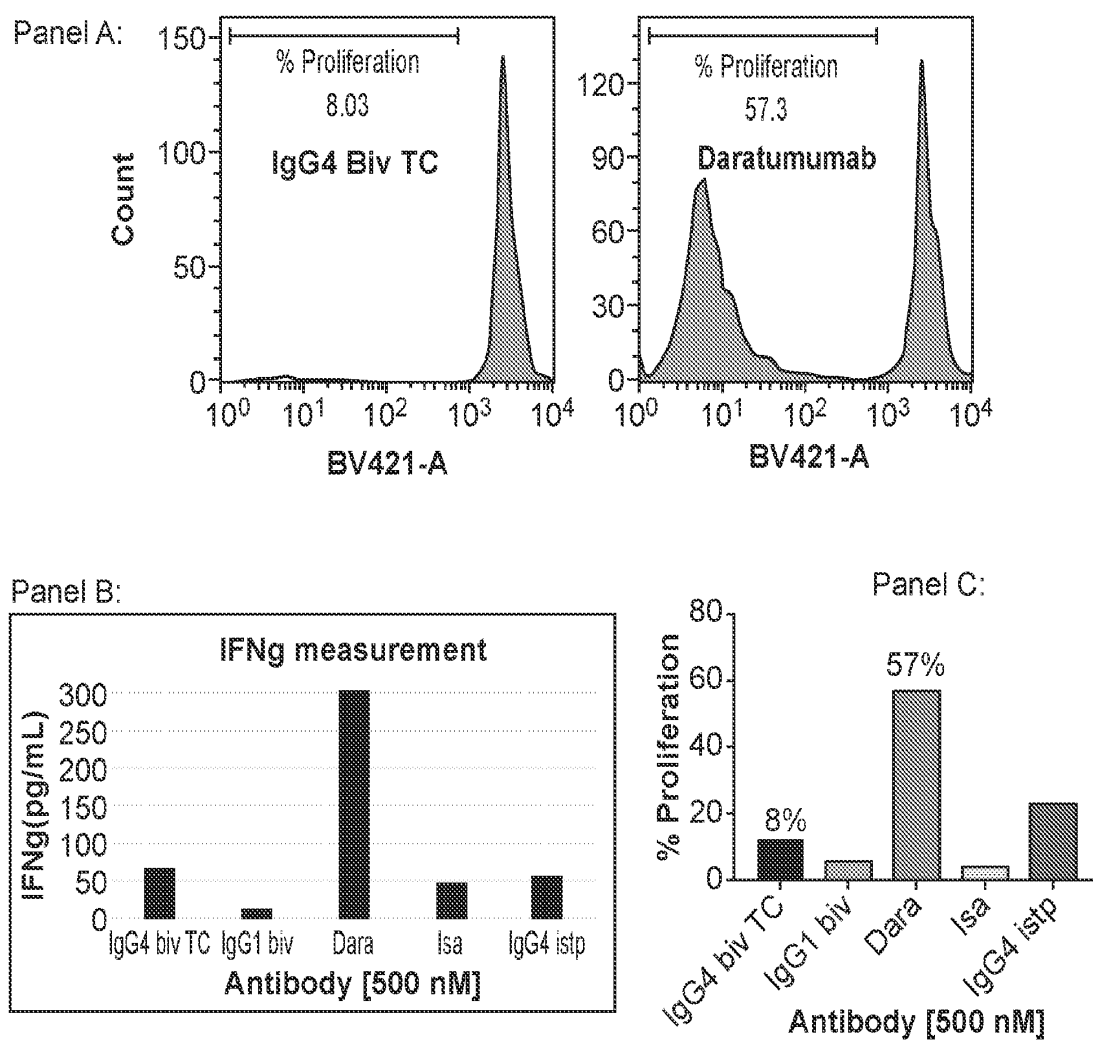
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FIG. 19



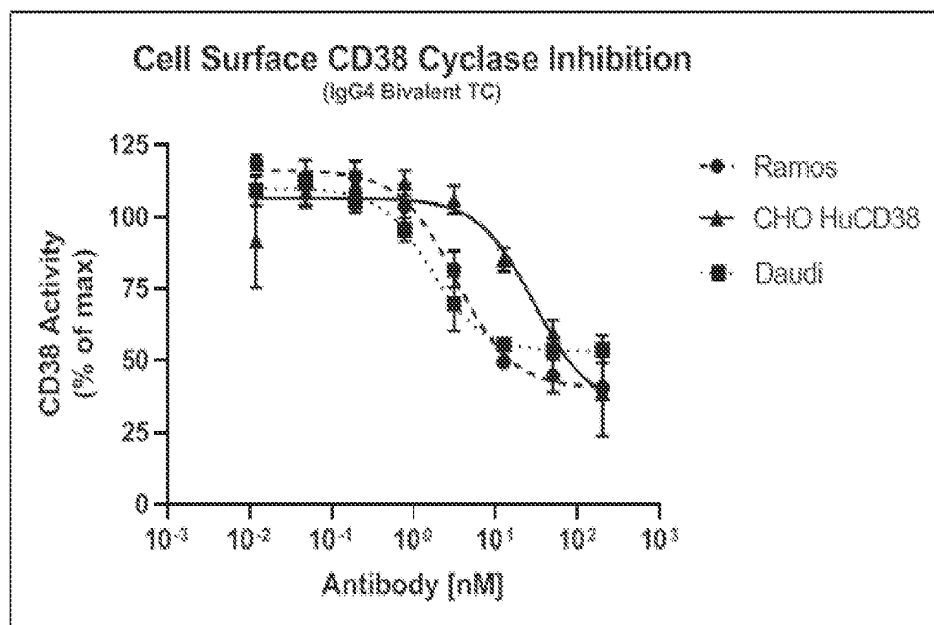
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FIG. 20



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FIG. 21



Cell Line	EC50 [nM]	Max Inhibition (%)
Ramos	3.3	60
Daudi	1.6	57
CHO HuCD38	29.2	61

FIG. 22

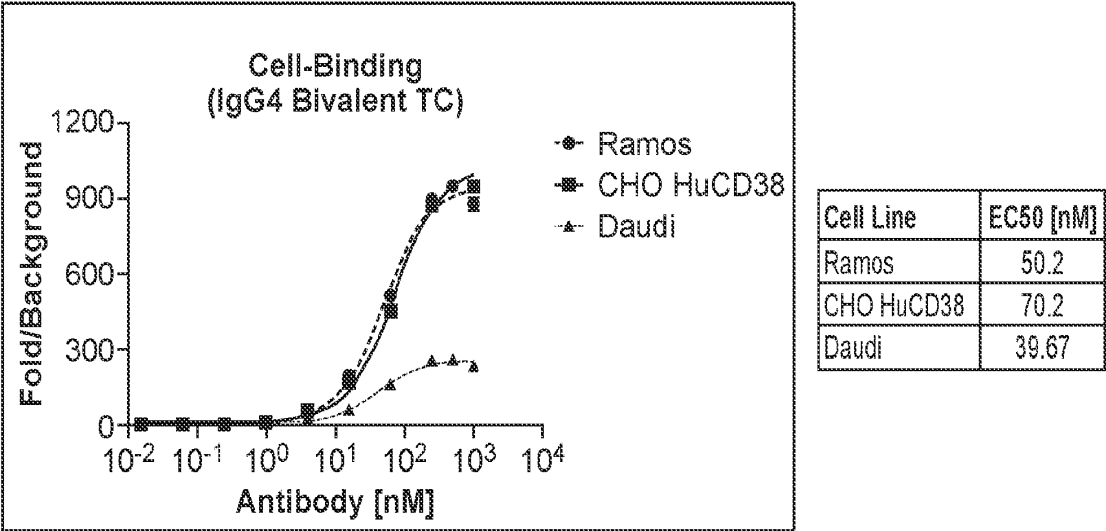
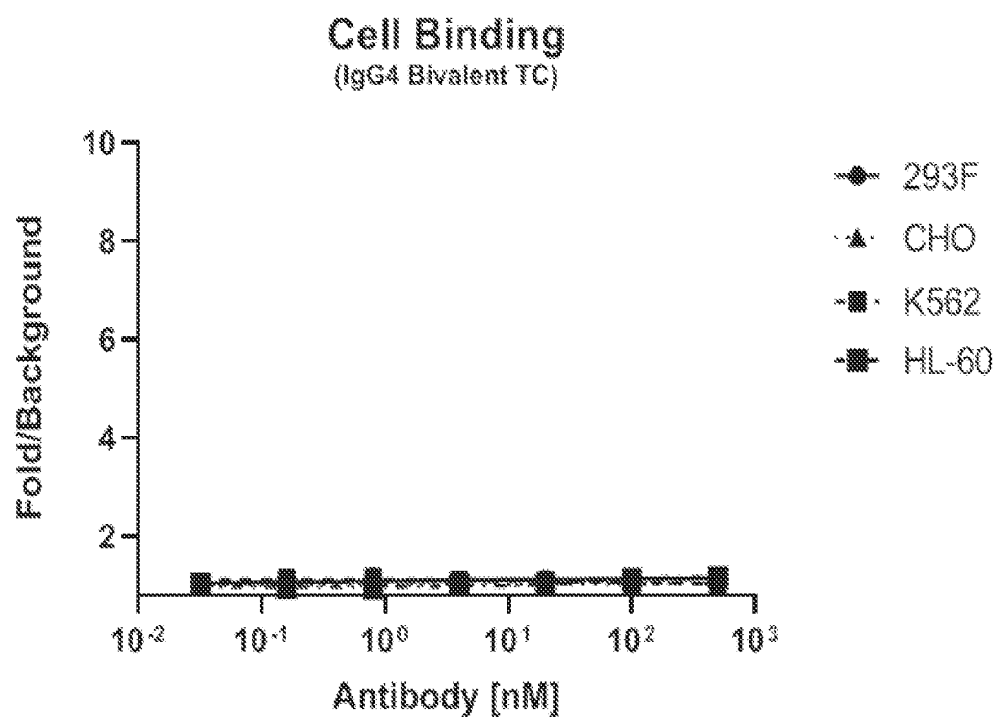


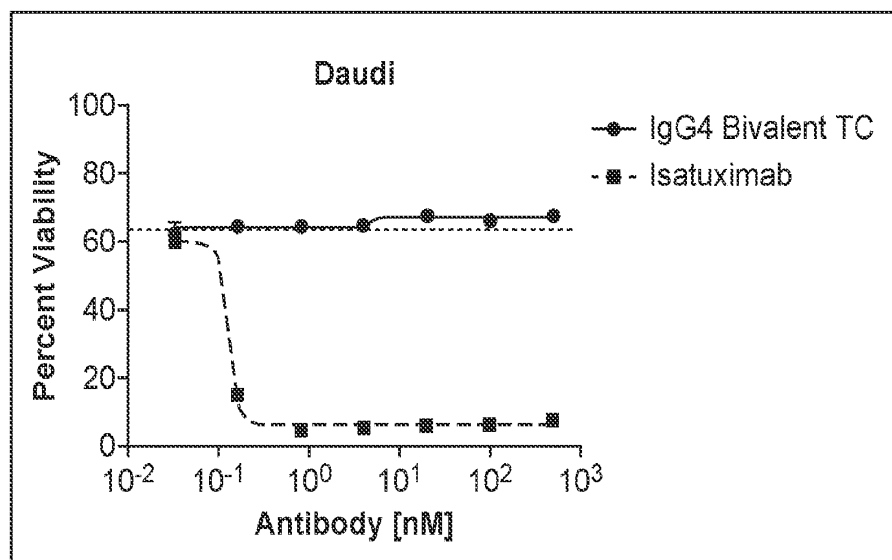
FIG. 23



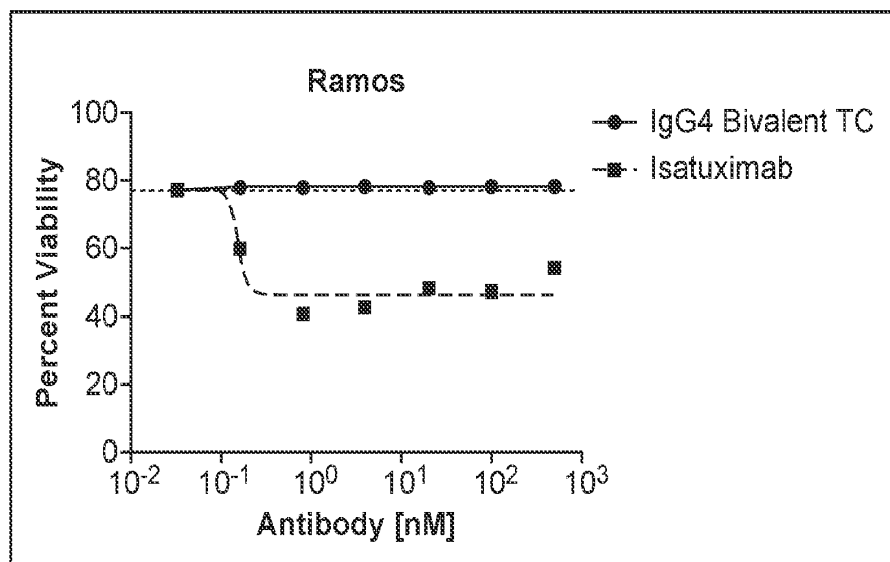
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FIG. 24

Panel A:



Panel B:



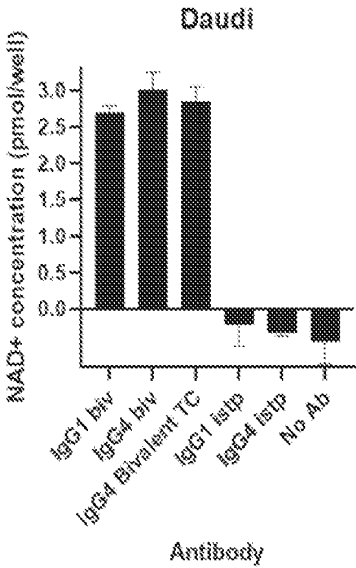
Panel C:

	Daudi		Ramos	
	EC50 [nM]	Max Apoptosis (%)	EC50 [nM]	Max Apoptosis (%)
IgG4 Bivalent TC	NA	NA	NA	NA
Isatuximab	0.13	57	0.16	37

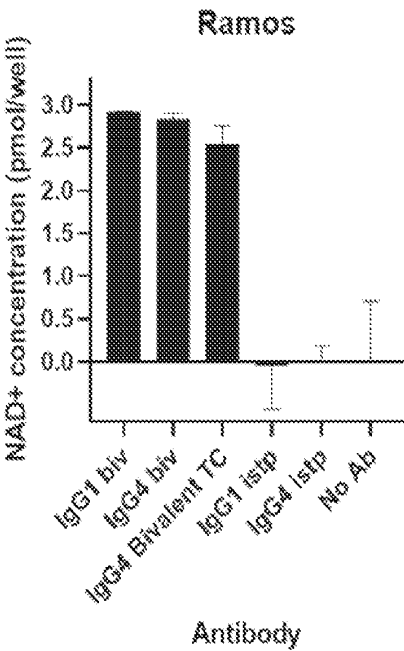
SUBSTITUTE SHEET (RULE 26)

FIG. 25

Panel A:



Panel B:



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FIG. 26

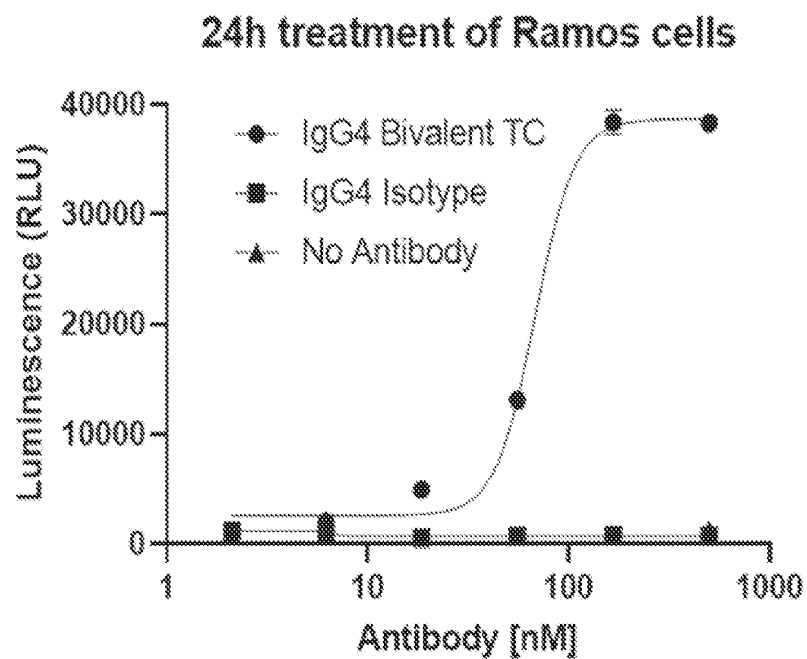
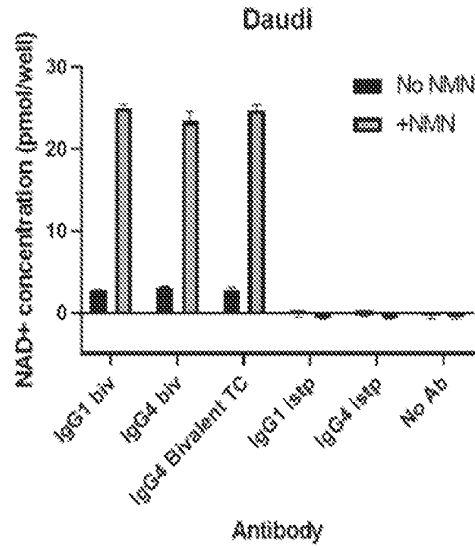
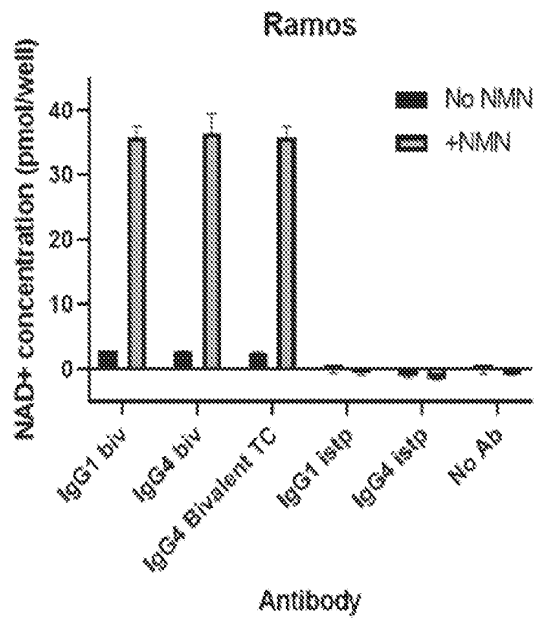


FIG. 27

Panel A:

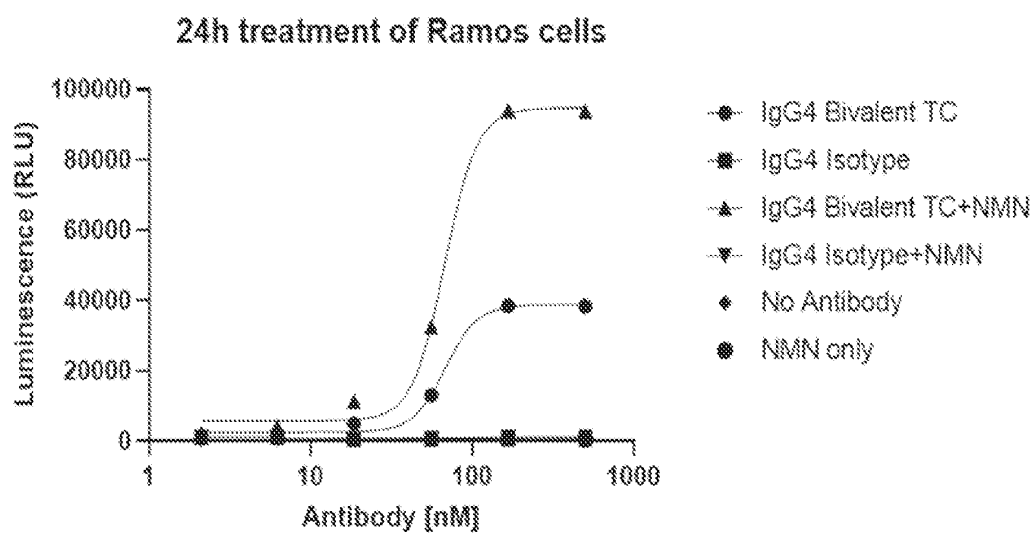


Panel B:



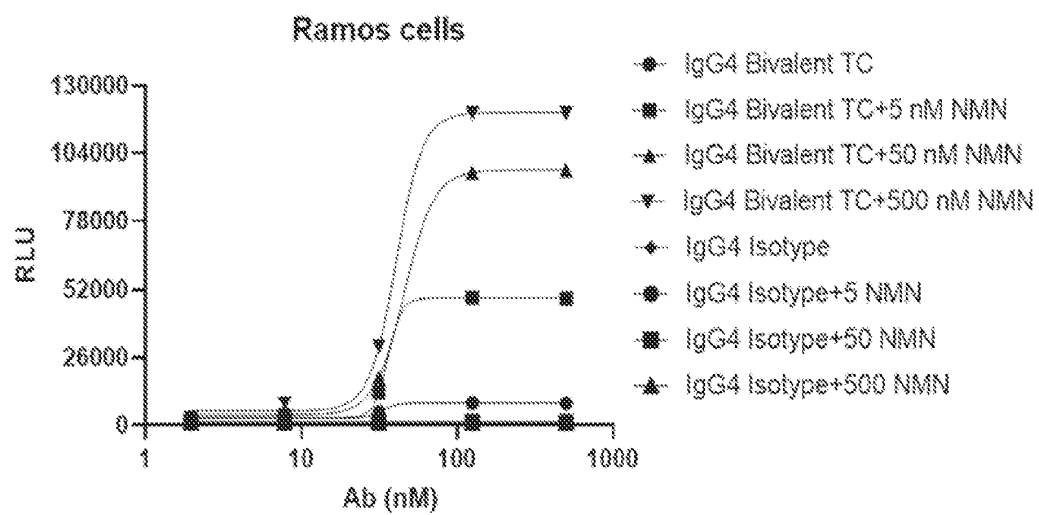
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FIG. 28



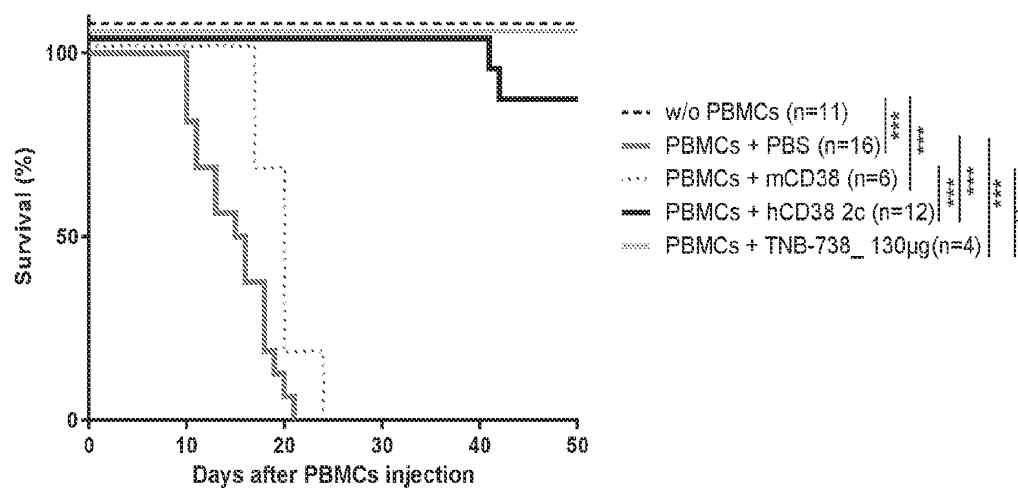
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FIG. 29



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FIG. 30



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FIG. 31

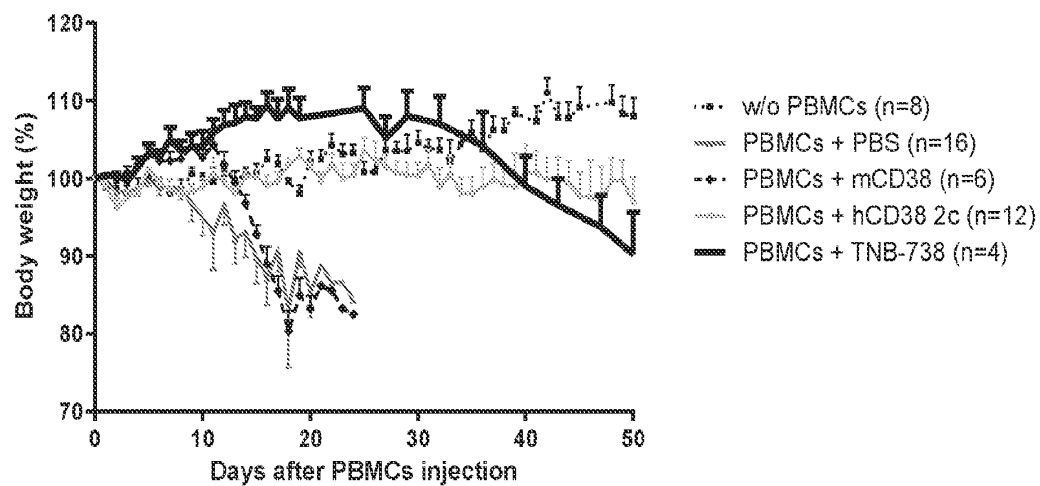


FIG. 32

