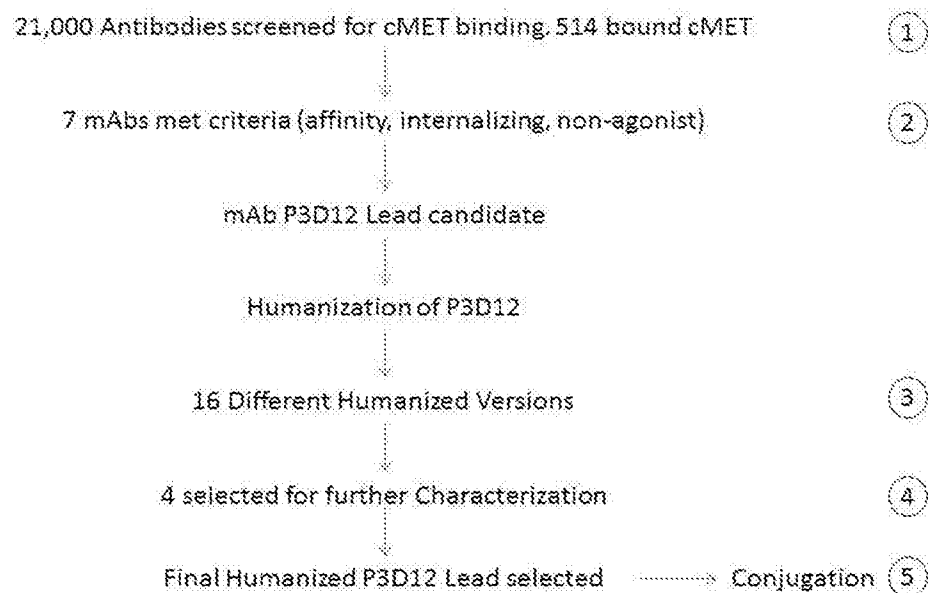


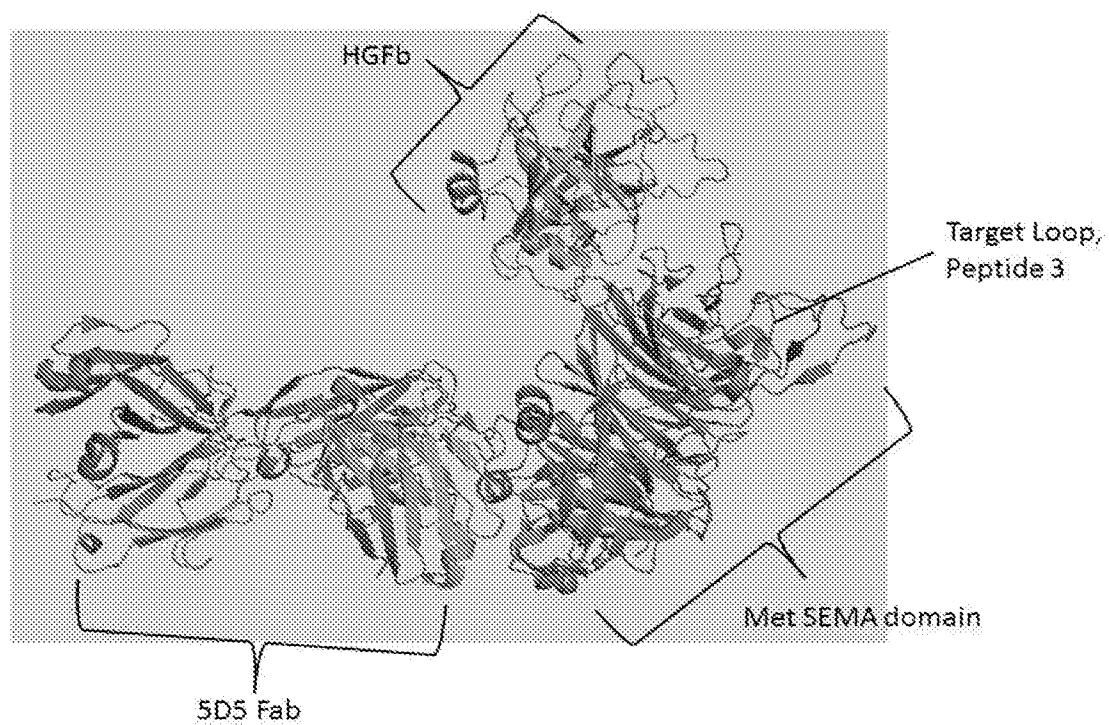
[Fig. 1]

FIG. 1

MET Antibodies Work Flow

[Fig. 3]

FIG. 3



[Fig. 4]

2

FIG. 4

Well name	Description	FACS Geom. Mean	MET BINDING ELISA OD450nm
Well_E01.fcs	negative control	103000	NA
Well_F01.fcs	negative control	116000	NA
Well_A01.fcs	positive control	83500	NA
Well_B01.fcs	positive control	81800	NA
Well_E09.fcs	hybridoma	61000	4.5319
Well_D12.fcs	hybridoma	67300	4.3803
Well_E02.fcs	hybridoma	69800	4.596
Well_F04.fcs	hybridoma	77300	3.0801
Well_B10.fcs	hybridoma	97200	0.0211
Well_H06.fcs	hybridoma	97600	6.1209
Well_F06.fcs	hybridoma	97800	-0.0005
Well_G10.fcs	hybridoma	98800	0.0079
Well_E07.fcs	hybridoma	98900	0.0011
Well_H10.fcs	hybridoma	98900	1.7236
Well_E06.fcs	hybridoma	99300	5.2925
Well_F10.fcs	hybridoma	99700	0.0185
Well_F07.fcs	hybridoma	99800	0.235

[Fig. 5]

2

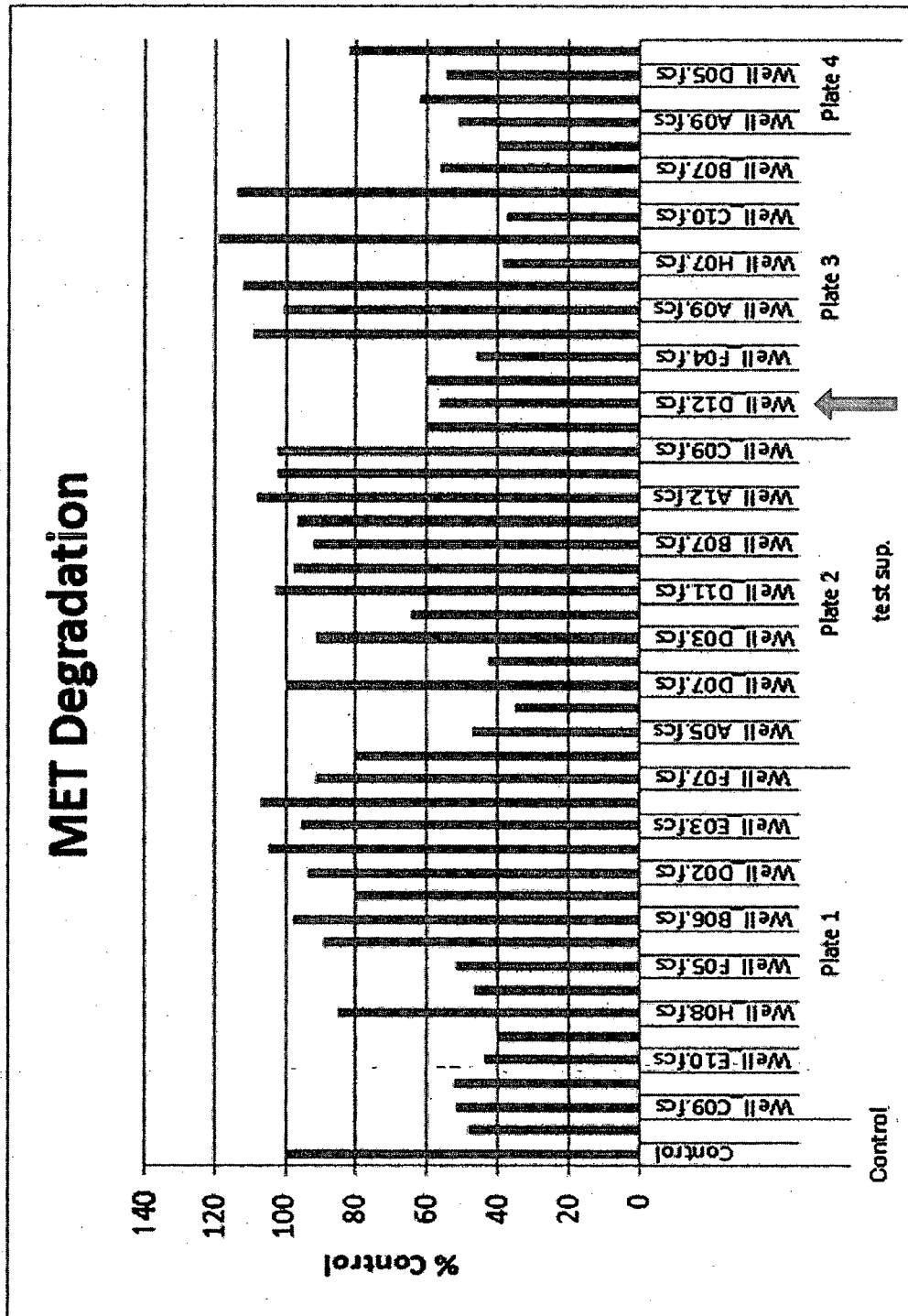
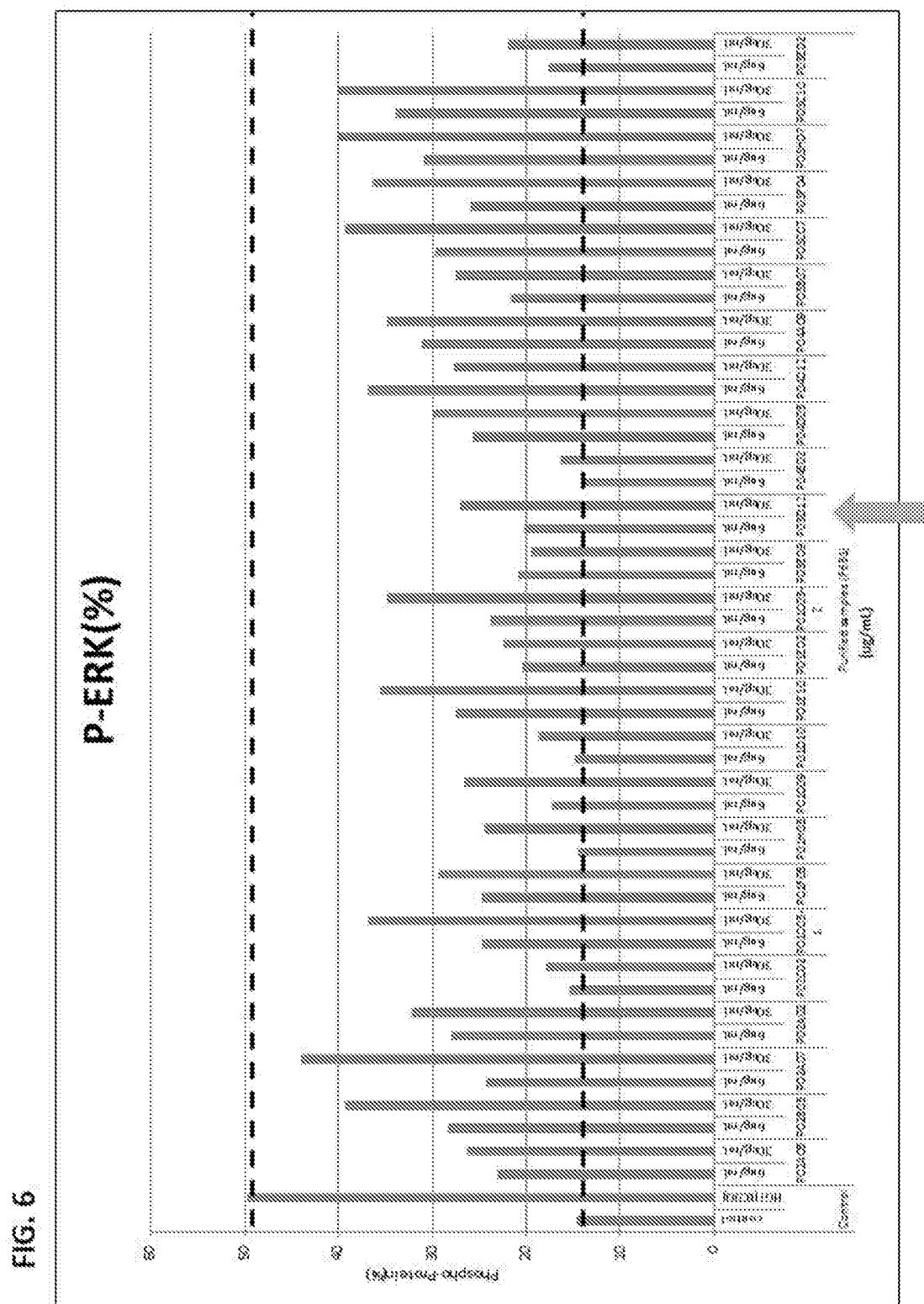
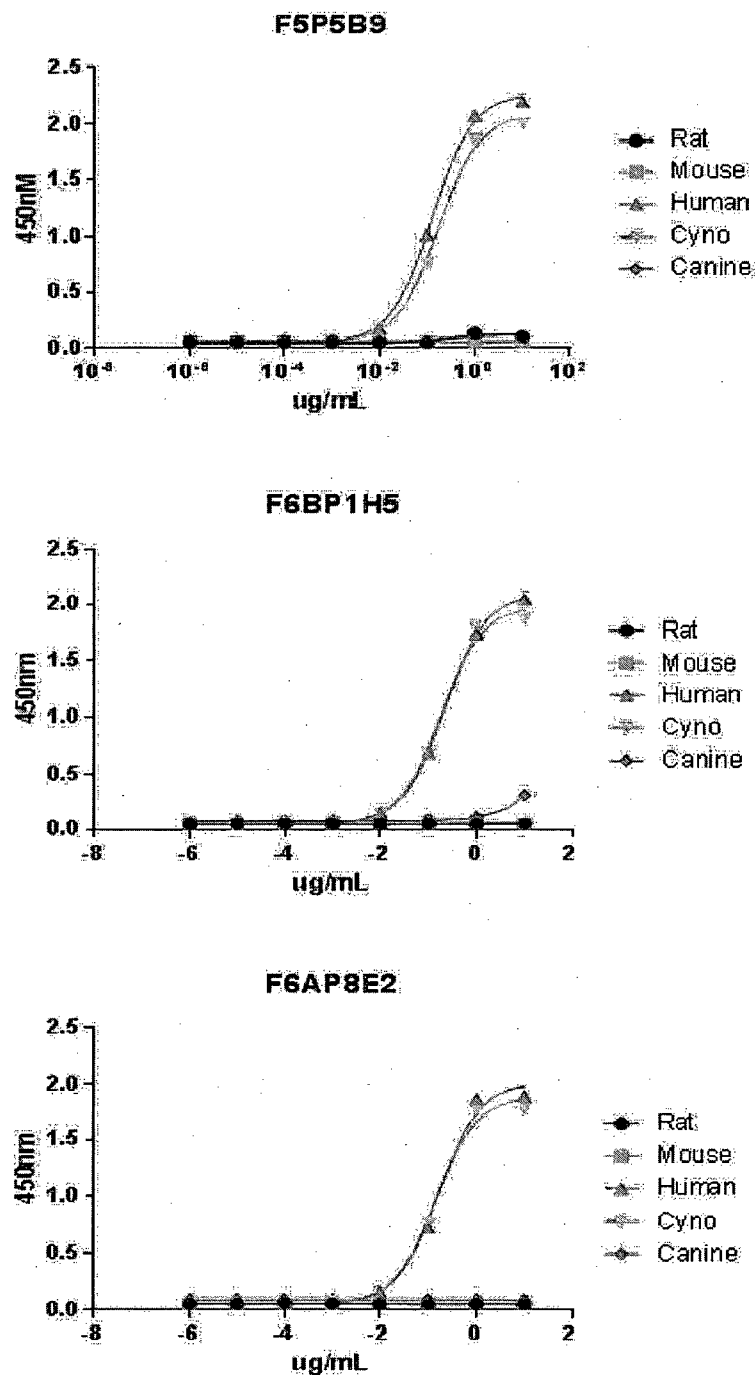


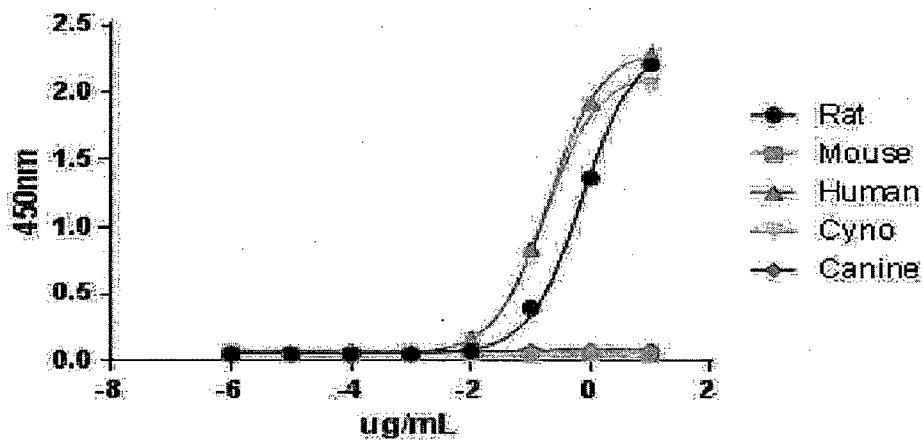
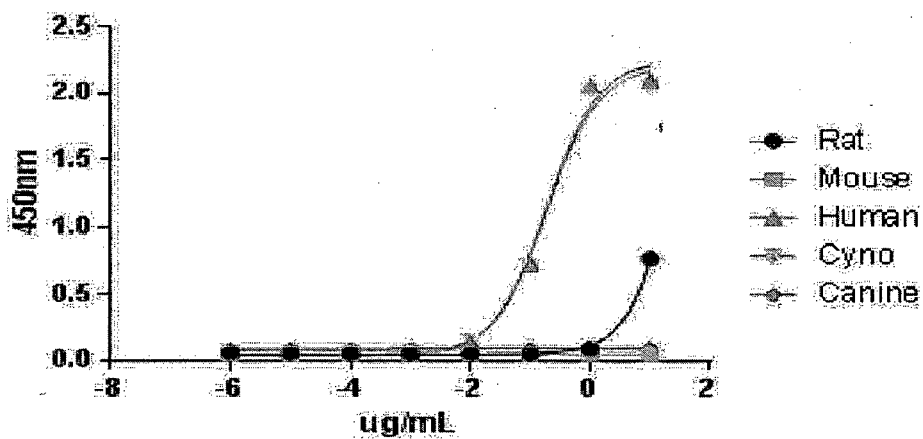
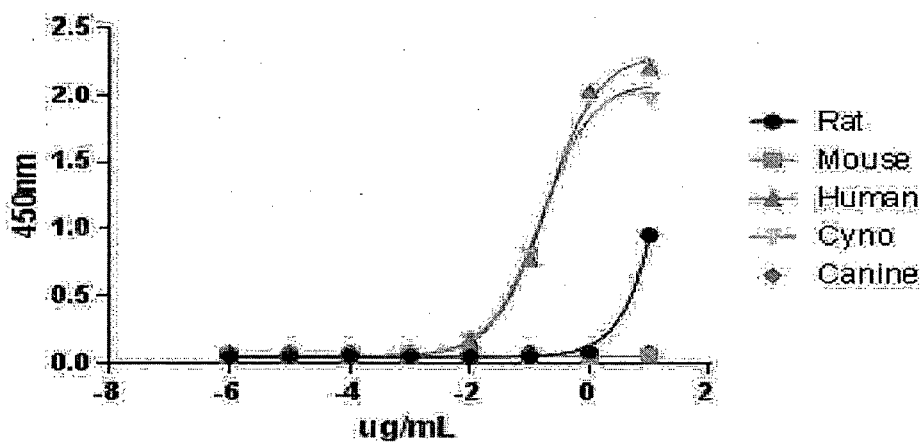
FIG. 5

[Fig. 6]



[Fig. 7]

FIG. 7 Anti-Met antibodies species cross-reactivity

F6B1P3D12**F6B1P1E2****F6BP2D4**

[Fig. 8]

Sequences of top 9 murine clones. Two clones were duplicated giving 7 unique sequences

FIG. 8A

Light Chain		SEQ ID NO:	1	10	20	30	40	50	60	70	80	90	100	110	117
F5_P5_B9_L (1)	--DVLMTQPLSLPVSIGDQASISCRSSQ--TIVHGTGNT--YLEWYQKPGQSPKLLIYKSNRFGSGGSDFTFLKISRVEAEDLGWYVYFCQSHVPTFGGKLEIKR	37													
F6A_P8_E2_L (1)	--DIVMTQSPKSMMSVGERVTLSCAS-----ENVGT--YYSWYQKPGQSPKLLIYGASNRVTGVPDRFTGSGSANDFTLTISSVQAEDLADYHCGQSYSPYPLTFGAGTKLEIKR	38													
F6A_P12F12_L (1)	--DIVMSQSPSSSLAVSYGGERVMTSCRSSOSILYXSINQKN--YLAWYQKIPGQSPKLLIYWASTRESGVDPDRFTGSGGSDFTLTISSRVAEDLADLYCQYYTYPLTFGAGTKLEIKR	39													
F6B_P1_H5_L (1)	RCDIQMTQSPASLSVSGEIVTITCRASENIYN-----TLAWYQKQKSPQLLIYAATNLADGVPSRFGSGSGGTQYSLKINSIQSEDFGSYVCQHFHWGTPYTFGGGKLEIKR	40													
F6B1_P3_D12_L (1)	--QIVLTQSPAIMSASPEGEKVTITCSASSSVTS-----NYLYWYQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISMEAEADAASYFCHQWSSYPPTFGSGTKLEIKR	41													
F6B1_P3_B9_L (1)	--QIVLTQSPAIMSASPEGEKVTITCSASSSVTS-----NYLYWYQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISMEAEADAASYFCHQWSSYPPTFGSGTKLEIKR	41													
F6B_P2_D4_L (1)	--QIVLTQSPAIMSASPEGEKVTITCSASSSVSS-----NYLYWYQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISMEAEADAASYFCHQWSSYPPTFGSGTKLEIKR	42													
F6B1_P1_E2_L (1)	--QIVLTQSPAIMSASPEGEKVTITCSASSSVSS-----NYLYWYHQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISMEAEADAASYFCHQWSSYPPTFGSGTKLEIKR	43													
F6B_P3_E2_L (1)	--QIVLTQSPAIMSASPEGEKVTITCSASSSVSS-----NYLYWYHQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISMEAEADAASYFCHQWSSYPPTFGSGTKLEIKR	43													

LC F6B1P1E2=F6BP3E2
LC F6B1P3D12=F6B1P3E9

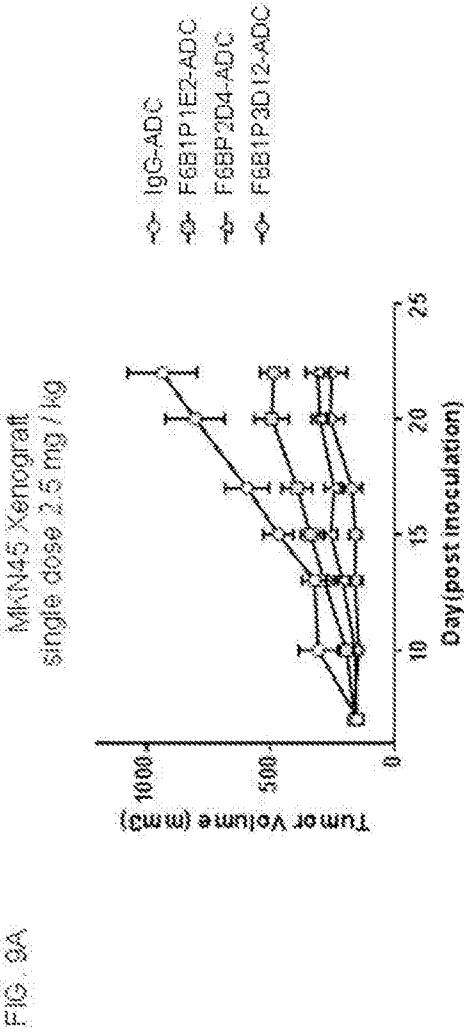
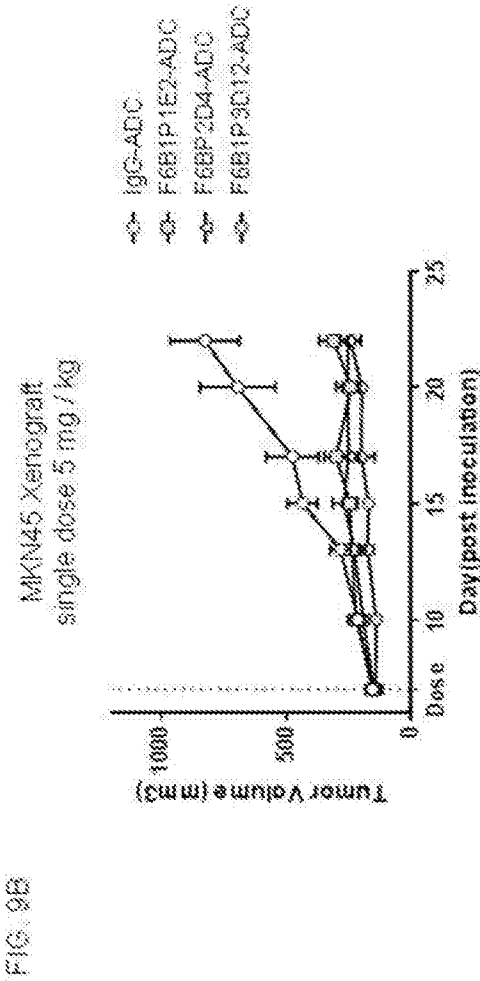
FIG. 8B

Heavy Chain

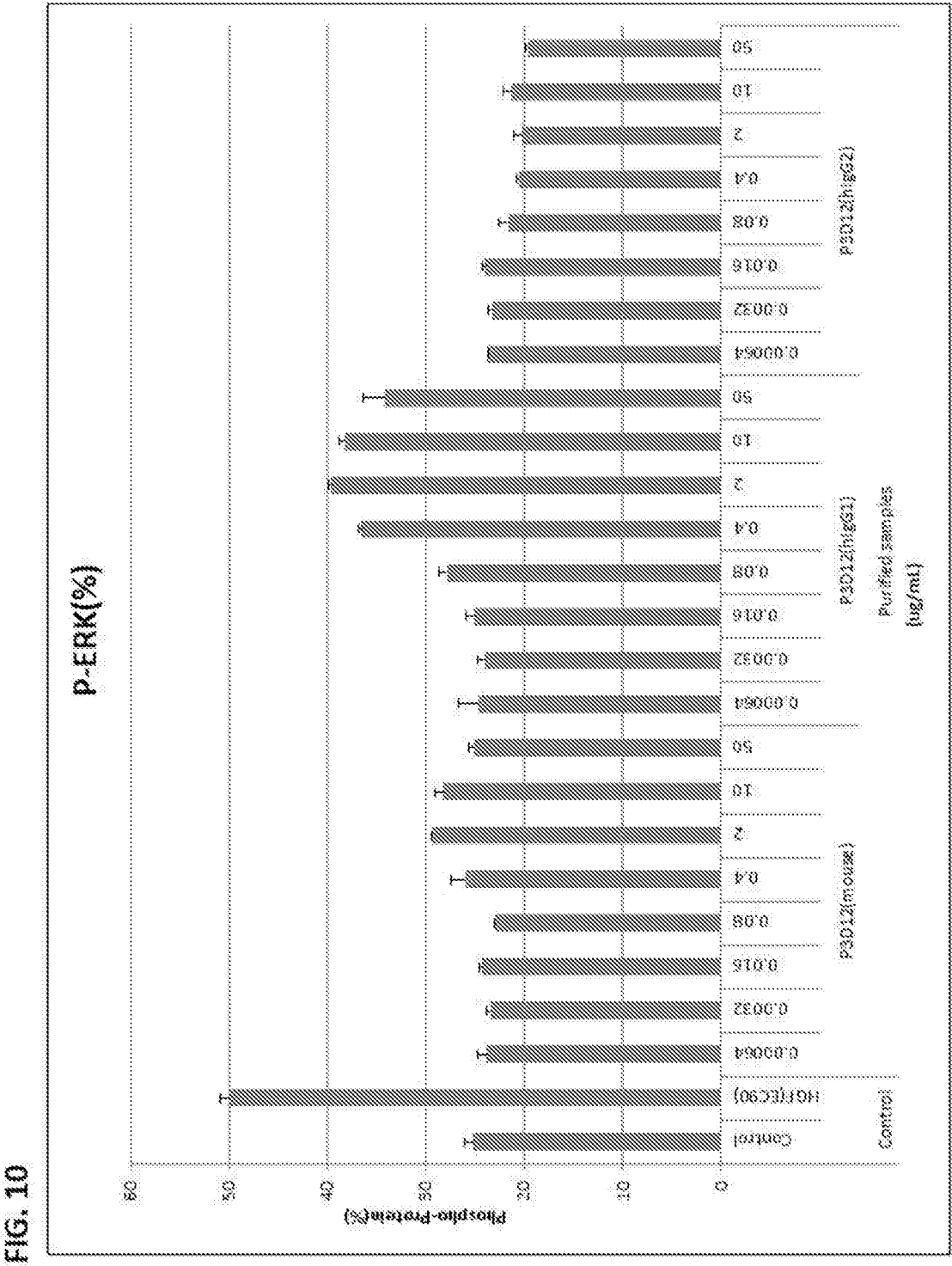
Heavy Chain		SEQ ID NO:	1	10	20	30	40	50	60	70	80	90	100	110	120	131
F5_P5_B9_H (1)	---	QVQLKESGPGLVAPFQSLSIQTCTVSGFSLTNYGAVNVRQPPGKGLWLGILWG---	94													
F6A_P12_F12_H (1)	---	EVLKVESGGGLVQPGGSLRLSCATSGFTFTDYIMSNVRQPPGKALEWLGFINNKANGYTTKYSASVKGRTISRDNSSQ---	95													
F6A_P8_E2_H (1)	VNSEVQLQSGAELVRPGALVKLSCKASGNINDYFMHWVQRPEQGLEWIGWIDP--	ENGNTIYDPKFPQKASITADTSN--TAYLQLSLTSEDTAVYCARGGNYLRSEYIYAMDYWGQGTSTVTVSS	96													
F6B_P1_H5_H (1)	VLSEVLLQSGPELVKPGASVKLPCKASGYTFTDYNMDVQKSHGKSLWIGDINP--	NNGGTIYNQKFKKATLITVDKSS--TAYMELSLTSEDTAVYRAGDYGSSRYIYAMDYWGQGTSTVTVSS	97													
F6B1_P3_D12_H_79_13 (1)	---	QVQLQSGAELAKPGASVRMSCRASGYTFTSYMHWVQRPGQGLDWIGYIRP--	98													
F6B1P3E9_H (1)	---	QVQLQSGAELAKPGASVRMSCRASGYTFTSYMHWVQRPGQGLDWIGYIRP--	99													
F6B1_P1_E2_H_78_19 (1)	---	QVQLQSGAELAKPGASVRMSCRASGYTFTSYMHWVQRPGQGLEWIGYINP--	100													
F6B_P3_E2_H (1)	---	QVQLQSGAELAKPGASVRMSCRASGYTFTSYMHWVQRPGQGLEWIGYINP--	101													
F6B_P2_D4_H (1)	---	QVQLQSGAELAKPGASVRMSCRASGYTFTSYMHWVQRPGQGLEWIGYINP--	102													

HC F6B1P3D12H7913=F6B1P3E9
HC F6B1P1E2H7819=F6B1P3E2

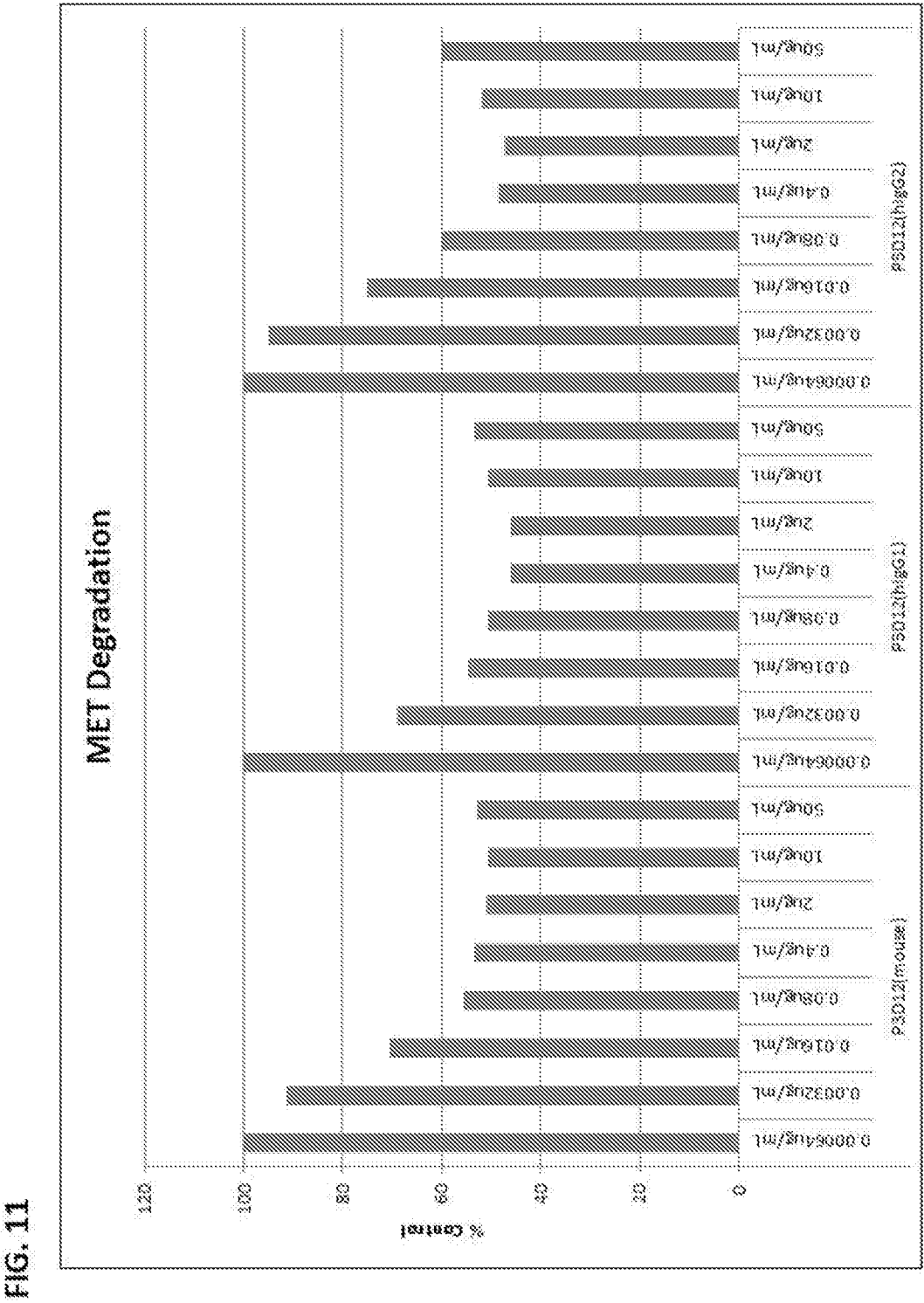
[Fig. 9]



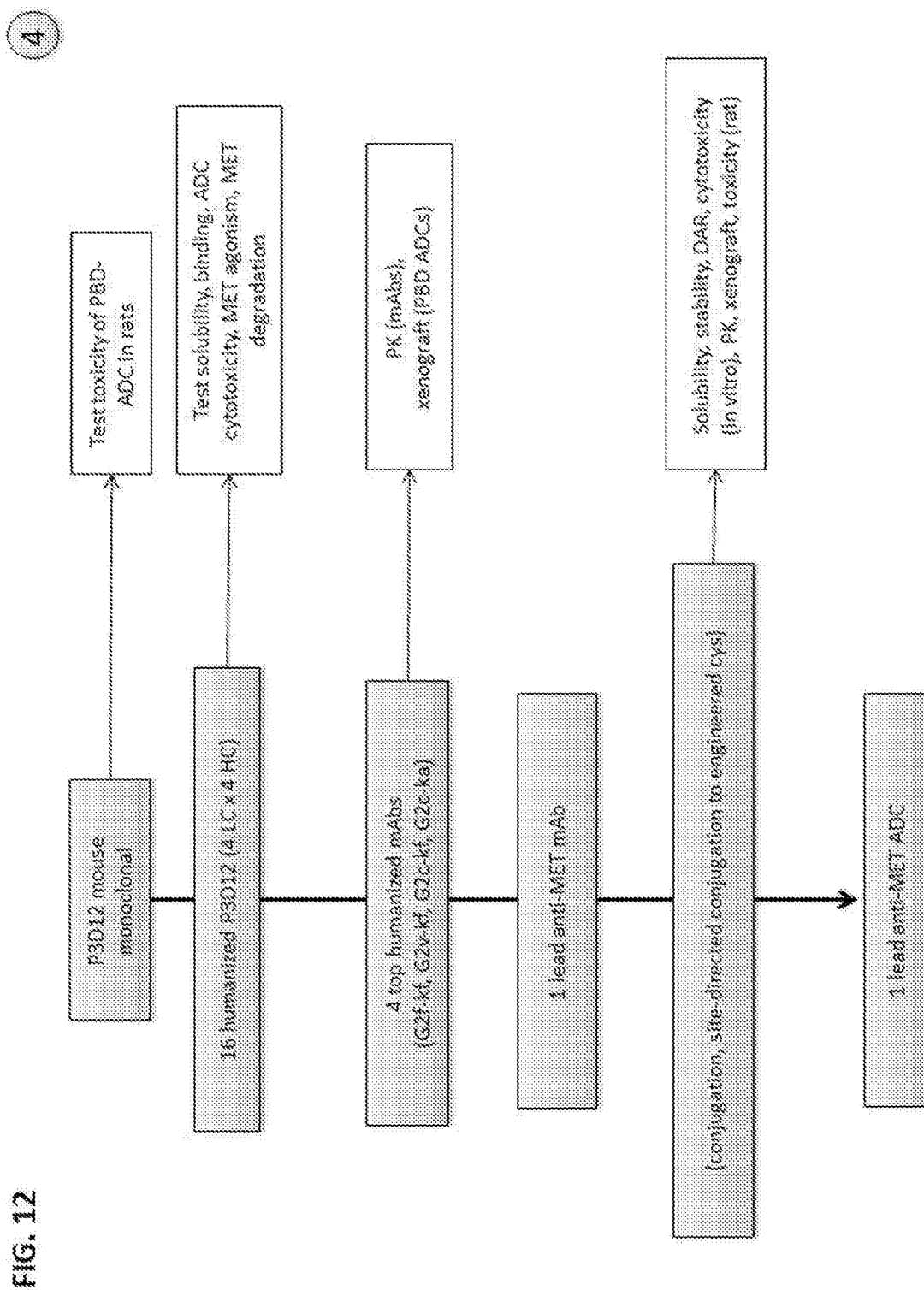
[Fig. 10]



[Fig. 11]



[Fig. 12]



[Fig. 13]

3

FIG. 13

HUMANIZED LIGHT CHAIN VARIABLE REGIONS

	SEQ ID NO.	1	50
P3D12 VL 45 (1)		QIVLTQSPAIMSASPGERKVTLTCSASSSVTSNYLYWYQQKPGSSPKLIY	
P3D12 VL-ven 46 (1)		QIVLTQSPATMSASPGERVTLSCASSSVTSNYLYWYQQKPGSSPKLIY	
P3D12 VL-fra 47 (1)		QIVLTQSPAILSLSPGERATILSCASSSVTSNYLYWYQQKPGSSPKLIY	
P3D12 VL-abb/sdr 48 (1)		QIVLTQSPATLSLSPGERATILSCASQSVTSNYLYWYQQKPGSSPKLIY	
P3D12 VL-cdr 49 (1)		QIVLTQSPATLSLSPGERATILSCASSSVTSNYLYWYQQKPGSSPKLIY	
		51	100
P3D12 VL (51)		STSNLASGVPARFSGSGCTSYSLTISSEAEADAASYFCHQWSSYPPTFG	
P3D12 VL-ven (51)		STSNLASGVPARFSGSGCTSYTLTISRMEPEDAASYFCHQWSSYPPTFG	
P3D12 VL-fra (51)		STSNLASGVPARFSGSGCTSYTLTISSEAEADAASYFCHQWSSYPPTFG	
P3D12 VL-abb/sdr (51)		STSNLASGVPARFSGSGCTDYTLTISRLEPEDFASYFCHQWSSYPPTFG	
P3D12 VL-cdr (51)		STSNLASGVPARFSGSGCTSYTLTISRLEPEDFASYFCHQWSSYPPTFG	
		101	
P3D12 VL (101)		SGTKLEIKR	
P3D12 VL-ven (101)		SGTKLEIKR	
P3D12 VL-fra (101)		SGTKLEIKR	
P3D12 VL-abb/sdr (101)		SGTKLEIKR	
P3D12 VL-cdr (101)		SGTKLEIKR	

[Fig. 14]

3

FIG. 14

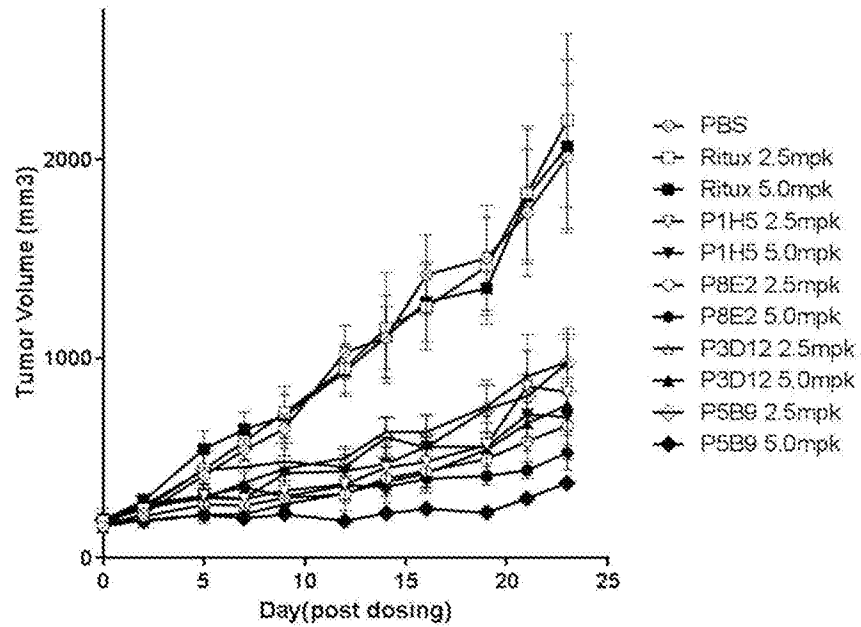
HUMANIZED HEAVY CHAIN VARIABLE REGIONS

SEQ ID NO.	1	50
P3D12 VH 104 (1)	QVQLQSGAEIAKPCASVKMSCHASGYTFTSYWMHWVKORPCQGLDNIGY	
P3D12 VH-fra 105 (1)	QVQLQSGAEVKKPCASVKVSKASGYTFTSYWMHWVKORPCQGLDNIGY	
P3D12 VH-ven 106 (1)	QVQLVQSGAEVAKPCASVKMSCHASGYTFTSYWMHWVKQAPCQGLDNIGY	
P3D12 VH-abb/sdr 107 (1)	QVQLVQSGAEVKKPCASVKVSKASGYTFTSYWMHWVKQAPCQGLDNMGY	
P3D12 VH-cdr 108 (1)	QVQLVQSGAEVKKPCASVKVSKASGYTFTSYWMHWVKQAPCQGLDNIGY	
	51	100
P3D12 VH (51)	IKPSTDNTEYNQKFHKDKATILTADKSSSTAYMQLSSLTSEISAVYYCARSY	
P3D12 VH-fra (51)	IKPSTDNTEYNQKFHDRVTILTADKSTSTAYMQLSNLISEDTAVYYCARSY	
P3D12 VH-ven (51)	IKPSTDNTEYNQKFHKDKATILTADKSTSTAYMQLSSLRSEDTAVYYCARSY	
P3D12 VH-abb/sdr (51)	IKPSTDNTEYAAQKFCQRRVTILTADKSTSTAYMELSSLRSEDTAVYYCARSY	
P3D12 VH-cdr (51)	IKPSTDNTEYNQKFHKDKATILTADKSTSTAYMELSSLRSEDTAVYYCARSY	
	101	119
P3D12 VH (101)	GNYPFLMDYWGCGTSVTVSS	
P3D12 VH-fra (101)	GNYPFLMDYWGCGTSVTVSS	
P3D12 VH-ven (101)	GNYPFLMDYWGCGTTVTVSS	
P3D12 VH-abb/sdr (101)	GNYPFLMDYWGCGTTVTVSS	
P3D12 VH-cdr (101)	GNYPFLMDYWGCGTTVTVSS	

[Fig. 15]

FIG. 15

MKN-45 xenograft



[Fig. 16]

FIG. 16

MET Binding ELISA

