

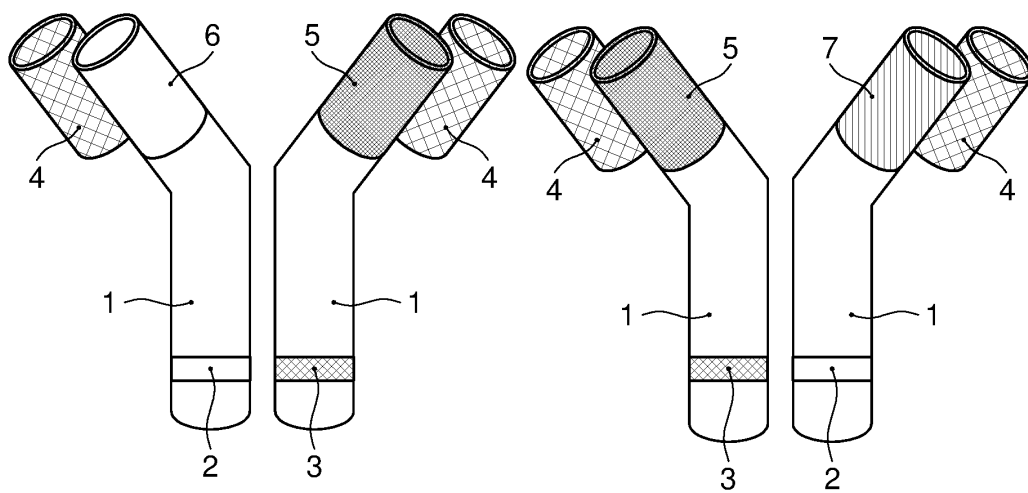


Fig. 1

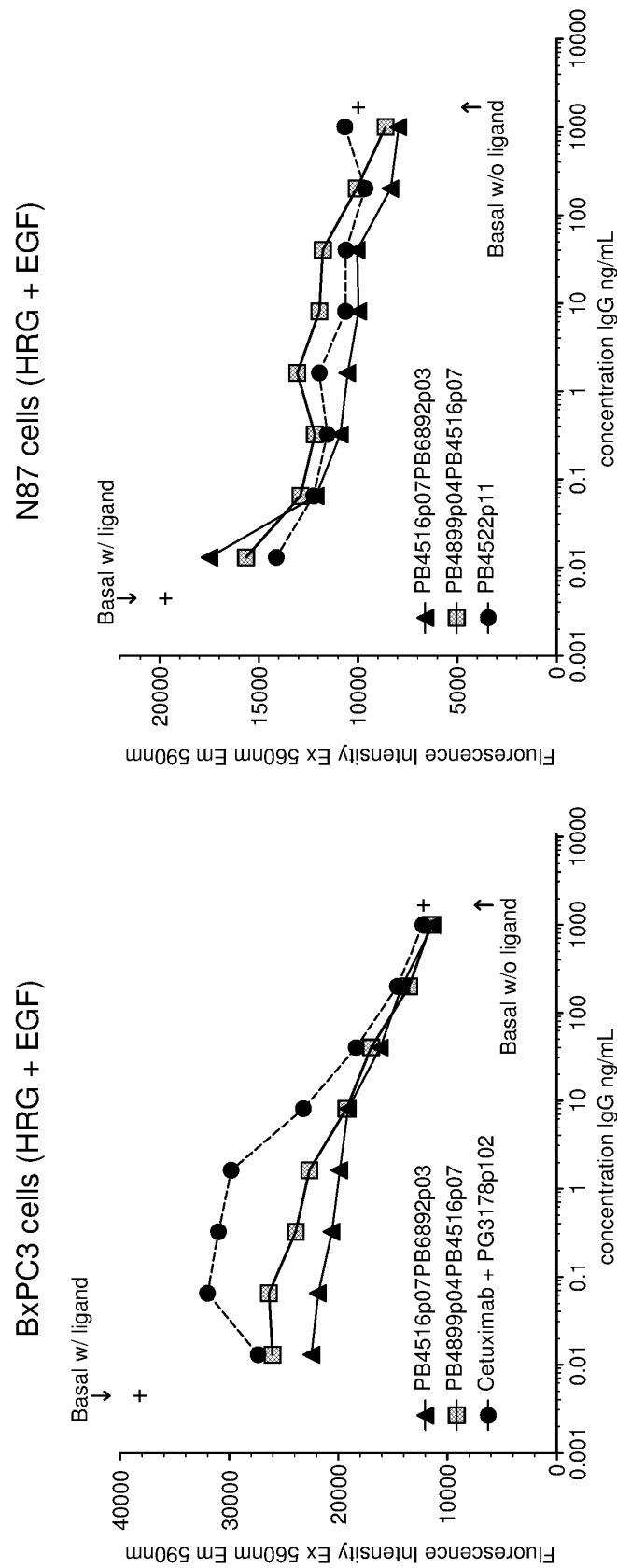


Fig. 2

ADCC Reporter Assay N87 Cells

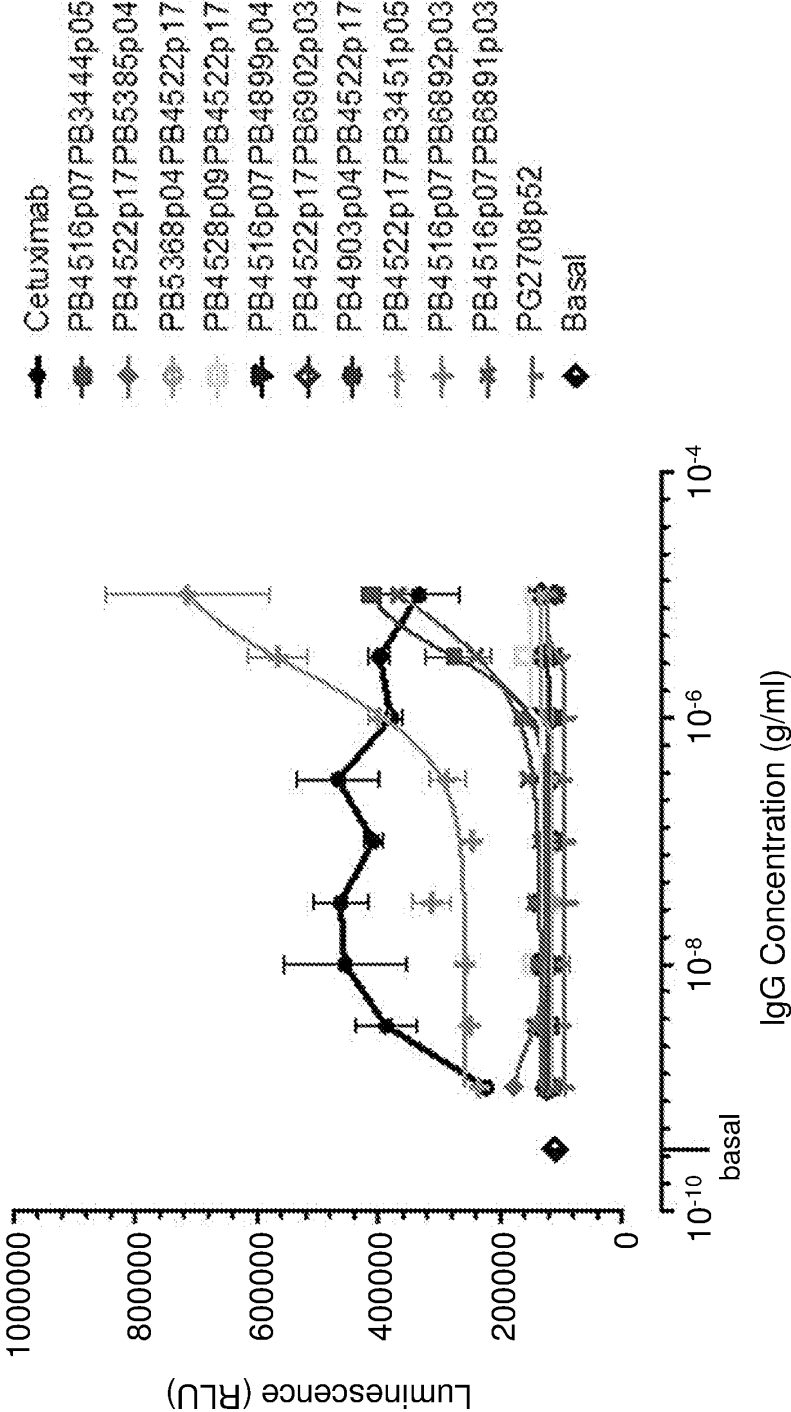


Fig. 3

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Fig. 4

A

Nb	Oligoclonic						ADCC activity	
	Bispecific 1	MF A	MF B	Bispecific 2	MF A	MF C	N87	BxPC3
1	PB4522	3178	4280	PB3451	3178	1871		
2	PB4522	4280	3178	PB6902	4280	1871		
3	PB4516	3755	3178	PB6891	3755	1847	++	
4	PB4516	3755	3178	PB6892	3755	1849	+++	
5	PB4528	3178	4003	PB4522	3178	4280		++
6	PB4522	3178	4280	PB5385	3178	4016		
7	PB4516	3755	3178	PB4899	3755	2703		

B

Bispecific	MF	MF
PB3444	3178	1847
PB5368	3178	4000
PB4903	2703	4290
PB11244	3755	2032

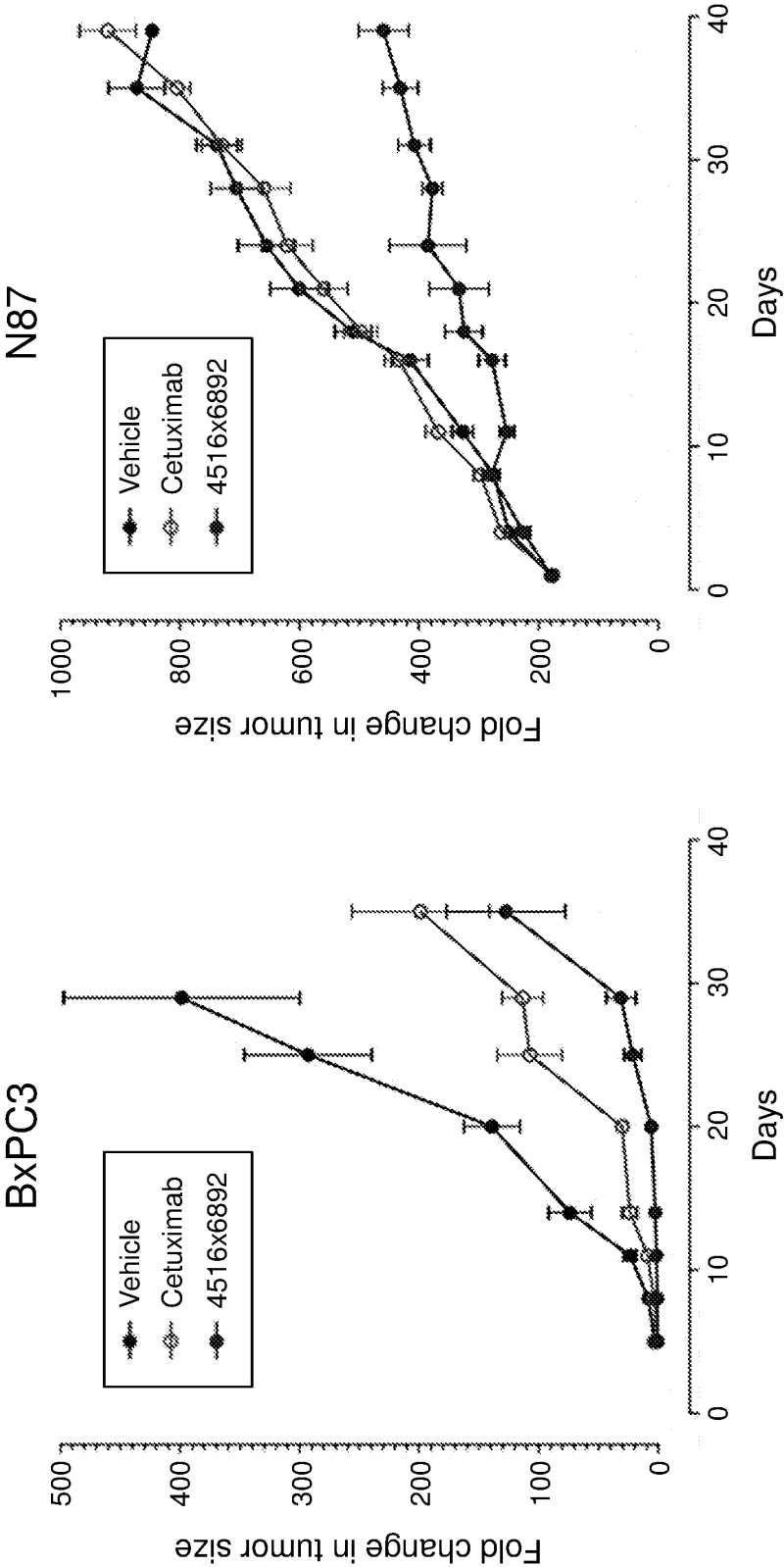


Fig. 5

GA0023

PDX Model	ERBB2	EGFR	ERBB3	NRG1	ERBB2 copy number	KRAS mut.	EGFR mut.	Cetuximab sensitivity	Trastuzumab sensitivity
GA0023-P5	4.28	1.18	5.16	-1.45	3			Res.	

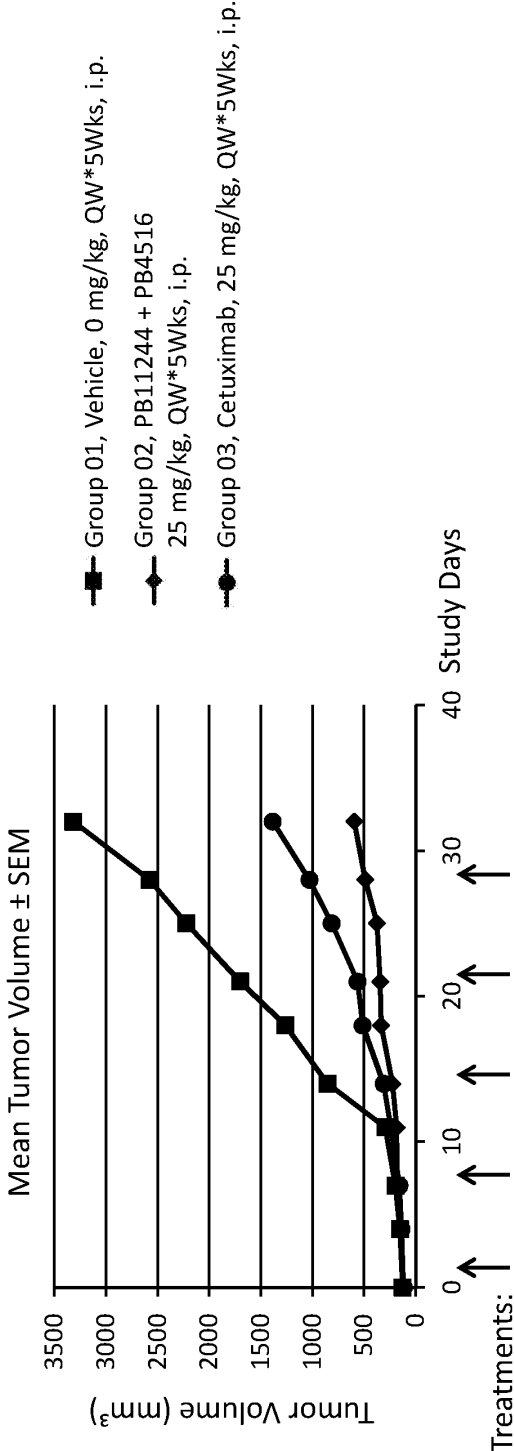


Fig. 6A

LU1206

PDX Model	ERBB2	EGFR	ERBB3	NRG1	ERBB2 copy number	KRAS mut.	EGFR mut.	Cetuximab sensitivity	Trastuzumab sensitivity
LU1206-P6	4.77	5.95	3.73	-0.11	3		R521K, W477fs	Res.	

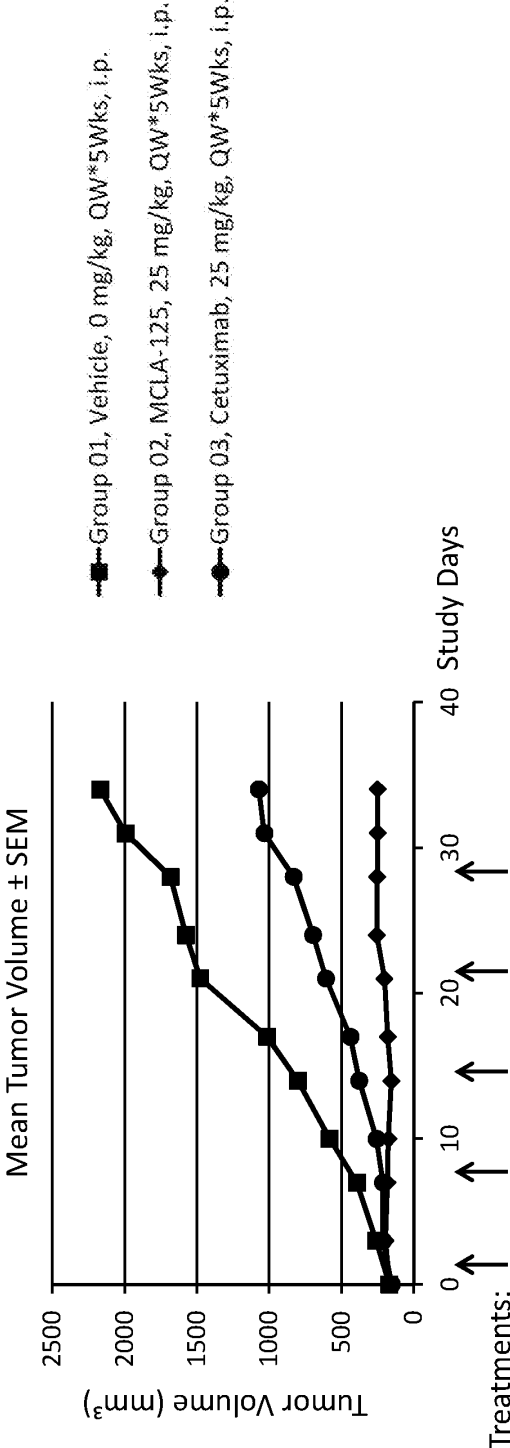


Fig. 6B

GA0055

PDX Model	ERBB2	EGFR	ERBB3	NRG1	ERBB2 copy number	KRAS mut.	EGFR mut.	Cetuximab sensitivity	Trastuzumab sensitivity
GA0055-P5	7.15	1.64	5.83	-2.57	14		R521K	Res.	Res.

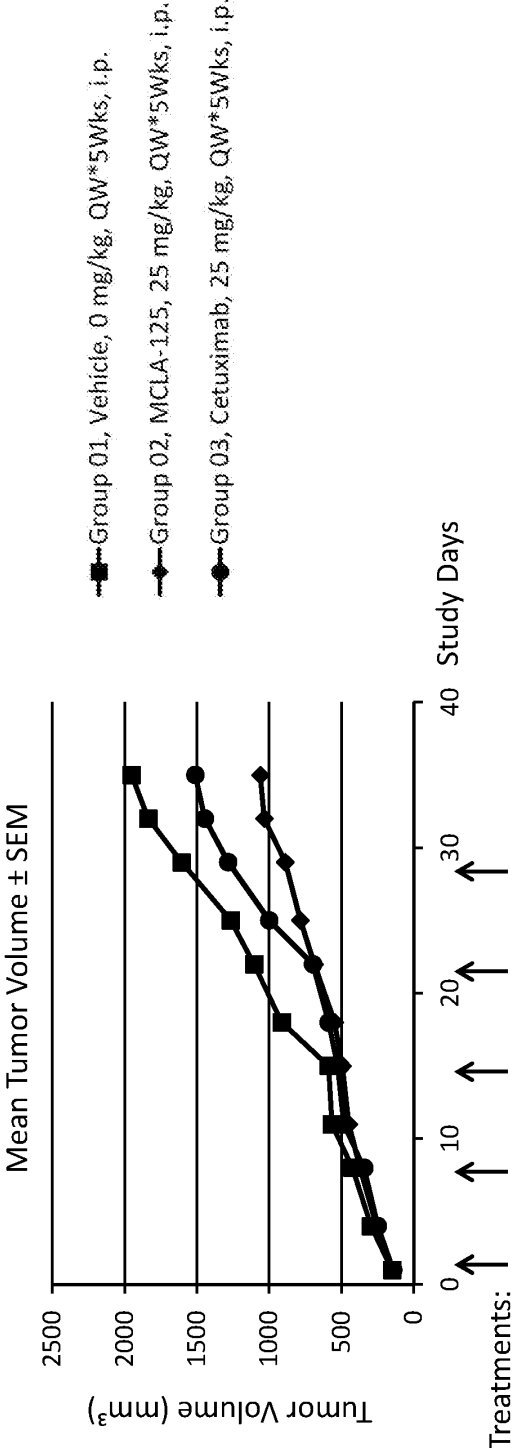


Fig. 6C

LU00009

PDX Model	ERBB2	EGFR	ERBB3	NRG1	ERBB2 copy number	KRAS mut.	EGFR mut.	Cetuximab sensitivity	Trastuzumab sensitivity
LU0009-P5	3.00	3.15	3.64	2.96	5			Part. Sens.	

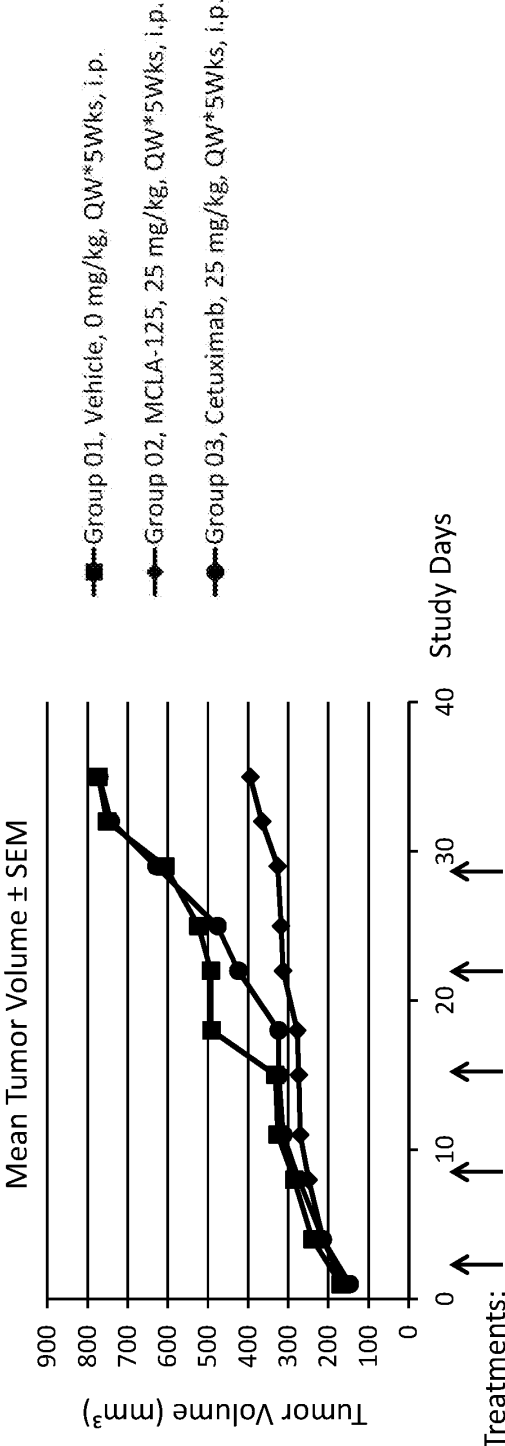


Fig. 6D

ES0026

PDX Model	ERBB2	EGFR	ERBB3	NRG1	ERBB2 copy number	KRAS mut.	EGFR mut.	Cetuximab sensitivity	Trastuzumab sensitivity
ES0026-P5	4.42	6.63	3.54	2.52	3			Part. Sens.	

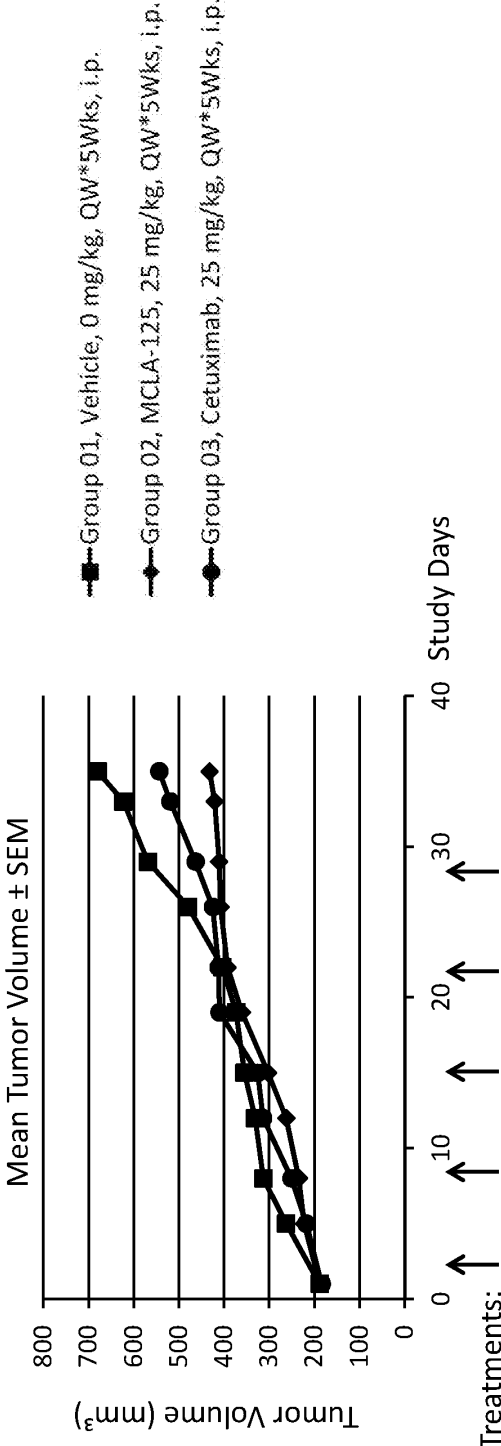


Fig. 6E

LU0357

PDX Model	ERBB2	EGFR	ERBB3	NRG1	ERBB2 copy number	KRAS mut.	EGFR mut.	Cetuximab sensitivity	Trastuzumab sensitivity
LU0357-P6	4.02	3.80	3.66	3.14	2		N528D	Part. Sens.	

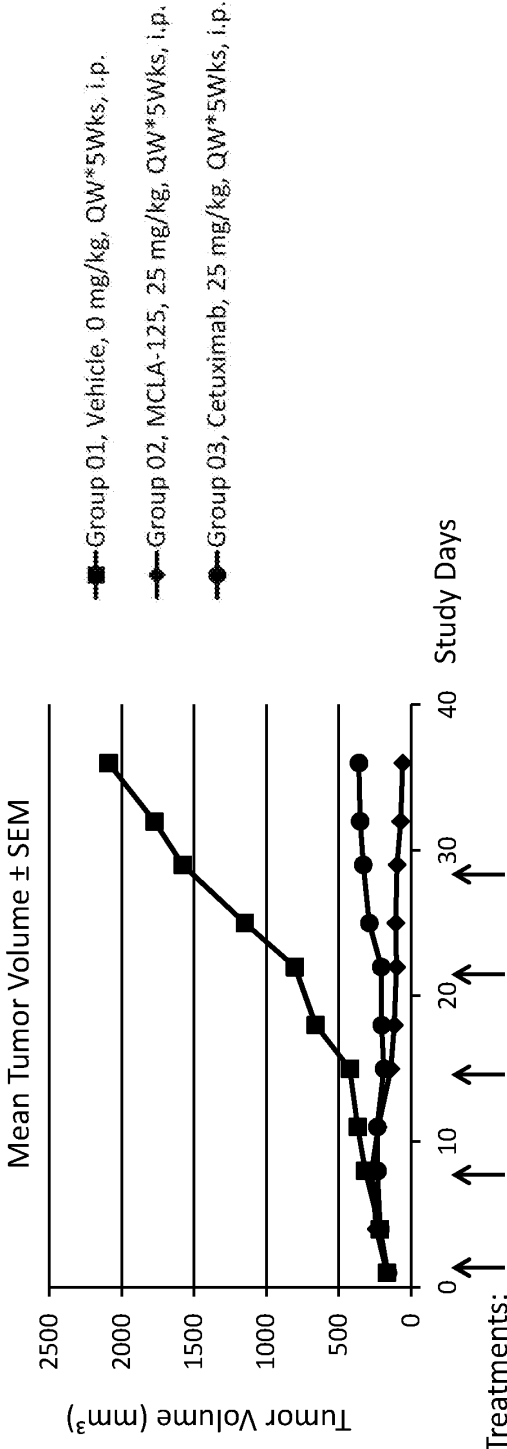


Fig. 6F

GA0006

PDX Model	ERBB2	EGFR	ERBB3	NRG1	ERBB2 copy number	KRAS mut.	EGFR mut.	Cetuximab sensitivity	Trastuzumab sensitivity
GA0006-P7	7.93	1.45	4.46	-2.90	14		R521K	Res.	Res.

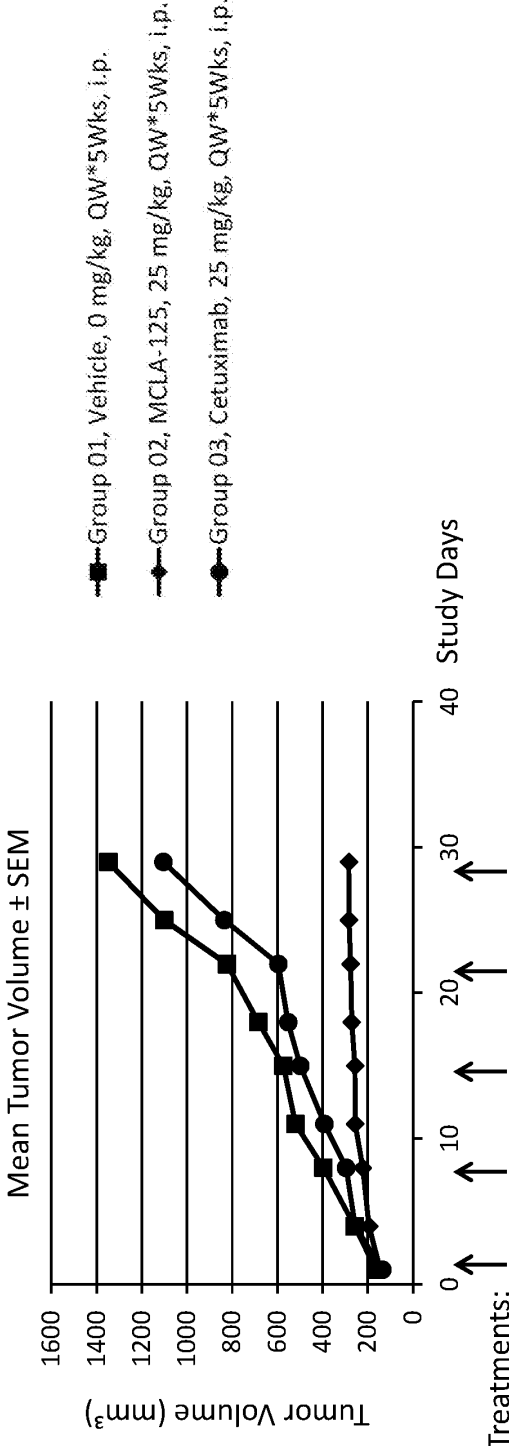


Fig. 6G

GA0151

PDX Model	ERBB2	EGFR	ERBB3	NRG1	ERBB2 copy number	KRAS mut.	EGFR mut.	Cetuximab sensitivity	Trastuzumab sensitivity
GA0151-P6	4.74	2.43	5.27	2.58	3		R521K	Res.	

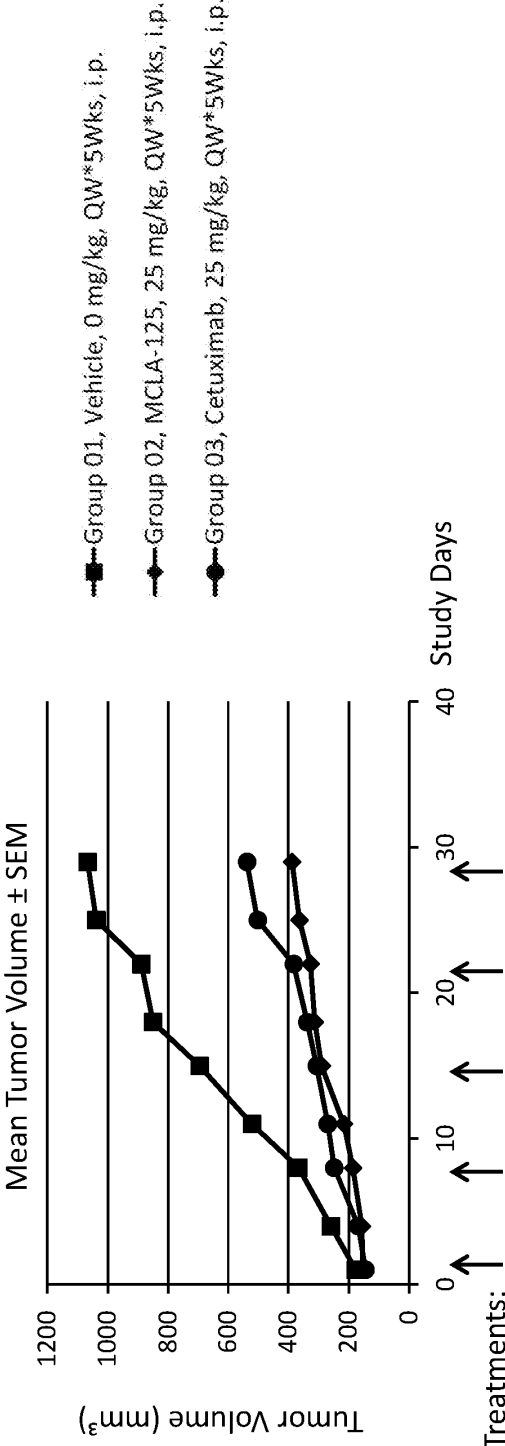


Fig. 6H

ES0172

PDX Model	ERBB2	EGFR	ERBB3	NRG1	ERBB2 copy number	KRAS mut.	EGFR mut.	Cetuximab sensitivity	Trastuzumab sensitivity
ES0172-P6	5.39	3.35	5.08	1.14	4		R521K	Res.	

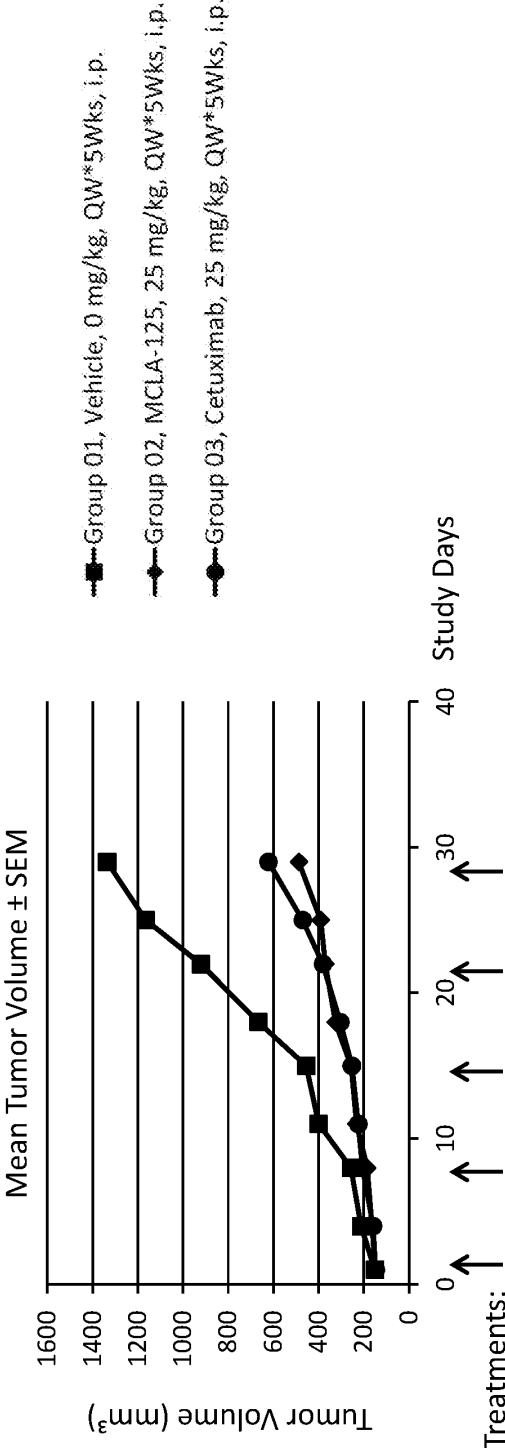


Fig. 6I

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Fig. 7

Amino acid sequences of the heavy chain variable regions of the various variable domains indicated by the MF number SEQ ID NO: 1-21 and the CDRs and light chain variable regions of SEQ ID NO: 22-27.

SEQUENCE LISTING SUMMARY

1	HER3-MF3178	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGGLEWMGWINPN SGGTNYAQKFQGRVTMTSDTSISTAYMELSLRSLRSDTAVYYCARDHGSRHFWSY WGFYWGQGTILVTVSS
2	HER2-MF1849	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYD GSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGDYGSYSSYA FDYWGQGTILVTVSS
3	EGFR-MF3755	QVQLVQSGSELKKPGASVKISCKASGYDFTNYAMNWVRQAPGHGLEWMGWINAN TGDPTYAQGFTGRFVFLSDTSVSTAYLQISSLKAEDSAVYYCTRERFLEWLHFD YWGQGTILVTVSS
4	EGFR-MF4280	QVQLVQSGAEVKKPGASVKVSCKASGYTLTSLMHWVRQAPGKGLEWMGGFDPE YKTFFAQNFQGRVTMTEDTSADTAYMELSSLRSED TAVYYCATEGYYETTTY YNLFDSWGQGTILVTVSS
5	EGFR-MF4003	QVQLVQSGSELKKPGASVKVSCKASGYTFPSFAMNWLQAPGGLEWMGWITTN TGDPTYAQGFSGRFVFLSDTSVSTAYLQISSLKAEDTAVYYCARVYNWIRGFDY WGQGTILVTVSS
6	HER2-MF2032	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYD GSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDYYRRTARAG FDYWGQGTILVTVSS
7	VL CDR1	QSISSY
8	VL CDR2	AASSLQS
9	VL CDR3	QQSYSTP
10	IgVk1-39*01	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP
11	Common Light Chain IgKV1*39/jk1	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYSTPPTFGQGTKVEIK
12	Common Light Chain IgKV1*39/jk5	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPK LLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ SYSTPPTFGQGTIRLEIK
13	IgG1 CH1 Hinge	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRV EPKSCDKHTCPCP
14	IgG1 CH2	APELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISK AK
15	IgG1 CH3 KK	GQPREPQVYTKPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
16	IgG1 CH3 DE	GQPREPQVYTKPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

MF Nr :	Specificity	VH sequence
3755	EGFR	QVQLVQSGSELKPKGASVKISCKASGYDTNYYAMNWVRQAPGQGLEWMGWINANTGDDITYAQGFTGRVFLSDTSVSTAYLIQISSIKAEKDSAVYYCTRERFLEWLFHFDYWGQGLITVTSS
3178	HER3	QVQLVQSGAEVRKPKGASVKVSKCKASGYTFGYIMHWVRQAPGQGLEWMGWINPNSGGNTNYAKQFCQVMTTRDTSISTAYMELSRISGSDTAVYYCARDHGSRIHFYSWGFYWGQGLITVTSS
1847	HER2	QVQLVESGGGVQPKRSIRLSCAASGFTSSYGIMHWVRQAPGKGLEWVAISYDGSNKYYADSVKGRFTISRDNSKNTLIYMQMNSIRAEADTAVYYCAKGWHPILSGDFYWGQGLITVTSS
1849	HER2	QVQLVESGGGVQPKRSIRLSCAASGFTSSYGIMHWVRQAPGKGLEWVAISYDGSNKYYADSVKGRFTISRDNSKNTLIYMQMNSIRAEADTAVYYCAKGRDYSGSYSAFDYWGQGLITVTSS
1871	HER2	EVQLVQSGAEVRKPKGSIRLISCKGSGYFTSWIGVRQMPKGLIEWMGIYPGSDSTRYSFSGQVITIYSGADKSISTAYLIQWSSIKASDIAVCGRVDILMWYGFDFYWGQGLITVTSS
2032	HER2	QVQLVESGGGVQPKRSIRLSCAASGFTSSYGIMHWVRQAPGKGLEWVAISYDGSNKYYADSVKGRFTISRDNSKNTLIYMQMNSIRAEADTAVYYCAKDYVRRRTARAGDFYWGQGLITVTSS
4280	EGFR	QVQLVQSGAEVRKPKGASVKVSKCKVSGYTLITELISMHWVRQAPGKGLEWMGDPPEYKGTFFAQNFCQVMTMETDSADTAYMELSSIRAEADTAVYYCATEGYETITTYTNYIFDSWGQGLITVTSS
4003	EGFR	QVQLVQSGSELKPKGASVKVSKCKASGYTFPSFAMNLIHQAPGQGLEWMGWIITNTDGSYIYADSVKGRFTISRDNAKNSIYIYQMSIRADDTAVYYCARGVCAPIAFDIWGQGLITVTSS
4000	EGFR	EVQLVESGGGLVQPKGSIRLSCAASGFTFNSYSIIHWVRQAPGEGLEWYSFISSSSEYIYADSVKGRFTISRDNAKNSIYIYQMSIRADDTAVYYCARGVCAPIAFDIWGQGLITVTSS
4290	EGFR	QMQVLVQSGAEVRKPKGASVKVSKCKISGYTLITELISMHWVRQAPGKPEWMGDPPEYKGTFFAQNFCQVMTMETDSADTAYMELSSIRAEADTAVYYCATEGYETITTYTNYIFDYWGQGLITVTSS
4016	EGFR	EVQLVESGGDLVQPKGSIRLSCAASGFTSSYAMNWVRQAPGKGLEWVAISYDGSNSTYADSVKGRFTISRDNSKNTLIYMQMNSIRAEADTAVYYCAKPNYVGGSGSPHYFYMVGKGTITVTSS
2703	HER3	EVQLVESGGGLVQPKGSIRLSCAASGFTSSYAMSWVRQAPGKGLEWYSYTSFGDNTNYADSVKGRFTISRDNSKNNIYLQMSIRAEADTAVYYCAKSDSYSSGHWYGFPTDYFDYWGQGLITVTSS
2708	HER3	EVQLVESGGGVQPKRSIRLSCAASGFTSNYGMHWVRQAPGKGLEWVAISYDGSNTKYASDLKGRFTISRDNSKNTLIYMQMNSIRADDTAVYYCAREKWSFDSSGYSRWFDSWGQGLITVTSS
1337	Tetanus toxoid	EVQLVETGAEVRKPKGASVKVSKCKASDYIFTKYDINWVRQAPGQGLEWMGWSANTGNTGTYAQKFGQVMTTRDTSINTAYMELSSLTSGDTAVYFCARSLFKTETAPYYHFALDVMGQGLITVTSS
MF Nr :	Specificity	VH sequence
3755	EGFR	QVQLVQSGSELKPKGASVKISCKASGYDFTNYAMNIWVRQAPGQGLEWMGWINANTGDDITYAQGFTGRVFLSDTSVSTAYLIQISSIKAEKDSAVYYCTRERFLEWLFHFDYWGQGLITVTSS
3178	HER3	QVQLVQSGAEVRKPKGASVKVSKCKASGYTFTGYIMHWVRQAPGQGLEWMGWINPNSGGNTNYAKQFCQVMTTRDTSISTAYMELSRISGSDTAVYYCARDHGSRIHFYSWGFYWGQGLITVTSS
1849	HER2	QVQLVESGGGVQPKRSIRLSCAASGFTSSYGIMHWVRQAPGKGLEWVAISYDGSNKYYADSVKGRFTISRDNSKNTLIYMQMNSIRAEADTAVYYCAKGWHPILSGDFYWGQGLITVTSS
2032	HER2	QVQLVESGGGVQPKRSIRLSCAASGFTSSYGIMHWVRQAPGKGLEWVAISYDGSNKYYADSVKGRFTISRDNSKNTLIYMQMNSIRAEADTAVYYCAKGRDYSGSYSAFDYWGQGLITVTSS
1337	TT	EVQLVETGAEVRKPKGASVKVSKCKASDYIFTKYDINWVRQAPGQGLEWMGWINANTGNTGTYAQKFGQVMTTRDTSINTAYMELSSLTSGDTAVYFCARSLFKTETAPYYHFALDVMGQGLITVTSS



Fig. 9A

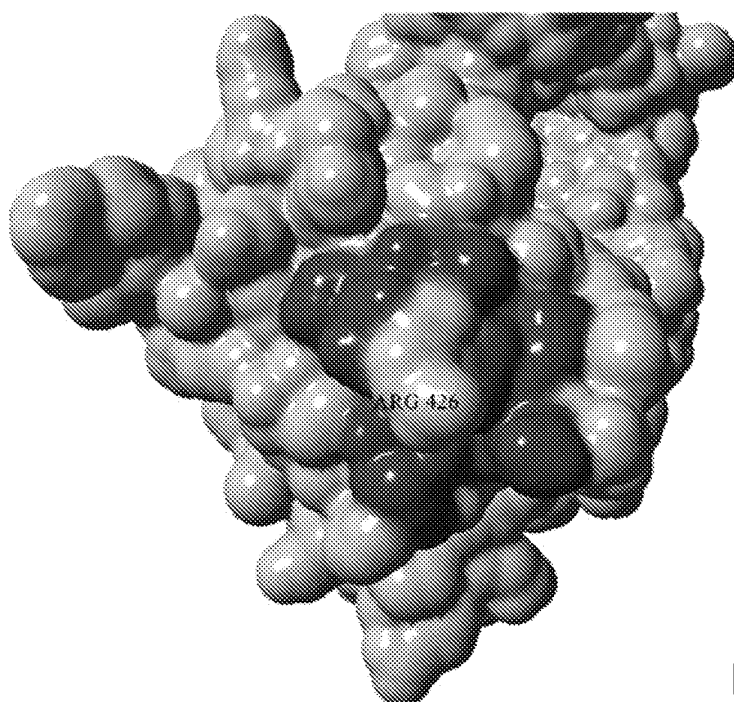


Fig. 9B

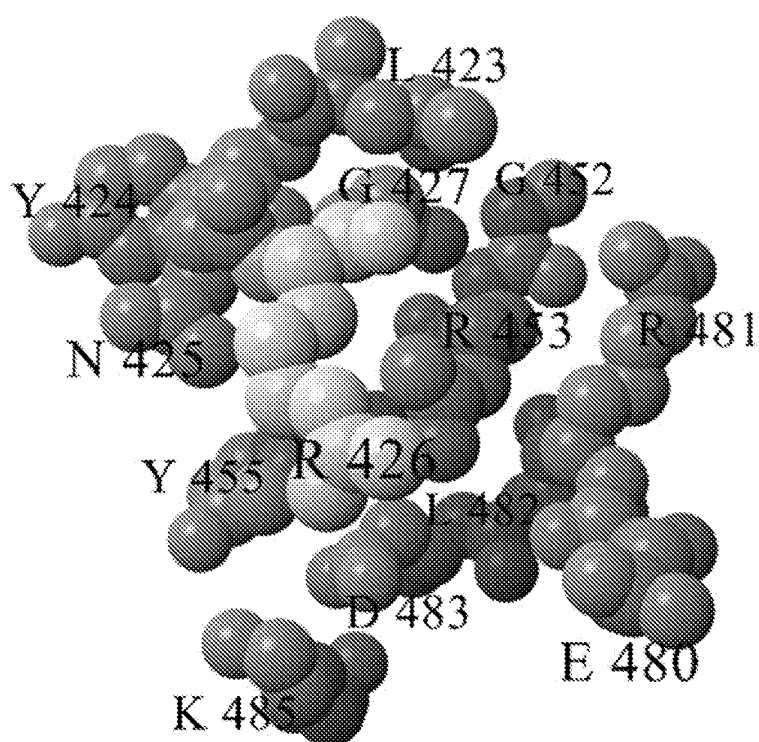


Fig. 9C