

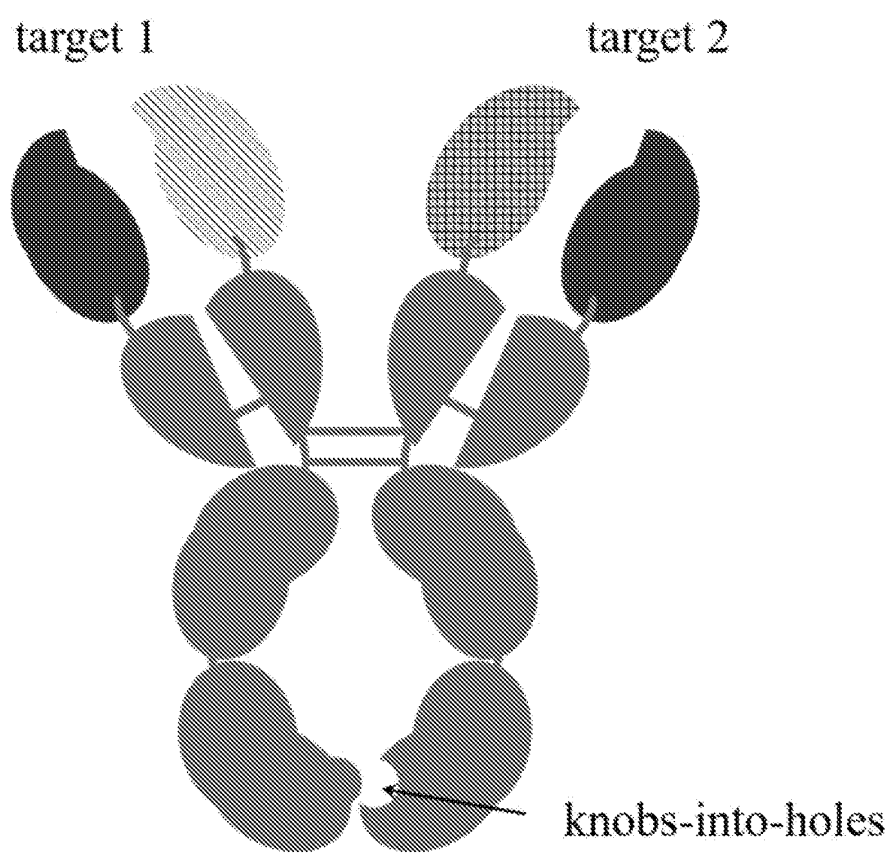


FIG. 1

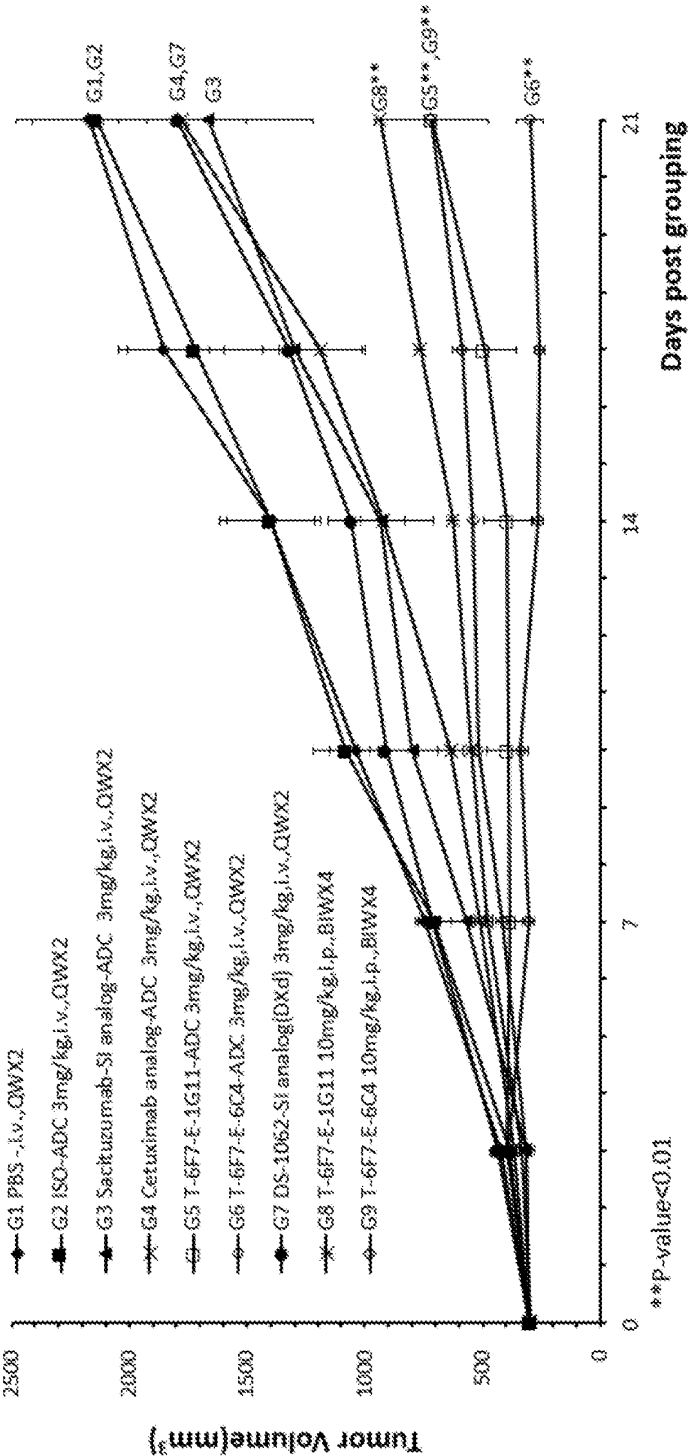


FIG. 2

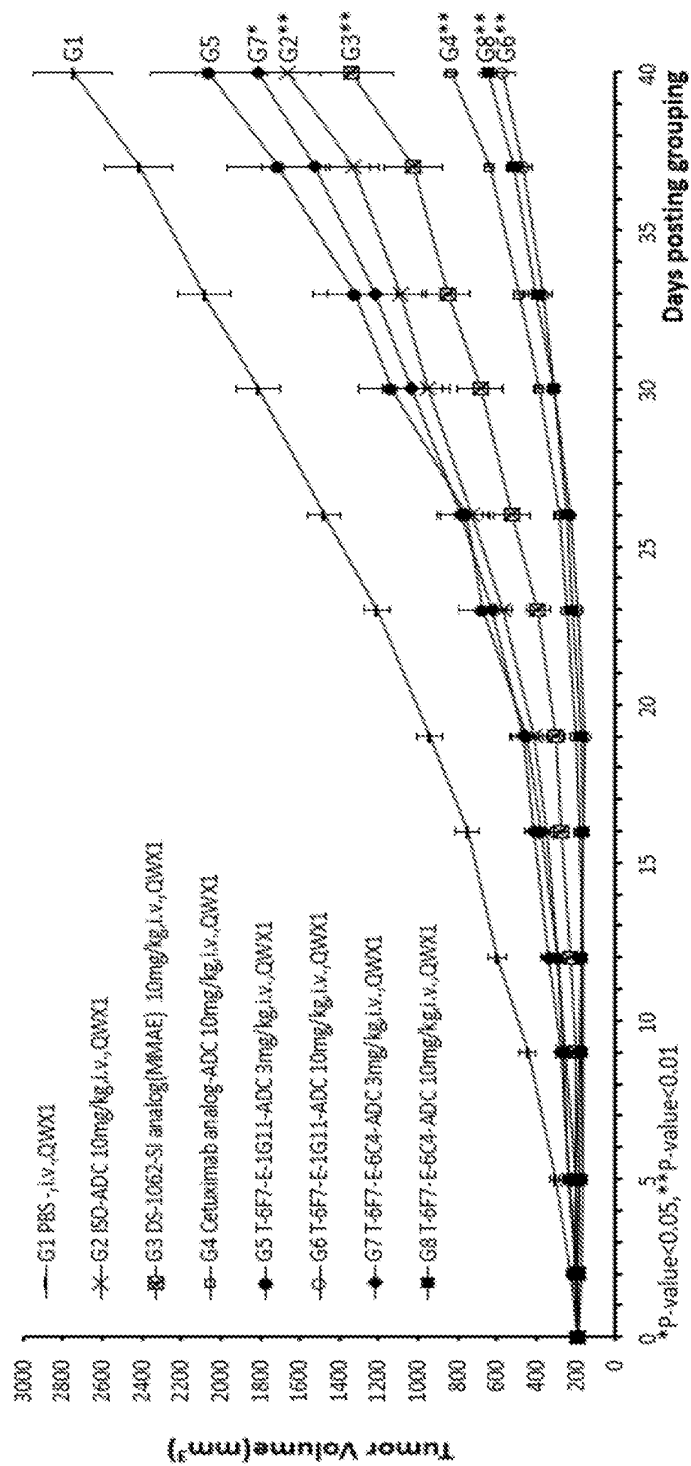


FIG. 3

Kabat CDR in anti-TROP2/EGFR antibodies

Ab	VH CDR1	SEQ ID NO:	VH CDR2	SEQ ID NO:	VH CDR3	SEQ ID NO:
T-6F7	SGYYWG	4	SIYIGTTYIYPSLKS	5	QPITVAGHDAFDI	6
E-1G11	SYEMN	7	YISSAGSTIYYADSVKG	8	VWYSSGWSGCFAY	9
E-6C4	SGDYWS	10	YIYSGSTYYNPSLKS	11	ERVYSSSLDY	12

FIG. 4

Chothia CDR in anti-TROP2/EGFR antibodies

Ab	VH CDR1	SEQ ID NO:	VH CDR2	SEQ ID NO:	VH CDR3	SEQ ID NO:
T-6F7	GGSIDSGYY	13	YYIGT	14	QPITVAGHDAFDI	15
E-1G11	GFTFSSY	16	SSAGST	17	VWYSSGWSGCFAY	18
E-6C4	GGSINSGDY	19	YYSGS	20	ERVYSSSLDY	21

FIG. 5

Kabat and Chothia CDR for common light chain

Ab	VL CDR1	SEQ ID NO:	VL CDR2	SEQ ID NO:	VL CDR3	SEQ ID NO:
Common light chain	RASQSVSYLA	1	DASNRAT	2	QQRSNWPPT	3

FIG. 6

Ab	Description	Amino acid sequence	SEQ ID NO:
Common light chain	light chain variable region in anti-TROP2/EGFR antibodies	EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPKGQAPRLIYDASNRATGIPARFSGSGGTDFLTITSSLEPEDFAVYYCQQRSNWPPTEGGQTKVEIK	22
E-1G11	heavy chain variable region in anti-TROP2/EGFR antibodies	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGMGLEWVSYISAGSTIYVADSVKGRFTISRDNAMNSLYLEMNLSRAEDTAVYYCVRVWYSSGWSGCFAYWGQGSLVTVSS	23
E-6C4	heavy chain variable region in anti-TROP2/EGFR antibodies	QVQLQQWGPGLVKPQSQTLSLTCTVSGGSINSGDYYWSWIRQPPGKGLESIGYIYSGSTIYNPSLKSRTISADTSKNQFSKLTSVTAADTAVYYCARERYVSSSLDYWGQGTLLVTVSS	24
T-6F7	heavy chain variable region in anti-TROP2/EGFR antibodies	EVQLVQSGPGLVKPSETLSLTCTVSGGSIDSGYYWGWIQQPPGKGLEWIGSIYIYGTYYIPSLKSRTISVDTSKNRFSKLTSVTAADTAVYYCARQPIVAGHDAFDIWGQGTMTVTVSS	25

FIG. 7

FIG. 8

Name/Description	Amino acid sequence	SEQ ID NO:
Common light chain constant region	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSLTLSKA DYEKHKVYACEVTHQGLSPVTKSNRGECC	26
IgG1 heavy chain constant region with knob	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCVMHEALHNHYTQKSLSLSPGK	27
IgG1 heavy chain constant region with hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPSSREEMTKNQVSLCAVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCVMHEALHNHYTQKSLSLSPGK	28
Cetuximab heavy chain (HC)	QVQLKQSGPGLVQPSSLSITCTVSGFSLTNYGVHWVRQSPGKGLWLVGVWGGNTDYNTPFTRLSINKDNSK SQVFFKMNSLQSNDAIYCARALTYDYEFAYWGGQGLTVTVAASATKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKTHCTC PPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK	29
Cetuximab light chain (LC)	DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLIKYASESISGPSRFSGSGSGTDFTLINSVSE DIADYYCQNNNNWPTTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSYLSLSLTLSKADYEKHKVYACEVTHQGLSPVTKSNRGECC	30
Sacituzumab-S1 analog HC	QVQLQQSGSELKPGASVKVCKASGYTFNTYGMNHWVKAAPGQGLKWMGMWINTYTGTEPTTDDFKGRFAFSL DTSVSTAYLQISLKADDTAVYFCARGGFGSSYWFVDVWGQGSLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCD KTHCTCPCPAPPELLGGPDVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQY	31

	NSTVRVSVLTVLHQDWLNGKEYCKVSNKALPAPKEETISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK	
Sacituzumab-5J analog LC	DIQLTQSPSSLSASVGDGRVSIITCKASQDVSIJAVAWYQQKPGKAPKLLIYSASVRYTGVPDRFSGSGSGTDFTLTISL QPEDFAVYCCQHQHTPLTFGAGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC	32
DS-1062 HC	QVQLVQSGAEVKKPGASVKVSCKASQYFTFTAGMQWVRQAPGQGLEWMGWINTHSGVPKYAEDEFKGRVTISA DTSTAYLQLSLKSEDTAVVYCARGSGSSVWFYEDVWGQGTITVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCL VKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDK THTCPPCPAPPELLGGPDVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPKEETISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK	33
DS-1062-S1 LC	DIQMTQSPSSLSASVGDRTITTCASQDVSTAVAWYQQKPGKAPKLLIYSASVRYTGVPDRFSGSGSGTDFTLTISL QPEDFAVYCCQHQHTPLTFGQGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC	34
MIRG003 HC	QVQLQESGPGLVKPSETLSLTCTVSGFSLSNVDVHWVRQAPGKGLEWILGVWSSGNTDYNTPFTSRLTISVDTSK NQFSLKLSSTVAADTAVYYCARALDYDYEFAYWGQGTITVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYF PEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCP PCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK	35
MIRG003 LC	EIVLTQSPDFQSVTPKEKVTITCRASQSIGTNIHWYQQKPDQSPKLLIKIYASESISGIPSRFSGSGSGTDFTLTINSLEA EDAATYYCQQNNWPTSFQGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC	36

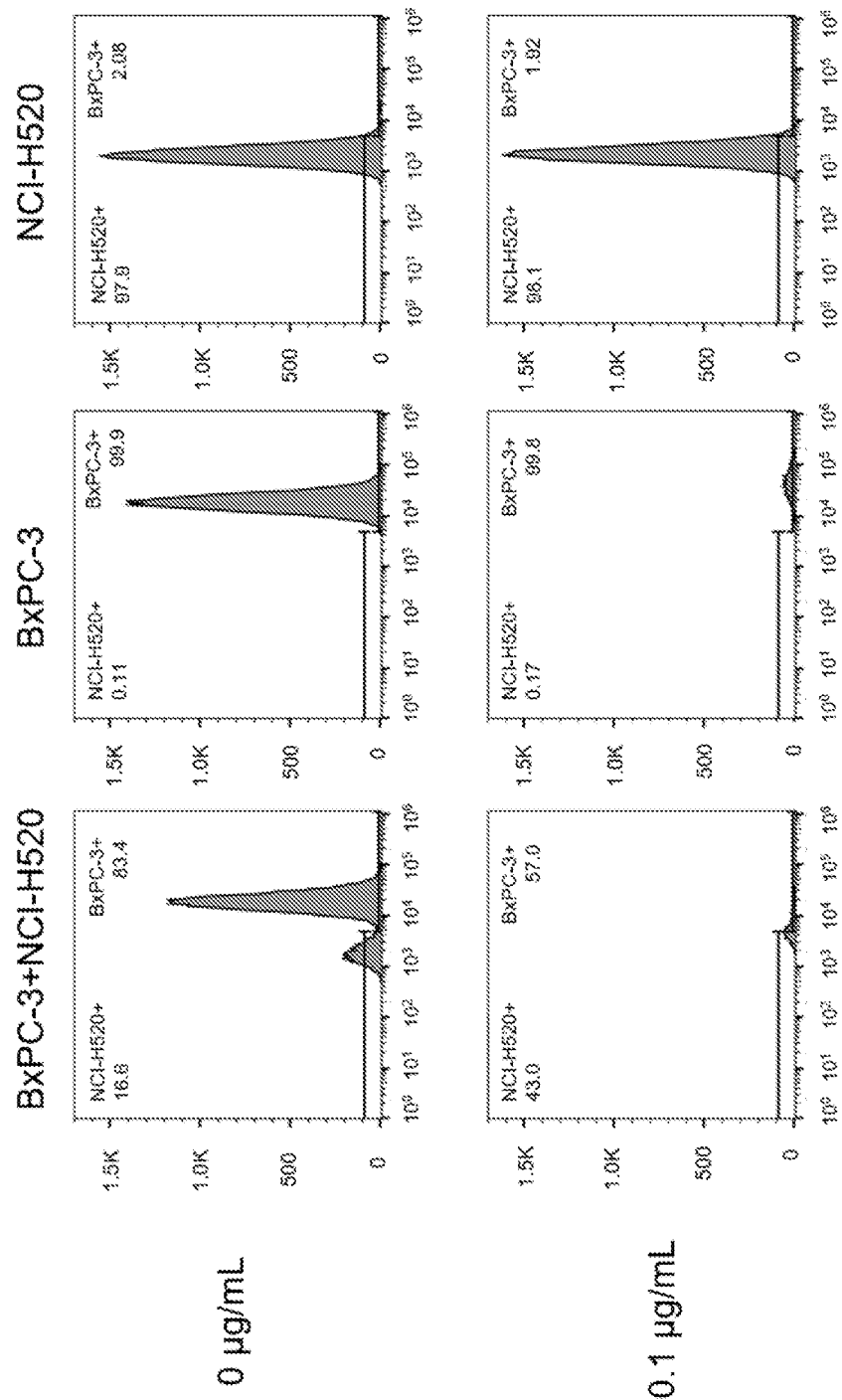


FIG. 9A

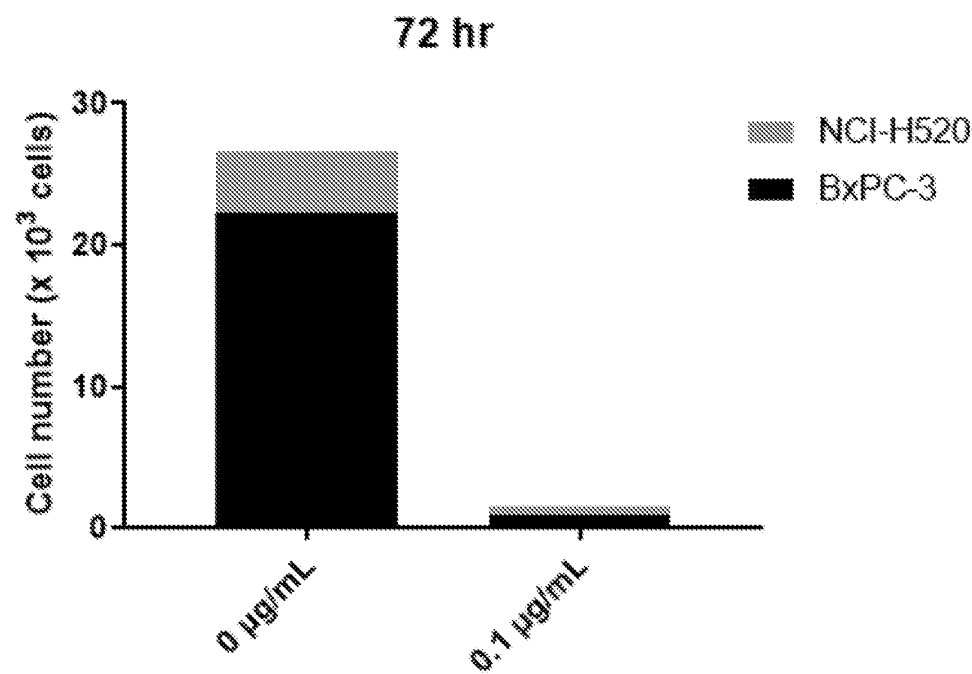


FIG. 9B

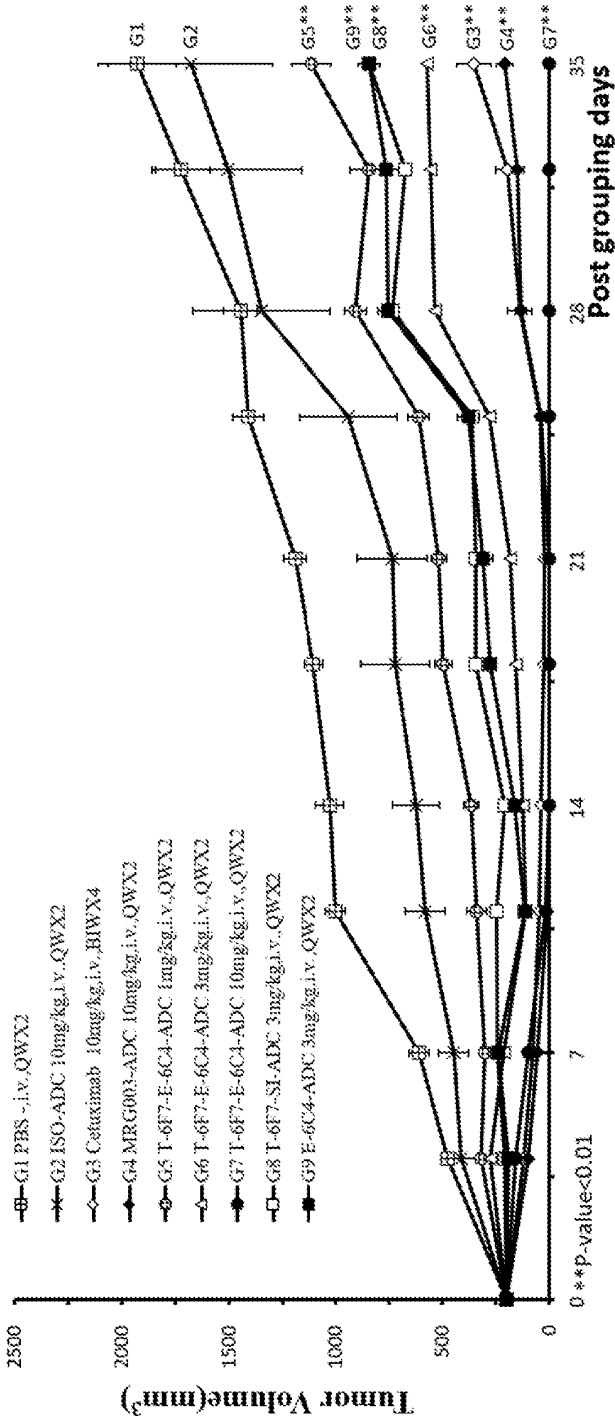


FIG. 10

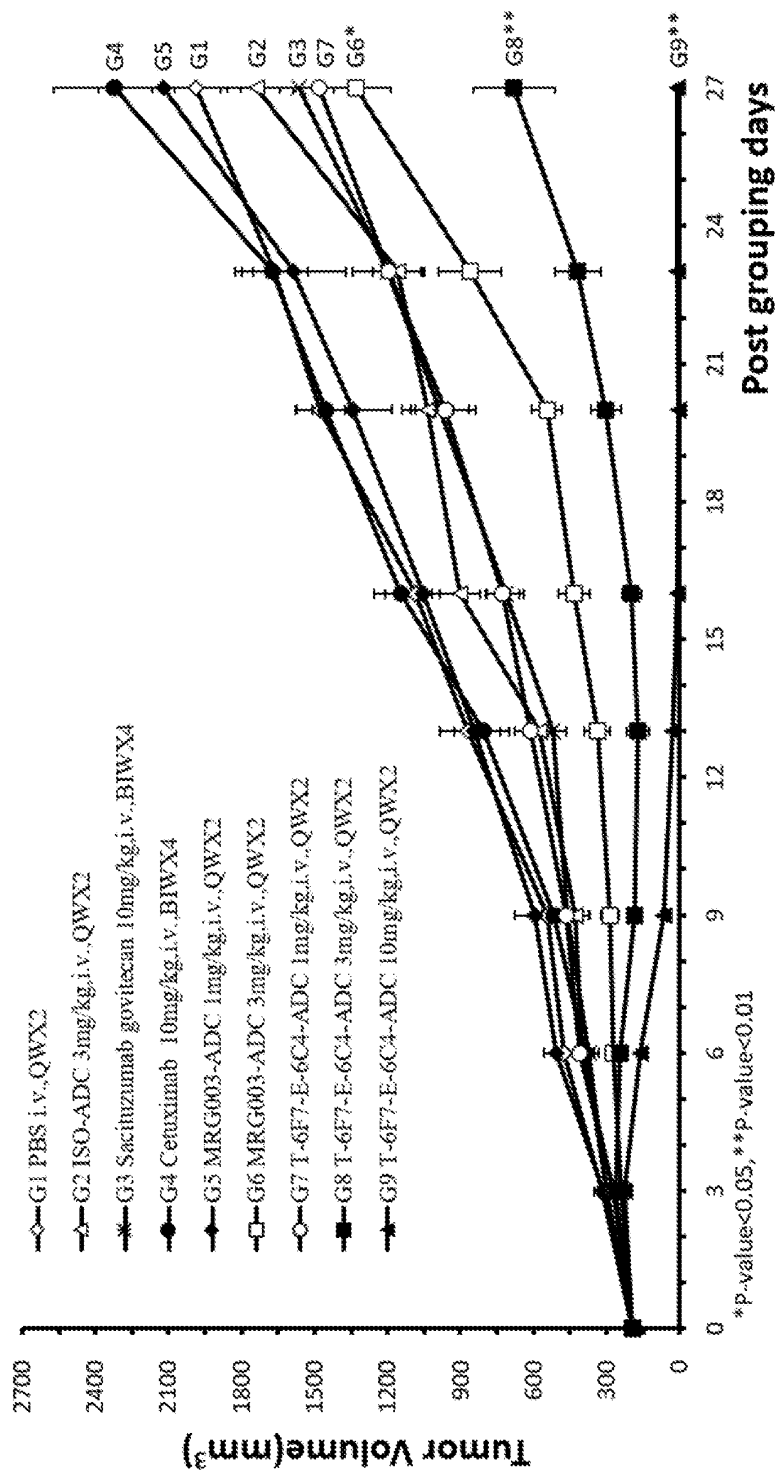


FIG. 11

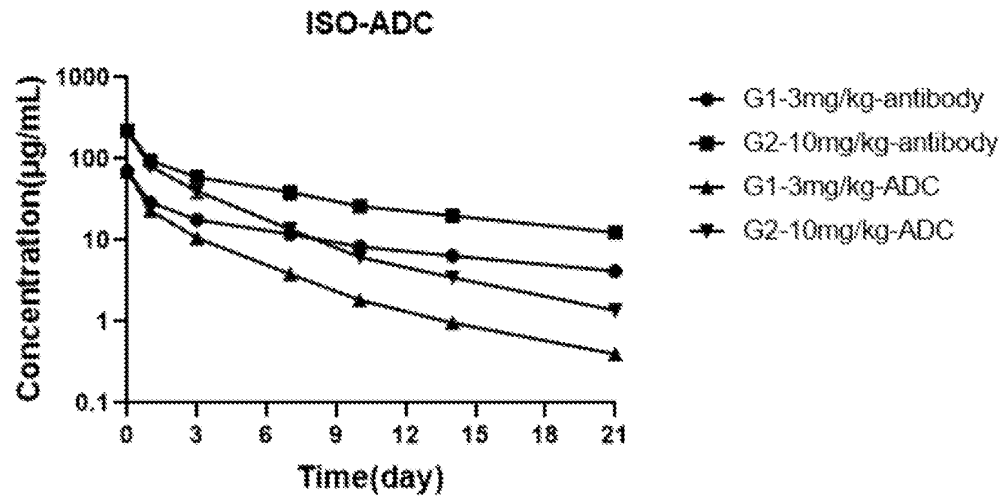


FIG. 12A

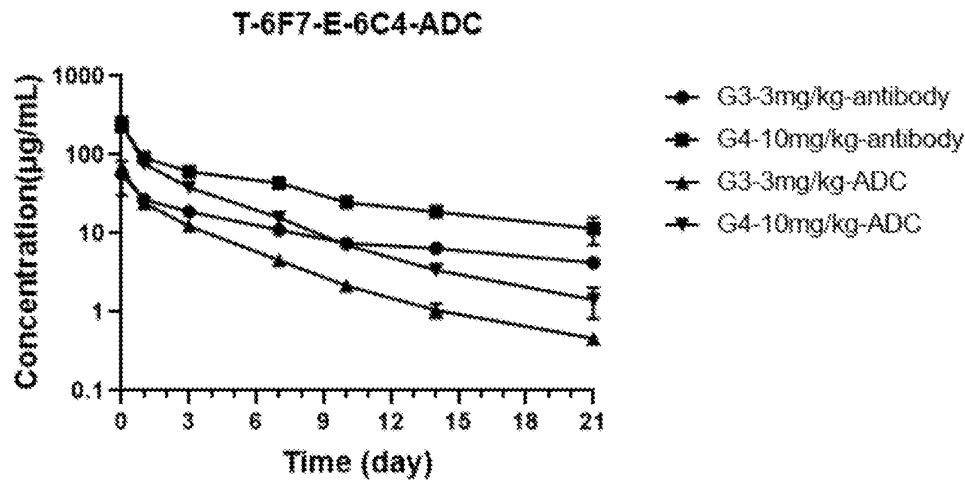


FIG. 12B

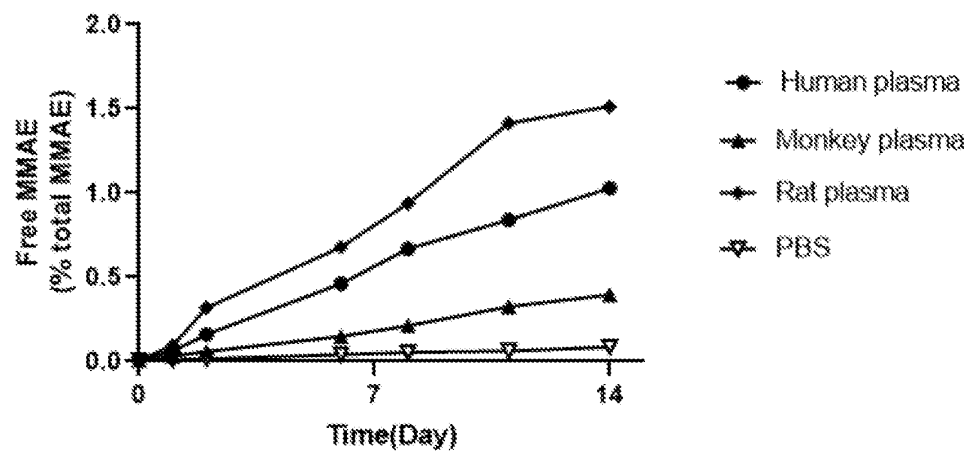


FIG. 13

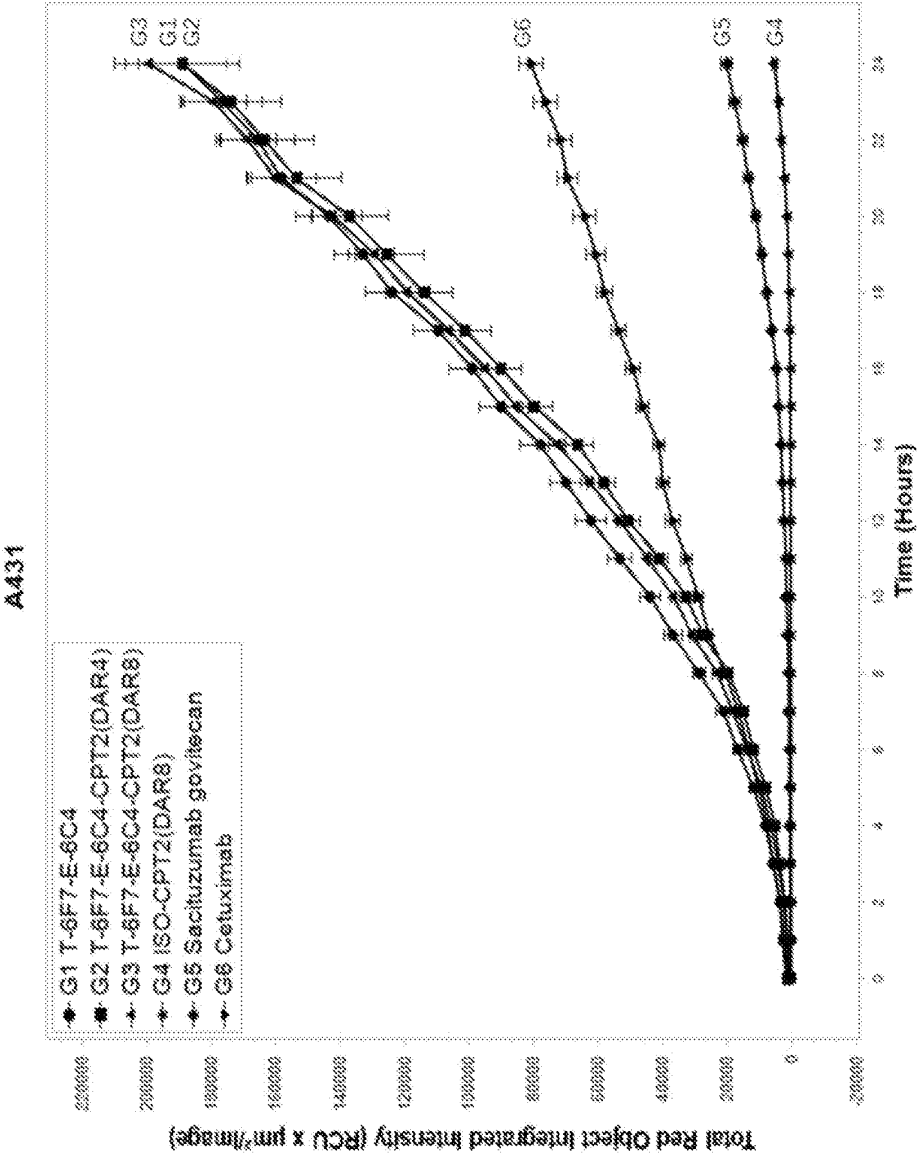


FIG. 14A

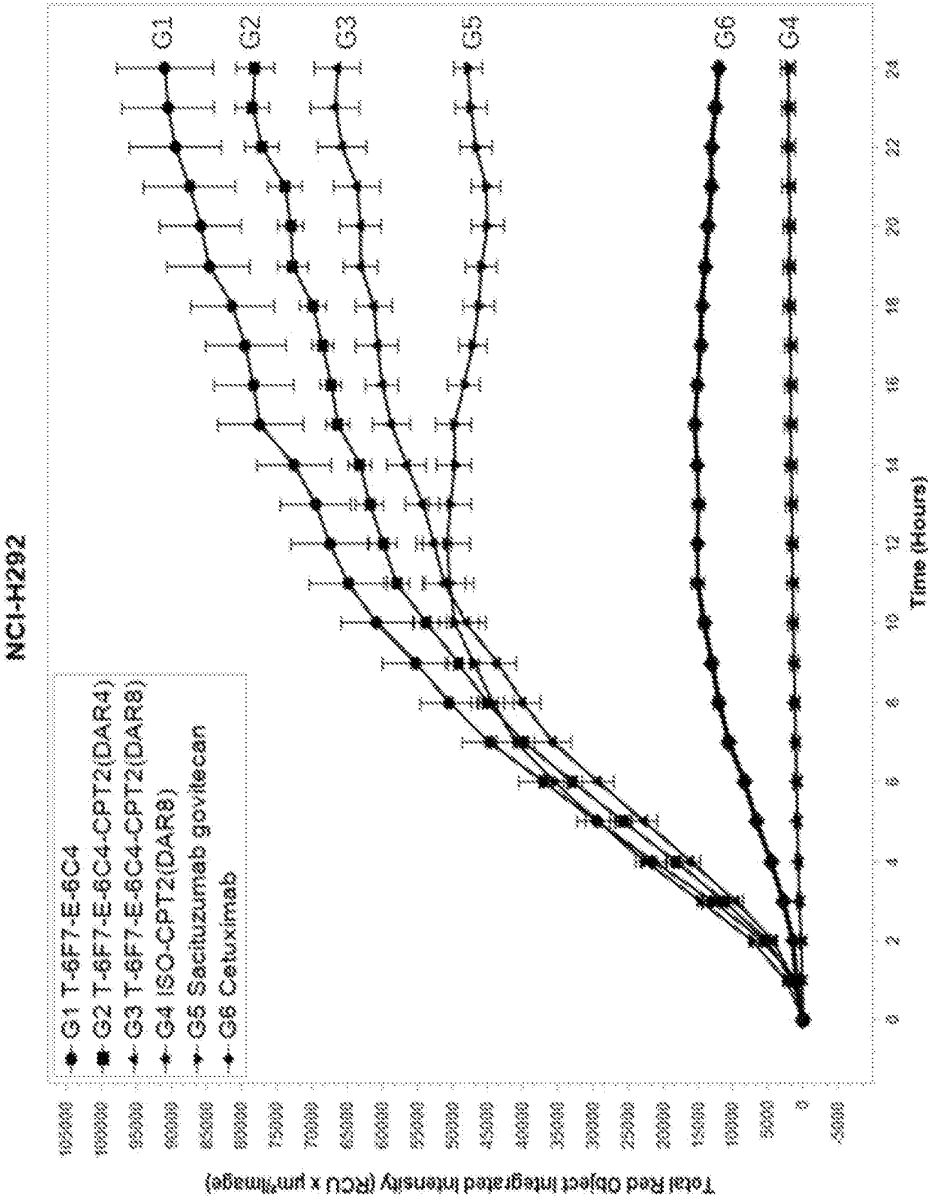


FIG. 14B

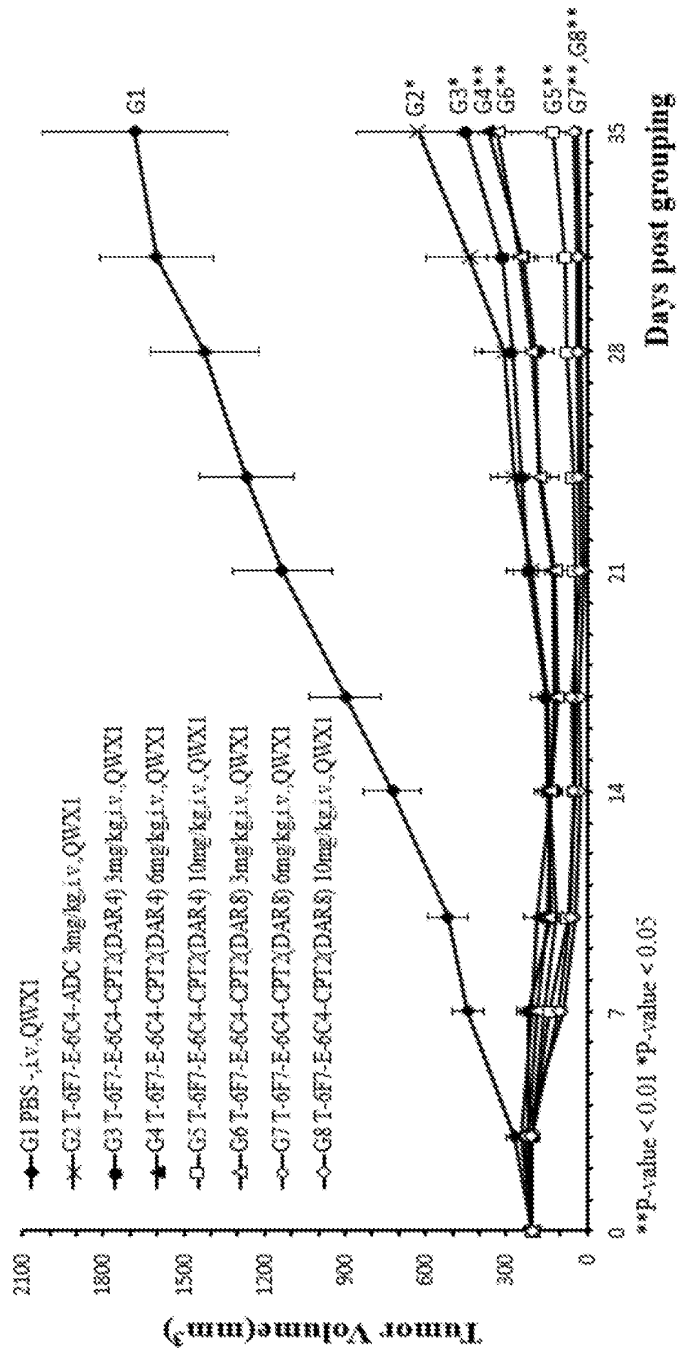


FIG. 15

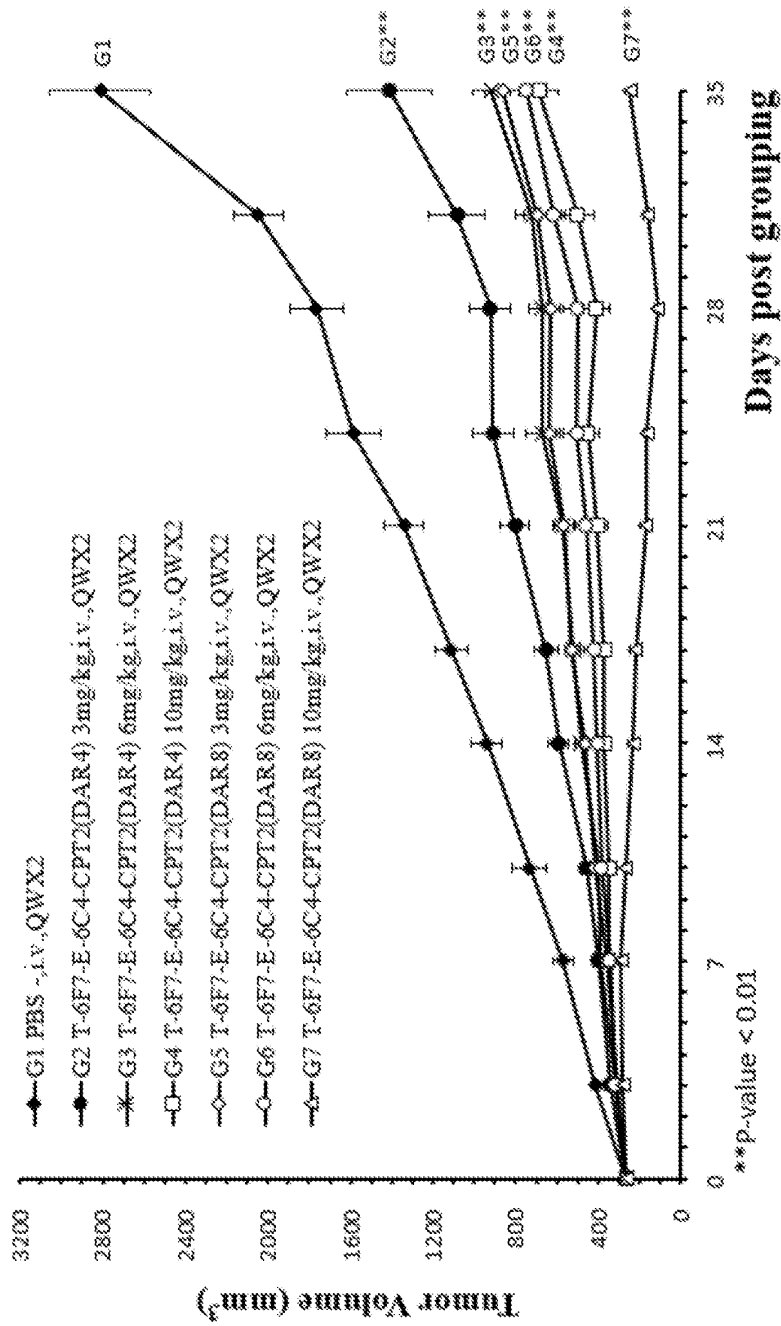


FIG. 16

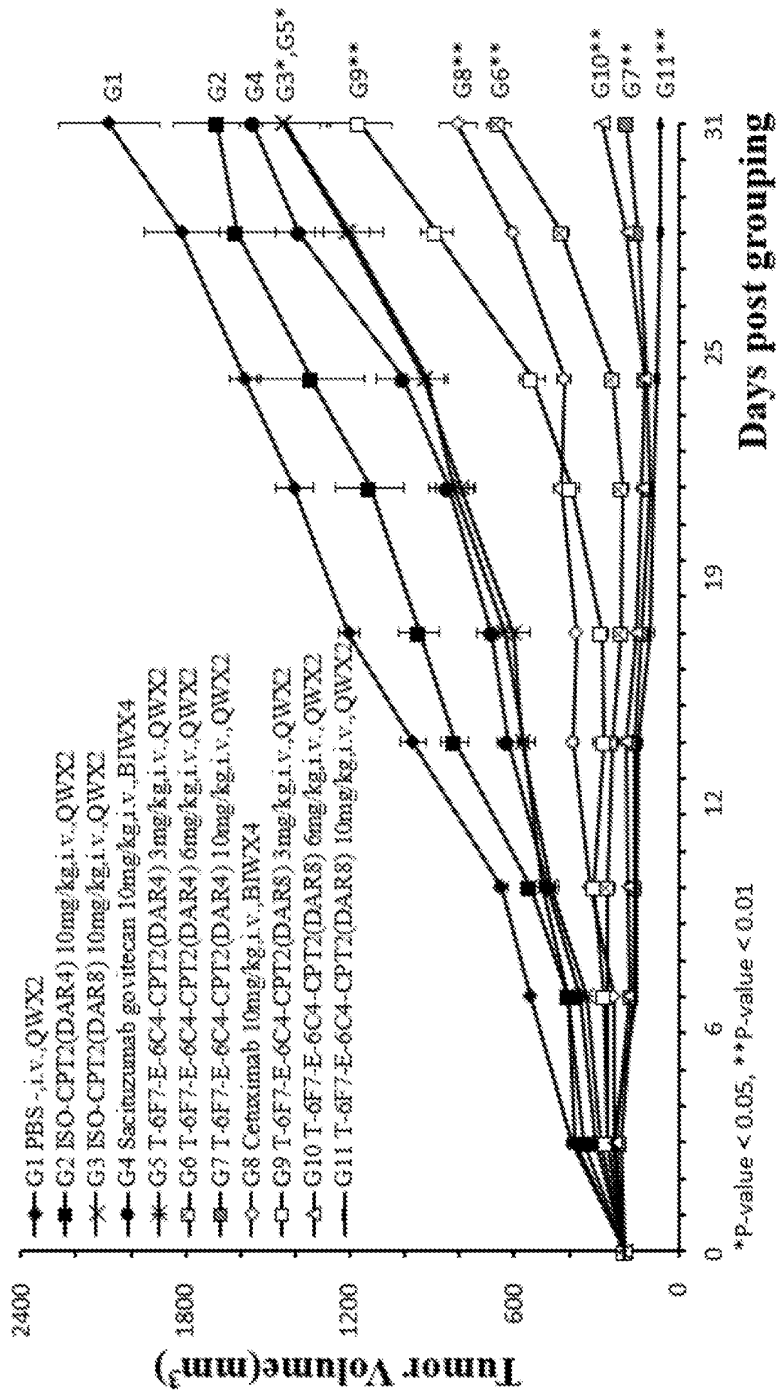


FIG. 17

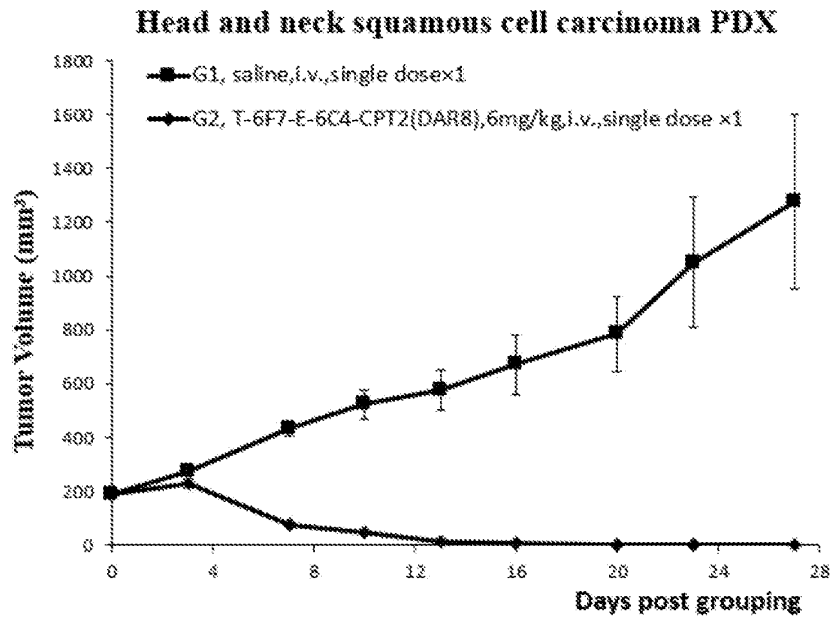


FIG. 18A

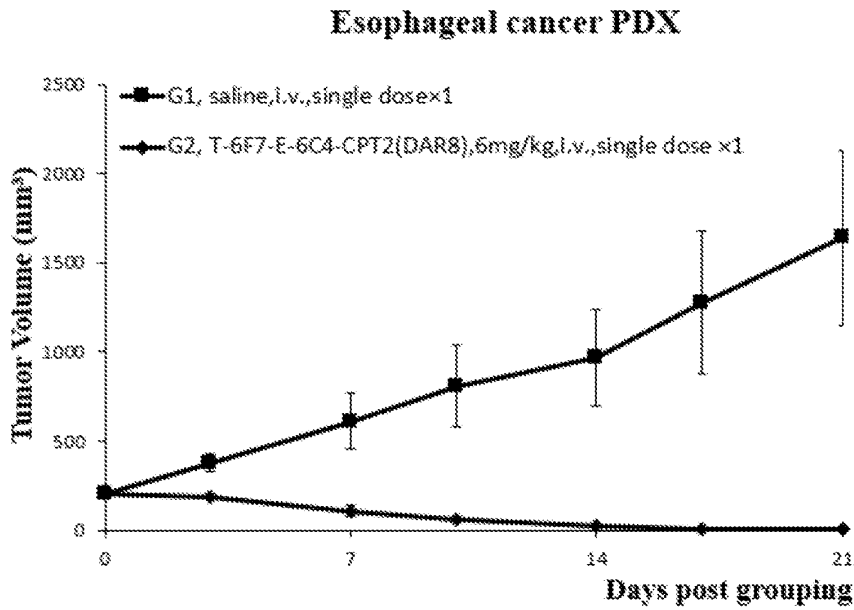


FIG. 18B

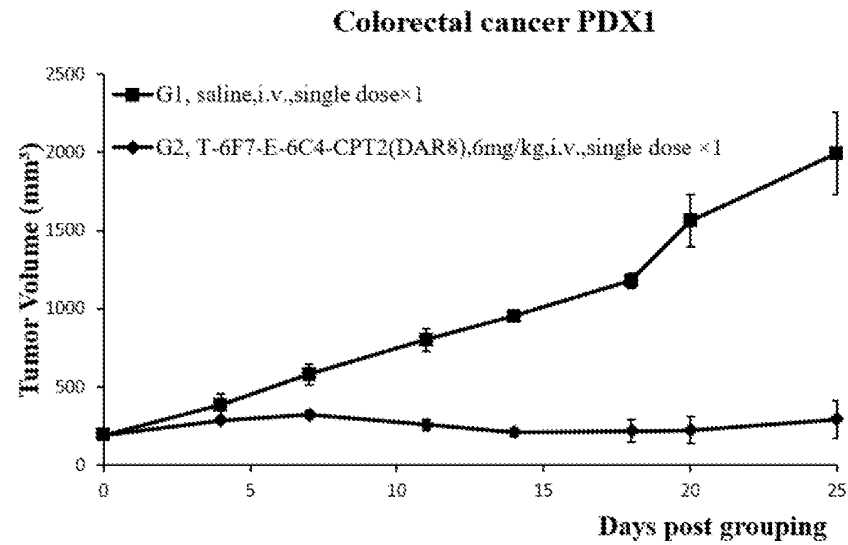


FIG. 18C

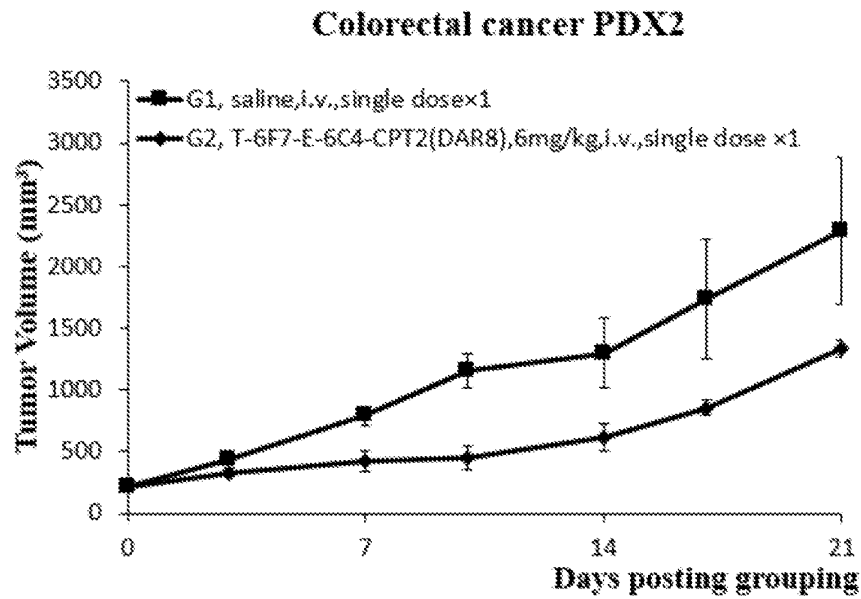


FIG. 18D

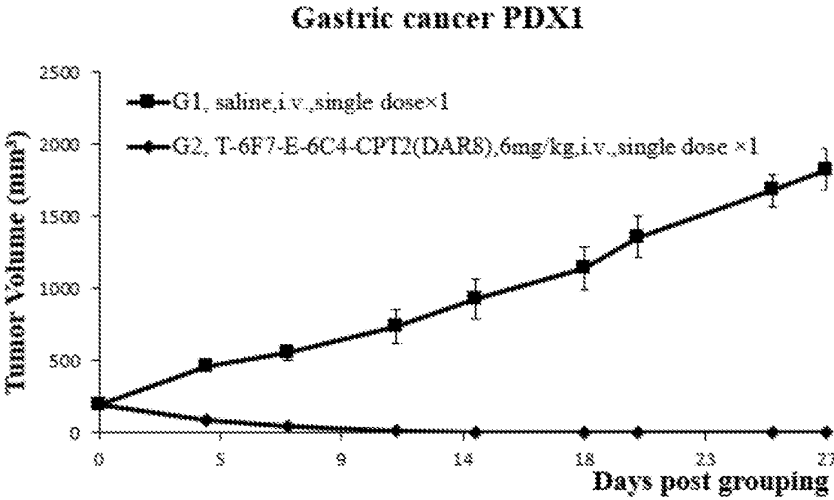


FIG. 18E

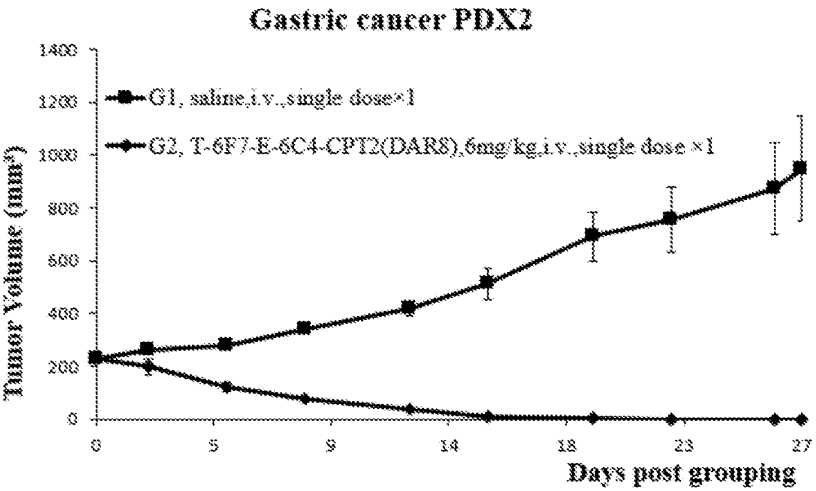


FIG. 18F

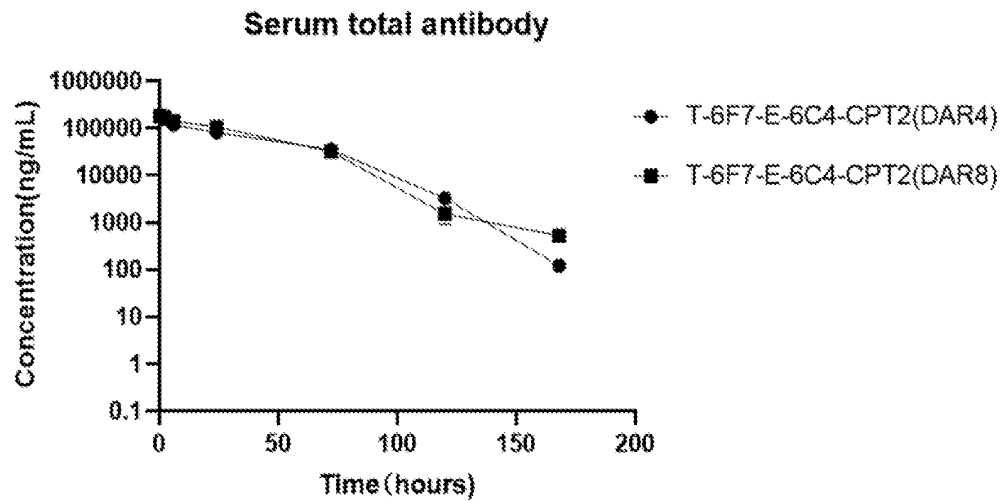


FIG. 19A

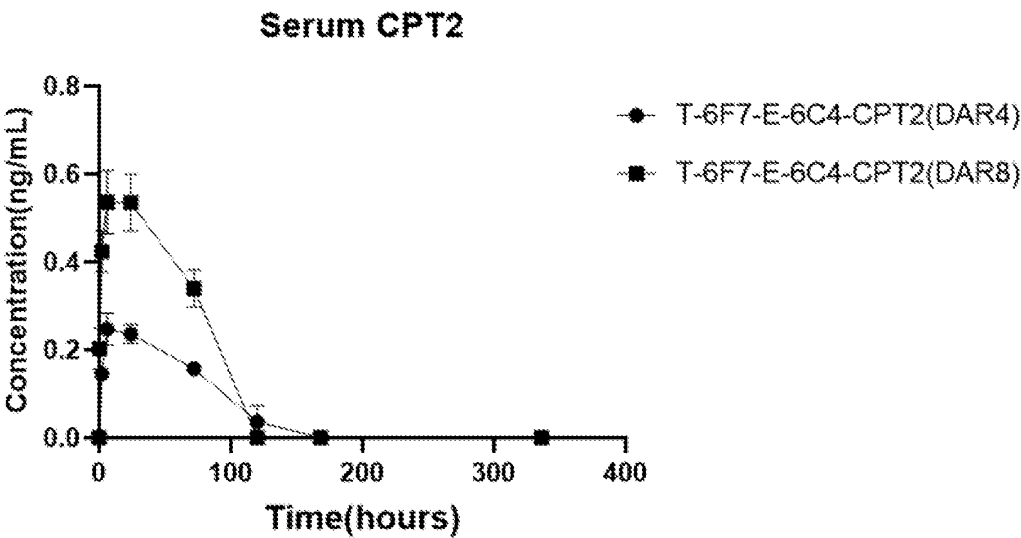


FIG. 19B

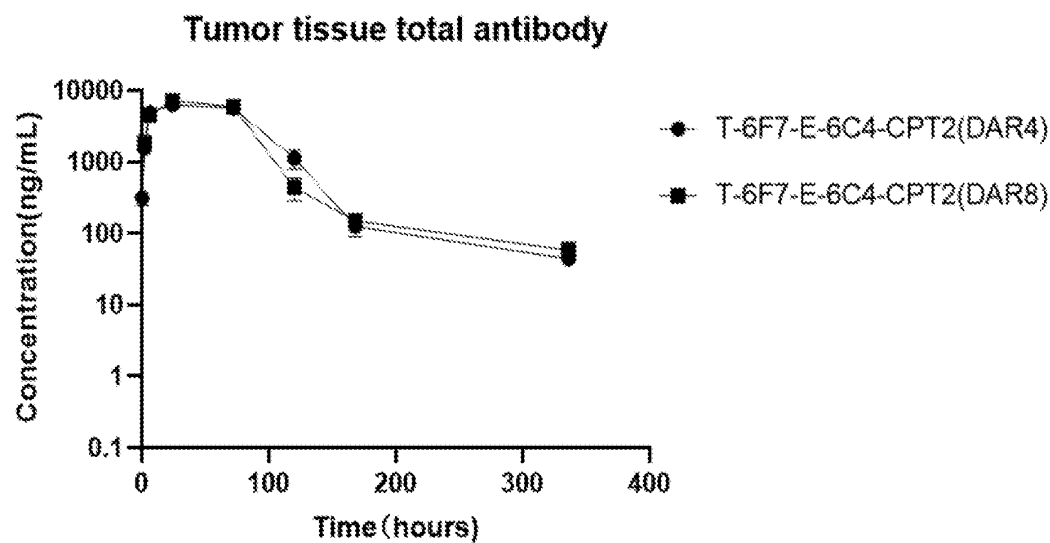


FIG. 19C

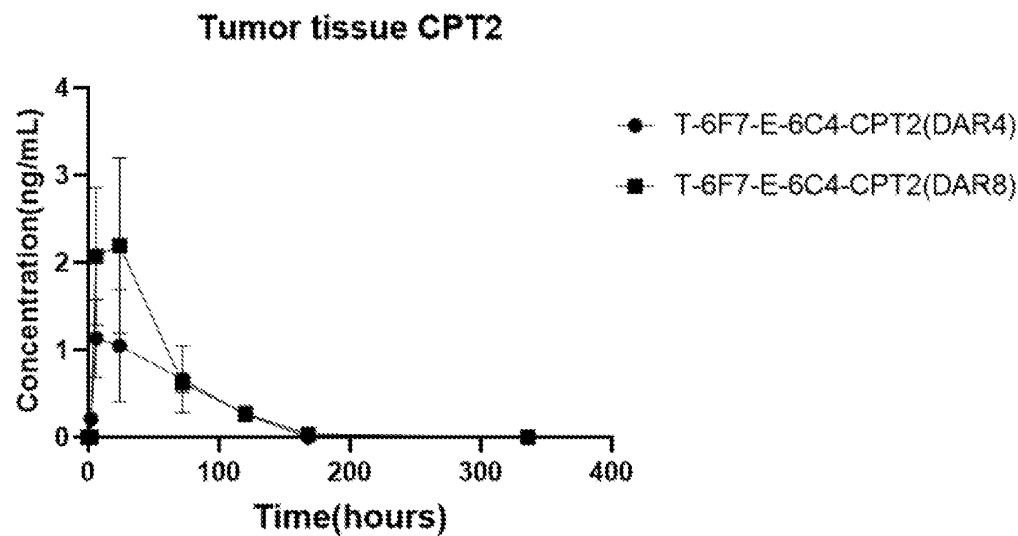


FIG. 19D

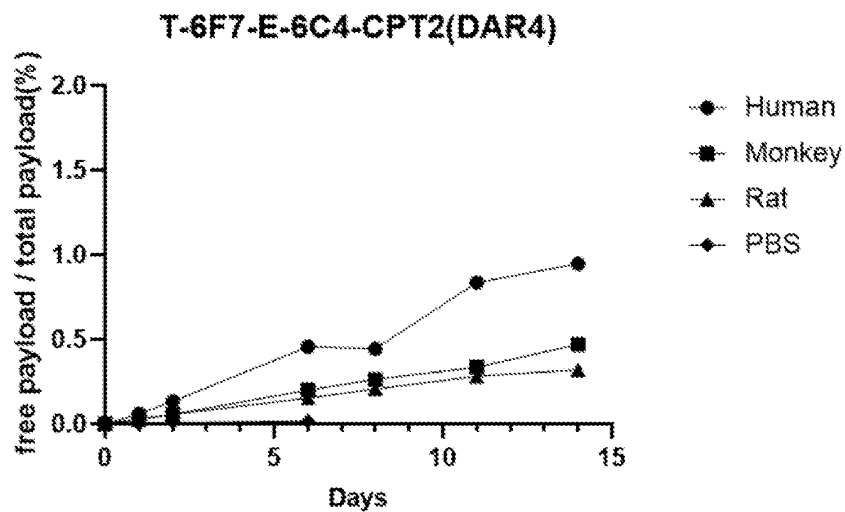


FIG. 20A

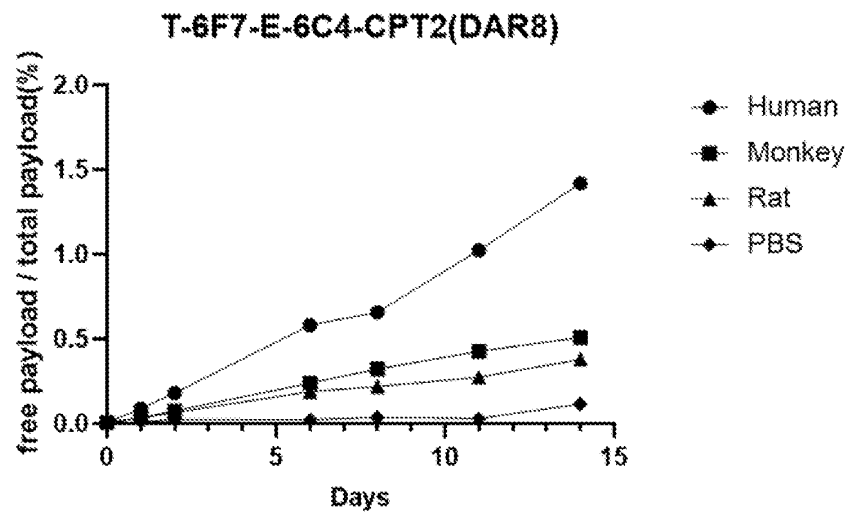


FIG. 20B