A

```
            1           2           3
 123456789 0123456789 0123456789 0123456789
 QVQLQQSGA DLMKPGASVK ISCKATGYTF SGNWIEWVKQ

4           5  a        6           7
0123456789 01223456789 0123456789 0123456789
RPGHGLEWIG EILPGSGNTNY NEKFKGKATF TADTSSNTAY

8  abc         9          10abc          11
0122223456789 0123456789 0000123456789 0123
MQLSSLTSEDSAV YYCARGGHYY GSSWDYWGQGTTL TVSS
```

B

```
           1           2           3
 123456789 0123456789 0123456789 0123456789
 NIVMTQSPK SMSMSVGERV TLTCKASENV VTYVSWYQQK

4           5           6           7
0123456789 0123456789 0123456789 0123456789
PEQSPKLLIY GASNRYTGVP DRFTGSGSAT DFTLTISSVQ

8           9          10
0123456789 0123456789 012345678
AEDLADYHCG QGYSYPYTFG GGTKLEIKR
```

FIGURE 1

A

```
                        1           2           3
                123456789 0123456789 0123456789 0123456789
L2G7            QVQLQQSGA DLMKPGASVK ISCKATGYTF SGNWIEWVKQ
HuL2G7          EVQLVQSGA EVKKPGASVK VSCKVSGYTF SGNWIEWVRQ
AAC18323        QVQLVQSGA EVKKPGASVK VSCKVSGYTL TelsmhWVRQ

                4           5  a        6           7
                0123456789 01223456789 0123456789 0123456789
L2G7            RPGHGLEWIG EILPGSGNTNY NEKFKGKATF TADTSSNTAY
HuL2G7          APGKGLEWIG EILPGSGNTNY NEKFKGKATM TADTSTDTAY
AAC18323        APGKGLEWMG gfdpedgetiy aqkfqgRVTM TEDTSTDTAY

                8  abc        9          10abc         11
                0122223456789 0123456789 0000123456789 0123
L2G7            MQLSSLTSEDSAV YYCARGGHYY GSSWDYWGQGTTL TVSS
HuL2G7          MELSSLRSEDTAV YYCARGGHYY GSSWDYWGQGTLV TVSS
AAC18323        MELSSLRSEDTAV YYCATpvgrc sst*dyWGQGTLV TVSS
```

* insertion of scyhpl between sst and dyW

B

```
                        1           2           3
                123456789 0123456789 0123456789 0123456789
L2G7            NIVMTQSPK SMSMSVGERV TLTCKASENV VTYVSWYQQK
HuL2G7          DIVMTQSPS SLSASVGDRV TITCKASENV VTYVSWYQQK
BAC01726        DIQMTQSPS SLSASVGDRV TITCrasqsi ssylnWYQQK

                4           5           6           7
                0123456789 0123456789 0123456789 0123456789
L2G7            PEQSPKLLIY GASNRYTGVP DRFTGSGSAT DFTLTISSVQ
HuL2G7          PGKAPKLLIY GASNRYTGVP DRFSGSGSGT DFTLTISSLQ
BAC01726        PGKAPKLLIY AasslqsGVP SRFSGSGSGT DFTLTISSLQ

                8           9          10
                0123456789 0123456789 012345678
L2G7            AEDLADYHCG QGYSYPYTFG GGTKLEIKR
HuL2G7          PEDFATYYCG QGYSYPYTFG QGTKLEIKR
BAC01726        PEDFATYYCq qsystpytFG QGTKLEIKR
```

FIGURE 2

A

																	1									
-19	M	D	C	T	W	R	I	L	F	L	V	A	A	A	T	G	T	H	A	E	V	Q	L	V	Q	S	G	A	E	V
12	K	K	P	G	A	S	V	K	V	S	C	K	V	S	G	Y	T	F	S	G	N	W	I	E	W	V	R	Q	A	P
42	G	K	G	L	E	W	I	G	E	I	L	P	G	S	G	N	T	N	Y	N	E	K	F	K	G	K	A	T	M	T
72	A	D	T	S	T	D	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R	G	G	H
102	Y	Y	G	S	S	W	D	Y	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S	V	F	P	L
132	A	P	S	S	K	S	T	S	G	G	T	A	A	L	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W
162	N	S	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G	L	Y	S	L	S	S	V	V	T	V
192	P	S	S	S	L	G	T	Q	T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	R	V	E	P	K
222	S	C	D	K	T	H	T	C	P	P	C	P	A	P	E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K
252	D	T	L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H	E	D	P	E	V	K	F	N	W	Y
282	V	D	G	V	E	V	H	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S	V	L	T	V
312	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K	V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K
342	A	K	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	E	E	M	T	K	N	Q	V	S	L	T	C	L
372	V	K	G	F	Y	P	S	D	I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T	P	P	V	L
402	D	S	D	G	S	F	F	L	Y	S	K	L	T	V	D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M
432	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P	G	K												

B

																		1								
-20	M	E	A	P	A	Q	L	L	F	L	L	L	L	W	L	P	D	T	H	G	D	I	V	M	T	Q	S	P	S	S
11	L	S	A	S	V	G	D	R	V	T	I	T	C	K	A	S	E	N	V	V	T	Y	V	S	W	Y	Q	Q	K	P
41	G	K	A	P	K	L	L	I	Y	G	A	S	N	R	Y	T	G	V	P	D	R	F	S	G	S	G	S	G	T	D
71	F	T	L	T	I	S	S	L	Q	P	E	D	F	A	T	Y	Y	C	G	Q	G	Y	S	Y	P	Y	T	F	G	Q
101	G	T	K	L	E	I	K	R	T	V	A	A	P	S	V	F	I	F	P	P	S	D	E	Q	L	K	S	G	T	A
131	S	V	V	C	L	L	N	N	F	Y	P	R	E	A	K	V	Q	W	K	V	D	N	A	L	Q	S	G	N	S	Q
161	E	S	V	T	E	Q	D	S	K	D	S	T	Y	S	L	S	S	T	L	T	L	S	K	A	D	Y	E	K	H	K
191	V	Y	A	C	E	V	T	H	Q	G	L	S	S	P	V	T	K	S	F	N	R	G	E	C						

FIGURE 3

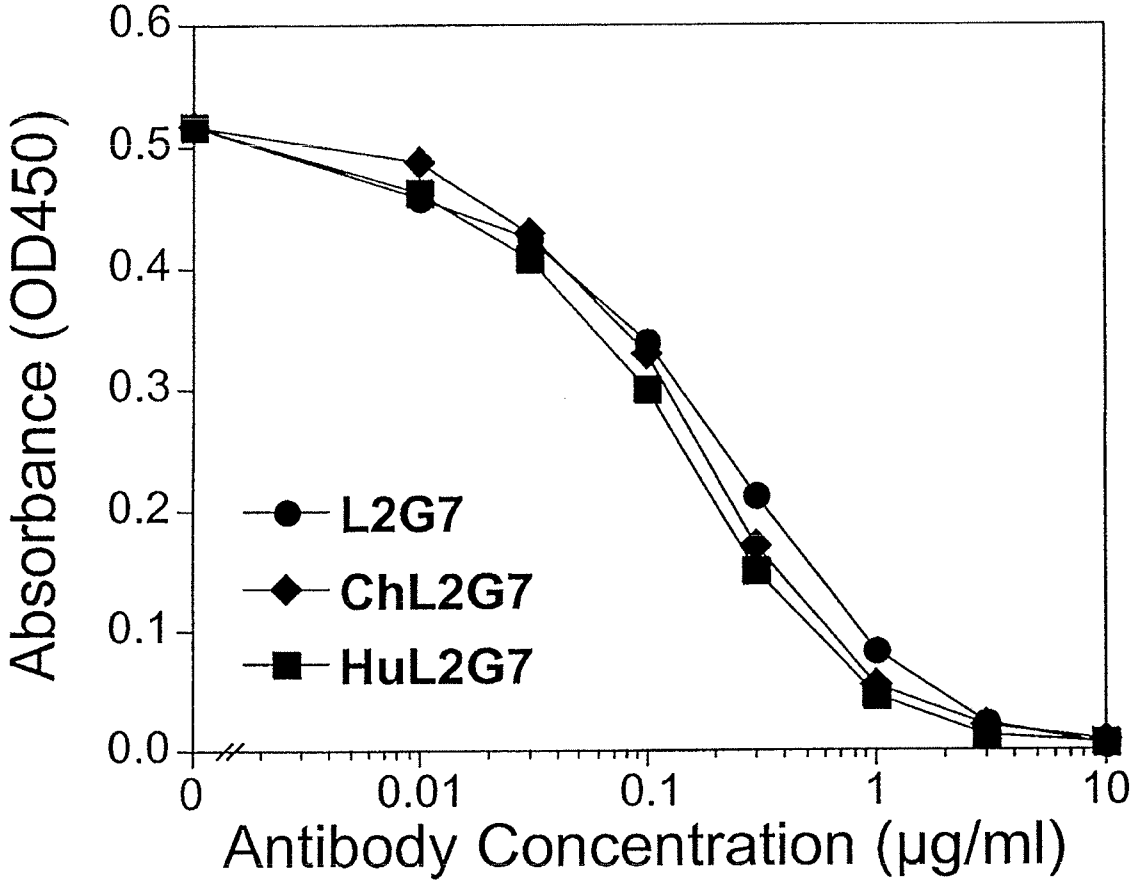

0.6
0.5
0.4
0.3
0.2
0.1
0.0
Absorbance (OD450)
L2G7
ChL2G7
HuL2G7
0
0.01
0.1
1
10
Antibody Concentration (µg/ml)

FIGURE 4

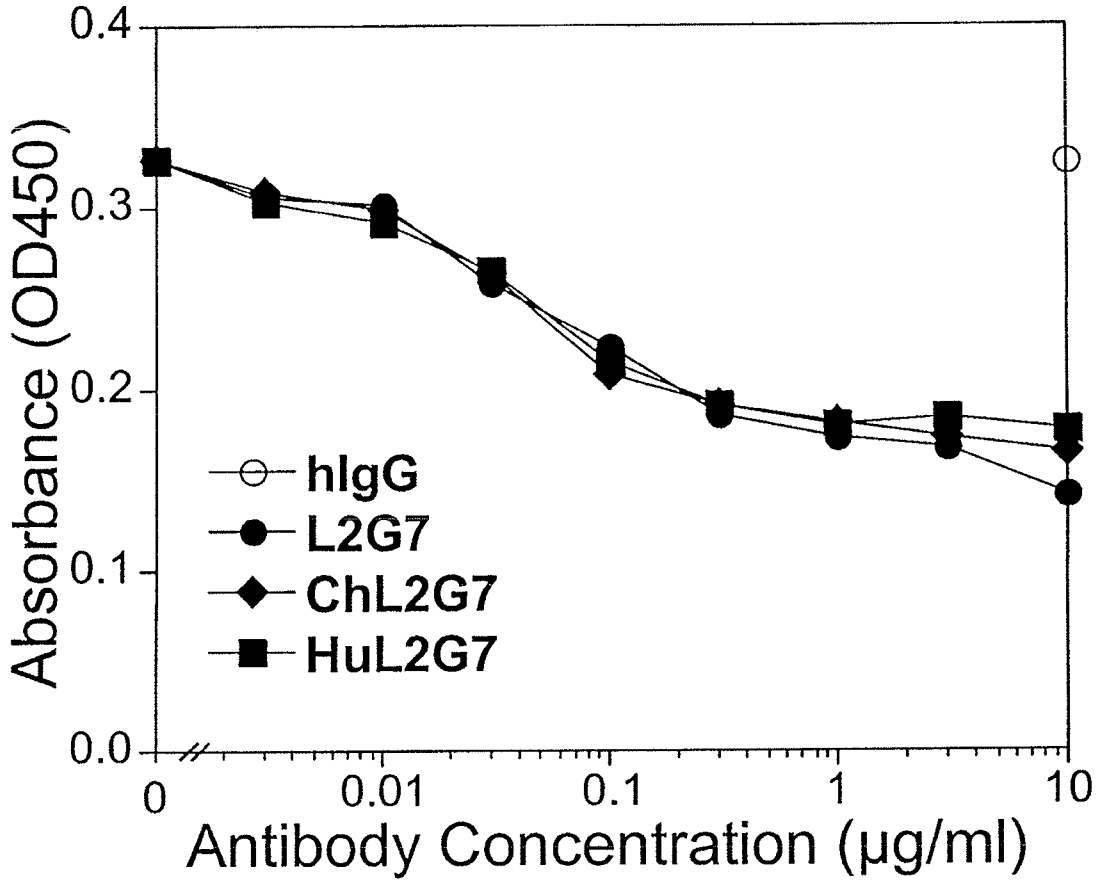

0.4
0.3
0.2
0.1
0.0
Absorbance (OD450)
hIgG
L2G7
ChL2G7
HuL2G7
0
0.01
0.1
1
10
Antibody Concentration (µg/ml)

FIGURE 5

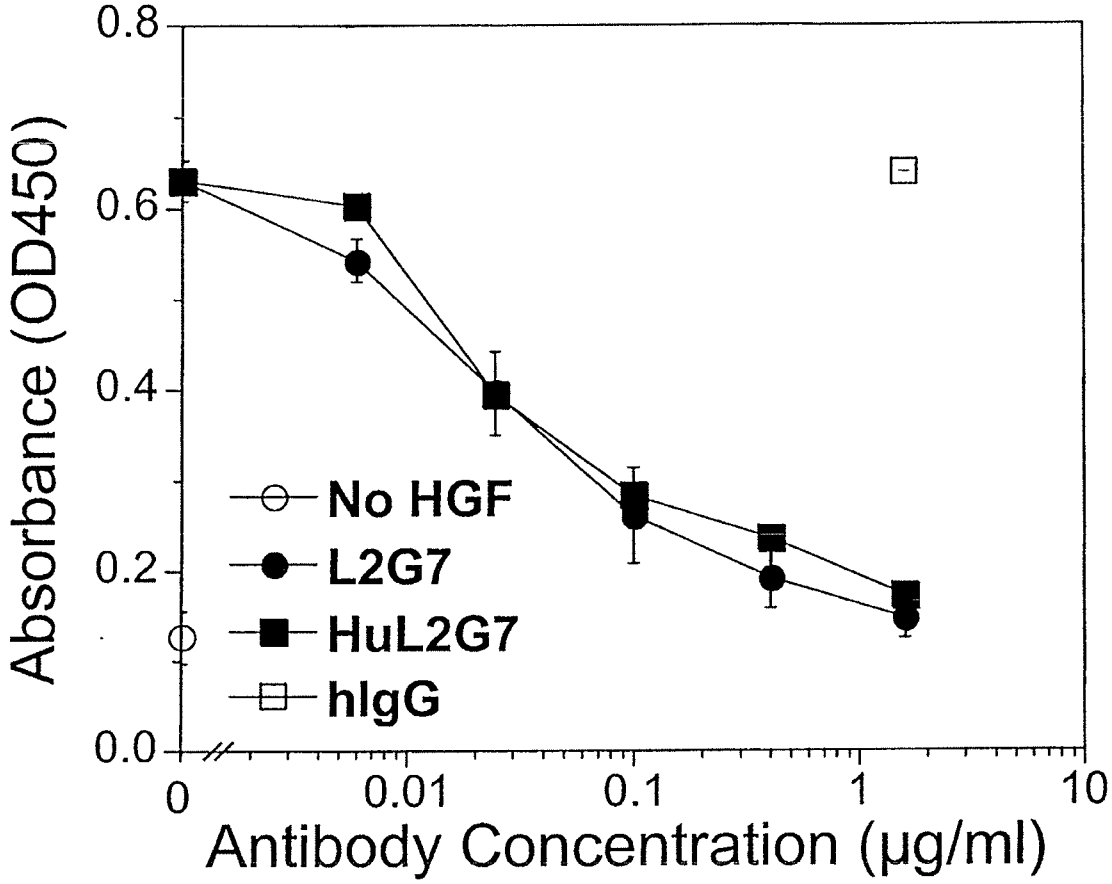

0.8
0.6
0.4
0.2
0.0
Absorbance (OD450)
No HGF
L2G7
HuL2G7
hIgG
0
0.01
0.1
1
10
Antibody Concentration (µg/ml)

FIGURE 6

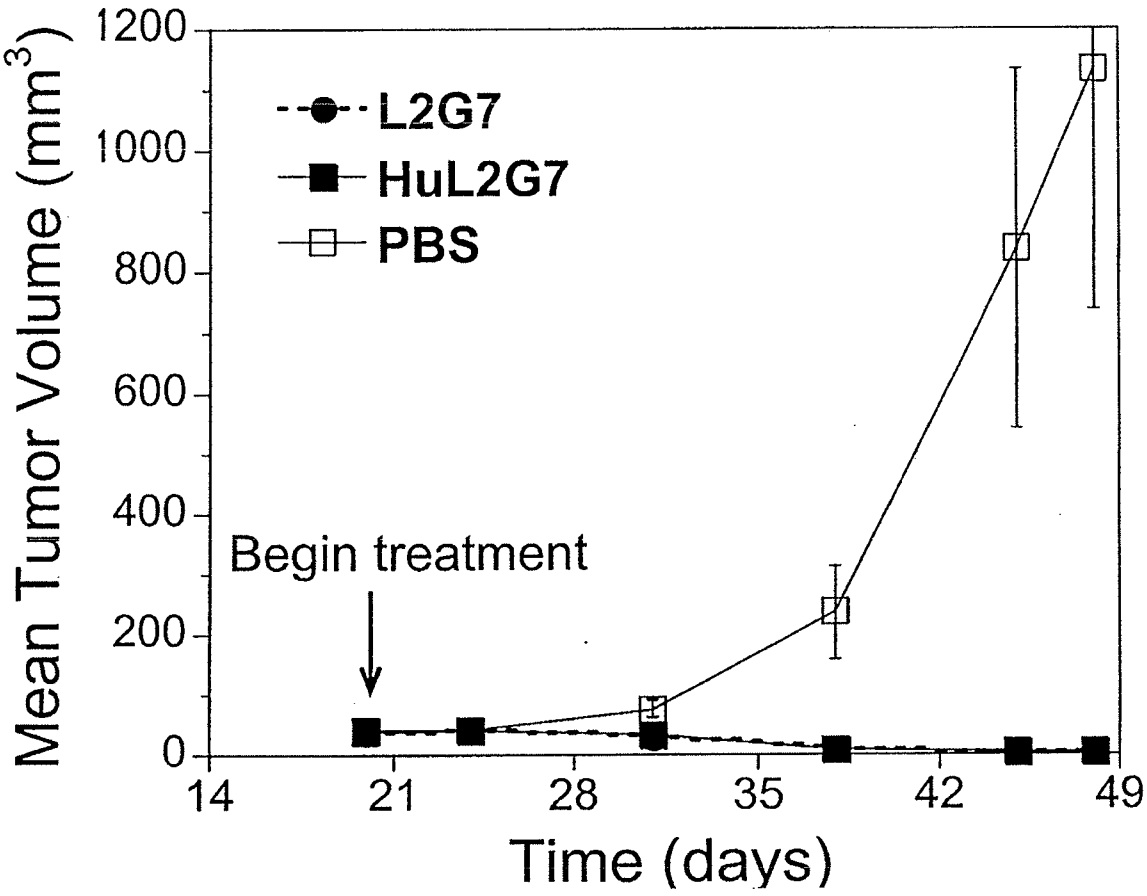

Mean Tumor Volume (mm3)
1200
1000
800
600
400
200
0
L2G7
HuL2G7
PBS
Begin treatment
14
21
28
35
42
49
Time (days)

FIGURE 7

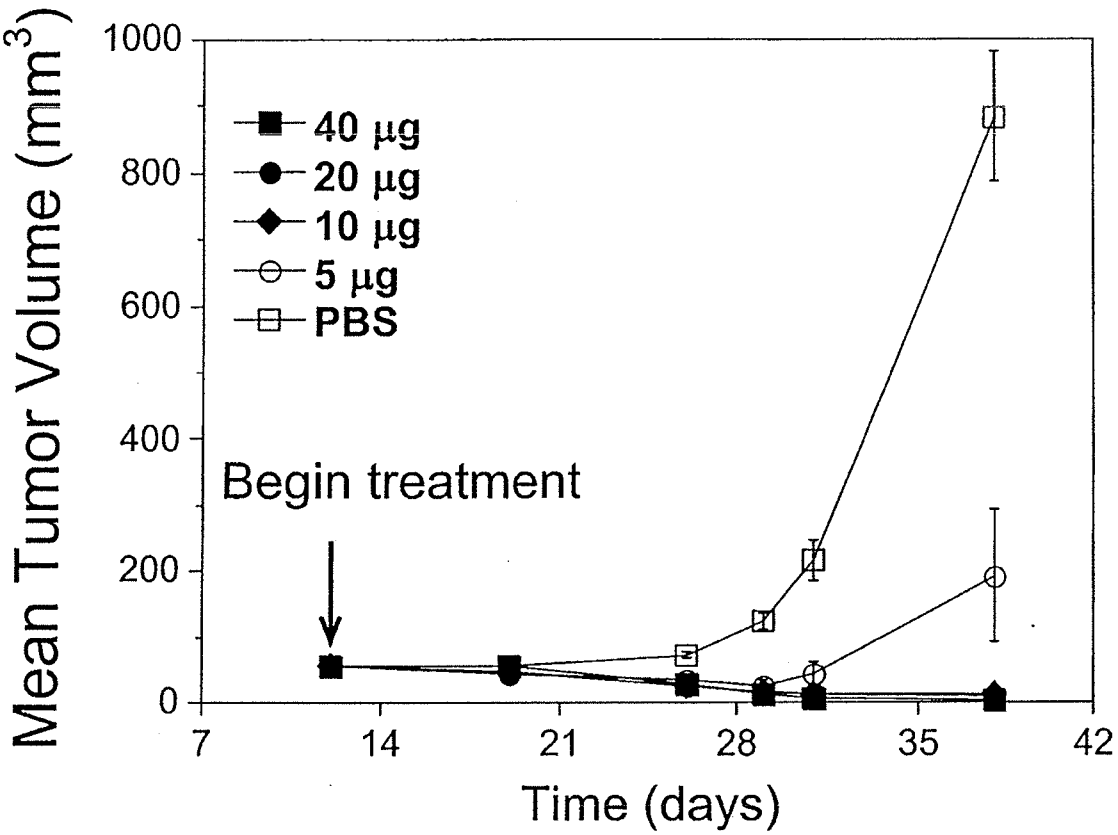

Mean Tumor Volume (mm3)
1000
800
600
400
200
0
40 µg
20 µg
10 µg
5 µg
PBS
Begin treatment
7
14
21
28
35
42
Time (days)

FIGURE 8