Fig. 1

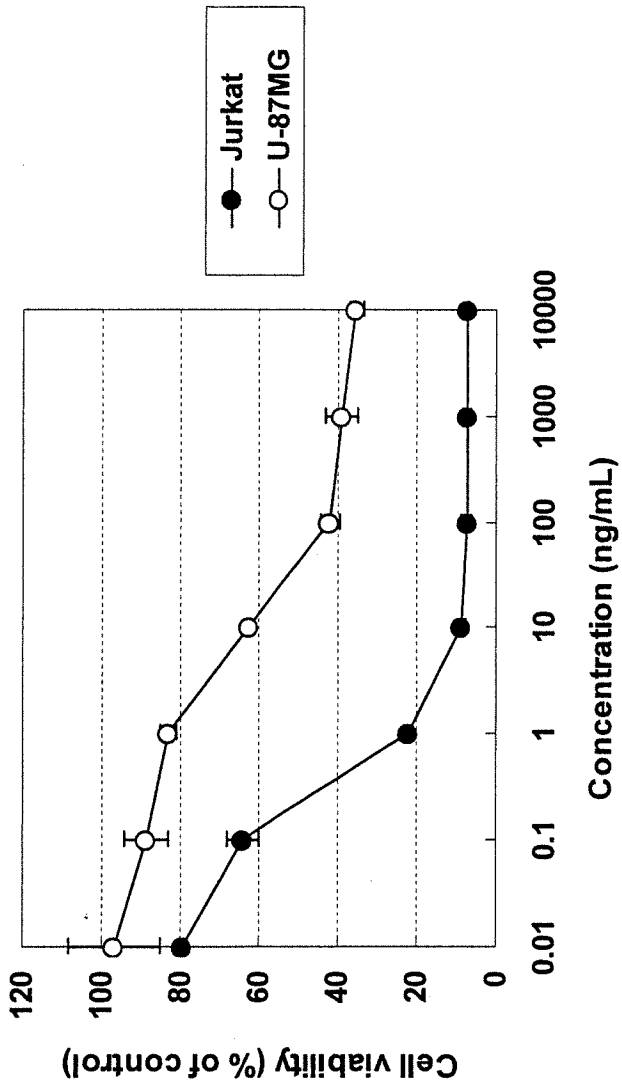

Jurkat
U-87MG
Cell viability (% of control)
120
100
80
60
40
20
0
0.01
0.1
1
10
100
1000
10000
Concentration (ng/mL)

Fig. 2

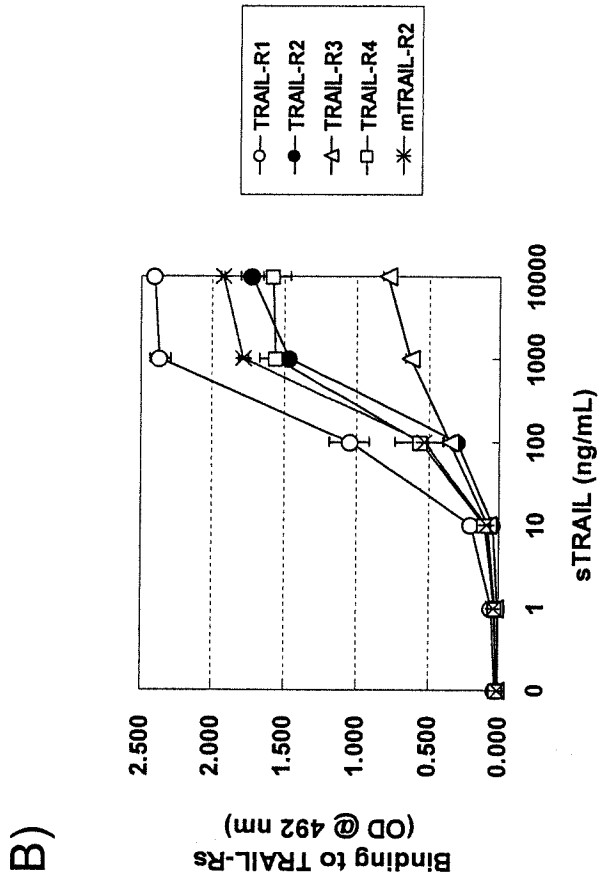
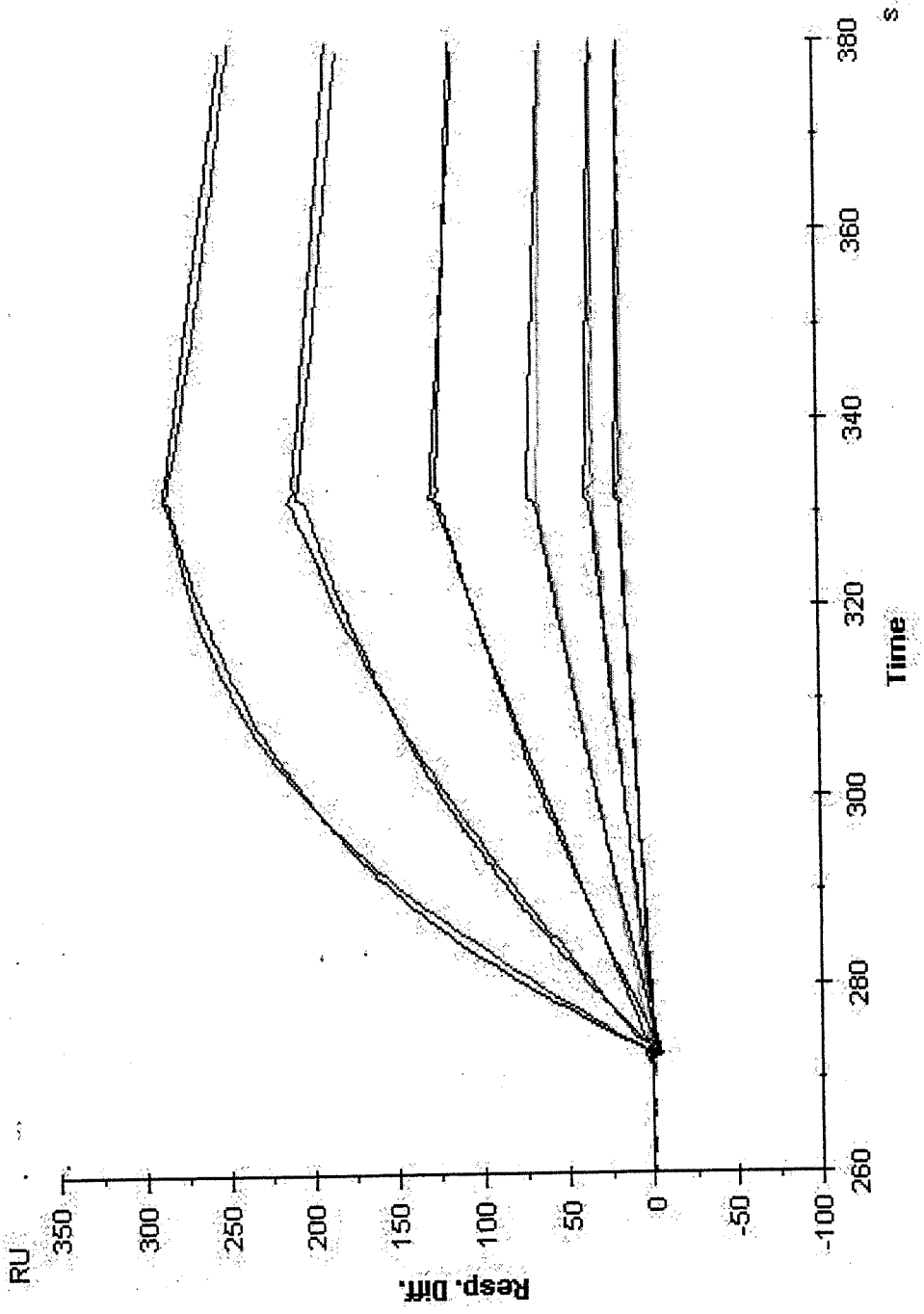

A)
Binding to TRAIL-Rs
(OD @ 492 nm)
2.500
2.000
1.500
1.000
0.500
0.000
0
1
10
100
1000
10000
cB273 (ng/mL)
B)
Binding to TRAIL-Rs
(OD @ 492 nm)
2.500
2.000
1.500
1.000
0.500
0.000
0
1
10
100
1000
10000
sTRAIL (ng/mL)
TRAIL-R1
TRAIL-R2
TRAIL-R3
TRAIL-R4
mTRAIL-R2

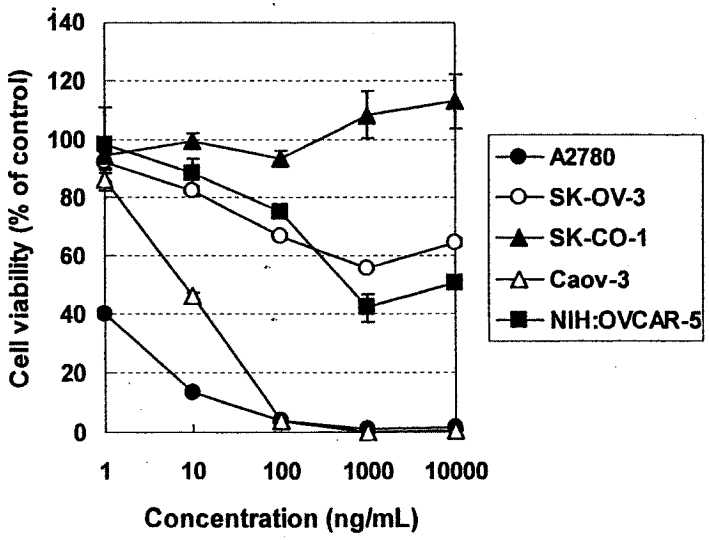
Fig. 3



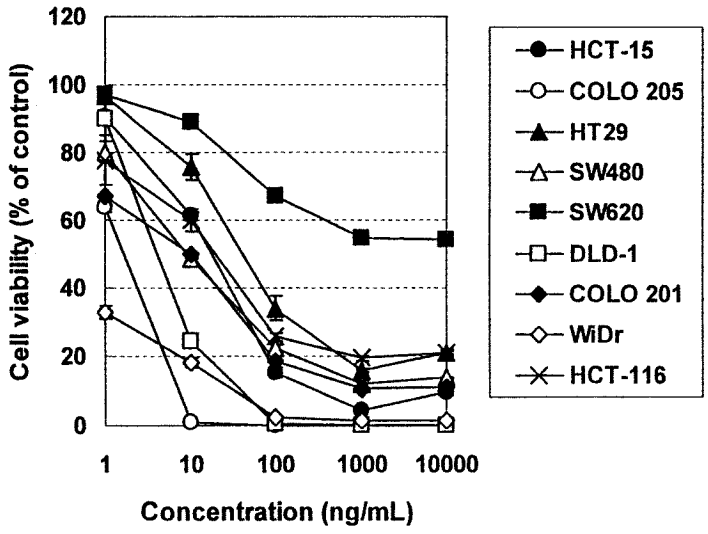
Kon (1/Ms)	Koff (1/d)	KD (nM)
1.69E+06	2.79E-03	1.65

Fig. 4

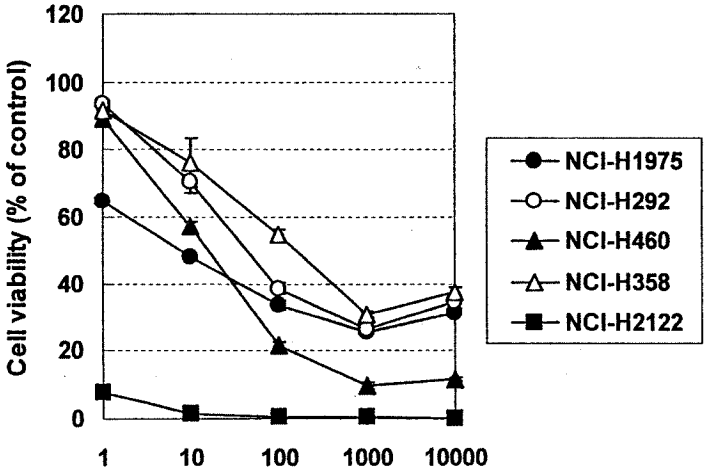
A) Human ovarian cancer cell line



B) Human colon cancer cell line



C) Human lung cancer cell line



D) Human breast cancer cell line

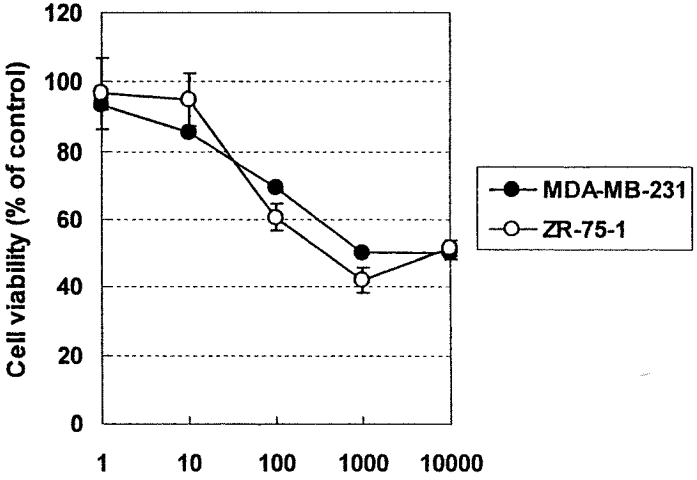
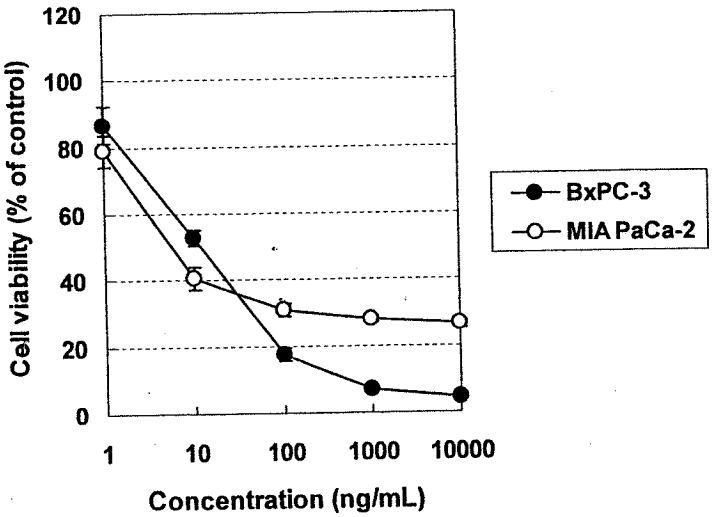
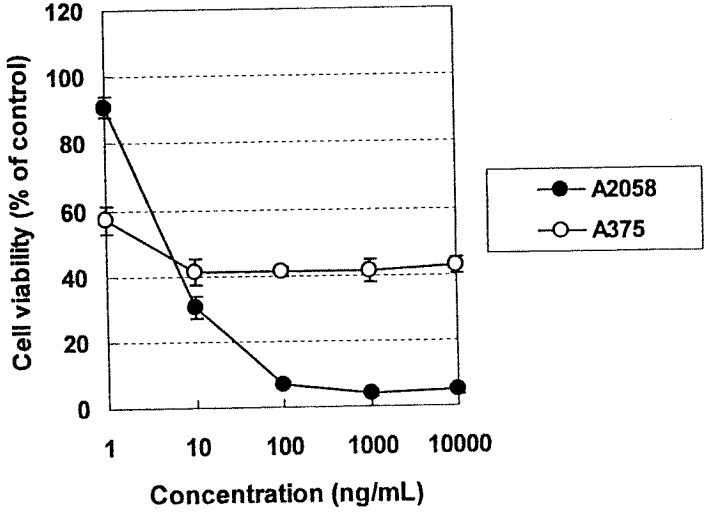


Fig. 5

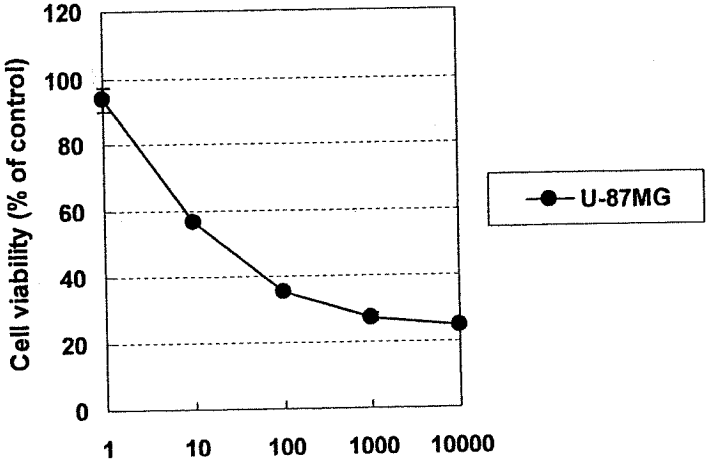
A) Human pancreatic cancer cell line



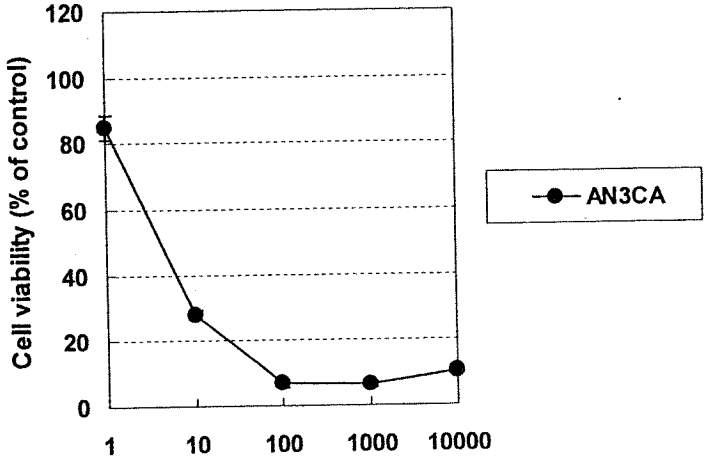
B) Human melanoma cell line



C) Human glioblastoma cell line



D) Human endometrial cancer cell line



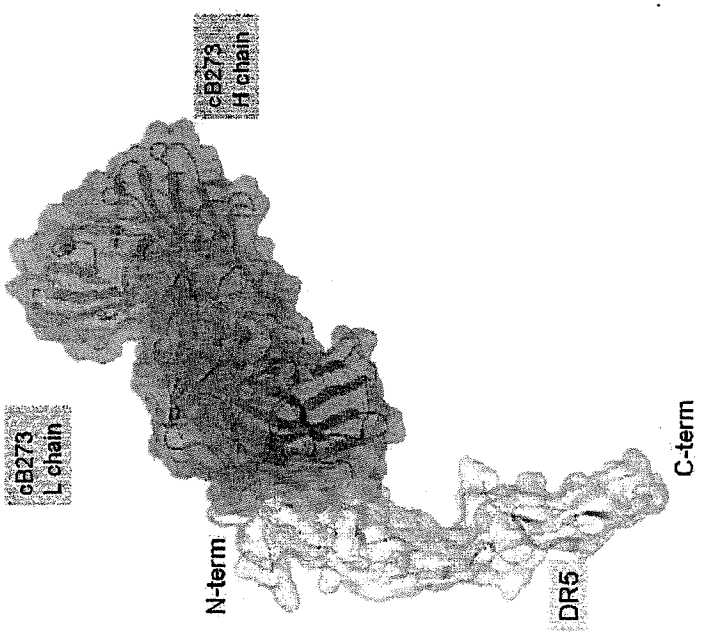


Fig. 6

Fig. 7

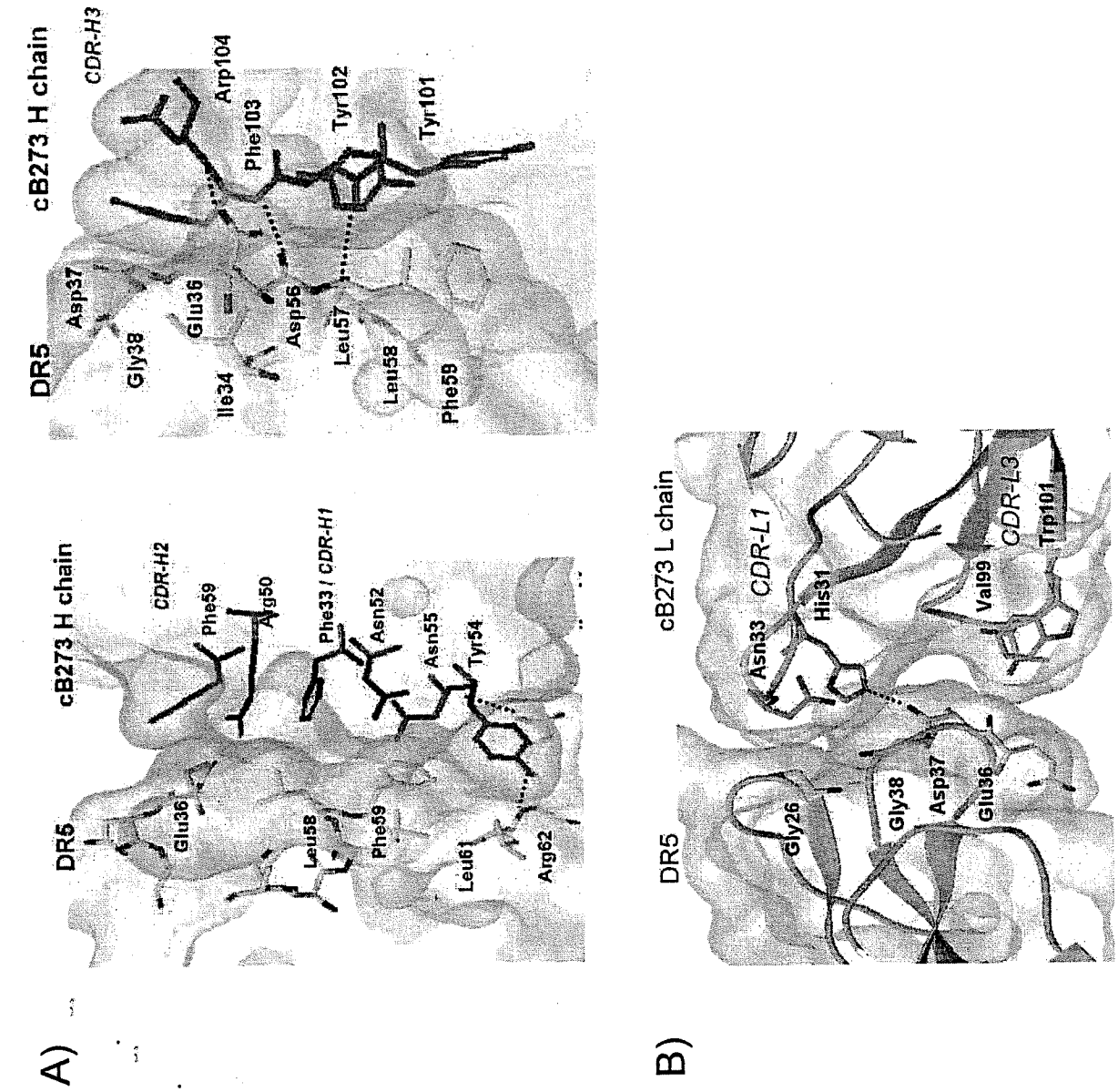

A)
DR5
cB273 H chain
Asp37
Gly38
Glu36
Ile34
Asp56
Leu57
Leu58
Phe59
Phe103
Arp104
Tyr102
Tyr101
CDR-H3
DR5
cB273 H chain
Glu36
Phe59
CDR-H2
Arg50
Leu58
Phe59
Phe33 / CDR-H1
Asn52
Asn55
Tyr54
Leu61
Arg62
B)
DR5
cB273 L chain
Gly26
Gly38
Asp37
Glu36
Asn33
CDR-L1
His31
Val99
CDR-L3
Trp101

Fig. 8-1

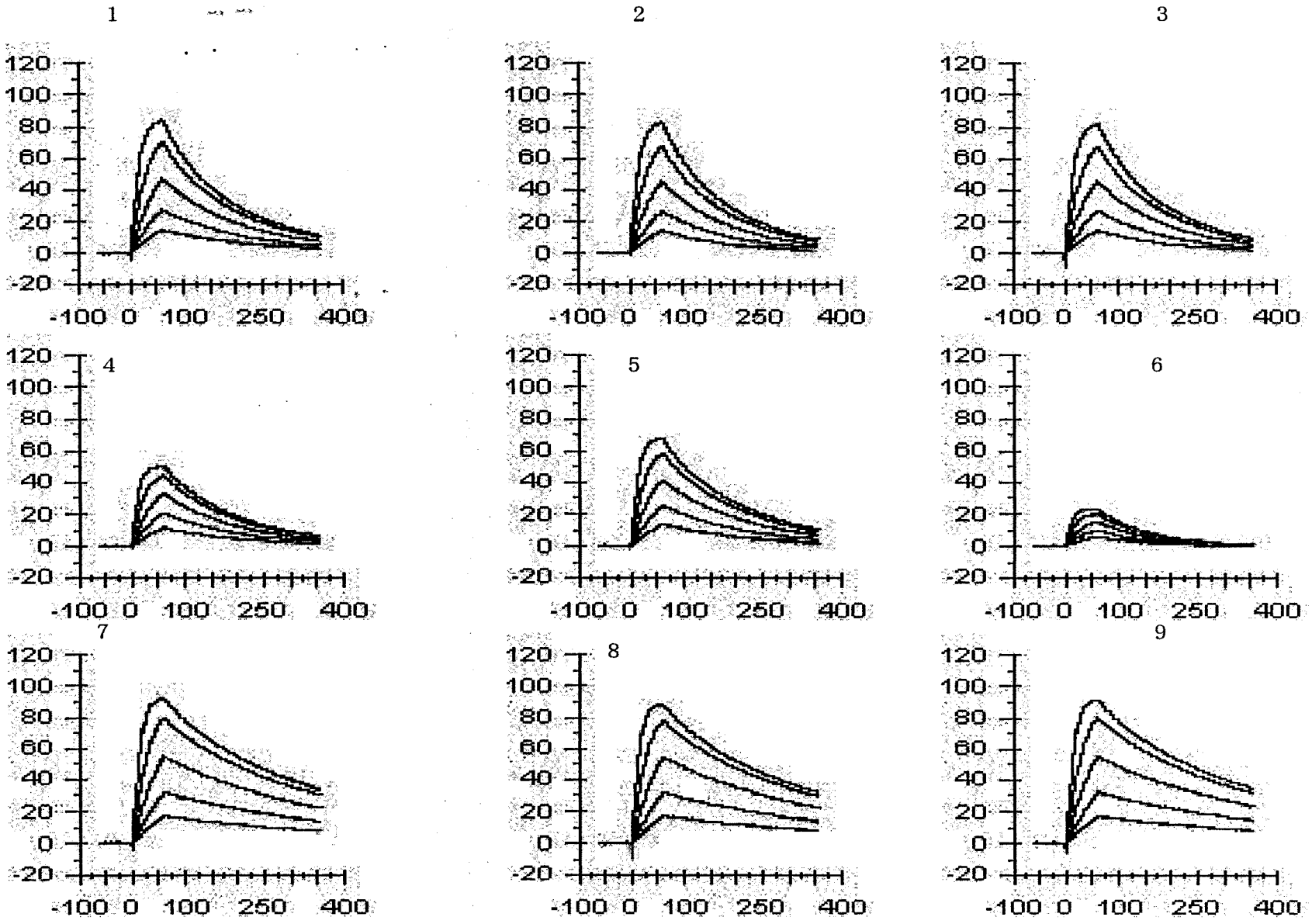


Fig. 8-2

EntryNo.	Neme	Kon (1/Ms)	Koff (1/d)	KD (nM)
1	hB273_H1/hB273_L1	1.804E+06	9.837E-03	5.45
2	hB273_H1/hB273_L2	1.441E+06	9.409E-03	6.53
3	hB273_H1/hB273_L3	1.527E+06	9.218E-03	6.04
4	hB273_H2/hB273_L1	1.853E+06	8.087E-03	4.36
5	hB273_H2/hB273_L2	1.711E+06	7.694E-03	4.47
6	hB273_H2/hB273_L3	1.889E+06	1.020E-02	5.40
7	hB273_H3/hB273_L1	1.809E+06	4.340E-03	2.40
8	hB273_H3/hB273_L2	2.117E+06	4.645E-03	2.19
9	hB273_H3/hB273_L3	2.027E+06	4.363E-03	2.15

Fig. 9

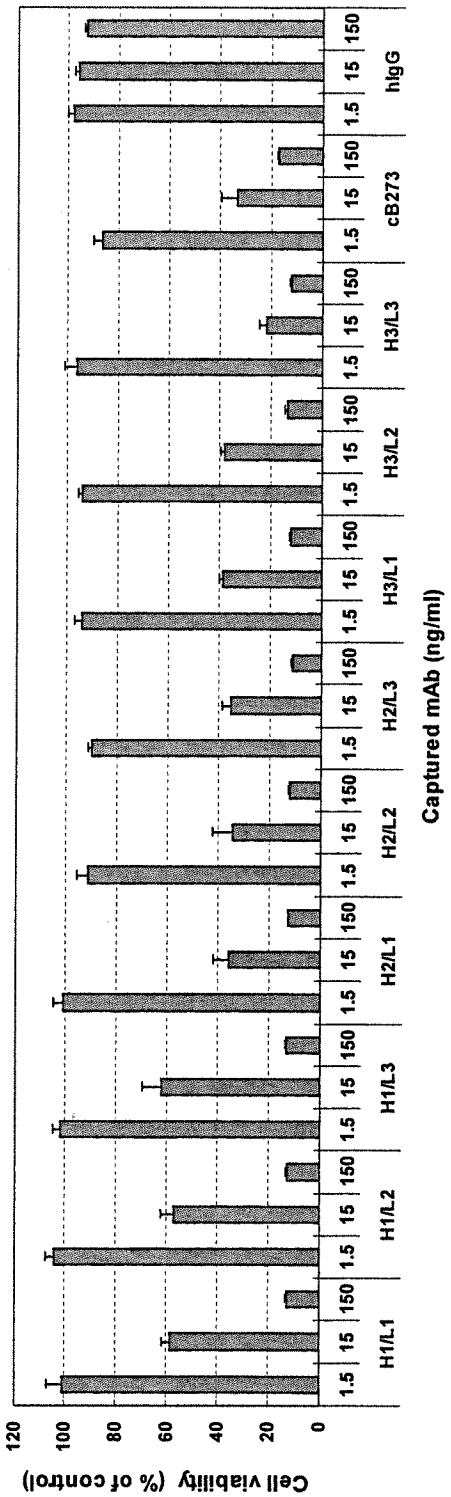
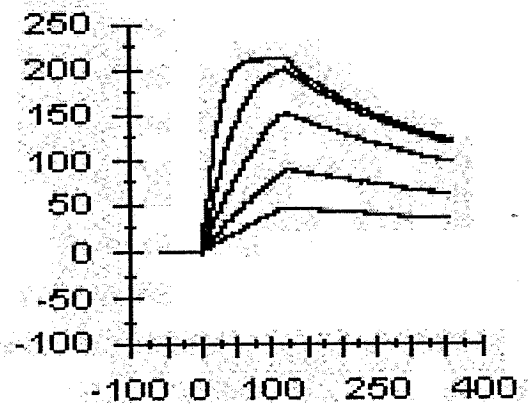
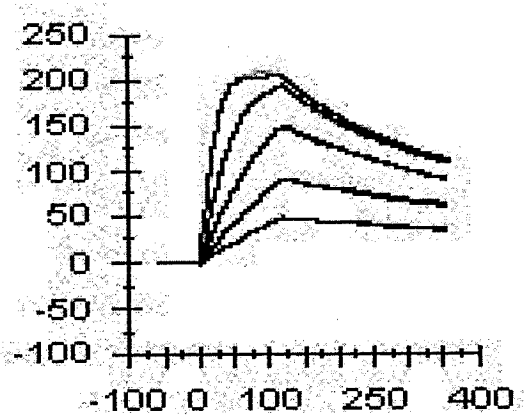

Cell viability (% of control)
120
100
80
60
40
20
0
Captured mAb (ng/ml)
1.5
15
150
H1/L1
H1/L2
H1/L3
H2/L1
H2/L2
H2/L3
H3/L1
H3/L2
H3/L3
cB273
hIgG

Fig. 10-1

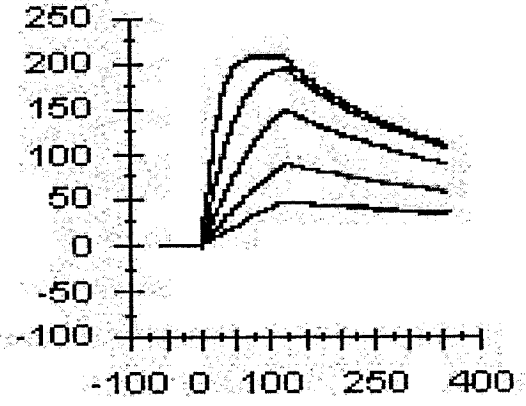
1.



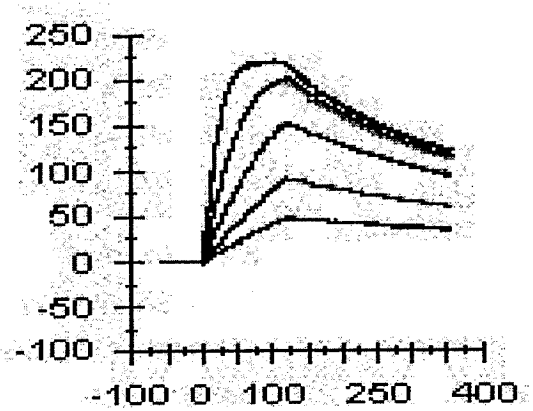
2.



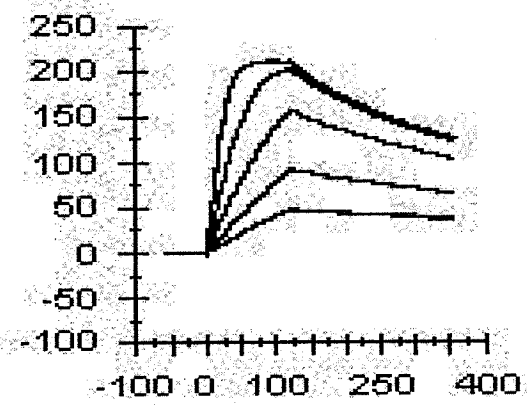
3.



4.



5.



6.

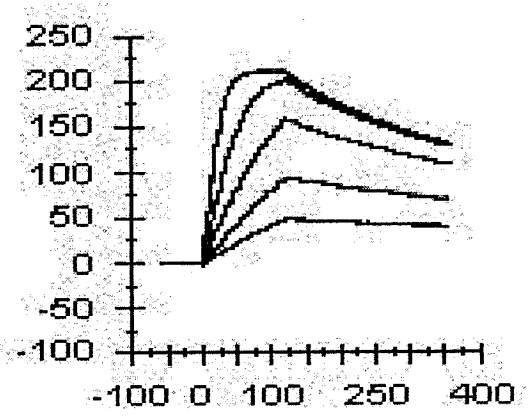


Fig. 10-2

Entry No	Name	Kon (1/Ms)	Koff (1/d)	KD (nM)
1	hB273_H1-1/hB273_L1	2.074E+06	3.787E-03	1.83
2	hB273_H2-1/hB273_L1	2.014E+06	4.015E-03	1.99
3	hB273_H2-2/hB273_L1	2.036E+06	4.359E-03	2.14
4	hB273_H2-3/hB273_L1	1.770E+06	3.755E-03	2.12
5	hB273_H2-4/hB273_L1	2.327E+06	3.595E-03	1.55
6	hB273_H2-5/hB273_L1	2.196E+06	3.024E-03	1.38

Fig. 11

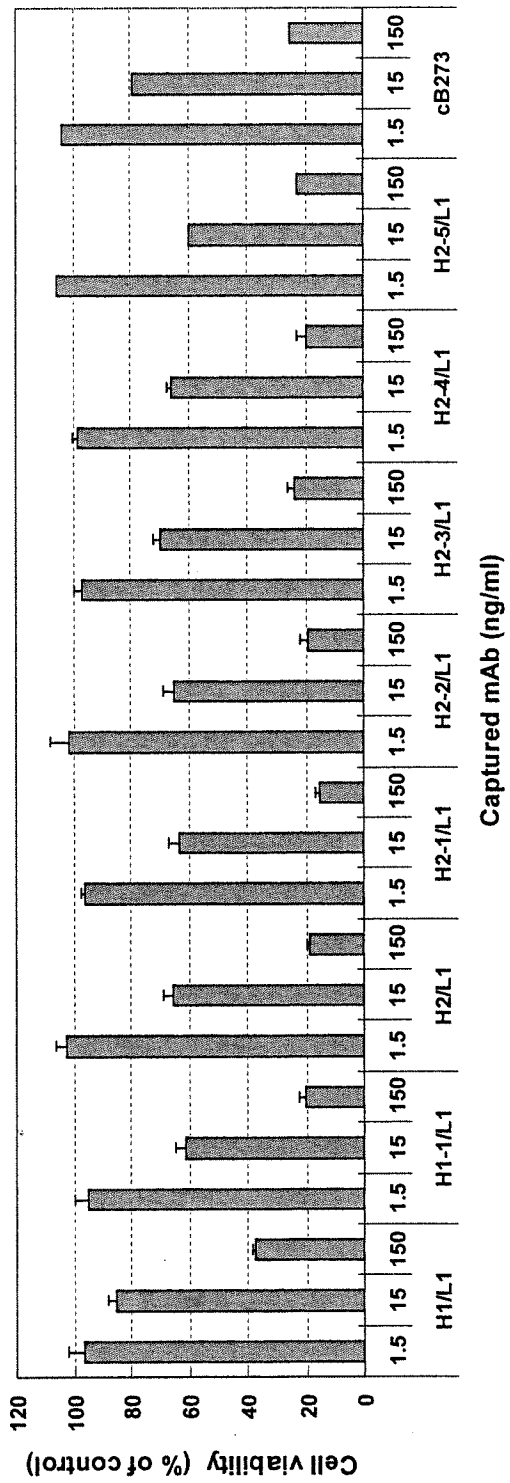

Cell viability (% of control)
120
100
80
60
40
20
0
1.5
15
150
H1/L1
H1-1/L1
H2/L1
H2-1/L1
H2-2/L1
H2-3/L1
H2-4/L1
H2-5/L1
cB273
Captured mAb (ng/ml)

Fig. 12-1

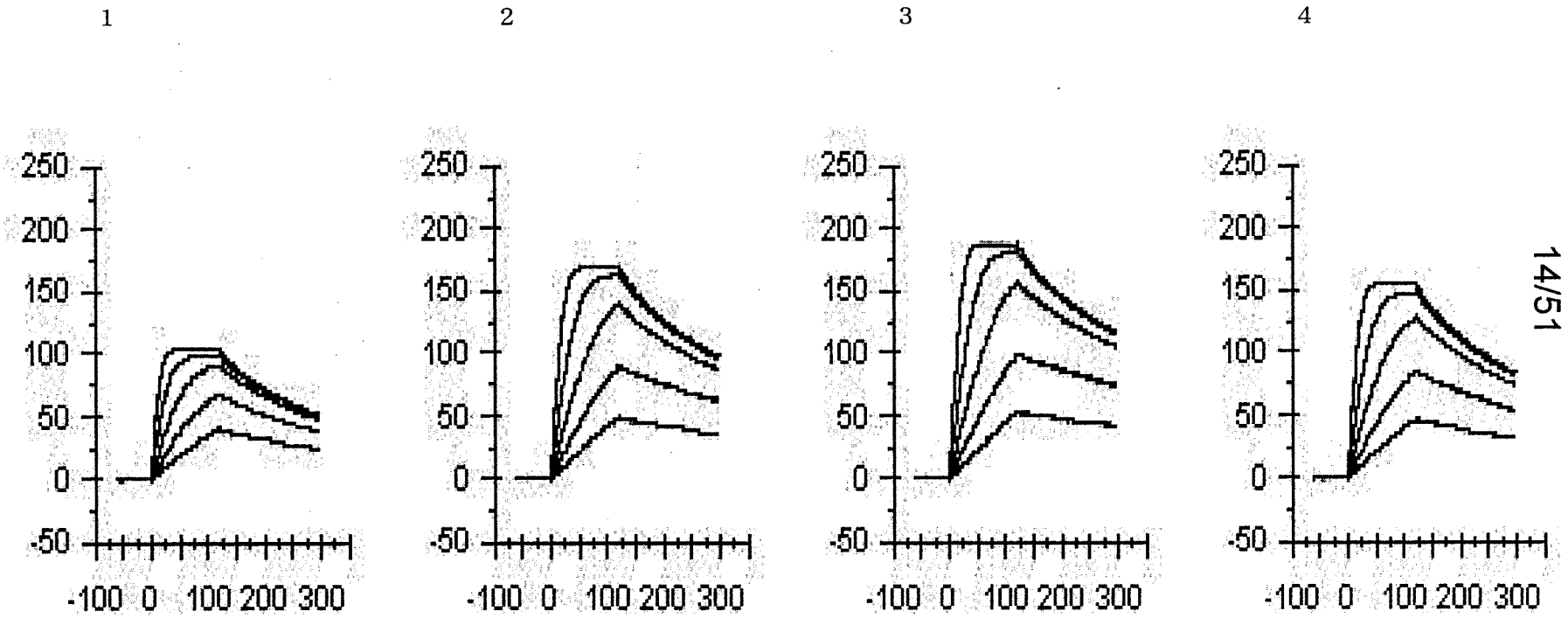


Fig. 12-2

Entry No	Name	kon (1/Ms)	koff (1/d)	KD (nM)
1	hB273_H2-1-NE/hB273_L1-NE	2.77E+06	5.59E-03	2.02
2	hB273_H2-1-NE/hB273_L1-NF	2.92E+06	5.14E-03	1.76
3	hB273_H2-1-NE/hB273_L1-NK	3.34E+06	4.63E-03	1.39
4	hB273_H2-1-NE/hB273_L1-NL	3.34E+06	5.90E-03	1.76

Fig. 13-1

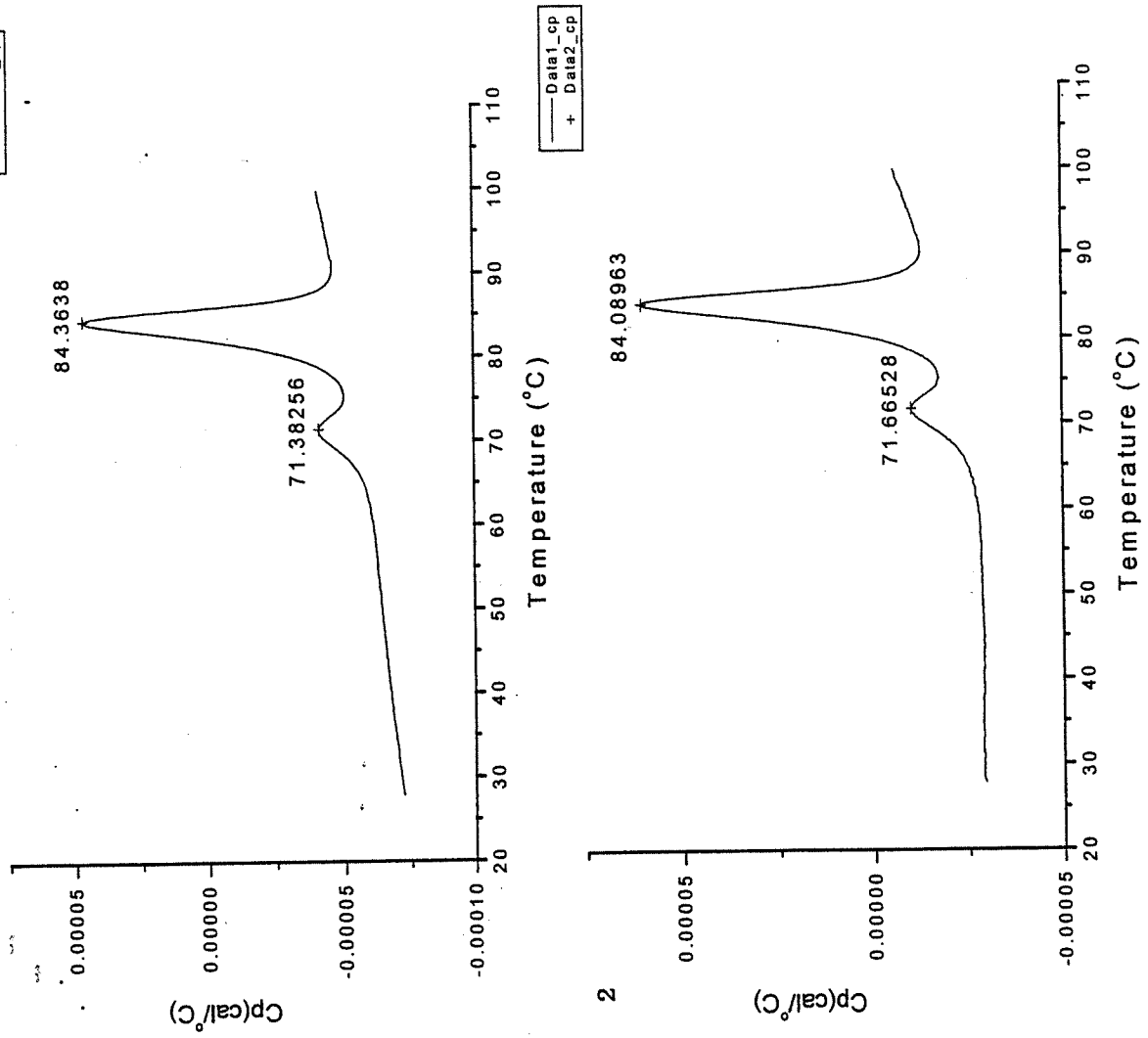

Data1_cp
Data2_cp
84.3638
71.38256
0.00005
0.00000
-0.00005
-0.00010
Cp(cal/°C)
20
30
40
50
60
70
80
90
100
110
Temperature (°C)
Data1_cp
Data2_cp
84.08963
71.66528
0.00005
0.00000
-0.00005
Cp(cal/°C)
20
30
40
50
60
70
80
90
100
110
Temperature (°C)

Fig. 13-2

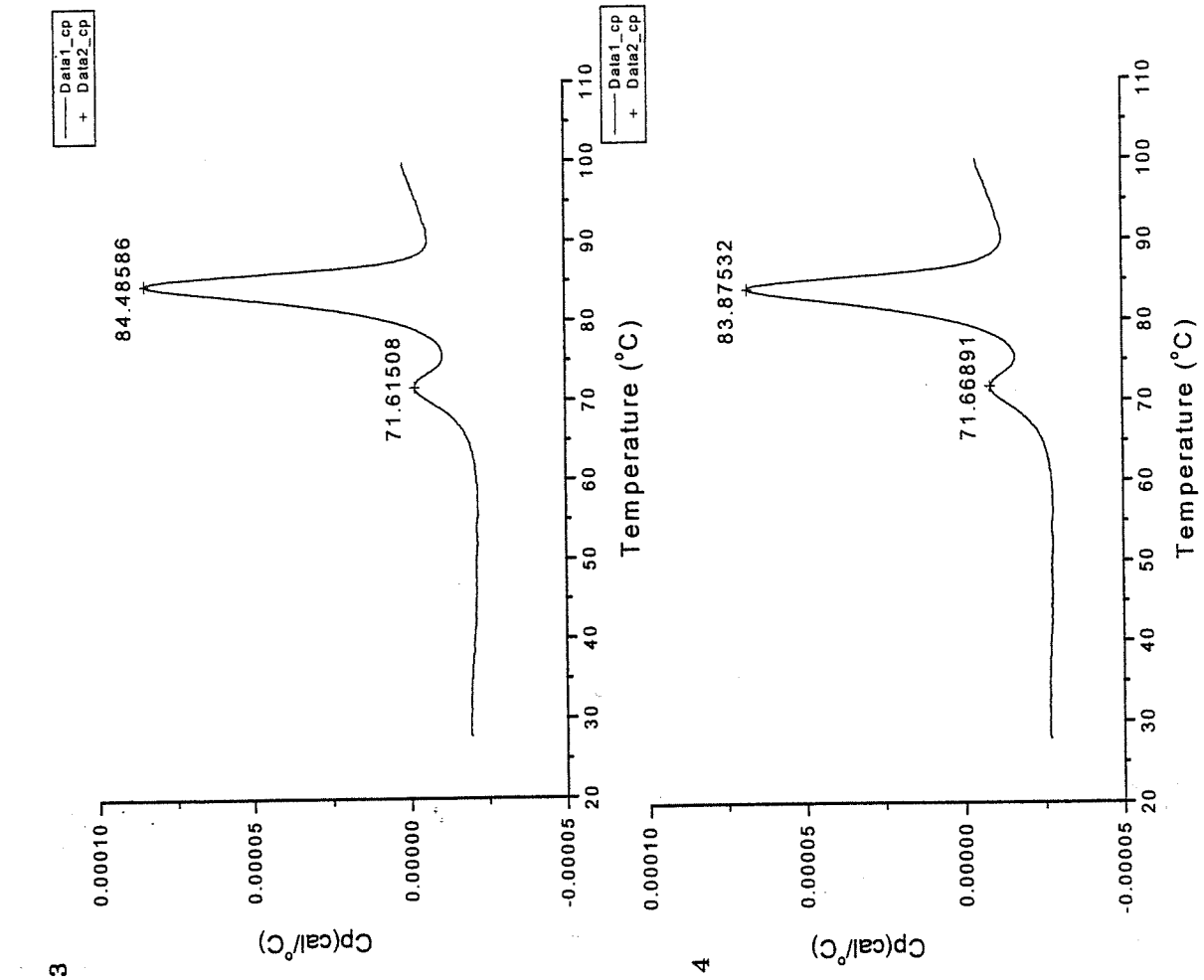

Data1_cp
Data2_cp
84.48586
71.61508
0.00010
0.00005
0.00000
-0.00005
Cp(cal/°C)
20
30
40
50
60
70
80
90
100
110
Temperature (°C)
3
Data1_cp
Data2_cp
83.87532
71.66891
0.00010
0.00005
0.00000
-0.00005
Cp(cal/°C)
20
30
40
50
60
70
80
90
100
110
Temperature (°C)
4

Fig. 13-3

Entry No	Name	Tm (℃)
1	hB273_H2-1-NE/hB273_L1-NE	83.9
2	hB273_H2-1-NE/hB273_L1-NF	84.1
3	hB273_H2-1-NE/hB273_L1-NK	84.5
4	hB273_H2-1-NE/hB273_L1-NL	84.4

Fig. 14

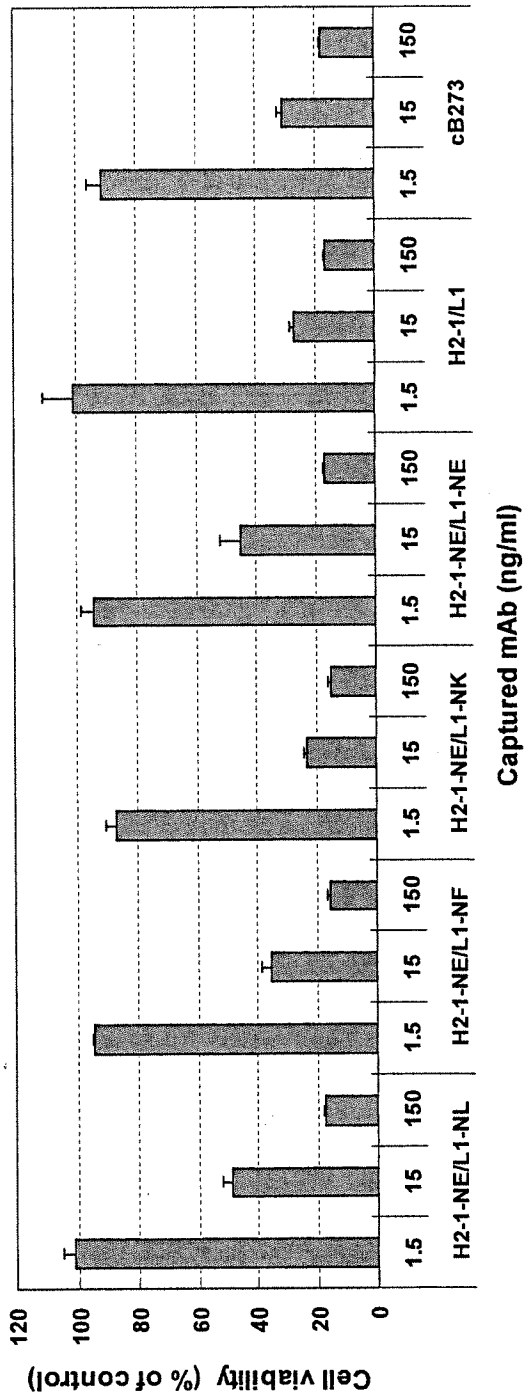

Cell viability (% of control)
120
100
80
60
40
20
0
1.5
15
150
H2-1-NE/L1-NL
1.5
15
150
H2-1-NE/L1-NF
1.5
15
150
H2-1-NE/L1-NK
1.5
15
150
H2-1-NE/L1-NE
1.5
15
150
H2-1/L1
1.5
15
150
cB273
Captured mAb (ng/ml)

Fig. 15

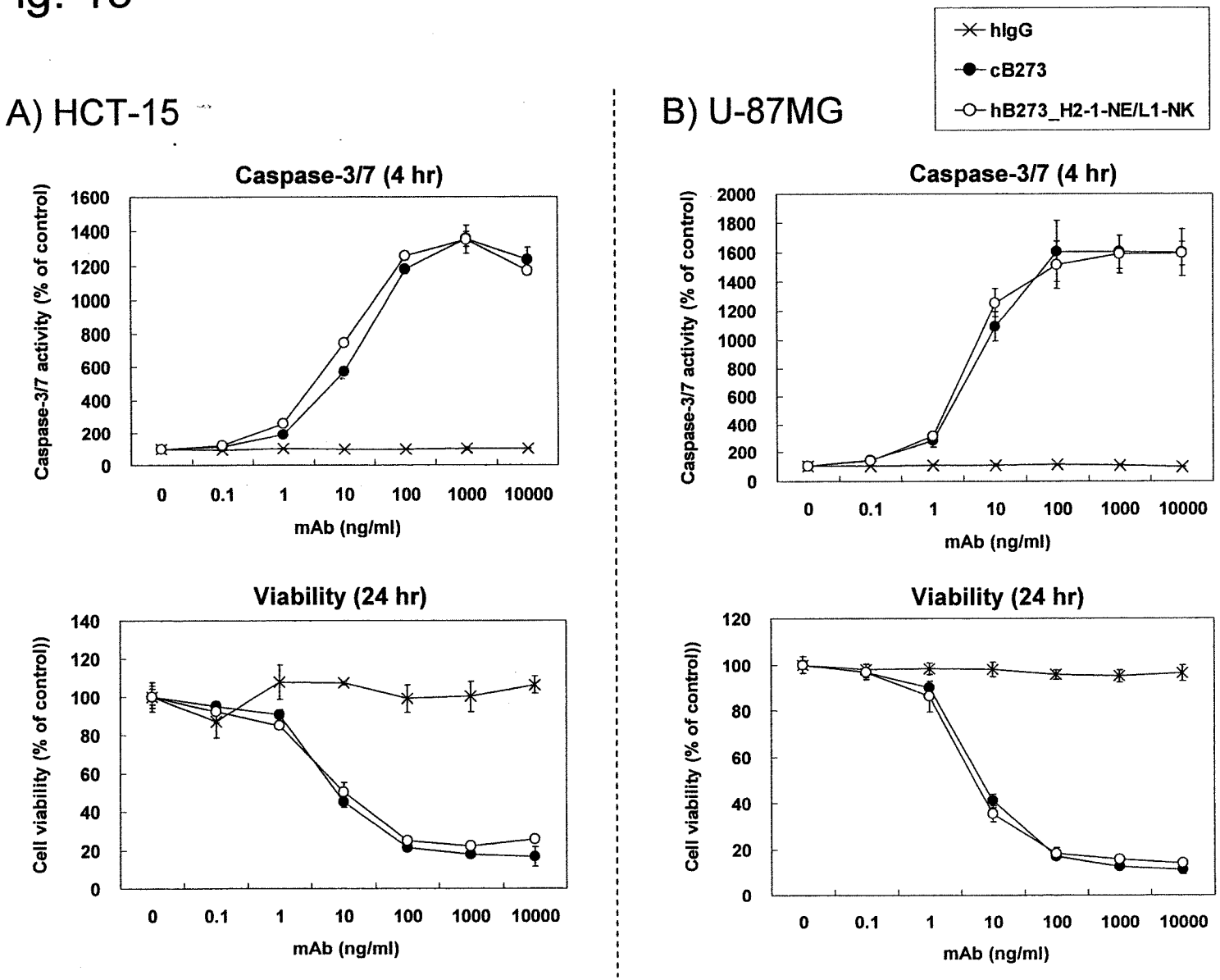

A) HCT-15
B) U-87MG
hIgG
cB273
hB273_H2-1-NE/L1-NK
Caspase-3/7 (4 hr)
Caspase-3/7 activity (% of control)
mAb (ng/ml)
Viability (24 hr)
Cell viability (% of control))
0
0.1
1
10
100
1000
10000

Fig. 16

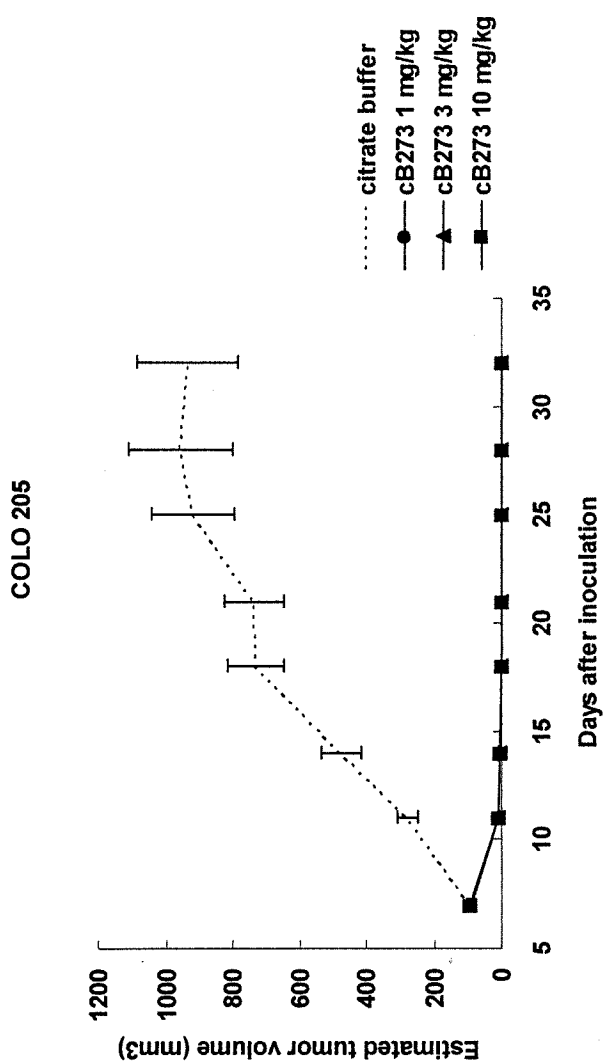

COLO 205
Estimated tumor volume (mm3)
Days after inoculation
citrate buffer
cB273 1 mg/kg
cB273 3 mg/kg
cB273 10 mg/kg
0
200
400
600
800
1000
1200
5
10
15
20
25
30
35

Fig. 17

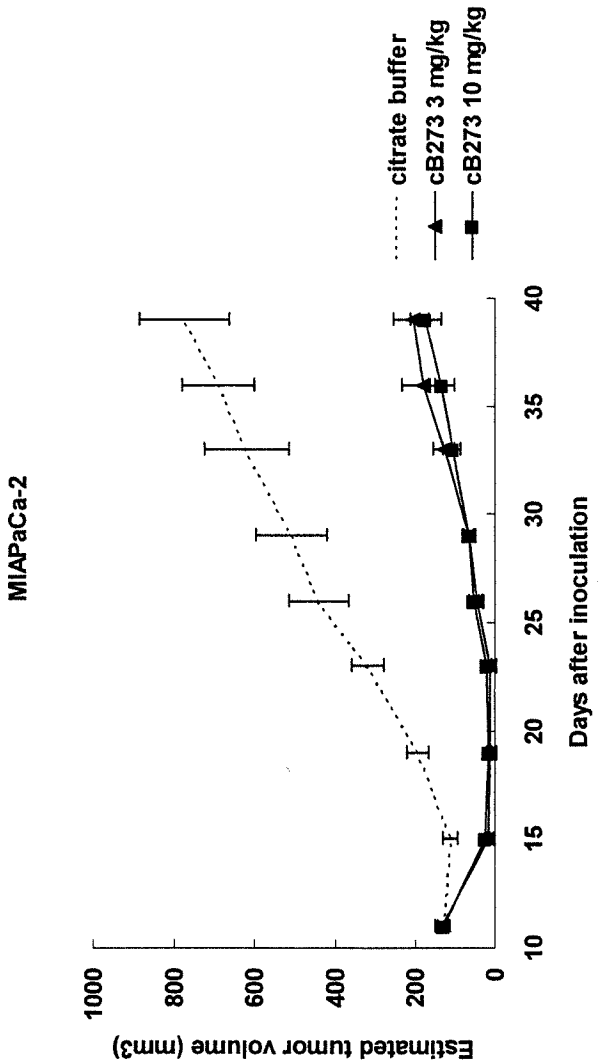

MIAPaCa-2
Estimated tumor volume (mm3)
Days after inoculation
citrate buffer
cB273 3 mg/kg
cB273 10 mg/kg
0
200
400
600
800
1000
10
15
20
25
30
35
40

Fig. 18

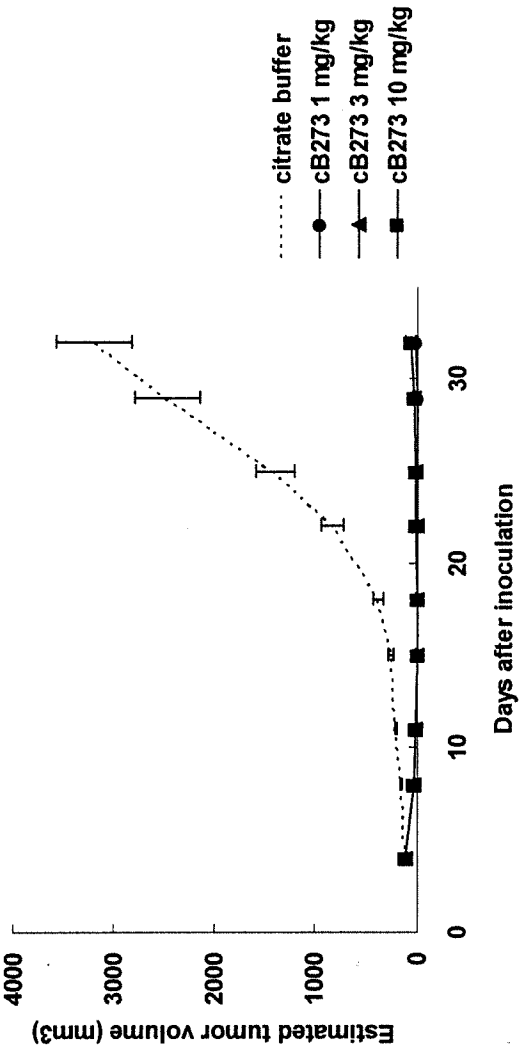

U-87MG
citrate buffer
cB273 1 mg/kg
cB273 3 mg/kg
cB273 10 mg/kg
Estimated tumor volume (mm3)
Days after inoculation
0
1000
2000
3000
4000
0
10
20
30

Fig. 19

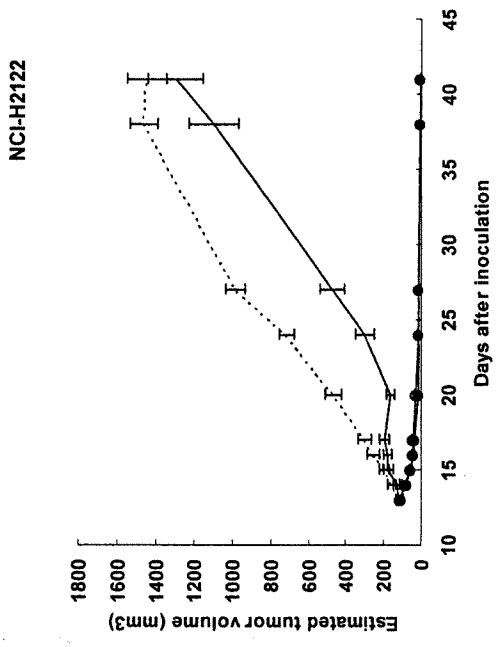

NCI-H2122
untreated
cB273
cB273 + paclitaxel + carboplatin
paclitaxel + carboplatin
Estimated tumor volume (mm3)
Days after inoculation
0
200
400
600
800
1000
1200
1400
1600
1800
10
15
20
25
30
35
40
45

Fig. 20

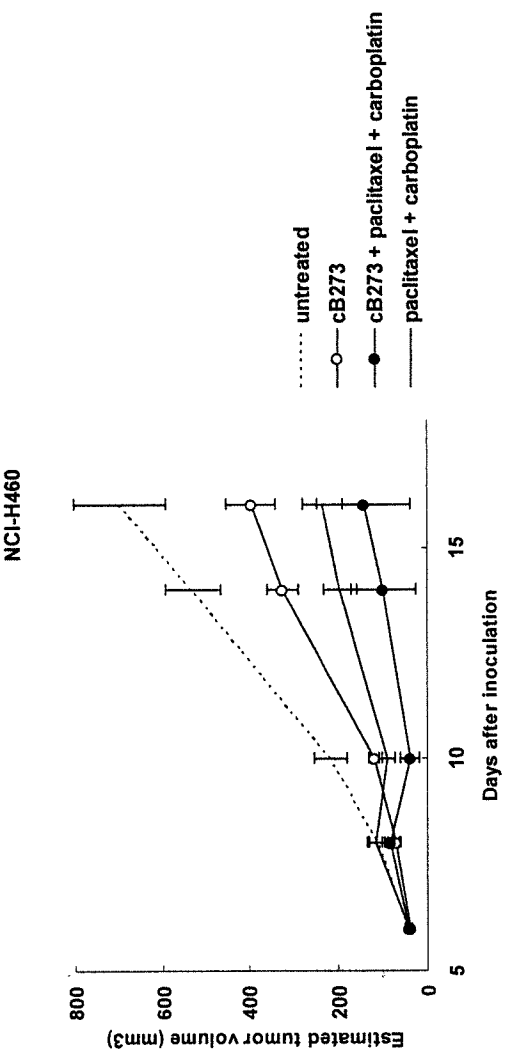

NCI-H460
untreated
cB273
cB273 + paclitaxel + carboplatin
paclitaxel + carboplatin
Estimated tumor volume (mm3)
0
200
400
600
800
5
10
15
Days after inoculation

Fig. 21

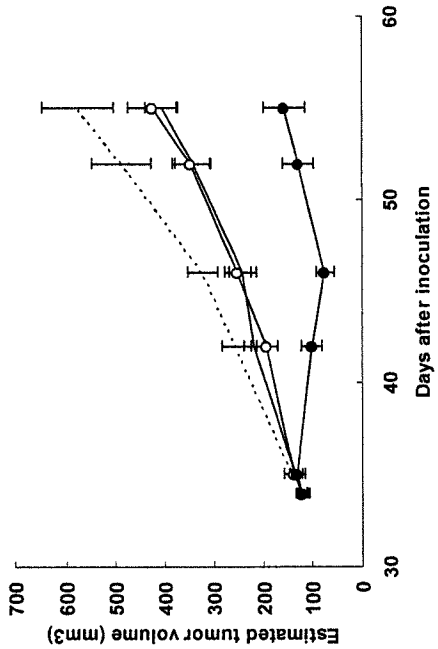

DLD-1
untreated
cB273
cB273 + CPT-11
CPT-11
Estimated tumor volume (mm3)
0
100
200
300
400
500
600
700
30
40
50
60
Days after inoculation

Fig. 22

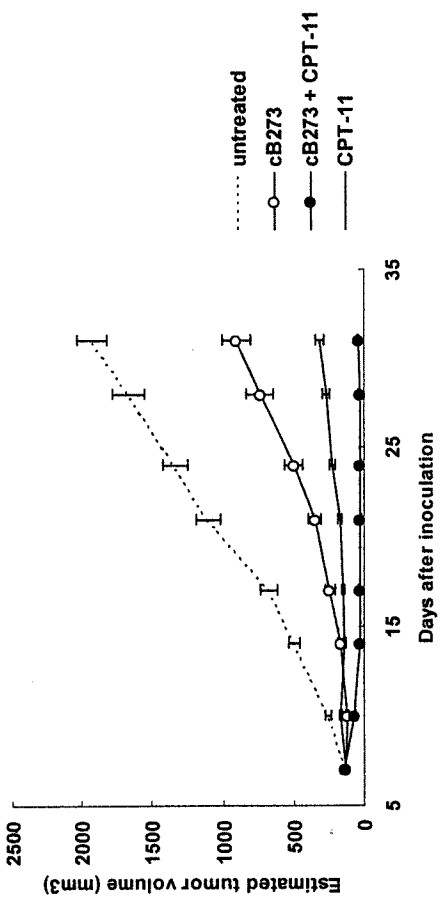

HCT-15
untreated
cB273
cB273 + CPT-11
CPT-11
Estimated tumor volume (mm3)
2500
2000
1500
1000
500
0
5
15
25
35
Days after inoculation

Fig. 23

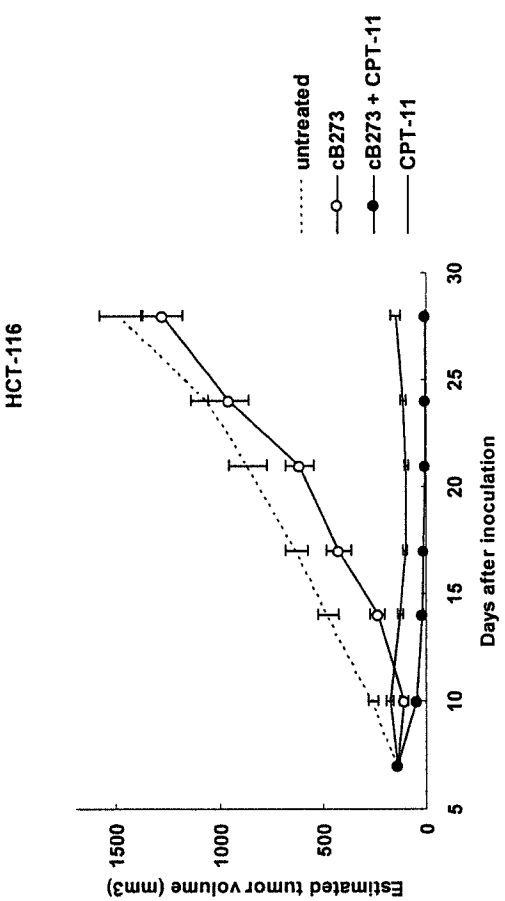

HCT-116
untreated
cB273
cB273 + CPT-11
CPT-11
Estimated tumor volume (mm3)
1500
1000
500
0
5
10
15
20
25
30
Days after inoculation

Fig. 24

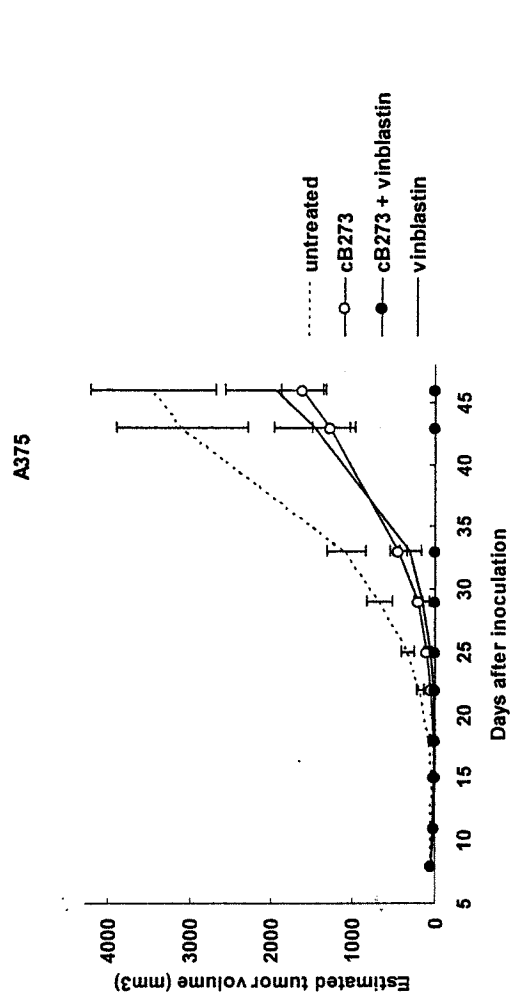

A375
untreated
cB273
cB273 + vinblastin
vinblastin
Estimated tumor volume (mm3)
Days after inoculation
0
1000
2000
3000
4000
5
10
15
20
25
30
35
40
45

Fig. 25

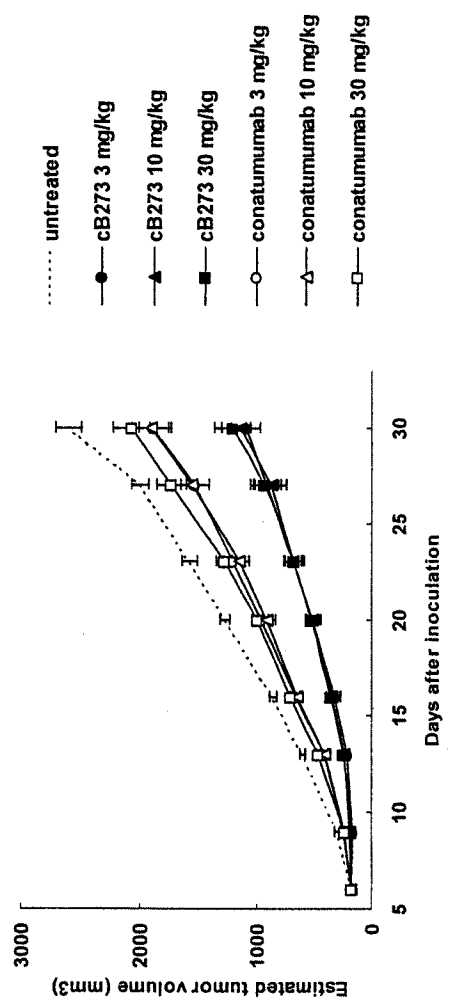

HCT-15
untreated
cB273 3 mg/kg
cB273 10 mg/kg
cB273 30 mg/kg
conatumumab 3 mg/kg
conatumumab 10 mg/kg
conatumumab 30 mg/kg
Estimated tumor volume (mm3)
Days after inoculation
0
1000
2000
3000
5
10
15
20
25
30

Fig. 26

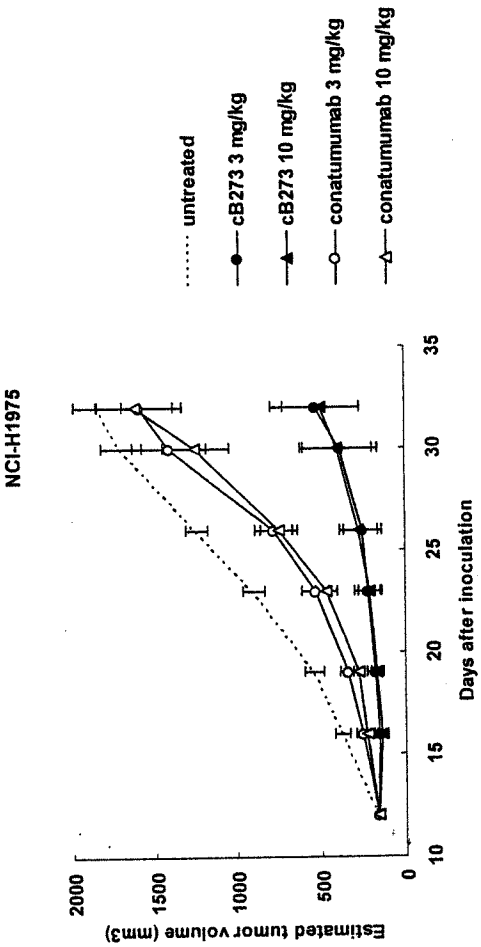

NCI-H1975
untreated
cB273 3 mg/kg
cB273 10 mg/kg
conatumumab 3 mg/kg
conatumumab 10 mg/kg
Estimated tumor volume (mm3)
Days after inoculation
0
500
1000
1500
2000
10
15
20
25
30
35

Fig. 27

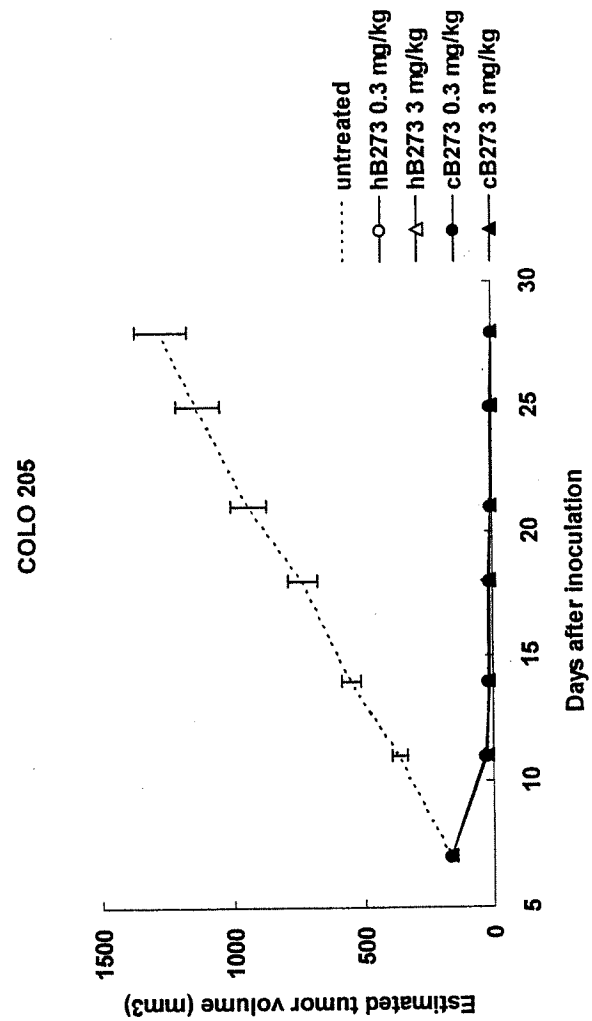

COLO 205
untreated
hB273 0.3 mg/kg
hB273 3 mg/kg
cB273 0.3 mg/kg
cB273 3 mg/kg
Estimated tumor volume (mm3)
Days after inoculation
0
500
1000
1500
5
10
15
20
25
30

Fig. 28

SEQ ID NO: 7: Nucleotide sequence of cDNA encoding mouse antibody B273 heavy chain

atgggatggagctgtatctttctctttctcctgtcagtaactgtaggtgtgttctctgaggttcagc
tgcagcagtctggacctgagctggtgaagcctggggcttcagtgaagatatcctgcaaggcttctgg
ttactcatttattggctactttatgaactggatgaagcagagccatggaaagagccttgagtggatt
ggacgttttaatccatacaatggtgatactttctacaaccagaagttcaagggcaaggccacattga
ctgtagacaaatcctctaccacagcccacatggagctcctgagcctgacatctgaggactctgcagt
ctatttttgtggaagatcggcgtattacttcgatagtgggggctactttgactactggggccaaggc
accactctcacagtctcctcagccaaaacgacacccccatctgtctatccactggcccctggatctg
ctgcccaaactaactccatggtgaccctgggatgcctggtcaagggctatttccctgagccagtgac
agtgacctggaactctggatccctgtccagcggtgtgcacaccttcccagctgtcctgcagtctgac
ctctacactctgagcagctcagtgactgtcccctccagcacctggcccagcgagaccgtcacctgca
acgttgcccacccggccagcagcaccaaggtggacaagaaaattgtgcccagggattgtggttgtaa
gccttgcatatgtacagtcccagaagtatcatctgtcttcatcttccccccaaagcccaaggatgtg
ctcaccattactctgactcctaaggtcacgtgtgttgtggtagacatcagcaaggatgatcccgagg
tccagttcagctggtttgtagatgatgtggaggtgcacacagctcagacgcaaccccgggaggagca
gttcaacagcactttccgctcagtcagtgaacttcccatcatgcaccaggactggctcaatggcaag
gagttcaaatgcagggtcaacagtgcagctttccctgcccccatcgagaaaaccatctccaaaacca
aaggcagaccgaaggctccacaggtgtacaccattccacctcccaaggagcagatggccaaggataa
agtcagtctgacctgcatgataacagacttcttccctgaagacattactgtggagtggcagtggaat
gggcagccagcggagaactacaagaacactcagcccatcatggacacagatggctcttacttcgtct
acagcaagctcaatgtgcagaagagcaactgggaggcaggaaatactttcacctgctctgtgttaca
tgagggcctgcacaaccaccatactgagaagagcctctcccactctcctggtaaa

Signal sequence (1-57), Variable region (58-423), Constant region (424-1395)

SEQ ID NO: 8: Amino acid sequence of mouse antibody B273 heavy chain

MGWSCIFLFLLSVTVGVFSEVQLQQSGPELVKPGASVKISCKASGYSFIGYFMNWMKQSHGKSLEWI
GRFNPYNGDTFYNQKFKGKATLTVDKSSTTAHMELLSLTSEDSAVYFCGRSAYYFDSGGYFDYWGQG
TTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD
LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDV
LTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGK
EFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWN
GQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK

Signal sequence (1-19), Variable region (20-141), Constant region (142-465)

Fig. 29

SEQ ID NO: 9: Nucleotide sequence of cDNA encoding mouse antibody B273 light chain

atgaagttgcctgttaggctgttggtgctgatgttctggattcctgcttccagcagtgatgttgtga
tgacccaaactccactctccctgcctgtcagtcttggagatcaagcctccatctcttgcagatctag
tcagagccttgtacacagtaatggaaacacctatctacattggtacctgcagaagccaggccagtct
ccaaagctcctgatctacaaagtttccaaccgattttctggggtcccagacaggttcagtggcagtg
gatcagggacagatttcacactcaagatcagcagagtggaggctgaggatctgggaatttatttctg
ctctcaaagtacacatgttccgtggacgttcggtggaggcaccaagctggaaatcaaacgggctgat
gctgcaccaactgtatccatcttcccaccatccagtgagcagttaacatctggaggtgcctcagtcg
tgtgcttcttgaacaacttctaccccaaagacatcaatgtcaagtggaagattgatggcagtgaacg
acaaaatggcgtcctgaacagttggactgatcaggacagcaaagacagcacctacagcatgagcagc
accctcacgttgaccaaggacgagtatgaacgacataacagctatacctgtgaggccactcacaaga
catcaacttcacccattgtcaagagcttcaacaggaatgagtgt

Signal sequence (1-57), Variable region (58-399), Constant region (400-714)

SEQ ID NO: 10: Amino acid sequence of mouse antibody B273 light chain

MKLPVRLLVLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQS
PKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQSTHVPWTFGGGTKLEIKRAD
AAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSS
TLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

Signal sequence (1-19), Variable region (20-133), Constant region (134-238)

Fig. 30

SEQ ID NO: 15: Nucleotide sequence of B273 chimera-type light chain

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcatatggcgatgttg
tgatgacccaaactccactctccctgcctgtcagtcttggagatcaagcctccatctcttgcagatc
tagtcagagccttgtacacagtaatggaaacacctatctacattggtacctgcagaagccaggccag
tctccaaagctcctgatctacaaagtttccaaccgattttctggggtcccagacaggttcagtggca
gtggatcagggacagatttcacactcaagatcagcagagtggaggctgaggatctgggaatttattt
ctgctctcaaagtacacatgttccgtggacgttcggtggaggcaccaagctggaaatcaaacgtacg
gtggccgcccccctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccgcctccg
tggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtggacaacgccct
gcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacctacagcctgagc
agcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcctgcgaggtgacccacc
agggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt

Signal sequence (1-60), Variable region (61-402), Constant region (403-717)

SEQ ID NO: 16: Amino acid sequence of B273 chimera-type light chain

MVLQTQVFISLLLWISGAYGDVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQ
SPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQSTHVPWTFGGGTKLEIKRT
VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-134), Constant region (135-239)

Fig. 31

SEQ ID NO: 19: Nucleotide sequence of B273 chimera-type heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagcgaggttcagc
tgcagcagtctggacctgagctggtgaagcctggggcttcagtgaagatatcctgcaaggcttctgg
ttactcatttattggctactttatgaactggatgaagcagagccatggaaagagccttgagtggatt
ggacgttttaatccatacaatggtgatactttctacaaccagaagttcaagggcaaggccacattga
ctgtagacaaatcctctaccacagcccacatggagctcctgagcctgacatctgaggactctgcagt
ctatttttgtggaagatcggcgtattacttcgatagtgggggctactttgactactggggccaaggc
accactctcacagtcagctcagcctccaccaagggcccaagcgtcttcccccctggcaccctcctcca
agagcacctctggcggcacagccgccctgggctgcctggtcaaggactacttccccgaacccgtgac
cgtgagctggaactcaggcgccctgaccagcggcgtgcacaccttccccgctgtcctgcagtcctca
ggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatct
gcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgtgacaa
aactcacacatgcccaccctgcccagcacctgaactcctgggggggaccctcagtcttcctcttcccc
ccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtga
gccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagac
aaagccccgggaggagcagtacaacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccag
gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgaga
aaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccatcccggga
ggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgcc
gtggagtgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccg
acggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtctt
ctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctccc
ggcaaa

Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 20: Amino acid sequence of B273 chimera-type heavy chain

MKHLWFFLLLVAAPRWVLSEVQLQQSGPELVKPGASVKISCKASGYSFIGYFMNWMKQSHGKSLEWI
GRFNPYNGDTFYNQKFKGKATLTVDKSSTTAHMELLSLTSEDSAVYFCGRSAYYFDSGGYFDYWGQG
TTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 32

SEQ ID NO: 27: Nucleotide sequence of hB273_L1-type light chain
atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcatatggcgacatcg
taatgacccagtctccgctgagtcttcctgtgactccaggggagcccgcaagcatctcttgtcgcag
cagtcagtcactggtccatagcaatgggaacacttacctgcattggtacctccaaaaaccagggcag
tccccacagctcttgatctacaaggtgtccaatcggttcagtggtgtgcctgaccgcttctccggaa
gtggctccgggacagatttcactcttaagatttcaagagtggaggcagaagacgttggagtctatta
ttgctcacagagcacacatgtcccctggactttcggtcccggcacaaaagtcgagatcaagcgtacg
gtggccgccccctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccgcctccg
tggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtggacaacgccct
gcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacctacagcctgagc
agcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcctgcgaggtgacccacc
agggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt
Signal sequence (1-60), Variable region (61-402), Constant region (403-717)

SEQ ID NO: 28: Amino acid sequence of hB273_L1-type light chain
MVLQTQVFISLLLWISGAYGDIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGNTYLHWYLQKPGQ
SPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPWTFGPGTKVEIKRT
VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Signal sequence (1-20), Variable region (21-134), Constant region (135-239)

Fig. 33

SEQ ID NO: 29: Nucleotide sequence of hB273_L2-type light chain
atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcatatggcgacgtcg
tcatgacacagacacctctgagcctgcccgtgtctctgggcgaacccgccagtatttcttgtaggtc
atctcagtctctggtgcacagtaacggaaacacatatctccattggtacctgcagaagccaggtcag
tccccaaagctcctgatctataaggtgagcaacagattctccggagtgcctgatcgattcagcggga
gtggttcagggaccgacttcaccttgaagattagccgggtcgaggccgaggatgttggagtgtattt
ctgtagccagagtacacacgtgccctggaccttcggacctgggactaaagtcgagattaaacgtacg
gtggccgccccctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccgcctccg
tggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtggacaacgccct
gcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacctacagcctgagc
agcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcctgcgaggtgacccacc
agggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt
Signal sequence (1-60), Variable region (61-402), Constant region (403-717)

SEQ ID NO: 30: Amino acid sequence of hB273_L2-type light chain
MVLQTQVFISLLLWISGAYGDVVMTQTPLSLPVSLGEPASISCRSSQSLVHSNGNTYLHWYLQKPGQ
SPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTHVPWTFGPGTKVEIKRT
VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Signal sequence (1-20), Variable region (21-134), Constant region (135-239)

Fig. 34

SEQ ID NO: 31: Nucleotide sequence of hB273_L3-type light chain
atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcatatggcgacgtgg
tgatgacgcagactccgctgtcactgcccgtatctctgggagagcctgccagcatcagctgcaggag
ctctcaatcactggtgcactctaacggtaatacctacctccactggtatctccagaagccaggacaa
tccccaaagttgctcatatataaagtgtccaaccggttctcaggagtccctgaccggtttagcggta
gtggctctggtacagatttcaccctgaaaatatcaagggttgaagcggaagacgtaggagtgtattt
ttgcagccagagcacccatgtcccctggacatttgggggcggcaccaaggtcgaaatcaagcgtacg
gtggccgcccccctccgtgttcatcttcccccccctccgacgagcagctgaagtccggcaccgcctccg
tggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtggacaacgccct
gcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacctacagcctgagc
agcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcctgcgaggtgacccacc
agggcctgagctccccgtcaccaagagcttcaacaggggggagtgt
Signal sequence (1-60), Variable region (61-402), Constant region (403-717)

SEQ ID NO: 32: Amino acid sequence of hB273_L3-type light chain
MVLQTQVFISLLLWISGAYGDVVMTQTPLSLPVSLGEPASISCRSSQSLVHSNGNTYLHWYLQKPGQ
SPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTHVPWTFGGGTKVEIKRT
VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Signal sequence (1-20), Variable region (21-134), Constant region (135-239)

Fig. 35

SEQ ID NO: 33: Nucleotide sequence of hB273_H1-type heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCtgagcCAAGTTCAGC
TCGTGCAGTCCGGCGCGGAGGTTAAGAAACCAGGCGCATCCGTTAAAGTGTCATGTAAGGCCAGCGG
GTACTCCTTTATCGGCTACTTTATGAACTGGGTGCGGCAGGCCCCTGGTATGGGCCTGGAGTGGATG
GGACGGTTTAATCCATATAATGGCGATACTTTTTACAACCAGAAATTTAAAGGAAGGGTCACTCTCA
CAGTGGATAAAAGCACTAGTACGGCTTACATGGAACTGTCCTCCCTCAGATCAGAAGATACTGCCGT
CTACTACTGCGCCCGAAGTGCTTACTATTTCGACAGCGGGGGCTACTTTGATTATTGGGGCCAGGGG
ACCCTGGTAACTGTGagcTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCACCCTCCTCCA
AGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGAC
CGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCA
GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
GCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
AACTCACACATGCCCACCCTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCC
CCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
AAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAG
GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA
AAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTGCCCCCATCCCGGGA
GGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
GTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTT
CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCC
GGCAAA

Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 34: Amino acid sequence of hB273_H1-type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYSFIGYFMNWVRQAPGMGLEWM
GRFNPYNGDTFYNQKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCARSAYYFDSGGYFDYWGQG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 36

SEQ ID NO: 35: Nucleotide sequence of hB273_H2-type heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtccagc
tggtgcagagtggagccgaggtaaaaaaaccaggggctagtgtcaaggtctcctgtaaggcatctgg
ttactcttttataggatacttcatgaactggatgaagcagtctcccggtatgtctctggagtggatt
ggcagattcaacccctacaacggggacacttttataatcagaagttcaaagggaaagccactctga
ccgtggacaagtcaacttccacagcatacatggaattgtcctcactgaggtccgaagataccgccgt
gtacttctgcgctcggagtgcttattatttcgatagcggagggtattttgactattgggggcaaggg
acccttgtaaccgtgagctcagcctccaccaagggcccaagcgtcttcccccctggcaccctcctcca
agagcacctctggcggcacagccgccctgggctgcctggtcaaggactacttccccgaacccgtgac
cgtgagctggaactcaggcgccctgaccagcggcgtgcacaccttccccgctgtcctgcagtcctca
ggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatct
gcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgtgacaa
aactcacacatgcccaccctgcccagcacctgaactcctgggggggaccctcagtcttcctcttcccc
ccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtga
gccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagac
aaagccccgggaggagcagtacaacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccag
gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgaga
aaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccatcccggga
ggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgcc
gtggagtgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccg
acggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtctt
ctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctccc
ggcaaa

Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 36: Amino acid sequence of hB273_H2-type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYSFIGYFMNWMKQSPGMSLEWI
GRFNPYNGDTFYNQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYFCARSAYYFDSGGYFDYWGQG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 37

SEQ ID NO: 37: Nucleotide sequence of hB273_H3-type heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagcgaagtgcagc
tcgtgcaaagcggcgctgaagtgaaaaaaccaggagcctcagtcaaagtgtcctgtaaggcctccgg
gtatagcttcatcggctattttatgaactggatgaagcagagcccgggcaaaagcctcgaatggatc
gggagattcaatccatacaatggtgacacctttacaatcagaaattcaaaggcaaggccacgctga
ctgtagacaaatccaccagcacagcccacatggaattgtcttccctgaggtctgaggataccgcggt
gtacttttgtggccgaagtgcgtattatttcgattcaggcgggtacttcgattactggggtcagggg
acgctcgtcaccgtaagctcagcctccaccaagggcccaagcgtcttcccccctggcaccctcctcca
agagcacctctggcggcacagccgccctgggctgcctggtcaaggactacttccccgaacccgtgac
cgtgagctggaactcaggcgccctgaccagcggcgtgcacaccttccccgctgtcctgcagtcctca
ggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatct
gcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgtgacaa
aactcacacatgcccaccctgcccagcacctgaactcctgggggggaccctcagtcttcctcttcccc
ccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtga
gccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagac
aaagccccgggaggagcagtacaacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccag
gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgaga
aaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccatcccggga
ggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgcc
gtggagtgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccg
acggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtctt
ctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctccc
ggcaaa

Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 38: Amino acid sequence of hB273_H3-type heavy chain

MKHLWFFLLLVAAPRWVLSEVQLVQSGAEVKKPGASVKVSCKASGYSFIGYFMNWMKQSPGKSLEWI
GRFNPYNGDTFYNQKFKGKATLTVDKSTSTAHMELSSLRSEDTAVYFCGRSAYYFDSGGYFDYWGQG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 38

SEQ ID NO: 39: Nucleotide sequence of hB273_H1-1-type heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagc
tggtgcagtctggcgccgaagtgaagaaacctggcgcttctgtgaaggtgtcctgcaaggccagcgg
ctacagcttcatcggctacttcatgaactggatgcggcaggcccctggcatgggactggaatggatg
ggccggttcaaccctacaacggcgacaccttctacaaccagaaattcaagggcagagtgaccctga
ccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggagcgaggataccgccgt
gtatttctgcggcagaagcgcctactacttcgacagcggcggctacttcgactactggggccagggc
accctggtgacagtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctcca
agagcacctctggcggcacagccgccctgggctgcctggtcaaggactacttccccgaacccgtgac
cgtgagctggaactcaggcgccctgaccagcggcgtgcacaccttccccgctgtcctgcagtcctca
ggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatct
gcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgtgacaa
aactcacacatgcccaccctgcccagcacctgaactcctgggggggaccctcagtcttcctcttcccc
ccaaaacccaaggacaccctcatgatctcccggaccctgaggtcacatgcgtggtggtggacgtga
gccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagac
aaagccccgggaggagcagtacaacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccag
gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgaga
aaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccatcccggga
ggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgcc
gtggagtgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccg
acggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtctt
ctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctccc
ggcaaa

Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 40: Amino acid sequence of hB273_H1-1-type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYSFIGYFMNWMRQAPGMGLEWM
GRFNPYNGDTFYNQKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYFCGRSAYYFDSGGYFDYWGQG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 39

SEQ ID NO: 41: Nucleotide sequence of hB273_H2-1-type heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagcgaggtgcagc
tggtgcagtctggcgccgaagtgaagaaacctggagccagcgtgaaggtgtcctgcaaggccagcgg
ctacagcttcatcggctacttcatgaactggatgaagcagagccccggcatgagcctggaatggatc
ggccggttcaacccctacaacggcgacaccttctacaaccagaagttcaagggaaaggccaccctga
cagtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggagcgaggataccgccgt
gtacttctgcgccagaagcgcctactacttcgacagcggcggctacttcgactactggggccagggc
accctggtgacagtgagctcagcctccaccaagggcccaagcgtcttcccccctggcaccctcctcca
agagcacctctggcggcacagccgccctgggctgcctggtcaaggactacttccccgaacccgtgac
cgtgagctggaactcaggcgccctgaccagcggcgtgcacaccttccccgctgtcctgcagtcctca
ggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatct
gcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgtgacaa
aactcacacatgcccaccctgcccagcacctgaactcctgggggggaccctcagtcttcctcttcccc
ccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtga
gccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagac
aaagccccgggaggagcagtacaacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccag
gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgaga
aaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccatcccggga
ggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgcc
gtggagtgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccg
acggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtctt
ctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctccc
ggcaaa

Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 42: Amino acid sequence of hB273_H2-1-type heavy chain

MKHLWFFLLLVAAPRWVLSEVQLVQSGAEVKKPGASVKVSCKASGYSFIGYFMNWMKQSPGMSLEWI
GRFNPYNGDTFYNQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYFCARSAYYFDSGGYFDYWGQG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 40

SEQ ID NO: 43: Nucleotide sequence of hB273_H2-2-type heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagc
tggtgcagtctggcgccgaagtgaagaaacctggagccagcgtgaaggtgtcctgcaaggccagcgg
ctacagcttcatcggctacttcatgaactggatgaagcagagccccggcatgagcctggaatggatc
ggccggttcaacccctacaacggcgacaccttctacaaccagaagttcaagggaaaggccaccctga
cagtggacaagagcaccagcaccgcccacatggaactgagcagcctgcggagcgaggataccgccgt
gtacttctgcgccagaagcgcctactacttcgacagcggcggctacttcgactactggggccagggc
accctggtgacagtgagctcagcctccaccaagggcccaagcgtcttcccccctggcaccctcctcca
agagcacctctggcggcacagccgccctgggctgcctggtcaaggactacttccccgaacccgtgac
cgtgagctggaactcaggcgccctgaccagcggcgtgcacaccttccccgctgtcctgcagtcctca
ggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatct
gcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgtgacaa
aactcacacatgcccaccctgcccagcacctgaactcctgggggggaccctcagtcttcctcttcccc
ccaaaacccaaggacaccctcatgatctcccggaccccctgaggtcacatgcgtggtggtggacgtga
gccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagac
aaagccccgggaggagcagtacaacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccag
gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgaga
aaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccatcccggga
ggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgcc
gtggagtgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccg
acggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtctt
ctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctccc
ggcaaa

Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 44: Amino acid sequence of hB273_H2-2-type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYSFIGYFMNWMKQSPGMSLEWI
GRFNPYNGDTFYNQKFKGKATLTVDKSTSTAHMELSSLRSEDTAVYFCARSAYYFDSGGYFDYWGQG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 41

SEQ ID NO: 45: Nucleotide sequence of hB273_H2-3-type heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagcgaggtgcagc
tggtgcagtctggcgccgaagtgaagaaacctggagccagcgtgaaggtgtcctgcaaggccagcgg
ctacagcttcatcggctacttcatgaactggatgaagcagagccccggcatgagcctggaatggatc
ggccggttcaacccctacaacggcgacaccttctacaaccagaagttcaagggaaaggccaccctga
cagtggacaagagcaccagcaccgcccacatggaactgagcagcctgcggagcgaggataccgccgt
gtacttctgcgccagaagcgcctactacttcgacagcggcggctacttcgactactggggccagggc
accctggtgacagtgagctcagcctccaccaagggcccaagcgtcttcccccctggcaccctcctcca
agagcacctctggcggcacagccgccctgggctgcctggtcaaggactacttccccgaacccgtgac
cgtgagctggaactcaggcgccctgaccagcggcgtgcacaccttccccgctgtcctgcagtcctca
ggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatct
gcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgtgacaa
aactcacacatgcccaccctgcccagcacctgaactcctgggggggaccctcagtcttcctcttcccc
ccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtga
gccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagac
aaagccccgggaggagcagtacaacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccag
gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgaga
aaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccatcccggga
ggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgcc
gtggagtgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccg
acggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtctt
ctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctccc
ggcaaa

Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 46: Amino acid sequence of hB273_H2-3-type heavy chain

MKHLWFFLLLVAAPRWVLSEVQLVQSGAEVKKPGASVKVSCKASGYSFIGYFMNWMKQSPGMSLEWI
GRFNPYNGDTFYNQKFKGKATLTVDKSTSTAHMELSSLRSEDTAVYFCARSAYYFDSGGYFDYWGQG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 42

SEQ ID NO: 47: Nucleotide sequence of hB273_H2-4-type heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagc
tggtgcagtctggcgccgaagtgaagaaacctggagccagcgtgaaggtgtcctgcaaggccagcgg
ctacagcttcatcggctacttcatgaactggatgaagcagagccccggcatgagcctggaatggatc
ggccggttcaacccctacaacggcgacaccttctacaaccagaagttcaagggaaaggccaccctga
cagtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggagcgaggataccgccgt
gtacttctgcggcagaagcgcctactacttcgacagcggcggctacttcgactactggggccagggc
accctggtgacagtgagctcagcctccaccaagggcccaagcgtcttcccccctggcaccctcctcca
agagcacctctggcggcacagccgccctgggctgcctggtcaaggactacttccccgaacccgtgac
cgtgagctggaactcaggcgccctgaccagcggcgtgcacaccttccccgctgtcctgcagtcctca
ggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatct
gcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgtgacaa
aactcacacatgcccaccctgcccagcacctgaactcctgggggggaccctcagtcttcctcttcccc
ccaaaacccaaggacaccctcatgatctcccggaccccctgaggtcacatgcgtggtggtggacgtga
gccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagac
aaagccccgggaggagcagtacaacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccag
gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgaga
aaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccatcccggga
ggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgcc
gtggagtgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccg
acggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtctt
ctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctccc
ggcaaa

Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 48: Amino acid sequence of hB273_H2-4-type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYSFIGYFMNWMKQSPGMSLEWI
GRFNPYNGDTFYNQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYFCGRSAYYFDSGGYFDYWGQG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 43

SEQ ID NO: 49: Nucleotide sequence of hB273_H2-5-type heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagc
tggtgcagtctggcgccgaagtgaagaaacctggagccagcgtgaaggtgtcctgcaaggccagcgg
ctacagcttcatcggctacttcatgaactggatgaagcagagccccggcaagagcctggaatggatc
ggccggttcaacccctacaacggcgacaccttctacaaccagaagttcaagggaaaggccaccctga
cagtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggagcgaggataccgccgt
gtacttctgcggcagaagcgcctactacttcgacagcggcggctacttcgactactggggccagggc
accctggtgacagtgagctcagcctccaccaagggcccaagcgtcttcccccctggcaccctcctcca
agagcacctctggcggcacagccgccctgggctgcctggtcaaggactacttccccgaacccgtgac
cgtgagctggaactcaggcgccctgaccagcggcgtgcacaccttccccgctgtcctgcagtcctca
ggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatct
gcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgtgacaa
aactcacacatgcccaccctgcccagcacctgaactcctgggggggaccctcagtcttcctcttcccc
ccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtga
gccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagac
aaagccccgggaggagcagtacaacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccag
gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgaga
aaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccatcccggga
ggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgcc
gtggagtgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccg
acggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtctt
ctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctccc
ggcaaa

Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 50: Amino acid sequence of hB273_H2-5-type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYSFIGYFMNWMKQSPGKSLEWI
GRFNPYNGDTFYNQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYFCGRSAYYFDSGGYFDYWGQG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 44

SEQ ID NO: 51: Nucleotide sequence of hB273_L1-NE-type light chain

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcatatggcgacatcg
taatgacccagtctccgctgagtcttcctgtgactccaggggagcccgcaagcatctcttgtcgcag
cagtcagtcactggtccatagcaatgagaacacttacctgcattggtacctccaaaaaccagggcag
tccccacagctcttgatctacaaggtgtccaatcggttcagtggtgtgcctgaccgcttctccggaa
gtggctccgggacagatttcactcttaagatttcaagagtggaggcagaagacgttggagtctatta
ttgctcacagagcacacatgtcccctggactttcggtcccggcacaaaagtcgagatcaagcgtacg
gtggccgcccccctccgtgttcatcttcccccccctccgacgagcagctgaagtccggcaccgcctccg
tggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtggacaacgccct
gcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacctacagcctgagc
agcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcctgcgaggtgacccacc
agggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt

Signal sequence (1-60), Variable region (61-402), Constant region (403-717)

SEQ ID NO: 52: Amino acid sequence of hB273_L1-NE-type light chain

MVLQTQVFISLLLWISGAYGDIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNENTYLHWYLQKPGQ
SPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPWTFGPGTKVEIKRT
VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-134), Constant region (135-239)

Fig. 45

SEQ ID NO: 57: Nucleotide sequence of hB273_L1-NF-type light chain
atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcatatggcgacatcg
taatgacccagtctccgctgagtcttcctgtgactccaggggagcccgcaagcatctcttgtcgcag
cagtcagtcactggtccatagcaatttcaacacttacctgcattggtacctccaaaaaccagggcag
tccccacagctcttgatctacaaggtgtccaatcggttcagtggtgtgcctgaccgcttctccggaa
gtggctccgggacagatttcactcttaagatttcaagagtggaggcagaagacgttggagtctatta
ttgctcacagagcacacatgtcccctggactttcggtcccggcacaaaagtcgagatcaagcgtacg
gtggccgccccctccgtgttcatcttcccccccctccgacgagcagctgaagtccggcaccgcctccg
tggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtggacaacgccct
gcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacctacagcctgagc
agcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcctgcgaggtgacccacc
agggcctgagctccccgtcaccaagagcttcaacaggggggagtgt
Signal sequence (1-60), Variable region (61-402), Constant region (403-717)

SEQ ID NO: 58: Amino acid sequence of hB273_L1-NF-type light chain
MVLQTQVFISLLLWISGAYGDIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNFNTYLHWYLQKPGQ
SPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPWTFGPGTKVEIKRT
VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Signal sequence (1-20), Variable region (21-134), Constant region (135-239)

Fig. 46

SEQ ID NO: 61: Nucleotide sequence of hB273_L1-NK-type light chain

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcatatggcgacatcg
taatgacccagtctccgctgagtcttcctgtgactccaggggagcccgcaagcatctcttgtcgcag
cagtcagtcactggtccatagcaataagaacacttacctgcattggtacctccaaaaaccagggcag
tccccacagctcttgatctacaaggtgtccaatcggttcagtggtgtgcctgaccgcttctccggaa
gtggctccgggacagatttcactcttaagatttcaagagtggaggcagaagacgttggagtctatta
ttgctcacagagcacacatgtcccctggactttcggtcccggcacaaaagtcgagatcaagcgtacg
gtggccgccccctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccgcctccg
tggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtggacaacgccct
gcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacctacagcctgagc
agcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcctgcgaggtgacccacc
agggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt

Signal sequence (1-60), Variable region (61-402), Constant region (403-717)

SEQ ID NO: 62: Amino acid sequence of hB273_L1-NK-type light chain

MVLQTQVFISLLLWISGAYGDIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNKNTYLHWYLQKPGQ
SPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPWTFGPGTKVEIKRT
VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-134), Constant region (135-239)

Fig. 47

SEQ ID NO: 65: Nucleotide sequence of hB273_L1-NL-type light chain
atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcatatggcgacatcg
taatgacccagtctccgctgagtcttcctgtgactccaggggagcccgcaagcatctcttgtcgcag
cagtcagtcactggtccatagcaatctgaacacttacctgcattggtacctccaaaaaccagggcag
tccccacagctcttgatctacaaggtgtccaatcggttcagtggtgtgcctgaccgcttctccggaa
gtggctccgggacagatttcactcttaagatttcaagagtggaggcagaagacgttggagtctatta
ttgctcacagagcacacatgtcccctggactttcggtcccggcacaaaagtcgagatcaagcgtacg
gtggccgccccctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccgcctccg
tggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtggacaacgccct
gcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacctacagcctgagc
agcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcctgcgaggtgacccacc
agggcctgagctccccgtcaccaagagcttcaacaggggggagtgt
Signal sequence (1-60), Variable region (61-402), Constant region (403-717)

SEQ ID NO: 66: Amino acid sequence of hB273_L1-NL-type light chain
MVLQTQVFISLLLWISGAYGDIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNLNTYLHWYLQKPGQ
SPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPWTFGPGTKVEIKRT
VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Signal sequence (1-20), Variable region (21-134), Constant region (135-239)

Fig. 48

SEQ ID NO: 69: Nucleotide sequence of hB273_H2-1-NE-type heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagcgaggtgcagc
tggtgcagtctggcgccgaagtgaagaaacctggagccagcgtgaaggtgtcctgcaaggccagcgg
ctacagcttcatcggctacttcatgaactggatgaagcagagccccggcatgagcctggaatggatc
ggccggttcaacccctacaacgaggacaccttctacaaccagaagttcaagggaaaggccaccctga
cagtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggagcgaggataccgccgt
gtacttctgcgccagaagcgcctactacttcgacagcggcggctacttcgactactggggccagggc
accctggtgacagtgagctcagcctccaccaagggcccaagcgtcttcccccctggcaccctcctcca
agagcacctctggcggcacagccgccctgggctgcctggtcaaggactacttccccgaacccgtgac
cgtgagctggaactcaggcgccctgaccagcggcgtgcacaccttccccgctgtcctgcagtcctca
ggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatct
gcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgtgacaa
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ggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgcc
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acggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtctt
ctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctccc
ggcaaa

Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 70: Amino acid sequence of hB273_H2-1-NE-type heavy chain

MKHLWFFLLLVAAPRWVLSEVQLVQSGAEVKKPGASVKVSCKASGYSFIGYFMNWMKQSPGMSLEWI
GRFNPYNEDTFYNQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYFCARSAYYFDSGGYFDYWGQG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 49

SEQ ID NO: 75: Nucleotide sequence of cDNA encoding conatumumab light chain

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcatatggcgaaatcg
tgttgacacagagtcccggcactcttagccttagcccgggtgaacgcgccaccctgtcctgccgcgc
ctctcagggaatctctcgctcttacctcgcgtggtaccagcagaaacccggccaggcccccagtttg
ctgatatacggtgcctctagccgagcaactggcatcccagaccggttctcaggatctggctccggga
ctgacttcactctgaccatctccagactggagcccgaggatttcgcggtatattactgccagcagtt
cggcagcagtccttggaccttcggacagggtactaaggtggagattaaacgtacggtggccgccccc
tccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccgcctccgtggtgtgcctgc
tgaataacttctaccccagagaggccaaggtgcagtggaaggtggacaacgccctgcagtccgggaa
ctcccaggagagcgtgaccgagcaggacagcaaggacagcacctacagcctgagcagcaccctgacc
ctgagcaaagccgactacgagaagcacaaggtgtacgcctgcgaggtgacccaccagggcctgagct
cccccgtcaccaagagcttcaacaggggggagtgt

Signal sequence (1-60), Variable region (61-390), Constant region (400-705)

SEQ ID NO: 76: Amino acid sequence of conatumumab light chain

MVLQTQVFISLLLWISGAYGEIVLTQSPGTLSLSPGERATLSCRASQGISRSYLAWYQQKPGQAPSL
LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPWTFGQGTKVEIKRTVAAP
SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT
LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-130), Constant region (131-235)

Fig. 50

SEQ ID NO: 77: Nucleotide sequence of cDNA encoding conatumumab heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagc
ttcaggaaagcgggcccggcctcgtgaagccctcccagaccctgtctcttacttgtacagtgagcgg
tggcagcatttcttcaggcgattacttctggagttggattcgccaactgcctggtaaagggctggaa
tggatcgggcatattcacaattcaggaaccacatattataacccttcactgaagagccgggtaacta
tctccgttgacactagcaagaaacagttctccctccggctgtcttctgtcacagccgctgacaccgc
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accaccgtaacagtgagctcagcctccaccaagggcccaagcgtcttcccccctggcaccctcctcca
agagcacctctggcggcacagccgccctgggctgcctggtcaaggactacttccccgaacccgtgac
cgtgagctggaactcaggcgccctgaccagcggcgtgcacaccttccccgctgtcctgcagtcctca
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gcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgtgacaa
aactcacacatgcccaccctgcccagcacctgaactcctgggggggaccctcagtcttcctcttcccc
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gccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagac
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gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgaga
aaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccatcccggga
ggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgcc
gtggagtgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccg
acggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtctt
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ggcaaa

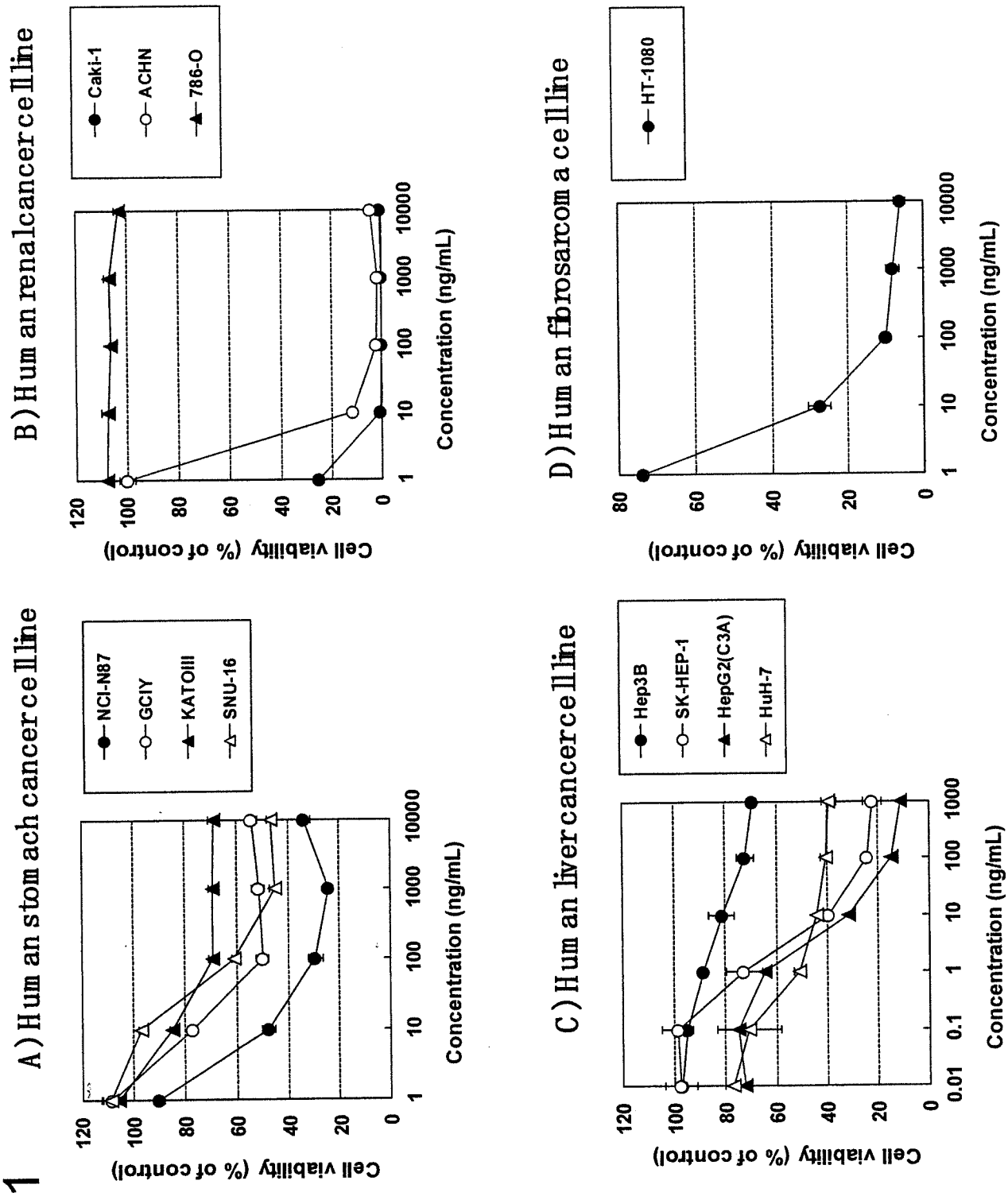
Signal sequence (1-57), Variable region (58-423), Constant region (424-1413)

SEQ ID NO: 78: Amino acid sequence of conatumumab heavy chain

MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYFWSWIRQLPGKGLE
WIGHIHNSGTTYYNPSLKSRVTISVDTSKKQFSLRLSSVTAADTAVYYCARDRGGDYYYGMDVWGQG
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

Signal sequence (1-19), Variable region (20-141), Constant region (142-471)

Fig. 51


A) Human stomach cancer cell line
NCI-N87
GCIY
KATOIII
SNU-16
Cell viability (% of control)
Concentration (ng/mL)
B) Human renal cancer cell line
Caki-1
ACHN
786-O
Cell viability (% of control)
Concentration (ng/mL)
C) Human liver cancer cell line
Hep3B
SK-HEP-1
HepG2(C3A)
HuH-7
Cell viability (% of control)
Concentration (ng/mL)
D) Human fibrosarcoma cell line
HT-1080
Cell viability (% of control)
Concentration (ng/mL)

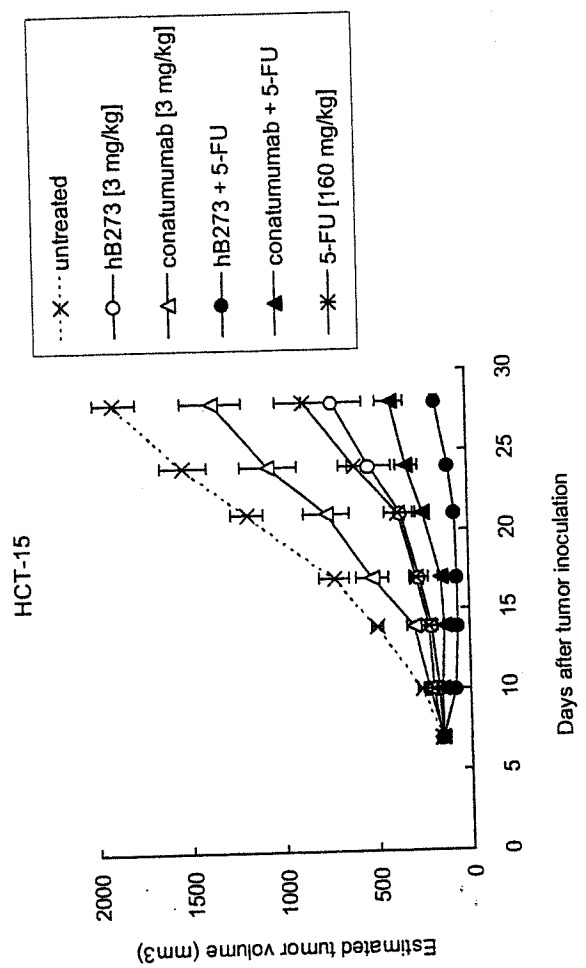

HCT-15
untreated
hB273 [3 mg/kg]
conatumumab [3 mg/kg]
hB273 + 5-FU
conatumumab + 5-FU
5-FU [160 mg/kg]
Estimated tumor volume (mm3)
Days after tumor inoculation
0
500
1000
1500
2000
0
5
10
15
20
25
30

Fig. 52

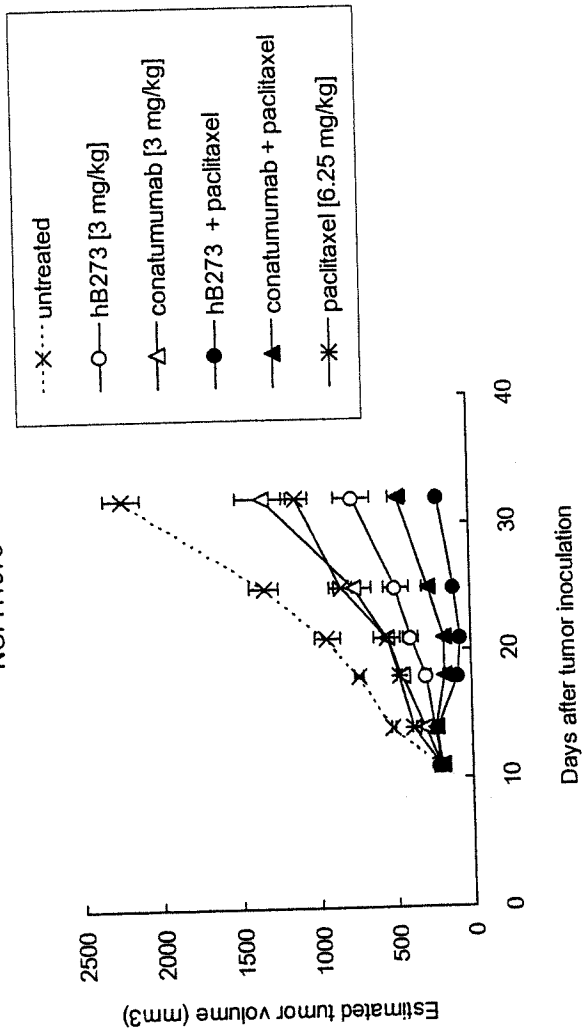

NCI-H1975
untreated
hB273 [3 mg/kg]
conatumumab [3 mg/kg]
hB273 + paclitaxel
conatumumab + paclitaxel
paclitaxel [6.25 mg/kg]
Estimated tumor volume (mm3)
Days after tumor inoculation
0
500
1000
1500
2000
2500
0
10
20
30
40

Fig. 53