FIG. 1

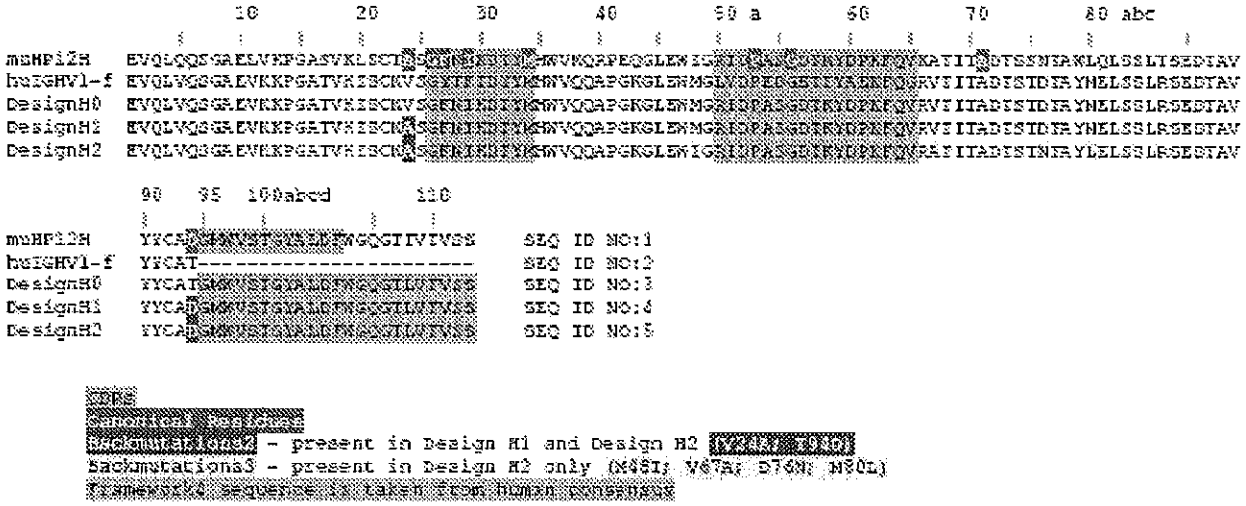

10 20 30 40 50 a 60 70 80 abc
muHPi2H
huIGHV1-f
DesignH0
DesignH1
DesignH2
90 95 100abcd 110
SEQ ID NO:1
SEQ ID NO:2
SEQ ID NO:3
SEQ ID NO:4
SEQ ID NO:5
CDRs
Framework regions
backmutations1 - present in Design H1 and Design H2
backmutations3 - present in Design H2 only
framework sequence is taken from human consensus

FIG. 2

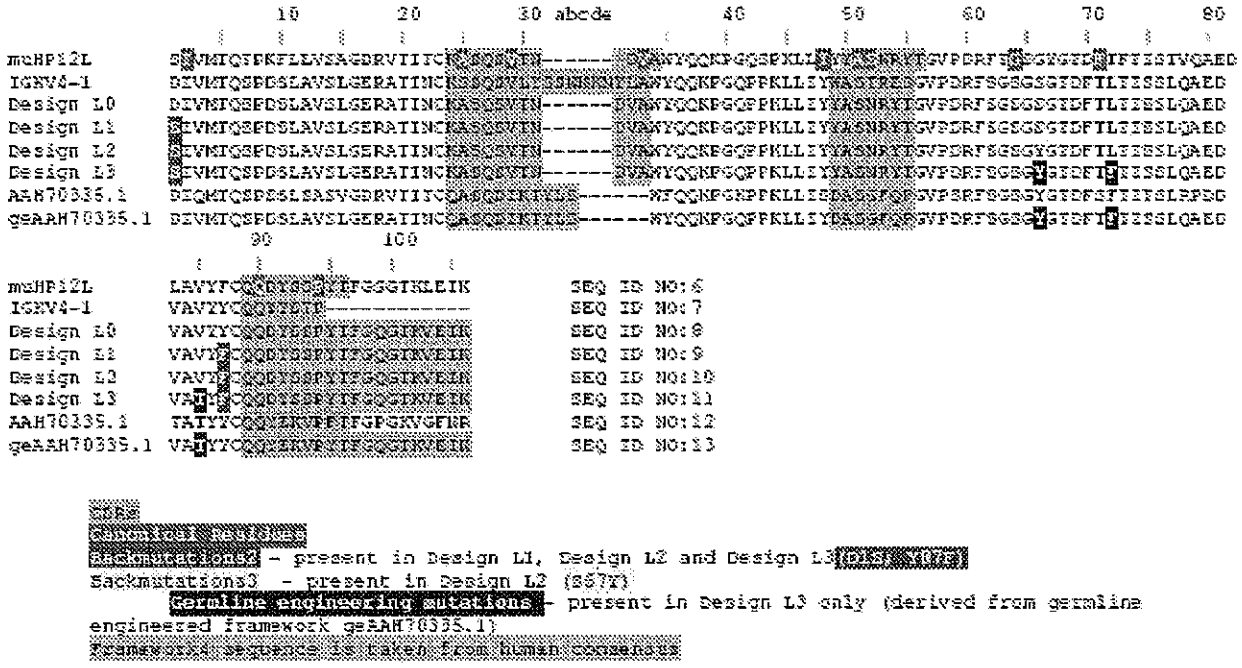

muHP12L
IGNV4-1
Design L0
Design L1
Design L2
Design L3
AAH70335.1
geAAH70335.1
SEQ ID NO:6
SEQ ID NO:7
SEQ ID NO:8
SEQ ID NO:9
SEQ ID NO:10
SEQ ID NO:11
SEQ ID NO:12
SEQ ID NO:13
Backmutations4 - present in Design L1, Design L2 and Design L3
Backmutations3 - present in Design L2
Germline engineering mutations - present in Design L3 only (derived from germline engineered framework geAAH70335.1)
Framework sequence is taken from human consensus

FIG. 3

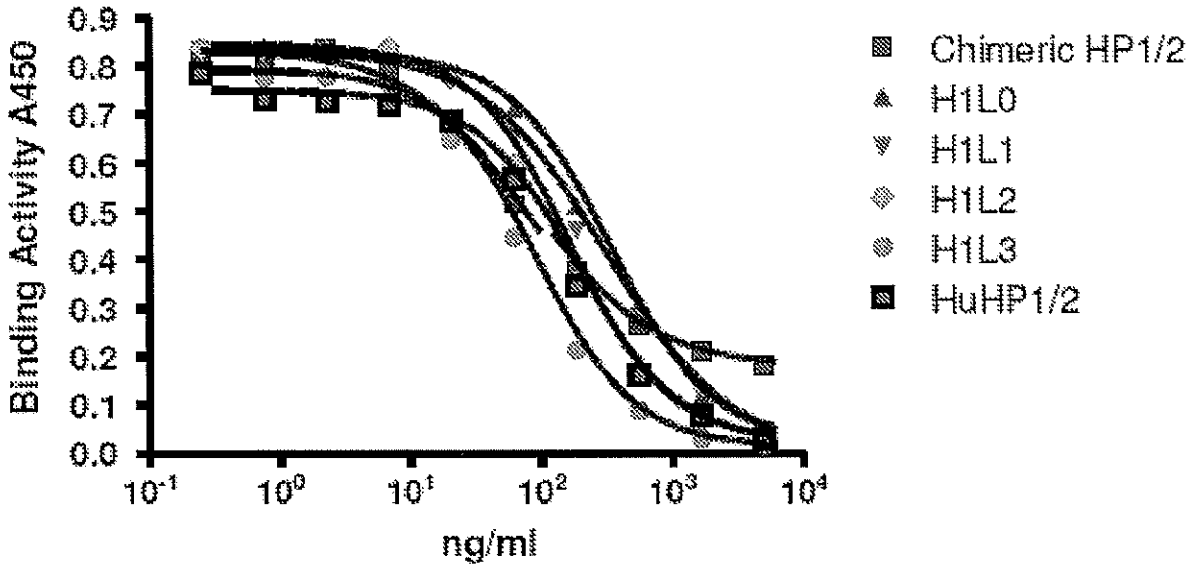

Binding Activity A450
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
10^{4}
ng/ml
Chimeric HP1/2
H1L0
H1L1
H1L2
H1L3
HuHP1/2

FIG. 4

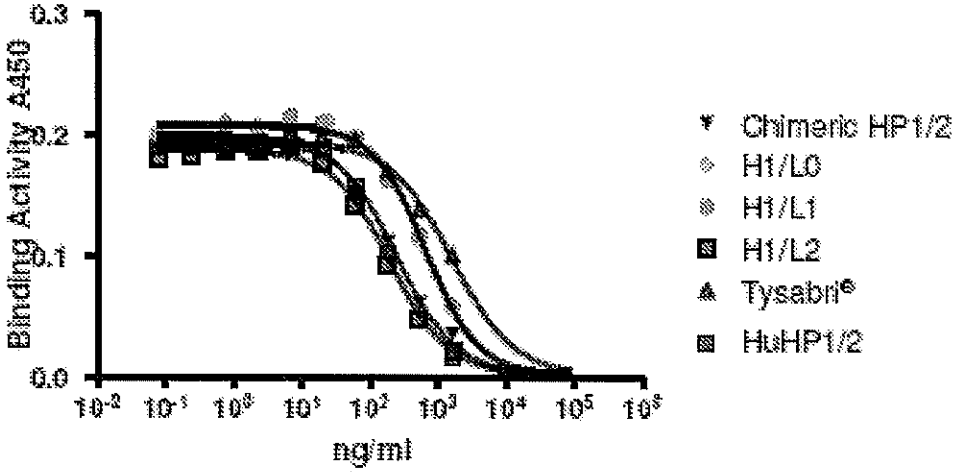

Binding Activity A450
0.3
0.2
0.1
0.0
10^{-2} 10^{-1} 10^{0} 10^{1} 10^{2} 10^{3} 10^{4} 10^{5} 10^{6}
ng/ml
Chimeric HP1/2
H1/L0
H1/L1
H1/L2
Tysabri®
HuHP1/2

FIG. 5

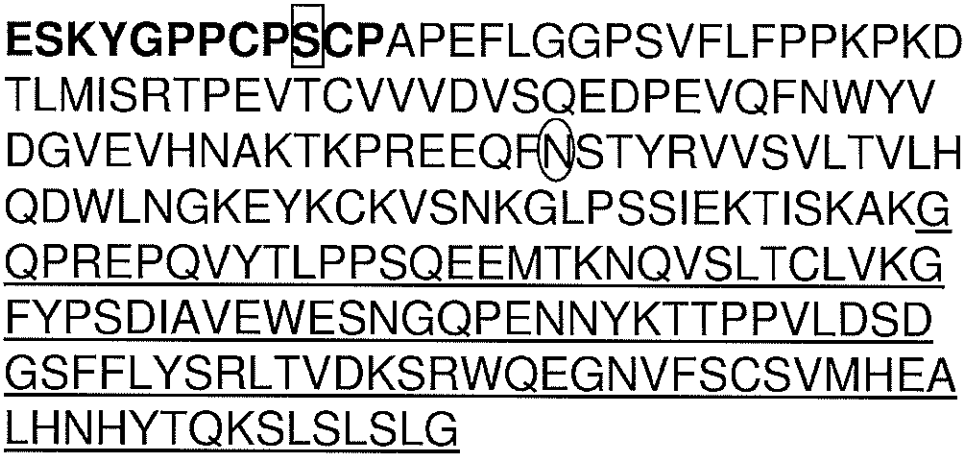

ESKYGPPCPSCPAPEFLGGPSVFLFPPKPKD
TLMISRTPEVTCVVVDVSQEDPEVQFNWYV
DGVEVHNAKTKPREEQFNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKGLPSSIEKTISKAKG
QPREPQVYTLPPSQEEMTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSD
GSFFLYSRLTVDKSRWQEGNVFSCSVMHEA
LHNHYTQKSLSLSLG

FIG. 6

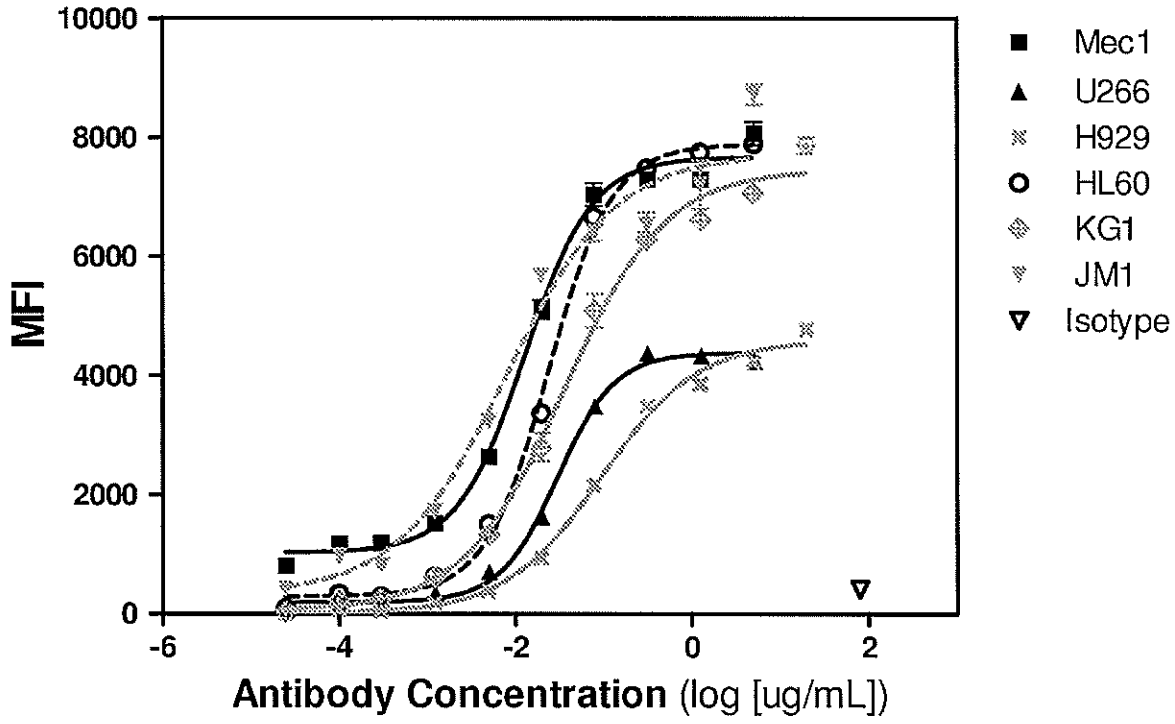

10000
8000
6000
4000
2000
0
MFI
-6
-4
-2
0
2
Antibody Concentration (log [ug/mL])
Mec1
U266
H929
HL60
KG1
JM1
Isotype

FIG. 7A

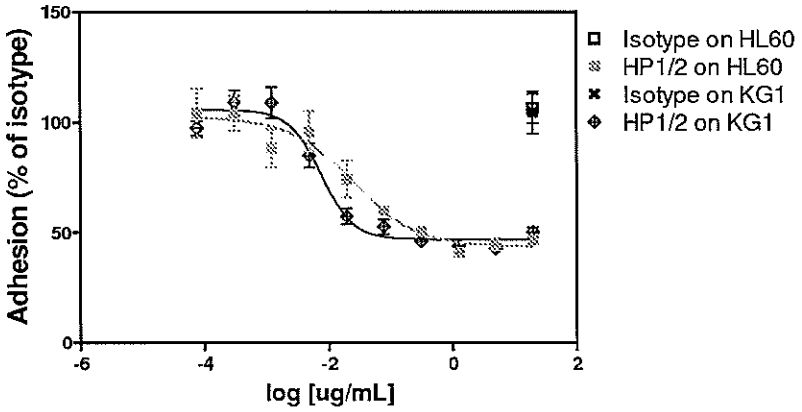


FIG. 7B

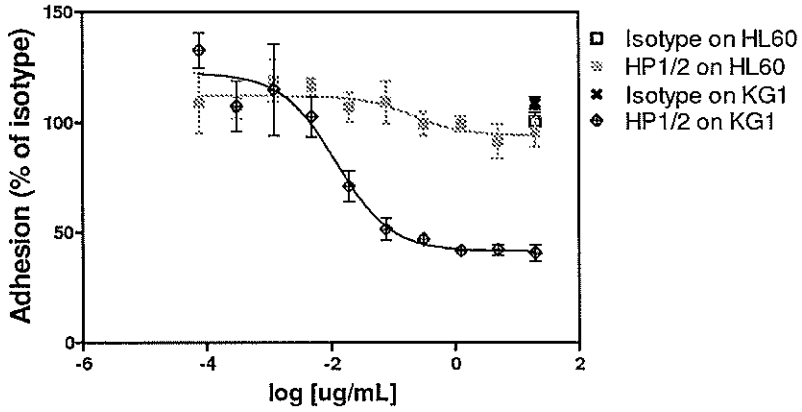


FIG. 7C

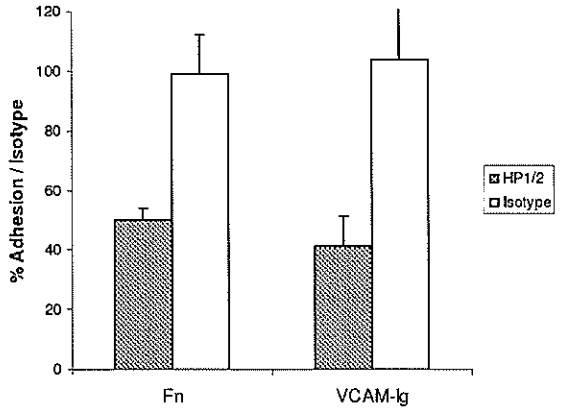


FIG. 8A

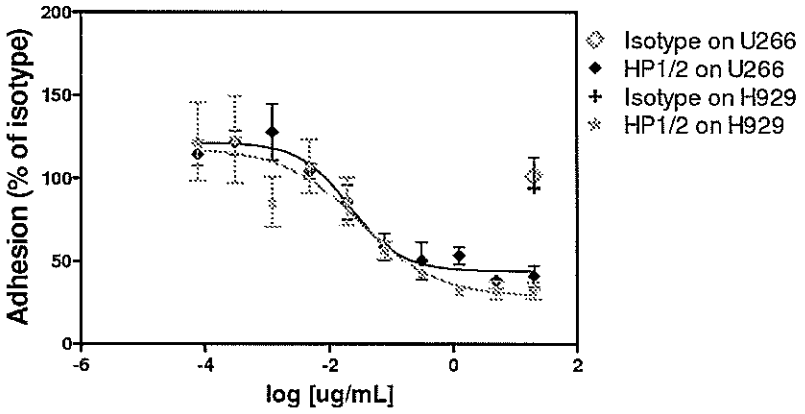


FIG. 8B

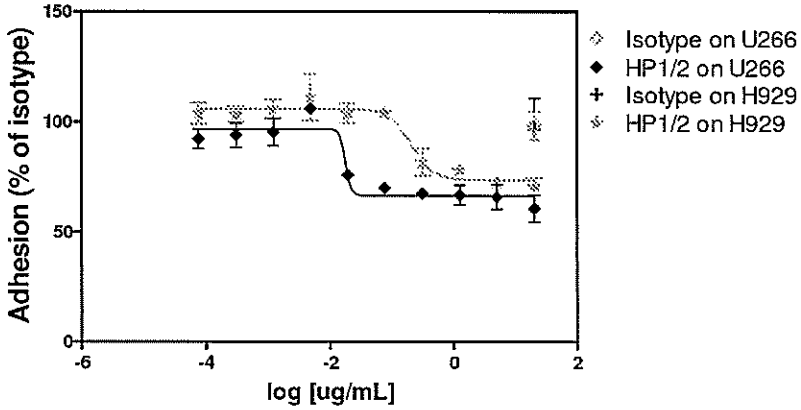


FIG. 8C

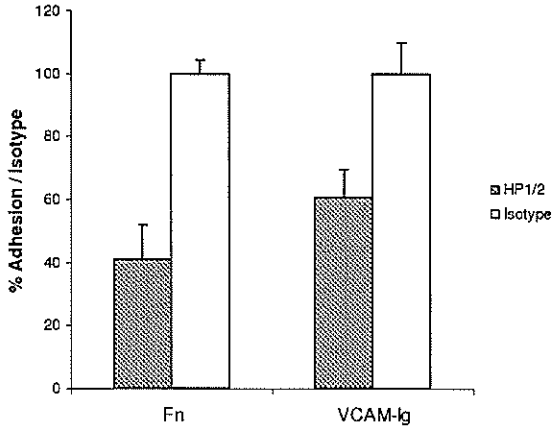


FIG. 9A

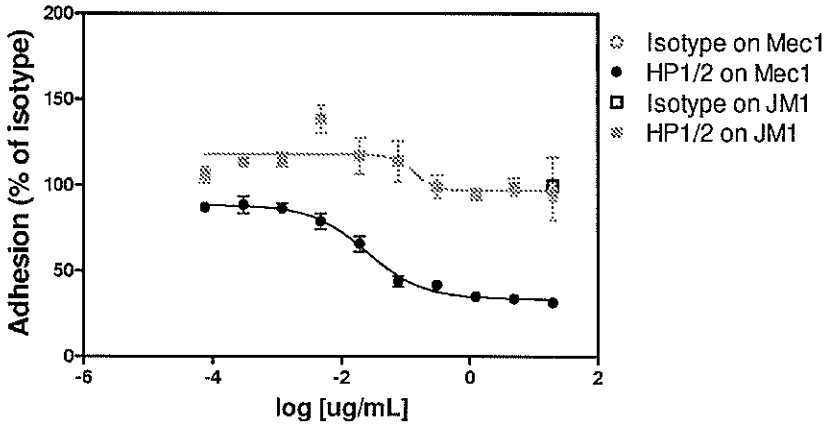


FIG. 9B

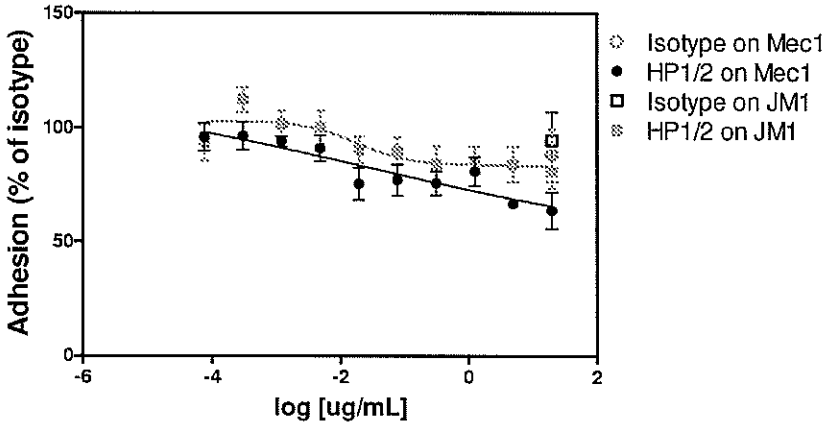


FIG. 9C

