```
HSAA1 (SEQ ID NO: 98)     1   MKLLTGLVFC SLVLGVSSRS FFSFLGEAFD GARDMWRAYS DMREANYIGS
HSAA2 (SEQ ID NO: 99)     1   MKLLTGLVFC SLVLSVSSRS FFSFLGEAFD GARDMWRAYS DMREANYIGS
HSAA3 (SEQ ID NO: 100)    1   MKLSTGIIFC SLVLGVSSQG WLTFLKAAGQ GAKDMWRAYS DMKEANYKKS
HSAA4 (SEQ ID NO: 101)    1   MRLFTGIVFC SLVMGVTSES WRSFFKEALQ GVGDMGRAYw DIMISNHQNS

HSAA1 (SEQ ID NO: 98)    51   DKYFHARGNY DAAKRGPGGV WAAEAISDAR ENIQRFFGHG A--------E
HSAA2 (SEQ ID NO: 99)    51   DKYFHARGNY DAAKRGPGGA WAAEVISNAR ENIQRLTGHG A--------E
HSAA3 (SEQ ID NO: 100)   51   DKYFHARGNY DAVQRGPGGV WATEVISDAR ENVQRLTGdh A--------E
HSAA4 (SEQ ID NO: 101)   51   NRYLYARGNY DAAQRGPGGV WAAKLISRSR vylqglidyy lfgnsstvlE

HSAA1 (SEQ ID NO: 98)    93   DSLADQAANE WGRSGKDPNH FRPAGLPEKY
HSAA2 (SEQ ID NO: 99)    93   DSLADQAANK WGRSGRDPNH FRPAGLPEKY
HSAA3 (SEQ ID NO: 100)   93   DSLAGQATNK WGQSGKDPNH FRPAGLPEKY
HSAA4 (SEQ ID NO: 101)  101   DSKSNEKAEE WGRSGKDPDR FRPDGLPKKY
```

FIG. 1

```
HSAA1  (SEQ ID NO: 98)              1   mkiltglvfc slvlgvssRS FFSFLGEAFD GARDMWRAYS DMREANYIGS
HAA1  (SEQ ID NO: 102)              1   ---------- --------RS FFSFLGEAFD GARDMWRAYS DMREANYIGS

HSAA1  (SEQ ID NO: 98)             51   DKYFHARGNY DAAKRGPGGV WAAEAISDAR ENIQRFFGHG AEDsladqaa
HAA1   (SEQ ID NO: 102)            33   DKYFHARGNY DAAKRGPGGV WAAEAISDAR ENIQRFFGHG AEDS------

HSAA1  (SEQ ID NO: 98)           101   newgrsgkdp nhfrpaglpe ky
HAA1   (SEQ ID NO: 102)                ---------- ---------- --
```

FIG. 2

```
HSAA2(alpha)  (SEQ ID NO: 99)       1   mkllтglvfc slvlsvssRS FFSFLGEAFD GARDMWRAYS DMREANYIGS
HAA2(alpha)   (SEQ ID NO: 103)      1   ---------- --------RS FFSFLGEAFD GARDMWRAYS DMREANYIGS


HSAA2(alpha)  (SEQ ID NO:  99)     51   DKYFHARGNY DAAKRGPGGA WAAEVISNAR ENIQRLTGHG AEDSladqaa
HAA2(alpha)   (SEQ ID NO:  103)    33   DKYFHARGNY DAAKRGPGGA WAAEVISNAR ENIQRLTGHG AEDS------


HSAA2(alpha)  (SEQ ID NO:  99)    101   nkwgrsgrdp nhfrpaglpe ky
HAA2(alpha)   (SEQ ID NO:  103)         ---------- ---------- --
```


FIG. 3

```
HSAA3   (SEQ ID NO: 100)      1   mklstgiifc slvlgvssQG WLTFLKAAGQ GAKDMWRAYS DMKEANYKKS
HAA3    (SEQ ID NO: 104)      1   ---------- --------QG WLTFLKAAGQ GAKDMWRAYS DMKEANYKKS

HSAA3   (SEQ ID NO: 100)     51   DKYFHARGNY DAVQRGPGGV WATEVISDAR ENVQRLTGDH AEDSlagqat
HAA3    (SEQ ID NO: 104)     33   DKYFHARGNY DAVQRGPGGV WATEVISDAR ENVQRLTGDH AEDS------

HSAA3   (SEQ ID NO: 100)    101   nkwgqsgkdp nhfrpaglpe ky
HAA3    (SEQ ID NO: 104)          ---------- ---------- --
```

FIG. 4

```
HSAA4  (SEQ ID NO: 101)            1   mrlftgivfc slvmgvtsES WRSFFKEALQ GVGDMGRAYW DIMISNHQNS
HAA4   (SEQ ID NO: 105)            1   ---------- --------ES WRSFFKEALQ GVGDMGRAYW DIMISNHQNS

HSAA4  (SEQ ID NO: 101)           51   NRYLYARGNY DAAQRGPGGV WAAKLISRSR VYLQGLIDYY LFGNSstvle
HAA4   (SEQ ID NO: 105)           33   NRYLYARGNY DAAQRGPGGV WAAKLISRSR VYLQGLIDYY LFGNS-----

HSAA4  (SEQ ID NO: 101)          101   dsksnekaee wgrsgkdpdr frpdglpkky
HAA4   (SEQ ID NO: 105)                ---------- ---------- ----------
```

FIG. 5

```
HAA1  (SEQ ID NO: 102)      1   RSFFSFLGEA FDGARDMWRA YSDMREANYI GSDKYFHARG NYDAAKRGPG
HAA2  (SEQ ID NO: 103)      1   RSFFSFLGEA FDGARDMWRA YSDMREANYI GSDKYFHARG NYDAAKRGPG
HAA3  (SEQ ID NO: 104)      1   QGWLTFLKAA GQGAKDMWRA YSDMKEANYK KSDKYFHARG NYDAVQRGPG
HAA4  (SEQ ID NO: 105)      1   ESWRSFFKEA LQGVGDMGRA YWDIMISNHQ NSNRYLYARG NYDAAQRGPG

HAA1  (SEQ ID NO: 102)     51   GVWAAEAISD ARENIQRF-- ---FGHGA-- -EDS
HAA2  (SEQ ID NO: 103)     51   GAWAAEVISN ARENIQRL-- ---TGHGA-- -EDS
HAA3  (SEQ ID NO: 104)     51   GVWATEVISD ARENVQRL-- ---TGdhA-- -EDS
HAA4  (SEQ ID NO: 105)     51   GVWAAKLISR SRVYLQGLid yylFGNSStv lEDS
```


FIG. 6

HAA1	(SEQ ID NO: 102)	70	GHGAEDS
HAA2	(SEQ ID NO: 103)	70	GHGAEDS
HAA3	(SEQ ID NO: 104)	70	GdhAEDS
HAA4	(SEQ ID NO: 105)	78	stvlEDS

FIG. 7

```
Mouse SAA1  (SEQ ID NO: 106)      1   MKLLTSLVFC SLLLGVCHGG FFSFVHEAFQ GAGDMWRAYT DMKEANWKNS
Mouse SAA2  (SEQ ID NO: 107)      1   MKLLTSLVFC SLLLGVCHGG FFSFIGEAFQ GAGDMWRAYT DMKEAGWKDG
Mouse SAA3  (SEQ ID NO: 108)      1   MKPSIAIILC ILILGVDSQR WVQFMKEAGQ GSRDMWRAYS DMKKANWKNS
Mouse SAA4  (SEQ ID NO: 109)      1   MRLATVIVLC SLFLGVSGDG WYSFFREAVQ GTWDLWRAYR DnlEANYQNA

Mouse SAA1  (SEQ ID NO: 106)     51   DKYFHARGNY DAAQRGPGGV WAAEKISDGR EAFQE----- FFG---RGHE
Mouse SAA2  (SEQ ID NO: 107)     51   DKYFHARGNY DAAQRGPGGV WAAEKISDAR ESFQE----- FFG---RGHE
Mouse SAA3  (SEQ ID NO: 108)     51   DKYFHARGNY DAARRGPGGA WAAKVISDAR EAVQK----- FTG---HGAE
Mouse SAA4  (SEQ ID NO: 109)     51   DQYFYARGNY EAQQRGSGGI WAAKIISTSR KYFqgllnry YFGirnHGLE

Mouse SAA1  (SEQ ID NO: 106)     93   DTIADQEANR HGRSGKDPNY YRPPGLPDKY
Mouse SAA2  (SEQ ID NO: 107)     93   DTMADQEANR HGRSGKDPNY YRPPGLPAKY
Mouse SAA3  (SEQ ID NO: 108)     93   DSRADQFANE WGRSGKDPNH FRPAGLPKRY
Mouse SAA4  (SEQ ID NO: 109)    101   TLQATQKAEE WGRSGKNPNH FRPEGLPEKF
```

FIG. 8

```
MSAA1   (SEQ ID NO: 106)          1   mkllltslvfc slllgvchgG FFSFVHEAFQ GAGDMWRAYT DMKEANWKNS
MAA1    (SEQ ID NO: 110)          1   ---------- ---------G FFSFVHEAFQ GAGDMWRAYT DMKEANWKNS

MSAA1   (SEQ ID NO: 106)         51   DKYFHARGNY DAAQRGPGGV WAAEKISDGR EAFQEFFGRG HEDTiadqea
MAA1    (SEQ ID NO: 110)         32   DKYFHARGNY DAAQRGPGGV WAAEKISDGR EAFQEFFGRG HEDT------

MSAA1   (SEQ ID NO: 106)        101   nrhgrsgkdp nyyrppglpd ky
MAA1    (SEQ ID NO: 110)             ---------- ---------- --
```

FIG. 9

```
MSAA2   (SEQ ID NO: 107)      1   mkllltslvfc slllgvchgG FFSFIGEAFQ GAGDMWRAYT DMKEAGWKDG
MAA2    (SEQ ID NO: 111)      1   ---------- ---------G FFSFIGEAFQ GAGDMWRAYT DMKEAGWKDG

MSAA2   (SEQ ID NO: 107)     51   DKYFHARGNY DAAQRGPGGV WAAEKISDAR ESFQEFFGRG HEDTmadqea
MAA2    (SEQ ID NO: 111)     32   DKYFHARGNY DAAQRGPGGV WAAEKISDAR ESFQEFFGRG HEDT------

MSAA2   (SEQ ID NO: 107)    101   nrhgrsgkdp nyyrppglpa ky
MAA2    (SEQ ID NO: 111)          ---------- ---------- --
```

FIG. 10

```
MSAA3 (SEQ ID NO: 108)      1   mkpsiaiilc ililgvdsqr wvqfmkEAGQ GSRDMWRAYS DMKKANWKNS
MAA3  (SEQ ID NO: 112)      1   ---------- ---------- ------EAGQ GSRDMWRAYS DMKKANWKNS

MSAA3 (SEQ ID NO: 108)     51   DKYFHARGNY DAARRGPGGA WAAKVISDAR EAVQKFTGHG AEDSradqfa
MAA3  (SEQ ID NO: 112)     25   DKYFHARGNY DAARRGPGGA WAAKVISDAR EAVQKFTGHG AEDS------

MSAA3 (SEQ ID NO: 108)    101   newgrsgkdp nhfrpaglpk ry
MAA3  (SEQ ID NO: 112)          ---------- ---------- --
```

FIG. 11

```
MSAA4  (SEQ ID NO: 109)      1   mrlatvivlc slflgvsgdg WYSFFREAVQ GTWDLWRAYR DNLEANYQNA
MAA4   (SEQ ID NO: 113)      1   ---------- ---------- WYSFFREAVQ GTWDLWRAYR DNLEANYQNA

MSAA4  (SEQ ID NO: 109)     51   DQYFYARGNY EAQQRGSGGI WAAKIISTSR KYFQGLLNRY YFGIRNHGLE
MAA4   (SEQ ID NO: 113)     31   DQYFYARGNY EAQQRGSGGI WAAKIISTSR KYFQGLLNRY YFGIRNHGLE

MSAA4  (SEQ ID NO: 109)    101   TLqatqkaee wgrsgknpnh frpeglpekf
MAA4   (SEQ ID NO: 113)     81   TL-------- ---------- ----------
```

FIG. 12

```
MAA1  (SEQ ID NO: 110)          1   GFFSFVHEAF QGAGDMWRAY TDMKEANWKN SDKYFHARGN YDAAQRGPGG
MAA2  (SEQ ID NO: 111)          1   GFFSFIGEAF QGAGDMWRAY TDMKEAGWKD GDKYFHARGN YDAAQRGPGG
MAA3  (SEQ ID NO: 112)          1   -------EAG QGSRDMWRAY SDMKKANWKN SDKYFHARGN YDAARRGPGG
MAA4  (SEQ ID NO: 113)          1   -WYSFFREAV QGTWDLWRAY RDNLEANYQN ADQYFYARGN YEAQQRGSGG

MAA1  (SEQ ID NO: 110)         51   VWAAEKISDG REAFQE---- -FFG---RGH EDT
MAA2  (SEQ ID NO: 111)         51   VWAAEKISDA RESFQE---- -FFG---RGH EDT
MAA3  (SEQ ID NO: 112)         44   AWAAKVISDA REAVQK---- -FTG---HGA EDS
MAA4  (SEQ ID NO: 113)         50   IWAAKIISTS RKYFQgllnr yYFGirnHGL ETL
```


FIG. 13

MAA1	(SEQ ID NO: 110)	69	GRGHEDT
MAA2	(SEQ ID NO: 111)	69	GRGHEDT
MAA3	(SEQ ID NO: 112)	62	GHGAEDS
MAA4	(SEQ ID NO: 113)	76	nHGLETL

FIG. 14

```
HSAA1 (SEQ ID NO: 98)          1   MKLLTGLVFC SLVLGVSSRS FFSFLGEAFD GARDMWRAYS DMREANYIGS
MSAA1 (SEQ ID NO: 106)         1   MKLLTSLVFC SLLLGVCHGG FFSFVHEAFQ GAGDMWRAYT DMKEANWKNS

HSAA1 (SEQ ID NO: 98)         51   DKYFHARGNY DAAKRGPGGV WAAEAISDAR eniQRFFGHG AEDSLADQAA
MSAA1 (SEQ ID NO: 106)        51   DKYFHARGNY DAAQRGPGGV WAAEKISDGR eafQEFFGRG HEDTIADQEA

HSAA1 (SEQ ID NO: 98)        101   NEWGRSGKDP NHFRPAGLPE KY
MSAA1 (SEQ ID NO: 106)       101   NRHGRSGKDP NYYRPPGLPD KY
```

FIG. 15

```
HAA1 (SEQ ID NO: 102)      1   rsFFSFLGEA FDGARDMWRA YSDMREANYi gSDKYFHARG NYDAAKRGPG
MAA1 (SEQ ID NO: 110)      1   g-FFSFVHEA FQGAGDMWRA YTDMKEANWk nSDKYFHARG NYDAAQRGPG

HAA1 (SEQ ID NO: 102)     51   GVWAAEAISD AREniQRFFG HGAEDS
MAA1 (SEQ ID NO: 110)     50   GVWAAEKISD GREafQEFFG RGHEDT
```

FIG. 16

```
HAA1   (SEQ ID NO: 102)          1   GHGAEDS
MAA1   (SEQ ID NO: 110)          1   GRGHEDT
```

FIG. 17

```
HSAA1alpha   (SEQ ID NO: 114)      1   mKLLTGLVFC SLVLGVSSRS FFSFLGEAFD GARDMWRAYS DMREANYIGS
HSAA1beta    (SEQ ID NO: 115)      1   mKLLTGLVFC SLVLGVSSRS FFSFLGEAFD GARDMWRAYS DMREANYIGS
HSAA1gamma   (SEQ ID NO: 116)      1   mKLLTGLVFC SLVLGVSSRS FFSFLGEAFD GARDMWRAYS DMREANYIGS

HSAA1alpha   (SEQ ID NO: 114)     51   DKYFHARGNY DAAKRGPGGV WAAEAISDAR ENIQRFFGHG AEDSLADQAA
HSAA1beta    (SEQ ID NO: 115)     51   DKYFHARGNY DAAKRGPGGA WAAEVISDAR ENIQRFFGHD AEDSLADQAA
HSAA1gamma   (SEQ ID NO: 116)     51   DKYFHARGNY DAAKRGPGGV WAAEAISDAR ENIQRFFGHD AEDSLADQAA

HSAA1alpha   (SEQ ID NO: 114)    101   NEWGRSGKDP NHFRPAGLPE KY
HSAA1beta    (SEQ ID NO: 115)    101   NEWGRSGKDP NHFRPAGLPE KY
HSAA1gamma   (SEQ ID NO: 116)    101   NEWGRSGKDP NHFRPAGLPE KY
```


FIG. 18

```
HSAA2alpha (SEQ ID NO: 114)      1   mKLLTGLVFC SLVLSVSSRS FFSFLGEAFD GARDMWRAYS DmREANYIGS
HSAA2beta  (SEQ ID NO: 115)      1   mKLLTGLVFC SLVLSVSSRS FFSFLGEAFD GARDMWRAYS DmREANYIGS

HSAA2alpha  (SEQ ID NO: 114)    51   DKYFHARGNY DAAKRGPGGA WAAEVISNAR ENIQRLTGHG AEDSLADQAA
HSAA2beta   (SEQ ID NO: 115)    51   DKYFHARGNY DAAKRGPGGA WAAEVISNAR ENIQRLTGRG AEDSLADQAA

HSAA2alpha  (SEQ ID NO: 114)   101   NKWGRSGRDP NHFRPAGLPE KY
HSAA2beta   (SEQ ID NO: 115)   101   NKWGRSGRDP NHFRPAGLPE KY
```


FIG. 19

		10	20	30	40
Human	(SEQ ID NO: 119):	RSFFSFLGEA	FDGARDMWRA	YSDMREANYI	GSDKYFHARG
Mouse	(SEQ ID NO: 120):	G FFSFIGEA	FQGAGDMWRA	YTDMKEAGWK	DGDKYFHARG
Shar Pei	(SEQ ID NO: 121):	E WYSFVGEA	AQGAWDMLRA	YSDMREANYK	NSDKYFHARG

		50	60	70	80
Human	(SEQ ID NO: 119):	NYDAAKRGPG	GVWAAEAISD	ARENIQRFFG	HGAEDSLADQ
Mouse	(SEQ ID NO: 120):	NYDAAQRGPG	GVWAAEKISD	ARESFQEFFG	RGHEDTMADQ
Shar Pei	(SEQ ID NO: 121):	NYDAAQRGPG	GAWAAKVISD	ARENSQRDSG	HGAEDSKADQ

ITDLLRFG

		90	100	104
Human	(SEQ ID NO: 119):	AANEWGRSGK	DPNHFRPAGL	PEKY
Mouse	(SEQ ID NO: 120):	EANRHGRSGK	DPNYYRPPGL	PAKY
Shar Pei	(SEQ ID NO: 121):	AANEWG		

FIG. 20

```
                        0          1          2               3     3          4         5
                        1          1          1      abc def  0     5          5         4
kp1a (SEQ ID NO:123) DIQMTQSPST LSASVGDRVT ITCRASQSI* *****SSWLA WYQQKPGKAP KLLIYKASSL
kp1b (SEQ ID NO:124) .........S .......... ...Q...D.. ......NY.N .......... .....D..N.
kp1c (SEQ ID NO:125) .........S .......... .......... .......Y.N .......... .....A....
kp1d (SEQ ID NO:126) .........S .......... .......G.. .....RND.G .......... .R...A....
kp1e (SEQ ID NO:127) .........S .......... .......G.. ......NY.. .F........ .S...A....
kp1f (SEQ ID NO:128) A..L.....S .......... .......G.. .......A.. .......... .....D....
kp1g (SEQ ID NO:129) .........S V......... .......G.. .......... .......... .....A....
kp2a (SEQ ID NO:130) ..V...T.LS .PVTP.EPAS .S..S...LL DSDDGNTY.D ..L....QS. Q....TL.YR
kp2b (SEQ ID NO:131) ..V.....LS .PVTP.EPAS .S..S...LL HS.NGYNY.D ..L....QS. Q....LG.NR
kp2c (SEQ ID NO:132) ..V...T.LS ..VTP.QPAS .S.KS...LL HS.DGKTY.Y ..L....QP. Q....EV.NR
kp3a (SEQ ID NO:133) E.V.....A. ..V.P.E.A. LS......V. .......N.. .......Q.. R....G..TR
kp3b (SEQ ID NO:134) E.VL....G. ..L.P.E.A. LS......VS .......Y.. .......Q.. R....G...R
kp3c (SEQ ID NO:135) E.VL....A. ..L.P.E.A. LS......VS .......Y.. .......Q.. R....D..NR
kp4  (SEQ ID NO:136) ..V.....DS .AV.L.E.A. .N.KS...VL YSSNNKNY.. .......QP. .....W..TR
kp5  (SEQ ID NO:137) ETTL....AF M..TP..K.N .S.K...D.. .....DDDMN .......E.A IFI.QE.TT.

                        5          6          7          8          9
                        5          5 ab       3          3          3
kp1a (SEQ ID NO:123) ESGVPSRFSG SG**SGTEFT LTISSLQPDD FATYYCQQYN SYS****
kp1b (SEQ ID NO 124) .T........ .......D.. F.......E. I........D NLP....
kp1c (SEQ ID NO:125) Q......... .......D.. .........E. .........SY .TP....
kp1d (SEQ ID NO:126) Q......... .......... .........E. ......L.H. ..P....
kp1e (SEQ ID NO:127) Q......... .......D.. .........E. .......... ..P....
kp1f (SEQ ID NO:128) .......... .......D.. .........E. .........F. N.P....
kp1g (SEQ ID NO:129) Q......... .......D.. .........E. .........A. .FP....
kp2a (SEQ ID NO:130) A....D.... .......D.. .K..RVEAE. VGV...M.RI EFP....
kp2b (SEQ ID NO:131) A....D.... .......D.. .K..RVEAE. VGV...M.AL QTP....
kp2c (SEQ ID NO:132) F....D.... .......D.. .K..RVEAE. VGV...M.SI QLP....
kp3a (SEQ ID NO:133) AT.I.A.... .......... .......SE. ..V....... NWP....
kp3b (SEQ ID NO:134) AT.I.D.... .......D.. ....R.E.E. ..V......G .SP....
kp3c (SEQ ID NO:135) AT.I.A.... .......D.. .......E.E. ..V.....RS NWP....
kp4  (SEQ ID NO:136) .....D.... .......D.. .......AE. V.V......Y .TP....
kp5  (SEQ ID NO:137) VP.I.P.... ....Y..D.. ...NNIESE. A.Y.F.L.HD NFP....
```

FIG. 21

```
                        0          1          2                3     3          4         5
                        1          1          1      abc def   0     5          5         4
lm1a (SEQ ID NO:138) QSVLTQPPS* VSAAPGQKVT ISCSGSSSNI G****NNYVS WYQQLPGTAP KLLIYENNKR
lm1b (SEQ ID NO:139) .......... A.GT...R.. .......... .....S...Y .......... .....R..Q.
lm1c (SEQ ID NO:140) ...V...... ..G....R.. ...T...... .A...GYD.H .......... .....G.SN.
lm2a (SEQ ID NO:141) ..A....A.. ..GS...SI. ...T.T..DV .S...Y.L.. ....H..K.. ..M...GS..
lm2b (SEQ ID NO:142) ..A....R.. ..GS...VI. ...T.T..DV .G...Y.... ....H..K.. ..M..DVS..
lm3a (SEQ ID NO;143) SY........ ..V...KTAR .T.G.NNIG* *....SKS.H ....K..Q.. V.VV.DDSD.
lm3b (SEQ ID NO:144) SYE....... ..VS...TAR .T...DALP* *....KQ.AY ....K..Q.. V.V..KDSE.
lm3c (SEQ ID NO:145) SYE....... ..VS...TAS .T...DKLG* *....DK.AC ....K..QS. V.V..QDS..
lm4  (SEQ ID NO:146) S.E...D.A. ..V.L..T.R .T.Q.D.LR* *....SY.A. ....K..Q.. V.V..GK.N.
lm6  (SEQ ID NO:147) NFM....H.. ..ES..KT.. ...TR..GS. A....S...Q ....R..SS. TTV...D.Q.
lm7  (SEQ ID NO:148) .T.V..E... LTVS..GT.. LT.AS.TGAV TS...GY.PN .F..K..Q.. RA...STSNK
lm8  (SEQ ID NO:149) .L....S... A..SL.AS.K LT.TL..G** *..HSSYAIA .H..Q.EKG. RY.MKL.SDG

                        5          6          7          8          9
                        5          5 ab       3          3          3
lm1a (SEQ ID NO:138) PSGIPDRFSG SK**SGTSAT LGITGLQTGD EADYYCGTWD SSLSA**
lm1b (SEQ ID NO:139) ...V...... .........S .A.S..RSE. ......AA.. D...G..
lm1c (SEQ ID NO:140) ...V...... .........S .A.....AE. ......QSY. ....G..
lm2a (SEQ ID NO:141) ...VSN.... ......NT.S .T.S...AE. ......CSYA G.STL..
lm2b (SEQ ID NO:142)...V...... ......NT.S .T.S...AE. ......CSYA G.YTF..
lm3a (SEQ ID NO:143)  .....E.... .N....NT.. .T.SRVEA.. ......QV.. ..SDH..
lm3b (SEQ ID NO:144) .....E.... .S.....TV. .T.S.V.AE. ......QSA. ..G**..
lm3c (SEQ ID NO:145) .....E.... .N....NT.. .T.S.T.AM. ......QA.. ..TAH..
lm4  (SEQ ID NO:146) .......... .S....NT.S .T...A.AE. ......NSR. ..GNH..
lm6  (SEQ ID NO:147)...V...... .IDS.SN..S .T.S..K.E. ......QSY. ..N**..
lm7  (SEQ ID NO:148) H.WT.A.... .L..L.GK.A .TLS.V.PE. ..E...LLYY GGAQ*..
lm8  (SEQ ID NO:149) GD........ .S....AERY .T.SS..SE. ......Q..G TGI**..
```

FIG. 22

1	10	21	31	35	
NFLLTQPHS	VSESPGKTVT	ISCTRSSGSI	A****NNYVH	WYQQRPGSSP	
45	55	65AB	73	82	93
TTVIFEDDHR	PSGVPDRFSG	SVDTSSNSAS	LTISGLKTED	EADYYCQSYD	HNN

$V_{\lambda}6$ Wil (SEQ ID NO: 150)

FIG. 23

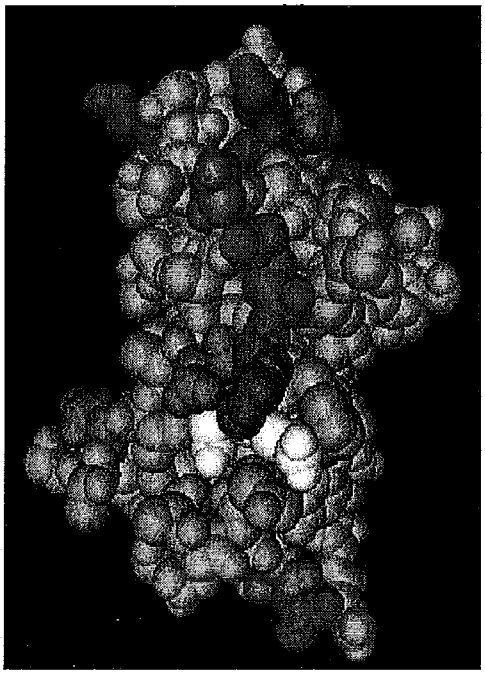
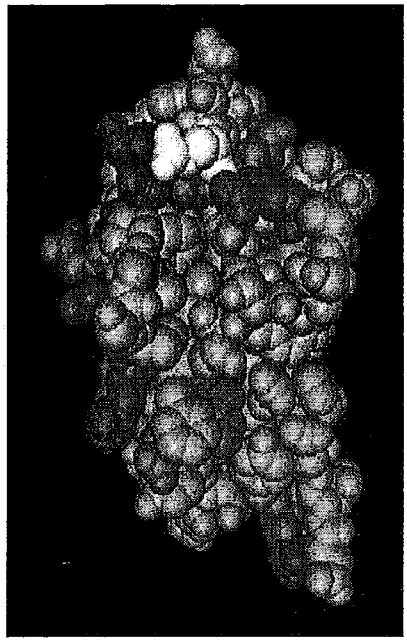
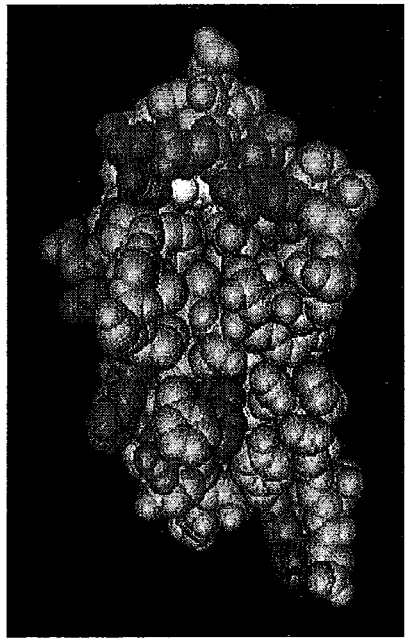


FIG. 24



V_λ6 Wil Glu81



V_λ6 Wil Asp82

FIG. 25

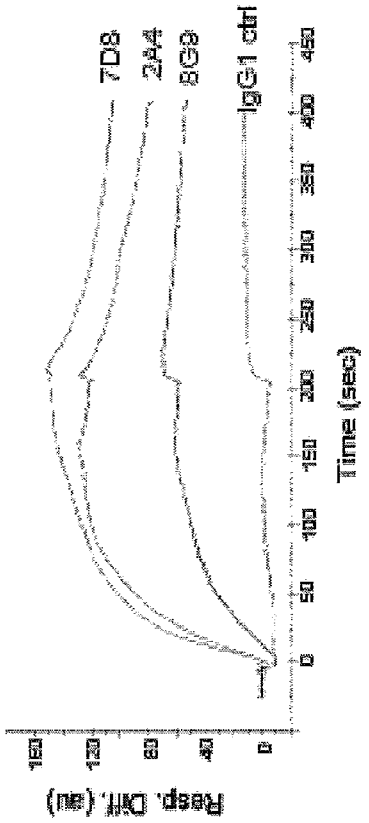

7D8
2A4
8G8
IgG1 ctrl
Resp. Diff. (au)
0
40
80
120
160
Time (sec)
0
50
100
150
200
250
300
350
400
450

FIG. 26

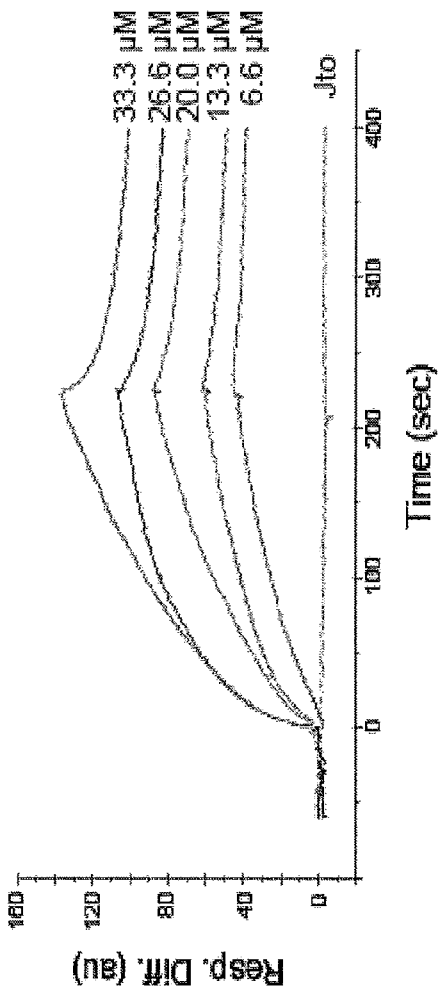

33.3 µM
26.6 µM
20.0 µM
13.3 µM
6.6 µM
Jto
Resp. Diff. (au)
Time (sec)
160
120
80
40
0
0
100
200
300
400

FIG. 27

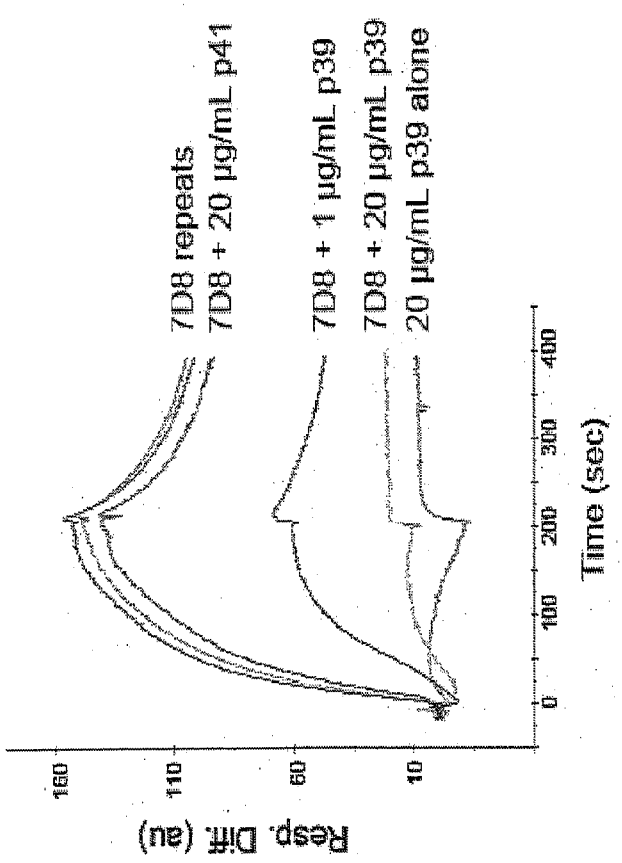

7D8 repeats
7D8 + 20 µg/mL p41
7D8 + 1 µg/mL p39
7D8 + 20 µg/mL p39
20 µg/mL p39 alone
Resp. Diff. (au)
160
110
60
10
0
100
200
300
400
Time (sec)

FIG. 28

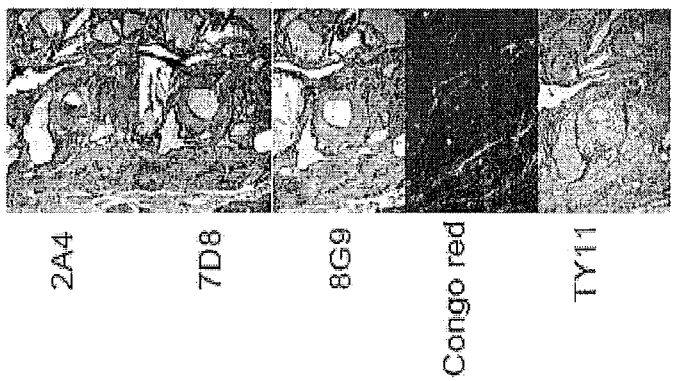


FIG. 29

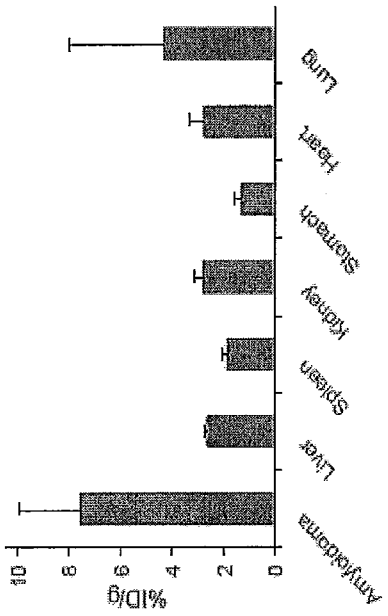

%ID/g
10
8
6
4
2
0
Xenograft
Liver
Spleen
Kidney
Stomach
Heart
Lung

FIG. 30

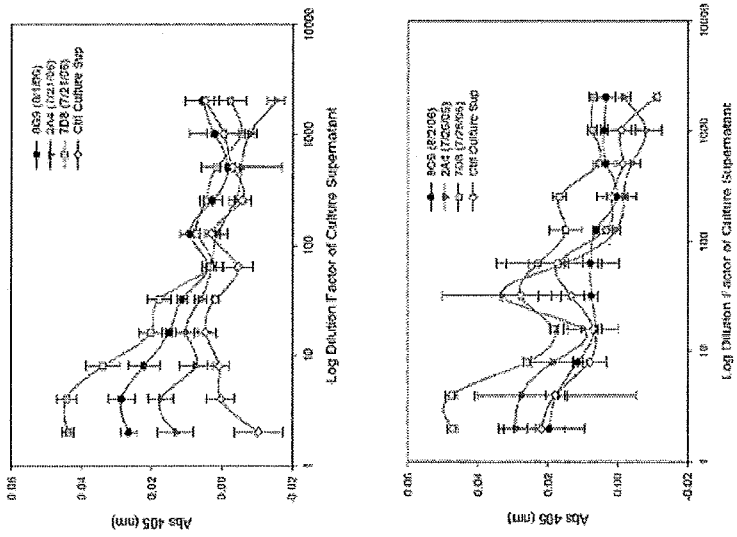

Abs 405 (nm)
Log Dilution Factor of Culture Supernatant
Abs 405 (nm)
Log Dilution Factor of Culture Supernatant

FIG. 31

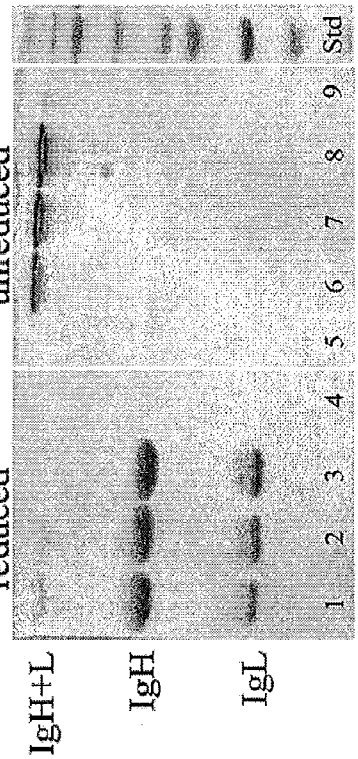


FIG. 32

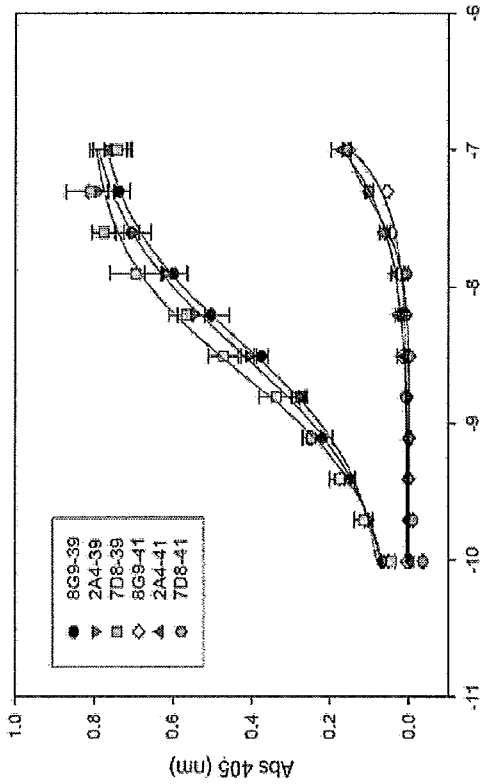

Abs 405 (nm)
1.0
0.8
0.6
0.4
0.2
0.0
-11
-10
-9
-8
-7
-6
log [Ab] (M)
8G9-39
2A4-39
7D8-39
8G9-41
2A4-41
7D8-41

FIG. 33

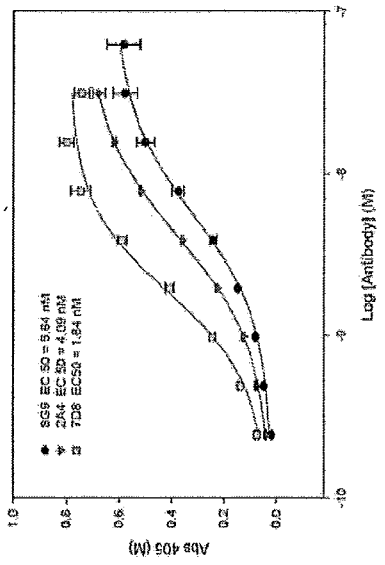

Abs 405 (M)
1.0
0.8
0.6
0.4
0.2
0.0
-10
-9
-8
-7
Log [Antibody] (M)
SG6 EC 50 = 5.64 nM
2A4 EC 50 = 4.09 nM
7D8 EC50 = 1.84 nM

FIG. 34

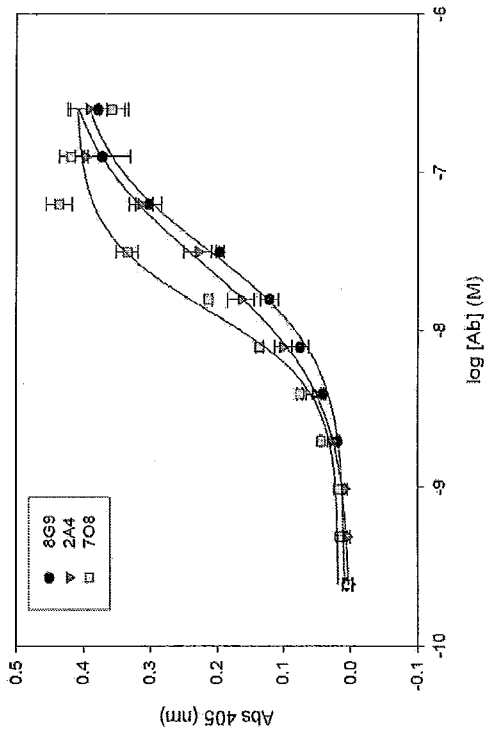


FIG. 35

Murine VL(2A4 and 8G9)
MKLPVRLLVLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSLVHSTGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGS
GSGTYFTLKISRVEAEDLGVYFCSQSTHVPFTFGGGTKLEIK (SEQ ID NO: 152)

Murine VL(7D8)
MKLPVRLLVLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSLSLVHSTGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGS
GSGTYFTLKISRVEAEDLGVYFCSQSTHVPFTFGGGTKLEIK (SEQ ID NO: 153)

Murine VH (2A4, 7D8, 8G9)
MVLGLKWVFFVVFYQGVHCEVQLVESGGRLVQPKGSLKLSCAASGFTFNTYAMYWIRQAPGKGLEWVARIRSKSNNYAIYYADSVK
DRFTIFRDDSQSMLYLQMNNLKTEDTAMYYCVRPYSDSFAYWGQGTLVTVSA (SEQ ID NO: 154)

FIG. 36A

Hum2A4 VL Version 1
DVVMTQSPLSLPVTPGEPASISCRSSQSLVHSTGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTyFTLKISRVEAEDVGV
YfCSQSTHVPFTFGGGTKVEIK (SEQ ID NO: 155)

Hum2A4 VL Version 2
DVVMTQSPLSLPVTPGEPASISCRSSQSLVHSTGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGV
YfCSQSTHVPFTFGGGTKVEIK (SEQ ID NO: 156)

Hum2A4 VL Version 3
DVVMTQSPLSLPVTPGEPASISCRSSQSLVHSTGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGV
YYCSQSTHVPFTFGGGTKVEIK (SEQ ID NO: 157)

FIG. 36B

Hum7D8 VL Version 1
DVVMTQSPLSLPVTPGEPASISCRSSLSLVHSTGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTyFTLKISRVEAEDVGV
YfCSQSTHVPFTFGQGTKLEIK (SEQ ID NO: 158)

Hum7D8 VL Version 2
DVVMTQSPLSLPVTPGEPASISCRSSLSLVHSTGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGV
YfCSQSTHVPFTFGQGTKLEIK (SEQ ID NO: 159)

Hum7D8 VL Version 3
DVVMTQSPLSLPVTPGEPASISCRSSLSLVHSTGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGV
YYCSQSTHVPFTFGQGTKLEIK (SEQ ID NO: 160)

Hum7D8 VL Version 4
DVVMTQSPLSLPVTPGEPASISCRSSLSLVHSTGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTyFTLKISRVEAEDVGV
YfCSQSTHVPFTFGGGTKLEIK (SEQ ID NO: 174)

Hum7D8 VL Version 5
DVVMTQSPLSLPVTPGEPASISCRSSLSLVHSTGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGV
YfCSQSTHVPFTFGGGTKLEIK (SEQ ID NO: 175)

Hum7D8 VL Version 6
DVVMTQSPLSLPVTPGEPASISCRSSLSLVHSTGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGV
YYCSQSTHVPFTFGGGTKLEIK (SEQ ID NO: 176)

FIG. 36C

Framework VL Gen Bank Accession No. BAC01562
DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGV
YYCMQALQTPLTFGGGTKVEIKR (SEQ ID NO: 166)

Framework VL Gen Bank Accession No. BAC01733
MKYLLPTAAAGLLLLAAQPAMADVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDR
FSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV
DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSARQSTPFVCEYQGQSSDLPQPPVN
AGGGSGGGSG (SEQ ID NO: 167)

FIG. 36D

Hum2A4/7D8/8G9 VH Version 1
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMYWiRQAPGKGLEWVaRIRSKSNNYAIYYADSVKDRFTIfRDDSKNSLYLQMNSL
KTEDTAVYYCvRPYSDSFAYWGQGTLVTVSS (SEQ ID NO: 161)

Hum2A4/7D8/8G9 VH Version 2
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMYWiRQAPGKGLEWVaRIRSKSNNYAIYYADSVKDRFTISRDDSKNSLYLQMNSL
KTEDTAVYYCvRPYSDSFAYWGQGTLVTVSS (SEQ ID NO: 162)

Hum2A4/7D8/8G9 VH Version 3
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMYWiRQAPGKGLEWVaRIRSKSNNYAIYYADSVKDRFTISRDDSKNSLYLQMNSL
KTEDTAVYYCARPYSDSFAYWGQGTLVTVSS (SEQ ID NO: 163)

2A4_8G9_7D8 H_chain_pro (murine 2A4 VH)
EVQLVESGGRLVQPKGSLKLSCAASGFTFNTYAMYWIRQAPGKGLEWVARIRSKSNNYAIYYADSVKDRFTIFRDDSQSMLYLQMNN
LKTEDTAMYYCVRPYSDSFAYWGQGTLVTVSA (SEQ ID NO: 164)

Framework VH Gen Bank Accession No. AAC51024
EVQLVESGGGLVQPGGSLRLSCAASGFTFSDHYMDWVRQAPGKGLEWVGRTRNKANSYTTEYAASVKGRFTISRDDSKNSLYLQMN
SLKTEDTAVYYCARYVVGATLDYWGQGTLVTVSS (SEQ ID NO: 165)

FIG. 36E