```
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

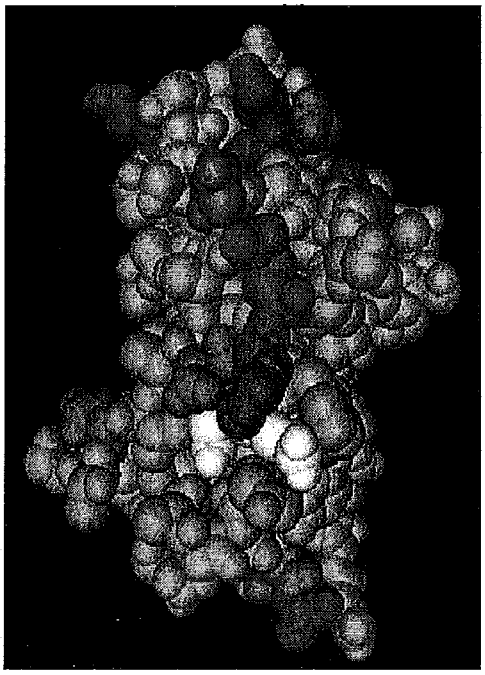
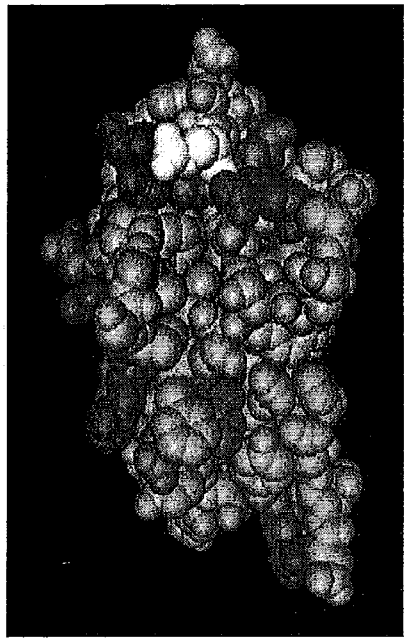
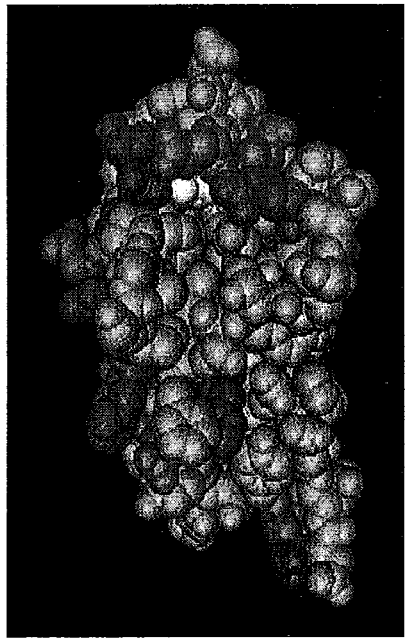


FIG. 24



V_λ6 Wil Glu81



V_λ6 Wil Asp82

FIG. 25

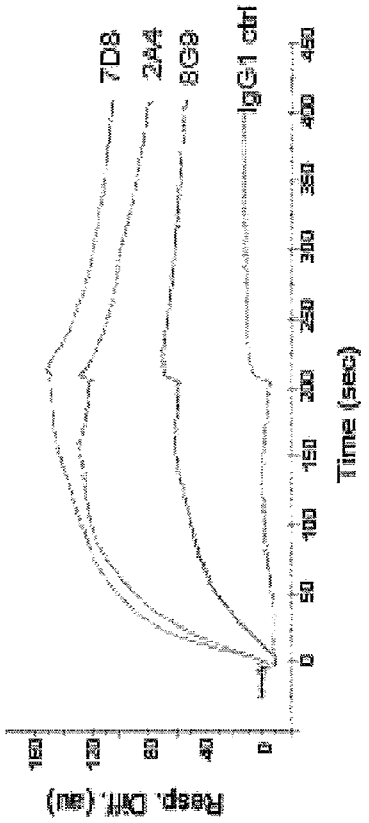

7D8
2A4
8G8
IgG1 ctrl
Resp. Diff. (au)
0
40
80
120
160
Time (sec)
0
50
100
150
200
250
300
350
400
450

FIG. 26

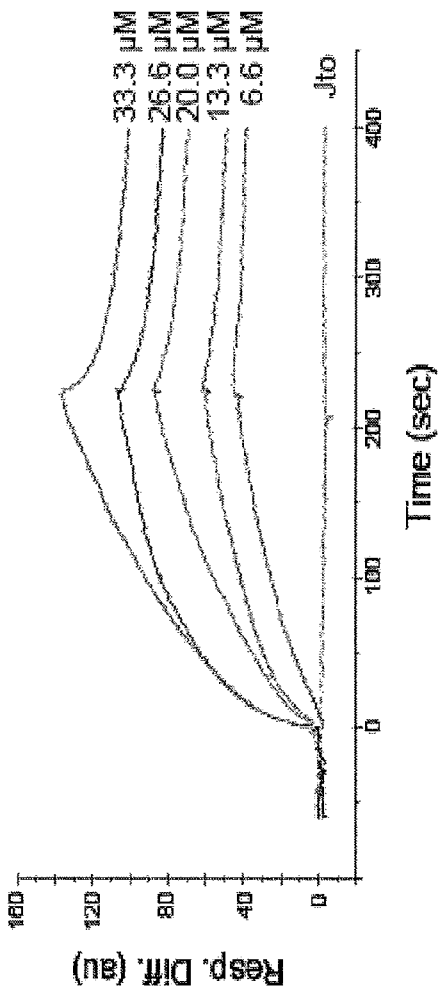

33.3 µM
26.6 µM
20.0 µM
13.3 µM
6.6 µM
Jto
Resp. Diff. (au)
Time (sec)
160
120
80
40
0
0
100
200
300
400

FIG. 27

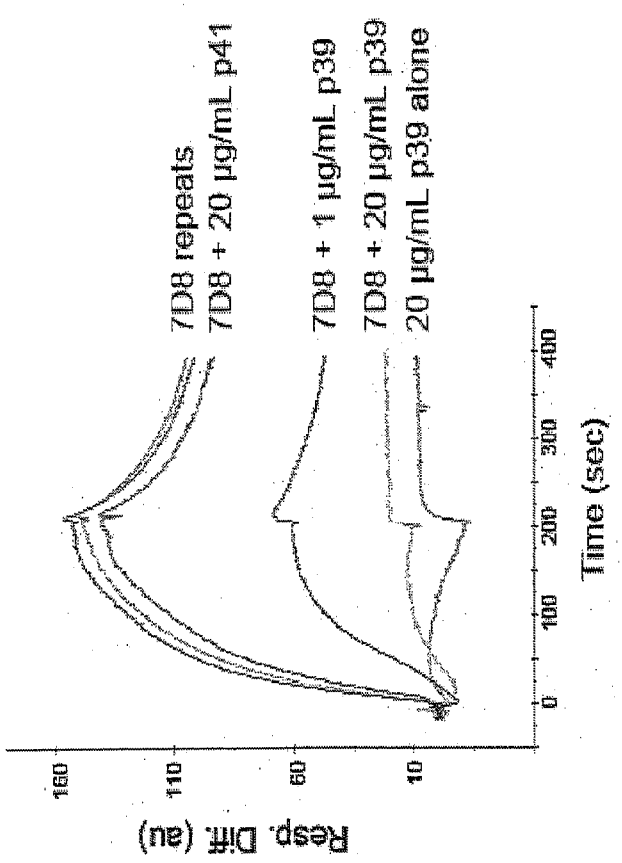

7D8 repeats
7D8 + 20 µg/mL p41
7D8 + 1 µg/mL p39
7D8 + 20 µg/mL p39
20 µg/mL p39 alone
Resp. Diff. (au)
160
110
60
10
0
100
200
300
400
Time (sec)

FIG. 28

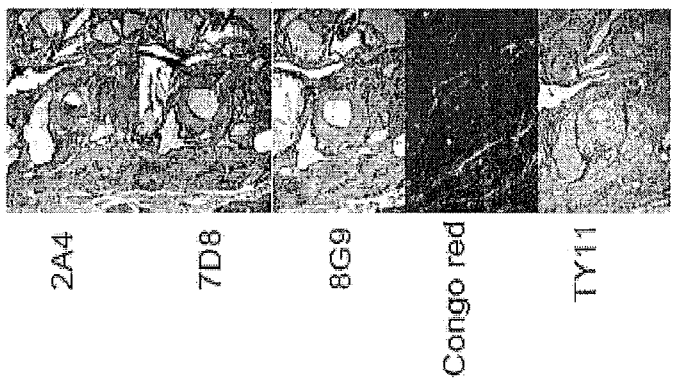


FIG. 29

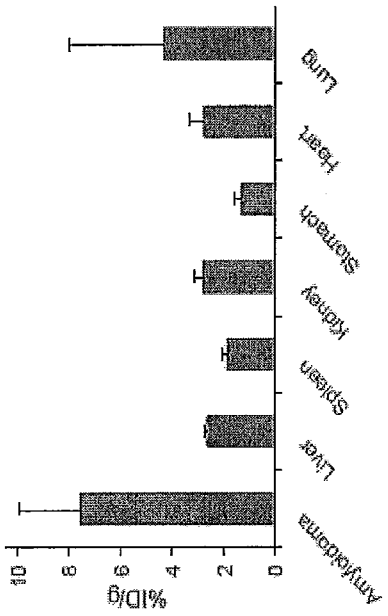

%ID/g
10
8
6
4
2
0
Xenograft
Liver
Spleen
Kidney
Stomach
Heart
Lung

FIG. 30

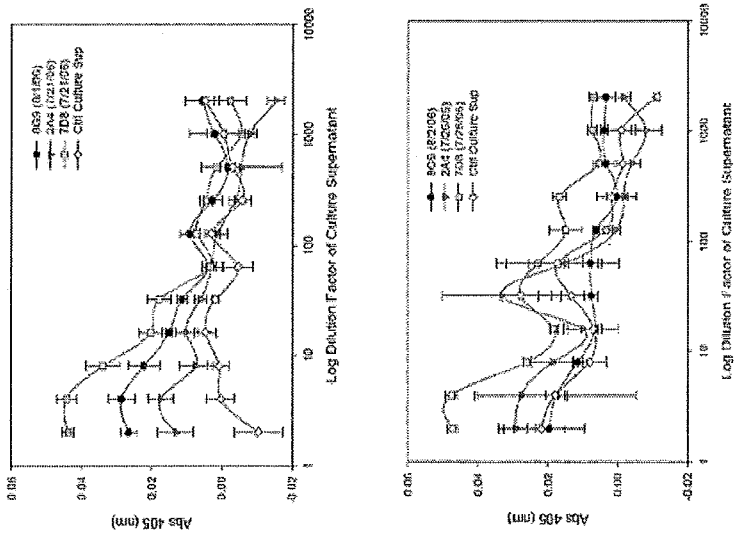

Abs 405 (nm)
Log Dilution Factor of Culture Supernatant
Abs 405 (nm)
Log Dilution Factor of Culture Supernatant

FIG. 31

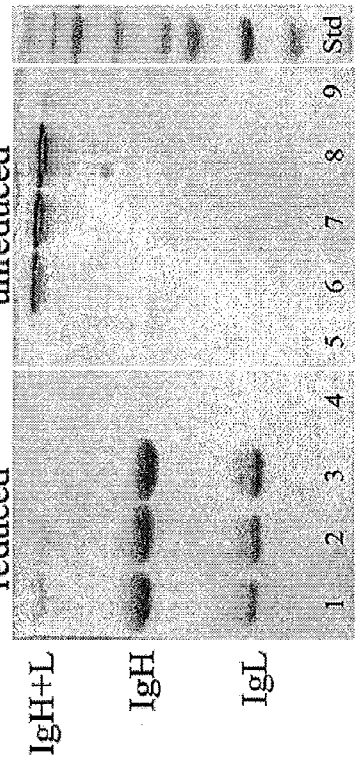


FIG. 32

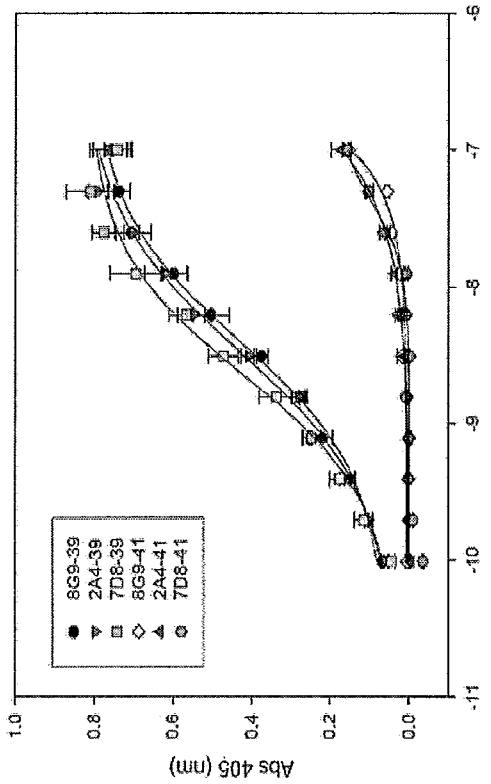

Abs 405 (nm)
1.0
0.8
0.6
0.4
0.2
0.0
-11
-10
-9
-8
-7
-6
log [Ab] (M)
8G9-39
2A4-39
7D8-39
8G9-41
2A4-41
7D8-41

FIG. 33

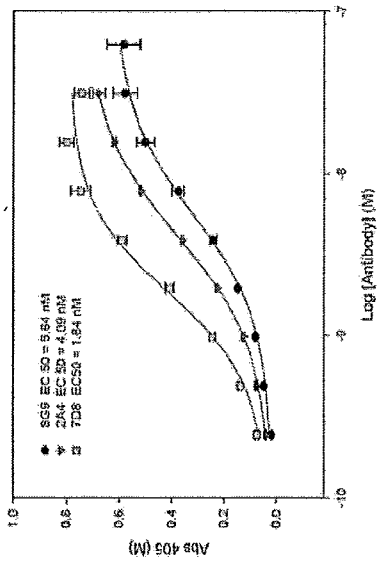

Abs 405 (M)
1.0
0.8
0.6
0.4
0.2
0.0
-10
-9
-8
-7
Log [Antibody] (M)
SG6 EC 50 = 5.64 nM
2A4 EC 50 = 4.09 nM
7D8 EC50 = 1.84 nM

FIG. 34

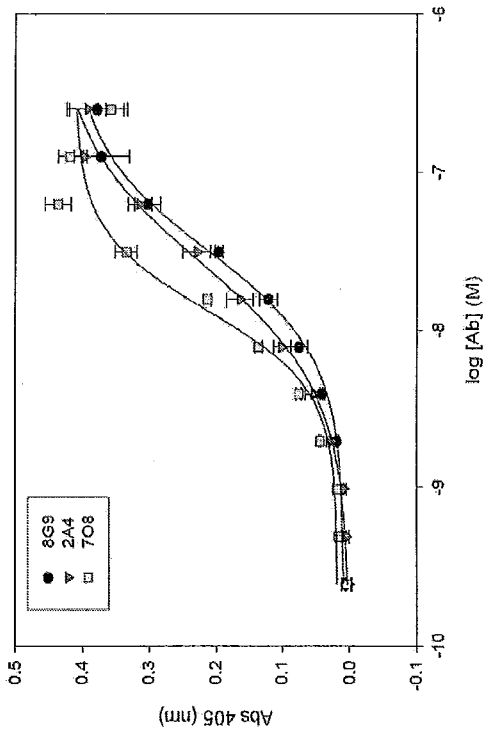


FIG. 35

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

SEQUENCE LISTING

<110> University of Tennessee Research Foundation
Elan Pharmaceuticals, Inc.

<120> Treatment and Prophylaxis of Amyloidosis

<130> SG1812A

<150> 61/007,544
<151> 2007-12-28

<150> 61/095,932
<151> 2008-09-10

<160> 177

<170> PatentIn version 3.4

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<211> 122
<212> PRT
<213> Homo sapiens

<400> 1

Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
1 5 10 15

Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
20 25 30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
35 40 45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
50 55 60

Arg Gly Pro Gly Gly Ala Trp Ala Ala Glu Val Ile Ser Asp Ala Arg
65 70 75 80

Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
85 90 95

Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
100 105 110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
115 120

<210> 2
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<212> PRT
<213> Homo sapiens

<220>

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<223> Human amyloid protein A peptide

<400> 2

Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala Arg Asp
1 5 10 15

Met Tyr Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile Gly Ser
20 25 30

Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys Arg Gly
35 40 45

Pro Gly Gly Ala Tyr Ala Ala Glu Val Ile Ser Asp Ala Arg Glu Asn
50 55 60

Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser
65 70 75

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<220>
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1 5

<210> 4
<211> 7
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<220>
<223> Derived from amyloid A protein

<400> 4

Gly His Gly Ala Glu Asp Ser
1 5

<210> 5
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Derived from amyloid A protein

<400> 5

Gly His Asp Ala Glu Asp Ser
1 5

<210> 6

<211> 7
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<220>
<223> Derived from amyloid protein

<400> 6

Gly His Gly Ala Glu Asp Ser
1 5

<210> 7
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<220>
<223> Derived from amyloid A protein

<400> 7

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1 5

<210> 8
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Derived from amyloid A protein

<400> 8

Ser Thr Val Ile Glu Asp Ser
1 5

<210> 9
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Derived from amyloid A protein

<400> 9

Gly Arg Gly His Glu Asp Thr
1 5

<210> 10
<211> 7
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<220>
<223> Derived from amyloid A protein

<400> 10

Gly His Gly Ala Glu Asp Ser
1 5

<210> 11
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Derived from amyloid A protein

<400> 11

Asn His Gly Leu Glu Thr Leu
1 5

<210> 12
<211> 4
<212> PRT
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<220>
<223> Derived from amyloidosis peptide

<400> 12

His Glu Asp Thr
1

<210> 13
<211> 4
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<220>
<223> Consensus sequence derived from human amyloidogenic proteins

<400> 13

Ala Glu Asp Ser
1

<210> 14
<211> 4
<212> PRT
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<220>
<223> Consensus sequence derived from human amyloidogenic proteins

<400> 14

Ala Glu Asp Thr
1

<210> 15
<211> 4
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<400> 15

His Glu Asp Ala

1

<210> 16
<211> 4
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<220>
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<400> 16

Thr Glu Asp Glu
1

<210> 17
<211> 4
<212> PRT
<213> Artificial

<220>
<223> AL V lambda fragment from amyloid protein

<400> 17

Phe Glu Asp Asp
1

<210> 18
<211> 4
<212> PRT
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<220>
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<400> 18

Ser Glu Asp Glu
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<210> 19
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<400> 19

Ala Glu Asp Glu
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<220>
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<400> 20

Pro Glu Asp Glu
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<210> 21
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Pro Glu Asp Ile
1

<210> 22
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<400> 22

Pro Glu Asp Phe
1

<210> 23
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Ala Glu Asp Val
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<210> 24
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<400> 25

Ser Glu Asp Ala
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<210> 26
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Pro Glu Asp Leu
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Thr Glu Asp Val
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<210> 29
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Ser Glu Asp Ile
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Thr Glu Asp Thr
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<400> 31

Leu Glu Asp Gly
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Ala Glu Asp Met
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His Glu Asp Ser
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Cys Glu Asp Asp
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<400> 35

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Arg Glu Asp Ser
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<400> 41

Glu Glu Asp Pro
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Leu Glu Asp Leu

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<400> 43

Lys Glu Asp Ala
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<210> 44
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<400> 44

Ser Glu Asp Cys
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<210> 45
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Glu Glu Asp Asp
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<210> 46
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Ser Glu Asp Lys
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Asp Glu Asp Asp
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<210> 48
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Asp Glu Asp Gly
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<400> 49

Leu Glu Asp Glu
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<210> 50
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Gly Glu Asp Ala
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<210> 51
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<400> 51

Val Glu Asp Phe
1

<210> 52
<211> 4
<212> PRT
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<400> 52

Tyr Glu Asp Glu
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<400> 53

Ile Glu Asp Leu
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<210> 54
<211> 4
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<400> 54

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Asp Glu Asp Trp
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<210> 56
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<400> 56

Ser Glu Asp Leu
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<210> 57
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Tyr Glu Asp Gln
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<210> 58
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<400> 58

Leu Glu Asp Trp
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<210> 59
<211> 4
<212> PRT
<213> Artificial

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<400> 59

Tyr Glu Asp Arg
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<210> 60
<211> 4
<212> PRT
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<223> Consensus sequence derived from human amyloidogenic proteins

<400> 60

Pro Glu Asp Lys
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<210> 61
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Non-amyloid portion of serum amyloid A protein

<400> 61

Gly His Glu Asp Thr Met Ala Asp Gln Glu
1 5 10

<210> 62
<211> 4
<212> PRT

<213> Artificial

<220>
<223> Consensus sequence derived from human amyloidogenic proteins

<400> 62

Ala Glu Asp Ala
1

<210> 63
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Consensus sequence derived from human amyloidogenic proteins

<400> 63

Gln Glu Asp Leu
1

<210> 64
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<212> PRT
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<220>
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<400> 64

Val Glu Asp Leu
1

<210> 65
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Consensus sequence derived from human amyloidogenic proteins

<400> 65

Leu Glu Asp Ala
1

<210> 66
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Consensus sequence derived from human amyloidogenic proteins

<400> 66

Ser Glu Asp Gly
1

<210> 67

<211> 16
<212> PRT
<213> Artificial

<220>
<223> Derived from Malaria CS

<220>
<221> MISC_FEATURE
<223> T3 epitope

<400> 67

Glu Lys Lys Ile Ala Lys Met Glu Lys Ala Ser Ser Val Phe Asn Val
1 5 10 15

<210> 68
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Derived from Hepititis B surface antigen residues 19-28

<400> 68

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
1 5 10

<210> 69
<211> 19
<212> PRT
<213> Artificial

<220>
<223> Derived from mycobacterium heat shock protein 65 residues 153-171

<400> 69

Asp Gln Ser Ile Gly Asp Leu Ile Ala Glu Ala Met Asp Lys Val Gly
1 5 10 15

Asn Glu Gly

<210> 70
<211> 14
<212> PRT
<213> Bicille calmette-guerin

<400> 70

Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu
1 5 10

<210> 71
<211> 15
<212> PRT
<213> Artificial

<220>
<223> Derived from Tetanus toxoid residues 830-844

<400> 71

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 72
<211> 21
<212> PRT
<213> Artificial

<220>
<223> Derived from Tetanus toxoid residues 947-967

<400> 72

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

Ala Ser His Leu Glu
20

<210> 73
<211> 16
<212> PRT
<213> HIV

<220>
<221> MISC_FEATURE
<223> HIV gb120 T1

<400> 73

Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala
1 5 10 15

<210> 74
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Pan DR epitope

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<400> 74

Ala Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10

<210> 75
<211> 36
<212> PRT
<213> Artificial

<220>
<223> Fusion protein derived from Tetanus toxoid residues 830-844 and

947-967

<400> 75

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Phe
1 5 10 15

Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala
20 25 30

Ser His Leu Glu
35

<210> 76
<211> 17
<212> PRT
<213> Artificial

<220>
<223> Derived from ovalbumin residues 323-389

<400> 76

Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
1 5 10 15

Arg

<210> 77
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Derived from hemagglutinin influenza A virus

<400> 77

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

<210> 78
<211> 65
<212> PRT
<213> Artificial

<220>
<223> Fusion protein derived from hemagglutinin influenza A residues 307-319, Malaria CD: T3 epitope, tetanus toxoid residues 830-844 and 947-967

<400> 78

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr Glu Lys Lys
1 5 10 15

Ile Ala Lys Met Glu Lys Ala Ser Ser Val Phe Asn Val Gln Tyr Ile
20 25 30

Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Phe Asn Asn Phe
35 40 45

Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu
50 55 60

Glu
65

<210> 79
<211> 37
<212> PRT
<213> Artificial

<220>
<223> Fusion protein

<400> 79

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Cys
1 5 10 15

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
20 25 30

Ala Ser His Leu Glu
35

<210> 80
<211> 15
<212> PRT
<213> Artificial

<220>
<223> Derived from human amyloid A protein

<400> 80

Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala Arg
1 5 10 15

<210> 81
<211> 15
<212> PRT
<213> Artificial

<220>
<223> Derived from human amyloid A protein

<400> 81

Gln Gly Trp Leu Thr Phe Leu Lys Ala Ala Gly Gln Gly Ala Lys
1 5 10 15

<210> 82
<211> 10
<212> PRT
<213> Artificial

<220>

<223> Derived from mouse amyloid A protein

<400> 82

Glu Ser Trp Arg Ser Phe Phe Lys Glu Ala
1 5 10

<210> 83
<211> 15
<212> PRT
<213> Artificial

<220>
<223> Derived from mouse amyloid A protein

<400> 83

Gly Phe Phe Ser Phe Val His Glu Ala Phe Gln Gly Ala Gly Asp
1 5 10 15

<210> 84
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Derived from mouse amyloid A protein

<400> 84

Glu Ala Gly Gln Gly Ser Arg Asp
1 5

<210> 85
<211> 14
<212> PRT
<213> Artificial

<220>
<223> Derived from mouse amyloid A protein

<400> 85

Trp Tyr Ser Phe Phe Arg Glu Ala Val Gln Gly Thr Trp Asp
1 5 10

<210> 86
<211> 99
<212> PRT
<213> Homo Sapiens

<220>
<221> MISC_FEATURE
<223> Lambda 2 fragments from human amyloid deposits

<400> 86

Gly Ser Val Val Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Arg Gln
1 5 10 15

Thr Val Ala Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

```
Ala Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Val Leu
        35                  40                  45

Ile Tyr Tyr Asp Asp Leu Leu Pro Ala Gly Val Ser Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln
65                  70                  75                  80

Ser Glu Asp Glu Gly Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Ser Ala Leu
```

<210> 87
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Derived from serum amyloid A protein

<400> 87

```
Cys Gly Gly His Glu Asp Thr
1               5
```

<210> 88
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Derived from serum amyloid A protein

<400> 88

```
Cys Gly Gly Ala Glu Asp Ser
1               5
```

<210> 89
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Derived from serum amyloid A protein

<400> 89

```
Gly His Glu Asp Thr Ile Ala Asp Gln Glu
1               5                   10
```

<210> 90
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Derived from serum amyloid A protein

<400> 90

Cys Gly Gly Ala Glu Asp Thr
1   5

<210> 91
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Derived from serum amyloid A protein

<400> 91

Cys Gly Gly His Ala Asp Thr
1   5

<210> 92
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Derived from serum amyloid A protein

<400> 92

Cys Gly Gly His Glu Ala Thr
1   5

<210> 93
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Derived from serum amyloid A protein

<400> 93

Cys Gly Gly His Glu Asp Ala
1   5

<210> 94
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Derived from serum amyloid A protein

<400> 94

Cys Gly Gly His Glu Asp Thr Met
1   5

<210> 95
<211> 9

<212> PRT
<213> Artificial

<220>
<223> Derived from serum amyloid A protein

<400> 95

Cys Gly Gly His Glu Asp Thr Met Ala
1 5

<210> 96
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Derived from serum amyloid A protein

<400> 96

Cys Gly Gly His Glu Asp Thr Met Ala Asp
1 5 10

<210> 97
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Derived from serum amyloid A protein

<400> 97

Cys Gly Gly His Glu Asp
1 5

<210> 98
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> HSAA1

<400> 98

Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
1 5 10 15

Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
20 25 30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
35 40 45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
50 55 60

```
Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
65                  70                  75                  80

Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
                85                  90                  95

Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
            100                 105                 110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
        115                 120
```

<210> 99
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> HSAA2

<400> 99

```
Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Ser Val
1               5                   10                  15

Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
            20                  25                  30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
        35                  40                  45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
    50                  55                  60

Arg Gly Pro Gly Gly Ala Trp Ala Ala Glu Val Ile Ser Asn Ala Arg
65                  70                  75                  80

Glu Asn Ile Gln Arg Leu Thr Gly His Gly Ala Glu Asp Ser Leu Ala
                85                  90                  95

Asp Gln Ala Ala Asn Lys Trp Gly Arg Ser Gly Arg Asp Pro Asn His
            100                 105                 110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
        115                 120
```

<210> 100
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

<223> HSAA3

<400> 100

Met Lys Leu Ser Thr Gly Ile Ile Phe Cys Ser Leu Val Leu Gly Val
1 5 10 15

Ser Ser Gln Gly Trp Leu Thr Phe Leu Lys Ala Ala Gly Gln Gly Ala
20 25 30

Lys Asp Met Trp Arg Ala Tyr Ser Asp Met Lys Glu Ala Asn Tyr Lys
35 40 45

Lys Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Val Gln
50 55 60

Arg Gly Pro Gly Gly Val Trp Ala Thr Glu Val Ile Ser Asp Ala Arg
65 70 75 80

Glu Asn Val Gln Arg Leu Thr Gly Asp His Ala Glu Asp Ser Leu Ala
85 90 95

Gly Gln Ala Thr Asn Lys Trp Gly Gln Ser Gly Lys Asp Pro Asn His
100 105 110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
115 120

<210> 101
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> HSAA4

<400> 101

Met Arg Leu Phe Thr Gly Ile Val Phe Cys Ser Leu Val Met Gly Val
1 5 10 15

Thr Ser Glu Ser Trp Arg Ser Phe Phe Lys Glu Ala Leu Gln Gly Val
20 25 30

Gly Asp Met Gly Arg Ala Tyr Trp Asp Ile Met Ile Ser Asn His Gln
35 40 45

Asn Ser Asn Arg Tyr Leu Tyr Ala Arg Gly Asn Tyr Asp Ala Ala Gln
50 55 60

Arg Gly Pro Gly Gly Val Trp Ala Ala Lys Leu Ile Ser Arg Ser Arg
65 70 75 80

```
Val Tyr Leu Gln Gly Leu Ile Asp Tyr Tyr Leu Phe Gly Asn Ser Ser
                85                  90                  95

Thr Val Leu Glu Asp Ser Lys Ser Asn Glu Lys Ala Glu Glu Trp Gly
            100                 105                 110

Arg Ser Gly Lys Asp Pro Asp Arg Phe Arg Pro Asp Gly Leu Pro Lys
        115                 120                 125

Lys Tyr
    130
```

<210> 102
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> HAA1

<400> 102

```
Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala Arg Asp
1               5                   10                  15

Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile Gly Ser
            20                  25                  30

Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys Arg Gly
        35                  40                  45

Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg Glu Asn
    50                  55                  60

Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser
65                  70                  75
```

<210> 103
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> HAA2

<400> 103

```
Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala Arg Asp
1               5                   10                  15

Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile Gly Ser
            20                  25                  30
```

Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys Arg Gly
        35   40   45

Pro Gly Gly Ala Trp Ala Ala Glu Val Ile Ser Asn Ala Arg Glu Asn
    50   55   60

Ile Gln Arg Leu Thr Gly His Gly Ala Glu Asp Ser
65   70   75

<210> 104
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> HAA3

<400> 104

Gln Gly Trp Leu Thr Phe Leu Lys Ala Ala Gly Gln Gly Ala Lys Asp
1   5   10   15

Met Trp Arg Ala Tyr Ser Asp Met Lys Glu Ala Asn Tyr Lys Lys Ser
            20   25   30

Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Val Gln Arg Gly
        35   40   45

Pro Gly Gly Val Trp Ala Thr Glu Val Ile Ser Asp Ala Arg Glu Asn
    50   55   60

Val Gln Arg Leu Thr Gly Asp His Ala Glu Asp Ser
65   70   75

<210> 105
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> HAA4

<400> 105

Glu Ser Trp Arg Ser Phe Phe Lys Glu Ala Leu Gln Gly Val Gly Asp
1   5   10   15

Met Gly Arg Ala Tyr Trp Asp Ile Met Ile Ser Asn His Gln Asn Ser
            20   25   30

Asn Arg Tyr Leu Tyr Ala Arg Gly Asn Tyr Asp Ala Ala Gln Arg Gly
        35   40   45

Pro Gly Gly Val Trp Ala Ala Lys Leu Ile Ser Arg Ser Arg Val Tyr
50 55 60

Leu Gln Gly Leu Ile Asp Tyr Tyr Leu Phe Gly Asn Ser Ser Thr Val
65 70 75 80

Ile Glu Asp Ser

<210> 106
<211> 117
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> MSAA1

<400> 106

Met Lys Leu Leu Thr Ser Leu Val Phe Cys Ser Leu Leu Leu Gly Val
1 5 10 15

Cys His Gly Gly Phe Phe Ser Phe Val His Glu Ala Phe Gln Gly Ala
20 25 30

Gly Asp Met Trp Arg Ala Tyr Thr Asp Met Lys Glu Ala Asn Trp Lys
35 40 45

Asn Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Gln
50 55 60

Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Lys Ile Ser Asp Gly Arg
65 70 75 80

Glu Ala Phe Gln Glu Phe Phe Gly Arg Ile Ala Asp Gln Glu Ala Asn
85 90 95

Arg His Gly Arg Ser Gly Lys Asp Pro Asn Tyr Tyr Arg Pro Pro Gly
100 105 110

Leu Pro Asp Lys Tyr
115

<210> 107
<211> 122
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> MSAA2

<400> 107

```
Met Lys Leu Leu Thr Ser Leu Val Phe Cys Ser Leu Leu Leu Gly Val
1               5                  10                  15

Cys His Gly Gly Phe Phe Ser Phe Ile Gly Glu Ala Phe Gln Gly Ala
            20                  25                  30

Gly Asp Met Trp Arg Ala Tyr Thr Asp Met Lys Glu Ala Gly Trp Lys
        35                  40                  45

Asp Gly Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Gln
    50                  55                  60

Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Lys Ile Ser Asp Ala Arg
65                  70                  75                  80

Glu Ser Phe Gln Glu Phe Phe Gly Arg Gly His Glu Asp Thr Met Ala
                85                  90                  95

Asp Gln Glu Ala Asn Arg His Gly Arg Ser Gly Lys Asp Pro Asn Tyr
            100                 105                 110

Tyr Arg Pro Pro Gly Leu Pro Ala Lys Tyr
        115                 120
```

<210> 108
<211> 122
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> MSAA3

<400> 108

```
Met Lys Pro Ser Ile Ala Ile Ile Leu Cys Ile Leu Ile Leu Gly Val
1               5                  10                  15

Asp Ser Gln Arg Trp Val Gln Phe Met Lys Glu Ala Gly Gln Gly Ser
            20                  25                  30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Lys Lys Ala Asn Trp Lys
        35                  40                  45

Asn Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Arg
    50                  55                  60

Arg Gly Pro Gly Gly Ala Trp Ala Ala Lys Val Ile Ser Asp Ala Arg
65                  70                  75                  80

Glu Ala Val Gln Lys Phe Thr Gly His Gly Ala Glu Asp Ser Arg Ala
                85                  90                  95
```

Asp Gln Phe Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
100 105 110

Phe Arg Pro Ala Gly Leu Pro Lys Arg Tyr
115 120

<210> 109
<211> 130
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> MSAA4

<400> 109

Met Arg Leu Ala Thr Val Ile Val Leu Cys Ser Leu Phe Leu Gly Val
1 5 10 15

Ser Gly Asp Gly Trp Tyr Ser Phe Phe Arg Glu Ala Val Gln Gly Thr
20 25 30

Trp Asp Leu Trp Arg Ala Tyr Arg Asp Asn Leu Glu Ala Asn Tyr Gln
35 40 45

Asn Ala Asp Gln Tyr Phe Tyr Ala Arg Gly Asn Tyr Glu Ala Gln Gln
50 55 60

Arg Gly Ser Gly Gly Ile Trp Ala Ala Lys Ile Ile Ser Thr Ser Arg
65 70 75 80

Lys Tyr Phe Gln Gly Leu Leu Asn Arg Tyr Tyr Phe Gly Ile Arg Asn
85 90 95

His Gly Leu Glu Thr Leu Gln Ala Thr Gln Lys Ala Glu Glu Trp Gly
100 105 110

Arg Ser Gly Lys Asn Pro Asn His Phe Arg Pro Glu Gly Leu Pro Glu
115 120 125

Lys Phe
130

<210> 110
<211> 85
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> MAA1

<400> 110

```
Gly Phe Phe Ser Phe Val His Glu Ala Phe Gln Gly Ala Gly Asp Met
1               5                   10                  15

Trp Arg Ala Tyr Thr Asp Met Lys Glu Ala Asn Trp Lys Asn Ser His
            20                  25                  30

Glu Asp Thr Ile Ala Asp Gln Glu Ala Asp Lys Tyr Phe His Ala Arg
        35                  40                  45

Gly Asn Tyr Asp Ala Ala Gln Arg Gly Pro Gly Gly Val Trp Ala Ala
    50                  55                  60

Glu Lys Ile Ser Asp Gly Arg Glu Ala Phe Gln Glu Phe Phe Gly Arg
65                  70                  75                  80

Gly His Glu Asp Thr
                85
```

<210> 111
<211> 75
<212> PRT
<213> Mouse

<220>
<221> MISC_FEATURE
<223> MAA2

<400> 111

```
Gly Phe Phe Ser Phe Ile Gly Glu Ala Phe Gln Gly Ala Gly Asp Met
1               5                   10                  15

Trp Arg Ala Tyr Thr Asp Met Lys Glu Ala Gly Trp Lys Asp Gly Asp
            20                  25                  30

Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Gln Arg Gly Pro
        35                  40                  45

Gly Gly Val Trp Ala Ala Glu Lys Ile Ser Asp Ala Arg Glu Ser Phe
    50                  55                  60

Gln Glu Phe Phe Gly Arg Gly His Glu Asp Thr
65                  70                  75
```

<210> 112
<211> 68
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> MAA3

<400> 112

```
Glu Ala Gly Gln Gly Ser Arg Asp Met Trp Arg Ala Tyr Ser Asp Met
1               5                   10                  15

Lys Lys Ala Asn Trp Lys Asn Ser Asp Lys Tyr Phe His Ala Arg Gly
            20                  25                  30

Asn Tyr Asp Ala Ala Arg Arg Gly Pro Gly Gly Ala Trp Ala Ala Lys
        35                  40                  45

Val Ile Ser Asp Ala Arg Glu Ala Val Gln Lys Phe Thr Gly His Gly
    50                  55                  60

Ala Glu Asp Ser
65
```

<210> 113
<211> 82
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> MAA4

<400> 113

```
Trp Tyr Ser Phe Phe Arg Glu Ala Val Gln Gly Thr Trp Asp Leu Trp
1               5                   10                  15

Arg Ala Tyr Arg Asp Asn Leu Glu Ala Asn Tyr Gln Asn Ala Asp Gln
            20                  25                  30

Tyr Phe Tyr Ala Arg Gly Asn Tyr Glu Ala Gln Gln Arg Gly Ser Gly
        35                  40                  45

Gly Ile Trp Ala Ala Lys Ile Ile Ser Thr Ser Arg Lys Tyr Phe Gln
    50                  55                  60

Gly Leu Leu Asn Arg Tyr Tyr Phe Gly Ile Arg Asn His Gly Leu Glu
65                  70                  75                  80

Thr Leu
```

<210> 114
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> HSAA1 alpha

<400> 114

Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
1 5 10 15

Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
20 25 30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
35 40 45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
50 55 60

Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
65 70 75 80

Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
85 90 95

Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
100 105 110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
115 120

<210> 115
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> HSSA1 beta

<400> 115

Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
1 5 10 15

Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
20 25 30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
35 40 45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
50 55 60

Arg Gly Pro Gly Gly Ala Trp Ala Ala Glu Val Ile Ser Asp Ala Arg
65 70 75 80

Glu Asn Ile Gln Arg Phe Phe Gly His Asp Ala Glu Asp Ser Leu Ala
85 90 95

```
Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
            100                 105                 110


Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
        115                 120


<210>  116
<211>  122
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  HSSA1 gamma

<400>  116

Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
1               5                   10                  15


Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
            20                  25                  30


Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
        35                  40                  45


Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
    50                  55                  60


Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
65                  70                  75                  80


Glu Asn Ile Gln Arg Phe Phe Gly His Asp Ala Glu Asp Ser Leu Ala
                85                  90                  95


Asp Gln Ala Ala Asn Lys Trp Gly Arg Ser Gly Arg Asp Pro Asn His
            100                 105                 110


Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
        115                 120


<210>  117
<211>  122
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  HSAA2 alpha

<400>  117

Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Ser Val
1               5                   10                  15
```

```
Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
            20                  25                  30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
        35                  40                  45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
    50                  55                  60

Arg Gly Pro Gly Gly Ala Trp Ala Ala Glu Val Ile Ser Asn Ala Arg
65                  70                  75                  80

Glu Asn Ile Gln Arg Leu Thr Gly His Gly Ala Glu Asp Ser Leu Ala
                85                  90                  95

Asp Gln Ala Ala Asn Lys Trp Gly Arg Ser Gly Arg Asp Pro Asn His
            100                 105                 110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
        115                 120


<210>  118
<211>  122
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  HSAA2 beta

<400>  118

Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Ser Val
1               5                   10                  15

Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
            20                  25                  30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
        35                  40                  45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
    50                  55                  60

Arg Gly Pro Gly Gly Ala Trp Ala Ala Glu Val Ile Ser Asn Ala Arg
65                  70                  75                  80

Glu Asn Ile Gln Arg Leu Thr Gly Arg Gly Ala Glu Asp Ser Leu Ala
                85                  90                  95

Asp Gln Ala Ala Asn Lys Trp Gly Arg Ser Gly Arg Asp Pro Asn His
            100                 105                 110
```

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
115 120

<210> 119
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> HAA1 beta isoform

<400> 119

Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala Arg Asp
1 5 10 15

Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile Gly Ser
20 25 30

Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys Arg Gly
35 40 45

Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg Glu Asn
50 55 60

Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala Asp Gln
65 70 75 80

Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His Phe Arg
85 90 95

Pro Ala Gly Leu Pro Glu Lys Tyr
100

<210> 120
<211> 102
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Serum amyloid A protein

<400> 120

Gly Phe Phe Ser Phe Ile Gly Glu Ala Phe Gln Gly Ala Gly Asp Met
1 5 10 15

Trp Arg Ala Tyr Thr Asp Met Lys Glu Ala Gly Trp Lys Asp Gly Asp
20 25 30

Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Gln Arg Gly Pro
35 40 45

Gly Gly Val Trp Ala Ala Glu Lys Ile Ser Asp Ala Arg Glu Ser Gln
50 55 60

Glu Phe Phe Gly Arg Gly His Glu Asp Thr Met Ala Asp Gln Glu Ala
65 70 75 80

Asn Arg His Gly Arg Ser Gly Lys Asp Pro Asn Tyr Tyr Arg Pro Pro
85 90 95

Gly Leu Pro Ala Lys Tyr
100

<210> 121
<211> 84
<212> PRT
<213> Canis lupus familiaris (Shar pei)

<220>
<221> MISC_FEATURE
<223> Serum amyloid A protein

<400> 121

Trp Tyr Ser Phe Val Gly Glu Ala Ala Gln Gly Ala Trp Asp Met Leu
1 5 10 15

Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Lys Asn Ser Asp Lys
20 25 30

Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Gln Arg Gly Pro Gly
35 40 45

Gly Ala Trp Ala Ala Lys Val Ile Ser Asp Ala Arg Glu Asn Ser Gln
50 55 60

Arg Asp Ser Gly His Gly Ala Glu Asp Ser Lys Ala Asp Gln Ala Ala
65 70 75 80

Asn Glu Trp Gly

<210> 122
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Amino acid insert between positions 67 and 68 of Shar Pei sequence

<400> 122

Ile Thr Asp Leu Leu Arg Phe Gly
1 5

<210> 123

<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kpla

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 123

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser
85 90 95

<210> 124
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kplb

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 124

Ser Gln Asp Asn Tyr Asn Asp Asn Thr Asp Phe Glu Ile Asp Asn Leu
1 5 10 15

Pro

<210> 125
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kplc

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 125

Ser Tyr Asn Ala Gln Asp Glu Ser Tyr Thr Pro
1   5   10

<210> 126
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kpld

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 126

Ser Gly Arg Asn Asp Gly Arg Ala Gln Glu Leu His Pro
1   5   10

<210> 127
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kple

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 127

Ser Gly Asn Tyr Phe Ser Ala Gln Asp Glu Pro
1   5   10

<210> 128
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kplf

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 128

Ala Leu Ser Gly Ala Asp Asp Glu Phe Asn Pro
1 5 10

<210> 129
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kplg

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 129

Ser Val Gly Ala Gln Asp Glu Ala Phe Pro
1 5 10

<210> 130
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kp2a

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 130

Val Thr Leu Ser Pro Val Thr Pro Glu Pro Ala Ser Ser Ser Leu Leu
1 5 10 15

Asp Ser Asp Asp Gly Asn Thr Tyr Asp Leu Gln Ser Gln Thr Leu Tyr
20 25 30

Arg Ala Asp Asp Lys Arg Val Glu Ala Glu Val Gly Val Met Arg Ile
35 40 45

Glu Phe Pro
50

<210> 131
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kp2b

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 131

Val Leu Ser Pro Val Thr Pro Glu Pro Ala Ser Ser Ser Leu Leu His
1   5   10   15

Ser Asn Gly Tyr Asn Tyr Asp Leu Gln Ser Gln Leu Gly Asn Arg Ala
            20   25   30

Asp Asp Lys Arg Val Glu Ala Glu Val Gly Val Met Ala Leu Gln Thr
        35   40   45

Pro

<210> 132
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kp2c

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 132

Val Thr Leu Ser Val Thr Pro Gln Pro Ala Ser Ser Lys Ser Leu Leu
1   5   10   15

His Ser Asp Gly Lys Thr Tyr Tyr Leu Gln Pro Gln Glu Val Asn Arg
            20   25   30

Phe Asp Asp Lys Arg Val Glu Ala Glu Val Gly Val Met Ser Ile Gln
        35   40   45

Leu Pro
    50

<210> 133
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kp3a

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 133

Glu Val Ala Val Pro Glu Ala Leu Ser Val Asn Gln Arg Gly Thr Arg
1 5 10 15

Ala Thr Ile Ala Ser Glu Val Asn Trp Pro
20 25

<210> 134
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kp3b

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 134

Glu Val Leu Gly Leu Pro Glu Ala Leu Ser Val Ser Tyr Gln Arg Gly
1 5 10 15

Arg Ala Thr Ile Asp Asp Arg Glu Glu Val Gly Ser Pro
20 25

<210> 135
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kp3c

<220>
<221> MISC_FEATURE
<223> Germline sequences of V kappa light chain

<400> 135

Glu Val Leu Ala Leu Pro Glu Ala Leu Ser Val Ser Tyr Gln Arg Asp
1 5 10 15

Asn Arg Ala Thr Ile Ala Asp Glu Glu Val Arg Ser Asn Trp Pro
20 25 30

<210> 136
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kp4

<220>
<221> MISC_FEATURE
<223> Germline sequences of V lambda light chain

<400> 136

Val Asp Ser Ala Val Leu Glu Ala Asn Lys Ser Val Leu Tyr Ser Ser
1   5   10   15

Asn Asn Lys Asn Tyr Gln Pro Trp Thr Arg Asp Asp Ala Glu Val Val
            20   25   30

Tyr Thr Pro
        35

<210> 137
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> kp5

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 137

Glu Thr Thr Leu Ala Phe Met Thr Pro Lys Asn Ser Lys Asp Asp Asp
1   5   10   15

Asp Met Asn Glu Ala Ile Phe Ile Gln Glu Thr Thr Val Pro Ile Pro
            20   25   30

Tyr Asp Asn Asn Ile Glu Ser Glu Ala Tyr Phe Leu His Asp Asn Phe
        35   40   45

Pro

<210> 138
<211> 97
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lmla

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 138

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln

1 5 10 15

Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr
20 25 30

Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Glu Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60

Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr
65 70 75 80

Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu Ser
85 90 95

Ala

<210> 139
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lmlb

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 139

Ala Gly Thr Arg Ser Tyr Arg Gln Val Ser Ala Ser Arg Ser Glu Ala
1 5 10 15

Ala Asp Gly

<210> 140
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lmlc

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 140

Val Gly Arg Thr Ala Gly Tyr Asp His Gly Ser Asn Val Ser Ala Ala

1 5 10 15

Glu Gln Ser Tyr Gly
20

<210> 141
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lm2a

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 141

Ala Ala Gly Ser Ser Ile Thr Thr Asp Val Ser Tyr Leu His Lys Met
1 5 10 15

Gly Ser Val Ser Ala Ala Glu Gln Ser Tyr Gly
20 25

<210> 142
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lm2b

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 142

Ala Arg Gly Ser Val Ile Thr Thr Asp Val Gly Tyr His Lys Met Asp
1 5 10 15

Val Ser Val Asn Thr Ser Thr Ser Ala Glu Cys Ser Tyr Ala Gly Tyr
20 25 30

Thr Phe

<210> 143
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lm3a

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 143

Ser Tyr Val Lys Thr Ala Arg Thr Gly Asn Asn Ile Gly Ser Lys Ser
1   5   10   15

His Lys Gln Val Val Val Asp Asp Ser Asp Glu Asn Asn Thr Thr Ser
            20   25   30

Arg Val Glu Ala Gln Val Ser Asp His
        35   40

<210> 144
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lm3b

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 144

Ser Tyr Glu Val Ser Thr Ala Arg Thr Asp Ala Leu Pro Lys Gln Ala
1   5   10   15

Tyr Lys Gln Val Val Lys Asp Ser Glu Glu Ser Thr Val Thr Ser Val
            20   25   30

Ala Glu Gln Ser Ala Gly
        35

<210> 145
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lm3c

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 145

Ser Tyr Glu Val Ser Thr Ala Ser Thr Asp Lys Leu Gly Asp Lys Ala
1   5   10   15

Cys Lys Gln Ser Val Val Gln Asp Ser Glu Asn Asn Thr Thr Ser Thr

20 25 30

Ala Met Gln Ala Thr Ala His
35

<210> 146
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lm4

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 146

Ser Glu Asp Ala Val Leu Thr Arg Thr Gln Asp Leu Arg Ser Tyr Ala
1 5 10 15

Lys Gln Val Val Gly Lys Asn
20

<210> 147
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lm6

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 147

Asn Phe Met His Glu Ser Lys Thr Thr Arg Gly Ser Ala Ser Gln Arg
1 5 10 15

Ser Ser Thr Thr Val Asp Gln Val Ile Asp Ser Ser Asn Ser Thr Ser
20 25 30

Lys Glu Gln Ser Tyr Asn
35

<210> 148
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lm7

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 148

Thr Val Glu Leu Thr Val Ser Gly Thr Leu Thr Ala Ser Thr Gly Ala
1   5   10   15

Val Thr Ser Gly Tyr Pro Asn Phe Lys Gln Arg Ala Ser Thr Ser Asn
            20   25   30

Lys His Trp Thr Ala Leu Leu Gly Lys Ala Thr Leu Ser Val Pro Glu
        35   40   45

Glu Leu Leu Tyr Tyr Gly Gly Ala Gln
    50   55

<210> 149
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> lm8

<220>
<221> MISC_FEATURE
<223> V lambda light chain

<400> 149

Leu Ser Ala Ser Leu Ala Ser Lys Leu Thr Thr Leu Gly His Ser Ser
1   5   10   15

Tyr Ala Ile Ala His Gln Glu Lys Gly Arg Tyr Met Lys Leu Ser Asp
            20   25   30

Gly Gly Asp Ser Ala Glu Arg Tyr Thr Ser Ser Ser Glu Gln Gly Thr
        35   40   45

Gly Ile
    50

<210> 150
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> V lambda Wil

<400> 150

Asn Phe Leu Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys

1 5 10 15

Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Asn Asn
20 25 30

Tyr Val His Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val
35 40 45

Ile Phe Glu Asp Asp His Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Val Asp Thr Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp His
85 90 95

Asn Asn

<210> 151
<211> 4
<212> PRT
<213> Artificial

<220>
<223> AL V kappa fragment from amyloid protein

<220>
<221> MISC_FEATURE
<223> Consensus sequence derived from human amyloidogenic proteins

<400> 151

Pro Glu Asp Val
1

<210> 152
<211> 131
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Murine 2A4 and 8G9 v kappa light chain

<220>
<221> SIGNAL
<222> (1)..(19)
<223> Leader sequence

<220>
<221> mat_peptide
<222> (20)..(131)

<220>
<221> MISC_FEATURE
<222> (43)..(58)

<223> CDR 1

<220>
<221> MISC_FEATURE
<222> (74)..(80)
<223> CDR 2

<220>
<221> MISC_FEATURE
<222> (113)..(121)
<223> CDR 3

<400> 152

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
-15 -10 -5

Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
-1 1 5 10

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
15 20 25

Val His Ser Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
30 35 40 45

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
50 55 60

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Tyr Phe Thr
65 70 75

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
80 85 90

Ser Gln Ser Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu
95 100 105

Glu Ile Lys
110

<210> 153
<211> 131
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Murine 7D8 v kappa light chain

<220>
<221> SIGNAL
<222> (1)..(19)
<223> Leader sequence

<220>
<221> mat_peptide
<222> (20)..(131)

<220>
<221> MISC_FEATURE
<222> (43)..(58)
<223> CDR 1

<220>
<221> MISC_FEATURE
<222> (74)..(80)
<223> CDR 2

<220>
<221> MISC_FEATURE
<222> (113)..(121)
<223> CDR 3

<400> 153

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
-15 -10 -5

Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
-1 1 5 10

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Leu Ser Leu
15 20 25

Val His Ser Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
30 35 40 45

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
50 55 60

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Tyr Phe Thr
65 70 75

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
80 85 90

Ser Gln Ser Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu
95 100 105

Glu Ile Lys
110

<210> 154
<211> 138
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Murine 2A4, 8G9 and 7D8 v heavy chain

<220>
<221> SIGNAL
<222> (1)..(19)
<223> Leader sequence

<220>
<221> mat_peptide
<222> (20)..(138)

<220>
<221> MISC_FEATURE
<222> (45)..(54)
<223> CDR 1

<220>
<221> MISC_FEATURE
<222> (69)..(87)
<223> CDR 2

<220>
<221> MISC_FEATURE
<222> (120)..(127)
<223> CDR 3

<400> 154

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Met Val Leu Gly Leu Lys Trp Val Phe Phe Val Val Phe Tyr Gln Gly
                -15                 -10                 -5


Val His Cys Glu Val Gln Leu Val Glu Ser Gly Gly Arg Leu Val Gln
        -1  1                5                  10


Pro Lys Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    15                  20                  25


Asn Thr Tyr Ala Met Tyr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
30                  35                  40                  45


Glu Trp Val Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr
                50                  55                  60


Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Phe Arg Asp Asp Ser
            65                  70                  75


Gln Ser Met Leu Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
        80                  85                  90


Ala Met Tyr Tyr Cys Val Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp
    95                  100                 105


Gly Gln Gly Thr Leu Val Thr Val Ser Ala
110                 115
```

<210> 155
<211> 112
<212> PRT
<213> Artificial

<220>
<223> Humanized 2A4 and 8G9 v kappa light chain version 1

<400> 155

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Tyr Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 156
<211> 112
<212> PRT
<213> Artificial

<220>
<223> Humanized 2A4 and 8G9 v kappa light chain version 2

<400> 156

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 157
<211> 112

<212> PRT
<213> Artificial

<220>
<223> Humanized 2A4 and 8G9 v kappa light chain version 3

<400> 157

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
85 90 95

Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 158
<211> 112
<212> PRT
<213> Artificial

<220>
<223> Humanized 7D8 v kappa light chain version 1

<400> 158

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Leu Ser Leu Val His Ser
20 25 30

Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Tyr Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

```
Thr His Val Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  159
<211>  112
<212>  PRT
<213>  Artificial

<220>
<223>  Humanized 7D8 v kappa light chain version 2

<400>  159

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1               5                   10                  15


Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Leu Ser Leu Val His Ser
            20                  25                  30


Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45


Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60


Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80


Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Ser Gln Ser
                85                  90                  95


Thr His Val Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  160
<211>  112
<212>  PRT
<213>  Artificial

<220>
<223>  Humanized 7D8 v kappa light chain version 3

<400>  160

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1               5                   10                  15


Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Leu Ser Leu Val His Ser
            20                  25                  30


Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45


Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60
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```
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80


Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
                85                  90                  95


Thr His Val Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  161
<211>  119
<212>  PRT
<213>  Artificial

<220>
<223>  Humanized 2A4, 8G9 and 7D8 heavy chain version 1

<400>  161

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30


Ala Met Tyr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Phe Arg Asp Asp Ser Lys Asn Ser
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  162
<211>  119
<212>  PRT
<213>  Artificial

<220>
<223>  Humanized 2A4, 8G9 and 7D8 heavy chain version 2

<400>  162

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20 25 30

Ala Met Tyr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 163
<211> 119
<212> PRT
<213> Artificial

<220>
<223> Humanized 2A4, 7D8 and 8g9 heavy chain version 3

<400> 163

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20 25 30

Ala Met Tyr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 164
<211> 119
<212> PRT
<213> Mus musculus

<400> 164

Glu Val Gln Leu Val Glu Ser Gly Gly Arg Leu Val Gln Pro Lys Gly
1   5   10   15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20   25   30

Ala Met Tyr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Thr Ile Phe Arg Asp Asp Ser Gln Ser Met
65   70   75   80

Leu Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Met Tyr
                85   90   95

Tyr Cys Val Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ala
        115

<210> 165
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Human heavy chain framework

<400> 165

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp His
            20   25   30

Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr Ala Ala

50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Tyr Val Val Gly Ala Thr Leu Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 166
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Human v kappa light chain framework

<400> 166

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg

<210> 167
<211> 276
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human v kappa light chain framework

<400> 167

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Asp Val Val Met Thr Gln Ser Pro Leu Ser
20 25 30

Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
35 40 45

Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu
50 55 60

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn
65 70 75 80

Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
85 90 95

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
100 105 110

Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly
115 120 125

Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
130 135 140

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
145 150 155 160

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
165 170 175

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
180 185 190

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
195 200 205

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
210 215 220

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
225 230 235 240

Cys Ser Ala Arg Gln Ser Thr Pro Phe Val Cys Glu Tyr Gln Gly Gln

245 250 255

Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala Gly Gly Gly Ser Gly
260 265 270

Gly Gly Ser Gly
275

<210> 168
<211> 16
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(16)
<223> 2A4 VL CDR1

<400> 168

Arg Ser Ser Gln Ser Leu Val His Ser Thr Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 169
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> 2A4 VL CDR2

<400> 169

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 170
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> 2A4 VL CDR3

<400> 170

Ser Gln Ser Thr His Val Pro Phe Thr
1 5

<210> 171
<211> 10
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> 2A4 VH CDR1

<400> 171

Gly Phe Thr Phe Asn Thr Tyr Ala Met Tyr
1 5 10

<210> 172
<211> 19
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(19)
<223> 2A4 VH CDR2

<400> 172

Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 173
<211> 8
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(8)
<223> 2A4 VH CDR3

<400> 173

Pro Tyr Ser Asp Ser Phe Ala Tyr
1 5

<210> 174
<211> 112
<212> PRT
<213> Artificial

<220>
<223> Humanized 7D8 v kappa light chain version 4

<400> 174

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Leu Ser Leu Val His Ser
20 25 30

Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser

```
        35                  40                  45

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Tyr Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Ser Gln Ser
                85                  90                  95

Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  175
<211>  112
<212>  PRT
<213>  Artificial

<220>
<223>  Humanized 7D8 v kappa light chain version 5

<400>  175

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1               5                   10                  15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Leu Ser Leu Val His Ser
            20                  25                  30

Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Ser Gln Ser
                85                  90                  95

Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  176
<211>  112
<212>  PRT
<213>  Artificial

<220>
<223>  Humanized 7D8 v kappa light chain version 6

<400>  176

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
```

```
1               5                   10                  15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Leu Ser Leu Val His Ser
            20                  25                  30

Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
                85                  90                  95

Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  177
<211>  16
<212>  PRT
<213>  Mus musculus

<400>  177

Arg Ser Ser Leu Ser Leu Val His Ser Thr Gly Asn Thr Tyr Leu His
1               5                   10                  15
```