Corresponding amino acid numbering conventions for hinge regions: hIgG1, hIgG2 and hIgG4

	Hinge															Hinge encoded by CH2 exon					
hIgG1 wt	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P	E	L	L	G
hIgG1 EU	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236
hIgG1 Kabat	226	227	228	232[a] 229[c]	233[a] 230[c]	234[a] 232[c]	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249
hIgG1 IMGT	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	1.6	1.5	1.4	1.3	1.2	1.1
hIgG2 wt	E	R	K	C	C	--	V	--	E	--	C	P	P	C	P	A	P	P	V	A	--
hIgG2 EU	216	217	218	219[a] 221[c]	220[a] -[c]		222		224		226	227	228	229	230	231[b]	232[b]	233[b]	234[b]	235[b]	236[b]
hIgG2 Kabat	226	227	228	232	233		235		237		239	240	241	242	243	244	245	246	247	248	249
hIgG2 IMGT	1	2	3	4	5		6		7		8	9	10	11	12	-	-	-	-	-	
hIgG4 wt	E	S	K	Y	G	--	--	--	P	P	C	P	S	C	P	A	P	E	F	L	G
hIgG4 EU	216	217	218	-[a] 219[c]	-[a] 220[c]				224	225	226	227	228	229	230	231[b]	232[b]	233[b]	234[b]	235[b]	236[b]
hIgG4 Kabat	226	227	228	229	230				237	238	239	240	241	242	243	244	245	246	247	248	249
hIgG4 IMGT	1	2	3	4	5				6	7	8	9	10	11	12	-	-	-	-	-	-

wt = wild-type

- means no corresponding number reported

-- means no corresponding amino acid

[a] numbering according to the last updated IMGT Scientific Chart (IMGT®, the international ImMunoGeneTics information system®, http://www.imgt.org/IMGTScientificChart/Numbering/Hu_IGHGnber.html, created: 17 May 2001, last updated:10 Jan 2013)

[b] numbering according to EU index as reported in Kabat, E.A. et al. Sequences of Proteins of Immunological interest, 5th ed. US Department of Health and Human Services, NIH publication No. 91-3242 (1991)

FIG. 1

Construction of chimeric hinge

	Upper Hinge												Lower Hinge								
IgG1 EU numbering	216	217	218	219	220	221	222	223	224	225	226	227									
IgG1 Kabat numbering	226	227	228	232[a] 229[b]	233[a] 230[b]	234[a] 232[b]	235	236	237	238	239	240									
IgG1	E	P	K	S	C	D	K	T	H	T	C	P	*IgG2*	*P*	*C*	*P*	*A*	*P*	*P*	*V*	*A*
IgG4	E	S	K	Y	G	--	--	--	P	P	C	P									
IgG4 EU numbering	216	217	218	-[a] 219[b]	-[a] 220[b]				224	225	226	227	*IgG2 EU numbering*	*228*	*229*	*230*	*231*	*232*	*233*	*234*	*235*
IgG4 Kabat numbering	226	227	228	229	230				237	238	239	240	*IgG2 Kabat numbering*	*241*	*242*	*243*	*244*	*245*	*246*	*247*	*248*

- means no corresponding number reported

-- means no corresponding amino acid

[a] numbering according to the last updated IMGT Scientific Chart (IMGT®, the international ImMunoGeneTics information system®, http://www.imgt.org/IMGTScientificChart/Numbering/Hu_IGHGnber.html, created: 17 May 2001, last updated:10 Jan 2013)

[b] numbering according to EU index as reported in Kabat, E.A. et al. Sequences of Proteins of Immunological interest. 5th ed. US Department of Health and Human Services, NIH publication No. 91-3242 (1991)

FIG. 2

```
        10         20         30         40         50         60
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS

                                  ←---- CH1 Hinge----→       CH2---→
        70         80         90        100        110        120
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG

       130        140        150        160        170        180
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN

                                                 CH3---→
       190        200        210        220        230        240
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE

       250        260        270        280        290        300
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW

       310        320        330
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK
```

Human IGHG1 heavy chain constant region UniProtKB/Swiss-Prot Accn. No. P01857 (SEQ ID NO:13)

FIG. 3

```
        10         20         30         40         50         60
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS

                                   <--CH1 Hinge-->       CH2-->
        70         80         90        100        110        120
GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTVER KCCVECPPCP APPVAGPSVF

       130        140        150        160        170        180
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTFR

                                         CH3-->
       190        200        210        220        230        240
VVSVLTVVHQ DWLNGKEYKC KVSNKGLPAP IEKTISKTKG QPREPQVYTL PPSREEMTKN

       250        260        270        280        290        300
QVSLTCLVKG FYPSDISVEW ESNGQPENNY KTTPPMLDSD GSFFLYSKLT VDKSRWQQGN

       310        320
VFSCSVMHEA LHNHYTQKSL SLSPGK
```

Human IGHG2 heavy chain constant region UniProtKB/Swiss-Prot Accn. No. P01859 (SEQ ID NO:14)

FIG. 4

```
        10         20         30         40         50         60
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS

                                  <--- CH1 Hinge--->       CH2--->
        70         80         90        100        110        120
GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPSCP APEFLGGPSV

       130        140        150        160        170        180
FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY

                                             CH3--->
       190        200        210        220        230        240
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK

       250        260        270        280        290        300
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG

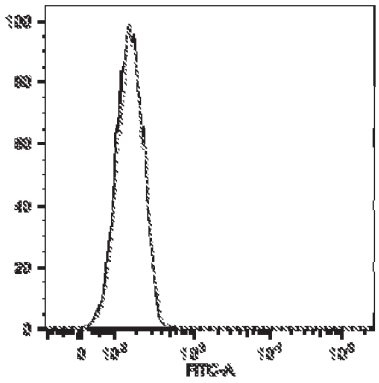
       310        320
NVFSCSVMHE ALHNHYTQKS LSLSLGK
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Human IGHG4 heavy chain constant region UniProtKB/Swiss-Prot Accn. No. P01861 (SEQ ID NO:15)

FIG. 5

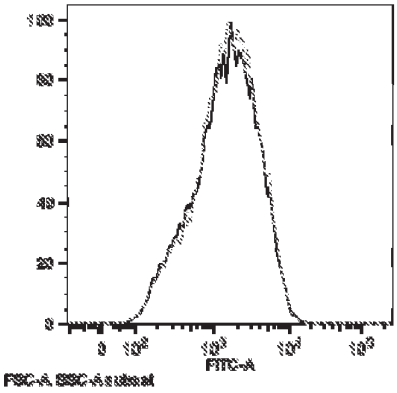
Comparison of Ab Binding on Jurkat Cells

(Chimeric Hinge Abs v. Control Abs)



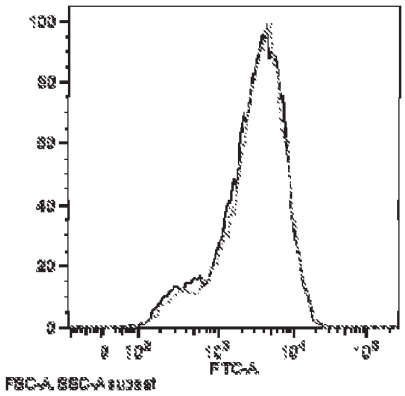
IgG type	Cell name	Geom. Mean:FITC-A
Sec	Jurkats	164
Unstained	Jurkats	155

FIG. 6A



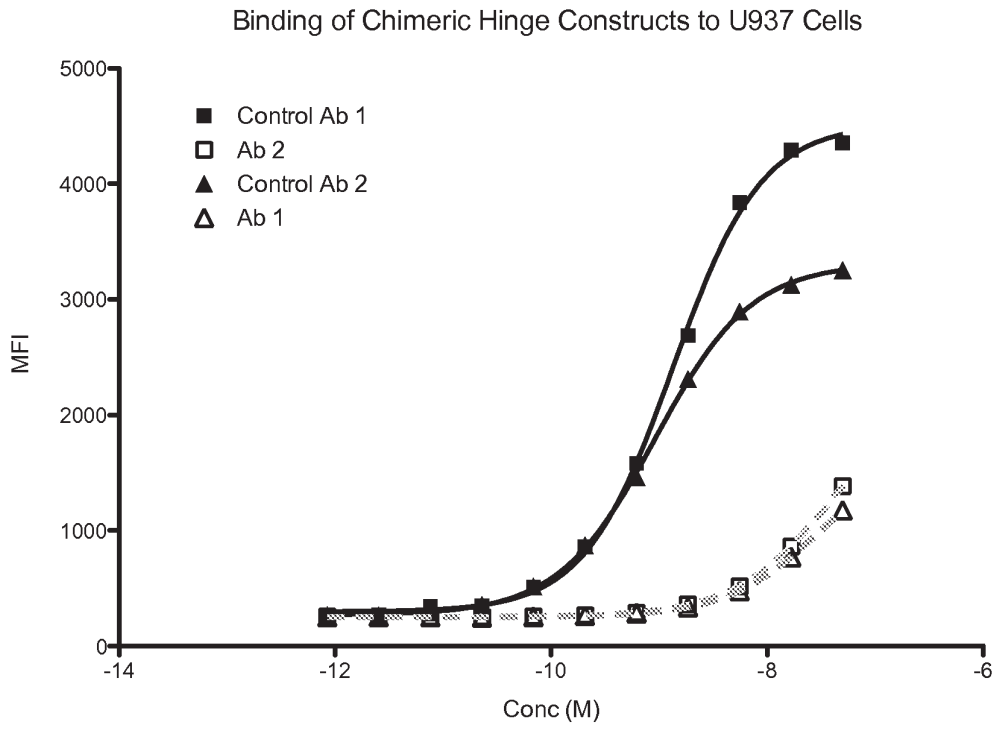
IgG type	Cell name	Geom. Mean:FITC-A
Ab 1	Jurkats	1387
Control Ab 2	Jurkats	1331

FIG. 6B



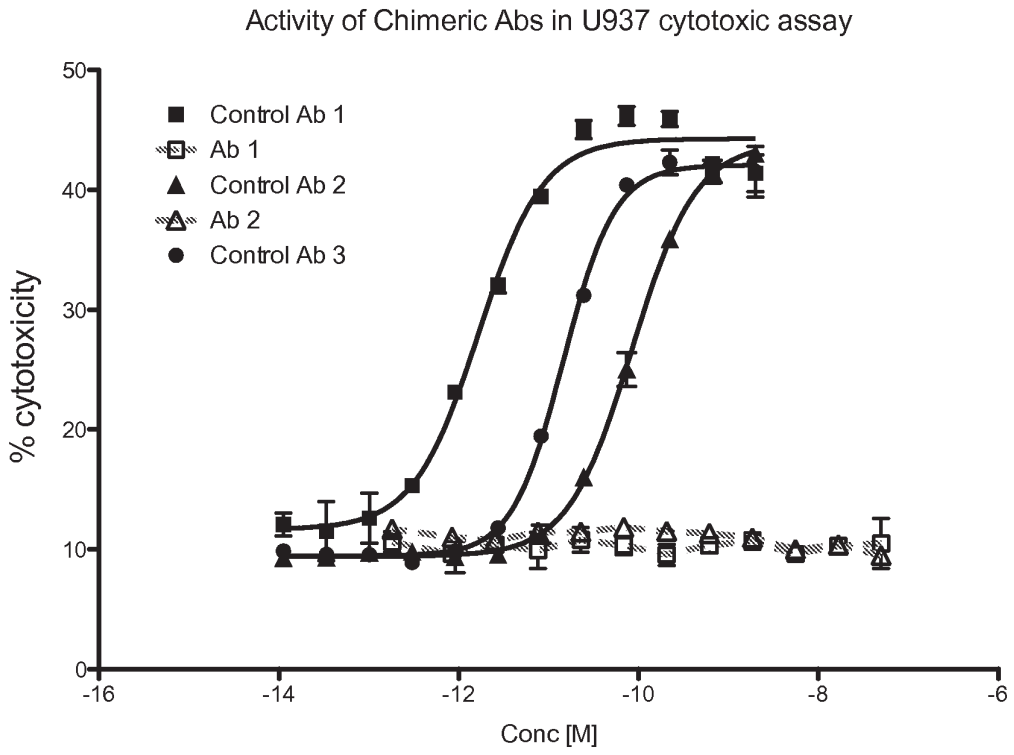
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Ab 2	Jurkats	2561
Control Ab 3	Jurkats	2598

FIG. 6C



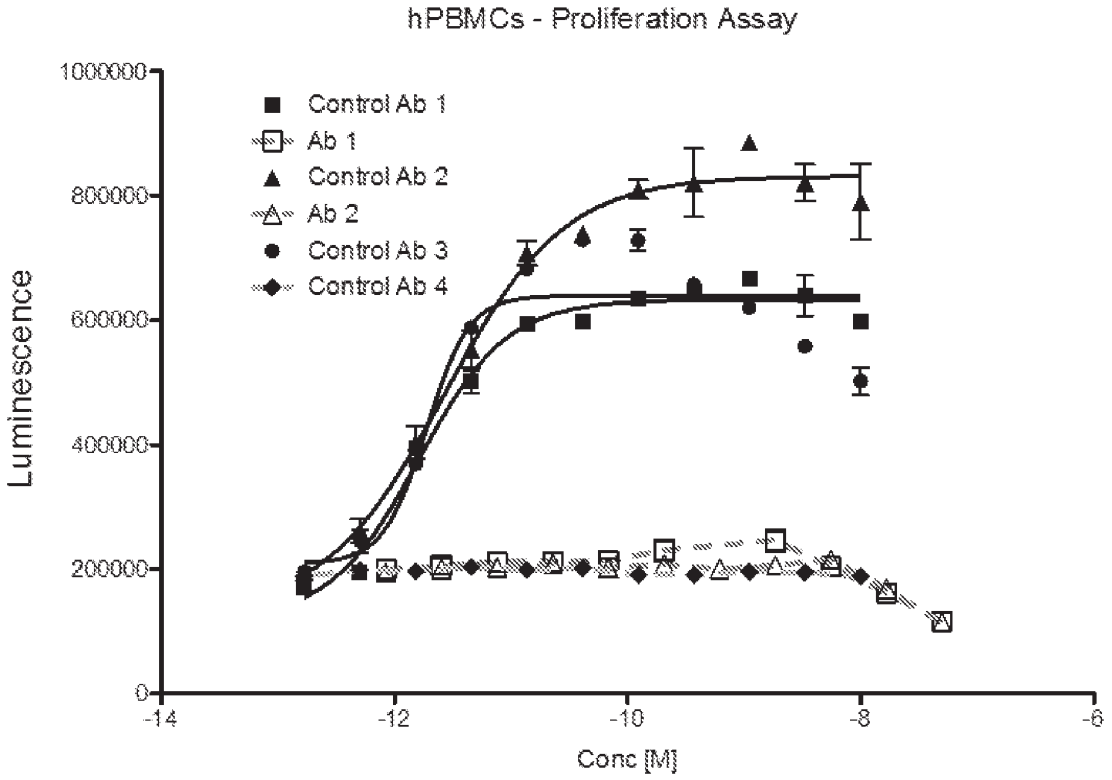
	EC50
Control Ab 1	1.338e-009
Ab 2	4.542e-008
Control Ab 2	9.138e-010
Ab 1	3.351e-008

FIG. 7



	EC50
Control Ab 1	1.656e-012
Control Ab 2	8.448e-011
Control Ab 3	1.465e-011

FIG. 8



	EC50
Control Ab 1	1.613e-012
Control Ab 2	2.691e-012
Control Ab 3	1.881e-012

FIG. 9

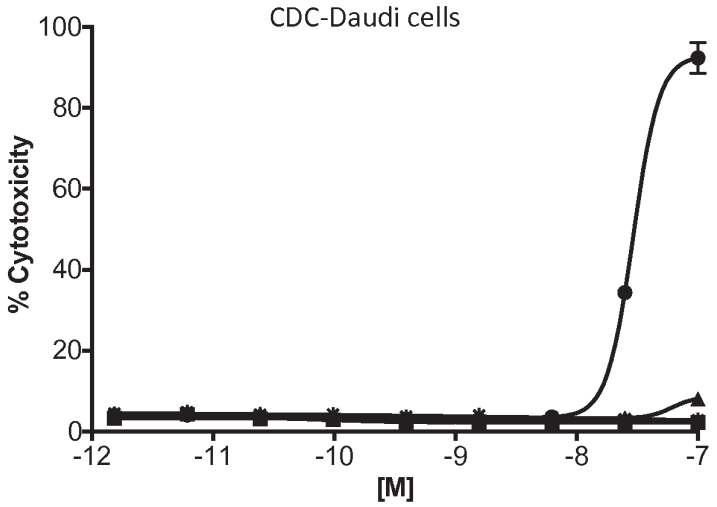


FIG. 10A

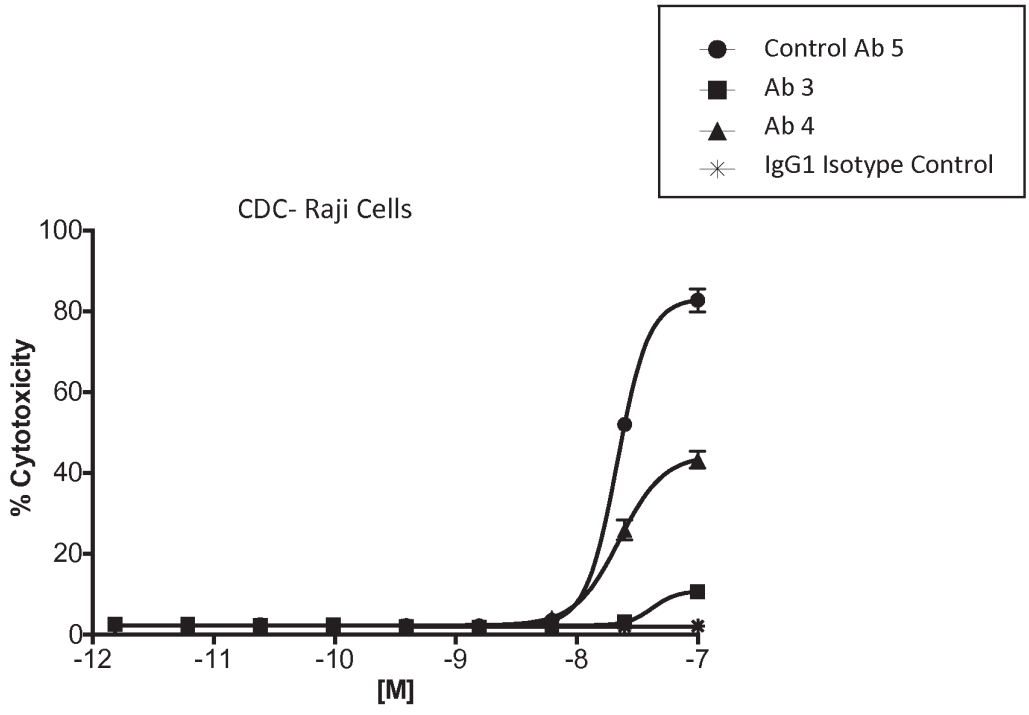


FIG. 10B

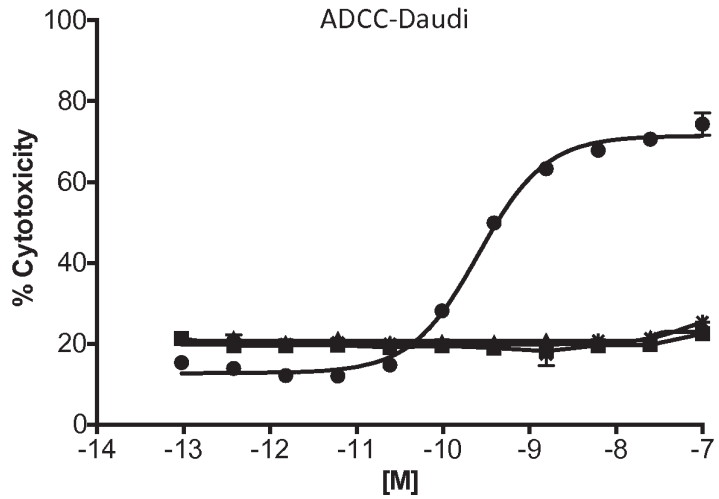
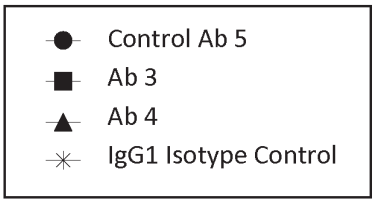


FIG. 11A



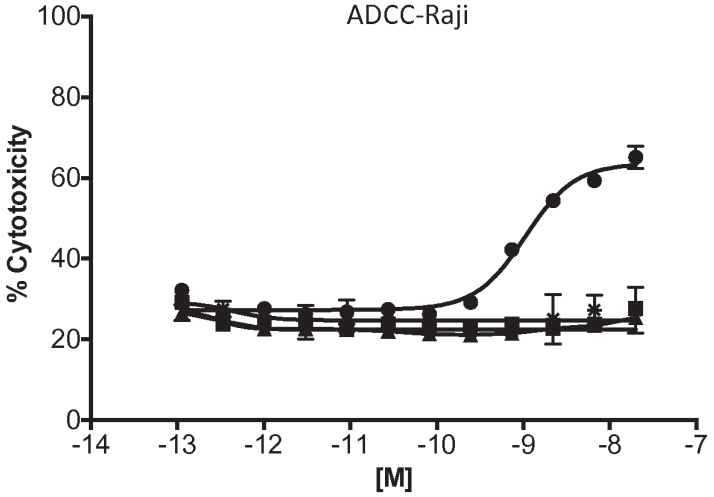


FIG. 11B

SEQUENCE LISTING

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<120> ANTIBODIES COMPRISING CHIMERIC CONSTANT DOMAINS

<130> 8550/PCT

<150> US 61/759,578
<151> 2013-02-01

<160> 44

<170> PatentIn version 3.5

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<211> 232
<212> PRT
<213> Artificial sequence

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<223> Synthetic

<400> 1

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Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
            100                 105                 110

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
```

```
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Leu Gly Lys
225                 230
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Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
            20                  25                  30

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        35                  40                  45

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
    50                  55                  60

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
65                  70                  75                  80

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
```

```
                85                  90                  95

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
            100                 105                 110

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
        115                 120                 125

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    130                 135                 140

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
145                 150                 155                 160

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                165                 170                 175

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            180                 185                 190

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        195                 200                 205

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    210                 215                 220

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225                 230                 235


<210>  3
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Pro Cys Pro Ala Pro Pro Val Ala
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<400> 8

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Pro Pro Val Ala
20

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<213> Artificial sequence

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1 5 10 15

Ala

<210> 10
<211> 104
<212> PRT
<213> Homo sapiens

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1 5 10 15

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
20 25 30

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
35 40 45

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr
50 55 60

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
65 70 75 80

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
85 90 95

Glu Lys Thr Ile Ser Lys Ala Lys
100

<210> 11
<211> 107
<212> PRT
<213> Homo sapiens

<400> 11

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

```
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65                  70                  75                  80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                85                  90                  95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            100                 105
```

<210> 12
<211> 107
<212> PRT
<213> Homo sapiens

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
65                  70                  75                  80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                85                  90                  95

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
```

100 105

<210> 13
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<213> Homo sapiens

<400> 13

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

```
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 14
<211> 326
<212> PRT
<213> Homo sapiens

<400> 14

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                   10                  15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
```

```
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130                 135                 140

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255

Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275                 280                 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
```

290 295 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

<210> 15
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<212> PRT
<213> Homo sapiens

<400> 15

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1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

```
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320

Leu Ser Leu Ser Leu Gly Lys
                325
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<210> 16
<211> 60
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 16
ttcgcgcagc ttaggtttat gccaggggggg acgggtggca cgggtcgtgg tggacaccgt 60

<210> 17
<211> 40

<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 17
aagcttatac tcgagctcta gattgggaac ccgggtctct 40

<210> 18
<211> 58
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 18
cccaccgtgc ccagcaccac ctgtggcagg accatcagtc ttcctgttcc ccccaaaa 58

<210> 19
<211> 44
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 19
tgtgtcttca gggagaggga cagagaccca tttactcgcc ggcg 44

<210> 20
<211> 60
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 20
ctcgggttta gaacactgtt ttgagtgtgt acgggtggca cgggtcgtgg tggacaccgt 60

<210> 21
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 21
aaatcttgtg acaaaactca cacatgccca ccgtgcccag caccacctgt g 51

<210> 22
<211> 54
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 22
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta cacc 54

<210> 23
<211> 54
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 23
ctcttttggt agaggtttcg gtttcccgtc ggggctcttg gtgtccacat gtgg 54

<210> 24
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial

<400> 24
cttcagggag agggacagag gcccatttac tcgccggcg 39

<210> 25
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 25
gctgacagac taacagactg 20

<210> 26
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 26
gacctcaggg gtccgggaga tcat 24

<210> 27
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 27
atacattata cgaagttata ccggta 26

<210> 28
<211> 990
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 28
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 60

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 120

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 240

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 300

aaatcttgtg acaaaactca cacatgccca ccgtgcccag caccacctgt ggcaggacca 360

tcagtcttcc tgttcccccc aaaacccaag gacactctca tgatctcccg gacccctgag 420

gtcacgtgcg tggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac 480

gtggatggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc 540

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa cggcaaggag 600

tacaagtgca aggtctccaa caaaggcctc ccgtcctcca tcgagaaaac catctccaaa 660

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 720

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 780

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 840

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 900

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 960

aagtccctct ccctgtctcc gggtaaatga 990

<210> 29
<211> 981
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 29
gccagcacaa aaggtcctag cgtttttcca cttgccccat gttcaaggtc aacctccgaa 60

agtaccgccg ctcttggctg tctcgtaaaa gattattttc ccgaacctgt aactgtctcc 120

tggaactccg gcgcactcac ttccggcgta cataccttcc ccgctgtcct ccaatcttcc 180

ggtctctact ccctgtcttc tgttgtcact gttccatcat cctcactcgg cacaaaaaca 240

tatacctgca acgttgatca caagccaagt aataccaaag ttgataagcg cgtcgaatcc 300

aaatacggtc ccccctgccc accgtgccca gcaccacctg tggcaggacc atcagtcttc 360

ctgttccccc caaaacccaa ggacactctc atgatctccc ggacccctga ggtcacgtgc 420

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 480

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 540

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 600

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 660

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac 720

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 780

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 840

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 900

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagtccctc 960

tccctgtctc tgggtaaatg a 981

<210> 30
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 30

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

```
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        115                 120                 125

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    130                 135                 140

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
145                 150                 155                 160

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                165                 170                 175

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            180                 185                 190

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        195                 200                 205

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    210                 215                 220

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
225                 230                 235                 240

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                245                 250                 255
```

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
260 265 270

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
275 280 285

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
290 295 300

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
305 310 315 320

Lys Ser Leu Ser Leu Ser Pro Gly Lys
325

<210> 31
<211> 326
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 31

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110

```
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130                 135                 140

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    210                 215                 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
225                 230                 235                 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
        275                 280                 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
    290                 295                 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305                 310                 315                 320

Ser Leu Ser Leu Gly Lys
                325
```

<210> 32
<211> 708
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 32
gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 60

ccacctgtgg caggaccatc agtcttcctg ttcccccaa aacccaagga cactctcatg 120

atctcccgga cccctgaggt cacgtgcgtg gtggtggacg tgagccagga agaccccgag 180

gtccagttca actggtacgt ggatggcgtg gaggtgcata atgccaagac aaagccgcgg 240

gaggagcagt tcaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 300

tggctgaacg gcaaggagta caagtgcaag gtctccaaca aaggcctccc gtcctccatc 360

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 420

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 480

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 540

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 600

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 660

cacaaccact acacgcagaa gtccctctcc ctgtctccgg gtaaatga 708

<210> 33
<211> 699
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 33
gataagcgcg tcgaatccaa atacggtccc ccctgcccac cgtgcccagc accacctgtg 60

gcaggaccat cagtcttcct gttcccccca aaacccaagg acactctcat gatctcccgg 120

acccctgagg tcacgtgcgt ggtggtggac gtgagccagg aagaccccga ggtccagttc 180

aactggtacg tggatggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240

ttcaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaac 300

ggcaaggagt acaagtgcaa ggtctccaac aaaggcctcc cgtcctccat cgagaaaacc 360

atctccaaag ccaaagggca gccccgagag ccacaggtgt acaccctgcc cccatcccag 420

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc 480

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540

cccgtgctgg actccgacgg ctccttcttc ctctacagca ggctcaccgt ggacaagagc 600

aggtggcagg aggggaatgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660

tacacacaga agtccctctc cctgtctctg ggtaaatga 699

<210> 34
<211> 357
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 34
gacgtccaac tggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctca 357

<210> 35
<211> 990
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 35
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 60

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 120

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 240

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 300

aaatcttgtg acaaaactca cacatgccca ccgtgcccag caccacctgt ggcaggacca 360

tcagtcttcc tgttcccccc aaaacccaag gacactctca tgatctcccg gacccctgag 420

gtcacgtgcg tggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac 480

gtggatggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc 540

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa cggcaaggag 600

tacaagtgca aggtctccaa caaaggcctc ccgtcctcca tcgagaaaac catctccaaa 660

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 720

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 780

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 840

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 900

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacag attcacgcag 960

aagtccctct ccctgtctcc gggtaaatga 990

<210> 36
<211> 981
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 36
gccagcacaa aaggtcctag cgtttttcca cttgccccat gttcaaggtc aacctccgaa 60

agtaccgccg ctcttggctg tctcgtaaaa gattattttc ccgaacctgt aactgtctcc 120

tggaactccg gcgcactcac ttccggcgta cataccttcc ccgctgtcct ccaatcttcc 180

ggtctctact ccctgtcttc tgttgtcact gttccatcat cctcactcgg cacaaaaaca 240

tatacctgca acgttgatca caagccaagt aataccaaag ttgataagcg cgtcgaatcc 300

aaatacggtc ccccctgccc accgtgccca gcaccacctg tggcaggacc atcagtcttc 360

ctgttccccc caaaacccaa ggacactctc atgatctccc ggacccctga ggtcacgtgc 420

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 480

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 540

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 600

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 660

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac 720

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 780

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 840

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 900

gtcttctcat gctccgtgat gcatgaggct ctgcacaaca gattcacaca gaagtccctc 960

tccctgtctc tgggtaaatg a 981

<210> 37
<211> 329
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 37

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
115 120 125

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
130 135 140

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
145 150 155 160

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
165 170 175

```
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            180                 185                 190

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        195                 200                 205

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    210                 215                 220

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
225                 230                 235                 240

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                245                 250                 255

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            260                 265                 270

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        275                 280                 285

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    290                 295                 300

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
305                 310                 315                 320

Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325
```

<210> 38
<211> 326
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 38

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                   10                  15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
```

```
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130                 135                 140

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    210                 215                 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
225                 230                 235                 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270
```

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
275 280 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
290 295 300

Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Leu Gly Lys
325

<210> 39
<211> 41
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 39
gtgagcgctc ttcggcagac gtccaactgg tgcagtcagg g 41

<210> 40
<211> 47
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 40
cagctagctc ttccggctga ggagacggtg accgtggtgc cttggcc 47

<210> 41
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 41

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

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

```
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65                  70                  75                  80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
                85                  90                  95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            100                 105
```

<210> 42
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 42

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
65                  70                  75                  80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
                85                  90                  95

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
            100                 105
```

<210> 43
<211> 98
<212> PRT
<213> Homo sapiens

<400> 43

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val

<210> 44
<211> 98
<212> PRT
<213> Homo sapiens

<400> 44

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

```
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val
```