Fig. 1

9E4 VH alignment

Kabat Numbering	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
m9E4VH	E	V	K	L	V	E	S	G	G	G	L	V	K	P	G	A	S	L	K	L
1791009	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L
Hu9E4VHv1	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L
Hu9E4VHv2	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L
Hu9E4VHv3	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L
Hu9E4VHv4	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L

Kabat Numbering	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
m9E4VH	S	C	A	A	S	G	F	T	F	S	***N***	***Y***	***G***	***M***	***S***	W	V	R	Q	T
1791009	S	C	A	A	S	G	F	T	F	S	***S***	***Y***	***W***	***M***	***S***	W	V	R	Q	A
Hu9E4VHv1	S	C	A	A	S	G	F	T	F	S	***N***	***Y***	***G***	***M***	***S***	W	V	R	Q	A
Hu9E4VHv2	S	C	A	A	S	G	F	T	F	S	***N***	***Y***	***G***	***M***	***S***	W	V	R	Q	A
Hu9E4VHv3	S	C	A	A	S	G	F	T	F	S	***N***	***Y***	***G***	***M***	***S***	W	V	R	Q	A
Hu9E4VHv4	S	C	A	A	S	G	F	T	F	S	***N***	***Y***	***G***	***M***	***S***	W	V	R	Q	A

Kabat Numbering	41	42	43	44	45	46	47	48	49	50	51	52	52A	53	54	55	56	57	58	59
m9E4VH	S	D	K	R	L	E	W	V	A	***S***	***I***	***S***	***S***	***G***	***G***	***G***	***S***	***T***	***Y***	***Y***
1791009	P	G	K	G	L	E	W	V	A	***N***	***I***	***K***	***Q***	***D***	***G***	***S***	***E***	***K***	***Y***	***Y***
Hu9E4VHv1	P	G	K	G	L	E	W	V	A	***S***	***I***	***S***	***S***	***G***	***G***	***G***	***S***	***T***	***Y***	***Y***
Hu9E4VHv2	P	G	K	G	L	E	W	V	A	***S***	***I***	***S***	***S***	***G***	***G***	***G***	***S***	***T***	***Y***	***Y***
Hu9E4VHv3	P	G	K	G	L	E	W	V	A	***S***	***I***	***S***	***S***	***G***	***G***	***G***	***S***	***T***	***Y***	***Y***
Hu9E4VHv4	P	G	K	G	L	E	W	V	A	***S***	***I***	***S***	***S***	***G***	***G***	***G***	***S***	***T***	***Y***	***Y***

Fig. 1 (cont.)

9E4 VH alignment

Kabat Numbering	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79
m9E4VH	***P***	***D***	***N***	***V***	***K***	***G***	R	F	T	I	S	R	E	D	A	K	N	T	L	Y
1791009	***V***	***D***	***S***	***V***	***K***	***G***	R	F	T	I	S	R	D	N	A	K	N	S	L	Y
Hu9E4VHv1	***P***	***D***	***N***	***V***	***K***	***G***	R	F	T	I	S	R	D	D	A	K	N	S	L	Y
Hu9E4VHv2	***P***	***D***	***N***	***V***	***K***	***G***	R	F	T	I	S	R	D	N	A	K	N	S	L	Y
Hu9E4VHv3	***P***	***D***	***N***	***V***	***K***	***G***	R	F	T	I	S	R	D	D	A	K	N	S	L	Y
Hu9E4VHv4	***P***	***D***	***N***	***V***	***K***	***G***	R	F	T	I	S	R	D	N	A	K	N	S	L	Y

Kabat Numbering	80	81	82	82A	82B	82C	83	84	85	86	87	88	89	90	91	92	93	94	95	96
m1H7VH	L	Q	M	S	S	L	R	S	E	D	T	A	L	Y	Y	C	S	R	***G***	***G***
1791009	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R	***G***	***S***
Hu9E4VHv1	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	S	R	***G***	***G***
Hu9E4VHv2	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	S	R	***G***	***G***
Hu9E4VHv3	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R	***G***	***G***
Hu9E4VHv4	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R	***G***	***G***

Kabat Numbering	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114
m9E4VH	***A***	***G***	***I***	-	***D***	***Y***	W	G	Q	G	T	T	L	T	V	S	S	-
1791009	***S***	***D***	***M***	-	***D***	***Y***	W	G	Q	G	T	L	V	T	V	S	S	-
Hu9E4VHv1	***A***	***G***	***I***	-	***D***	***Y***	W	G	Q	G	T	L	V	T	V	S	S	-
Hu9E4VHv2	***A***	***G***	***I***	-	***D***	***Y***	W	G	Q	G	T	L	V	T	V	S	S	-
Hu9E4VHv3	***A***	***G***	***I***	-	***D***	***Y***	W	G	Q	G	T	L	V	T	V	S	S	-
Hu9E4VHv4	***A***	***G***	***I***	-	***D***	***Y***	W	G	Q	G	T	L	V	T	V	S	S	-

Fig. 2

9E4 VL alignment

Kabat Numbering	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
m9E4VL	D	I	V	M	S	Q	S	P	S	S	L	A	V	S	V	G	E	K	V	T
63102889	D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T
Hu9E4VLv1	D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T
Hu9E4VLv2	D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T
Hu9E4VLv3	D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T

Kabat Numbering	21	22	23	24	25	26	27	27A	27B	27C	27D	27E	27F	28	29	30	31	32	33	34
m9E4VL	M	S	C	***K***	***S***	***I***	***Q***	***T***	***L***	***L***	***Y***	***S***	***S***	***N***	***Q***	***K***	***N***	***Y***	***L***	***A***
63102889	I	T	C	***R***	***A***	***S***	***Q***	-	-	-	-	-	-	***S***	***I***	***S***	***S***	***Y***	***L***	***N***
Hu9E4VLv1	I	T	C	***K***	***S***	***I***	***Q***	***T***	***L***	***L***	***Y***	***S***	***S***	***N***	***Q***	***K***	***N***	***Y***	***L***	***A***
Hu9E4VLv2	I	T	C	***K***	***S***	***I***	***Q***	***T***	***L***	***L***	***Y***	***S***	***S***	***N***	***Q***	***K***	***N***	***Y***	***L***	***A***
Hu9E4VLv3	I	T	C	***K***	***S***	***I***	***Q***	***T***	***L***	***L***	***Y***	***S***	***S***	***N***	***Q***	***K***	***N***	***Y***	***L***	***A***

Kabat Numbering	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54
m9E4VL	W	F	Q	Q	K	P	G	Q	S	P	K	L	L	I	Y	***W***	***A***	***S***	***I***	***R***
63102889	W	Y	Q	Q	K	P	G	K	A	P	K	L	L	I	Y	***A***	***A***	***S***	***S***	***L***
Hu9E4VLv1	W	F	Q	Q	K	P	G	K	A	P	K	L	L	I	Y	***W***	***A***	***S***	***I***	***R***
Hu9E4VLv2	W	Y	Q	Q	K	P	G	K	A	P	K	L	L	I	Y	***W***	***A***	***S***	***I***	***R***
Hu9E4VLv3	W	F	Q	Q	K	P	G	K	A	P	K	L	L	I	Y	***W***	***A***	***S***	***I***	***R***

Fig. 2 (cont.)

9E4 VL alignment

Kabat Numbering	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74
m9E4VL	K	S	G	V	P	D	R	F	T	G	S	G	S	G	T	D	F	T	L	T
63102889	Q	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T
Hu9E4VLv1	K	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T
Hu9E4VLv2	K	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T
Hu9E4VLv3	K	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T

Kabat Numbering	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
m9E4VL	I	S	S	V	K	A	E	D	L	A	V	Y	Y	C	Q	Q	Y	Y	S	Y
63102889	I	S	S	L	Q	P	E	D	F	A	T	Y	Y	C	Q	Q	S	Y	S	T
Hu9E4VLv1	I	S	S	L	Q	P	E	D	F	A	T	Y	Y	C	Q	Q	Y	Y	S	Y
Hu9E4VLv2	I	S	S	L	Q	P	E	D	F	A	T	Y	Y	C	Q	Q	Y	Y	S	Y
Hu9E4VLv3	I	S	S	L	Q	P	E	D	L	A	T	Y	Y	C	Q	Q	Y	Y	S	Y

Kabat Numbering	95	96	97	98	99	100	101	102	103	104	105	106	107
m9E4VL	P	L	T	F	G	A	G	T	K	L	E	L	K
63102889	P	L	T	F	G	G	G	T	K	L	E	I	K
Hu9E4VLv1	P	L	T	F	G	G	G	T	K	L	E	I	K
Hu9E4VLv2	P	L	T	F	G	G	G	T	K	L	E	I	K
Hu9E4VLv3	P	L	T	F	G	G	G	T	K	L	E	I	K

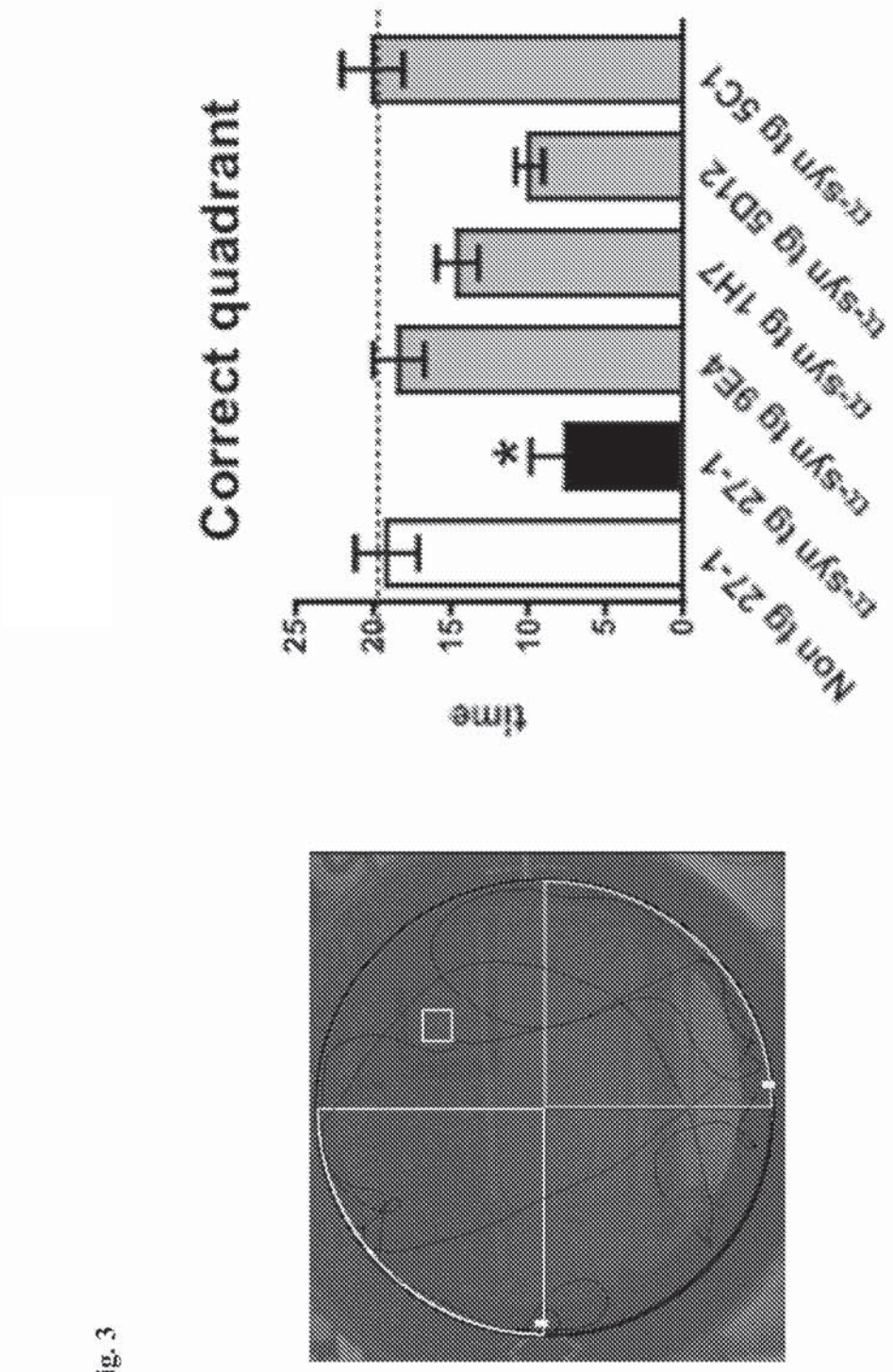
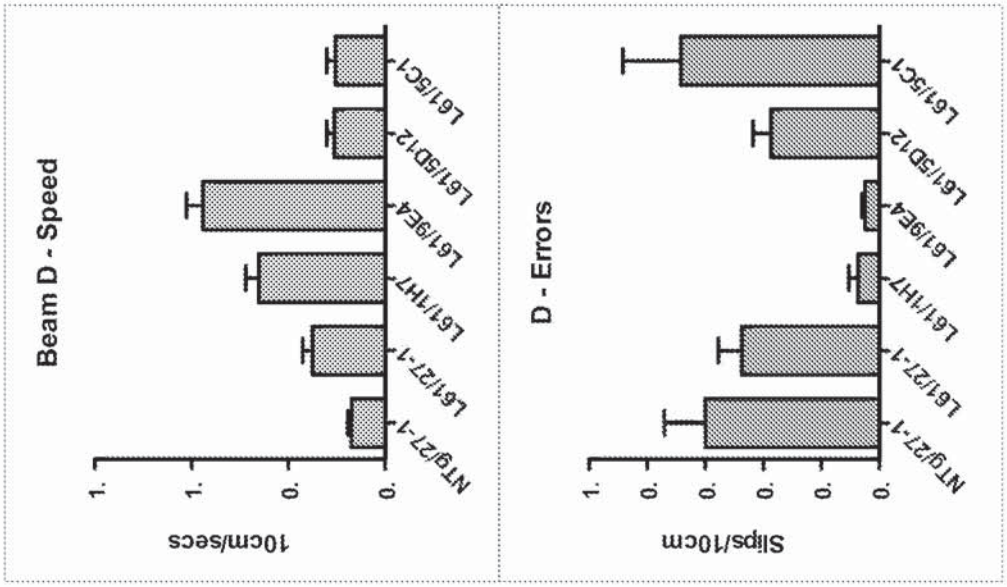

Correct quadrant
time
25
20
15
10
5
0
*
Non Ig 27-1
α-Syn Ig 27-1
α-Syn Ig 9E4
α-Syn Ig 1H7
α-Syn Ig 5D12
α-Syn Ig 5C1

Fig. 3


Beam D - Speed
10cm/secs
1.
1.
0.
0.
NTg/27-1
L61/27-1
L61/1H7
L61/9E4
L61/5D12
L61/5C1
D - Errors
Slips/10cm
1.
0.
0.
0.
0.
0.
NTg/27-1
L61/27-1
L61/1H7
L61/9E4
L61/5D12
L61/5C1

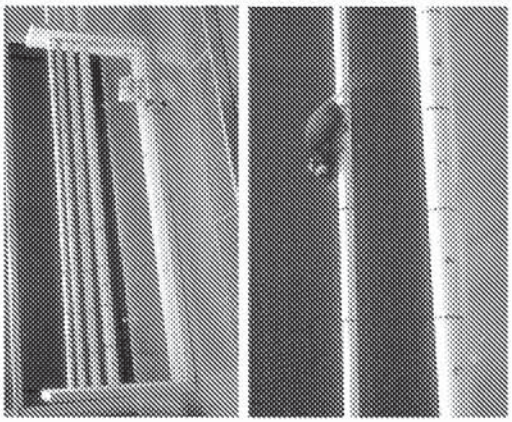


Fig. 4

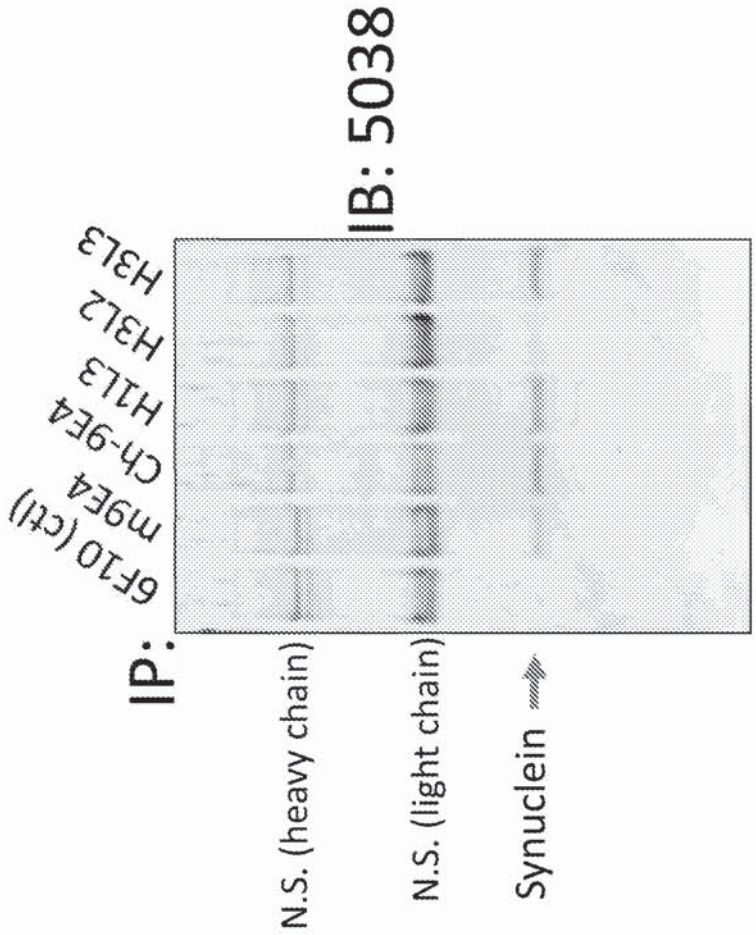

IB: 5038
IP:
6F10 (ctl)
m9E4
Ch-9E4
H1L3
H3L2
H3L3
N.S. (heavy chain)
N.S. (light chain)
Synuclein

Fig. 5

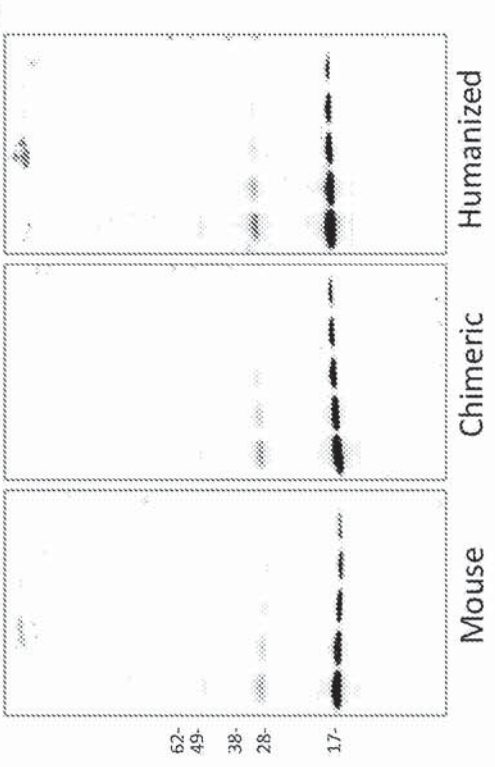

250 125 62.5 31.3 15.6
250 125 62.5 31.3 15.6
250 125 62.5 31.3 15.6
ng
62-
49-
38-
28-
17-
Mouse
Chimeric
Humanized

Fig. 6

SEQUENCE LISTING

<110> Prothena Biosciences Limited

<120> Humanized Antibodies that Recognize
Alpha-Synuclein

<130> SG4655A

<150> 61/553,131
<151> 2011-10-28

<160> 32

<170> FastSEQ for Windows Version 4.0

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Glu Lys Val Thr Met Ser Cys Lys Ser Ile Gln Thr Leu Leu Tyr Ser
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Ser Asn Gln Lys Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln
35 40 45
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Lys Ser Gly Val
50 55 60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
100 105 110
Lys

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
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Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

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Asp Arg Val Thr Ile Thr Cys Lys Ser Ile Gln Thr Leu Leu Tyr Ser
            20   25   30
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
        35   40   45
Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Lys Ser Gly Val
    50   55   60
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
                85   90   95
Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100   105   110
Lys

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Asp Arg Val Thr Ile Thr Cys Lys Ser Ile Gln Thr Leu Leu Tyr Ser
            20   25   30
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
        35   40   45
Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Lys Ser Gly Val
    50   55   60
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
                85   90   95
Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100   105   110
Lys

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Asp Arg Val Thr Ile Thr Cys Lys Ser Ile Gln Thr Leu Leu Tyr Ser
            20   25   30
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys

```
        35                  40                  45
Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Lys Ser Gly Val
    50                  55                  60
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80
Ile Ser Ser Leu Gln Pro Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln
                85                  90                  95
Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100                 105                 110
Lys
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            20                  25                  30
Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu Glu Trp Val
        35                  40                  45
Ala Ser Ile Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Asn Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Glu Asp Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95
Ser Arg Gly Gly Ala Gly Ile Asp Tyr Trp Gly Gln Gly Thr Thr Leu
            100                 105                 110
Thr Val Ser Ser
        115
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Ser Ser Asp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
Thr Val Ser Ser
        115
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<212> PRT
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Asn Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ser Arg Gly Gly Ala Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110
Thr Val Ser Ser
        115

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Asn Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ser Arg Gly Gly Ala Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110
Thr Val Ser Ser
        115

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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 Asn Tyr
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Asn Val
    50   55   60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Gly Ala Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
Thr Val Ser Ser
        115
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 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ala Ser Ile Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Asn Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Gly Ala Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
Thr Val Ser Ser
        115
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<210> 12
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 12

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Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val
 1               5                  10                  15
Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys
            20                  25                  30
Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
        35                  40                  45
Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr
    50                  55                  60
Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys
65                  70                  75                  80
Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys
                85                  90                  95
Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile
            100                 105                 110
Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro
        115                 120                 125
Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
    130                 135                 140
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<210> 13
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthesized

<400> 13
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 1   5   10   15
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
            20   25   30
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35   40   45
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50   55   60
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65   70   75   80
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85   90   95
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100   105

<210> 14
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 14
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
Arg 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 Val 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 Glu Glu
225   230   235   240
Met 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> 15
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 15
gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgcgtgacc 60
atcacctgca agtccatcca gaccctgctg tactcctcca accagaagaa ctacctggcc 120
tggttccagc agaagcccgg caaggccccc aagctgctga tctactgggc ctccatccgc 180
aagtccggcg tgccctcccg cttctccggc tccggctccg gcaccgactt caccctgacc 240
atctcctccc tgcagcccga ggacttcgcc acctactact gccagcagta ctactcctac 300
cccctgacct tcggcggcgg caccaagctg gagatcaag 339

<210> 16
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 16
gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgcgtgacc 60
atcacctgca agtccatcca gaccctgctg tactcctcca accagaagaa ctacctggcc 120
tggtaccagc agaagcccgg caaggccccc aagctgctga tctactgggc ctccatccgc 180
aagtccggcg tgccctcccg cttctccggc tccggctccg gcaccgactt caccctgacc 240
atctcctccc tgcagcccga ggacttcgcc acctactact gccagcagta ctactcctac 300
cccctgacct tcggcggcgg caccaagctg gagatcaag 339

<210> 17
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 17
gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgcgtgacc 60
atcacctgca agtccatcca gaccctgctg tactcctcca accagaagaa ctacctggcc 120
tggttccagc agaagcccgg caaggccccc aagctgctga tctactgggc ctccatccgc 180
aagtccggcg tgccctcccg cttctccggc tccggctccg gcaccgactt caccctgacc 240
atctcctccc tgcagcccga ggacctggcc acctactact gccagcagta ctactcctac 300
cccctgacct tcggcggcgg caccaagctg gagatcaag 339

<210> 18
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 18
gaggtgcagc tggtggagtc cggcggcggc ctggtgcagc ccggcggctc cctgcgcctg 60
tcctgcgccg cctccggctt caccttctcc aactacggca tgtcctgggt gcgccaggcc 120
cccggcaagg gcctggagtg ggtggcctcc atctcctccg gcggcggctc cacctactac 180
cccgacaacg tgaagggccg cttcaccatc tcccgcgacg acgccaagaa ctccctgtac 240
ctgcagatga actccctgcg cgccgaggac accgccgtgt actactgctc ccgcggcggc 300
gccggcatcg actactgggg ccagggcacc ctggtgaccg tgtcctcc 348

<210> 19
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 19
gaggtgcagc tggtggagtc cggcggcggc ctggtgcagc ccggcggctc cctgcgcctg 60
tcctgcgccg cctccggctt caccttctcc aactacggca tgtcctgggt gcgccaggcc 120
cccggcaagg gcctggagtg ggtggcctcc atctcctccg gcggcggctc cacctactac 180
cccgacaacg tgaagggccg cttcaccatc tcccgcgaca acgccaagaa ctccctgtac 240
ctgcagatga actccctgcg cgccgaggac accgccgtgt actactgctc ccgcggcggc 300
gccggcatcg actactgggg ccagggcacc ctggtgaccg tgtcctcc 348

<210> 20
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 20
gaggtgcagc tggtggagtc cggcggcggc ctggtgcagc ccggcggctc cctgcgcctg 60
tcctgcgccg cctccggctt caccttctcc aactacggca tgtcctgggt gcgccaggcc 120
cccggcaagg gcctggagtg ggtggcctcc atctcctccg gcggcggctc cacctactac 180
cccgacaacg tgaagggccg cttcaccatc tcccgcgacg acgccaagaa ctccctgtac 240
ctgcagatga actccctgcg cgccgaggac accgccgtgt actactgcgc ccgcggcggc 300
gccggcatcg actactgggg ccagggcacc ctggtgaccg tgtcctcc 348

<210> 21
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 21
gaggtgcagc tggtggagtc cggcggcggc ctggtgcagc ccggcggctc cctgcgcctg 60
tcctgcgccg cctccggctt caccttctcc aactacggca tgtcctgggt gcgccaggcc 120
cccggcaagg gcctggagtg ggtggcctcc atctcctccg gcggcggctc cacctactac 180
cccgacaacg tgaagggccg cttcaccatc tcccgcgaca acgccaagaa ctccctgtac 240
ctgcagatga actccctgcg cgccgaggac accgccgtgt actactgcgc ccgcggcggc 300
gccggcatcg actactgggg ccagggcacc ctggtgaccg tgtcctcc 348

<210> 22
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 22
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp
 1   5   10   15
Val Ser Gly Ser Ser Gly
            20

<210> 23
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 23
atggacatgc gcgtgcccgc ccagctgctg ggcctgctga tgctgtgggt gtccggctcc 60
tccggc 66

<210> 24
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 24
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
 1   5   10   15
Val Gln Cys

<210> 25
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 25
atggagttcg gcctgtcctg gctgttcctg gtggccatcc tgaagggcgt gcagtgc 57

<210> 26
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<220>
<221> VARIANT
<222> 42
<223> Xaa = Y or F

<220>
<221> VARIANT
<222> 89
<223> Xaa = F or L

<400> 26
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Lys Ser Ile Gln Thr Leu Leu Tyr Ser
            20   25   30
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Xaa Gln Gln Lys Pro Gly Lys
        35   40   45
Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Lys Ser Gly Val
    50   55   60
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Pro Glu Asp Xaa Ala Thr Tyr Tyr Cys Gln Gln
                85   90   95
Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100   105   110
Lys

<210> 27
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<220>
<221> VARIANT
<222> 74
<223> Xaa = N or D

<220>
<221> VARIANT
<222> 97
<223> Xaa = A or S

<400> 27
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 Asn Tyr
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Asn Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Xaa Ala Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Xaa Arg Gly Gly Ala Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110
Thr Val Ser Ser
        115

<210> 28
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 28
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100   105

<210> 29
<211> 220
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthesized

<400> 29
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Lys Ser Ile Gln Thr Leu Leu Tyr Ser
            20   25   30
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
        35   40   45
Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Lys Ser Gly Val
    50   55   60
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Pro Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln
                85   90   95
Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100   105   110
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115   120   125
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130   135   140
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145   150   155   160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165   170   175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180   185   190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
        195   200   205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210   215   220

<210> 30
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 30
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Lys Ser Ile Gln Thr Leu Leu Tyr Ser
            20   25   30
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
        35   40   45
Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Lys Ser Gly Val
    50   55   60
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Pro Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln
                85   90   95
Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100   105   110
Lys Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115   120   125
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130   135   140
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145   150   155   160
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165   170   175
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180   185   190
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195   200   205
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 31
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 31
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 Asn Tyr
20 25 30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Ser Ile Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Asn Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Ala Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205
Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225 230 235 240
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Val Lys Thr
275 280 285
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 32
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 32
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
Arg 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 Glu Glu
225   230   235   240
Met 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