8C10 V_L

```
  1 V  I  Q  L  T  Q  S  P  S  S  L  S  A  S  V  G  D  R  V  T
  1 gtcatccagttgacccagtctccatcctccctgtctgcatctgtaggagacagagtcacc
 21 I  T  C  R  A  S  Q  G  I  S  R  A  L  A  W  Y  Q  Q  K  P
 61 atcacttgccgggcaagtcagggcattagcagggctttagcctggtatcagcagaaacca
 41 G  K  G  P  K  L  L  I  Y  D  A  S  S  L  E  S  G  V  P  S
121 gggaaaggtcctaagctcctgatctatgatgcctccagtttggaaagtggggtcccatca
 61 R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S  S  L  Q  P
181 aggttcagcggcagtggatctgggacagatttcactctcaccatcagcagcctgcagcct
 81 E  D  F  A  T  Y  Y  C  Q  Q  F  N  S  Y  P  L  T  F  G  G
241 gaagattttgcaacttattactgtcaacagtttaatagttaccctctcactttcggcgga
101 G  T  K  V  E  I  K
301 gggaccaaggtggagatcaaa
```

Fig. 1A

8C10 V_H

```
  1 Q  V  Q  L  V  E  S  G  G  G  V  V  Q  P  G  R  S  L  R  L
  1 caggtgcaactggtggagtctgggggaggcgtggtccagcctgggaggtccctgagactc
 21 S  C  A  A  S  G  F  T  F  F  S  Y  A  M  H  W  V  R  Q  T
 61 tcctgtgcagcgtctggattcaccttctttagctatgccatgcactgggtccgccagact
 41 P  G  K  G  L  E  W  V  A  V  I  W  F  D  G  S  N  E  N  Y
121 ccaggcaaggggctggagtgggtggcagttatatggtttgatggaagtaatgaaaactat
 61 V  D  S  V  K  G  R  F  T  I  S  R  D  N  S  K  N  T  L  Y
181 gtagactccgtgaagggccgattcaccatctccagagacaattccaagaacacgctgtat
 81 L  Q  M  N  T  L  R  A  E  D  T  A  V  Y  Y  C  A  R  D  A
241 ctgcaaatgaacaccctgagagccgaggacacggctgtgtattactgtgcgagagatgcc
101 W  S  Y  F  D  Y  W  G  Q  G  T  L  V  T  V  S  S
301 tggagctactttgactactggggccagggaaccctggtcaccgtctcctca
```

Fig. 1B

8A4 V_L

```
  1 E  I  V  L  T  Q  S  P  A  T  L  S  L  S  P  G  E  R  A  T
  1 gaaattgtgttgacacagtctccagccaccctgtctttgtctccaggggaaagagccacc
 21 L  S  C  R  A  S  Q  S  V  S  S  Y  L  A  W  Y  Q  Q  K  P
 61 ctctcctgcagggccagtcagagtgttagcagctacttagcctggtaccaacagaaacct
 41 G  Q  A  P  R  L  L  I  Y  D  A  S  N  R  A  T  G  I  P  A
121 ggccaggctcccaggctcctcatctatgatgcatccaacagggccactggcatcccagcc
 61 R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S  S  L  E  P
181 aggttcagtggcagtgggtctgggacagacttcactctcaccatcagcagcctagagcct
 81 E  D  F  A  V  Y  Y  C  Q  Q  R  S  N  W  P  L  T  F  G  G
241 gaagattttgcagtttattactgtcagcagcgtagcaactggccgctcactttcggcgga
101 G  T  K  V  E  I  K
301 gggaccaaggtggagatcaaa
```

Fig. 2A

8A4 V_H

```
  1 E  V  Q  L  V  E  S  G  G  G  L  V  Q  P  G  G  S  L  R  L
  1 gaggtgcagctggtggagtctgggggaggcttggtccagcctgggggtccctgagactc
 21 S  C  A  A  S  G  F  I  F  S  N  Y  W  M  S  W  V  R  Q  A
 61 tcctgtgcagcctctggattcattttcagtaactattggatgagctgggtccgccaggct
 41 P  G  K  G  L  E  W  V  A  N  I  K  Q  D  G  S  E  K  Y  Y
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 81 L  Q  M  N  S  L  R  A  E  D  T  A  V  Y  Y  C  A  R  D  Y
241 ctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtgcgagggattac
101 F  G  S  G  T  Y  F  F  Y  F  D  Y  W  G  Q  G  T  L  V  T
301 tttggttcggggacttatttcttctactttgactactggggccagggaaccctggtcacc
121 F  S  S
361 ttctcctca
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Fig. 2B

3F10 V_L

```
  1 A  I  Q  L  T  Q  S  P  S  S  L  S  A  S  V  G  D  R  V  T
  1 gccatccagttgacccagtctccatcctccctgtctgcatctgtaggagacagagtcacc
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 61 atcacttgccgggcaagtcagggcattagcagagctttagcctggtatcagcagaaacca
 41 G  K  A  P  K  L  L  I  Y  D  A  S  N  L  E  R  G  V  P  S
121 gggaaagctcctaagctcctgatctatgatgcctccaatttggaaagaggggtcccatca
 61 R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S  S  L  Q  P
181 aggttcagcggcagtggatctgggacagatttcactctcaccatcagcagcctgcaacct
 81 E  D  F  A  T  Y  Y  C  Q  Q  F  N  S  F  P  L  T  F  G  G
241 gaggattttgcaacttattactgtcaacagtttaatagtttcccgctcactttcggcgga
101 G  T  K  V  E  I  K
301 gggaccaaggtggagatcaaa
```

Fig. 3A

3F10 V_H

```
  1 Q  V  Q  L  V  E  S  G  G  G  V  V  Q  P  G  R  S  L  R  L
  1 caggtgcagctggtggagtctgggggaggcgtggtccagcctgggaggtccctgagactc
 21 S  C  A  A  S  G  F  T  F  S  S  Y  A  M  H  W  V  R  Q  A
 61 tcctgtgcagcgtctggattcaccttcagtagctatgccatgcactgggtccgccaggct
 41 P  G  K  G  L  E  W  V  A  V  L  W  F  D  G  S  N  E  D  Y
121 ccaggcaaggggctggagtgggtggcagttttatggtttgatggaagtaatgaagactat
 61 A  D  S  V  K  G  R  F  T  I  S  R  D  N  S  K  N  T  L  Y
181 gcagactccgtgaagggccgattcaccatctccagagacaactccaagaacacgctgtat
 81 L  Q  M  N  S  L  R  A  E  D  T  A  V  Y  Y  C  A  R  D  G
241 ctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtgcgagagatggc
101 W  G  Y  F  D  Y  W  G  Q  G  T  L  V  T  V  S  S
301 tggggatactttgactactggggccagggaaccctggtcaccgtctcctca
```

Fig. 3B

5F12 V_L

```
  1 D  I  Q  M  T  Q  S  P  S  S  L  S  A  S  V  G  D  R  V  T
  1 gacatccagatgacccagtctccatcctcactgtctgcatctgtaggagacagagtcacc
 21 I  T  C  R  A  S  Q  G  I  S  S  W  L  A  W  Y  Q  Q  K  P
 61 atcacttgtcgggcgagtcagggtattagcagctggttagcctggtatcagcagaaacca
 41 E  K  A  P  K  S  L  I  Y  G  A  S  S  L  Q  S  G  V  P  S
121 gagaaagcccctaagtccctgatctatggtgcatccagtttgcaaagtggggtcccatca
 61 R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S  S  L  Q  P
181 aggttcagcggcagtggatctgggacagatttcactctcaccatcagcagcctgcagcct
 81 E  D  F  A  T  Y  Y  C  Q  Q  Y  N  S  Y  P  R  T  F  G  Q
241 gaagattttgcaacttattactgccaacagtataatagttaccctcggacgttcggccaa
101 G  T  K  V  E  I  K
301 gggaccaaggtggaaatcaaa
```

Fig. 4A

5F12 V_H

```
  1 Q  V  Q  L  V  D  S  G  G  D  V  V  Q  P  G  R  S  L  R  L
  1 caggtgcagctggtggactctgggggagacgtggtccagcctgggaggtccctgagactc
 21 S  C  A  A  S  G  F  S  F  S  R  S  G  I  H  W  V  R  Q  A
 61 tcctgtgcagcgtctggattcagtttcagtcggtctggcatacactgggtccgccaggct
 41 P  G  K  G  L  E  W  V  A  V  I  W  Y  D  G  I  Y  K  Y  Y
121 ccaggcaaggggctggagtgggtggcagttatatggtatgatggaatttataagtactat
 61 A  D  S  V  K  G  R  F  T  I  S  R  D  N  S  K  N  T  L  Y
181 gcagactccgtgaagggccgattcaccatctccagagacaattccaagaacacgctgtat
 81 L  Q  M  N  S  L  R  A  E  D  T  A  V  Y  Y  C  A  R  E  K
241 ctgcaaatgaacagcctgagggccgaggacacggctgtgtattactgtgcgagagagaag
101 N  W  G  I  D  Y  W  G  Q  G  T  L  V  T  V  S  S
301 aactggggaattgactactggggccagggaaccctggtcaccgtctcctca
```

Fig. 4B

4B3 V_L

```
  1 E  I  V  L  T  Q  S  P  G  T  L  S  L  S  P  G  D  R  A  T
  1 gaaattgtgttgacgcagtctccaggcaccctgtctttgtctccaggggatagagccacc
 21 L  S  C  R  A  S  Q  S  V  S  S  S  F  L  A  W  Y  Q  Q  K
 61 ctctcctgcagggccagtcagagtgttagcagcagcttcttagcctggtaccagcagaaa
 41 P  G  Q  A  P  R  L  L  I  Y  G  A  S  S  R  A  T  G  I  P
121 cctggccaggctcccaggctcctcatctatggtgcatccagcagggccactggcatccca
 61 D  R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S  R  L  E
181 gacaggttcagtggcagtgggtctgggacagacttcactctcaccatcagcagactggag
 81 P  E  D  F  A  V  Y  Y  C  Q  Q  Y  G  S  S  P  L  T  F  G
241 cctgaagattttgcagtgtattactgtcagcagtatggtagctcaccgctcactttcggc
101 G  G  T  K  V  E  I  K
301 ggagggaccaaggtggagatcaaa
```

Fig. 5A

4B3 V_H

```
  1 E  V  Q  L  V  Q  S  G  G  G  L  V  H  P  G  G  S  L  R  L
  1 gaggttcagctggtgcagtctgggggaggcttggtacatccgggggggtccctgagactc
 21 S  C  A  G  S  G  F  P  V  S  S  Y  G  M  H  W  V  R  Q  A
 61 tcctgtgcaggctctggattccccgtcagtagctatggaatgcactgggttcgccaggct
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101 F  G  E  V  Y  F  D  Y  W  G  Q  G  T  L  V  T  V  S  S
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Fig. 5B

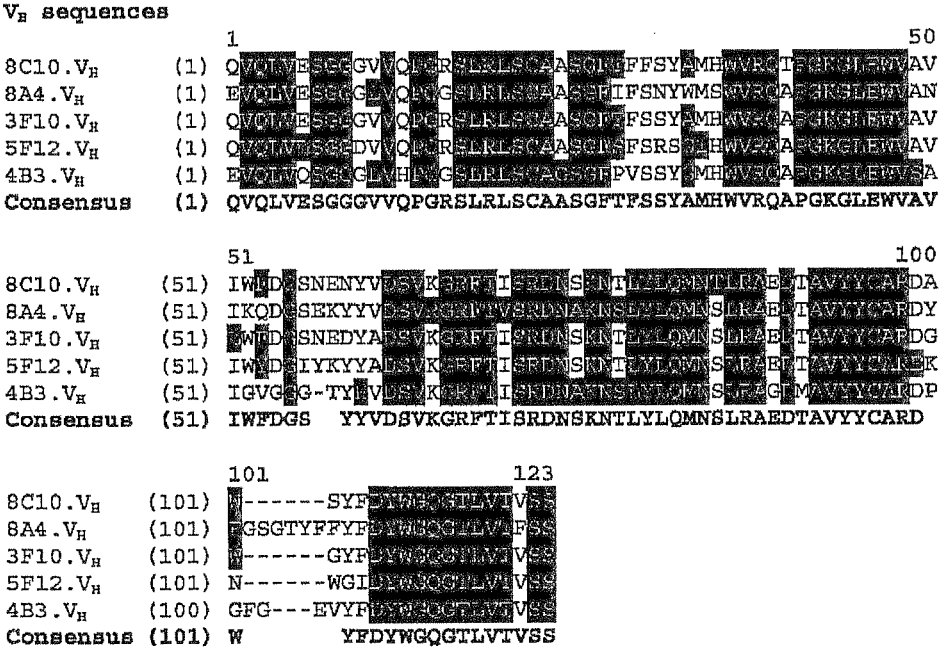


Fig. 6A

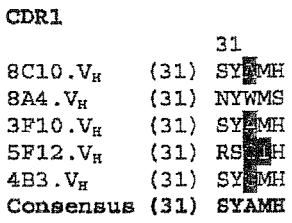


Fig. 6B

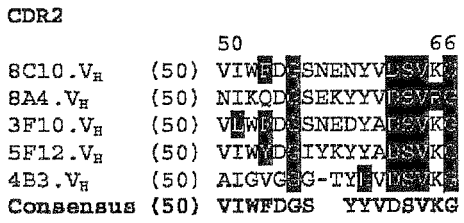


Fig. 6C

CDR3

```
                    99          112
8C10.VH     (99) DA------SYF
8A4.VH      (99) DYGSGTYFFYF
3F10.VH     (99) DG------GYF
5F12.VH     (99) EKN------WGI
4B3.VH      (98) DPGFG---EVYF
Consensus   (99) D W        YFDY
```

Fig. 6D

V_L sequences

```
                    1                                                  50
8C10.VL     (1)  VLQLTQSPSSLSASVGDRVTITCRASQGISS-FLAWYQQKPGKAPKLLIY
8A4.VL      (1)  LVVLTQSPAALSLSPGERATLSCRASQSVSS-YLAWYQQKPGQAPRLLIY
3F10.VL     (1)  ALQLTQSPSSLSASVGDRVTITCRASQGISR-ALAWYQQKPGKAPKLLIY
5F12.VL     (1)  DIQMTQSPSSLSASVGDRVTITCRASQGISS-WLAWYQQKPEKAFKSLIY
4B3.VL      (1)  EIVLTQSPGTLSLSPGDRATLSCRASQSVSSSFLAWYQQKPGQAPRLLIY
Consensus   (1)  EIQLTQSPSSLSASVGDRVTITCRASQGISS FLAWYQQKPGKAPKLLIY

                    51                                                 100
8C10.VL     (50) DASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPLTFG
8A4.VL      (50) DASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPLTFG
3F10.VL     (50) DASNLERGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSFPLTFG
5F12.VL     (50) GASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPRTFG
4B3.VL      (51) GASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFG
Consensus   (51) DASSL SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPLTFG

                    101
8C10.VL     (100) GGTKVEIK
8A4.VL      (100) GGTKVEIK
3F10.VL     (100) GGTKVEIK
5F12.VL     (100) QGTKVEIK
4B3.VL      (101) GGTKVEIK
Consensus   (101) GGTKVEIK
```

Fig. 6E

CDR1

```
                    24
8C10.VL     (24) RASQGISR-AL
8A4.VL      (24) RASQSVSS-YL
3F10.VL     (24) RASQGISR-AL
5F12.VL     (24) RASQGISS-WL
4B3.VL      (24) RASQSVSSSFL
Consensus   (24) RASQGISS FLA
```

Fig. 6F

CDR2

```
                    51
8C10.VL    (50)  DASSLES
8A4.VL     (50)  DASNRAT
3F10.VL    (50)  DASNLER
5F12.VL    (50)  GASSLQS
4B3.VL     (51)  SASSRAT
Consensus  (51)  DASSL S
```

Fig. 6G

CDR3

```
                    90
8C10.VL    (89)  QQENSWLL
8A4.VL     (89)  QQRSNWLL
3F10.VL    (89)  QQYNSWLL
5F12.VL    (89)  QQYNSWRL
4B3.VL     (90)  QQSGSSLL
Consensus  (90)  QQFNSYPLT
```

Fig. 6H

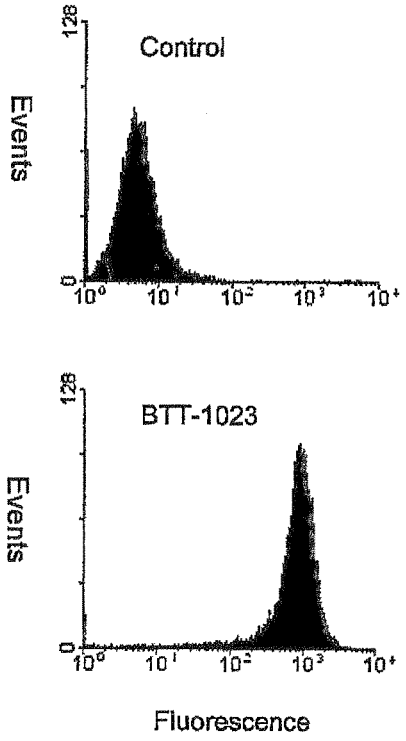

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Fluorescence

Fig. 7

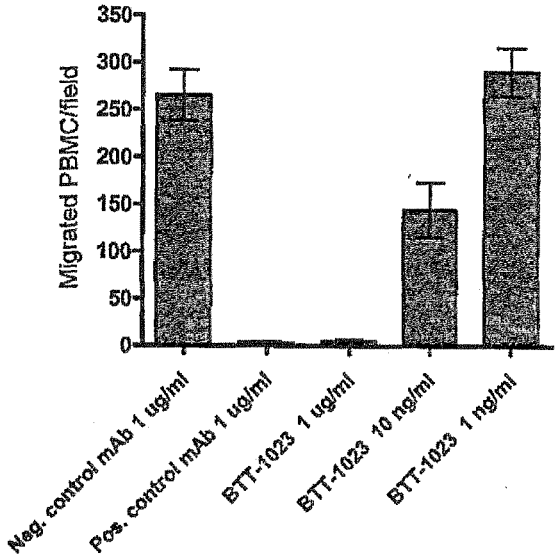

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BTT-1023 1 ng/ml

Figure 8

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BioTie Therapies Corp.
<112> Smith, David John
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<114> Mikkola, Jari
<115> Vuorio, PÄivi
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Val Leu Trp Phe Asp Gly Ser Asn Glu Asp Tyr Ala Asp Ser Val Lys
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Gly

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<213> Homo sapiens

<400> 12

Val Ile Trp Tyr Asp Gly Ile Tyr Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

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<212> PRT
<213> Homo sapiens

<400> 13

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

<210> 14
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<400> 14

Asp Ala Trp Ser Tyr Phe Asp Tyr
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<210> 15
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<400> 15

Asp Tyr Phe Gly Ser Gly Thr Tyr Phe Phe Tyr Phe Asp Tyr
1 5 10

<210> 16
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<400> 16

Asp Gly Trp Gly Tyr Phe Asp Tyr
1 5

<210> 17
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<400> 17

Glu Lys Asn Trp Gly Ile Asp Tyr
1 5

<210> 18
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<212> PRT
<213> Homo sapiens

<400> 18

Asp Pro Gly Phe Gly Glu Val Tyr Phe Asp Tyr
1 5 10

<210> 19
<211> 117
<212> PRT
<213> Homo sapiens

<400> 19

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

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

Ala Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Phe Asp Gly Ser Asn Glu Asn Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Trp Ser Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

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<211> 123
<212> PRT
<213> Homo sapiens

<400> 20

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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Asn 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

Arg Gly Arg Phe Thr Val 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 Asp Tyr Phe Gly Ser Gly Thr Tyr Phe Phe Tyr Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Phe Ser Ser
115 120

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<400> 21

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

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

Ala Val Leu Trp Phe Asp Gly Ser Asn Glu Asp Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Asp Gly Trp Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

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<213> Homo sapiens

<400> 22

Gln Val Gln Leu Val Asp Ser Gly Gly Asp Val Val Gln Pro Gly Arg
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Arg Ser
20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ile Tyr Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Glu Lys Asn Trp Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

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<400> 23

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

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Pro Val Ser Ser Tyr
20 25 30

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

Ser Ala Ile Gly Val Gly Gly Gly Thr Tyr His Val Asp Ser Val Lys
50 55 60

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

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

Arg Asp Pro Gly Phe Gly Glu Val Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

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<220>
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<223> A, F, W or Y

<400> 24

Arg Ala Ser Gln Xaa Xaa Ser Xaa Xaa Xaa Leu Ala
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<210> 25
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<213> Homo sapiens

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<223> S or N

<220>
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<222> (5)..(5)
<223> L or R

<220>
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<220>
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<223> S, T or R

<400> 25

Xaa Ala Ser Xaa Xaa Xaa Xaa
1 5

<210> 26
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<223> N, G or S

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> S or N

<220>
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<223> Y, F, W or S

<220>

<221> MISC_FEATURE
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<400> 26

Gln Gln Xaa Xaa Xaa Xaa Pro Xaa Thr
1 5

<210> 27
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<212> PRT
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<400> 27

Arg Ala Ser Gln Gly Ile Ser Arg Ala Leu Ala
1 5 10

<210> 28
<211> 11
<212> PRT
<213> Homo sapiens

<400> 28

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 29
<211> 11
<212> PRT
<213> Homo sapiens

<400> 29

Arg Ala Ser Gln Gly Ile Ser Arg Ala Leu Ala
1 5 10

<210> 30
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<212> PRT
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<400> 30

Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 31
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<400> 31

Arg Ala Ser Gln Ser Val Ser Ser Ser Phe Leu Ala
1 5 10

<210> 32
<211> 7
<212> PRT

<213> Homo sapiens

<400> 32

Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 33
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<212> PRT
<213> Homo sapiens

<400> 33

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 34
<211> 7
<212> PRT
<213> Homo sapiens

<400> 34

Asp Ala Ser Asn Leu Glu Arg
1 5

<210> 35
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<212> PRT
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<400> 35

Gly Ala Ser Ser Leu Gln Ser
1 5

<210> 36
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<212> PRT
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<400> 36

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 37
<211> 9
<212> PRT
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<400> 37

Gln Gln Phe Asn Ser Tyr Pro Leu Thr
1 5

<210> 38
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<400> 38

Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 39
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<400> 39

Gln Gln Phe Asn Ser Phe Pro Leu Thr
1 5

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<400> 40

Gln Gln Tyr Asn Ser Tyr Pro Arg Thr
1 5

<210> 41
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<400> 41

Gln Gln Tyr Gly Ser Ser Pro Leu Thr
1 5

<210> 42
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<212> PRT
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<400> 42

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

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

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

Tyr Asp Ala Ser Ser Leu Glu 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 Phe Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 43
<211> 107
<212> PRT
<213> Homo sapiens

<400> 43

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 44
<211> 107
<212> PRT
<213> Homo sapiens

<400> 44

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

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

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

Tyr Asp Ala Ser Asn Leu Glu Arg 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 Phe Asn Ser Phe Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 45
<211> 107
<212> PRT
<213> Homo sapiens

<400> 45

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 Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
35 40 45

Tyr Gly 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 Tyr Asn Ser Tyr Pro Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 46
<211> 108
<212> PRT
<213> Homo sapiens

<400> 46

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

Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

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

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

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

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 47
<211> 463
<212> PRT
<213> Homo sapiens

<400> 47

Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val Ala Leu Leu Arg Asp
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Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Phe Ser Tyr Ala Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Val Ile Trp Phe Asp Gly Ser Asn Glu Asn Tyr Val
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Asp Ala Trp Ser Tyr Phe Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
145 150 155 160

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
165 170 175

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
195 200 205

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Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
225                 230                 235                 240

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Ala Gly Gly Pro Ser Val
                245                 250                 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
        275                 280                 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
305                 310                 315                 320

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
            340                 345                 350

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        355                 360                 365

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    370                 375                 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385                 390                 395                 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                405                 410                 415

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
            420                 425                 430

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        435                 440                 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
    450                 455                 460
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<213> Homo sapiens

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Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
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Leu Pro Gly Ala Arg Cys Val Ile Gln Leu Thr Gln Ser Pro Ser Ser
            20                  25                  30

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

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

Gly Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val
65                  70                  75                  80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
                85                  90                  95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
            100                 105                 110

Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
        115                 120                 125

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

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

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

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

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

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
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Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
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agctatggaa tgcac 15

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<400> 57
gttatatggt atgatggaat ttataagtac tatgcagact ccgtgaaggg c 51

<210> 58
<211> 48
<212> DNA
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<400> 58
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<210> 59
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<212> DNA
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<400> 60
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<210> 61
<211> 24
<212> DNA
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<400> 61
gatggctggg gatactttga ctac 24

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<400> 62
gagaagaact ggggaattga ctac 24

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<212> DNA
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<400> 63
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ccaggcaagg ggctggagtg ggtggcagtt atatggtttg atggaagtaa tgaaaactat 180
gtagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
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ccagggaaag ggctggagtg ggtggccaac ataaagcaag atggaagtga gaagtactat 180
gtggactctg tgaggggccg attcaccgtc tccagagaca acgccaagaa ctcactgtat 240
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ttctcctca 369

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<211> 351
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ccaggcaagg ggctggagtg ggtggcagtt ttatggtttg atggaagtaa tgaagactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca actccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatggc 300
tggggatact ttgactactg gggccaggga accctggtca ccgtctcctc a 351

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<400> 67
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ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaattta taagtactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag ggccgaggac acggctgtgt attactgtgc gagagagaag 300

aactggggaa ttgactactg gggccaggga accctggtca ccgtctcctc a 351

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<400> 68
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ccaggaaaag gtctggagtg ggtatcagct attggtgttg gtggtggcac ataccatgta 180

gattccgtga agggccgatt caccatctcc agagacaatg ccaagaactc cttgtatctt 240

caaatgaaca gcctgagagc cggggacatg gctgtgtatt actgtgcaag agatcctggg 300

ttcggggagg tctactttga ctattggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 69
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<212> DNA
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<400> 69
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<210> 70
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<400> 70
agggccagtc agagtgttag cagctactta gcc 33

<210> 71
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<400> 71
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<400> 72
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<212> DNA
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<400> 73
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<210> 74
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<210> 78
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<210> 79
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aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

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ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

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gaggattttg caacttatta ctgtcaacag tttaatagtt tcccgctcac tttcggcgga 300

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aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

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<213> Homo sapiens

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gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

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<400> 90
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aaaccaggga aaggtcctaa gctcctgatc tatgatgcct ccagtttgga aagtggggtc 240

ccatcaaggt tcagcggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300

cagcctgaag attttgcaac ttattactgt caacagttta atagttaccc tctcactttc 360

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