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<110> REGENERON PHARMACEUTICALS, INC.
McWhirter, John
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Martin, Joel
Murphy, Andrew J.

<120> Non-Human Animals Expressing pH-Sensitive Immunoglobulin Sequences

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<150> 61/613,352

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28

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Gly Ile Ala Val Thr Thr Thr Ile Cys
1 5

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Gln Ser Pro Pro Gln Tyr Ala
1 5

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Asn Ser Ser His His His Asn Met
1 5

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31

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<400> 250

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1 5 10

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<400> 251

Pro Leu Gln Lys Ser
1 5

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Tyr Asn Asn His Ser Lys Asn Arg Asn
1 5

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ggtataataa ccactccaaa aatgctaata c

31

1900A-WO_SEQ_ST25

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<400> 254

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 1 5 10

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<400> 255

Pro Leu Gln Lys Cys
 1 5

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Tyr Asn Asn His Ser Lys Asn Ala Asn
 1 5

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gttataataa ccagtcaaaa tatcgtaata c

31

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Val Ile Ile Thr Ser Gln Asn Ile Val Ile
 1 5 10

1900A-WO_SEQ_ST25

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Pro Val Lys Ile Ser
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Tyr Asn Asn Gln Ser Lys Tyr Arg Asn
 1 5

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31

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<400> 263

Leu Pro Glu Pro
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1900A-WO_SEQ_ST25

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30

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<220>
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Val Ile Ile Thr Pro Arg Thr
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<210> 267
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<220>
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<400> 267

Leu Pro Glu His Ser Asn
 1 5

<210> 268
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Tyr Asn Asn Ser Pro Asn Ile Val Ile
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1900A-WO_SEQ_ST25

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<210> 270
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Gly Ile Ser Ile Thr Pro Pro Asn Val Ile Ile Ile
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<400> 271

Leu Pro Gln Thr
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Tyr Lys His Asn Ser Pro Lys Arg Asn His Asn
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31

1900A-WO_SEQ_ST25

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<400> 274

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 1 5 10

<210> 275
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<220>
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<400> 275

Pro Leu Leu Ser
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Ser Asn Asn His Tyr Tyr His Ser Asn
 1 5

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<220>
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1900A-WO_SEQ_ST25

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<400> 280
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16

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<400> 281

Ser His Arg Ser
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<400> 282
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<220>
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<400> 283

Gly val Thr Thr val val
 1 5

<210> 284
 <211> 4

<212> PRT
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<220>
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<400> 284

Glu Leu Pro Pro
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<210> 285
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<220>
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<400> 285

Ser Tyr His Arg Ser
1 5

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20

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<220>
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<400> 287

Val Thr Ile Ala Val Ser
1 5

<210> 288
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<220>
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<400> 288

Asn His Ser Cys Ile His
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<220>
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<400> 290

Val Ile Val Ala Thr Ile Ser
1 5

<210> 291
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<220>
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<400> 291

Pro Leu Tyr Pro
1

<210> 292
<211> 7
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<220>
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<400> 292

Asn Arg Ser His Tyr Ile His
1 5

<210> 293
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<220>
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1900A-WO_SEQ_ST25

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 1 5

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 <400> 295

Asn Cys Ser His Leu Tyr
 1 5

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<220>
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18

<210> 297
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<220>
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<400> 297

Gly Arg Ala Ala Ile Leu
 1 5

<210> 298
 <211> 5
 <212> PRT
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<220>
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<400> 298

Asp Glu Leu Leu Tyr
 1 5

<210> 299
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1900A-WO_SEQ_ST25

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<400> 299

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1 5

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<220>
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<400> 300
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<210> 301
<211> 7
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<220>
<223> Mamma1

<400> 301

Val Pro Ala Ala Ala Ile Pro
1 5

<210> 302
<211> 6
<212> PRT
<213> Unknown

<220>
<223> Mamma1

<400> 302

Tyr Gln Leu Leu Leu Tyr
1 5

<210> 303
<211> 6
<212> PRT
<213> Unknown

<220>
<223> Mamma1

<400> 303

Thr Ser Cys Cys Tyr Thr
1 5

<210> 304
<211> 21
<212> DNA
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<220>
<223> Mamma1

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21

<210> 305
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<220>
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<400> 305

Val Pro Ala Thr Ala Ile Pro
1 5

<210> 306
<211> 6
<212> PRT
<213> Unknown

<220>
<223> Mamma1

<400> 306

Tyr Gln Pro Leu Leu Tyr
1 5

<210> 307
<211> 6
<212> PRT
<213> Unknown

<220>
<223> Mamma1

<400> 307

Thr Ser His Cys Tyr Thr
1 5

<210> 308
<211> 18
<212> DNA
<213> Unknown

<220>
<223> Mamma1

<400> 308
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18

<210> 309
<211> 6
<212> PRT
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<220>

1900A-WO_SEQ_ST25

<223> Mammal

<400> 309

Val Ala Ala Ala Ile Pro
1 5

<210> 310

<211> 4

<212> PRT

<213> Unknown

<220>

<223> Mammal

<400> 310

Pro Leu Leu Tyr
1

<210> 311

<211> 5

<212> PRT

<213> Unknown

<220>

<223> Mammal

<400> 311

Ser Arg Cys Tyr Thr
1 5

<210> 312

<211> 366

<212> DNA

<213> Homo sapiens

<400> 312

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acctgcgctg tctatggtgg gtccttcagt ggttactact ggagctggat ccgccagccc	120
ccaggaagg ggctggagtg gattggggaa atcaatcata gtggaagcac caactacaac	180
ccgtccctca agatcgagt caccatatca gtagacacgt ccaagaacca gttctccctg	240
aagctgagct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcggg gcatagccat	300
ggctggtact actactacta cggtatggac gtctggggcc aagggaccac ggtcaccgtc	360
tcctca	366

<210> 313

<211> 122

<212> PRT

<213> Homo sapiens

<400> 313

Gln val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Asp
1 5 10 15

1900A-WO_SEQ_ST25

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

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

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Gly His Ser His Gly Trp Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val Trp
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 314
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 314

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

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

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

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

<210> 315
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 315

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcagc agtgggtggtt actactggag ctggatccgc 120

1900A-WO_SEQ_ST25

cagcaccag ggaagggcct ggagtggatt gggtagatct attacagtgg gagcacctac 180
tacaaccgt ccctcaagag tcgagttacc atatcagtag acacgtctaa gaaccagttc 240
tccctgaagc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgaggggg 300
gaccacggtc actacgacta ctggggccag ggaaccctgg tcaccgtctc ctcag 355

<210> 316
<211> 118
<212> PRT
<213> Homo sapiens

<400> 316

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

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

Leu Val Thr Val Ser Ser
115

<210> 317
<211> 98
<212> PRT
<213> Homo sapiens

<400> 317

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

1900A-WO_SEQ_ST25

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Ala

<210> 318
 <211> 370
 <212> DNA
 <213> Homo sapiens

<400> 318
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 cagccccag ggaaggggct ggagtggatt gggagtatct attatagtgg gagcacctac 180
 tacaaccctg ccctcaagag tcgagtcacc atatccgtag acacgtccaa gaaccagttc 240
 tccctgaagc tgagctctgt gaccgccgca gacacggctg tgtattactg tgcgagacat 300
 gaagggcata gccaccttaa ctggttcgac ccctggggcc aggggggaac cctggtcacc 360
 gtctcctcag 370

<210> 319
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 319
 Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
 20 25 30

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

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

1900A-WO_SEQ_ST25
 Cys Ala Arg His Glu Gly His Ser His Leu Asn Trp Phe Asp Pro Trp
 100 105 110

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

<210> 320
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 320

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
 20 25 30

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

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Ala Arg

<210> 321
 <211> 22
 <212> DNA
 <213> Unknown

<220>
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<400> 321
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22

<210> 322
 <211> 22
 <212> DNA
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<220>
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<400> 322
 ggaagacatt tgggaaggac tg

22

<210> 323

1900A-WO_SEQ_ST25

<211> 4
<212> PRT
<213> Unknown

<220>
<223> Mammal

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> wherein the "Xaa" represents any amino acid

<400> 323

Phe Gly Xaa Gly
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<210> 324
<211> 4
<212> PRT
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<220>
<223> Mammal

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> wherein the "Xaa" represents any amino acid

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<211> 95
<212> PRT
<213> Artificial

<220>
<223> Synthetic

<400> 325

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 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

1900A-WO_SEQ_ST25

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

<210> 326
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthetic

<220>
<221> CDS
<222> (1)..(21)

<400> 326
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Gln Gln Ser Tyr Ser Thr Pro
1 5

21

<210> 327
<211> 7
<212> PRT
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<220>
<223> Synthetic Construct

<400> 327
Gln Gln Ser Tyr Ser Thr Pro
1 5

<210> 328
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<220>
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<220>
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<222> (1)..(21)

<400> 328
cac cat agc cac agc acc cac
His His Ser His Ser Thr His
1 5

21

<210> 329
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 329
His His Ser His Ser Thr His

1

5

<210> 330
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<220>
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<220>
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 <222> (1)..(21)

<400> 330
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 His Gln Ser Tyr Ser Thr Pro
 1 5

21

<210> 331
 <211> 7
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<220>
 <223> Synthetic Construct

<400> 331
 His Gln Ser Tyr Ser Thr Pro
 1 5

<210> 332
 <211> 21
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 <213> Artificial

<220>
 <223> Synthetic

<220>
 <221> CDS
 <222> (1)..(21)

<400> 332
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 Gln His Ser Tyr Ser Thr Pro
 1 5

21

<210> 333
 <211> 7
 <212> PRT
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<220>
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<400> 333
 Gln His Ser Tyr Ser Thr Pro
 1 5

1900A-WO_SEQ_ST25

<210> 334
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<220>
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<220>
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 <222> (1)..(21)

<400> 334
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 Gln Gln Ser His Ser Thr Pro
 1 5

21

<210> 335
 <211> 7
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<220>
 <223> Synthetic Construct

<400> 335
 Gln Gln Ser His Ser Thr Pro
 1 5

<210> 336
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 <212> DNA
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<220>
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 <222> (1)..(21)

<400> 336
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 Gln Gln Ser Tyr Ser Thr His
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21

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 <211> 7
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<220>
 <223> Synthetic Construct

<400> 337
 Gln Gln Ser Tyr Ser Thr His
 1 5

<210> 338

<211> 21
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<220>
 <223> Synthetic

<220>
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 <222> (1)..(21)

<400> 338
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 His His Ser Tyr Ser Thr Pro
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21

<210> 339
 <211> 7
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 <213> Artificial

<220>
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<400> 339

His His Ser Tyr Ser Thr Pro
 1 5

<210> 340
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 <213> Artificial

<220>
 <223> Synthetic

<220>
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<400> 340
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 His Gln Ser His Ser Thr Pro
 1 5

21

<210> 341
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 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 341

His Gln Ser His Ser Thr Pro
 1 5

<210> 342
 <211> 21
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<213> Artificial

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1)..(21)

<400> 342

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His Gln Ser Tyr Ser Thr His
1 5

21

<210> 343

<211> 7

<212> PRT

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1 5

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1 5

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Gln His Ser His Ser Thr His
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 gcaaacaaaa accactggcc 20

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 gggcactgga tacgatgtat gg 22

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

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

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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 Pro
 85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
 100 105

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50