

SEQUENCE LISTING

<110> TOKO YAKUHHIN KOGYO CO., LTD.
JAPAN as represented by DIRECTOR GENERAL of National
Institute of Infectious Diseases

<120> Method of production of polymeric IgA-type antibody and
multispecific polymeric IgA-type antibody

<130> 676009

<150> 2020-051139
<151> 2020-03-23

<160> 16

<170> PatentIn version 3.5

<210> 1
<211> 353
<212> PRT
<213> Homo sapiens

<400> 1

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

Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
35 40 45

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

Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
65 70 75 80

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

Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro

100	105	110																	
Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Cys	Cys	His	Pro	Arg	Leu	Ser				
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Leu	His	Arg	Pro	Ala	Leu	Glu	Asp	Leu	Leu	Leu	Gly	Ser	Glu	Ala	Asn				
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Leu	Thr	Cys	Thr	Leu	Thr	Gly	Leu	Arg	Asp	Ala	Ser	Gly	Val	Thr	Phe				
145					150					155					160				
Thr	Trp	Thr	Pro	Ser	Ser	Gly	Lys	Ser	Ala	Val	Gln	Gly	Pro	Pro	Glu				
			165						170					175					
Arg	Asp	Leu	Cys	Gly	Cys	Tyr	Ser	Val	Ser	Ser	Val	Leu	Pro	Gly	Cys				
		180						185					190						
Ala	Glu	Pro	Trp	Asn	His	Gly	Lys	Thr	Phe	Thr	Cys	Thr	Ala	Ala	Tyr				
	195						200					205							
Pro	Glu	Ser	Lys	Thr	Pro	Leu	Thr	Ala	Thr	Leu	Ser	Lys	Ser	Gly	Asn				
	210					215					220								
Thr	Phe	Arg	Pro	Glu	Val	His	Leu	Leu	Pro	Pro	Pro	Ser	Glu	Glu	Leu				
225					230				235						240				
Ala	Leu	Asn	Glu	Leu	Val	Thr	Leu	Thr	Cys	Leu	Ala	Arg	Gly	Phe	Ser				
			245						250					255					
Pro	Lys	Asp	Val	Leu	Val	Arg	Trp	Leu	Gln	Gly	Ser	Gln	Glu	Leu	Pro				
		260						265					270						
Arg	Glu	Lys	Tyr	Leu	Thr	Trp	Ala	Ser	Arg	Gln	Glu	Pro	Ser	Gln	Gly				
	275						280					285							
Thr	Thr	Thr	Phe	Ala	Val	Thr	Ser	Ile	Leu	Arg	Val	Ala	Ala	Glu	Asp				
	290					295					300								

Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu
 305 310 315 320

Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro
 325 330 335

Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys
 340 345 350

Tyr

<210> 2
 <211> 340
 <212> PRT
 <213> Homo sapiens

<400> 2

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

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

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

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

Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Pro Asp Gly
 65 70 75 80

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

Val Thr Val Pro Cys Arg Val Pro Pro Pro Pro Pro Cys Cys His Pro
 100 105 110

Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser
115 120 125

Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly
130 135 140

Ala Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly
145 150 155 160

Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu
165 170 175

Pro Gly Cys Ala Gln Pro Trp Asn His Gly Glu Thr Phe Thr Cys Thr
180 185 190

Ala Ala His Pro Glu Leu Lys Thr Pro Leu Thr Ala Asn Ile Thr Lys
195 200 205

Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser
210 215 220

Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg
225 230 235 240

Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln
245 250 255

Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro
260 265 270

Ser Gln Gly Thr Thr Thr Tyr Ala Val Thr Ser Ile Leu Arg Val Ala
275 280 285

Ala Glu Asp Trp Lys Lys Gly Glu Thr Phe Ser Cys Met Val Gly His
290 295 300

Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Met Ala
 305 310 315 320

Gly Lys Pro Thr His Ile Asn Val Ser Val Val Met Ala Glu Ala Asp
 325 330 335

Gly Thr Cys Tyr
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<210> 3
 <211> 585
 <212> PRT
 <213> Homo sapiens

<400> 3

Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu Gly Asn
 1 5 10 15

Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His
 20 25 30

Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys Ile Thr
 35 40 45

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

Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn Ile Ala
 65 70 75 80

Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile
 85 90 95

Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser Gln Gly
 100 105 110

Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu Gly Arg
 115 120 125

Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln Lys Arg
130 135 140

Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val Ile Asp
145 150 155 160

Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg Leu Asp
165 170 175

Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn Gln Leu
180 185 190

Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp Asp Ser
195 200 205

Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro Glu Pro
210 215 220

Glu Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His Cys Ala
225 230 235 240

Leu Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg Gln Ser
245 250 255

Ser Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys Arg Ala
260 265 270

Pro Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys Asp Gly
275 280 285

Ser Phe Ser Val Val Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly Arg
290 295 300

Tyr Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly Ser Pro
305 310 315 320

Ile Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro Arg

Lys Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala Val
530 535 540

Glu Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala Lys Ala
545 550 555 560

Asp Ala Ala Pro Asp Glu Lys Val Leu Asp Ser Gly Phe Arg Glu Ile
565 570 575

Glu Asn Lys Ala Ile Gln Asp Pro Arg
580 585

<210> 4
<211> 224
<212> PRT
<213> Artificial

<220>
<223> SC12

<400> 4

Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu Gly Asn
1 5 10 15

Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His
20 25 30

Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys Ile Thr
35 40 45

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

Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn Ile Ala
65 70 75 80

Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile
85 90 95

Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser Gln Gly
100 105 110

Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu Gly Arg
115 120 125

Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln Lys Arg
130 135 140

Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val Ile Asp
145 150 155 160

Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg Leu Asp
165 170 175

Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn Gln Leu
180 185 190

Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp Asp Ser
195 200 205

Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro Glu Pro
210 215 220

<210> 5

<211> 618

<212> PRT

<213> Artificial

<220>

<223> wild-type SC containing signal sequence, thrombin site, His tag

<400> 5

Met Leu Leu Phe Val Leu Thr Cys Leu Leu Ala Val Phe Pro Ala Ile
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Ser Thr Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu
20 25 30

Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn
35 40 45

Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys
50 55 60

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

Arg Ala Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn
85 90 95

Ile Ala Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu
100 105 110

Gly Ile Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser
115 120 125

Gln Gly Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu
130 135 140

Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln
145 150 155 160

Lys Arg Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val
165 170 175

Ile Asp Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg
180 185 190

Leu Asp Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn
195 200 205

Gln Leu Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp
210 215 220

Asp Ser Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro

225		230		235		240									
Glu	Pro	Glu	Leu	Val	Tyr	Glu	Asp	Leu	Arg	Gly	Ser	Val	Thr	Phe	His
			245						250					255	
Cys	Ala	Leu	Gly	Pro	Glu	Val	Ala	Asn	Val	Ala	Lys	Phe	Leu	Cys	Arg
			260					265					270		
Gln	Ser	Ser	Gly	Glu	Asn	Cys	Asp	Val	Val	Val	Asn	Thr	Leu	Gly	Lys
		275					280					285			
Arg	Ala	Pro	Ala	Phe	Glu	Gly	Arg	Ile	Leu	Leu	Asn	Pro	Gln	Asp	Lys
	290					295					300				
Asp	Gly	Ser	Phe	Ser	Val	Val	Ile	Thr	Gly	Leu	Arg	Lys	Glu	Asp	Ala
305					310					315					320
Gly	Arg	Tyr	Leu	Cys	Gly	Ala	His	Ser	Asp	Gly	Gln	Leu	Gln	Glu	Gly
			325						330					335	
Ser	Pro	Ile	Gln	Ala	Trp	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ser	Thr	Ile
		340						345					350		
Pro	Arg	Ser	Pro	Thr	Val	Val	Lys	Gly	Val	Ala	Gly	Gly	Ser	Val	Ala
		355					360					365			
Val	Leu	Cys	Pro	Tyr	Asn	Arg	Lys	Glu	Ser	Lys	Ser	Ile	Lys	Tyr	Trp
	370					375					380				
Cys	Leu	Trp	Glu	Gly	Ala	Gln	Asn	Gly	Arg	Cys	Pro	Leu	Leu	Val	Asp
385					390					395					400
Ser	Glu	Gly	Trp	Val	Lys	Ala	Gln	Tyr	Glu	Gly	Arg	Leu	Ser	Leu	Leu
			405						410					415	
Glu	Glu	Pro	Gly	Asn	Gly	Thr	Phe	Thr	Val	Ile	Leu	Asn	Gln	Leu	Thr
			420					425					430		

Ser Arg Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu
435 440 445

Trp Arg Thr Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu
450 455 460

Lys Val Pro Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val
465 470 475 480

Pro Cys His Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys
485 490 495

Lys Trp Asn Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly
500 505 510

Pro Ser Lys Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser
515 520 525

Leu Thr Leu Asn Leu Val Thr Arg Ala Asp Glu Gly Trp Tyr Trp Cys
530 535 540

Gly Val Lys Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val
545 550 555 560

Ala Val Glu Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala
565 570 575

Lys Ala Asp Ala Ala Pro Asp Glu Lys Val Leu Asp Ser Gly Phe Arg
580 585 590

Glu Ile Glu Asn Lys Ala Ile Gln Asp Pro Arg Lys Leu Leu Val Pro
595 600 605

Arg Gly Ser Pro His His His His His His
610 615

<210> 6

<211> 257
<212> PRT
<213> Artificial

<220>

<223> SC12 containing signal sequence, thrombin site, His tag

<400> 6

Met Leu Leu Phe Val Leu Thr Cys Leu Leu Ala Val Phe Pro Ala Ile
1 5 10 15

Ser Thr Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu
20 25 30

Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn
35 40 45

Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys
50 55 60

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

Arg Ala Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn
85 90 95

Ile Ala Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu
100 105 110

Gly Ile Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser
115 120 125

Gln Gly Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu
130 135 140

Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln
145 150 155 160

Lys Arg Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val

165

170

175

Ile Asp Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg
 180 185 190

Leu Asp Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn
 195 200 205

Gln Leu Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp
 210 215 220

Asp Ser Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro
 225 230 235 240

Glu Pro Lys Leu Leu Val Pro Arg Gly Ser Pro His His His His His
 245 250 255

His

<210> 7
 <211> 1857
 <212> DNA
 <213> Artificial

<220>
 <223> wild-type SC containing signal sequence, thrombin site, His tag

<400> 7
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 cccatatttg gtcccgagga ggtgaatagt gtggaaggta actcagtgtc catcacgtgc 120
 tactaccac ccacctctgt caaccggcac acccggaagt actggtgccg gcaggagct 180
 agagggtggct gcataaccct catctcctcg gagggctacg tctccagcaa atatgcaggc 240
 agggctaacc tcaccaactt cccggagaac ggcacatttg tggatgaacat tgcccagctg 300
 agccaggatg actccggggcg ctacaagtgt ggcctgggca tcaatagccg aggcctgtcc 360
 tttgatgtca gcctggaggt cagccagggt cctgggctcc taaatgacac taaagtctac 420

acagtggacc tgggcagaac ggtgaccatc aactgccctt tcaagactga gaatgctcaa	480
aagaggaagt ccttgtacaa gcagataggc ctgtaccctg tgctgggtcat cgactccagt	540
ggttatgtaa atcccaacta tacaggaaga atacgccttg atattcaggg tactggccag	600
ttactgttca gcgttgtcat caaccaactc aggctcagcg atgctgggca gtatctctgc	660
caggctgggg atgattccaa tagtaataag aagaatgctg acctccaagt gctaaagccc	720
gagcccgagc tggtttatga agacctgagg ggctcagtga ccttccactg tgccctgggc	780
cctgagggtg caaacgtggc caaatttctg tgccgacaga gcagtgggga aaactgtgac	840
gtggtcgtca acaccctggg gaagagggcc ccagcctttg agggcaggat cctgctcaac	900
ccccaggaca aggatggctc attcagtgtg gtgatcacag gcctgaggaa ggaggatgca	960
gggcgctacc tgttgaggagc ccattcggat ggtcagctgc aggaaggctc gcctatccag	1020
gcctggcaac tcttcgtcaa tgaggagtcc acgattcccc gcagccccac tgtggtgaag	1080
ggggtggcag gaggctctgt ggccgtgctc tgcccctaca accgtaagga aagcaaaagc	1140
atcaagtact ggtgtctctg ggaaggggcc cagaatggcc gctgccccct gctggtggac	1200
agcgaggggt gggttaaggc ccagtacgag ggccgcctct ccctgctgga ggagccaggc	1260
aacggcacct tctgtgtcat cctcaaccag ctcaccagcc gggacgccgg cttctactgg	1320
tgtctgacca acggcgatac tctctggagg accaccgtgg agatcaagat tatcgaagga	1380
gaaccaaacc tcaaggtacc agggaatgtc acggctgtgc tgggagagac tctcaaggctc	1440
ccctgtcact ttccatgcaa attctcctcg tacgagaaat actggtgcaa gtggaataac	1500
acgggctgcc aggccctgcc cagccaagac gaaggcccca gcaaggcctt cgtgaactgt	1560
gacgagaaca gccggcttgt ctccctgacc ctgaacctgg tgaccagggc tgatgagggc	1620
tggtactggt gtggagtga gaggggccac ttctatggag agactgcagc cgtctatgtg	1680
gcagttgaag agaggaaggc agcgggggtcc cgcgatgtca gcctagcgaa ggcagacgct	1740
gctcctgatg agaagggtgt agactctggt tttcgggaga ttgagaacaa agccattcag	1800
gatcccagga agcttctggt gcctcgcggt tcccctcacc accaccacca ccactaa	1857

<211> 774
<212> DNA
<213> Artificial

<220>

<223> SC12 containing signal sequence, thrombin site, His tag

<400> 8

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tactaccac ccacctctgt caaccggcac acccggaagt actggtgccg gcaggagct      180
agaggtggct gcataaccct catctcctcg gagggctacg tctccagcaa atatgcaggc      240
agggctaacc tcaccaactt cccggagaac ggcacatttg tggatgaacat tgcccagctg      300
agccaggatg actccgggcg ctacaagtgt ggcctgggca tcaatagccg aggcctgtcc      360
tttgatgtca gcctggaggt cagccagggt cctgggctcc taaatgacac taaagtctac      420
acagtggacc tgggcagaac ggtgaccatc aactgccctt tcaagactga gaatgctcaa      480
aagaggaagt cttgtacaa gcagataggc ctgtaccctg tgctggtcat cgactccagt      540
ggttatgtaa atcccaacta tacaggaaga atacgccttg atattcaggg tactggccag      600
ttactgttca gcgttgtcat caaccaactc aggctcagcg atgctgggca gtatctctgc      660
caggctgggg atgattccaa tagtaataag aagaatgctg acctccaagt gctaaagccc      720
gagcccaagc ttctggtgcc tcgcggttcc cctcaccacc accaccacca ctaa      774
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<210> 9
<211> 390
<212> DNA
<213> Homo sapiens

<400> 9

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cagaccctgt ccctcacctg cgttgtctct ggtggctcca tcaatcttgg taatgactac      120
tggaactgga tccggcagcc cgccgggaag gggctggagt gggttgggcg tatctattcc      180
agtgggagtg ccaagtacaa tccctccctc aagagtcgag tcaccatttc actagacacg      240
tccaagaacc agttctccct ggagctgacc tccgtgaccg ccgcagacac ggccgtgtat      300
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tactgtgcga gattttcggg gagttaccaa gatcatgatg cttttgatgt gtggggccag 360

gggacaatgg tcaccgtctc ttcagctagc 390

<210> 10

<211> 130

<212> PRT

<213> Homo sapiens

<400> 10

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

Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Val Val Ser Gly Gly
20 25 30

Ser Ile Asn Leu Gly Asn Asp Tyr Trp Asn Trp Ile Arg Gln Pro Ala
35 40 45

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

Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp Thr
65 70 75 80

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

Thr Ala Val Tyr Tyr Cys Ala Arg Phe Ser Gly Ser Tyr Gln Asp His
100 105 110

Asp Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

Ala Ser
130

<210> 11

<211> 330
 <212> DNA
 <213> Homo sapiens

<400> 11
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 ggagacagag tcaccatcac ttgccgggcg actcaggaca ttaacattgg tttagcctgg 120
 tatcagcaaa aaccagggaa agccccaagg ctctgtctcc attctgcgtc cacattggag 180
 agtgggggtcc catccagggtt cagtggcagt ggatctggga cggattacac tctcaccatc 240
 agcagcctac agcctgaaga ttttgcaact tattactgtc aacaatattt cagttccccg 300
 tacacttttg gccaggggac caagctggag 330

<210> 12
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 12

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

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

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

Pro Arg Leu Leu Leu His Ser Ala Ser Thr Leu Glu Ser Gly Val Pro
 50 55 60

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

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

Phe Ser Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu

100

105

110

<210> 13
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 13
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 tgggtccggc agccccagg gaagggactg gagtggattg gaaatatcta ttacagtggg 180
 accagcagcg acatccccta cagtgggagc tccagttaca acccctccct cgagagtcgc 240
 gtcaccatgt cagtagacac gtccaagaac cagttctccc tgacgctgag ctctgtgacc 300
 gctgcggaca cggccgttta ttactgtgcg agacttactc tgattcgggg agttattccc 360
 ccgtaccact ttgactgctg gggccaggga accctggtca ccgtctcctc agctagc 417

<210> 14
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 14

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

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ile Val Ser Asp Asp
 20 25 30

Ser Ile Arg Ser Ser Ser Trp Ser Trp Val Arg Gln Pro Pro Gly Lys
 35 40 45

Gly Leu Glu Trp Ile Gly Asn Ile Tyr Tyr Ser Gly Thr Ser Ser Asp
 50 55 60

Ile Pro Tyr Ser Gly Ser Ser Ser Tyr Asn Pro Ser Leu Glu Ser Arg
 65 70 75 80

Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu
85 90 95

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu
100 105 110

Thr Leu Ile Arg Gly Val Ile Pro Pro Tyr His Phe Asp Cys Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
130 135

<210> 15
<211> 399
<212> DNA
<213> Homo sapiens

<400> 15
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Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu
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Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu
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Phe Pro Pro Ser Ser
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