

SEQUENCE LISTING

<110> Glaxosmithkline Intellectual Property
Development Limited
Inserm
Institut Jean Paoli & Irene Calmettes
Universite dAix-Marseille
Centre National De La Recherche Scientifique

<120> ICOS BINDING PROTEINS

<130> PU65846

<150> 62/247,355
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<151> 2015-01-28

<160> 24

<170> FastSEQ for Windows Version 4.0

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<213> Murine

<400> 1
Asp Tyr Ala Met His
1 5

<210> 2
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Leu Ile Ser Ile Tyr Ser Asp His Thr Asn Tyr Asn Gln Lys Phe Gln
1 5 10 15
Gly

<210> 3
<211> 12
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<213> Murine

<400> 3

Asn Asn Tyr Gly Asn Tyr Gly Trp Tyr Phe Asp Val
1 5 10

<210> 4

<211> 10

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Ser Ala Ser Ser Ser Val Ser Tyr Met His
1 5 10

<210> 5

<211> 7

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Asp Thr Ser Lys Leu Ala Ser
1 5

<210> 6

<211> 9

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<400> 6

Phe Gln Gly Ser Gly Tyr Pro Tyr Thr
1 5

<210> 7

<211> 121

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<213> Artificial Sequence

<220>

<223> Artificially Synthesized Sequence

<400> 7

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Leu Ile Ser Ile Tyr Ser Asp His Thr Asn Tyr Asn Gln Lys Phe

50						55						60			
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Gly	Arg	Asn	Asn	Tyr	Gly	Asn	Tyr	Gly	Trp	Tyr	Phe	Asp	Val	Trp	Gly
		100						105					110		
Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser							
		115					120								

<210> 8
 <211> 106
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<220>
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<400> 8															
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	Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met
		20						25				30			
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr
		35					40				45				
Asp	Thr	Ser	Lys	Leu	Ala	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser
	50					55				60					
Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu
65				70					75					80	
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	Gly	Tyr	Pro	Tyr	Thr
			85					90					95		
Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys						
		100					105								

<210> 9
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<220>
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<400> 9															
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1			5					10						15	
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
		20						25					30		
Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
	35					40					45				
Thr	Asp	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
	50				55						60				

Glu	Trp	Met	Gly	Leu	Ile	Ser	Ile	Tyr	Ser	Asp	His	Thr	Asn	Tyr	Asn	65	70	75	80
Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser		85	90	95
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	100	105	110	
Tyr	Tyr	Cys	Gly	Arg	Asn	Asn	Tyr	Gly	Asn	Tyr	Gly	Trp	Tyr	Phe	Asp	115	120	125	
Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	130	135	140	
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	145	150	155	160
Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	165	170	175	
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	180	185	190	
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	195	200	205	
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	210	215	220	
Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	225	230	235	240
Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	245	250	255	
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	260	265	270	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	275	280	285	
Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	290	295	300	
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	305	310	315	320
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	325	330	335	
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	340	345	350	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	355	360	365	
Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	370	375	380	
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	385	390	395	400
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	405	410	415	
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	420	425	430	
Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	435	440	445	
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	450	455	460	
Leu	Gly	Lys														465			

<210> 10
 <211> 168
 <212> PRT
 <213> Homo Sapien

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

<210> 11
 <211> 19
 <212> PRT
 <213> Homo Sapien

<400> 11
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 Val His Ser

<210> 12
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Sequence

<400> 12
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1				5				10					15			
Val	His	Ser	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	
			20					25					30			
Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Ser	Ala	Ser	Ser	Ser	Val	
		35					40					45				
Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	
	50					55					60					
Leu	Ile	Tyr	Asp	Thr	Ser	Lys	Leu	Ala	Ser	Gly	Ile	Pro	Ala	Arg	Phe	
65					70					75					80	
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	
				85					90					95		
Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	Gly	Tyr	
			100					105					110			
Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val	
		115					120						125			
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	
	130					135					140					
Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	
145					150					155					160	
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	
				165				170						175		
Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	
			180					185					190			
Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	
	195					200						205				
Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	
	210					215					220					
Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys									
225					230											

<210> 13
 <211> 124
 <212> PRT
 <213> Murine

<400> 13																
Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	
1				5				10						15		
Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Ser	Tyr	
		20						25					30			
Trp	Ile	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	
		35					40					45				
Gly	Asn	Ile	Tyr	Pro	Ser	Asp	Ser	Tyr	Thr	Asn	Tyr	Asn	Gln	Met	Phe	
	50					55					60					
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Asn	Thr	Ala	Tyr	
65					70					75					80	
Met	Gln	Leu	Thr	Ser	Pro	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	
				85				90						95		
Thr	Arg	Trp	Asn	Leu	Ser	Tyr	Tyr	Phe	Asp	Asn	Asn	Tyr	Tyr	Leu	Asp	
			100					105					110			
Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser					
		115					120									

<210> 14
 <211> 109
 <212> PRT
 <213> Murine

<400> 14
 Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu
 1 5 10 15
 Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30
 Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
 35 40 45
 Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe
 50 55 60
 Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
 65 70 75 80
 Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Asn Asn
 85 90 95
 His Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> 15
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Sequence

<400> 15
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Leu Ile Ser Ile Tyr Ser Asp His Thr Asn Tyr Asn Gln Lys Phe
 50 55 60
 Gln Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Gly Arg Asn Asn Tyr Gly Asn Tyr Gly Trp Tyr Phe Asp Val Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 16
 <211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Sequence

<400> 16

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1			5					10					15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr
		20					25					30			
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Leu	Ile	Ser	Ile	Tyr	Ser	Asp	His	Thr	Asn	Tyr	Asn	Gln	Lys	Phe
	50				55					60					
Gln	Gly	Arg	Ala	Thr	Met	Thr	Val	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
65					70				75					80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Gly	Arg	Asn	Asn	Tyr	Gly	Asn	Tyr	Gly	Trp	Tyr	Phe	Asp	Val	Trp	Gly
		100						105					110		
Gln	Gly	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
		115				120					125				
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
	130				135					140					
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
145					150				155					160	
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
			165					170					175		
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
		180					185					190			
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
	195				200						205				
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
	210				215					220					
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
225					230				235					240	
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			245					250					255		
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
		260					265					270			
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	275					280					285				
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290				295					300					
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310				315					320	
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
			325					330					335		
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
		340					345					350			
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
		355					360					365			

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys
 450

<210> 17
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Sequence

<400> 17
 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 Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
 35 40 45
 Asp Thr Ser Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
 65 70 75 80
 Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Tyr Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 18
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Sequence

<400> 18
 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 Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr

<400> 20

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

<210> 21

<211> 1401

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Sequence

<400> 21

atgggctggt	cctgcatcat	cctgtttctg	gtggccaccg	ccaccggcgt	gcacagccag	60
gtgcagctgg	tgcagagcgg	agccgaggtg	aaaaagcccc	gctcaagcgt	gaaggtgagc	120
tgcaaggcca	gcggctacac	cttcaccgac	tacgctatgc	actgggtgag	gcaggccccc	180
ggccagggcc	tggagtggat	gggcctgata	agcatctaca	gcgaccacac	caactacaac	240
cagaagtcc	agggcagggc	gaccatcacc	gccgataaga	gcaccagcac	agcctacatg	300
gagctgagca	gcctgaggag	cgaagacacc	gccgtgtact	attgcggcag	gaacaactac	360
ggcaactacg	gctggtactt	cgacgtgtgg	ggccagggaa	ccactgtcac	cgtgagcagc	420
gccagcacca	agggccccag	cgtgttcccc	ctggccccct	gcagcagaag	caccagcgag	480
agcacagccg	ccctgggctg	cctgggtgaag	gactacttcc	ccgagcccgt	gaccgtgagc	540
tggaacagcg	gagccctgac	cagcggcgtg	cacaccttcc	ccgccgtgct	gcagagcagc	600
ggcctgtaca	gcctgagcag	cgtgggtgac	gtgcccagca	gcagcctggg	caccaagacc	660
tacacctgca	acgtggacca	caagcccagc	aacaccaagg	tggacaagcg	ggtggagagc	720
aagtacggcc	ctccctgccc	cccctgccct	gcccccgagt	tcgagggcgg	accctccgtg	780
ttcctgttcc	cccccaagcc	caaggacacc	ctgatgatca	gccggacccc	cgaggtgacc	840
tgcgtggtgg	tggacgtgag	ccaggaagat	cccgaggtcc	agttcaattg	gtacgtggac	900
ggcgtggagg	tgcacaacgc	caagaccaag	ccccgggagg	aacagttcaa	cagcacctac	960
cgggtggtgt	ccgtgctgac	cgtgctgcac	caggactggc	tgaacggcaa	agaatacaag	1020
tgcaaggtgt	ccaacaaggg	cctgcccagc	tccatcgaga	aaaccatcag	caaggccaag	1080
ggccagcctc	gggagcccca	ggtgtacacc	ctgcccccat	cccaggaaga	gatgaccaag	1140
aaccaggtgt	ccctgacctg	tctggtgaag	ggcttctacc	ccagcgacat	cgccgtggag	1200
tgggagagca	acggccagcc	cgagaacaac	tacaagacca	ccccccctgt	gctggacagc	1260
gacggcagct	tcttcctgta	cagcaggctg	accgtggaca	agagccggtg	gcaggaaggc	1320
aacgtcttta	gctgcagcgt	gatgcacgag	gccctgcaca	accactacac	ccagaagagc	1380
ctgagcctgt	ccctgggcaa	g				1401

<210> 22

<211> 696
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Sequence

<400> 22
 atgggctggt cctgcatcat cctgtttctg gtggccaccg ccaccggcgt gcacagcgag 60
 attgtgctga cccagagccc cgccaccctg agcctgagcc ccggcgaaaag ggcaaccctc 120
 agctgcagcg ccagcagcag cgtgagctac atgcactggt accagcagaa gcccggccag 180
 gcccctaggc tgctgatcta cgacacctcc aagctggcca gcggcatccc agccaggttc 240
 tcaggcagcg gcagcggcac cgactatact ctgaccatca gcagcctgga gcccaggagac 300
 ttcgccgtgt actactgctt ccagggaagc ggctaccctt acaccttcgg ccagggcacc 360
 aagctggaga tcaagcgtac ggtggccgcc cccagcgtgt tcattcttccc ccccagcgat 420
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 <212> PRT
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<220>
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 Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Leu Ile Ser Ile Tyr Ser Asp His Thr Asn Tyr Asn Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Gly Arg Asn Asn Tyr Gly Asn Tyr Gly Trp Tyr Phe Asp Val Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

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Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His		
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Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly		
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Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	Gly	Pro	Ser		
225					230					235					240		
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg		
			245						250					255			
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro		
		260						265					270				
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala		
	275						280					285					
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val		
	290				295						300						
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr		
305					310					315					320		
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr		
			325					330						335			
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu		
		340						345					350				
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys		
	355						360					365					
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser		
	370				375					380							
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp		
385				390						395				400			
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser		
			405						410				415				
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala		
		420					425					430					
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<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Sequence

<400> 24

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

65					70					75					80
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	Gly	Tyr	Pro	Tyr	Thr
				85					90					95	
Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro
			100					105					110		
Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr
		115					120					125			
Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys
	130					135					140				
Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu
145					150					155					160
Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser
				165					170					175	
Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala
			180				185						190		
Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe
	195						200					205			
Asn	Arg	Gly	Glu	Cys											
	210														