

SEQUENCE LISTING

<110> GILEAD BIOLOGICS, Inc.
 Fan, Peidong
 Yao, Lina
 Kang, Jong

<120> METHODS FOR TREATING CARDIOVASCULAR DISEASES

<130> 1068.PF

<150> US 62/010,929

<151> 2014-06-11

<160> 51

<170> PatentIn version 3.5

<210> 1

<211> 16

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

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Ser Arg Val Asp Gly Met Val Gly Asp Asp Pro Tyr Asn Pro Tyr Lys
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<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

<400> 2

Asp Thr Tyr Glu Arg Pro Arg Pro Gly Gly Arg Tyr Arg Pro Gly
 1 5 10 15

<210> 3

<211> 24

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

<400> 3

Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn Gly Gln Ser
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Asp Phe Arg Pro Lys Asn Gly Arg
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<210> 4
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 4
Glu Asp Thr Ser Cys Asp Tyr Gly Tyr His Arg Arg Phe Ala
1 5 10

<210> 5
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

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<210> 6
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<220>
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Asp Pro Tyr Tyr Ile Gln Ala Ser Thr Tyr Val Gln Lys Met Ser Met
1 5 10 15

Tyr Asn Leu Arg Cys
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<210> 7
<211> 21
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<213> Artificial Sequence

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Phe Met Leu Gln Cys
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<220>
 <223> Description of Artificial Sequence: Synthetic peptide

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<210> 9
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<400> 9
 Trp Glu Trp His Ser Cys His Gln His Tyr His
 1 5 10

<210> 10
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<400> 10
 Trp Glu Trp His Ser Cys His Gln His Tyr His
 1 5 10

<210> 11
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<220>
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<400> 11
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<210> 12
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<220>

<223> Description of Artificial Sequence: Synthetic peptide

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<210> 13

<211> 11

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<210> 14

<211> 17

<212> PRT

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<223> Description of Artificial Sequence: Synthetic peptide

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Tyr

<210> 15

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<212> PRT

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1 5 10 15

Tyr

<210> 16

<211> 17

<212> PRT

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Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp Val Pro Pro Gly Asp
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Tyr

<210> 17

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<212> PRT

<213> Artificial Sequence

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Tyr

<210> 18

<211> 17

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

<400> 18

Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp Val Gly Pro Gly Asn
1 5 10 15

Tyr

<210> 19

<211> 417

<212> PRT

<213> Homo sapiens

<400> 19

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

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

Tyr

<210> 20
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 <212> PRT
 <213> Homo sapiens

<400> 20

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

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65	Asn	Arg	Thr	Ala	Ala	70	Ala	Arg	Thr	Arg	Thr	75	Ala	Gly	Ser	Ser	80	Gly	Val
				85	Pro	Arg	Pro	Thr	Ala	100	Arg	His	Trp	Phe	Gln	95	Ala	Gly	
				100	Arg	Ala	Arg	Glu	Ala	105	Gly	Ala	Ser	Arg	Ala	110	Glu	Asn	
				115	Pro	Gly	Glu	Val	Pro	120	Ala	Leu	Ser	Asn	Leu	Arg	Pro	Pro	
				130	Val	Asp	Gly	Met	Val	135	Gly	Asp	Asp	Pro	Tyr	Asn	Pro	Tyr	
				145	Arg	Val	Asp	Asn	Pro	150	Tyr	Tyr	Asn	Tyr	Tyr	Asp	Thr	Glu	
				165	Asp	Asp	Asn	Pro	Tyr	170	Tyr	Tyr	Asp	Thr	Tyr	Asp	Thr	Glu	
				180	Gly	Arg	Tyr	Arg	Pro	185	Gly	Tyr	Gly	Thr	Gly	Thr	Tyr	Phe	
				195	Leu	Pro	Asp	Leu	Val	200	Ala	Asp	Pro	Tyr	Tyr	Ile	Gln	Ala	
				210	Tyr	Val	Gln	Lys	Met	215	Ser	Met	Tyr	Asn	Leu	Arg	Cys	Ala	
				225	Glu	Asn	Cys	Leu	Ala	230	Ser	Thr	Ala	Tyr	Arg	Ala	Asp	Val	
				245	Val	Leu	Leu	Arg	Phe	250	Pro	Gln	Arg	Val	Lys	Asn	Gln	Asp	
				260	Thr	Ser	Asp	Phe	Leu	265	Pro	Arg	Tyr	Ser	Trp	Glu	Trp	Gln	
				275	Ser	Cys	His	Gln	His	280	Ser	Met	Asp	Glu	Phe	Ser	His	Tyr	
				290	Leu	Leu	Asp	Ala	Asn	295	Thr	Gln	Arg	Arg	Val	Ala	Glu	Gly	
				305	Ala	Ser	Phe	Cys	Leu	310	Glu	Asp	Thr	Ser	Cys	Asp	Tyr	Gly	
				325	Arg	Phe	Ala	Cys	Thr	330	Ala	His	Thr	Gln	Gly	Leu	Ser	Pro	
				340	Asp	Thr	Tyr	Gly	Ala	345	Asp	Ile	Asp	Cys	Gln	Trp	Ile	Asp	
				355	Val	Lys	Pro	Gly	Asn	360	Tyr	Ile	Leu	Lys	Val	Ser	Val	Asn	
				370	Leu	Val	Pro	Glu	Ser	375	Thr	Asn	Asn	Val	Val	Arg	Cys	Asp	
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					Tyr														

<210> 21
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 <213> Homo sapiens

<400> 21

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

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Phe Pro Gln Arg Val Lys Asn Gln Gly Thr Ser Asp Phe Leu Pro Ser
 Arg Pro Arg Tyr Ser Trp Glu Trp His Ser Cys His Gln His Tyr His
 Ser Met Asp Glu Phe Ser His Tyr Asp Leu Leu Asp Ala Asn Thr Gln
 Arg Arg Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu Asp Thr
 Ser Cys Asp Tyr Gly Tyr His Arg Arg Phe Ala Cys Thr Ala His Thr
 Gln Gly Leu Ser Pro Gly Cys Tyr Asp Thr Tyr Gly Ala Asp Ile Asp
 Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn Tyr Ile Leu
 Lys Val Ser Val Asn Pro Ser Tyr Leu Val Pro Glu Ser Asp Tyr Thr
 Asn Asn Val Val Arg Cys Asp Ile Arg Tyr Thr Gly His His Ala Tyr
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<210> 22

<211> 774

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<213> Homo sapiens

<400> 22

Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu
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 Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu Tyr His Gln Pro Gln
 Ala Pro Ala Asn Val Ala Lys Ile Gln Leu Arg Leu Ala Gly Gln Lys
 Arg Lys His Ser Glu Gly Arg Val Glu Val Tyr Tyr Asp Gly Gln Trp
 Gly Thr Val Cys Asp Asp Phe Ser Ile His Ala Ala His Val Val
 Cys Arg Glu Leu Gly Tyr Val Glu Ala Lys Ser Trp Thr Ala Ser Ser
 Ser Tyr Gly Lys Gly Glu Gly Pro Ile Trp Leu Asp Asn Leu His Cys
 Thr Gly Asn Glu Ala Thr Leu Ala Ala Cys Thr Ser Asn Gly Trp Gly
 Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val Cys Ser Asp
 Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile Asn Gln Ile
 Glu Asn Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg Ala Ile Leu
 Ser Thr Tyr Arg Lys Arg Thr Pro Val Met Glu Gly Tyr Val Glu Val
 Lys Glu Gly Lys Thr Trp Lys Gln Ile Cys Asp Lys His Trp Thr Ala
 Lys Asn Ser Arg Val Val Cys Gly Met Phe Gly Phe Pro Gly Glu Arg
 Thr Tyr Asn Thr Lys Val Tyr Lys Met Phe Ala Ser Arg Arg Lys Gln
 Arg Tyr Trp Pro Phe Ser Met Asp Cys Thr Gly Thr Glu Ala His Ile
 Ser Ser Cys Lys Leu Gly Pro Gln Val Ser Leu Asp Pro Met Lys Asn

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Val	Thr	Cys	Glu	Asn	Gly	Leu	Pro	Ala	Val	Val	Ser	Cys	Val	Pro	Gly
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Gln	Val	Phe	Ser	Pro	Asp	Gly	Pro	Ser	Arg	Phe	Arg	Lys	Ala	Tyr	Lys
305					310					315					320
Pro	Glu	Gln	Pro	Leu	Val	Arg	Leu	Arg	Gly	Gly	Ala	Tyr	Ile	Gly	Glu
				325					330					335	
Gly	Arg	Val	Glu	Val	Leu	Lys	Asn	Gly	Glu	Trp	Gly	Thr	Val	Cys	Asp
			340					345					350		
Asp	Lys	Trp	Asp	Leu	Val	Ser	Ala	Ser	Val	Val	Cys	Arg	Glu	Leu	Gly
		355					360					365			
Phe	Gly	Ser	Ala	Lys	Glu	Ala	Val	Thr	Gly	Ser	Arg	Leu	Gly	Gln	Gly
	370					375					380				
Ile	Gly	Pro	Ile	His	Leu	Asn	Glu	Ile	Gln	Cys	Thr	Gly	Asn	Glu	Lys
385					390					395					400
Ser	Ile	Ile	Asp	Cys	Lys	Phe	Asn	Ala	Glu	Ser	Gln	Gly	Cys	Asn	His
				405					410					415	
Glu	Glu	Asp	Ala	Gly	Val	Arg	Cys	Asn	Thr	Pro	Ala	Met	Gly	Leu	Gln
			420					425					430		
Lys	Lys	Leu	Arg	Leu	Asn	Gly	Gly	Arg	Asn	Pro	Tyr	Glu	Gly	Arg	Val
		435					440					445			
Glu	Val	Leu	Val	Glu	Arg	Asn	Gly	Ser	Leu	Val	Trp	Gly	Met	Val	Cys
	450					455					460				
Gly	Gln	Asn	Trp	Gly	Ile	Val	Glu	Ala	Met	Val	Val	Cys	Arg	Gln	Leu
465					470					475					480
Gly	Leu	Gly	Phe	Ala	Ser	Asn	Ala	Phe	Gln	Glu	Thr	Trp	Tyr	Trp	His
				485					490					495	
Gly	Asp	Val	Asn	Ser	Asn	Lys	Val	Val	Met	Ser	Gly	Val	Lys	Cys	Ser
			500					505					510		
Gly	Thr	Glu	Leu	Ser	Leu	Ala	His	Cys	Arg	His	Asp	Gly	Glu	Asp	Val
		515					520					525			
Ala	Cys	Pro	Gln	Gly	Gly	Val	Gln	Tyr	Gly	Ala	Gly	Val	Ala	Cys	Ser
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Glu	Thr	Ala	Pro	Asp	Leu	Val	Leu	Asn	Ala	Glu	Met	Val	Gln	Gln	Thr
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Thr	Tyr	Leu	Glu	Asp	Arg	Pro	Met	Phe	Met	Leu	Gln	Cys	Ala	Met	Glu
				565					570					575	
Glu	Asn	Cys	Leu	Ser	Ala	Ser	Ala	Ala	Gln	Thr	Asp	Pro	Thr	Thr	Gly
			580					585					590		
Tyr	Arg	Arg	Leu	Leu	Arg	Phe	Ser	Gln	Ile	His	Asn	Asn	Gly	Gln	
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Ser	Asp	Phe	Arg	Pro	Lys	Asn	Gly	Arg	His	Ala	Trp	Ile	Trp	His	Asp
	610					615					620				
Cys	His	Arg	His	Tyr	His	Ser	Met	Glu	Val	Phe	Thr	His	Tyr	Asp	Leu
625					630					635					640
Leu	Asn	Leu	Asn	Gly	Thr	Lys	Val	Ala	Glu	Gly	His	Lys	Ala	Ser	Phe
				645					650					655	
Cys	Leu	Glu	Asp	Thr	Glu	Cys	Glu	Gly	Asp	Ile	Gln	Lys	Asn	Tyr	Glu
			660					665					670		
Cys	Ala	Asn	Phe	Gly	Asp	Gln	Gly	Ile	Thr	Met	Gly	Cys	Trp	Asp	Met
		675					680					685			
Tyr	Arg	His	Asp	Ile	Asp	Cys	Gln	Trp	Val	Asp	Ile	Thr	Asp	Val	Pro
	690					695					700				
Pro	Gly	Asp	Tyr	Leu	Phe	Gln	Val	Val	Ile	Asn	Pro	Asn	Phe	Glu	Val
705					710					715					720
Ala	Glu	Ser	Asp	Tyr	Ser	Asn	Asn	Ile	Met	Lys	Cys	Arg	Ser	Arg	Tyr
				725					730					735	
Asp	Gly	His	Arg	Ile	Trp	Met	Tyr	Asn	Cys	His	Ile	Gly	Gly	Ser	Phe
			740					745					750		
Ser	Glu	Glu	Thr	Glu	Lys	Lys	Phe	Glu	His	Phe	Ser	Gly	Leu	Leu	Asn
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Asn	Gln	Leu	Ser	Pro	Gln										
770															

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<210> 23
 <211> 1604
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
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ctgcgcgct agtgcaactgc gccccctccc ccgcccggcca acagcagccc ccgcccgcgagc 180
cgccggcgcc tccggggcgcc tggcgccagc agatccaatg ggagaacaac gggcaggtgt 240
tcagcttgct gaggctgggc tcacagtacc agcctcagcg ccgcccgggac ccgggcgccc 300
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gccgccccag gccaccgcgc cgtcactggt tccaagctgg ctactcgaca tctagagccc 480
ggaacgtgg cgcctcgcgc gcggagaacc agacagcgcc gggagaagtt cctgcgctca 540
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ctgggggcag gtaccggccc ggatacggca ctggctactt ccagtacggt ctcccagacc 720
tggtggccga cccctactac atccaggcgt ccacgtacgt gcagaagatg tccatgtaca 780
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caacaaaaga atttttgttt ggactgtttt caataacaaa gcacataact ggattttgaa 1500
cgcttaagtc aatcattact tggaaatttn taatgtttat tattttacatc aactttgtga 1560
attaacacag tgtttcaatt ctgtaatttc atatttgact cttt 1604
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<210> 24
 <211> 417
 <212> PRT
 <213> Homo sapiens

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<400> 24
Met Arg Phe Ala Trp Thr Val Leu Leu Leu Gly Pro Leu Gln Leu Cys
1      5      10      15
Ala Leu Val His Cys Ala Pro Pro Ala Ala Gly Gln Gln Gln Pro Pro
20      25      30
Arg Glu Pro Pro Ala Ala Pro Gly Ala Trp Arg Gln Gln Ile Gln Trp
35      40      45
Glu Asn Asn Gly Gln Val Phe Ser Leu Leu Ser Leu Gly Ser Gln Tyr
50      55      60
Gln Pro Gln Arg Arg Arg Asp Pro Gly Ala Ala Val Pro Gly Ala Ala
65      70      75      80
Asn Ala Ser Ala Gln Gln Pro Arg Thr Pro Ile Leu Leu Ile Arg Asp
85      90      95
Asn Arg Thr Ala Ala Ala Arg Thr Arg Thr Ala Gly Ser Ser Gly Val
100     105     110
Thr Ala Gly Arg Pro Arg Pro Thr Ala Arg His Trp Phe Gln Ala Gly
115     120     125
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Tyr	Ser	Thr	Ser	Arg	Ala	Arg	Glu	Arg	Gly	Ala	Ser	Arg	Ala	Glu	Asn
130	130					135					140				
Gln	Thr	Ala	Pro	Gly	Glu	Val	Pro	Ala	Leu	Ser	Asn	Leu	Arg	Pro	Pro
145				150						155					160
Ser	Arg	Val	Asp	Gly	Met	Val	Gly	Asp	Asp	Pro	Tyr	Asn	Pro	Tyr	Lys
			165					170						175	
Tyr	Ser	Asp	Asp	Asn	Pro	Tyr	Tyr	Asn	Tyr	Tyr	Asp	Thr	Tyr	Glu	Arg
		180						185					190		
Pro	Arg	Pro	Gly	Gly	Arg	Tyr	Arg	Pro	Gly	Tyr	Gly	Thr	Gly	Tyr	Phe
		195					200					205			
Gln	Tyr	Gly	Leu	Pro	Asp	Leu	Val	Ala	Asp	Pro	Tyr	Tyr	Ile	Gln	Ala
	210					215					220				
Ser	Thr	Tyr	Val	Gln	Lys	Met	Ser	Met	Tyr	Asn	Leu	Arg	Cys	Ala	Ala
225					230					235					240
Glu	Glu	Asn	Cys	Leu	Ala	Ser	Thr	Ala	Tyr	Arg	Ala	Asp	Val	Arg	Asp
			245						250					255	
Tyr	Asp	His	Arg	Val	Leu	Leu	Arg	Phe	Pro	Gln	Arg	Val	Lys	Asn	Gln
		260						265					270		
Gly	Thr	Ser	Asp	Phe	Leu	Pro	Ser	Arg	Pro	Arg	Tyr	Ser	Trp	Glu	Trp
		275					280					285			
His	Ser	Cys	His	Gln	His	Tyr	His	Ser	Met	Asp	Glu	Phe	Ser	His	Tyr
	290					295					300				
Asp	Leu	Leu	Asp	Ala	Asn	Thr	Gln	Arg	Arg	Val	Ala	Glu	Gly	His	Lys
305					310					315					320
Ala	Ser	Phe	Cys	Leu	Glu	Asp	Thr	Ser	Cys	Asp	Tyr	Gly	Tyr	His	Arg
			325						330					335	
Arg	Phe	Ala	Cys	Thr	Ala	His	Thr	Gln	Gly	Leu	Ser	Pro	Gly	Cys	Tyr
			340					345					350		
Asp	Thr	Tyr	Gly	Ala	Asp	Ile	Asp	Cys	Gln	Trp	Ile	Asp	Ile	Thr	Asp
		355					360					365			
Val	Lys	Pro	Gly	Asn	Tyr	Ile	Leu	Lys	Val	Ser	Val	Asn	Pro	Ser	Tyr
	370					375					380				
Leu	Val	Pro	Glu	Ser	Asp	Tyr	Thr	Asn	Asn	Val	Val	Arg	Cys	Asp	Ile
385					390					395					400
Arg	Tyr	Thr	Gly	His	His	Ala	Tyr	Ala	Ser	Gly	Cys	Thr	Ile	Ser	Pro
				405					410					415	

Tyr

<210> 25
 <211> 1254
 <212> DNA
 <213> Homo sapiens

<400> 25

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gcctggcgcc	agcagatcca	atgggagaac	aacgggcagg	tggtcagctt	gctgagcctg	180
ggctcacagt	accagcctca	gcgccgccg	gacccgggcg	ccgccgtccc	tggtgcagcc	240
aacgcctccg	cccagcagcc	ccgcactccg	atcctgctga	tccgcgacaa	ccgcaccgcc	300
gcggcgcgaa	cgcgacggc	cggtcatct	ggagtcaccg	ctggccgccc	caggcccacc	360
gcccgtcact	ggttccaagc	tggctactcg	acatctagag	cccgcgaacg	tggcgccctg	420
cgcgcgagaa	accagacagc	gccgggagaa	gttcctgcgc	tcagtaacct	gcggccgccc	480
agccgcgtgg	acggcatggt	gggcgacgac	ccttacaacc	cctacaagta	ctctgacgac	540
aacccttatt	acaactacta	cgatacttat	gaaaggccca	gacctggggg	caggtaccgg	600
cccggatacg	gcactggcta	cttccagtac	ggctctccag	acctgggtgg	cgacccttac	660
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gaggaaaact	gtctggccag	tacagcatac	agggcagatg	tcagagatta	tgatcacagg	780
gtgctgctca	gatttcccca	aagagtgaag	aaccaaggga	catcagattt	cttaccacag	840
cgaccaagat	attcctggga	atggcacagt	tgatcatcaac	attaccacag	tatggatgag	900
tttagccact	atgacctgct	tgatgccaac	acccagagga	gagtggctga	aggccacaaa	960
gcaagtttct	gtcttgaaga	cacatcctgt	gactatggct	accacaggcg	atttgcattgt	1020

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actgcacaca	cacagggatt	gagtcctggc	tgttatgata	cctatggtgc	agacatagac	1080
tgccagtgga	ttgatattac	agatgtaaaa	cctggaaact	atatacctaaa	ggtcagtgta	1140
aaccccagct	acctgggttc	tgaatctgac	tataccaaca	atgttgtgcg	ctgtgacatt	1200
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<210> 26

<211> 417

<212> PRT

<213> Homo sapiens

<400> 26

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

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405 410 415

Tyr

<210> 27
 <211> 1780
 <212> DNA
 <213> Homo sapiens

<400> 27

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gctcgcctcc	ttggttgaag	atcttctcctt	ccctcacgtg	atctgagccc	cgttttttatt	180
ttctgtgagc	cacgtcctcc	tcgagcgggg	tcaatctggc	aaaaggagtg	atgcgcttcg	240
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accagcctca	gcgccgccgg	gacccgggcg	ccgccgtccc	tggtgcagcc	aacgcctccg	480
cccagcagcc	ccgcactccg	atcctgctga	tccgcgacaa	ccgcaccgcc	gcggggcgaa	540
cgcggaaggc	gggtcctatc	ggagtcaccg	ctggccgccc	caggcccacc	gcccgtcact	600
ggttccaagc	tggctactcg	acatctagag	cccgcgaagc	tgggccctcg	cgcgcgagga	660
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cgtccacgta	cgtgcagaag	atgtccatgt	acaacctgag	atgcgcggcg	gaggaaaact	960
gtctggccag	tacagcatac	agggcagatg	tcagagatta	tgatcacagg	gtgctgctca	1020
gatttcccca	aagagtgaag	aaccaaggga	catcagattt	cttaccagc	cgaccaagat	1080
attcctggga	atggcacagt	tgatcatcaac	attaccacag	tatggatgag	tttagccact	1140
tgtacctgct	tgatgccaac	acccagagga	gatgggctga	aggccacaaa	gcaagtttct	1200
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cacagggatt	gagtcctggc	tggttatgata	cctatggtgc	agacatagac	tgccagtggg	1320
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gacatcatgc	gtatgcctca	ggctgcacaa	tttcaccgta	ttagaaggca	aagcaaaaact	1500
cccaatggat	aaatcagtag	ctggtgttct	gaagtgggaa	aaaatagact	aacttcagta	1560
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<210> 28
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 28

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

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

Tyr

<210> 29
 <211> 1935
 <212> DNA
 <213> Homo sapiens

<400> 29

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actgagatac	ccgtgctccg	ctcgccctct	tggttgaaga	tttctccttc	cctcacgtga	180
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cggccgccc	gccgcgtgga	cggcatgggtg	ggcgacgacc	cttacaaccc	ctacaagtac	780
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aggtaccggc	ccggatacgg	cactggctac	ttccagtagc	gtctcccaga	cctggtggcc	900
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gatcacaggg	tgctgctcag	atttcccca	agagtgaaaa	accaagggac	atcagatttc	1080
ttaccagcc	gaccaagata	ttcctgggaa	tggcacagtt	gtcatcaaca	ttaccacagt	1140
atggatgagt	ttagccacta	tgacctgctt	gatgccaaca	cccagaggag	agtggctgaa	1200
ggccacaaag	caagtttctg	tcttgaagac	acatcctgtg	actatggcta	ccacaggcga	1260
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gtcagtgtaa	accccagcta	cctggttcct	gaatctgact	ataccaacaa	tgttgtgcgc	1440
tgtgacattc	gctacacagg	acatcatgcg	tatgcctcag	gctgcacaat	ttcaccgtat	1500
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ccttttgaaa	ttgtagtgc	aaatgggtcag	tattatctaa	atgaatgagc	caaatgtgact	1860
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<210> 30
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 30
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 35 40 45
 Glu Asn Asn Gly Gln Val Phe Ser Leu Leu Ser Leu Gly Ser Gln Tyr
 50 55 60
 Gln Pro Gln Arg Arg Arg Asp Pro Gly Ala Ala Val Pro Gly Ala Ala
 65 70 75 80
 Asn Ala Ser Ala Gln Gln Pro Arg Thr Pro Ile Leu Leu Ile Arg Asp
 85 90 95
 Asn Arg Thr Ala Ala Ala Arg Thr Arg Thr Ala Gly Ser Ser Gly Val
 100 105 110
 Thr Ala Gly Arg Pro Arg Pro Thr Ala Arg His Trp Phe Gln Ala Gly
 115 120 125
 Tyr Ser Thr Ser Arg Ala Arg Glu Ala Gly Ala Ser Arg Ala Glu Asn
 130 135 140
 Gln Thr Ala Pro Gly Glu Val Pro Ala Leu Ser Asn Leu Arg Pro Pro
 145 150 155 160
 Ser Arg Val Asp Gly Met Val Gly Asp Asp Pro Tyr Asn Pro Tyr Lys
 165 170 175
 Tyr Ser Asp Asp Asn Pro Tyr Tyr Asn Tyr Tyr Asp Thr Tyr Glu Arg
 180 185 190
 Pro Arg Pro Gly Gly Arg Tyr Arg Pro Gly Tyr Gly Thr Gly Tyr Phe
 195 200 205
 Gln Tyr Gly Leu Pro Asp Leu Val Ala Asp Pro Tyr Tyr Ile Gln Ala
 210 215 220
 Ser Thr Tyr Val Gln Lys Met Ser Met Tyr Asn Leu Arg Cys Ala Ala
 225 230 235 240
 Glu Glu Asn Cys Leu Ala Ser Thr Ala Tyr Arg Ala Asp Val Arg Asp
 245 250 255
 Tyr Asp His Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln
 260 265 270
 Gly Thr Ser Asp Phe Leu Pro Ser Arg Pro Arg Tyr Ser Trp Glu Trp
 275 280 285
 His Ser Cys His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr
 290 295 300

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Asp	Leu	Leu	Asp	Ala	Asn	Thr	Gln	Arg	Arg	Val	Ala	Glu	Gly	His	Lys
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Ala	Ser	Phe	Cys	Leu	Glu	Asp	Thr	Ser	Cys	Asp	Tyr	Gly	Tyr	His	Arg
				325					330					335	
Arg	Phe	Ala	Cys	Thr	Ala	His	Thr	Gln	Gly	Leu	Ser	Pro	Gly	Cys	Tyr
			340					345					350		
Asp	Thr	Tyr	Gly	Ala	Asp	Ile	Asp	Cys	Gln	Trp	Ile	Asp	Ile	Thr	Asp
		355				360						365			
Val	Lys	Pro	Gly	Asn	Tyr	Ile	Leu	Lys	Val	Ser	Val	Asn	Pro	Ser	Tyr
	370					375					380				
Leu	Val	Pro	Glu	Ser	Asp	Tyr	Thr	Asn	Asn	Val	Val	Arg	Cys	Asp	Ile
385					390					395					400
Arg	Tyr	Thr	Gly	His	His	Ala	Tyr	Ala	Ser	Gly	Cys	Thr	Ile	Ser	Pro
				405					410					415	

Tyr

<210> 31
 <211> 1322
 <212> DNA
 <213> Homo sapiens

<400> 31

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cgagccgccc	gcggctccgg	gcgcctggcg	ccagcagatc	caatgggaga	acaacgggca	180
ggtgttcagc	ttgctgagcc	tgggtcacac	gtaccagcct	cagcgccgcc	gggacccggg	240
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cgctggccgc	cccaggccca	ccgcccgtca	ctggttccaa	gctggctact	cgacatctag	420
agccccgcga	gctggcgctt	cgcgcgcgga	gaaccagaca	gcgccgggag	aagttcctgc	480
gctcagtaac	ctgcggccgc	ccagccgcgt	ggacggcatg	gtgggcgacg	acccttaca	540
cccctacaag	tactctgacg	acaaccctta	ttacaactac	tacgatactt	atgaaaggcc	600
cagacctggg	ggcaggtacc	ggcccggata	cggcactggc	tacttccagt	acggtctccc	660
agacctggtg	gccgaccctt	actacatcca	ggcgtccacg	tacgtgcaga	agatgtccat	720
gtacaacctg	agatgcgcgg	cggaggaaaa	ctgtctggcc	agtacagcat	acagggcaga	780
tgctcagagat	tatgatcaca	gggtgctgct	cagatttccc	caaagagtga	aaaaccaagg	840
gacatcagat	ttcttaccca	gccgaccaag	atattcctgg	gaatggcaca	gttgatcatca	900
acattaccac	agtatggatg	agtttagcca	ctatgacctg	cttgatgcca	acaccagag	960
gagagtggct	gaaggccaca	aagcaagttt	ctgtcttgaa	gacacatcct	gtgactatgg	1020
ctaccacagg	cgatttgcat	gtactgcaca	cacacagggg	ttgagtcctg	gctgttatga	1080
tacctatggt	gcagacatag	actgccagtg	gattgatatt	acagatgtaa	aacctggaaa	1140
ctatatccta	aaggtcagtg	taaaccaccg	ctacctgggt	cctgaatctg	actataccaa	1200
caatgtttgtg	cgctgtgaca	ttcgctacac	aggacatcat	gcgtatgcct	caggctgcac	1260
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ct						1322

<210> 32
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 32

Met	Arg	Phe	Ala	Trp	Thr	Val	Leu	Leu	Leu	Gly	Pro	Leu	Gln	Leu	Cys
1			5					10					15		
Ala	Leu	Val	His	Cys	Ala	Pro	Pro	Ala	Ala	Gly	Gln	Gln	Gln	Pro	Pro
			20					25				30			
Arg	Glu	Pro	Pro	Ala	Ala	Pro	Gly	Ala	Trp	Arg	Gln	Gln	Ile	Gln	Trp
		35				40					45				
Glu	Asn	Asn	Gly	Gln	Val	Phe	Ser	Leu	Leu	Ser	Leu	Gly	Ser	Gln	Tyr
50					55			60							

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

Tyr

<210> 33
 <211> 1325
 <212> DNA
 <213> Homo sapiens

<400> 33

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cgagccgccc	gcggctccgg	gcgcctggcg	ccagcagatc	caatgggaga	acaacgggca	180
ggtgttcagc	ttgctgagcc	tgggctcaca	gtaccagcct	cagcgccgcc	gggacccggg	240
cgccgcccgc	cctggtgcag	ccaacgcctc	cgcccagcag	ccccgcactc	cgatcctgct	300
gatccgcgac	aaccgcaccg	ccgcggcgcg	aacgcggacg	gccggctcat	ctggagtcac	360
cgctggccgc	cccaggccca	ccgcccgtca	ctggttccaa	gctggctact	cgacatctag	420
agcccgcgaa	gctggcgccct	cgcgcgcgga	gaaccagaca	gcgccgggag	aagttcctgc	480
gctcagtaac	ctgcggccgc	ccagccgcgt	ggacggcatg	gtgggcgacg	acccttaca	540
cccctacaag	tactctgacg	acaaccctta	ttacaactac	tacgatactt	atgaaaggcc	600
cagacctggg	ggcaggtacc	ggcccggata	cggcactggc	tacttccagt	acggtctccc	660

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agacctgggtg	gccgaccct	actacatcca	ggcgtccacg	tacgtgcaga	agatgtccat	720
gtacaacctg	agatgcgcgg	cggaggaaaa	ctgtctggcc	agtacagcat	acagggcaga	780
tgtcagagat	tatgatcaca	gggtgctgct	cagatttccc	caaagagtga	aaaaccaagg	840
gacatcagat	ttcttaccca	gccgaccaag	atattcctgg	gaatggcaca	gttgatcatca	900
acattaccac	agtatggatg	agtttagcca	ctatgacctg	cttgatgcca	acaccagag	960
gagagtggct	gaaggccaca	aagcaagttt	ctgtcttgaa	gacacatcct	gtgactatgg	1020
ctaccacagg	cgatttgcag	gtactgcaca	cacacagggg	ttgagtcctg	gctgttatga	1080
tacctatggt	gcagacatag	actgccagtg	gattgatatt	acagatgtaa	aacctggaaa	1140
ctatatccta	aaggtcagtg	taaaccaccag	ctacctgggt	cctgaatctg	actataccaa	1200
caatgtttgtg	cgctgtgaca	ttcgctacac	aggacatcat	gcgtatgcct	caggctgcac	1260
aatttcaccg	tattagaagg	caaagcaaaa	ctcccaatgg	ataaatcagt	gcctgggtgtt	1320
ctgaa						1325

<210> 34
 <211> 407
 <212> PRT
 <213> Homo sapiens

<400> 34

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

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Trp	Ile	Asp	Ile	Thr	Asp	Val	Lys	Pro	Gly	Asn	Tyr	Ile	Leu	Lys	Val
		355					360					365			
Ser	Val	Asn	Pro	Ser	Tyr	Leu	Val	Pro	Glu	Ser	Asp	Tyr	Thr	Asn	Asn
	370					375					380				
Val	Val	Arg	Cys	Asp	Ile	Arg	Tyr	Thr	Gly	His	His	Ala	Tyr	Ala	Ser
385					390					395					400
Gly	Cys	Thr	Ile	Ser	Pro	Tyr									
				405											

<210> 35
 <211> 842
 <212> DNA
 <213> Homo sapiens

<400> 35

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cgccgtccct	ggtgcagcca	acgcctccgc	ccagcagccc	cgactccga	tcctgctgat	120
ccgcgacaac	cgcaccgccg	cggcgcgaaac	gcggacggcc	ggctcatctg	gagtcaccgc	180
tgccgcccc	aggcccaccg	cccgtcactg	gttccaagct	ggctactcga	catctagagc	240
ccgcaagct	ggcgctcgc	gcgcggagaa	ccagacagcg	ccgggagaag	ttcctgcgct	300
cagtaacctg	cgccgcccc	gccgcgtgga	cggcatggtg	ggcgacgacc	cttacaaccc	360
ctacaagtac	tctgacgaca	acccttatta	caactactac	gatacttatg	aaaggccag	420
acctgggggc	aggtaccggc	ccggatacgg	caactggtac	ttccagtacg	gtaagtaccc	480
ccaagtccgc	tggaagcacc	cgtgcacctg	gtccccagct	atgtggcttc	ttctcgacgt	540
ggctgcctgg	gcgcggcggg	ccccggtcct	cgcagatccg	acccctcccc	acgcgcctgc	600
agtggcagcc	ctggaatcca	gtgcaaaccg	cgcgctctggc	ccctcctgct	tccttttcac	660
attgctttgc	agtcccgggg	gtccccagtt	ctcttgctgt	cctccgctcc	actctgcagt	720
cccgggtggc	gaaggggtgag	gagtaagggg	cctagagggg	tagggagttg	gagcgggggg	780
cgccgggttg	tttactgct	gcgcccgtcg	cctgctgacg	tttaggtctc	ccagacctgg	840
tg						842

<210> 36
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 36

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

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<210> 37
 <211> 135
 <212> PRT
 <213> Mus sp.

<400> 37
 Met Glu Trp Ser Arg Val Phe Ile Phe Leu Leu Ser Val Thr Ala Gly
 1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
 20 25 30

Pro Gly Thr Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe
 35 40 45

Thr Tyr Tyr Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn
 65 70 75 80

Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
 100 105 110

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

Thr Thr Leu Thr Val Ser Ser
 130 135

<210> 38
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 38
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Ala
 1 5 10 15

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

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

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Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asn Trp Met Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 39

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 39

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

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

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

Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu 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 Phe Cys
85 90 95

Ala Arg Asn Trp Met Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

467600_1

<210> 40
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 40
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Ala 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 Phe Cys
85 90 95

Ala Arg Asn Trp Met Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 41
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 41
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys 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

Ala Arg Asn Trp Met Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 42
<211> 132
<212> PRT
<213> Mus sp.

<400> 42
Met Arg Cys Leu Ala Glu Phe Leu Gly Leu Leu Val Leu Trp Ile Pro
1 5 10 15

Gly Ala Ile Gly Asp Ile Val Met Thr Gln Ala Ala Pro Ser Val Ser
20 25 30

Val Thr Pro Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45

Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg
50 55 60

Pro Gly Gln Ser Pro Gln Phe Leu Ile Tyr Arg Met Ser Asn Leu Ala
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe
85 90 95

Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

Cys Met Gln His Leu Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
115 120 125

Leu Glu Ile Lys
130

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<210> 43
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 43
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Phe Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
85 90 95
Leu Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 44
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 44
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Phe Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
85 90 95

Leu Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 45
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 45
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Phe Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
85 90 95

Leu Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 46
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 46
Gly Tyr Ala Phe Thr Tyr Tyr Leu Ile Glu
1 5 10

467600_1

<210> 47
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 47
Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 48
Asn Trp Met Asn Phe Asp Tyr
1 5

<210> 49
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 49
Arg Ser Ser Lys Ser Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr
1 5 10 15

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 50
Arg Met Ser Asn Leu Ala Ser
1 5

<210> 51
<211> 9
<212> PRT

467600_1

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 51

Met Gln His Leu Glu Tyr Pro Tyr Thr
1 5