

SEQUENCE LISTING

<110> CG Discovery, Inc.
LUO, Chun

<120> COMPOSITIONS OF INFLUENZA HEMAGGLUTININ WITH HETEROLOGOUS EPITOPES AND/OR
ALTERED MATURATION CLEAVAGE SITES AND METHODS OF USE THEREOF

<130> 758252000140

<140> Not Yet Assigned

<141> Concurrently Herewith

<150> US 62/290,894

<151> 2016-02-03

<160> 62

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 566

<212> PRT

<213> Influenza A virus

<400> 1

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Val	Asp	Thr	Val	Leu	Glu	Lys	Asn	Val	Thr	Val	Thr	His	Ser	Val	Asn
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Leu	Leu	Glu	Asp	Lys	His	Asn	Gly	Lys	Leu	Cys	Lys	Leu	Arg	Gly	Val
	50					55					60				
Ala	Pro	Leu	His	Leu	Gly	Lys	Cys	Asn	Ile	Ala	Gly	Trp	Ile	Leu	Gly
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Asn	Pro	Glu	Cys	Glu	Ser	Leu	Ser	Thr	Ala	Ser	Ser	Trp	Ser	Tyr	Ile
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Val	Glu	Thr	Pro	Ser	Ser	Asp	Asn	Gly	Thr	Cys	Tyr	Pro	Gly	Asp	Phe
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Ile	Asp	Tyr	Glu	Glu	Leu	Arg	Glu	Gln	Leu	Ser	Ser	Val	Ser	Ser	Phe
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Phe	Tyr	Lys	Asn	Leu	Ile	Trp	Leu	Val	Lys	Lys	Gly	Asn	Ser	Tyr	Pro
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Lys	Leu	Ser	Lys	Ser	Tyr	Ile	Asn	Asp	Lys	Gly	Lys	Glu	Val	Leu	Val
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Leu	Trp	Gly	Ile	His	His	Pro	Ser	Thr	Ser	Ala	Asp	Gln	Gln	Ser	Leu
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Tyr	Gln	Asn	Ala	Asp	Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser	Arg	Tyr	Ser
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Glu	Gly	Arg	Met	Asn	Tyr	Tyr	Trp	Thr	Leu	Val	Glu	Pro	Gly	Asp	Lys
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Ile	Thr	Phe	Glu	Ala	Thr	Gly	Asn	Leu	Val	Val	Pro	Arg	Tyr	Ala	Phe
			260					265					270		
Ala	Met	Glu	Arg	Asn	Ala	Gly	Ser	Gly	Ile	Ile	Ile	Ser	Asp	Thr	Pro
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Val	His	Asp	Cys	Asn	Thr	Thr	Cys	Gln	Thr	Pro	Lys	Gly	Ala	Ile	Asn
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Thr	Ser	Leu	Pro	Phe	Gln	Asn	Ile	His	Pro	Ile	Thr	Ile	Gly	Lys	Cys
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Pro	Lys	Tyr	Val	Lys	Ser	Thr	Lys	Leu	Arg	Leu	Ala	Thr	Gly	Leu	Arg
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Asn	Ile	Pro	Ser	Ile	Gln	Ser	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly
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Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly	Met	Val	Asp	Gly	Trp	Tyr	Gly	Tyr
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His	His	Gln	Asn	Glu	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp	Leu	Lys	Ser
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Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr	Asn	Lys	Val	Asn	Ser	Val	Ile
385					390					395					400
Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val	Gly	Lys	Glu	Phe	Asn	His
				405					410					415	
Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn	Lys	Lys	Val	Asp	Asp	Gly	Phe
			420					425					430		
Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn
		435					440					445			
Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser	Asn	Val	Lys	Asn	Leu	Tyr	Glu
	450					455					460				
Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Gly	Asn	Gly
465					470					475					480
Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn	Thr	Cys	Met	Glu	Ser	Val
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Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser	Glu	Glu	Ala	Lys	Leu
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Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys	Leu	Glu	Ser	Thr	Arg	Ile	Tyr
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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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Leu Leu Ser Thr Phe Leu Gly His His His His His His His His
35 40 45
His

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<213> Artificial Sequence

<220>
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Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
20 25

<210> 6
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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 6
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1 5 10

<210> 7
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 7
Met Lys Ala Ile Leu Val Val Leu Leu Tyr Thr Phe Ala Thr Ala Asn
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<210> 8
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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 8

Ile Pro Ser Ile Gln Ser Arg
1 5

<210> 9

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 9

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			20					25					30		
Thr	Asp	Thr	Val	Asp	Thr	Val	Leu	Glu	Lys	Asn	Val	Thr	Val	Thr	His
		35					40					45			
Ser	Val	Asn	Leu	Leu	Glu	Asp	Lys	His	Asn	Gly	Lys	Leu	Cys	Lys	Leu
	50				55					60					
Arg	Gly	Val	Ala	Pro	Leu	His	Leu	Gly	Lys	Cys	Asn	Ile	Ala	Gly	Trp
65					70					75					80
Ile	Leu	Gly	Asn	Pro	Glu	Cys	Glu	Ser	Leu	Ser	Thr	Ala	Ser	Ser	Trp
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Ser	Tyr	Ile	Val	Glu	Thr	Pro	Ser	Ser	Asp	Asn	Gly	Thr	Cys	Tyr	Pro
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Gly	Asp	Phe	Ile	Asp	Tyr	Glu	Glu	Leu	Arg	Glu	Gln	Leu	Ser	Ser	Val
		115				120						125			
Ser	Ser	Phe	Glu	Arg	Phe	Glu	Ile	Phe	Pro	Lys	Thr	Ser	Ser	Trp	Pro
	130					135					140				
Asn	His	Asp	Ser	Asn	Lys	Gly	Val	Thr	Ala	Ala	Cys	Pro	His	Ala	Gly
145					150					155					160
Ala	Lys	Ser	Phe	Tyr	Lys	Asn	Leu	Ile	Trp	Leu	Val	Lys	Lys	Gly	Asn
			165						170					175	
Ser	Tyr	Pro	Lys	Leu	Ser	Lys	Ser	Tyr	Ile	Asn	Asp	Lys	Gly	Lys	Glu
		180						185					190		
Val	Leu	Val	Leu	Trp	Gly	Ile	His	His	Pro	Ser	Thr	Ser	Ala	Asp	Gln
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Gln	Ser	Leu	Tyr	Gln	Asn	Ala	Asp	Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser
	210					215					220				
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225					230					235					240
Arg	Asp	Gln	Glu	Gly	Arg	Met	Asn	Tyr	Tyr	Trp	Thr	Leu	Val	Glu	Pro
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Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala	Thr	Gly	Asn	Leu	Val	Val	Pro	Arg
			260					265					270		
Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn	Ala	Gly	Ser	Gly	Ile	Ile	Ile	Ser
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Asp	Thr	Pro	Val	His	Asp	Cys	Asn	Thr	Thr	Cys	Gln	Thr	Pro	Lys	Gly
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Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe	Gln	Asn	Ile	His	Pro	Ile	Thr	Ile
305					310					315					320
Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys	Ser	Thr	Lys	Leu	Arg	Leu	Ala	Thr
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Tyr	Gly	Tyr	His	His	Gln	Asn	Glu	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp
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Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr	Asn	Lys	Val	Asn
385					390					395					400
Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val	Gly	Lys	Glu
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Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn	Lys	Lys	Val	Asp
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Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu
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Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser	Asn	Val	Lys	Asn
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Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile
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Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn	Thr	Cys	Met
			485						490					495	
Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser	Glu	Glu
			500					505					510		
Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys	Leu	Glu	Ser	Thr
		515					520					525			
Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Gly	Ser	Gly
	530					535					540				
Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp
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Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	His	His	His	His	His
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His	His	His	His	His											
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<210> 10

<211> 1757

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 10

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<210> 11

<211> 584

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 11

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Thr Asp Thr Val Asp Thr Val Leu Glu Lys Asn Val Thr Val Thr His
      35             40            45
Ser Val Asn Leu Leu Glu Asp Lys His Asn Gly Lys Leu Cys Lys Leu
      50             55            60
Arg Gly Val Ala Pro Leu His Leu Gly Lys Cys Asn Ile Ala Gly Trp
65             70             75            80
Ile Leu Gly Asn Pro Glu Cys Glu Ser Leu Ser Thr Ala Ser Ser Trp

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Gly	Asp	Phe	Ile	Asp	Tyr	Glu	Glu	Leu	Arg	Glu	Gln	Leu	Ser	Ser	Val		
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Ser	Ser	Phe	Glu	Arg	Phe	Glu	Ile	Phe	Pro	Lys	Thr	Ser	Ser	Trp	Pro		
		130				135					140						
Asn	His	Asp	Ser	Asn	Lys	Gly	Val	Thr	Ala	Ala	Cys	Pro	His	Ala	Gly		
145					150				155						160		
Ala	Lys	Ser	Phe	Tyr	Lys	Asn	Leu	Ile	Trp	Leu	Val	Lys	Lys	Gly	Asn		
			165					170						175			
Ser	Tyr	Pro	Lys	Leu	Ser	Lys	Ser	Tyr	Ile	Asn	Asp	Lys	Gly	Lys	Glu		
			180					185					190				
Val	Leu	Val	Leu	Trp	Gly	Ile	His	His	Pro	Ser	Thr	Ser	Ala	Asp	Gln		
		195				200						205					
Gln	Ser	Leu	Tyr	Gln	Asn	Ala	Asp	Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser		
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Arg	Asp	Gln	Glu	Gly	Arg	Met	Asn	Tyr	Tyr	Trp	Thr	Leu	Val	Glu	Pro		
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Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala	Thr	Gly	Asn	Leu	Val	Val	Pro	Arg		
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Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn	Ala	Gly	Ser	Gly	Ile	Ile	Ile	Ser		
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Asp	Thr	Pro	Val	His	Asp	Cys	Asn	Thr	Thr	Cys	Gln	Thr	Pro	Lys	Gly		
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			340					345					350				
Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly	Met	Val		
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Asp	Gly	Trp	Tyr	Gly	Tyr	His	Gln	Asn	Glu	Gln	Gly	Ser	Gly	Tyr			
	370				375				380								
Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr	Asn		
385					390				395						400		
Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val		
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Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser	Asn		
	450					455					460						
Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn	Ala		
465					470					475					480		
Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn		

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Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr		
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Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys	Leu		
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Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln	Gly		
		530				535					540						
Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr	Val		
545					550					555					560		
Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	His	His		
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 12
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<210> 13
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

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<210> 14

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 14

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Ser Ala Phe Ala Asp Thr Leu Cys Ile Gly Tyr His Ala Asn Asn Ser
 20              25              30
Thr Asp Thr Val Asp Thr Val Leu Glu Lys Asn Val Thr Val Thr His
 35              40              45
Ser Val Asn Leu Leu Glu Asp Lys His Asn Gly Lys Leu Cys Lys Leu
 50              55              60
Arg Gly Val Ala Pro Leu His Leu Gly Lys Cys Asn Ile Ala Gly Trp
 65              70              75              80
Ile Leu Gly Asn Pro Glu Cys Glu Ser Leu Ser Thr Ala Ser Ser Trp
 85              90              95
Ser Tyr Ile Val Glu Thr Pro Ser Ser Asp Asn Gly Thr Cys Tyr Pro
 100             105             110
Gly Asp Phe Ile Asp Tyr Glu Glu Leu Arg Glu Gln Leu Ser Ser Val
 115             120             125
Ser Ser Phe Glu Arg Phe Glu Ile Phe Pro Lys Thr Ser Ser Trp Pro
 130             135             140
Asn His Asp Ser Asn Lys Gly Val Thr Ala Ala Cys Pro His Ala Gly
 145             150             155             160
Ala Lys Ser Phe Tyr Lys Asn Leu Ile Trp Leu Val Lys Lys Gly Asn
 165             170             175
Ser Tyr Pro Lys Leu Ser Lys Ser Tyr Ile Asn Asp Lys Gly Lys Glu

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			180				185				190				
Val	Leu	Val	Leu	Trp	Gly	Ile	His	Pro	Ser	Thr	Ser	Ala	Asp	Gln	
			195				200				205				
Gln	Ser	Leu	Tyr	Gln	Asn	Ala	Asp	Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser
			210				215				220				
Arg	Tyr	Ser	Lys	Lys	Phe	Lys	Pro	Glu	Ile	Ala	Ile	Arg	Pro	Lys	Val
225				230				235				240			
Arg	Asp	Gln	Glu	Gly	Arg	Met	Asn	Tyr	Tyr	Trp	Thr	Leu	Val	Glu	Pro
			245				250				255				
Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala	Thr	Gly	Asn	Leu	Val	Val	Pro	Arg
			260				265				270				
Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn	Ala	Gly	Ser	Gly	Ile	Ile	Ile	Ser
			275				280				285				
Asp	Thr	Pro	Val	His	Asp	Cys	Asn	Thr	Thr	Cys	Gln	Thr	Pro	Lys	Gly
			290				295				300				
Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe	Gln	Asn	Ile	His	Pro	Ile	Thr	Ile
305				310				315				320			
Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys	Ser	Thr	Lys	Leu	Arg	Leu	Ala	Thr
			325				330				335				
Gly	Leu	Arg	Asn	Ile	Pro	Arg	Arg	Arg	Arg	Arg	Gly	Leu	Phe	Gly	Ala
			340				345				350				
Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly	Met	Val	Asp	Gly	Trp
			355				360				365				
Tyr	Gly	Tyr	His	His	Gln	Asn	Glu	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp
			370				375				380				
Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr	Asn	Lys	Val	Asn
385				390				395				400			
Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val	Gly	Lys	Glu
			405				410				415				
Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn	Lys	Lys	Val	Asp
			420				425				430				
Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu
			435				440				445				
Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser	Asn	Val	Lys	Asn
			450				455				460				
Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile
465				470				475				480			
Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn	Thr	Cys	Met
			485				490				495				
Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser	Glu	Glu
			500				505				510				
Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys	Leu	Glu	Ser	Thr
			515				520				525				
Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Gly	Ser	Gly
			530				535				540				
Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp
545				550				555				560			
Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	His	His	His	His	His
			565				570				575				
His	His	His	His	His											

<210> 15
 <211> 1757
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

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 tggagaagaa tgtgaccgtg acccactctg tgaatctgct ggaggataag cacaatggca 180
 agctgtgtaa gctgagagga gttgcccctc tgcacctggg caaatgtaat attgccggct 240
 ggattctggg aaatcctgaa tgtgaaaagg tgtctacagc cagcagctgg tcttatatcg 300
 tggaaaacccc tagcagcgac aatggcacct gttaccctgg cgacttcatc gattacgagg 360
 agctgagaga acagctgtct agcgtgtcca gcttcgagag attcgagatc ttccctaaga 420
 caagcagctg gcctaatac gattctaata agggagtgac agccgcctgt cctcatgccg 480
 gagccaagtc cttttacaag aacctgatct ggctggtgaa gaagggaac agctacccta 540
 agctgtctaa gagctacatc aacgacaagg gcaaagaagt gctggtgctg tggggaatcc 600
 accaccctag cacaagcgcc gatcagcaga gcctgtacca gaatgccgat gcctatgtgt 660
 ttgtgggcag cagcagatac agcaaaaaagt tcaagcctga aattgccatt agacccaaag 720
 tgagagatca ggaaggcaga atgaattact actggaccct ggtggaacct ggcgataaga 780
 tcacatttga ggccaccgga aatctggtgg tgcctagata tgcatttgct atggagagaa 840
 atgctggctc tggcatcatt atctctgata cccctgtgca cgactgtaat accacctgtc 900
 agacacctaa gggcgccatt aataccagcc tgcccttcca gaatattcac cctatcacca 960
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 gatggaccgg aatgggtggat ggctggtagc gctatcacca ccagaatgag cagggatccg 1140
 gatatgccgc cgatctgaag tctacacaga acgccatcga cgagatcaca aacaaggatga 1200
 acagcgtgat cgagaagatg aacacccagt ttacagctgt gggcaaggag ttcaaccacc 1260
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 cctacaatgc cgagctgctc gtgctcctgg agaagagag aacctggac taccacgaca 1380
 gcaatgtgaa gaacctgtac gagaaggatga gaagccagct gaagaacaat gccaaggaga 1440
 tcggcaacgg ctgctttgag ttctaccaca agtgtgacaa cacctgtatg gagtctgtga 1500
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<210> 16
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 16

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

Tyr	Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr
385					390				395					400	
Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala
			405					410					415		
Val	Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn
			420					425					430		
Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu
		435					440					445			
Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser
	450					455					460				
Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn
465				470					475						480
Ala	Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp
				485					490					495	
Asn	Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys
		500						505				510			
Tyr	Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys
		515					520					525			
Leu	Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln
	530					535					540				
Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr
545					550					555					560
Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	His
			565					570						575	
His	His	His	His	His	His	His	His	His							
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<210> 17

<211> 1769

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 17

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tggagaagaa	tgtgaccgtg	accactctg	tgaatctgct	ggaggataag	cacaatggca	180
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caagcagctg	gcctaatac	gattctaata	agggagtgc	agccgcctgt	cctcatgccg	480
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accaccctag	cacaagcgcc	gatcagcaga	gcctgtacca	gaatgccgat	gcctatgtgt	660
ttgtgggcag	cagcagatac	agcaaaaagt	tcaagcctga	aattgccatt	agacccaaag	720
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atgctggctc tggcatcatt atctctgata cccctgtgca cgactgtaat accacctgtc 900
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accatcacca tcatcactga taaaagctt 1769

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<210> 18

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 18

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Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala Ala His
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Ser Ala Phe Ala Asp Thr Leu Cys Ile Gly Tyr His Ala Asn Asn Ser
 20             25             30
Thr Asp Thr Val Asp Thr Val Leu Glu Lys Asn Val Thr Val Thr His
 35             40             45
Ser Val Asn Leu Leu Glu Asp Lys His Asn Gly Lys Leu Cys Lys Leu
 50             55             60
Arg Gly Val Ala Pro Leu His Leu Gly Lys Cys Asn Ile Ala Gly Trp
 65             70             75             80
Ile Leu Gly Asn Pro Glu Cys Glu Ser Leu Ser Thr Ala Ser Ser Trp
 85             90             95
Ser Tyr Ile Val Glu Thr Pro Ser Ser Asp Asn Gly Thr Cys Tyr Pro
 100            105            110
Gly Asp Phe Ile Asp Tyr Glu Glu Leu Arg Glu Gln Leu Ser Ser Val
 115            120            125
Ser Ser Phe Glu Arg Phe Glu Ile Phe Pro Lys Thr Ser Ser Trp Pro
 130            135            140
Asn His Asp Ser Asn Lys Gly Val Thr Ala Ala Cys Pro His Ala Gly
 145            150            155            160
Ala Lys Ser Phe Tyr Lys Asn Leu Ile Trp Leu Val Lys Lys Gly Asn
 165            170            175
Ser Tyr Pro Lys Leu Ser Lys Ser Tyr Ile Asn Asp Lys Gly Lys Glu

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			180					185				190			
Val	Leu	Val	Leu	Trp	Gly	Ile	His	Pro	Ser	Thr	Ser	Ala	Asp	Gln	
		195					200				205				
Gln	Ser	Leu	Tyr	Gln	Asn	Ala	Asp	Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser
	210					215					220				
Arg	Tyr	Ser	Lys	Lys	Phe	Lys	Pro	Glu	Ile	Ala	Ile	Arg	Pro	Lys	Val
225					230					235					240
Arg	Asp	Gln	Glu	Gly	Arg	Met	Asn	Tyr	Tyr	Trp	Thr	Leu	Val	Glu	Pro
				245					250					255	
Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala	Thr	Gly	Asn	Leu	Val	Val	Pro	Arg
			260					265					270		
Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn	Ala	Gly	Ser	Gly	Ile	Ile	Ile	Ser
		275					280					285			
Asp	Thr	Pro	Val	His	Asp	Cys	Asn	Thr	Thr	Cys	Gln	Thr	Pro	Lys	Gly
	290					295					300				
Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe	Gln	Asn	Ile	His	Pro	Ile	Thr	Ile
305					310					315					320
Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys	Ser	Thr	Lys	Leu	Arg	Leu	Ala	Thr
				325					330					335	
Gly	Leu	Arg	Asn	Ile	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Leu	Phe	Gly	Ala
			340					345					350		
Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly	Met	Val	Asp	Gly	Trp
		355					360					365			
Tyr	Gly	Tyr	His	His	Gln	Asn	Glu	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp
					375						380				
Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr	Asn	Lys	Val	Asn
385					390					395					400
Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val	Gly	Lys	Glu
				405					410					415	
Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn	Lys	Lys	Val	Asp
			420					425				430			
Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu
		435					440					445			
Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser	Asn	Val	Lys	Asn
	450					455					460				
Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile
465					470					475					480
Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn	Thr	Cys	Met
				485					490					495	
Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser	Glu	Glu
			500					505					510		
Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys	Leu	Glu	Ser	Thr
		515					520					525			
Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Gly	Ser	Gly
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<210> 19
 <211> 1757
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 19
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<210> 20
 <211> 582
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 20

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

Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr	Asn	Lys	Val
385					390				395						400
Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val	Gly	Lys
			405						410					415	
Glu	Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn	Lys	Lys	Val
			420					425					430		
Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val
		435					440					445			
Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser	Asn	Val	Lys
	450					455					460				
Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn	Ala	Lys	Glu
465					470					475					480
Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn	Thr	Cys
			485						490					495	
Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser	Glu
			500					505					510		
Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys	Leu	Glu	Ser
		515					520					525			
Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Gly	Ser
	530					535					540				
Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys
545					550					555					560
Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	His	His	His	His
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His	His	His	His	His	His										
			580												

<210> 21

<211> 1760

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 21

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ggattctggg	aaatcctgaa	tgtgaaagcc	tgtctacagc	cagcagctgg	tcttatatcg	300
tggaaacccc	tagcagcgac	aatggcacct	gttaccctgg	cgacttcac	gattacgagg	360
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caagcagctg	gcctaatac	gattctaata	agggagtgc	agccgcctgt	cctcatgccg	480
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atcatcactg ataaaagctt                                1760

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<210> 22

<211> 584

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 22

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Ser Ala Phe Ala Asp Thr Leu Cys Ile Gly Tyr His Ala Asn Asn Ser
 20              25              30
Thr Asp Thr Val Asp Thr Val Leu Glu Lys Asn Val Thr Val Thr His
 35              40              45
Ser Val Asn Leu Leu Glu Asp Lys His Asn Gly Lys Leu Cys Lys Leu
 50              55              60
Arg Gly Val Ala Pro Leu His Leu Gly Lys Cys Asn Ile Ala Gly Trp
 65              70              75              80
Ile Leu Gly Asn Pro Glu Cys Glu Ser Leu Ser Thr Ala Ser Ser Trp
 85              90              95
Ser Tyr Ile Val Glu Thr Pro Ser Ser Asp Asn Gly Thr Cys Tyr Pro
 100             105             110
Gly Asp Phe Ile Asp Tyr Glu Glu Leu Arg Glu Gln Leu Ser Ser Val
 115             120             125
Ser Ser Phe Glu Arg Phe Glu Ile Phe Pro Lys Thr Ser Ser Trp Pro
 130             135             140
Asn His Asp Ser Asn Lys Gly Val Thr Ala Ala Cys Pro His Ala Gly
 145             150             155             160
Ala Lys Ser Phe Tyr Lys Asn Leu Ile Trp Leu Val Lys Lys Gly Asn
 165             170             175
Ser Tyr Pro Lys Leu Ser Lys Ser Tyr Ile Asn Asp Lys Gly Lys Glu

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Gln	Ser	Leu	Tyr	Gln	Asn	Ala	Asp	Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser
	210					215					220				
Arg	Tyr	Ser	Lys	Lys	Phe	Lys	Pro	Glu	Ile	Ala	Ile	Arg	Pro	Lys	Val
225					230					235					240
Arg	Asp	Gln	Glu	Gly	Arg	Met	Asn	Tyr	Tyr	Trp	Thr	Leu	Val	Glu	Pro
			245					250						255	
Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala	Thr	Gly	Asn	Leu	Val	Val	Pro	Arg
			260					265					270		
Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn	Ala	Gly	Ser	Gly	Ile	Ile	Ile	Ser
		275					280					285			
Asp	Thr	Pro	Val	His	Asp	Cys	Asn	Thr	Thr	Cys	Gln	Thr	Pro	Lys	Gly
	290					295					300				
Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe	Gln	Asn	Ile	His	Pro	Ile	Thr	Ile
305					310					315					320
Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys	Ser	Thr	Lys	Leu	Arg	Leu	Ala	Thr
			325					330						335	
Gly	Leu	Arg	Asn	Ile	Pro	Ser	Ile	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Leu
			340					345					350		
Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly	Met	Val
	355						360					365			
Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Gln	Asn	Glu	Gln	Gly	Ser	Gly	Tyr
	370					375					380				
Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr	Asn
385					390					395					400
Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val
			405					410						415	
Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn	Lys
			420					425					430		
Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu
		435					440					445			
Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser	Asn
	450					455					460				
Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn	Ala
465					470					475					480
Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn
			485					490						495	
Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr
			500					505					510		
Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys	Leu
		515					520					525			
Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln	Gly
	530					535					540				
Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr	Val
545					550					555					560
Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	His	His
			565					570						575	
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<210> 23
 <211> 1766
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 23
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 gagccaagtc cttttacaag aacctgatct ggctggtgaa gaagggaac agctacccta 540
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<210> 24
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 24

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			20					25					30		
Thr	Asp	Thr	Val	Asp	Thr	Val	Leu	Glu	Lys	Asn	Val	Thr	Val	Thr	His
		35					40					45			
Ser	Val	Asn	Leu	Leu	Glu	Asp	Lys	His	Asn	Gly	Lys	Leu	Cys	Lys	Leu
	50					55					60				
Arg	Gly	Val	Ala	Pro	Leu	His	Leu	Gly	Lys	Cys	Asn	Ile	Ala	Gly	Trp
65					70					75					80
Ile	Leu	Gly	Asn	Pro	Glu	Cys	Glu	Ser	Leu	Ser	Thr	Ala	Ser	Ser	Trp
				85					90					95	
Ser	Tyr	Ile	Val	Glu	Thr	Pro	Ser	Ser	Asp	Asn	Gly	Thr	Cys	Tyr	Pro
			100					105					110		
Gly	Asp	Phe	Ile	Asp	Tyr	Glu	Glu	Leu	Arg	Glu	Gln	Leu	Ser	Ser	Val
		115					120					125			
Ser	Ser	Phe	Glu	Arg	Phe	Glu	Ile	Phe	Pro	Lys	Thr	Ser	Ser	Trp	Pro
	130					135					140				
Asn	His	Asp	Ser	Asn	Lys	Gly	Val	Thr	Ala	Ala	Cys	Pro	His	Ala	Gly
145					150					155					160
Ala	Lys	Ser	Phe	Tyr	Lys	Asn	Leu	Ile	Trp	Leu	Val	Lys	Lys	Gly	Asn
				165					170					175	
Ser	Tyr	Pro	Lys	Leu	Ser	Lys	Ser	Tyr	Ile	Asn	Asp	Lys	Gly	Lys	Glu
			180					185					190		
Val	Leu	Val	Leu	Trp	Gly	Ile	His	His	Pro	Ser	Thr	Ser	Ala	Asp	Gln
		195				200							205		
Gln	Ser	Leu	Tyr	Gln	Asn	Ala	Asp	Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser
	210					215					220				
Arg	Tyr	Ser	Lys	Lys	Phe	Lys	Pro	Glu	Gly	Met	Ile	Asp	Tyr	Glu	Gly
225					230					235					240
Thr	Gly	Gln	Ala	Ala	Gly	Arg	Met	Asn	Tyr	Tyr	Trp	Thr	Leu	Val	Glu
				245					250					255	
Pro	Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala	Thr	Gly	Asn	Leu	Val	Val	Pro
			260					265					270		
Arg	Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn	Ala	Gly	Ser	Gly	Ile	Ile	Ile
		275				280						285			
Ser	Asp	Thr	Pro	Val	His	Asp	Cys	Asn	Thr	Thr	Cys	Gln	Thr	Pro	Lys
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Gly	Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe	Gln	Asn	Ile	His	Pro	Ile	Thr
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Ile	Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys	Ser	Thr	Lys	Leu	Arg	Leu	Ala
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Thr	Gly	Leu	Arg	Asn	Ser	Pro	Gln	Arg	Glu	Arg	Arg	Lys	Lys	Arg	Gly
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Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly	Met
		355					360					365			
Val	Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Gln	Asn	Glu	Gln	Gly	Ser	Gly
	370					375					380				

Tyr	Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr
385					390					395					400
Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala
			405						410						415
Val	Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn
			420					425							430
Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu
		435					440					445			
Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser
	450					455					460				
Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn
465					470					475					480
Ala	Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp
				485					490						495
Asn	Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys
			500					505					510		
Tyr	Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys
		515					520					525			
Leu	Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln
	530					535					540				
Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr
545					550					555					560
Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	His
			565						570					575	
His	His	His	His	His	His	His	His	His							
			580					585							

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 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 25
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 1 5

<210> 26
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 26

Glu Gly Thr Gly Gln Ala Ala
1 5

<210> 27
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 27
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<210> 28
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<213> Artificial Sequence

<220>
<223> Synthetic

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agctgtgtaa gctgagagga gttgcccctc tgcacctggg caaatgtaat attgccggct 240
ggattctggg aaatcctgaa tgtgaaaagc tgtctacagc cagcagctgg tcttatatcg 300
tggaaacccc tagcagcgac aatggcacct gttaccctgg cgacttcacg gattacgagg 360
agctgagaga acagctgtct agcgtgtcca gcttcgagag attcgagatc ttccctaaga 420
caagcagctg gcctaatac gattctaata agggagtgac agccgcctgt cctcatgccg 480
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acgttcgtaa agacggtgaa tgggttctgc tgtctacctt cctgggtcac catcatcacc 1740
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<210> 29

<211> 583

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 29

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

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Arg	Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn	Ala	Gly	Ser	Gly	Ile	Ile	Ile
		275					280					285			
Ser	Asp	Thr	Pro	Val	His	Asp	Cys	Asn	Thr	Thr	Cys	Gln	Thr	Pro	Lys
		290				295					300				
Gly	Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe	Gln	Asn	Ile	His	Pro	Ile	Thr
305					310					315					320
Ile	Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys	Ser	Thr	Lys	Leu	Arg	Leu	Ala
			325						330					335	
Thr	Gly	Leu	Arg	Asn	Ser	Pro	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Leu	Phe
			340					345					350		
Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly	Met	Val	Asp
		355					360					365			
Gly	Trp	Tyr	Gly	Tyr	His	His	Gln	Asn	Glu	Gln	Gly	Ser	Gly	Tyr	Ala
	370				375						380				
Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr	Asn	Lys
385					390					395					400
Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val	Gly
			405						410					415	
Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn	Lys	Lys
			420					425					430		
Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu
	435						440					445			
Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser	Asn	Val
	450					455					460				
Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn	Ala	Lys
465					470					475					480
Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn	Thr
			485						490					495	
Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser
		500						505					510		
Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys	Leu	Glu
		515					520					525			
Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Gly
	530				535						540				
Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg
545					550					555					560
Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	His	His	His
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His	His	His	His	His	His	His									
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<210> 30

<211> 1763

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 30

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caagcagctg gcctaatacac gattctaata agggagtgc agccgcctgt cctcatgccg 480
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accatcatca ctgataaaag ctt 1763
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<210> 31

<211> 590

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 31

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Ser Ala Phe Ala Asp Thr Leu Cys Ile Gly Tyr His Ala Asn Asn Ser
          20             25             30
Thr Asp Thr Val Asp Thr Val Leu Glu Lys Asn Val Thr Val Thr His
          35             40             45
Ser Val Asn Leu Leu Glu Asp Lys His Asn Gly Lys Leu Cys Lys Leu
          50             55             60
Arg Gly Val Ala Pro Leu His Leu Gly Lys Cys Asn Ile Ala Gly Trp
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65					70					75					80
Ile	Leu	Gly	Asn	Pro	Glu	Cys	Glu	Ser	Leu	Ser	Thr	Ala	Ser	Ser	Trp
				85					90					95	
Ser	Tyr	Ile	Val	Glu	Thr	Pro	Ser	Ser	Asp	Asn	Gly	Thr	Cys	Tyr	Pro
			100					105					110		
Gly	Asp	Phe	Ile	Asp	Tyr	Glu	Glu	Leu	Arg	Glu	Gln	Leu	Ser	Ser	Val
		115					120					125			
Ser	Ser	Phe	Glu	Arg	Phe	Glu	Ile	Phe	Pro	Lys	Thr	Ser	Ser	Trp	Pro
	130					135					140				
Asn	His	Asp	Ser	Asn	Lys	Gly	Val	Thr	Ala	Ala	Cys	Pro	His	Ala	Gly
145					150				155					160	
Ala	Lys	Ser	Phe	Tyr	Lys	Asn	Leu	Ile	Trp	Leu	Val	Glu	Gly	Met	Ile
			165						170					175	
Asp	Tyr	Glu	Gly	Thr	Gly	Gln	Ala	Ala	Tyr	Pro	Lys	Leu	Ser	Lys	Ser
		180					185					190			
Tyr	Ile	Asn	Asp	Lys	Gly	Lys	Glu	Val	Leu	Val	Leu	Trp	Gly	Ile	His
	195					200						205			
His	Pro	Ser	Thr	Ser	Ala	Asp	Gln	Gln	Ser	Leu	Tyr	Gln	Asn	Ala	Asp
	210					215					220				
Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser	Arg	Tyr	Ser	Lys	Lys	Phe	Lys	Pro
225					230					235					240
Glu	Ile	Ala	Ile	Arg	Pro	Lys	Val	Arg	Asp	Gln	Glu	Gly	Arg	Met	Asn
			245						250					255	
Tyr	Tyr	Trp	Thr	Leu	Val	Glu	Pro	Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala
		260						265					270		
Thr	Gly	Asn	Leu	Val	Val	Pro	Arg	Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn
	275						280					285			
Ala	Gly	Ser	Gly	Ile	Ile	Ile	Ser	Asp	Thr	Pro	Val	His	Asp	Cys	Asn
	290					295					300				
Thr	Thr	Cys	Gln	Thr	Pro	Lys	Gly	Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe
305					310					315					320
Gln	Asn	Ile	His	Pro	Ile	Thr	Ile	Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys
			325						330					335	
Ser	Thr	Lys	Leu	Arg	Leu	Ala	Thr	Gly	Leu	Arg	Asn	Ser	Pro	Glu	Asn
		340						345					350		
Leu	Tyr	Phe	Gln	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly
	355					360					365				
Gly	Trp	Thr	Gly	Met	Val	Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Gln	Asn
	370					375					380				
Glu	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala
385					390					395					400
Ile	Asp	Glu	Ile	Thr	Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn
			405						410					415	
Thr	Gln	Phe	Thr	Ala	Val	Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg
		420						425					430		
Ile	Glu	Asn	Leu	Asn	Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp
	435					440						445			
Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu
	450					455					460				
Asp	Tyr	His	Asp	Ser	Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser

465		470		475		480									
Gln	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe
			485				490							495	
Tyr	His	Lys	Cys	Asp	Asn	Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr
		500						505					510		
Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu
	515						520					525			
Ile	Asp	Gly	Val	Lys	Leu	Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu
	530					535					540				
Asn	Leu	Tyr	Phe	Gln	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg
545				550				555						560	
Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser
			565					570						575	
Thr	Phe	Leu	Gly	His	His	His	His	His	His	His	His	His	His		
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<210> 32
 <211> 1785
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

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 ctgaaattgc cattagaccc aaagtgtgag atcaggaagg cagaatgaat tactactgga 780
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gtgacgggtca ggcttacgtt cgtaaagacg gtgaatgggt tctgctgtct accttcctgg 1740
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<210> 33

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 33

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

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Ala	Thr	Gly	Asn	Leu	Val	Val	Pro	Arg	Tyr	Ala	Phe	Ala	Met	Glu	Arg
		275					280					285			
Asn	Ala	Gly	Ser	Gly	Ile	Ile	Ile	Ser	Asp	Thr	Pro	Val	His	Asp	Cys
	290					295					300				
Asn	Thr	Thr	Cys	Gln	Thr	Pro	Lys	Gly	Ala	Ile	Asn	Thr	Ser	Leu	Pro
305					310					315					320
Phe	Gln	Asn	Ile	His	Pro	Ile	Thr	Ile	Gly	Lys	Cys	Pro	Lys	Tyr	Val
			325						330					335	
Lys	Ser	Thr	Lys	Leu	Arg	Leu	Ala	Thr	Gly	Leu	Arg	Asn	Ser	Pro	Glu
		340					345						350		
Asn	Leu	Tyr	Phe	Gln	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu
		355					360					365			
Gly	Gly	Trp	Thr	Gly	Met	Val	Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Gln
	370					375					380				
Asn	Glu	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn
385					390					395					400
Ala	Ile	Asp	Glu	Ile	Thr	Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met
			405						410					415	
Asn	Thr	Gln	Phe	Thr	Ala	Val	Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys
		420					425						430		
Arg	Ile	Glu	Asn	Leu	Asn	Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile
	435					440						445			
Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr
	450					455					460				
Leu	Asp	Tyr	His	Asp	Ser	Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg
465					470					475					480
Ser	Gln	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu
			485						490					495	
Phe	Tyr	His	Lys	Cys	Asp	Asn	Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly
		500						505					510		
Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu
		515					520					525			
Glu	Ile	Asp	Gly	Val	Lys	Leu	Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala
	530					535					540				
Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro
545					550					555					560
Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu
			565						570					575	
Ser	Thr	Phe	Leu	Gly	His	His	His	His	His	His	His	His	His	His	His
			580					585						590	

<210> 34

<211> 1787

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 34

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agctgtgtaa gctgagagga gttgcccctc tgcacctggg caaatgtaat attgccggct 240
ggattctggg aaatcctgaa tgtgaaagcc tgtctacagc cagcagctgg tcttataatcg 300
tggaaacccc tagcagcgac aatggcacct gttaccctgg cgacttcacg gattacgagg 360
agctgagaga acagctgtct agcgtgtcca gcttcgagag attcgagatc ttccctgaag 420
gcatgattga ttacgaaggc acaggccagg cagcctggcc taatcacgat tctaataagg 480
gagtgacagc cgctgtcct catgccggag ccaagtccct ttacaagaac ctgatctggc 540
tgggtaagaa gggcaacagc taccctaagc tgtctaagag ctacatcaac gacaagggca 600
aagaagtgtc ggtgctgtgg ggaatccacc accctagcac aagcgccgat cagcagagcc 660
tgtaccagaa tgccgatgcc tatgtgtttg tgggcagcag cagatacagc aaaaagttca 720
agcctgaaat tgccattaga cccaaagtga gagatcagga aggcagaatg aattactact 780
ggaccctggt ggaacctggc gataagatca catttgaggc caccggaaat ctggtggtgc 840
ctagatatgc atttgctatg gagagaaatg ctggctctgg catcattatc tctgataccc 900
ctgtgcacga ctgtaatacc acctgtcaga cacctaaggg cgccattaat accagcctgc 960
ccttccagaa tattcacccct atcaccatcg gcaagtgtcc taagtatgtg aagagcacca 1020
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gctatcacca ccagaatgag cagggatccg gatatgccgc cgatctgaag tctacacaga 1200
acgccatcga cgagatcaca aacaaggatg acagcgtgat cgagaagatg aacaccagg 1260
ttacagctgt gggcaaggag ttcaaccacc tggagaagag aatcgagaac ctgaacaaga 1320
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agaatgagag aaccctggac taccacgaca gcaatgtgaa gaacctgtac gagaaggtga 1440
gaagccagct gaagaacaat gccaaaggaga tcggcaacgg ctgctttgag ttctaccaca 1500
agtgtgacaa cacctgtatg gagtctgtga agaacggcac ctacgactac cctaagtata 1560
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tctatcaggg cgctgaaaac ctgtattttc agggcggttc tggttacatc ccggaagctc 1680
cgcgtgacgg tcaggcttac gttcgtaaag acggtgaatg gggttctgctg tctaccttcc 1740
tgggtcacca tcatcaccac catcaccatc atcactgata aaagctt 1787
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<210> 35

<211> 586

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 35

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 1             5             10             15
Ser Ala Phe Ala Asp Thr Leu Cys Ile Gly Tyr His Ala Asn Asn Ser
      20             25             30
Thr Asp Thr Val Asp Thr Val Leu Glu Lys Asn Val Thr Val Thr His
      35             40             45
Ser Val Asn Leu Leu Glu Asp Lys His Asn Gly Lys Leu Cys Lys Leu
      50             55             60
Arg Gly Val Ala Pro Leu His Leu Gly Lys Cys Asn Ile Ala Gly Trp
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65					70					75					80
Ile	Leu	Gly	Asn	Pro	Glu	Cys	Glu	Ser	Leu	Ser	Thr	Ala	Ser	Ser	Trp
				85					90					95	
Ser	Tyr	Ile	Val	Glu	Thr	Pro	Ser	Ser	Asp	Asn	Gly	Thr	Cys	Tyr	Pro
			100					105					110		
Gly	Asp	Phe	Ile	Asp	Tyr	Glu	Glu	Leu	Arg	Glu	Gln	Leu	Ser	Ser	Val
		115					120					125			
Ser	Ser	Phe	Glu	Arg	Phe	Glu	Ile	Phe	Pro	Lys	Thr	Ser	Ser	Trp	Pro
	130					135					140				
Asn	His	Asp	Ser	Asn	Lys	Gly	Val	Thr	Ala	Ala	Cys	Pro	His	Ala	Gly
145					150				155					160	
Ala	Lys	Ser	Phe	Tyr	Lys	Asn	Leu	Ile	Trp	Leu	Val	Lys	Lys	Gly	Asn
			165						170					175	
Ser	Tyr	Pro	Lys	Leu	Ser	Lys	Ser	Tyr	Ile	Asn	Asp	Lys	Gly	Lys	Glu
			180					185					190		
Val	Leu	Val	Leu	Trp	Gly	Ile	His	His	Pro	Ser	Thr	Ser	Ala	Asp	Gln
	195					200						205			
Gln	Ser	Leu	Tyr	Gln	Asn	Ala	Asp	Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser
	210					215					220				
Arg	Tyr	Ser	Lys	Lys	Phe	Lys	Pro	Glu	Ile	Ala	Ile	Gly	Ile	Phe	Gly
225					230					235					240
Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Arg	Met	Asn	Tyr	Tyr	Trp	Thr
			245						250					255	
Leu	Val	Glu	Pro	Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala	Thr	Gly	Asn	Leu
			260					265					270		
Val	Val	Pro	Arg	Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn	Ala	Gly	Ser	Gly
	275						280					285			
Ile	Ile	Ile	Ser	Asp	Thr	Pro	Val	His	Asp	Cys	Asn	Thr	Thr	Cys	Gln
	290					295					300				
Thr	Pro	Lys	Gly	Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe	Gln	Asn	Ile	His
305					310					315					320
Pro	Ile	Thr	Ile	Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys	Ser	Thr	Lys	Leu
			325						330					335	
Arg	Leu	Ala	Thr	Gly	Leu	Arg	Asn	Ser	Pro	Glu	Asn	Leu	Tyr	Phe	Gln
			340					345					350		
Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly
	355						360					365			
Met	Val	Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Gln	Asn	Glu	Gln	Gly	Ser
	370					375					380				
Gly	Tyr	Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile
385					390					395					400
Thr	Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr
			405						410					415	
Ala	Val	Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu
			420					425					430		
Asn	Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala
	435					440						445			
Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp
	450					455					460				
Ser	Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn

465		470		475		480									
Asn	Ala	Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys
			485					490						495	
Asp	Asn	Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro
			500					505					510		
Lys	Tyr	Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val
		515					520					525			
Lys	Leu	Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe
	530					535					540				
Gln	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala
545				550				555						560	
Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly
			565					570						575	
His	His	His	His	His	His	His	His	His	His						
			580					585							

<210> 36
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 36
 Gly Ile Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly
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<210> 37
 <211> 1772
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 37
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 cggatacact gtgtattggc taccacgcca acaatagcac cgataccgtg gatacagtgc 120
 tggagaagaa tgtgaccgtg acccactctg tgaatctgct ggaggataag cacaatggca 180
 agctgtgtaa gctgagagga gttgcccctc tgcacctggg caaatgtaat attgccggct 240
 ggattctggg aaatcctgaa tgtgaaagcc tgtctacagc cagcagctgg tcttatatcg 300
 tggaaacccc tagcagcgac aatggcacct gttaccctgg cgacttcac gattacgagg 360
 agctgagaga acagctgtct agcgtgtcca gcttcgagag attcgagatc ttccctaaga 420
 caagcagctg gcctaatacac gattctaata agggagtgac agccgcctgt cctcatgccg 480
 gagccaagtc cttttacaag aacctgatct ggctggtgaa gaagggcaac agctacccta 540
 agctgtctaa gagctacatc aacgacaagg gcaaagaagt gctgggtgctg tgggggaatcc 600
 accaccctag cacaagcgcc gatcagcaga gcctgtacca gaatgccgat gcctatgtgt 660

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ttgtgggcag cagcagatac agcaaaaagt tcaagcctga aattgccatt ggcatttttcg 720
gcgctatcgc cggcttcatt gagggaggca gaatgaatta ctactggacc ctggtggaac 780
ctggcgataa gatcacattt gagggcaccg gaaatctggt ggtgcctaga tatgcatttg 840
ctatggagag aaatgctggc tctggcatca ttatctctga taccctgtg cacgactgta 900
ataccacctg tcagacacct aagggcgcca ttaataccag cctgcccttc cagaatattc 960
accctatcac catcggcaag tgtcctaagt atgtgaagag caccaagctg agactggcta 1020
ccggtctgag aaatagccct gaaaacctgt attttcaagg cctgtttgga gccatcgccg 1080
gctttattga gggaggatgg accggaatgg tggatggctg gtacggctat caccaccaga 1140
atgagcaggg atccggatat gccgccgac tgaagtctac acagaacgcc atcgacgaga 1200
tcacaaacaa ggtgaacagc gtgatcgaga agatgaacac ccagtttaca gctgtgggca 1260
aggagttcaa ccacctggag aagagaatcg agaacctgaa caagaaaagtg gacgacggct 1320
tcctggatat ttggacctac aatgccgagc tgctcgtgct cctggagaat gagagaaccc 1380
tggtactacca cgacagcaat gtgaagaacc tgtacgagaa ggtgagaagc cagctgaaga 1440
acaatgccaa ggagatcggc aacggctgct ttgagttcta ccacaagtgt gacaacacct 1500
gtatggagtc tgtgaagaac ggcacctacg actaccctaa gtatagcgag gaggccaagc 1560
tgaatagaga ggagatcgac ggcgtgaaac tggaaaagcac aagaatctat cagggcgctg 1620
aaaacctgta ttttcagggc ggttctgggt acatcccgga agctccgcgt gacggtcagg 1680
cttacgttcg taaagacggg gaatgggttc tgctgtctac cttcctgggt caccatcatc 1740
accaccatca ccatcatcac tgataaaaagc tt 1772

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<210> 38

<211> 588

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 38

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

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				165				170				175			
Leu	Val	Lys	Lys	Gly	Asn	Ser	Tyr	Pro	Lys	Leu	Ser	Lys	Ser	Tyr	Ile
			180					185					190		
Asn	Asp	Lys	Gly	Lys	Glu	Val	Leu	Val	Leu	Trp	Gly	Ile	His	His	Pro
		195					200					205			
Ser	Thr	Ser	Ala	Asp	Gln	Gln	Ser	Leu	Tyr	Gln	Asn	Ala	Asp	Ala	Tyr
		210				215					220				
Val	Phe	Val	Gly	Ser	Ser	Arg	Tyr	Ser	Lys	Lys	Phe	Lys	Pro	Glu	Ile
225					230					235					240
Ala	Ile	Arg	Pro	Lys	Val	Arg	Asp	Gln	Glu	Gly	Arg	Met	Asn	Tyr	Tyr
				245					250					255	
Trp	Thr	Leu	Val	Glu	Pro	Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala	Thr	Gly
			260					265					270		
Asn	Leu	Val	Val	Pro	Arg	Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn	Ala	Gly
		275					280					285			
Ser	Gly	Ile	Ile	Ile	Ser	Asp	Thr	Pro	Val	His	Asp	Cys	Asn	Thr	Thr
	290					295					300				
Cys	Gln	Thr	Pro	Lys	Gly	Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe	Gln	Asn
305					310					315					320
Ile	His	Pro	Ile	Thr	Ile	Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys	Ser	Thr
				325					330					335	
Lys	Leu	Arg	Leu	Ala	Thr	Gly	Leu	Arg	Asn	Ser	Pro	Glu	Asn	Leu	Tyr
			340					345					350		
Phe	Gln	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp
		355					360					365			
Thr	Gly	Met	Val	Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Gln	Asn	Glu	Gln
	370					375					380				
Gly	Ser	Gly	Tyr	Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp
385					390					395					400
Glu	Ile	Thr	Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln
			405						410					415	
Phe	Thr	Ala	Val	Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu
			420					425					430		
Asn	Leu	Asn	Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr
		435					440					445			
Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr
	450					455					460				
His	Asp	Ser	Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu
465					470					475					480
Lys	Asn	Asn	Ala	Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His
				485					490					495	
Lys	Cys	Asp	Asn	Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp
			500					505					510		
Tyr	Pro	Lys	Tyr	Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp
		515					520						525		
Gly	Val	Lys	Leu	Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu
	530					535					540				
Tyr	Phe	Gln	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly
545					550					555					560
Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe

	565	570	575
Leu Gly His His His His His His His His His His			
	580	585	

<210> 39
 <211> 1778
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 39
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 cggatacact gtgtattggc taccacgcca acaatagcac cgataccgtg gatacagtgc 120
 tggagaagaa tgtgaccgtg acccactctg tgaatctgct ggaggataag cacaatggca 180
 agctgtgtaa gctgagagga gttgcccctc tgcacctggg caaatgtaat attgccggct 240
 ggattctggg aaatcctgaa tgtgaaaagcc tgtctacagc cagcagctgg tcttatatcg 300
 tggaaacccc tagcagcgac aatggcacct gttaccctgg cgacttcacg gattacgagg 360
 agctgagaga acagctgtct agcgtgtcca gcttcgagag attcgagatc ttccctaaga 420
 caagcagctg gcctaatacac gattctaata agggagtgac agccgcctgt cctggcattt 480
 tcggcgctat cgccggcttc attgagggat tttacaagaa cctgatctgg ctggtgaaga 540
 agggcaacag ctaccctaag ctgtctaaga gctacatcaa cgacaagggc aaagaagtgc 600
 tgggtgctgtg gggaaatccac caccctagca caagcgccga tcagcagagc ctgtaccaga 660
 atgccgatgc ctatgtgttt gtgggcagca gcagatacag caaaaagttc aagcctgaaa 720
 ttgccattag acccaaagtg agagatcagg aaggcagaat gaattactac tggaccctgg 780
 tggaacctgg cgataagatc acatttgagg ccaccggaaa tctggtggtg cctagatatg 840
 catttgctat ggagagaaat gctggctctg gcatcattat ctctgatacc cctgtgcacg 900
 actgtaatac cacctgtcag acacctaagg gcgccattaa taccagcctg cccttccaga 960
 atattcacc tatcaccatc ggcaagtgtc ctaagtatgt gaagagcacc aagctgagac 1020
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 tcgccggctt tattgaggga ggatggaccg gaatggtgga tggctggtac ggctatcacc 1140
 accagaatga gcagggatcc ggatatgccg ccgatctgaa gtctacacag aacgccatcg 1200
 acgagatcac aaacaagggtg aacagcgtga tcgagaagat gaacacccag ttacagctg 1260
 tgggcaagga gttcaaccac ctggagaaga gaatcgagaa cctgaacaag aaagtggacg 1320
 acggcttcct ggataatttg acctacaatg ccgagctgct cgtgctcctg gagaatgaga 1380
 gaaccctgga ctaccacgac agcaatgtga agaacctgta cgagaagggtg agaagccagc 1440
 tgaagaacaa tgccaaggag atcggcaacg gctgctttga gttctaccac aagtgtgaca 1500
 acacctgtat ggagtctgtg aagaacggca cctacgacta ccctaagtat agcgaggagg 1560
 ccaagctgaa tagagaggag atcgacggcg tgaaactgga aagcacaaga atctatcagg 1620
 gcgctgaaaa cctgtatttt cagggcgggt ctggttacat cccggaagct ccgcgtgacg 1680
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<210> 40
 <211> 589
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 40

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

Trp	Thr	Gly	Met	Val	Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Gln	Asn	Glu
370						375					380				
Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile
385					390					395					400
Asp	Glu	Ile	Thr	Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr
				405					410					415	
Gln	Phe	Thr	Ala	Val	Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg	Ile
			420					425					430		
Glu	Asn	Leu	Asn	Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr
	435						440					445			
Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp
	450					455					460				
Tyr	His	Asp	Ser	Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln
465					470					475					480
Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr
				485					490					495	
His	Lys	Cys	Asp	Asn	Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr
			500					505					510		
Asp	Tyr	Pro	Lys	Tyr	Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile
		515					520					525			
Asp	Gly	Val	Lys	Leu	Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn
	530					535					540				
Leu	Tyr	Phe	Gln	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp
545					550					555					560
Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr
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Phe	Leu	Gly	His	His	His	His	His	His	His	His	His	His			
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<210> 41
 <211> 1781
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 41
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 tggagaagaa tgtgaccgtg acccactctg tgaatctgct ggaggataag cacaatggca 180
 agctgtgtaa gctgagagga gttgccctc tgcacctggg caaatgtaat attgccggct 240
 ggattctggg aaatcctgaa tgtgaaagcc tgtctacagc cagcagctgg tcttatatcg 300
 tggaaacccc tagcagcgac aatggcacct gttaccctgg cgacttcac gattacgagg 360
 agctgagaga acagctgtct agcgtgtcca gcttcgagag attcgagatc ttccctaaga 420
 caagcagctg gcctaatac gattctaata agggagtgac agccgcctgt cctcatgccg 480
 gagccaagtc cttttacaag aacctgatct ggctgggtgg cattttcggc gctatcgccg 540
 gcttcattga gggataccct aagctgtcta agagctacat caacgacaag ggcaaagaag 600
 tgctgggtgct gtggggaatc caccacccta gcacaagcgc cgatcagcag agcctgtacc 660

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aaattgccat tagacccaaa gtgagagatc aggaaggcag aatgaattac tactggaccc 780
tggtggaacc tggcgataag atcacatttg aggccaccgg aaatctggtg gtgcctagat 840
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acgactgtaa taccacctgt cagacaccta agggcgccat taataccagc ctgcccttcc 960
agaatattca ccctatcacc atcggcaagt gtcctaagta tgtgaagagc accaagctga 1020
gactggctac cggctctgaga aatagccctg aaaacctgta ttttcaaggc ctgtttggag 1080
ccatcgccgg ctttattgag ggaggatgga ccggaatggt ggatggctgg tacggctatc 1140
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tcgacgagat cacaacaag gtgaacagcg tgatcgagaa gatgaacacc cagtttacag 1260
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acgacggctt cctggatatt tggacctaca atgccgagct gctcgtgctc ctggagaatg 1380
agagaaccct ggactaccac gacagcaatg tgaagaacct gtacgagaag gtgagaagcc 1440
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acaacacctg tatggagtct gtgaagaacg gcacctacga ctaccctaag tatacgagg 1560
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agggcgctga aaacctgtat tttcagggcg gttctgggta catcccgga gctccgcgtg 1680
acggtcaggc ttacgttcgt aaagacgggtg aatgggttct gctgtctacc ttcctgggtc 1740
accatcatca ccaccatcac catcatcact gataaaaagct t 1781

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<210> 42

<211> 590

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 42

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

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				165					170				175				
Ile	Trp	Leu	Val	Lys	Lys	Gly	Asn	Ser	Tyr	Pro	Lys	Leu	Ser	Lys	Ser		
			180					185					190				
Tyr	Ile	Asn	Asp	Lys	Gly	Lys	Glu	Val	Leu	Val	Leu	Trp	Gly	Ile	His		
		195					200					205					
His	Pro	Ser	Thr	Ser	Ala	Asp	Gln	Gln	Ser	Leu	Tyr	Gln	Asn	Ala	Asp		
		210				215					220						
Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser	Arg	Tyr	Ser	Lys	Lys	Phe	Lys	Pro		
225					230					235					240		
Glu	Ile	Ala	Ile	Arg	Pro	Lys	Val	Arg	Asp	Gln	Glu	Gly	Arg	Met	Asn		
				245					250					255			
Tyr	Tyr	Trp	Thr	Leu	Val	Glu	Pro	Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala		
			260					265					270				
Thr	Gly	Asn	Leu	Val	Val	Pro	Arg	Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn		
		275					280					285					
Ala	Gly	Ser	Gly	Ile	Ile	Ile	Ser	Asp	Thr	Pro	Val	His	Asp	Cys	Asn		
		290				295					300						
Thr	Thr	Cys	Gln	Thr	Pro	Lys	Gly	Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe		
305					310					315					320		
Gln	Asn	Ile	His	Pro	Ile	Thr	Ile	Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys		
				325					330					335			
Ser	Thr	Lys	Leu	Arg	Leu	Ala	Thr	Gly	Leu	Arg	Asn	Ser	Pro	Glu	Asn		
			340					345					350				
Leu	Tyr	Phe	Gln	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly		
		355					360					365					
Gly	Trp	Thr	Gly	Met	Val	Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Gln	Asn		
		370				375					380						
Glu	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala		
385					390					395					400		
Ile	Asp	Glu	Ile	Thr	Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn		
				405					410					415			
Thr	Gln	Phe	Thr	Ala	Val	Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg		
			420					425					430				
Ile	Glu	Asn	Leu	Asn	Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp		
		435					440					445					
Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu		
		450				455					460						
Asp	Tyr	His	Asp	Ser	Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser		
465					470				475					480			
Gln	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe		
				485					490					495			
Tyr	His	Lys	Cys	Asp	Asn	Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr		
			500					505					510				
Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu		
		515					520					525					
Ile	Asp	Gly	Val	Lys	Leu	Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu		
		530				535					540						
Asn	Leu	Tyr	Phe	Gln	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg		
545					550					555					560		
Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser		

		565						570					575
Thr	Phe	Leu	Gly	His	His	His	His	His	His	His	His	His	His
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<210> 43
 <211> 1784
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

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 tggagaagaa tgtgaccgtg acccactctg tgaatctgct ggaggataag cacaatggca 180
 agctgtgtaa gctgagagga gttgcccctc tgcacctggg caaatgtaat attgccggct 240
 ggattctggg aaatcctgaa tgtgaaaagcc tgtctacagc cagcagctgg tcttatatcg 300
 tggaaacccc tagcagcgac aatggcacct gttaccctgg cgacttcacg gattacgagg 360
 agctgagaga acagctgtct agcgtgtcca gcttcgagag attcgagatc ttccctggca 420
 ttttcggcgc tatcgccggc ttcataggag gatggcctaa tcacgattct aataagggag 480
 tgacagccgc ctgtcctcat gccggagcca agtcctttta caagaacctg atctggctgg 540
 tgaagaaggg caacagctac cctaagctgt ctaagagcta catcaacgac aaggggcaaaag 600
 aagtgtctgg gctgtgggga atccaccacc ctagcacaag cgccgatcag cagagcctgt 660
 accagaatgc cgatgcctat gtgtttgtgg gcagcagcag atacagcaaa aagttcaagc 720
 ctgaaattgc cattagaccc aaagtgagag atcaggaagg cagaatgaat tactactgga 780
 ccctgggtgga acctggcgat aagatcacat ttgaggccac cggaaatctg gtggtgccta 840
 gatatgcatt tgctatggag agaaaatgctg gctctggcat cattatctct gataccctg 900
 tgcacgactg taataccacc tgtcagacac ctaaggcgc cattaatacc agcctgccct 960
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 tggacgacgg cttcctggat atttggacct acaatgccga gctgctcgtg ctcctggaga 1380
 atgagagaac cctggactac cacgacagca atgtgaagaa cctgtacgag aaggtgagaa 1440
 gccagctgaa gaacaatgcc aaggagatcg gcaacggctg ctttgagttc taccacaagt 1500
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 atcagggcgc tgaaaacctg tattttcagg gcggttctgg ttacatcccg gaagctccgc 1680
 gtgacggtca ggcttacgtt cgtaaagacg gtgaatgggt tctgctgtct accttcctgg 1740
 gtcaccatca tcaccacat caccatcatc actgataaaa gctt 1784

<210> 44
 <211> 584
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 44

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

Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Gln	Asn	Glu	Gln	Gly	Ser	Gly	Tyr
370						375					380				
Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr	Asn
385					390					395					400
Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val
				405					410					415	
Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn	Lys
			420					425					430		
Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu
		435					440					445			
Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser	Asn
		450				455					460				
Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn	Ala
465					470					475					480
Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn
				485					490					495	
Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr
			500					505					510		
Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys	Leu
		515					520					525			
Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln	Gly
	530					535					540				
Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr	Val
545					550					555					560
Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	His	His
				565					570					575	
His	His	His	His	His	His	His	His								
				580											

<210> 45
 <211> 1766
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

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<210> 46

<211> 584

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 46

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Thr Asp Thr Val Asp Thr Val Leu Glu Lys Asn Val Thr Val Thr His
 35              40              45
Ser Val Asn Leu Leu Glu Asp Lys His Asn Gly Lys Leu Cys Lys Leu
 50              55              60
Arg Gly Val Ala Pro Leu His Leu Gly Lys Cys Asn Ile Ala Gly Trp
 65              70              75              80
Ile Leu Gly Asn Pro Glu Cys Glu Ser Leu Ser Thr Ala Ser Ser Trp
              85              90              95
Ser Tyr Ile Val Glu Thr Pro Ser Ser Asp Asn Gly Thr Cys Tyr Pro
              100             105             110
Gly Asp Phe Ile Asp Tyr Glu Glu Leu Arg Glu Gln Leu Ser Ser Val
              115             120             125
Ser Ser Phe Glu Arg Phe Glu Ile Phe Pro Lys Thr Ser Ser Trp Pro
              130             135             140
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Val	Leu	Val	Leu	Trp	Gly	Ile	His	His	Pro	Ser	Thr	Ser	Ala	Asp	Gln	
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Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr	Asn	
385					390					395					400	
Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val	
				405					410					415		
Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn	Lys	
			420					425					430			
Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	
		435					440					445				
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Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn	
				485					490					495		
Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	
			500					505					510			
Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys	Leu	
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Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	
	530					535					540					
Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr	Val	
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565

570

575

His His His His His His His His
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<210> 47

<211> 1766

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 47

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<211> 592

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 48

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			20					25					30		
Thr	Asp	Thr	Val	Asp	Thr	Val	Leu	Glu	Lys	Asn	Val	Thr	Val	Thr	His
		35					40					45			
Ser	Val	Asn	Leu	Leu	Glu	Asp	Lys	His	Asn	Gly	Lys	Leu	Cys	Lys	Leu
	50					55				60					
Arg	Gly	Val	Ala	Pro	Leu	His	Leu	Gly	Lys	Cys	Asn	Ile	Ala	Gly	Trp
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Ile	Leu	Gly	Asn	Pro	Glu	Cys	Glu	Ser	Leu	Ser	Thr	Ala	Ser	Ser	Trp
				85					90					95	
Ser	Tyr	Ile	Val	Glu	Thr	Pro	Ser	Ser	Asp	Asn	Gly	Thr	Cys	Tyr	Pro
			100					105					110		
Gly	Asp	Phe	Ile	Asp	Tyr	Glu	Glu	Leu	Arg	Glu	Gln	Leu	Ser	Ser	Val
		115				120						125			
Ser	Ser	Phe	Glu	Arg	Phe	Glu	Ile	Phe	Pro	Lys	Thr	Ser	Ser	Trp	Pro
	130					135					140				
Asn	His	Asp	Ser	Asn	Lys	Gly	Val	Thr	Ala	Ala	Cys	Pro	His	Ala	Gly
145					150					155					160
Ala	Lys	Ser	Phe	Tyr	Lys	Asn	Leu	Ile	Trp	Leu	Val	Arg	Lys	Lys	Arg
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			180					185					190		
Gly	Lys	Glu	Val	Leu	Val	Leu	Trp	Gly	Ile	His	His	Pro	Ser	Lys	Glu
	195						200					205			
Ser	Thr	Gln	Lys	Ala	Ile	Asp	Gly	Val	Thr	Asn	Lys	Val	Asn	Ser	Asp
	210					215					220				
Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser	Arg	Tyr	Ser	Lys	Lys	Phe	Lys	Pro
225					230					235					240
Glu	Ile	Ala	Ile	Arg	Pro	Lys	Val	Arg	Asp	Gln	Glu	Gly	Arg	Met	Asn
				245					250					255	
Tyr	Tyr	Trp	Thr	Leu	Val	Glu	Pro	Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala
			260					265					270		
Thr	Gly	Asn	Leu	Val	Val	Pro	Arg	Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn
		275					280					285			
Ala	Gly	Ser	Gly	Ile	Ile	Ile	Ser	Asp	Thr	Pro	Val	His	Asp	Cys	Asn
	290					295					300				
Thr	Thr	Cys	Gln	Thr	Pro	Lys	Gly	Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe
305					310					315					320
Gln	Asn	Ile	His	Pro	Ile	Thr	Ile	Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys
				325					330					335	
Ser	Thr	Lys	Leu	Arg	Leu	Ala	Thr	Gly	Leu	Arg	Asn	Ser	Pro	Gln	Arg
			340					345					350		
Glu	Arg	Arg	Lys	Lys	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile
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<400> 50

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Ser

<210> 51

<211> 1790

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 51

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<211> 589

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

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			20					25					30		
Thr	Asp	Thr	Val	Asp	Thr	Val	Leu	Glu	Lys	Asn	Val	Thr	Val	Thr	His
			35				40					45			
Ser	Val	Asn	Leu	Leu	Glu	Asp	Lys	His	Asn	Gly	Lys	Leu	Cys	Lys	Leu
	50					55				60					
Arg	Gly	Val	Ala	Pro	Leu	His	Leu	Gly	Lys	Cys	Asn	Ile	Ala	Gly	Trp
65					70					75					80
Ile	Leu	Gly	Asn	Pro	Glu	Cys	Glu	Ser	Leu	Ser	Thr	Ala	Ser	Ser	Trp
				85					90					95	
Ser	Tyr	Ile	Val	Glu	Thr	Pro	Ser	Ser	Asp	Asn	Gly	Thr	Cys	Tyr	Pro
			100					105					110		
Gly	Asp	Phe	Ile	Asp	Tyr	Glu	Glu	Leu	Arg	Glu	Gln	Leu	Ser	Ser	Val
	115					120						125			
Ser	Ser	Phe	Glu	Arg	Phe	Glu	Ile	Phe	Pro	Lys	Thr	Ser	Ser	Trp	Pro
	130					135					140				
Asn	His	Asp	Ser	Asn	Lys	Gly	Val	Thr	Ala	Ala	Cys	Pro	His	Ala	Gly
145					150					155					160
Ala	Lys	Ser	Phe	Tyr	Lys	Asn	Leu	Ile	Trp	Leu	Val	Arg	Lys	Lys	Arg
			165						170					175	
Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Tyr	Ile	Asn	Asp	Lys
			180					185					190		
Gly	Lys	Glu	Val	Leu	Val	Leu	Trp	Gly	Ile	His	His	Pro	Ser	Lys	Glu
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Ser	Thr	Gln	Lys	Ala	Ile	Asp	Gly	Val	Thr	Asn	Lys	Val	Asn	Ser	Asp
	210					215					220				
Ala	Tyr	Val	Phe	Val	Gly	Ser	Ser	Arg	Tyr	Ser	Lys	Lys	Phe	Lys	Pro
225					230					235					240
Glu	Ile	Ala	Ile	Arg	Pro	Lys	Val	Arg	Asp	Gln	Glu	Gly	Arg	Met	Asn
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Tyr	Tyr	Trp	Thr	Leu	Val	Glu	Pro	Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala
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Thr	Gly	Asn	Leu	Val	Val	Pro	Arg	Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn
	275						280					285			
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Gln	Asn	Ile	His	Pro	Ile	Thr	Ile	Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys
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agggcgctga aaacctgtat tttcagggcg gttctgggta catcccgga gctccgcgtg 1680
acggtcaggc ttacgttcgt aaagacgggtg aatgggttct gctgtctacc ttcctgggtc 1740
accatcatca ccaccatcac catcatcact gataaaagct t 1781

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<210> 54

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 54

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

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Asn	His	Asp	Ser	Asn	Lys	Gly	Val	Thr	Ala	Ala	Cys	Pro	His	Ala	Gly
145					150					155					160
Ala	Lys	Ser	Phe	Tyr	Lys	Asn	Leu	Ile	Trp	Leu	Val	Arg	Lys	Lys	Arg
				165					170						175
Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Tyr	Ile	Asn	Asp
			180					185					190		
Lys	Gly	Lys	Glu	Val	Leu	Val	Leu	Trp	Gly	Ile	His	His	Pro	Ser	Thr
		195					200					205			
Ser	Ala	Asp	Gln	Gln	Ser	Leu	Tyr	Gln	Asn	Ala	Asp	Ala	Tyr	Val	Phe
	210					215					220				
Val	Gly	Ser	Ser	Arg	Tyr	Ser	Lys	Lys	Phe	Lys	Pro	Glu	Ile	Ala	Ile
225					230					235					240
Arg	Pro	Lys	Val	Arg	Asp	Gln	Glu	Gly	Arg	Met	Asn	Tyr	Tyr	Trp	Thr
				245					250						255
Leu	Val	Glu	Pro	Gly	Asp	Lys	Ile	Thr	Phe	Glu	Ala	Thr	Gly	Asn	Leu
			260					265					270		
Val	Val	Pro	Arg	Tyr	Ala	Phe	Ala	Met	Glu	Arg	Asn	Ala	Gly	Ser	Gly
		275					280					285			
Ile	Ile	Ile	Ser	Asp	Thr	Pro	Val	His	Asp	Cys	Asn	Thr	Thr	Cys	Gln
	290					295					300				
Thr	Pro	Lys	Gly	Ala	Ile	Asn	Thr	Ser	Leu	Pro	Phe	Gln	Asn	Ile	His
305					310					315					320
Pro	Ile	Thr	Ile	Gly	Lys	Cys	Pro	Lys	Tyr	Val	Lys	Ser	Thr	Lys	Leu
				325					330					335	
Arg	Leu	Ala	Thr	Gly	Leu	Arg	Asn	Ile	Glu	Asn	Leu	Tyr	Phe	Gln	Gly
			340					345					350		
Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly	Met
		355					360					365			
Val	Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Gln	Asn	Glu	Gln	Gly	Ser	Gly
	370					375					380				
Tyr	Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Asn	Ala	Ile	Asp	Glu	Ile	Thr
385					390					395					400
Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala
				405					410					415	
Val	Gly	Lys	Glu	Phe	Asn	His	Leu	Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn
			420					425					430		
Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu
		435					440					445			
Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser
						455					460				
Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn
465					470					475					480
Ala	Lys	Glu	Ile	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp
				485					490					495	
Asn	Thr	Cys	Met	Glu	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys
			500					505					510		
Tyr	Ser	Glu	Glu	Ala	Lys	Leu	Asn	Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys
		515					520					525			
Leu	Glu	Ser	Thr	Arg	Ile	Tyr	Gln	Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln
	530					535					540				

Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr
545					550					555					560
Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	Leu	Ser	Thr	Phe	Leu	Gly	His
			565					570						575	
His	His	His	His	His	His	His	His	His							
			580					585							

<210> 55
 <211> 1769
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 55
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 tggagaagaa tgtgaccgtg acccactctg tgaatctgct ggaggataag cacaatggca 180
 agctgtgtaa gctgagagga gttgcccctc tgcacctggg caaatgtaat attgccggct 240
 ggattctggg aaatcctgaa tgtgaaagcc tgtctacagc cagcagctgg tcttatatcg 300
 tggaaacccc tagcagcgac aatggcacct gttaccctgg cgacttcacg gattacgagg 360
 agctgagaga acagctgtct agcgtgtcca gcttcgagag attcgagatc ttccctaaga 420
 caagcagctg gcctaatacac gattctaata agggagtgac agccgcctgt cctcatgccg 480
 gagccaagtc cttttacaag aacctgatct ggctgggtgag aaagaagaga ggccctgttcg 540
 gcgctatcgc cggcttcatt gagggataca tcaacgacaa gggcaaagaa gtgctgggtgc 600
 tgtggggaat ccaccaccct agcacaagcg ccgatcagca gagcctgtac cagaatgccg 660
 atgcctatgt gtttgtgggc agcagcagat acagcaaaaa gttcaagcct gaaattgcc 720
 ttagacccaa agtgagagat caggaaggca gaatgaatta ctactggacc ctggtggaac 780
 ctggcgataa gatcacattt gagggcaccg gaaatctggt ggtgcctaga tatgcatttg 840
 ctatggagag aaatgctggc tctggcatca ttatctctga taccctgtg cacgactgta 900
 ataccacctg tcagacacct aagggcgcca ttaataccag cctgcccttc cagaatattc 960
 accctatcac catcggcaag tgtcctaagt atgtgaagag caccaagctg agactggcta 1020
 ccggtctgag aaatatcgaa aacctgtatt ttcaaggcct gtttggagcc atcgccggct 1080
 ttattgaggg aggatggacc ggaatggtgg atggctggta cggctatcac caccagaatg 1140
 agcagggatc cggatatgcc gccgatctga agtctacaca gaacgccatc gacgagatca 1200
 caaacaaggt gaacagcgtg atcgagaaga tgaacacca gtttacagct gtgggcaagg 1260
 agttcaacca cctggagaag agaatcgaga acctgaacaa gaaagtggac gacggcttcc 1320
 tggatatttg gacctacaat gccgagctgc tcgtgctcct ggagaatgag agaaccctgg 1380
 actaccacga cagcaatgtg aagaacctgt acgagaaggt gagaagccag ctgaagaaca 1440
 atgccaagga gatcggcaac ggctgctttg agttctacca caagtgtgac aacacctgta 1500
 tggagtctgt gaagaacggc acctacgact accctaagta tagcgaggag gccaagctga 1560
 atagagagga gatcgacggc gtgaaactgg aaagcacaag aatctatcag ggcgctgaaa 1620
 acctgtattt tcagggcggt tctgggttaca tcccggaaag tccgcgtgac ggtcaggctt 1680
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 accatcacca tcatcactga taaaagctt 1769

<210> 56
 <211> 593

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 56

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

<210> 58
<211> 1793
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 58
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tggagaagaa tgtgaccgtg acccactctg tgaatctgct ggaggataag cacaatggca 180
agctgtgtaa gctgagagga gttgccctc tgcacctggg caaatgtaat attgccggct 240
ggattctggg aaatcctgaa tgtgaaagcc tgtctacagc cagcagctgg tcttatatcg 300
tggaaacccc tagcagcgac aatggcacct gttaccctgg cgacttcac gattacgagg 360
agctgagaga acagctgtct agcgtgtcca gcttcgagag attcgagatc ttccctaaga 420
caagcagctg gcctaatac gattctaata agggagtgc agccgcctgt cctcatgccg 480
gagccaagtc cttttacaag aacctgatct ggctggtgaa gaagggaac agctacccta 540
agctgtctaa gagctacatc aacgacaagg gcaaagaagt gctggtgctg tggggaatcc 600
accaccctag cacaagcgcc gatcagcaga gcctgtacca gaatgccgat gcctatgtgt 660
ttgtgggcag cagcagatac agcaaaaagt tcaagccttc cctgctgacc gaggtggaga 720
ccccaccag gaacggctgg gagtgcgaagt gctccgactc cggcagaatg aattactact 780
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ccttcagaa tattcaccct atcaccatcg gcaagtgtcc taagtatgtg aagagcacca 1020
agctgagact ggctaccggt ctgagaaata gccctcagag ggagagacgc aagaagagag 1080
gcctgtttgg agccatcgcc ggctttattg agggaggatg gaccggaatg gtggatggct 1140
ggtagggcta tcaccaccag aatgagcagg gatccggata tgccgccgat ctgaagtcta 1200
cacagaacgc catcgacgag atcacaaaca aggtgaacag cgtgatcgag aagatgaaca 1260
cccagtttac agctgtgggc aaggagttca accacctgga gaagagaatc gagaacctga 1320
acaagaaaagt ggacgacggc ttcttgata tttggaccta caatgccgag ctgctcgtgc 1380
tcctggagaa tgagagaacc ctggactacc acgacagcaa tgtgaagaac ctgtacgaga 1440
agggtgagaag ccagctgaag aacaatgcca aggagatcgg caacggctgc tttgagttct 1500
accacaagtg tgacaacacc tgtatggagt ctgtgaagaa cggcacctac gactacccta 1560
agtatagcga ggaggccaag ctgaatagag aggagatcga cggcgtgaaa ctggaaagca 1620
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aagctccgag tgacggtcag gcttacgttc gtaaagacgg tgaatgggtt ctgctgtcta 1740
ccttcctggg tcaccatcat caccaccatc accatcatca ctgataaaag ctt 1793

<210> 59
<211> 593
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 59
Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala Ala His

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

				405					410					415			
Lys	Met	Asn	Thr	Gln	Phe	Thr	Ala	Val	Gly	Lys	Glu	Phe	Asn	His	Leu		
				420					425					430			
Glu	Lys	Arg	Ile	Glu	Asn	Leu	Asn	Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu		
		435						440					445				
Asp	Ile	Trp	Thr	Tyr	Asn	Ala	Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Glu		
	450					455						460					
Arg	Thr	Leu	Asp	Tyr	His	Asp	Ser	Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys		
465					470					475					480		
Val	Arg	Ser	Gln	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Gly	Asn	Gly	Cys		
			485						490					495			
Phe	Glu	Phe	Tyr	His	Lys	Cys	Asp	Asn	Thr	Cys	Met	Glu	Ser	Val	Lys		
			500					505					510				
Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	Lys	Tyr	Ser	Glu	Glu	Ala	Lys	Leu	Asn		
	515						520					525					
Arg	Glu	Glu	Ile	Asp	Gly	Val	Lys	Leu	Glu	Ser	Thr	Arg	Ile	Tyr	Gln		
	530					535					540						
Gly	Ala	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu		
545					550					555					560		
Ala	Pro	Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val		
			565						570					575			
Leu	Leu	Ser	Thr	Phe	Leu	Gly	His	His	His	His	His	His	His	His	His		
			580					585						590			

His

<210> 60
 <211> 1793
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 60
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 tggagaagaa tgtgaccgtg acccactctg tgaatctgct ggaggataag cacaatggca 180
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 ggattctggg aaatcctgaa tgtgaaagcc tgtctacagc cagcagctgg tcttatatcg 300
 tggaaacccc tagcagcgac aatggcacct gttaccctgg cgacttcac gattacgagg 360
 agctgagaga acagctgtct agcgtgtcca gcttcgagag attcgagatc ttccctaaga 420
 caagcagctg gcctaatac gattctaata agggagtgc agccgcctgt cctcatgccg 480
 gagccaagtc cttttacaag aacctgatct ggctggtgaa gaagggaac agctacccta 540
 agctgtctaa gagctacatc aacgacaagg gcaaagaagt gctggtgctg tggggaatcc 600
 accaccctag ctccctgctg accgaggtgg agacccccac caggaacggc tgggagtgc 660
 agtgctccga ctccgatgcc tatgtgtttg tgggcagcag cagatacagc aaaaagttca 720
 agcctgaaat tgccattaga cccaaagtga gagatcagga aggcagaatg aattactact 780
 ggaccctggt ggaacctggc gataagatca catttgaggc caccggaaat ctggtggtgc 840

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ctagatatgc atttgctatg gagagaaatg ctggctctgg catcattatc tctgataccc 900
ctgtgcacga ctgtaatacc acctgtcaga cacctaaggg cgccattaat accagcctgc 960
ccttccagaa tattcaccct atcaccatcg gcaagtgtcc taagtatgtg aagagcacca 1020
agctgagact ggctaccggt ctgagaaaata gccctcagag ggagagacgc aagaagagag 1080
gcctgttttg agccatcgcc ggcttttattg agggaggatg gaccggaatg gtggatggct 1140
ggtagcggcta tcaccaccag aatgagcagg gatccggata tgccgccgat ctgaagtcta 1200
cacagaacgc catcgacgag atcacaaaca aggtgaacag cgtgatcgag aagatgaaca 1260
cccagtttac agctgtgggc aaggagttca accacctgga gaagagaatc gagaacctga 1320
acaagaaagt ggacgacggc ttcctggata tttggacct caatgccgag ctgctcgtgc 1380
tcctggagaa tgagagaacc ctggactacc acgacagcaa tgtgaagaac ctgtacgaga 1440
aggtgagaag ccagctgaag aacaatgcca aggagatcgg caacggctgc tttgagttct 1500
accacaagtg tgacaacacc tgtatggagt ctgtgaagaa cggcacctac gactacccta 1560
agtatagcga ggaggccaag ctgaatagag aggagatcga cggcgtgaaa ctggaaagca 1620
caagaatcta tcagggcgct gaaaacctgt attttcaggg cggttctggt tacatcccgg 1680
aagctccgcg tgacggtcag gcttacgttc gtaaagacgg tgaatgggtt ctgctgtcta 1740
ccttcctggg tcaccatcat caccaccatc accatcatca ctgataaaaag ctt 1793

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<210> 61

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 61

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

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