

SEQUENCE LISTING

<110> PhagoMed Biopharma GmbH

<120> Novel Gardnerella endolysins and uses thereof

<130> AC1230 PCT S3

<150> EP19 17 3389.8

<151> 2019-05-08

<160> 97

<170> BiSSAP 1.3.6

<210> 1

<211> 196

<212> PRT

<213> Artificial Sequence

<220>

<223> H1

<400> 1

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

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195

<210> 2
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<213> Artificial Sequence

<220>
<223> H2

<400> 2
Met Ser Lys Arg Gly Ile Asp Val Ser Glu Trp Gln Gly Asp Ile Asp
1 5 10 15
Phe Asn Ala Val Lys Ala Ser Gly Val Glu Phe Val Ile Ile Arg Ala
20 25 30
Gly Tyr Gly Ile Gly Cys Lys Asp Lys Trp Phe Glu Gln Asn Tyr Arg
35 40 45
Lys Ala Lys Thr Cys Gly Leu Asp Val Gly Ala Tyr Trp Tyr Ser Tyr
50 55 60
Ala Asn Ser Gly Phe Glu Ala Ala Glu Glu Ala Gln Ser Cys Val Asn
65 70 75 80
Met Leu Ser Gly Lys Ser Phe Glu Tyr Pro Val Tyr Phe Asp Leu Glu
85 90 95
Glu Lys Ser Gln Leu Asn Arg Gly Arg Ala Phe Cys Asp Ser Leu Ile
100 105 110
Thr Gly Phe Cys Asn Lys Leu Glu Ser Cys Gly Tyr Tyr Ala Gly Phe
115 120 125
Tyr Thr Ser Leu Ser Thr Ala Asn Asn Leu Val Ser Ala His Val Arg
130 135 140
Asn Arg Tyr Ala Leu Trp Ile Ala Gln Trp Asn Thr His Cys Ser Tyr
145 150 155 160
Gln Gly Ser Tyr Gly Leu Trp Gln Tyr Ser Ser Ser Gly Ser Val Pro
165 170 175
Gly Val Ala Gly Arg Val Asp Met Asp Tyr Ala Tyr Val Asp Tyr Pro
180 185 190
Ser Ile Ile Lys
195

<210> 3
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<213> Artificial Sequence

<220>
<223> H3

<400> 3
Met Ser Lys Lys Gly Ile Asp Val Ser Val Trp Gln Gly Asp Ile Asp

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

<210> 4

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<212> PRT

<213> Artificial Sequence

<220>

<223> H4

<400> 4

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

<210> 6
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<213> Artificial Sequence

<220>
<223> H6

<400> 6
Met Ser Lys Lys Gly Ile Asp Val Ser Val Trp Gln Gly Asp Ile Asp
1 5 10 15
Phe Asn Ala Val Lys Ala Ser Gly Val Glu Phe Val Ile Ile Arg Ala
20 25 30
Gly Tyr Gly Ile Gly Cys Lys Asp Lys Trp Phe Glu Gln Asn Tyr Arg
35 40 45
Lys Ala Lys Thr Cys Gly Leu Asp Val Gly Ala Tyr Trp Tyr Ser Tyr
50 55 60
Ala Asn Ser Gly Phe Glu Ala Ala Glu Glu Ala Gln Ser Cys Val Asn
65 70 75 80
Met Leu Ser Gly Lys Ser Phe Glu Tyr Pro Val Tyr Phe Asp Leu Glu
85 90 95
Glu Lys Ser Gln Leu Asn Arg Gly Arg Ala Phe Cys Asp Ser Leu Ile
100 105 110
Thr Ser Phe Cys Ser Lys Leu Glu Ser Cys Gly Tyr Tyr Ala Gly Phe
115 120 125
Tyr Thr Ser Leu Ser Thr Ala Asn Asn Leu Val Ser Ala His Val Arg
130 135 140
Asn Arg Tyr Ala Leu Trp Ile Ala Gln Trp Asn Thr His Cys Asp Tyr
145 150 155 160
Gln Gly Ser Tyr Gly Leu Trp Gln Tyr Ser Ser Ser Gly Ser Val Pro
165 170 175
Gly Val Ala Gly Arg Val Asp Met Asp Tyr Ala Tyr Lys Asn Tyr Pro
180 185 190
Ser Ile Ile Lys
195

<210> 7
<211> 196
<212> PRT
<213> Artificial Sequence

<220>
<223> H7

<400> 7
Met Ser Lys Lys Gly Ile Asp Val Ser Glu Trp Gln Gly Asp Ile Asp
1 5 10 15
Phe Asn Ala Val Lys Ala Ser Gly Val Glu Phe Val Ile Ile Arg Ala

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

<210> 8

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> EL8

<400> 8

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

Tyr	Thr	Ser	Leu	Ser	Thr	Ala	Asn	Asn	Leu	Val	Ser	Ser	His	Val	Arg
130						135					140				
Asn	Arg	Tyr	Ala	Leu	Trp	Ile	Ala	Gln	Trp	Asn	Thr	His	Cys	Ser	Tyr
145					150					155					160
Gln	Gly	Ser	Tyr	Gly	Leu	Trp	Gln	Tyr	Ser	Ser	Asn	Gly	Ser	Val	Pro
				165					170					175	
Gly	Val	Ala	Gly	Arg	Val	Asp	Met	Asp	Tyr	Ala	Tyr	Val	Asp	Tyr	Pro
			180					185					190		
Ser	Ile	Ile	Lys	Asn	Ala	Gly	Leu	Asn	Gly	Tyr	Lys	Asn	Gly	Gly	Ser
	195					200						205			
Tyr	Thr	Ala	Pro	Gln	Thr	Ser	Ser	Ile	Asp	Asp	Val	Ala	Arg	Glu	Val
	210					215					220				
Ile	Asn	Gly	Ala	Trp	Gly	Asn	Gly	Asn	Glu	Arg	Lys	Gln	Arg	Leu	Thr
225					230					235					240
Gln	Ala	Gly	Tyr	Asp	Tyr	Thr	Ser	Val	Gln	Asn	Lys	Val	Asn	Lys	Leu
				245					250					255	
Leu	Gly	Val	Lys	Ala	Cys	Arg	Lys	Ser	Val	Asp	Glu	Leu	Ala	Arg	Glu
			260					265					270		
Val	Ile	Arg	Gly	Thr	Trp	Gly	Asn	Gly	Asn	Glu	Arg	Lys	Asn	Arg	Leu
	275					280						285			
Thr	Gln	Ala	Gly	Tyr	Asp	Tyr	Asp	Thr	Val	Gln	Lys	Arg	Val	Asn	Glu
	290					295					300				
Leu	Leu														
305															

<210> 9
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 <213> Artificial Sequence

<220>
 <223> EL9

<400> 9

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

Gly	Ile	Ala	Gly	Arg	Val	Asp	Met	Asp	Tyr	Ala	Tyr	Val	Asp	Tyr	Pro
			180					185					190		
Ser	Val	Ile	Lys												
			195												

<210> 11
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H11

<400> 11

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

<210> 12
 <211> 196
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H12

<400> 12

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Met Ser Lys Lys Gly Ile Asp Val Ser Val Trp Gln Gly Asp Ile Asp
1      5      10      15
Phe Asn Ala Val Lys Ala Ser Gly Val Glu Phe Val Ile Ile Arg Ala
      20      25      30
Gly Tyr Gly Ile Gly His Lys Asp Lys Trp Phe Glu Glu Asn Tyr Arg
      35      40      45
Lys Ala Lys Lys Thr Ala Gly Leu Asp Val Gly Ser Tyr Trp Tyr Ser Tyr
      50      55      60
Ala Ser Ser Ala Gly Glu Val Ala Leu Glu Ala Gln Ser Cys Val Asn
65      70      75      80
Ile Leu Ser Gly Lys Ser Phe Glu Tyr Pro Val Tyr Phe Asp Leu Glu
      85      90      95
Glu Lys Ser Gln Leu Asn Arg Gly Arg Asp Phe Cys Asp Ser Leu Ile
      100     105     110
Thr Ser Phe Cys Asn Lys Leu Glu Ala Cys Gly Tyr Tyr Ala Gly Phe
      115     120     125
Tyr Thr Ser Leu Ser Val Ala Asn Asn Leu Val Ser Ser His Val Arg
      130     135     140
Asp Arg Tyr Ala Leu Trp Ile Ala Gln Trp Asn Thr His Cys Ser Tyr
145     150     155     160
Gln Gly Ser Tyr Gly Leu Trp Gln Tyr Ser Ser Ser Gly Ser Val Asn
      165     170     175
Gly Ile Ala Gly Arg Val Asp Met Asp Tyr Ala Tyr Val Asp Tyr Pro
      180     185     190
Ser Val Ile Lys
      195
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<210> 13

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> EL13

<400> 13

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

<210> 14

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> EL14

<400> 14

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

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

<220>
<223> B1_C

<400> 16
Gly Val Lys Ala Cys Arg Lys Ser Val Asp Glu Leu Ala Arg Glu Val
1 5 10 15
Ile Arg Gly Ala Trp Gly Asn Gly Ser Thr Arg Lys Gln Arg Leu Ala
20 25 30
Gln Ala Gly Tyr Asp Tyr Asp Thr Val Gln Lys Arg Val Asn Glu Leu
35 40 45
Leu

<210> 17
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> B2_N

<400> 17
Asp Gln Ala Ala Arg Thr Ser Ser Ile Asp Glu Val Ala Arg Glu Val
1 5 10 15
Ile Asn Gly Ala Trp Gly Asn Gly Asn Glu Arg Lys Gln Arg Leu Thr
20 25 30
Ser Ala Gly Tyr Asp Tyr Ala Ser Val Gln Asn Lys Val Asn Glu Leu
35 40 45
Leu

<210> 18
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> B2_C

<400> 18
Gly Val Lys Ala Cys Arg Lys Ser Val Asp Glu Ile Ala Arg Glu Val
1 5 10 15

Ile	Arg	Gly	Thr	Trp	Gly	Asn	Gly	Ser	Thr	Arg	Lys	Gln	Arg	Leu	Thr
			20					25					30		
Gln	Ala	Gly	Tyr	Asp	Tyr	Asp	Thr	Val	Gln	Lys	Arg	Val	Asn	Glu	Leu
		35					40					45			
Leu															

<210> 19
 <211> 49
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> B3_N

<400> 19															
Tyr	Thr	Ala	Pro	Gln	Thr	Ser	Ser	Ile	Asp	Glu	Val	Ala	Arg	Glu	Val
1				5				10					15		
Ile	Asn	Gly	Asp	Trp	Gly	Asn	Gly	Asn	Asp	Arg	Lys	Asn	Arg	Leu	Ile
		20					25					30			
Ser	Ala	Gly	Tyr	Asp	Tyr	Ala	Ser	Val	Gln	Asn	Lys	Val	Asn	Glu	Leu
		35					40					45			
Leu															

<210> 20
 <211> 49
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> B3_C

<400> 20															
Gly	Val	Lys	Ala	Tyr	Arg	Lys	Ser	Val	Asp	Glu	Leu	Ala	Arg	Glu	Val
1				5				10					15		
Ile	Arg	Gly	Thr	Trp	Gly	Asn	Gly	Ser	Met	Arg	Lys	His	Arg	Leu	Thr
		20					25					30			
Gln	Ala	Gly	Tyr	Asp	Tyr	Asp	Ala	Val	Gln	Lys	Arg	Val	Asn	Glu	Leu
		35					40					45			
Leu															

<210> 21
 <211> 49
 <212> PRT
 <213> Artificial Sequence

<220>

<223> B4_N

<400> 21

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

Leu

<210> 22

<211> 49

<212> PRT

<213> Artificial Sequence

<220>

<223> B4_C

<400> 22

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

Leu

<210> 23

<211> 49

<212> PRT

<213> Artificial Sequence

<220>

<223> B5_N

<400> 23

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

Leu

<210> 24
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> B5_C

<400> 24
Gly Val Lys Ala Cys Arg Lys Ser Val Asp Glu Leu Ala Arg Glu Val
1 5 10 15
Ile Arg Gly Thr Trp Gly Asn Gly Asn Glu Arg Lys Asn Arg Leu Thr
20 25 30
Gln Ala Gly Tyr Asp Tyr Asp Thr Val Gln Lys Arg Val Asn Glu Leu
35 40 45
Leu

<210> 25
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> B6_N

<400> 25
Asn Gln Ala Ala Arg Thr Ser Ser Ile Asp Asp Val Ala Arg Glu Val
1 5 10 15
Ile Asn Gly Ala Trp Gly Asn Gly Asn Glu Arg Lys Gln Arg Leu Thr
20 25 30
Gln Ala Gly Tyr Asp Tyr Ala Ser Val Ala Lys
35 40

<210> 26
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> B7_N

<400> 26
Asp Gln Ala Ala Arg Thr Ser Ser Ile Asp Glu Val Ala Arg Glu Val
1 5 10 15

Ile	Asn	Gly	Ala	Trp	Gly	Asn	Gly	Asn	Glu	Arg	Lys	Gln	Arg	Leu	Thr
			20					25					30		
Gln	Ala	Gly	Tyr	Asp	Tyr	Thr	Ser	Val	Gln	Asn	Lys	Val	Asn	Lys	Leu
		35					40					45			
Leu															

<210> 27
 <211> 49
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> B7_C

<400> 27															
Gly	Val	Lys	Ala	Cys	Arg	Lys	Ser	Val	Asp	Glu	Leu	Ala	Arg	Glu	Val
1				5					10					15	
Ile	Arg	Gly	Thr	Trp	Gly	Asn	Gly	Asn	Glu	Arg	Lys	Asn	Arg	Leu	Thr
			20					25					30		
Gln	Ala	Gly	Tyr	Asp	Tyr	Asp	Thr	Val	Gln	Lys	Arg	Val	Asn	Glu	Leu
		35					40					45			
Leu															

<210> 28
 <211> 49
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> B10_N

<400> 28															
Tyr	Thr	Ala	Pro	Gln	Ile	Ser	Ser	Ile	Asp	Glu	Val	Ala	Arg	Glu	Val
1				5					10					15	
Ile	Asn	Gly	Asp	Trp	Gly	Asn	Gly	Asn	Glu	Arg	Lys	Gln	Arg	Leu	Thr
			20					25					30		
Ser	Ala	Gly	Tyr	Asp	Tyr	Ala	Ser	Val	Gln	Asn	Lys	Val	Asn	Glu	Leu
		35					40					45			
Leu															

<210> 29
 <211> 49
 <212> PRT
 <213> Artificial Sequence

<220>

<223> B10_C

<400> 29

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

Leu

<210> 30

<211> 49

<212> PRT

<213> Artificial Sequence

<220>

<223> B11_N

<400> 30

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

Leu

<210> 31

<211> 49

<212> PRT

<213> Artificial Sequence

<220>

<223> B11_C

<400> 31

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

Leu

<210> 32
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> B12_N

<400> 32
Tyr Thr Ala Pro Gln Thr Ser Ser Ile Asp Glu Val Ala Arg Glu Val
1 5 10 15
Ile Asn Gly Asp Trp Gly Asn Gly Ile Glu Arg Lys Asn Arg Leu Thr
20 25 30
Ser Ala Gly Tyr Asp Tyr Thr Ser Val Gln Asn Lys Val Asn Glu Leu
35 40 45
Leu

<210> 33
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> B12_C

<400> 33
Gly Val Lys Ala Tyr Arg Lys Ser Val Asp Glu Leu Ala Arg Glu Val
1 5 10 15
Ile Arg Gly Thr Trp Gly Asn Gly Lys Thr Arg Lys Gln Arg Leu Thr
20 25 30
Gln Ala Gly Tyr Asp Tyr Asn Ala Val Gln Lys Arg Val Asn Glu Leu
35 40 45
Leu

<210> 34
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> linker polypeptide

<220>

<221> VARIANT
<222> 1
<223> Asn = Lys

<220>
<221> VARIANT
<222> 8
<223> Xaa = Lys or Gln

<400> 34
Asn Ala Gly Leu Asn Gly Tyr Xaa Asn Gly Gly Ser
1 5 10

<210> 35
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<220>
<221> VARIANT
<222> 1..6
<223> Xaa = Gly, Ala or Ser

<400> 35
Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 36
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<220>
<221> VARIANT
<222> 1..9
<223> Xaa = Gly, Ala or Ser

<400> 36
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 37

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

<220>
<223> linker

<220>
<221> VARIANT
<222> 1..12
<223> Xaa = Gly, Ala or Ser

<400> 37
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 38
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<220>
<221> VARIANT
<222> 1..15
<223> Xaa = Gly, Ala or Ser

<400> 38
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

<210> 39
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<220>
<221> VARIANT
<222> 1..18
<223> Xaa = Gly, Ala or Ser

<400> 39

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa

<210> 40
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 40
Gly Gly Ser Gly Gly Ser
1 5

<210> 41
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 41
Gly Gly Ser Gly Gly Ser Gly Gly Ser
1 5

<210> 42
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 42
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
1 5 10

<210> 43
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> linker

<400> 43

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
1 5 10 15

<210> 44

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 44

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15
Gly Ser

<210> 45

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 45

Asn Ala Gly Leu Asn Gly Tyr Lys Asn Gly Gly Ser
1 5 10

<210> 46

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<220>

<221> VARIANT

<222> 1

<223> Xaa = Asn or Lys

<220>

<221> VARIANT
<222> 2
<223> Xaa = Ala or Val

<220>
<221> VARIANT
<222> 7
<223> Xaa = Tyr or Cys

<220>
<221> VARIANT
<222> 8
<223> Xaa = Lys or Gln

<400> 46
Xaa Xaa Gly Leu Asn Gly Xaa Xaa Asn Gly Gly Ser
1 5 10

<210> 47
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> CW_7 motif

<220>
<221> VARIANT
<222> 38
<223> Xaa is Ile for motif No. 1 and No. 2
Xaa is Leu for motif No. 3

<400> 47
Thr Val Ala Asn Glu Val Ile Gln Gly Leu Trp Gly Asn Gly Gln Glu
1 5 10 15
Arg Tyr Asp Ser Leu Ala Asn Ala Gly Tyr Asp Pro Gln Ala Val Gln
20 25 30
Asp Lys Val Asn Glu Xaa Leu
35

<210> 48
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> primer T7casette-16-rev

<400> 48
aacagggtctc aatacaatcc ggatatagtt cctcctttca gc 42

<210> 49
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> primer T7casette-01-for

<400> 49
aacagggtctc aacctccgcg aaattaatac gactcactat agg 43

<210> 50
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer EL_H1-rev

<400> 50
aacagggtctc aagccggcat ttttgatgat gctcggg 37

<210> 51
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> primer EL_H2-rev

<400> 51
aacagggtctc aagccaacat ttttaataat gctcgataa tcc 43

<210> 52
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> primer EL_H3-rev

<400> 52

aacaggtctc aagccggcgt ttttgataac gctcggg

37

<210> 53

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer EL_H4-rev

<400> 53

aacaggtctc aagcccacgt tcttgatgat gctcgg

36

<210> 54

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer EL_H5-rev

<400> 54

aacaggtctc aagccggcgt ttttgatgat gctcgg

36

<210> 55

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> primer EL_H6-rev

<400> 55

aacaggtctc aagccggcat tcttaataat gctcggata

39

<210> 56

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> primer EL_H7-rev

<400> 56

aacaggtctc aagccggcgt ttttaatgat gctcggataa tc

42

<210> 57

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer EL_H10-rev

<400> 57

aacaggtctc aagccggcgt ttttgatcac gctcgg

36

<210> 58

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> primer EL_H11-rev

<400> 58

aacaggtctc aagccggcct tcttgataac gctcggataa tc

42

<210> 59

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer EL_H12-rev

<400> 59

aacaggtctc aagccggcat tcttgatcac gctcgg

36

<210> 60

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer EL_B6-for

<400> 60

aacaggtctc aggcttaaac ggctgcaaaa atggcgg

37

<210> 61

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer EL_B7-for

<400> 61

aacaggtctc aggcttaaac ggctgcaaaa acggtgg

37

<210> 62

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer EL_B10-for

<400> 62

aacaggtctc aggcttaaac ggctataaaa acggcggc

38

<210> 63

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer EL_B11-for

<400> 63

aacaggtctc aggcttaa at ggttacaaga atggcggcag

40

<210> 64

<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer EL_B12-for

<400> 64
aacaggtctc aggcttaa at ggctaccaga acggcgg 37

<210> 65
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer EL_B1-for

<400> 65
aacaggtctc aggcttaa ac ggctgcaaga atggtgg 37

<210> 66
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer EL_B2-for

<400> 66
aacaggtctc aggcttaa at ggttgcaaga acggcgg 37

<210> 67
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer EL_B3-for

<400> 67
aacaggtctc aggcttaa at ggctaccaga atggcggc 38

<210> 68
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer EL_B4-for

<400> 68
aacagggtctc aggcttaaataa ggctgcaaaa acgggtggc 38

<210> 69
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer T7term-STOP-for

<400> 69
aacagggtctc atgacgccat taacctgatg ttctggg 37

<210> 70
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> linker region L10

<400> 70
Asn Ala Gly Leu Asn Gly Tyr Lys Asn Gly Gly Ser
1 5 10

<210> 71
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminus of B-domains

<400> 71

Val Asn Glu Leu Leu
1 5

<210> 72
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminus of B-domains

<400> 72
Val Asn Lys Leu Leu
1 5

<210> 73
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminus of CW_7 motifs

<400> 73
Val Asn Glu Ile Leu
1 5

<210> 74
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> L1

<400> 74
Asn Ala Gly Leu Asn Gly Cys Lys Asn Gly Gly Ser
1 5 10

<210> 75
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> L2

<400> 75
Asn Val Gly Leu Asn Gly Cys Lys Asn Gly Gly Ser
1 5 10

<210> 76
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> L3

<400> 76
Asn Ala Gly Leu Asn Gly Tyr Gln Asn Gly Gly Ser
1 5 10

<210> 77
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> L4

<400> 77
Asn Val Gly Leu Asn Gly Cys Lys Asn Gly Gly Ser
1 5 10

<210> 78
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> L5

<400> 78
Asn Ala Gly Leu Asn Gly Cys Lys Asn Gly Gly Ser
1 5 10

<210> 79
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> L6

<400> 79

Asn Ala Gly Leu Asn Gly Cys Lys Asn Gly Gly Ser
1 5 10

<210> 80

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> L7

<400> 80

Asn Ala Gly Leu Asn Gly Cys Lys Asn Gly Gly Ser
1 5 10

<210> 81

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> L10

<400> 81

Asn Ala Gly Leu Asn Gly Tyr Lys Asn Gly Gly Ser
1 5 10

<210> 82

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> L11

<400> 82

Lys Ala Gly Leu Asn Gly Tyr Lys Asn Gly Gly Ser
1 5 10

<210> 83

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> L12

<400> 83

Asn Ala Gly Leu Asn Gly Tyr Gln Asn Gly Gly Ser
1 5 10

<210> 84

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> EL11_strain_JCP8017A

<400> 84

Met Ser Lys Arg Gly Ile Asp Val Ser Val Trp Gln Gly Asp Ile Asp
1 5 10 15
Phe Asn Ala Val Lys Ala Ser Gly Val Glu Phe Val Ile Ile Arg Ala
20 25 30
Gly Tyr Gly Ile Gly His Lys Asp Lys Trp Phe Glu Gln Asn Tyr Arg
35 40 45
Lys Ala Lys Thr Thr Gly Leu Asp Val Gly Ala Tyr Trp Tyr Ser Tyr
50 55 60
Ala Ser Ser Ala Gly Glu Ala Ala Glu Glu Ala Gln Ser Cys Val Asn
65 70 75 80
Ile Leu Ser Gly Lys Ser Phe Glu Tyr Pro Val Tyr Phe Asp Leu Glu
85 90 95
Glu Lys Ser Gln Leu Asn Arg Gly Arg Asp Phe Cys Asp Ser Leu Ile
100 105 110
Thr Ser Phe Cys Asn Lys Leu Glu Thr Tyr Gly Tyr Tyr Ala Gly Phe
115 120 125
Tyr Thr Ser Leu Ser Val Ala Asn Asn Leu Val Ser Ser His Val Arg
130 135 140
Asp Arg Tyr Ala Leu Trp Ile Ala Gln Trp Asn Thr His Cys Asp Tyr
145 150 155 160
Gln Gly Ser Tyr Gly Leu Trp Gln Tyr Ser Ser Ser Gly Ser Val Asp
165 170 175
Gly Ile Ala Gly Arg Val Asp Met Asp Tyr Thr Tyr Val Asp Tyr Pro
180 185 190
Ser Val Ile Lys Lys Ala Gly Leu Asn Gly Tyr Lys Asn Gly Gly Ser
195 200 205
Tyr Thr Ala Pro Gln Thr Ser Ser Ile Asp Glu Val Ala Arg Glu Val
210 215 220
Ile Asn Gly Asp Trp Gly Asn Gly Asn Glu Arg Lys Asn Arg Leu Thr
225 230 235 240
Ser Ala Gly Tyr Asp Tyr Thr Ser Val Gln Asn Lys Val Asn Glu Leu

				245					250					255			
Leu	Gly	Val	Lys	Ala	Tyr	Arg	Lys	Ser	Val	Asp	Glu	Leu	Ala	Arg	Glu		
			260					265					270				
Val	Ile	Arg	Gly	Thr	Trp	Gly	Asn	Gly	Ser	Thr	Arg	Lys	Gln	Arg	Leu		
		275					280					285					
Thr	Gln	Ala	Gly	Tyr	Asp	Tyr	Asp	Ala	Val	Gln	Lys	Arg	Val	Asn	Glu		
	290					295					300						
Leu	Leu																
305																	

<210> 85
 <211> 306
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EL3_strain_Gv18-4

<400> 85

Met	Ser	Lys	Lys	Gly	Ile	Asp	Val	Ser	Val	Trp	Gln	Gly	Asp	Ile	Asp
1			5						10					15	
Phe	Asn	Ser	Val	Lys	Ala	Ser	Gly	Val	Glu	Phe	Val	Ile	Ile	Arg	Ala
		20					25					30			
Gly	Tyr	Gly	Ile	Gly	His	Lys	Asp	Lys	Trp	Phe	Glu	Glu	Asn	Tyr	Arg
	35					40					45				
Lys	Ala	Lys	Thr	Ala	Gly	Leu	Asp	Val	Gly	Ser	Tyr	Trp	Tyr	Ser	Tyr
	50					55				60					
Ala	Ser	Ser	Ala	Gly	Glu	Ala	Ser	Glu	Glu	Ala	Gln	Ser	Cys	Val	Asn
65				70					75					80	
Ile	Leu	Ser	Gly	Lys	Ser	Phe	Glu	Tyr	Pro	Ile	Tyr	Phe	Asp	Leu	Glu
			85					90					95		
Glu	Lys	Ser	Gln	Leu	Asn	Arg	Gly	Arg	Asp	Phe	Cys	Asp	Ser	Leu	Ile
		100					105						110		
Thr	Ser	Phe	Cys	Asn	Lys	Leu	Glu	Ala	Cys	Gly	Tyr	Tyr	Ala	Gly	Phe
	115					120					125				
Tyr	Thr	Ser	Leu	Ser	Val	Ala	Asn	Asn	Leu	Val	Ser	Ser	His	Val	Arg
	130					135					140				
Asp	Arg	Tyr	Ala	Leu	Trp	Ile	Ala	Gln	Trp	Asn	Thr	His	Cys	Ser	Tyr
145				150					155					160	
Gln	Gly	Ser	Tyr	Gly	Leu	Trp	Gln	Tyr	Ser	Ser	Ser	Gly	Ser	Val	Asn
			165				170						175		
Gly	Ile	Ala	Gly	Arg	Val	Asp	Met	Asp	Tyr	Ala	Tyr	Val	Asp	Tyr	Pro
	180						185					190			
Ser	Val	Ile	Lys	Asn	Ala	Gly	Leu	Asn	Gly	Tyr	Gln	Asn	Gly	Gly	Ser
	195					200					205				
Tyr	Thr	Ala	Pro	Gln	Thr	Ser	Ser	Ile	Asp	Glu	Val	Ala	Arg	Glu	Val
	210					215					220				
Ile	Asn	Gly	Asp	Trp	Gly	Asn	Gly	Asn	Asp	Arg	Lys	Asn	Arg	Leu	Ile
225				230					235					240	

Ser Ala Gly Tyr Asp Tyr Ala Ser Val Gln Asn Lys Val Asn Glu Leu
245 250 255
Leu Gly Val Lys Ala Tyr Arg Lys Ser Val Asp Glu Leu Ala Arg Glu
260 265 270
Val Ile Arg Gly Thr Trp Gly Asn Gly Ser Met Arg Lys His Arg Leu
275 280 285
Thr Gln Ala Gly Tyr Asp Tyr Asp Ala Val Gln Lys Arg Val Asn Glu
290 295 300
Leu Leu
305

<210> 86
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> EL10_strain_G30-4

<400> 86
Met Ser Lys Arg Gly Ile Asp Val Ser Val Trp Gln Gly Asp Ile Asp
1 5 10 15
Phe Asn Ala Val Lys Ala Ser Gly Val Glu Phe Val Ile Ile Arg Ala
20 25 30
Gly Tyr Gly Ile Gly His Lys Asp Lys Trp Phe Glu Glu Asn Tyr Arg
35 40 45
Lys Ala Lys Thr Val Gly Leu Asp Val Gly Ala Tyr Trp Tyr Ser Tyr
50 55 60
Ala Ser Ser Ala Gly Glu Ala Ser Glu Glu Ala Gln Ser Cys Val Asn
65 70 75 80
Ile Leu Ser Gly Lys Ser Phe Glu Tyr Pro Val Tyr Phe Asp Leu Glu
85 90 95
Glu Lys Ser Gln Leu Asn Arg Gly Arg Asp Phe Cys Asp Ser Leu Ile
100 105 110
Thr Ser Phe Cys Asn Lys Leu Glu Ala Cys Gly Tyr Tyr Ala Gly Phe
115 120 125
Tyr Thr Ser Leu Ser Val Ala Asn Asn Leu Val Ser Ser His Val Arg
130 135 140
Asp Arg Tyr Ala Leu Trp Ile Ala Gln Trp Asn Thr His Cys Ser Tyr
145 150 155 160
Gln Gly Ser Tyr Gly Leu Trp Gln Tyr Ser Ser Ser Gly Ser Val Asn
165 170 175
Gly Ile Ala Gly Arg Val Asp Met Asp Tyr Ala Tyr Val Asp Tyr Pro
180 185 190
Ser Val Ile Lys Asn Ala Gly Leu Asn Gly Tyr Lys Asn Gly Gly Ser
195 200 205
Tyr Thr Ala Pro Gln Ile Ser Ser Ile Asp Glu Val Ala Arg Glu Val
210 215 220
Ile Asn Gly Asp Trp Gly Asn Gly Asn Glu Arg Lys Gln Arg Leu Thr

225		230		235		240									
Ser	Ala	Gly	Tyr	Asp	Tyr	Ala	Ser	Val	Gln	Asn	Lys	Val	Asn	Glu	Leu
		245		250		255									
Leu	Gly	Val	Lys	Ala	Tyr	Arg	Lys	Ser	Val	Asp	Glu	Leu	Ala	Arg	Glu
		260		265		270									
Val	Ile	Arg	Gly	Thr	Trp	Gly	Asn	Gly	Ser	Thr	Arg	Lys	Gln	Arg	Leu
		275		280		285									
Thr	Gln	Ala	Gly	Tyr	Asp	Tyr	Asn	Ala	Val	Gln	Lys	Arg	Val	Asn	Glu
	290			295		300									
Leu	Leu														
305															

<210> 87
 <211> 306
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EL12_strain_3549624_non-prophage

<400> 87

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

Ile	Asn	Gly	Asp	Trp	Gly	Asn	Gly	Ile	Glu	Arg	Lys	Asn	Arg	Leu	Thr
225					230					235					240
Ser	Ala	Gly	Tyr	Asp	Tyr	Thr	Ser	Val	Gln	Asn	Lys	Val	Asn	Glu	Leu
				245					250						255
Leu	Gly	Val	Lys	Ala	Tyr	Arg	Lys	Ser	Val	Asp	Glu	Leu	Ala	Arg	Glu
			260					265						270	
Val	Ile	Arg	Gly	Thr	Trp	Gly	Asn	Gly	Lys	Thr	Arg	Lys	Gln	Arg	Leu
	275						280					285			
Thr	Gln	Ala	Gly	Tyr	Asp	Tyr	Asn	Ala	Val	Gln	Lys	Arg	Val	Asn	Glu
	290					295					300				
Leu	Leu														
305															

<210> 88
 <211> 306
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EL8_strain_JCP7719

<400> 88

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

210		215		220
Ile Asn Gly Ala Trp Gly Asn Gly Asn Glu Arg Lys Gln Arg Leu Thr				
225		230		240
Gln Ala Gly Tyr Asp Tyr Thr Ser Val Gln Asn Lys Val Asn Lys Leu				
	245		250	255
Leu Gly Val Lys Ala Cys Arg Lys Ser Val Asp Glu Leu Ala Arg Glu				
	260		265	270
Val Ile Arg Gly Thr Trp Gly Asn Gly Asn Glu Arg Lys Asn Arg Leu				
	275		280	285
Thr Gln Ala Gly Tyr Asp Tyr Asp Thr Val Gln Lys Arg Val Asn Glu				
	290		295	300
Leu Leu				
305				

<210> 89
 <211> 306
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EL5_strain_JCP7276

<400> 89

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

Asp	Gln	Ala	Ala	Arg	Thr	Ser	Ser	Ile	Asp	Glu	Val	Ala	Arg	Glu	Val
210						215					220				
Ile	Asn	Gly	Ala	Trp	Gly	Asn	Gly	Asn	Glu	Arg	Lys	Gln	Arg	Leu	Thr
225					230					235					240
Gln	Ala	Gly	Tyr	Asp	Tyr	Thr	Ser	Val	Gln	Asn	Lys	Val	Asn	Lys	Leu
				245						250				255	
Leu	Gly	Val	Lys	Ala	Cys	Arg	Lys	Ser	Val	Asp	Glu	Leu	Ala	Arg	Glu
			260					265					270		
Val	Ile	Arg	Gly	Thr	Trp	Gly	Asn	Gly	Asn	Glu	Arg	Lys	Asn	Arg	Leu
		275				280						285			
Thr	Gln	Ala	Gly	Tyr	Asp	Tyr	Asp	Thr	Val	Gln	Lys	Arg	Val	Asn	Glu
	290					295						300			
Leu	Leu														
305															

<210> 90
 <211> 306
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EL7_strain_AMD

<400> 90

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

	195		200		205										
Asp	Gln	Ala	Ala	Arg	Thr	Ser	Ser	Ile	Asp	Glu	Val	Ala	Arg	Glu	Val
	210					215					220				
Ile	Asn	Gly	Ala	Trp	Gly	Asn	Gly	Asn	Glu	Arg	Lys	Gln	Arg	Leu	Thr
225					230					235					240
Gln	Ala	Gly	Tyr	Asp	Tyr	Thr	Ser	Val	Gln	Asn	Lys	Val	Asn	Lys	Leu
				245						250				255	
Leu	Gly	Val	Lys	Ala	Cys	Arg	Lys	Ser	Val	Asp	Glu	Leu	Ala	Arg	Glu
			260					265					270		
Val	Ile	Arg	Gly	Thr	Trp	Gly	Asn	Gly	Asn	Glu	Arg	Lys	Asn	Arg	Leu
		275					280					285			
Thr	Gln	Ala	Gly	Tyr	Asp	Tyr	Asp	Thr	Val	Gln	Lys	Arg	Val	Asn	Glu
	290					295					300				
Leu	Leu														
305															

<210> 91

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> EL4_strain_Gv5-1

<400> 91

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

Ser Ile Ile Lys Asn Val Gly Leu Asn Gly Cys Lys Asn Gly Gly Ser
 195 200 205
 Asp Gln Ala Thr Arg Thr Ser Ser Ile Asp Glu Val Ala Arg Glu Val
 210 215 220
 Ile Asn Gly Ala Trp Gly Asn Gly Asn Glu Arg Lys Gln Arg Leu Thr
 225 230 235 240
 Ser Ala Gly Tyr Asp Tyr Ala Ser Val Gln Asn Lys Val Asn Lys Leu
 245 250 255
 Leu Gly Val Lys Ala Tyr Arg Lys Ser Val Asp Glu Leu Ala Arg Glu
 260 265 270
 Val Ile Arg Gly Thr Trp Gly Asn Gly Asn Glu Arg Lys Gln Arg Leu
 275 280 285
 Ala Gln Ala Gly Tyr Asp Tyr Asp Thr Val Gln Lys Arg Val Asn Glu
 290 295 300
 Leu Leu
 305

<210> 92
 <211> 251
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EL6_strain_1400E_frameshift

<400> 92
 Met Ser Lys Lys Gly Ile Asp Val Ser Val Trp Gln Gly Asp Ile Asp
 1 5 10 15
 Phe Asn Ala Val Lys Ala Ser Gly Val Glu Phe Val Ile Ile Arg Ala
 20 25 30
 Gly Tyr Gly Ile Gly Cys Lys Asp Lys Trp Phe Glu Gln Asn Tyr Arg
 35 40 45
 Lys Ala Lys Thr Cys Gly Leu Asp Val Gly Ala Tyr Trp Tyr Ser Tyr
 50 55 60
 Ala Asn Ser Gly Phe Glu Ala Ala Glu Glu Ala Gln Ser Cys Val Asn
 65 70 75 80
 Met Leu Ser Gly Lys Ser Phe Glu Tyr Pro Val Tyr Phe Asp Leu Glu
 85 90 95
 Glu Lys Ser Gln Leu Asn Arg Gly Arg Ala Phe Cys Asp Ser Leu Ile
 100 105 110
 Thr Ser Phe Cys Ser Lys Leu Glu Ser Cys Gly Tyr Tyr Ala Gly Phe
 115 120 125
 Tyr Thr Ser Leu Ser Thr Ala Asn Asn Leu Val Ser Ala His Val Arg
 130 135 140
 Asn Arg Tyr Ala Leu Trp Ile Ala Gln Trp Asn Thr His Cys Asp Tyr
 145 150 155 160
 Gln Gly Ser Tyr Gly Leu Trp Gln Tyr Ser Ser Ser Gly Ser Val Pro
 165 170 175
 Gly Val Ala Gly Arg Val Asp Met Asp Tyr Ala Tyr Lys Asn Tyr Pro

			180					185				190				
Ser	Ile	Ile	Lys	Asn	Ala	Gly	Leu	Asn	Gly	Cys	Lys	Asn	Gly	Gly	Ser	
		195					200					205				
Asn	Gln	Ala	Ala	Arg	Thr	Ser	Ser	Ile	Asp	Asp	Val	Ala	Arg	Glu	Val	
	210					215					220					
Ile	Asn	Gly	Ala	Trp	Gly	Asn	Gly	Asn	Glu	Arg	Lys	Gln	Arg	Leu	Thr	
225					230					235					240	
Gln	Ala	Gly	Tyr	Asp	Tyr	Ala	Ser	Val	Ala	Lys						
			245						250							

<210> 93
 <211> 306
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EL1_strain_HMP9231

<400> 93

Met	Ser	Lys	Lys	Gly	Ile	Asp	Val	Ser	Glu	Trp	Gln	Gly	Asp	Ile	Asp	
1				5					10					15		
Phe	Asn	Ala	Val	Lys	Ala	Ser	Gly	Val	Glu	Phe	Val	Ile	Ile	Arg	Ala	
		20					25					30				
Gly	Tyr	Gly	Ile	Gly	Cys	Lys	Asp	Lys	Trp	Phe	Glu	Gln	Asn	Tyr	Arg	
	35					40					45					
Lys	Ala	Lys	Thr	Ala	Gly	Leu	Asp	Val	Gly	Ala	Tyr	Trp	Tyr	Ser	Tyr	
	50				55					60						
Ala	Asn	Ser	Gly	Phe	Glu	Ala	Ala	Glu	Glu	Ala	Gln	Ser	Leu	Met	Asn	
65				70					75					80		
Met	Leu	Ser	Gly	Lys	Ser	Phe	Glu	Tyr	Pro	Val	Tyr	Phe	Asp	Leu	Glu	
			85					90					95			
Glu	Lys	Ser	Gln	Leu	Asn	Arg	Gly	Arg	Ala	Phe	Cys	Asp	Ser	Leu	Ile	
		100					105						110			
Thr	Ser	Phe	Cys	Asn	Lys	Leu	Glu	Ala	Cys	Gly	Tyr	Tyr	Ala	Gly	Phe	
	115					120						125				
Tyr	Thr	Ser	Leu	Ser	Thr	Ala	Asn	Asn	Leu	Val	Ser	Ala	His	Val	Arg	
	130				135					140						
Asn	Arg	Tyr	Ala	Leu	Trp	Ile	Ala	Gln	Trp	Asn	Thr	His	Cys	Asn	Tyr	
145				150					155					160		
Gln	Gly	Ser	Tyr	Gly	Leu	Trp	Gln	Tyr	Ser	Ser	Asn	Gly	Ser	Val	Pro	
			165					170					175			
Gly	Val	Ala	Gly	Arg	Val	Asp	Met	Asp	Tyr	Ala	Tyr	Val	Asp	Tyr	Pro	
	180					185						190				
Ser	Ile	Ile	Lys	Asn	Ala	Gly	Leu	Asn	Gly	Cys	Lys	Asn	Gly	Gly	Ser	
	195					200						205				
Asp	Gln	Ala	Ala	Arg	Thr	Ser	Ser	Ile	Asp	Glu	Val	Ala	Arg	Glu	Val	
	210					215					220					
Ile	Asn	Gly	Ala	Trp	Gly	Asn	Gly	Ser	Thr	Arg	Lys	Gln	Arg	Leu	Thr	
225					230					235					240	

Ser Ala Gly Tyr Asp Tyr Ala Ser Val Gln Asn Lys Val Asn Glu Leu
245 250 255
Leu Gly Val Lys Ala Cys Arg Lys Ser Val Asp Glu Leu Ala Arg Glu
260 265 270
Val Ile Arg Gly Ala Trp Gly Asn Gly Ser Thr Arg Lys Gln Arg Leu
275 280 285
Ala Gln Ala Gly Tyr Asp Tyr Asp Thr Val Gln Lys Arg Val Asn Glu
290 295 300
Leu Leu
305

<210> 94
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> EL9_strain_0288E_incomplete_contig

<400> 94
Met Ser Lys Lys Gly Ile Asp Val Ser Glu Trp Gln Gly Asp Ile Asp
1 5 10 15
Phe Asn Ala Val Lys Ala Ser Gly Val Glu Phe Val Ile Ile Arg Ala
20 25 30
Gly Tyr Gly Ile Gly Cys Lys Asp Lys Trp Phe Glu Gln Asn Tyr Arg
35 40 45
Lys Ala Lys Thr Cys Gly Leu Asp Val Gly Ala Tyr Trp Tyr Ser Tyr
50 55 60
Ala Asn Ser Gly Phe Glu Ala Ala Glu Glu Ala Gln Ser Cys Val Asn
65 70 75 80
Met Leu Ser Gly Lys Ser Phe Glu Tyr Pro Val Tyr Phe Asp Leu Glu
85 90 95
Glu Lys Ser Gln Leu Asn Arg Gly Arg Val Phe Cys Asp Ser Leu Ile
100 105 110
Thr Ser Phe Cys Asn Lys Leu Glu Ala Cys Gly Tyr Tyr Ala Gly Phe
115 120 125
Tyr Thr Ser Leu Ser Thr Ala Asn Asn Leu Val Ser Ser His Val Arg
130 135 140
Asn Arg Tyr Ala Leu Trp Ile Ala Gln Trp Asn Thr His Cys Asp Tyr
145 150 155 160
Gln Gly Ser Tyr Gly Leu Trp Gln Tyr Ser Ser Ser Gly Ser Val Pro
165 170 175
Gly Val Ala Gly Arg Val Asp Met Asp Tyr Ala Tyr Val Asp Tyr Pro
180 185 190
Ser Ile Ile Lys Asn Ala Gly Leu Asn Gly Cys Lys Asn Gly Gly Ser
195 200 205
Asp Gln Ala Ala Arg Thr Ser Ser Ile Asp Glu Val Ala Arg Glu Val
210 215 220
Ile Asn Gly Ala Trp Gly Asn Gly Ser Thr Arg Lys Gln Arg Leu Thr

225		230		235	240
Ser	Ala	Gly	Tyr	Asp	Tyr
					Ala
					Lys
		245		250	

<210> 95
 <211> 306
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EL2_strain_Gv18-4

<400> 95

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

Thr Gln Ala Gly Tyr Asp Tyr Asp Thr Val Gln Lys Arg Val Asn Glu
 290 295 300
 Leu Leu
 305

<210> 96
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 Phe Asn Ala Val Lys Ala Ser Gly Val Glu Phe Val Ile Ile Arg Ala
 20 25 30
 Gly Tyr Gly Ile Glu Cys Lys Asp Lys Trp Phe Glu Gln Asn Tyr Arg
 35 40 45
 Lys Ala Lys Thr Ala Gly Leu Asp Val Gly Ala Tyr Trp Tyr Ser Tyr
 50 55 60
 Ala Asn Ser Gly Phe Glu Ala Ala Glu Glu Ala Gln Ser Cys Val Asn
 65 70 75 80
 Met Leu Ser Gly Lys Ser Phe Glu Tyr Pro Val Tyr Phe Asp Leu Glu
 85 90 95
 Glu Lys Ser Gln Leu Asn Arg Gly Arg Ala Phe Cys Asp Ser Leu Ile
 100 105 110
 Thr Ser Phe Cys Asn Lys Leu Glu Ser Cys Gly Tyr Tyr Ala Gly Phe
 115 120 125
 Tyr Thr Ser Leu Ser Thr Ala Asn Asn Leu Val Pro Ala His Val Arg
 130 135 140
 Asn Arg Tyr Ala Leu Trp Ile Ala Gln Trp Asn Thr His Cys Asp Tyr
 145 150 155 160
 Gln Gly Ser Tyr Gly Leu Trp Gln Tyr Ser Ser Gly Ser Val Pro
 165 170 175
 Gly Val Ala Gly Arg Val Asp Met Asp Tyr Ala Tyr Val Asp Tyr Pro
 180 185 190
 Ser Ile Ile Lys Asn Ala Gly Leu Asn Gly Tyr Lys Asn Gly Glu Ser
 195 200 205
 His Gln Ala Thr Arg Thr Thr Ser Ile Asp Glu Val Ala Arg Glu Val
 210 215 220
 Ile Asn Gly Ala Trp Gly Asn Gly Asn Glu Arg Lys Gln Arg Leu Thr
 225 230 235 240
 Gln Ala Gly Tyr Asp Tyr Ala Ser Val Gln Asn Lys Val Asn Glu Leu
 245 250 255
 Leu Gly Val Lys Ala Cys Arg Lys Ser Val Asp Glu Leu Ala Arg Glu
 260 265 270
 Val Ile Arg Gly Thr Trp Gly Asn Gly Asn Glu Arg Lys Asn Arg Leu

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

[illegible]