SEQUENCE LISTING

<110> SAVILE, Christopher
MITCHELL, Vesna
ZHANG, Xiyun
HUISMAN, Gjalt

<120> ENONE REDUCTASES

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<150> 61/140,879
<151> 2008-12-25

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<170> PatentIn 3.5

<210> 1
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<212> DNA
<213> Artificial Sequence

<220>
<223> Old Yellow Enzyme 1 from Saccharomyces pastorianus

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taa 1203

<210> 2
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<212> PRT
<213> Artificial Sequence

<220>
<223> Old Yellow Enzyme 1 from Saccharomyces pastorianus

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

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            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Phe Met
    130                 135                 140
Asp Ala Glu Gln Glu Ala Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Leu Thr Lys Asp Glu Ile Lys Gln Tyr Ile Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Thr Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
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Thr Leu Glu Val Val Asp Ala Leu Val Glu Ala Ile Gly His Glu Lys
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Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Ala Gly Glu
            260                 265                 270
Leu Glu Lys Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
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Val Glu Pro Arg Val Thr Asn Pro Phe Leu Thr Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Glu Gly Gly Ser Asn Asp Phe Val Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Val Ile Arg Ala Gly Asn Phe Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Glu Val Lys Asp Lys Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Asp Arg Leu Glu Lys Gly Leu Pro Leu Asn
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<210> 3
<211> 1203
<212> DNA
<213> Artificial Sequence

<220>
<223> Old Yellow Enzyme 2 from Saccharomyces cerevisiae

<400> 3

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tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
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ttagaaaaag gtctgccact gaacaagtat gaccgtgata cgttctacaa aatgagcgcg 1140
gagggttaca tcgactaccc gacctacgaa gaagccttaa aactgggctg ggacaaaaac 1200
taa 1203

<210> 4
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> Old Yellow Enzyme 2 from Saccharomyces cerevisiae

<400> 4

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			20					25					30		
Val	Ile	Pro	Pro	Leu	Thr	Arg	Met	Arg	Ala	Gln	His	Pro	Gly	Asn	Ile
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Pro	Asn	Arg	Asp	Trp	Ala	Val	Glu	Tyr	Tyr	Ala	Gln	Arg	Ala	Gln	Arg
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Gly	Gly	Tyr	Asp	Asn	Ala	Pro	Gly	Ile	Trp	Ser	Glu	Glu	Gln	Ile	Lys
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Glu	Trp	Thr	Lys	Ile	Phe	Lys	Ala	Ile	His	Glu	Asn	Lys	Ser	Phe	Ala
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Ser	Ala	Asn	Gly	Tyr	Leu	Leu	Asn	Gln	Phe	Leu	Asp	Pro	His	Ser	Asn
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	210					215					220				
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225					230					235					240
Val	Gly	Leu	Arg	Leu	Ser	Pro	Tyr	Gly	Val	Phe	Asn	Ser	Met	Ser	Gly
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Gly	Ala	Glu	Thr	Gly	Ile	Val	Ala	Gln	Tyr	Ala	Tyr	Val	Leu	Gly	Glu
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Leu	Glu	Arg	Arg	Ala	Lys	Ala	Gly	Lys	Arg	Leu	Ala	Phe	Val	His	Leu
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Val	Glu	Pro	Arg	Val	Thr	Asn	Pro	Phe	Leu	Thr	Glu	Gly	Glu	Gly	Glu
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Tyr	Asn	Gly	Gly	Ser	Asn	Lys	Phe	Ala	Tyr	Ser	Ile	Trp	Lys	Gly	Pro
305					310					315					320
Ile	Ile	Arg	Ala	Gly	Asn	Phe	Ala	Leu	His	Pro	Glu	Val	Val	Arg	Glu
				325					330					335	
Glu	Val	Lys	Asp	Pro	Arg	Thr	Leu	Ile	Gly	Tyr	Gly	Arg	Phe	Phe	Ile
			340					345					350		
Ser	Asn	Pro	Asp	Leu	Val	Asp	Arg	Leu	Glu	Lys	Gly	Leu	Pro	Leu	Asn
		355					360					365			
Lys	Tyr	Asp	Arg	Asp	Thr	Phe	Tyr	Lys	Met	Ser	Ala	Glu	Gly	Tyr	Ile
	370					375					380				
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<210> 5
<211> 1203
<212> DNA
<213> Artificial Sequence

<220>
<223> Old Yellow Enzyme 3 from Saccharomyces cerevisiae

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cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
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taa 1203

<210> 6
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> Old Yellow Enzyme 3 from Saccharomyces cerevisiae

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

210 215 220
Thr Leu Glu Val Val Asp Ala Leu Ile Glu Thr Ile Gly Pro Glu Arg
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Thr Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Pro Gly Ile Ile Ala Gln Tyr Ser Tyr Val Leu Gly Glu
260 265 270
Leu Glu Lys Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
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<210> 7
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED chimera of Old Yellow Enzyme

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<210> 8
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED chimera of Old Yellow Enzyme

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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala

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    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
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Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 9
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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<210> 10
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 10

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

370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 11
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 11
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgctcg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
gggggggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgtac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 12
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 12
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Ser Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His

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            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Gly Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu Tyr Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 13
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 13

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggttgg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 14
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 14
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Leu Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 15
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 15
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggcggg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360

tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 16
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 16

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

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            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 17
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 17
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtggggtgg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 18
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 18
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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                   10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Val Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
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145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 19
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 19
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg tgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

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

<220>
<223> ERED variant

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

<210> 21
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 21
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120

cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgct tgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 22
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 22
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Leu Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro

305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 23
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 23
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactggc tgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactacac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 24
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 24
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ala Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu

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        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 25
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 25

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 26
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 26

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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                  10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Met Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 27
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 27
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactggc ggtcctgggc 360
tggaccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 28
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 28
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ala Val Leu Gly Trp Thr Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu

275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 29
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 29
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactggt ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
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aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 30
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

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

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


<210> 31
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 31
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat tgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 32
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 32

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

<210> 33
<211> 1200
<212> DNA

<213> Artificial Sequence

<220>
<223> ERED variant

<400> 33
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgga ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgacgaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 34
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 34
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Glu Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly

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


<210> 35
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 35
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgaa tgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200


<210> 36
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 36
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                   10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
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    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Asn Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 37
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 37

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgca ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
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aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 38
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 38

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

<210> 39
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 39
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt atcccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttcacgac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 40
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

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

```
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Pro Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Thr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 41
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 41

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gaatcgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 42
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 42

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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                   10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
```

```
            20                  25                  30
Val Met Pro Pro Leu Asn Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 43
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 43
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgccg gtccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600

cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggca aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 44
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 44

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

```
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 45
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 45
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgccc cgccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 46
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 46
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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                  10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Pro Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
```

```
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 47
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 47
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttgatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat cgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgccgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagtcg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 48
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 48
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Leu Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ile Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Pro Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 49
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 49
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gagccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat cgtcgttggc 360

tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 50
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

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

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            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 51
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 51
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactggc cgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggtgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 52
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 52
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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Ser Arg Tyr Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Ala Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
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145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 53
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 53
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gagccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactggc cgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gataactcca tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtac gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 54
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 54
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ala Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Asp Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 55
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 55
atgtctttcg ttaaggactt caagccgcag gcactgcgcg acaccaacct gttcgaacct 60
attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gagccgcatg 120

cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactggc cgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gcgaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 56
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 56
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ala Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ala Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro

305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 57
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 57
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat cgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcggaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt tggaactcta tgtcgggcgg cgcggaaacg 780
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
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<210> 58
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 58
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ile Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu

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        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Glu Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Trp Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Thr Phe Tyr Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 59
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 59

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat cgtcctgggc 360
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aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gcgaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caaacttttg gctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 60
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 60

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

<210> 61
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactggc cgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
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tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
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aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caacctttg gctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 62
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 62
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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ala Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Tyr Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu

275 280 285
Val Glu Pro Arg Val Thr Thr Phe Trp Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 63
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgct ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
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aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gcctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 64
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 64
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1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala

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


<210> 65
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat cgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caactgcttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 66
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 66
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ile Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Thr Ala Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 67
<211> 1200
<212> DNA

<213> Artificial Sequence

<220>
<223> ERED variant

<400> 67
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cgcgctacct atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
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atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
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aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg acccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 68
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 68
Met Ser Phe Val Glu Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20   25   30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr Tyr Pro Gly Asn Ile
        35   40   45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50   55   60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65   70   75   80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85   90   95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100   105   110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115   120   125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130   135   140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145   150   155   160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165   170   175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180   185   190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195   200   205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210   215   220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225   230   235   240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ala Asn Ser Met Ser Gly

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                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asn Pro Gly Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 69
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 69

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggca cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gcgaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgtac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 70
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 70

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

```
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ala Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu Tyr Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 71
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 71

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt cgcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
```

aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cccgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 72
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 72

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

<210> 73
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 73
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gcgaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccgag cctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 74
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 74
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1   5   10   15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20   25   30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35   40   45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50   55   60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65   70   75   80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85   90   95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100   105   110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115   120   125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130   135   140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145   150   155   160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165   170   175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180   185   190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195   200   205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe

```
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ala Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
```

<210> 75
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 75

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaggaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt tgcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttcaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 76
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 76

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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                   10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
```

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

<210> 77
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 77
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gtcacgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtt tgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600

cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt tcgaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 78
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 78

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

```
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 79
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 79
atgtctttcg ttaaggactt caagccgcag gcactgcgcg acaccaacct gttcgaacct 60
attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gtcacgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtt ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggag attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacgaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt tcgaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttcaagac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaact 1200

<210> 80
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

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

```
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asp Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ser Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Lys Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Thr
385                 390                 395                 400
```

<210> 81
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 81
atgtctttcg ttaaggactt caagccgcag gcactgcgcg acaccaacct gttcgaacct 60
attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gtcacgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt tcgaactcta tgtcgggcgg cgcggagacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagatgggtc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 82
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 82
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ser Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Gly Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 83
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 83
atgtctttcg ttaaggactt caagccgcag gcactgcgcg acaccaacct gttcgaacct 60
attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gtcacgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtt tgtcctgggc 360

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tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gtgaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttcattac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200


<210> 84
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 84
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                  10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Phe Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Val Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
```

```
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Ile Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 85
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 85
atgtctttcg ttaaggactt caagccgcag gcactgcgcg acaccaacct gttcgaacct 60
attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gtcacgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtt tgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt tcgaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caaatgggtt tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 86
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 86
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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                  10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Phe Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
```

```
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ser Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asn Gly Phe Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 87
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 87

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atgtctttcg ttaaggactt caagccgcag gcactgcgcg acaccaacct gttcgaacct 60
attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gtcacgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcacga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggctac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt tcgaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caacgtcgtt tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca tcgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 88
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 88
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ser Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Thr Ser Phe Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Ile
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 89
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
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cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gtgaactcta tgtcgggcgg cgcggaaacg 780
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cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 90
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

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

305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 91
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
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tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
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cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 92
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 92
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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Pro Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ala Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu

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        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
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Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
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Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Val Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
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Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 93
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 93

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cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgaa tgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 94
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 94

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

<210> 95
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
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tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
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<210> 96
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

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

275 280 285
Val Glu Pro Arg Val Thr Asp Arg Phe Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 97
<211> 1200
<212> DNA
<213> Artificial Sequence

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cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
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cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
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ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
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<210> 98
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 98
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20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala

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


<210> 99
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 99
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg tccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
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aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagattcgtt tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttcattac catgagcgcg 1140
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<210> 100
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

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

<210> 101
<211> 1200
<212> DNA

<213> Artificial Sequence

<220>
<223> ERED variant

<400> 101
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgaa tgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gtgaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 102
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 102
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1   5   10   15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20   25   30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35   40   45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50   55   60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65   70   75   80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85   90   95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100   105   110
Trp Val Gln Leu Asn Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115   120   125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130   135   140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145   150   155   160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165   170   175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180   185   190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195   200   205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210   215   220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225   230   235   240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Val Asn Ser Met Ser Gly

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

<210> 103
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
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atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt tcgaactcta tgtcgggcgg cgcggaaacg 780
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 104
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 104
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg

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    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ser Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Thr Gly Phe Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 105
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 105

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa gagctaacaa tccgcaacat 480
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cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gtgaactcta tgtcgggcgg cgcggaaacg 780
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 106
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 106

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

<210> 107
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 107
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc cggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
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cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 108
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 108
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1   5   10   15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20   25   30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35   40   45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50   55   60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65   70   75   80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85   90   95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100   105   110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115   120   125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130   135   140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145   150   155   160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165   170   175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180   185   190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195   200   205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe

210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ser Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 109
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 109
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acgggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ggtaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 110
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 110
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala

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            20                  25                  30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Arg Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Gly Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 111
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 111

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
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cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gctaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 112
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 112
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ala Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr

370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 113
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 113
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttgaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgggcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 114
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 114
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His

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            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Leu Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Gly Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 115
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 115

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt tgtaactcta tgtcgggcgg cgcggaaacg 780
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aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 116
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 116

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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Cys Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 117
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 117

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
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tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
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cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt cggaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactacac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 118
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 118
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Arg Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile

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            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 119
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 119
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
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cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
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<210> 120
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

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

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145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe His Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 121
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 121

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
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cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
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aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtgg cagggccttc tctggttgag 900
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 122
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 122
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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Ala Gly Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 123
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120

cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caacgccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
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cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 124
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 124
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Thr Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro

305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 125
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
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cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
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<210> 126
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 126
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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu

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        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Arg Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu Tyr Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 127
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
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aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
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cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 128
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 128

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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                  10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Gly Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 129
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcccgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
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cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
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<210> 130
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 130
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Pro Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu

275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 131
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgggcgcg 1140
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<210> 132
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 132
Met Ser Phe Val Lys Asp Phe Lys Pro Pro Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala

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                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Gly Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Gly Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 133
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 133

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgctcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagaccctgc gctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 134
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 134

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

<210> 135
<211> 1200
<212> DNA

<213> Artificial Sequence

<220>
<223> ERED variant

<400> 135
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtgcggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
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ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 136
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 136
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Cys Gly Val Phe Asn Ser Met Ser Gly

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                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Gly Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 137
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 137

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
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atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 138
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 138

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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
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    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Phe Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 139
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 139

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
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atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 140
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 140

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

<210> 141
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 141
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaggcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
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aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagaccctta tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 142
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 142
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1   5   10   15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20   25   30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35   40   45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50   55   60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65   70   75   80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85   90   95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100   105   110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115   120   125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130   135   140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145   150   155   160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165   170   175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180   185   190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195   200   205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe

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    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Tyr Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 143
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 143

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgcgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactggc ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
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cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 144
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 144

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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                   10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
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            20                  25                  30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Ala Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu Tyr Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 145
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 145
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600

cagttcctgg atccgcacag taacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagaccctta tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gatttcgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 146
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 146

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

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    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 147
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 147
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactggc ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 148
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 148
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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                  10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Ala Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
```

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            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 149
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 149

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggaagg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat cgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 150
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

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

<210> 151
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 151
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gagccgcgaa 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgtccatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat cgtcctgggc 360

tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga tggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 152
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 152
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Ser Arg Glu Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Ser Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ile Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile

```
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 153
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 153
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gagccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat cgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 154
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 154
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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                  10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Ser Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Ile Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
```

```
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 155
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 155
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtggggagg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat cgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg ccctgaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaagggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagctg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 156
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 156
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Glu Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ile Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Ala Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 157
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 157
atgtctttcg ttaaggactt caagccgcag gcactgcgcg acaccaacct gttcgaacct 60
attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120

cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggatcg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgat cgtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 158
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 158
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Ile Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Ile Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro

305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 159
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt agcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacgaagc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gaatttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 160
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 160
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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu

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        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ser Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Glu Ala Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Glu Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 161
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 161

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
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aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
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cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 162
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 162
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Ala Phe Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 163
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 163
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaga 720
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cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 164
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 164
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Arg
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ser Asn Ser Met Ser Gly
245 250 255
Gly Ala Gly Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu

275 280 285
Val Glu Pro Arg Val Thr Asp Gln Ala Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 165
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

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cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
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tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
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cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 166
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 166
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala

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                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ile Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Ser Phe Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 167
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 167

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
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cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggcttaccgc 1080
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 168
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 168
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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ser Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ile Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Ala Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 169
<211> 1200
<212> DNA

<213> Artificial Sequence

<220>
<223> ERED variant

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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacaaatc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactacac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttcgccac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 170
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 170
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly

```
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Lys Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Ala Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 171
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 171

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggaaggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gctaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacgctaa gctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacgaaaac 1200
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<210> 172
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 172

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

```
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ala Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Ala Lys Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Glu Asn
385                 390                 395                 400
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<210> 173
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 173

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
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aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatcctcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttcatcac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 174
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 174

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

<210> 175
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 175
atgtctttcg ttaaggactt caagccgcag gcactgcgcg acaccaacct gttcgaacct 60
attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt atcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacgaagc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttcatcac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 176
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 176
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1   5   10   15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20   25   30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35   40   45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50   55   60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65   70   75   80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85   90   95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100   105   110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115   120   125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130   135   140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145   150   155   160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165   170   175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180   185   190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195   200   205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe

```
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Ile Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Glu Ala Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Ile Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
```

<210> 177
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 177

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacattgc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagctg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttcgccac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 178
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 178

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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                   10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
```

```
            20                  25                  30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Ile Ala Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Ala Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Ala Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 179
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 179

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
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cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacgctgc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcgc cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtac gaccgttcta cgttcatcac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 180
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

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

370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 181
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 181
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gaaaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcgc cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttcatcac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 182
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 182
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His

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            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Glu Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu Arg Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Ile Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 183
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 183
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataatgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcggg acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacgcttt cctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcgc cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttcgaaac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 184
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 184
Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Gly Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Ala Phe Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu Arg Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Glu Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 185
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 185
atgtctttcg ttaaggactt caagccgcag gcactgcgcg acaccaacct gttcgaacct 60
attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360

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tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttt cctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacgagtat gaccgttcta cgttcaaaac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200
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<210> 186
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 186

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

```
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Glu Tyr Asp Arg Ser Thr Phe Lys Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 187
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 187
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggataa cctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt gaaaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 188
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED variant

<400> 188
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Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Arg Asp Thr Asn
1               5                   10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
```

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

<210> 189
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 189
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggtg cgttccctag cccgcagtca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagaagaac agattaaaga atggacgaaa 300
atcttcaagg ctattcatga aaataagtca tttgcgtggg tgcaactgtg gagcctgggc 360
tgggcctcct ttccggatgt gctggcgcgt gatgggttac gttacgattg tgcctccgat 420
cgtgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaacgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
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ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 190
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 190

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1               5                  10                  15
Leu Phe Lys Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Ala Phe Pro Ser Pro Gln Ser
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Glu Glu Gln Ile Lys
                85                  90                  95
Glu Trp Thr Lys Ile Phe Lys Ala Ile His Glu Asn Lys Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Ser Leu Gly Trp Ala Ser Phe Pro Asp Val Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Cys Ala Ser Asp Arg Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Lys Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Val Glu Gly Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asn Pro Phe Leu Thr Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 191
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 191

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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
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cgtgcacagc gtccggggac actgattatc acggagggta cgttccctag cccgcagtca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagaagaac agattaaaga atggacgaaa 300
atcttcaagg ctattcatga aaataagtca tttgtgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggatac gctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
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attatccgtg ccggcaacta cgcactacac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagatct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 192
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 192

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

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

<210> 193
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 193
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctctgc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggatgt gctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaccg 780
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ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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<210> 194
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 194
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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Leu His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Val Leu
115 120 125

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Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Pro Gly Ile Ile Ala Gln Tyr Ser Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Lys Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 195
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 195
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagaagaac agattaaaga atggacgaaa 300
atcttcaagg ctattcatga aaataagtca tttgcgtggg tgcaactgtg ggccctgggc 360
tgggccgcct ttccggatac gctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaacgc accgatgagt atgggggcac aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcgctgattg agaccatcgg cccagaacgc 720
gtgggtttac gtctgagtcc gtacggcact ttcaactcta tgtcgggcgg cgcggaaccg 780
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aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
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attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
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ttagaaaaag gtctgccact gaacaagtat gaccgtgata cgttctacaa aatgagcgcg 1140
gagggttaca tcgactaccc gacctacgaa gaagccttaa aactgggctg ggacaaaaac 1200
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<210> 196

<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 196
Met Pro Phe Val Lys Gly Phe Glu Pro Ile Ser Leu Arg Asp Thr Asn
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Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Glu Glu Gln Ile Lys
85 90 95
Glu Trp Thr Lys Ile Phe Lys Ala Ile His Glu Asn Lys Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Ala Leu Gly Trp Ala Ala Phe Pro Asp Thr Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Lys Arg Thr Asp Glu Tyr Gly Gly Thr Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Leu Ile Glu Thr Ile Gly Pro Glu Arg
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Thr Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Pro Gly Ile Ile Ala Gln Tyr Ser Tyr Val Leu Gly Glu
260 265 270
Leu Glu Lys Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Asp Arg Leu Glu Lys Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Asp Thr Phe Tyr Lys Met Ser Ala Glu Gly Tyr Ile
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Leu Lys Leu Gly Trp Asp Lys Asn
385 390 395 400

<210> 197
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 197
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga aaataagtca tttgtgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggatgt gctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
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aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caaacccttt tctgactgag 900
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cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggttgaccgc 1080
ttagaaaaag gtctgccact gaacaagtat gaccgtgata cgttctacaa aatgagcgcg 1140
gagggttaca tcgactaccc gacctacgaa gaagccttaa aactgggctg ggacaaaaac 1200

<210> 198
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 198
Met Pro Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Gly Asp Thr Asn
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Leu Phe Lys Pro Ile Lys Ile Gly Asn Asn Glu Leu Leu His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Glu Asn Lys Ser Phe Val
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Val Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285

Val Glu Pro Arg Val Thr Asn Pro Phe Leu Thr Glu Gly Glu Gly Glu
290 295 300
Tyr Asn Gly Gly Ser Asn Lys Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Phe Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Glu Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Asp Arg Leu Glu Lys Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Asp Thr Phe Tyr Lys Met Ser Ala Glu Gly Tyr Ile
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Leu Lys Leu Gly Trp Asp Lys Asn
385 390 395 400

<210> 199
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 199
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cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttccctag cccgcagtca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagaagaac agattaaaga atggacgaaa 300
atcttcaagg ctattcatga aaaaaagtca tttgcgtggg tgcaactgtg gagcctgggc 360
tgggcctcct ttccggatgt gctggcgcgt gatgggttac gttacgattg tgcctccgat 420
cgtgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaacgc accgatgagt atgggggcac aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcgctggttg aggccatcgg cccagaacgc 720
gtgggtttac gtctgagtcc gtacggcact ttcaactcta tgtcgggcgg cgcggaaccg 780
ggcattattg ctcagtatag ctatgtcctg ggtgagctgg agaaacgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 200
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 200
Met Pro Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Gly Asp Thr Asn
1 5 10 15
Leu Phe Lys Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Pro Ser Pro Gln Ser
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Glu Glu Gln Ile Lys
85 90 95

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Glu Trp Thr Lys Ile Phe Lys Ala Ile His Glu Lys Lys Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Ser Leu Gly Trp Ala Ser Phe Pro Asp Val Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Cys Ala Ser Asp Arg Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Lys Arg Thr Asp Glu Tyr Gly Gly Thr Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Leu Val Glu Ala Ile Gly Pro Glu Arg
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Thr Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Pro Gly Ile Ile Ala Gln Tyr Ser Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Lys Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400
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<210> 201
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 201
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg gagcctgggc 360
tgggcctcct ttccggatgt gctggcgcgt gatgggttac gttacgattg tgcctccgat 420
cgtgtgtata tgaatgcgac actgcaggaa aaagcgaaag acgctaacaa tctggaacat 480
agcttgacta aagacgatat taaacaatat atcaaagatt atattcatgc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaacgc accgatgagt atgggggcac aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcgctgattg agaccatcgg cccagaacgc 720
gtgggtttac gtctgagtcc gtacggcact ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caaacccttt tctgactgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
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gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 202
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 202
Met Pro Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Gly Asp Thr Asn
1 5 10 15
Leu Phe Lys Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Ser Leu Gly Trp Ala Ser Phe Pro Asp Val Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Cys Ala Ser Asp Arg Val Tyr Met
130 135 140
Asn Ala Thr Leu Gln Glu Lys Ala Lys Asp Ala Asn Asn Leu Glu His
145 150 155 160
Ser Leu Thr Lys Asp Asp Ile Lys Gln Tyr Ile Lys Asp Tyr Ile His
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Lys Arg Thr Asp Glu Tyr Gly Gly Thr Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Leu Ile Glu Thr Ile Gly Pro Glu Arg
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Thr Phe Asn Ser Met Ser Gly
245 250 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asn Pro Phe Leu Thr Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 203
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 203
atgcctttcg ttaagggctt cgagccgatt tcactgcgcg acaccaacct gttcgaacct 60
attaaaattg ggaacacact gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctcagc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttccctag cccgcagtca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagaagaac agattaaaga atggacgaaa 300
atcttcaagg ctattcatga aaataagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggatac gctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaacgc accgatgagt atgggggcac aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcgctgattg agaccatcgg cccagaacgc 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caaacccttt tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 204
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 204
Met Pro Phe Val Lys Gly Phe Glu Pro Ile Ser Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Leu Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Gln His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Pro Ser Pro Gln Ser
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Glu Glu Gln Ile Lys
85 90 95
Glu Trp Thr Lys Ile Phe Lys Ala Ile His Glu Asn Lys Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Thr Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205
Lys Arg Thr Asp Glu Tyr Gly Gly Thr Ile Glu Asn Arg Ala Arg Phe
210 215 220
Thr Leu Glu Val Val Asp Ala Leu Ile Glu Thr Ile Gly Pro Glu Arg
225 230 235 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
245 250 255

Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
260 265 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285
Val Glu Pro Arg Val Thr Asn Pro Phe Leu Val Glu Gly Glu Gly Glu
290 295 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
325 330 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
355 360 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
370 375 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385 390 395 400

<210> 205
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 205
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg gagcctgggc 360
tgggcctcct ttccggatgt gctggcgcgt gatgggttac gttacgattg tgcctccgat 420
cgtgtgtata tgaatgcgac actgcaggaa aaagcgaaag atgctaacaa tctggaacat 480
agcttgacta aagacgatat taaacaatat atcaaagatt atattcatgc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaacgc accgatgagt atgggggcac aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcgctgattg agaccatcgg cccagaacgc 720
gtgggtttac gtctgagtcc gtacggcact ttcaactcta tgtcgggcgg cgcggaaccg 780
ggcattattg ctcagtatag ctatgtcctg ggtgagctgg agaaacgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaactt cgcactgcac cctgaagttg tgcgcgaaga agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggttgaccgc 1080
ttagaaaaag gtctgccact gaacaagtat gaccgtgata cgttctacaa aatgagcgcg 1140
gagggttaca tcgactaccc gacctacgaa gaagccttaa aactgggctg ggacaaaaac 1200

<210> 206
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 206
Met Pro Phe Val Lys Gly Phe Glu Pro Ile Ser Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35 40 45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg
50 55 60

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Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Ser Leu Gly Trp Ala Ser Phe Pro Asp Val Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Cys Ala Ser Asp Arg Val Tyr Met
    130                 135                 140
Asn Ala Thr Leu Gln Glu Lys Ala Lys Asp Ala Asn Asn Leu Glu His
145                 150                 155                 160
Ser Leu Thr Lys Asp Asp Ile Lys Gln Tyr Ile Lys Asp Tyr Ile His
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Lys Arg Thr Asp Glu Tyr Gly Gly Thr Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Leu Ile Glu Thr Ile Gly Pro Glu Arg
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Thr Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Pro Gly Ile Ile Ala Gln Tyr Ser Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Lys Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Phe Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Glu Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Asp Arg Leu Glu Lys Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Asp Thr Phe Tyr Lys Met Ser Ala Glu Gly Tyr Ile
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Leu Lys Leu Gly Trp Asp Lys Asn
385                 390                 395                 400
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<210> 207
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 207

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attaaaattg ggaacaacga gctgctgcat cgcgcggtaa ttcctccgct gacccgcatg 120
cgcgctcagc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacgcccag 180
cgtgcacagc gtccggggac actgattatc acggagggta cgttcatcag cccgcagtca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagaagaac agattaaaga atggacgaaa 300
atcttcaagg ctattcatga aaataagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggatac gctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcgctgattg agaccatcgg cccagaacgc 720
gtgggtttac gtctgagtcc gtacggcact ttcaactcta tgtcgggcgg cgcggaaccg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caaacccttt tctgactgag 900
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ggggagggcg aatacaacgg gggcagcaac aaatttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaactt cgcactgcac cctgaagttg tgcgcgaaga agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggttgaccgc 1080
ttagaaaaag gtctgccact gaacaagtat gaccgtgata cgttctacaa aatgagcgcg 1140
gagggttaca tcgactaccc gacctacgaa gaagccctaa aactgggctg ggacaaaaac 1200

<210> 208
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 208

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

<210> 209
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 209
atgcctttcg ttaaggactt cgagccgcag gcactgggcg acaccaacct gttcaaacct 60
attaaaattg ggaacacaca gccggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacggccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg gagcctgggc 360
tgggcctcct ttccggatgt gctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggcgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaacgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caaaccctct tctgactgag 900
ggggagggcg aatacaacgg gggcagcaac aaatttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaactt cgcactgcac cctgaagttg tgcgcgaaga agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggttgaccgc 1080
ttagaaaaag gtctgccact gaacaagtat gaccgtgata cgttctacaa aatgagcgcg 1140
gagggttaca tcgactaccc gacctacgaa gaagccttaa aactgggctg ggacaaaaac 1200

<210> 210
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

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

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Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asn Pro Leu Leu Thr Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Asn Gly Gly Ser Asn Lys Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Phe Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Glu Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Asp Arg Leu Glu Lys Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Asp Thr Phe Tyr Lys Met Ser Ala Glu Gly Tyr Ile
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Leu Lys Leu Gly Trp Asp Lys Asn
385                 390                 395                 400
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<210> 211
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 211
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atgcctttcg ttaagggctt cgagccgatt tcactgcgcg acaccaacct gttcgaacct 60
attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac aaggagtggg ctgcggttta ctacacccag 180
cgtgcacagc gtccggggac aatgattatc acggagggtg cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg gagcctgggc 360
tgggccgcct ttccggatac gctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caaacccttt tctgactgag 900
ggggagggcg aatacaacgg gggcagcaac aaatttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaactt cgcactgcac cctgaagttg tgcgcgaaga agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggttgaccgc 1080
ttagaaaaag gtctgccact gaacaagtat gaccgtgata cgttctacaa aatgagcgcg 1140
gagggttaca tcgactaccc gacctacgaa gaagccttaa aactgggctg ggacaaaaac 1200
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<210> 212
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 212
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Met Pro Phe Val Lys Gly Phe Glu Pro Ile Ser Leu Arg Asp Thr Asn
1               5                   10                  15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
            20                  25                  30
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Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
        35                  40                  45
Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Thr Gln Arg Ala Gln Arg
    50                  55                  60
Pro Gly Thr Met Ile Ile Thr Glu Gly Ala Phe Ile Ser Pro Gln Ala
65                  70                  75                  80
Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Asp Glu Gln Val Ala
                85                  90                  95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
            100                 105                 110
Trp Val Gln Leu Trp Ser Leu Gly Trp Ala Ala Phe Pro Asp Thr Leu
        115                 120                 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
    130                 135                 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145                 150                 155                 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
                165                 170                 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
            180                 185                 190
Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asn Pro Phe Leu Thr Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Asn Gly Gly Ser Asn Lys Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Phe Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Glu Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Asp Arg Leu Glu Lys Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Asp Thr Phe Tyr Lys Met Ser Ala Glu Gly Tyr Ile
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Leu Lys Leu Gly Trp Asp Lys Asn
385                 390                 395                 400
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<210> 213
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 213
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctaccc atccgggcaa cattccgaac cgtgattggg ctgtggaata ctacacccag 180
cgtgcacagc gtccggggac aatgattatc acggagggtg cgttcatcag cccgcaggca 240
ggtgggtacg ataacgcgcc tggtgtttgg tcagaagaac agatggtcga atggacgaaa 300
atcttcaacg ctattcatga aaaaaagtca tttgtgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggatac gctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaccgc accgatgagt atgggggctc aattgaaaat 660

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cgtgcacgtt ttactctgga agtcgttgac gcggtggttg atgccatcgg cccagaaaaa 720
gtgggtttac gtctgagtcc gtacggcgtt ttcaactcta tgtcgggcgg cgcggaaacg 780
ggcattgttg ctcagtatgc ctatgtcctg ggtgagctgg agcgtcgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga caaacccttt tctgactgag 900
ggggagggcg aatacaacgg gggcagcaac aaatttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaactt cgcactgcac cctgaagttg tgcgcgaaga agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggttgaccgc 1080
ttagaaaaag gtctgccact gaacaagtat gaccgtgata cgttctacaa aatgagcgcg 1140
gagggttaca tcgactaccc gacctacgaa gaagccttaa aactgggctg ggacaaaaaa 1200
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<210> 214
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 214

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

<210> 215
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 215
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attaaaattg ggaacacaca gctggctcat cgcgcggtaa tgcctccgct gacccgcatg 120
cgcgctctgc atccgggcaa cattccgaac cgtgattggg ctgtggaata ctacacccag 180
cgtgcacagc gtccggggac aatgattatc acggagggta cgttccctag cccgcagtca 240
ggtgggtacg ataacgcgcc tggtatttgg tcagacgaac aggttgccga atggaagaac 300
atcttcctgg ctattcatga ctgtcagtca tttgcgtggg tgcaactgtg ggtcctgggc 360
tgggccgcct ttccggatac gctggcgcgt gatgggttac gttacgattc tgcctccgat 420
aatgtgtata tgaatgcgga acaggaggaa aaagcgaaaa aagctaacaa tccgcaacat 480
agcattacta aagacgaaat taaacaatat gtcaaagaat atgttcaggc agctaagaac 540
tcgatcgctg cgggtgcgga cggcgtggaa attcactcag ccaacggtta tctgttaaat 600
cagttcctgg atccgcacag caacaaacgc accgatgagt atgggggcac aattgaaaat 660
cgtgcacgtt ttactctgga agtcgttgac gcgctgattg agaccatcgg cccagaacgc 720
gtgggtttac gtctgagtcc gtacggcact ttcaactcta tgtcgggcgg cgcggaaccg 780
ggcattattg ctcagtatag ctatgtcctg ggtgagctgg agaaacgcgc caaggcgggg 840
aaacgcctgg cgtttgttca tttagtcgaa ccacgcgtga cagacccttc tctggttgag 900
ggggagggcg aatactcaga gggcaccaac gattttgctt attccatttg gaaaggtccg 960
attatccgtg ccggcaacta cgcactgcac cctgaagttg tgcgcgaaca agttaaggac 1020
cctcgcaccc tgatcggcta cggccgcttc tttatttcaa atccagacct ggtttaccgc 1080
ttagaagaag gtctgccact gaacaagtat gaccgttcta cgttctacac catgagcgcg 1140
gagggttaca ccgactaccc gacctacgaa gaagccgtag atctgggctg gaacaaaaac 1200

<210> 216
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> chimera of WT OYEs

<400> 216
Met Pro Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Gly Asp Thr Asn
1 5 10 15
Leu Phe Lys Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Thr Arg Met Arg Ala Leu His Pro Gly Asn Ile
35 40 45
Pro Asn Arg Asp Trp Ala Val Glu Tyr Tyr Thr Gln Arg Ala Gln Arg
50 55 60
Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Pro Ser Pro Gln Ser
65 70 75 80
Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Asp Glu Gln Val Ala
85 90 95
Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110
Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Thr Leu
115 120 125
Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met
130 135 140
Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His
145 150 155 160
Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln
165 170 175
Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190

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Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
        195                 200                 205
Lys Arg Thr Asp Glu Tyr Gly Gly Thr Ile Glu Asn Arg Ala Arg Phe
    210                 215                 220
Thr Leu Glu Val Val Asp Ala Leu Ile Glu Thr Ile Gly Pro Glu Arg
225                 230                 235                 240
Val Gly Leu Arg Leu Ser Pro Tyr Gly Thr Phe Asn Ser Met Ser Gly
                245                 250                 255
Gly Ala Glu Pro Gly Ile Ile Ala Gln Tyr Ser Tyr Val Leu Gly Glu
            260                 265                 270
Leu Glu Lys Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
        275                 280                 285
Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
    290                 295                 300
Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305                 310                 315                 320
Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu
                325                 330                 335
Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
            340                 345                 350
Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
        355                 360                 365
Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
    370                 375                 380
Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
385                 390                 395                 400


<210> 217
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> ERED Sequence with chimeric ERED backbone
      Synthetic Construct

<220>
<221> MISC_FEATURE
<222>(5)..(5)
<223> Xaa is a basic or acidic residue

<220>
<221> MISC_FEATURE
<222>(10)..(10)
<223> Xaa is a polar or constrained residue

<220>
<221> MISC_FEATURE
<222>(28)..(28)
<223> Xaa is an aliphatic or constrained residue

<220>
<221> MISC_FEATURE
<222>(38)..(38)
<223> Xaa is a polar or basic residue

<220>
<221> MISC_FEATURE
<222>(40)..(40)
<223> Xaa is a non-polar, aliphatic, aromatic, acidic or polar residue

<220>
<221> MISC_FEATURE
<222>(44)..(44)
<223> Xaa is a constrained or aromatic residue

<220>
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<221> MISC_FEATURE
<222>(75)..(75)
<223> Xaa is an aromatic, aliphatic or polar residue

<220>
<221> MISC_FEATURE
<222>(83)..(83)
<223> Xaa is an aromatic, aliphatic, acidic, or basic residue

<220>
<221> MISC_FEATURE
<222>(117)..(117)
<223> Xaa is a cysteine or nonpolar, aliphatic, basic, acidic, polar, or aromatic residue

<220>
<221> MISC_FEATURE
<222>(119)..(119)
<223> Xaa is a constrained or aliphatic residue

<220>
<221> MISC_FEATURE
<222>(122)..(122)
<223> Xaa is an aliphatic or polar residue

<220>
<221> MISC_FEATURE
<222>(124)..(124)
<223> Xaa is an aromatic, non-polar or a constrained residue

<220>
<221> MISC_FEATURE
<222>(147)..(147)
<223> Xaa is an acidic or non-polar residue

<220>
<221> MISC_FEATURE
<222>(148)..(148)
<223> Xaa is a polar or basic residue

<220>
<221> MISC_FEATURE
<222>(153)..(153)
<223> Xaa is a basic or acidic residue

<220>
<221> MISC_FEATURE
<222>(154)..(154)
<223> Xaa is a basic residue

<220>
<221> MISC_FEATURE
<222>(179)..(179)
<223> Xaa is a basic residue

<220>
<221> MISC_FEATURE
<222>(209)..(209)
<223> Xaa is a polar or acidic residue

<220>
<221> MISC_FEATURE
<222>(240)..(240)
<223> Xaa is a basic residue

<220>
<221> MISC_FEATURE
<222>(248)..(248)

<223> Xaa is an aromatic residue or cysteine

<220>
<221> MISC_FEATURE
<222>(251)..(251)
<223> Xaa is a cysteine, or aromatic, non-polar, aliphatic, acidic, basic, or polar residue

<220>
<221> MISC_FEATURE
<222>(252)..(252)
<223> Xaa is a polar, aromatic or constrained residue

<220>
<221> MISC_FEATURE
<222>(255)..(255)
<223> Xaa is a polar or constrained residue

<220>
<221> MISC_FEATURE
<222>(259)..(259)
<223> Xaa is an acidic or non-polar residue

<220>
<221> MISC_FEATURE
<222>(294)..(294)
<223> Xaa is a polar or aliphatic residue

<220>
<221> MISC_FEATURE
<222>(295)..(295)
<223> Xaa is an acidic, polar, basic, or non-polar residue

<220>
<221> MISC_FEATURE
<222>(296)..(296)
<223> Xaa is a constrained, aromatic, non-polar, aliphatic, basic, acidic, or polar residue

<220>
<221> MISC_FEATURE
<222>(297)..(297)
<223> Xaa is a polar, aromatic, non-polar, aliphatic, or basic residue

<220>
<221> MISC_FEATURE
<222>(302)..(302)
<223> Xaa is an acidic or non-polar residue

<220>
<221> MISC_FEATURE
<222>(304)..(304)
<223> Xaa is an acidic or basic residue

<220>
<221> MISC_FEATURE
<222>(305)..(305)
<223> Xaa is an aromatic or polar residue

<220>
<221> MISC_FEATURE
<222>(311)..(311)
<223> Xaa is an acidic residue

<220>
<221> MISC_FEATURE
<222>(315)..(315)
<223> Xaa is a constrained residue

<220>
<221> MISC_FEATURE
<222>(330)..(330)
<223> Xaa is a constrained, aromatic or basic residue

<220>
<221> MISC_FEATURE
<222>(333)..(333)
<223> Xaa is an aliphatic residue

<220>
<221> MISC_FEATURE
<222>(339)..(339)
<223> Xaa is a basic or polar residue

<220>
<221> MISC_FEATURE
<222>(358)..(358)
<223> Xaa is an aliphatic residue

<220>
<221> MISC_FEATURE
<222>(369)..(369)
<223> Xaa is a basic or acidic residue

<220>
<221> MISC_FEATURE
<222>(376)..(376)
<223> Xaa is an aromatic, non-polar, aliphatic, basic or acidic residue

<220>
<221> MISC_FEATURE
<222>(379)..(379)
<223> Xaa is a polar or nonpolar residue

<220>
<221> MISC_FEATURE
<222>(384)..(384)
<223> Xaa is a polar or aliphatic residue

<220>
<221> MISC_FEATURE
<222>(386)..(386)
<223> Xaa is an aromatic or acidic residue

<220>
<221> MISC_FEATURE
<222>(397)..(397)
<223> Xaa is an aromatic or basic residue

<220>
<221> MISC_FEATURE
<222>(399)..(399)
<223> Xaa is a basic or acidic residue

<220>
<221> MISC_FEATURE
<222>(400)..(400)
<223> Xaa is a polar residue

<400> 217
Met Ser Phe Val Xaa Asp Phe Lys Pro Xaa Ala Leu Arg Asp Thr Asn
1 5 10 15
Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Xaa Ala His Arg Ala
20 25 30
Val Met Pro Pro Leu Xaa Arg Xaa Arg Ala Thr Xaa Pro Gly Asn Ile
35 40 45

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