

SEQUENCE LISTING

<110> CODEXIS, INC.

<120> KETOREDUCTASE POLYPEPTIDES AND POLYNUCLEOTIDES

<130> CX2-166USP1

<140> NOT YET ASSIGNED

<141> 2017-04-27

<160> 260

<210> 1

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 1

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<210> 2

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 2

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

<210> 3

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 3

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gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
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cacgctatca aaatggctca ggtttctccg acctctaaca tctgctgat cggtgctggg 540
ggctctgggt gtaacgctat ccaggttgct aaagcattcg gtgctaaagt taccgttctg 600
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<210> 4
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-NADH-102 variant

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<400> 4
Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
1      5      10      15
Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
20      25      30
Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
35      40      45
His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
50      55      60
His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
65      70      75      80
Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
85      90      95
Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
100     105     110
Phe Gly Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr
115     120     125
Leu Leu Val Thr Arg Pro Arg Asn Leu Ser Arg Ile Pro Asp Asn Val
130     135     140
Ser Ala Asp Val Ala Ala Ala Ser Thr Asp Ala Val Leu Thr Pro Tyr
145     150     155     160
His Ala Ile Lys Met Ala Gln Val Ser Pro Thr Ser Asn Ile Leu Leu
165     170     175
Ile Gly Ala Gly Gly Leu Gly Gly Asn Ala Ile Gln Val Ala Lys Ala
180     185     190
Phe Gly Ala Lys Val Thr Val Leu Asp Lys Lys Lys Glu Ala Arg Asp
195     200     205
Gln Ala Lys Lys Leu Gly Ala Asp Ala Val Tyr Glu Thr Leu Pro Glu
210     215     220
Ser Ile Ser Pro Gly Ser Phe Ser Ala Cys Phe Asp Phe Val Ser Val
225     230     235     240
Gln Ala Thr Phe Asp Val Cys Gln Lys Tyr Val Glu Pro Lys Gly Val
245     250     255
Ile Met Pro Val Gly Leu Gly Ala Pro Asn Leu Ser Phe Asn Leu Gly
260     265     270
Asp Leu Ala Leu Arg Glu Ile Arg Ile Leu Gly Ser Phe Trp Gly Thr
275     280     285
Thr Asn Asp Leu Asp Asp Val Leu Lys Leu Val Ser Glu Gly Lys Val
290     295     300
Lys Pro Val Val Phe Ser Ala Lys Leu Lys Glu Leu Pro Glu Tyr Ile
305     310     315     320
Glu Lys Leu Arg Asn Asn Ala Tyr Glu Gly Arg Val Val Phe Asn Pro
325     330     335

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<210> 5
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 5
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 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactt gggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgcctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatgggtca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
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<210> 6
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

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

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

<210> 7
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 7

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gaaaaactgc	gtaacaacgc	ttacgaaggt	cgtgttggtt	tcaaccgta	a	1011

<210> 8
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 8

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

<210> 9

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 9

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<210> 10
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-NADH-102 variant

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

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				245						250					255				
Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Ser	Phe	Asn	Leu	Val				
				260					265					270					
Asp	Leu	Ala	Leu	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr				
				275				280						285					
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val				
				290				295					300						
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile				
305						310				315					320				
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro				
				325					330					335					

<210> 11
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 11
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 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgtatg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 12
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 12
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60

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

<210> 13
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 13
 atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtcttg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccgggt 780

```

ggctctgggtg ctccgaacct gtcttttaac ctgggtgacc tggcttttcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

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<210> 14
<211> 336
<212> PRT
<213> Artificial Sequence

```

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<220>
<223> KRED-NADH-102 variant

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```

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

```

<210> 15
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 15
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 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggacat tggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatgggtca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
 ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 16
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 16
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Ile Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80
 Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
 85 90 95
 Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
 100 105 110
 Phe Gly Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr
 115 120 125
 Leu Leu Val Thr Arg Pro Arg Asn Leu Ser Arg Ile Pro Asp Asn Val
 130 135 140
 Ser Ala Asp Val Ala Ala Ser Thr Asp Ala Val Leu Thr Pro Tyr
 145 150 155 160

His	Ala	Ile	Lys	Met	Ala	Gln	Val	Ser	Pro	Thr	Ser	Asn	Ile	Leu	Leu
				165					170					175	
Ile	Gly	Ala	Gly	Gly	Leu	Gly	Gly	Asn	Ala	Ile	Gln	Val	Ala	Lys	Ala
			180					185					190		
Phe	Gly	Ala	Lys	Val	Thr	Val	Leu	Asp	Lys	Lys	Lys	Glu	Ala	Arg	Asp
		195					200					205			
Gln	Ala	Lys	Lys	Leu	Gly	Ala	Asp	Ala	Val	Tyr	Glu	Thr	Leu	Pro	Glu
	210					215					220				
Ser	Ile	Ser	Pro	Gly	Ser	Phe	Ser	Ala	Cys	Phe	Asp	Phe	Val	Ser	Val
225					230					235				240	
Gln	Ala	Thr	Phe	Asp	Val	Cys	Gln	Lys	Tyr	Val	Glu	Pro	Lys	Gly	Val
			245					250						255	
Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Ser	Phe	Asn	Leu	Gly
			260					265					270		
Asp	Leu	Ala	Leu	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr
		275					280					285			
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
	290					295					300				
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305					310					315					320
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
				325					330					335	

<210> 17
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 17
 atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatac tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctgtt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgccagacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 18
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 18

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

<210> 19

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 19

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atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
cgcaacgatc tgccagtaca caagccgaaa gctggtcaac tgctgctgaa agtagatgca 120
```

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gtaggctctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
tacaaagtag gtgaccgtgt agcttggtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggtt cggtctgggt 360
tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
ggtctgggtg ctccgaacct gtcttttaac ctggttgacc tggctctgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaaag ttaaacgggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

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<210> 20
<211> 336
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> KRED-NADH-102 variant

```

```

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

```

Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Ser	Phe	Asn	Leu	Leu
			260					265					270		
Asp	Leu	Ala	Leu	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr
		275					280					285			
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
	290					295					300				
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305					310					315					320
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
				325					330					335	

<210> 21
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 21

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gtaggctctgt	gccactctga	tctgcacggt	atctacgaag	gcctggactg	cggtgacaac	180
tacgttatgg	gtcacgaaat	cgctgggtacc	gttgctgctg	ttggtgatga	cgttatcaac	240
tacaaagtag	gtgaccgtgt	agcttgtggt	gggtccgaacg	gttgcggtgg	ttgcaaatac	300
tgccgtgggtg	ctatcgacaa	cgtttgcaaa	aacgctttca	tggtactgggt	cggtctgggt	360
tatgatgggtg	gctatcaaca	atacctgctg	gtaactcgcc	cgcgtaacct	gtctcgtatc	420
ccggataacg	tatctgctga	tggtgctgct	gcttctaccg	acgctgttct	gactccgtac	480
cacgctatca	aaatgggtca	ggtttctccg	acctctaaca	tcctgctgat	cggtgctgggt	540
gggtctgggtg	gtaacgctat	ccagggttgc	aaagcattcg	gtgctaaagt	taccgttctg	600
gacaaaaaaa	aagaagctcg	tgaccaggct	aaaaaactgg	gtgctgacgc	tgtttacgaa	660
accctgccgg	aatctatctc	tccgggttct	ttctctgctt	gcttcgactt	cgtttctggt	720
caggctacct	tcgacgtttg	ccagaaatac	gttgaaccga	aagggtgttat	catgccgggt	780
gggtctgggtg	ctccgaacct	gtcttttaac	ctgggtgacc	tggtctctgcg	tgaatccgt	840
atcctgggtt	ctttctgggg	taccaccaac	gacctggacg	acgttctgaa	actggtttct	900
gaaggtaaag	ttaaaccggt	tgtacgttct	gctaaactga	aagaactgcc	ggaatacatc	960
gaaaaactgc	gtaacaacgc	ttacgaaggt	cgtgttggtt	tcaaccgta	a	1011

<210> 22
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 22

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

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

<210> 23
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 23
 atgtctatcc cgtctttctca gtatgggtttc gtattttaaca aacagtcttg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggt ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggt gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccgggt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgagtgcac tggctctgcg tgaaatccgt 840

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atcctggggtt ctttctggggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

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<210> 24
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-NADH-102 variant

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

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<210> 25
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 25
 atgtctatcc cgtctttctca gtatgggtttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttgggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgcttttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatgggtca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
 ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctgtt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgcaagacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011

<210> 26
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 26
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80
 Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
 85 90 95
 Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
 100 105 110
 Phe Gly Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr
 115 120 125
 Leu Leu Val Thr Arg Pro Arg Asn Leu Ser Arg Ile Pro Asp Asn Val
 130 135 140
 Ser Ala Asp Val Ala Ala Ser Thr Asp Ala Val Leu Thr Pro Tyr
 145 150 155 160
 His Ala Ile Lys Met Ala Gln Val Ser Pro Thr Ser Asn Ile Leu Leu

<400> 28

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

<210> 29
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 29
 atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcctggactg cggtgacaac 180

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tacgttatgg gtcacgaaat cgctggtacc gttgctgctg ttggtgatga cgttatcaac 240
tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
ggctctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctgtt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
ggctctgggtg ctccgaacct gtcttttaac ctgacagacc tggctctgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaaag ttaaacgggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

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<210> 30
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-NADH-102 variant

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

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			260					265					270				
Asp	Leu	Ala	Leu	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr		
		275					280					285					
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val		
	290					295					300						
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile		
305					310					315					320		
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro		
				325					330					335			

<210> 31
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 31
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 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcc atgactgggt cggctctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatgggtca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 32
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 32
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80

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

<210> 33
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 33
 atgtctatcc cgtctttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcgggtg ttgcaaatac 300
 tgccgtgggt ctatcgacaa cgtttgcaaa aacgcttttcg gtgactgggt cggtctgggt 360
 tatgatgggt gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcttgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccgggt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgattgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900

gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 34
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 34
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80
 Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
 85 90 95
 Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
 100 105 110
 Phe Gly Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr
 115 120 125
 Leu Leu Val Thr Arg Pro Arg Asn Leu Ser Arg Ile Pro Asp Asn Val
 130 135 140
 Ser Ala Asp Val Ala Ala Ala Ser Thr Asp Ala Val Leu Thr Pro Tyr
 145 150 155 160
 His Ala Ile Lys Met Ala Gln Val Ser Pro Thr Ser Asn Ile Leu Leu
 165 170 175
 Ile Gly Ala Gly Gly Leu Gly Gly Asn Ala Ile Gln Val Ala Lys Ala
 180 185 190
 Phe Gly Ala Lys Val Thr Val Leu Asp Lys Lys Lys Glu Ala Arg Asp
 195 200 205
 Gln Ala Lys Lys Leu Gly Ala Asp Ala Val Tyr Glu Thr Leu Pro Glu
 210 215 220
 Ser Ile Ser Pro Gly Ser Phe Ser Ala Cys Phe Asp Phe Val Ser Val
 225 230 235 240
 Gln Ala Thr Phe Asp Val Cys Gln Lys Tyr Val Glu Pro Lys Gly Val
 245 250 255
 Ile Met Pro Val Gly Leu Gly Ala Pro Asn Leu Ser Phe Asn Leu Ile
 260 265 270
 Asp Leu Ala Leu Arg Glu Ile Arg Ile Leu Gly Ser Phe Trp Gly Thr
 275 280 285
 Thr Asn Asp Leu Asp Asp Val Leu Lys Leu Val Ser Glu Gly Lys Val
 290 295 300
 Lys Pro Val Val Arg Ser Ala Lys Leu Lys Glu Leu Pro Glu Tyr Ile
 305 310 315 320
 Glu Lys Leu Arg Asn Asn Ala Tyr Glu Gly Arg Val Val Phe Asn Pro
 325 330 335

<210> 35

<211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 35
 atgtctatcc cgtctttctca gtatgggtttc gtattttaaca aacagtcttg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttgggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
 ggtctgggtg gtaacgctat ccaggttgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctgtt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgtgggacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011

<210> 36
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 36
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80
 Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
 85 90 95
 Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
 100 105 110
 Phe Gly Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr
 115 120 125
 Leu Leu Val Thr Arg Pro Arg Asn Leu Ser Arg Ile Pro Asp Asn Val
 130 135 140
 Ser Ala Asp Val Ala Ala Ser Thr Asp Ala Val Leu Thr Pro Tyr
 145 150 155 160
 His Ala Ile Lys Met Ala Gln Val Ser Pro Thr Ser Asn Ile Leu Leu
 165 170 175

Ile	Gly	Ala	Gly	Gly	Leu	Gly	Gly	Asn	Ala	Ile	Gln	Val	Ala	Lys	Ala		
			180					185					190				
Phe	Gly	Ala	Lys	Val	Thr	Val	Leu	Asp	Lys	Lys	Lys	Glu	Ala	Arg	Asp		
		195					200					205					
Gln	Ala	Lys	Lys	Leu	Gly	Ala	Asp	Ala	Val	Tyr	Glu	Thr	Leu	Pro	Glu		
	210					215					220						
Ser	Ile	Ser	Pro	Gly	Ser	Phe	Ser	Ala	Cys	Phe	Asp	Phe	Val	Ser	Val		
225					230					235					240		
Gln	Ala	Thr	Phe	Asp	Val	Cys	Gln	Lys	Tyr	Val	Glu	Pro	Lys	Gly	Val		
				245					250					255			
Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Ser	Phe	Asn	Leu	Trp		
			260					265					270				
Asp	Leu	Ala	Leu	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr		
	275						280					285					
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val		
	290					295					300						
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile		
305					310					315					320		
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro		
				325					330					335			

<210> 37
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 37
 atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatac tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgcccg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgtgggacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 38
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

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<400> 38
Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
1      5      10      15
Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
20      25      30
Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
35      40      45
His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
50      55      60
His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
65      70      75      80
Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
85      90      95
Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
100     105     110
Phe Gly Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr
115     120     125
Leu Leu Val Thr Arg Pro Arg Asn Leu Ser Arg Ile Pro Asp Asn Val
130     135     140
Ser Ala Asp Val Ala Ala Ala Ser Thr Asp Ala Val Leu Thr Pro Tyr
145     150     155     160
His Ala Ile Lys Met Ala Gln Val Ser Pro Thr Ser Asn Ile Leu Leu
165     170     175
Ile Gly Ala Gly Gly Leu Gly Gly Asn Ala Ile Gln Val Ala Lys Ala
180     185     190
Phe Gly Ala Lys Val Thr Val Leu Asp Lys Lys Lys Glu Ala Arg Asp
195     200     205
Gln Ala Lys Lys Leu Gly Ala Asp Ala Val Tyr Glu Thr Leu Pro Glu
210     215     220
Ser Ile Ser Pro Gly Ser Phe Ser Ala Cys Phe Asp Phe Val Ser Val
225     230     235     240
Gln Ala Thr Phe Asp Val Cys Gln Lys Tyr Val Glu Pro Lys Gly Val
245     250     255
Ile Met Pro Val Gly Leu Gly Ala Pro Asn Leu Ser Phe Asn Leu Trp
260     265     270
Asp Leu Ala Leu Arg Glu Ile Arg Ile Leu Gly Ser Phe Trp Gly Thr
275     280     285
Thr Asn Asp Leu Asp Asp Val Leu Lys Leu Val Ser Glu Gly Lys Val
290     295     300
Lys Pro Val Val Arg Ser Ala Lys Leu Lys Glu Leu Pro Glu Tyr Ile
305     310     315     320
Glu Lys Leu Arg Asn Asn Ala Tyr Glu Gly Arg Val Val Phe Asn Pro
325     330     335

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<210> 39
<211> 1011
<212> DNA
<213> Artificial Sequence

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<220>
<223> KRED-NADH-102 variant

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<400> 39
atgtctatcc cgtcttctca gtatggtttc gtatttaaca aacagtctgg tctgaaactg 60
cgcaacgatc tgccagtaca caagccgaaa gctggtcaac tgctgctgaa agtagatgca 120
gtaggctctgt gccactctga tctgcacgtt atctacgaag gcctggactg cggtgacaac 180
tacgttatgg gtcacgaaat cgctggtacc gttgctgctg ttggtgatga cgttatcaac 240

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tacaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaacatcgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaacgggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011

```

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<210> 40
<211> 336
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> KRED-NADH-102 variant

```

```

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

```

Asp	Leu	Ala	Leu	Arg	Glu	His	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr
	275						280					285			
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
	290					295					300				
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305					310					315					320
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
				325					330					335	

<210> 41
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 41
 atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatgggtca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgcatg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 42
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 42
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80
 Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly

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

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<220>
<223> KRED-NADH-102 variant
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gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a

1011

<210> 44

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 44

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

<210> 45

<211> 1011

<212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 45
 atgtctatcc cgtctttctca gtatgggtttc gtattttaaca aacagtcttg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttgggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgcttttc gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatgggtca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
 ggtctgggtg gtaacgctat ccaggttgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gatgtttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011

<210> 46
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

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

			180					185					190				
Phe	Gly	Ala	Lys	Val	Thr	Val	Leu	Asp	Lys	Lys	Lys	Glu	Ala	Arg	Asp		
		195					200					205					
Gln	Ala	Lys	Lys	Leu	Gly	Ala	Asp	Ala	Val	Tyr	Glu	Thr	Leu	Pro	Glu		
	210					215					220						
Ser	Ile	Ser	Pro	Gly	Ser	Phe	Ser	Ala	Cys	Phe	Asp	Phe	Val	Ser	Val		
225					230					235					240		
Gln	Ala	Thr	Phe	Asp	Val	Cys	Gln	Lys	Tyr	Val	Glu	Pro	Lys	Gly	Val		
			245					250						255			
Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Met	Phe	Asn	Leu	Gly		
		260						265					270				
Asp	Leu	Ala	Leu	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr		
	275						280					285					
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val		
	290					295					300						
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile		
305					310					315					320		
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro		
			325						330					335			

<210> 47
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 47
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 cgcaacgatac tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaaa cgtttgcaaa aacgcttttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtggtttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011

<210> 48
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 48

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

<210> 49
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 49
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 cgcaacgatc tgccagtaca caagccgaaa gctggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcttggaactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300

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tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggtt cggtctgggt 360
tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
ggctctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctgtt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
ggctctgggtg ctccgaacct gtcttttaac ctgggtgacg ttgctctgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

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<210> 50
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-NADH-102 variant

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

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		275					280					285			
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
	290					295					300				
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305					310					315					320
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
				325					330					335	

<210> 51
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 51
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 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 taaaaaattg gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgcttttc gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatgggtca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011

<210> 52
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 52
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80
 Tyr Lys Ile Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
 85 90 95

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

<210> 53
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 53
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 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atcgatgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcgggtg ttgcaaatac 300
 tgccgtgggt ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggt gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccgggt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaacccgta a 1011

<210> 54
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

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

<210> 55
 <211> 1011
 <212> DNA

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 55

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cgcaacgata tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
gtaggctctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttgggtgatga cgttatcaac 240
tacaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
tgccgtgggtg ctatcgacaa cgtttgcaaa aacgcttttc gtgactgggt cggtctgggt 360
tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
ggctctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
ggctctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaaggcgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011
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<210> 56

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 56

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

<210> 57
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 57

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cgcaacgata	tgccagtaca	caagccgaaa	gctgggtcaac	tgctgctgaa	agtagatgca	120
gtaggctctgt	gccactctga	tctgcacgtt	atcagtgaag	gcctggactg	cggtgacaac	180
tacgttatgg	gtcacgaaat	cgctgggtacc	gttgctgctg	ttggtgatga	cgttatcaac	240
tacaaaagtag	gtgaccgtgt	agcttgtggt	gggtccgaacg	ggtgcggtgg	ttgcaaatac	300
tgccgtgggtg	ctatcgacaa	cgtttgcaaa	aacgctttcg	gtgactgggt	cggtctgggt	360
tatgatgggtg	gctatcaaca	atacctgctg	gtaactcgcc	cgcgtaacct	gtctcgtatc	420
ccggataacg	tatctgctga	tggtgctgct	gcttctaccg	acgctgttct	gactccgtac	480
cacgctatca	aaatggctca	ggtttctccg	acctctaaca	tcctgctgat	cggtgctggg	540
gggtctgggtg	gtaacgctat	ccagggttgc	aaagcattcg	gtgctaaagt	taccgttctg	600
gacaaaaaaa	aagaagctcg	tgaccaggct	aaaaaactgg	gtgctgacgc	tgtttacgaa	660
accctgccgg	aatctatctc	tccgggttct	ttctctgctt	gcttcgactt	cgtttctggt	720
caggctacct	tcgacgtttg	ccagaaatac	ggtgaaccga	aaggtgttat	catgccgggt	780
gggtctgggtg	ctccgaacct	gtcttttaac	ctgggtgacc	tggctctgcg	tgaaatccgt	840
atcctgggtt	ctttctgggg	taccaccaac	gacctggacg	acgttctgaa	actggtttct	900
gaaggtaaag	ttaaaccggt	tgtacgttct	gctaaactga	aagaactgcc	ggaatacatc	960
gaaaaactgc	gtaacaacgc	ttacgaaggt	cgtgttggtt	tcaaccgta	a	1011

<210> 58
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 58

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

<210> 59
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 59
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 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcttggtgactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactggtt cggtctgggt 360

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tatgatggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
ggctctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgcccg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctgtt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
ggctctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaacaacgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

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<210> 60
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-NADH-102 variant

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

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Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
290						295					300				
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305					310					315					320
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
				325					330					335	

<210> 61
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 61
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 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatgggtca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
 ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgaca ttgctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 62
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 62
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80
 Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
 85 90 95
 Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala

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

<210> 63
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 63
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 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctgctttg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccaggttgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccgggt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011

<210> 64
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 64
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Leu Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80
 Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
 85 90 95
 Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
 100 105 110
 Phe Gly Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr
 115 120 125
 Leu Leu Val Thr Arg Pro Arg Asn Leu Ser Arg Ile Pro Asp Asn Val
 130 135 140
 Ser Ala Asp Val Ala Ala Ala Ser Thr Asp Ala Val Leu Thr Pro Tyr
 145 150 155 160
 His Ala Ile Lys Met Ala Gln Val Ser Pro Thr Ser Asn Ile Leu Leu
 165 170 175
 Ile Gly Ala Gly Gly Leu Gly Gly Asn Ala Ile Gln Val Ala Lys Ala
 180 185 190
 Phe Gly Ala Lys Val Thr Val Leu Asp Lys Lys Lys Glu Ala Arg Asp
 195 200 205
 Gln Ala Lys Lys Leu Gly Ala Asp Ala Val Tyr Glu Thr Leu Pro Glu
 210 215 220
 Ser Ile Ser Pro Gly Ser Phe Ser Ala Cys Phe Asp Phe Val Ser Val
 225 230 235 240
 Gln Ala Thr Phe Asp Val Cys Gln Lys Tyr Val Glu Pro Lys Gly Val
 245 250 255
 Ile Met Pro Val Gly Leu Gly Ala Pro Asn Leu Ser Phe Asn Leu Gly
 260 265 270
 Asp Leu Ala Leu Arg Glu Ile Arg Ile Leu Gly Ser Phe Trp Gly Thr
 275 280 285
 Thr Asn Asp Leu Asp Asp Val Leu Lys Leu Val Ser Glu Gly Lys Val
 290 295 300
 Lys Pro Val Val Arg Ser Ala Lys Leu Lys Glu Leu Pro Glu Tyr Ile
 305 310 315 320
 Glu Lys Leu Arg Asn Asn Ala Tyr Glu Gly Arg Val Val Phe Asn Pro
 325 330 335

<210> 65
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 65

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cgcaacgata tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
gtaggctctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
tacaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
tgccgtgggtg ctatcgacaa cgtttgcaca aacgctttcg gtgactgggt cggtctgggt 360
tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
ggctctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
ggctctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaacgggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011
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<210> 66

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 66

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

	195		200		205										
Gln	Ala	Lys	Lys	Leu	Gly	Ala	Asp	Ala	Val	Tyr	Glu	Thr	Leu	Pro	Glu
	210					215					220				
Ser	Ile	Ser	Pro	Gly	Ser	Phe	Ser	Ala	Cys	Phe	Asp	Phe	Val	Ser	Val
225					230					235				240	
Gln	Ala	Thr	Phe	Asp	Val	Cys	Gln	Lys	Tyr	Val	Glu	Pro	Lys	Gly	Val
				245					250					255	
Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Ser	Phe	Asn	Leu	Gly
			260					265					270		
Asp	Leu	Ala	Leu	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr
	275						280					285			
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
	290					295					300				
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305					310					315				320	
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
				325					330					335	

<210> 67
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 67
 atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgcttttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tagtggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 68
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 68
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15


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ccggataacg tatcttcgga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
ggctctgggtg gtaacgctat ccagggttgct aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctgtt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat cgtgccggtt 780
ggctctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccagcaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

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<210> 70
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 70

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

290		295		300
Lys Pro Val Val Arg Ser Ala Lys Leu Lys Glu Leu Pro Glu Tyr Ile				
305		310		315
Glu Lys Leu Arg Asn Asn Ala Tyr Glu Gly Arg Val Val Phe Asn Pro				
	325		330	335

<210> 71
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 71
 atgtc gatcc cgtcttctca gtatgggttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttgggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatgggtca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
 ggtctgggtg gtaacgctat ccagggttgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaaa aagaagctcg tgaccaggct agaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaacccgta a 1011

<210> 72
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 72
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80
 Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
 85 90 95
 Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
 100 105 110

Phe	Gly	Asp	Trp	Phe	Gly	Leu	Gly	Tyr	Asp	Gly	Gly	Tyr	Gln	Gln	Tyr
		115					120					125			
Leu	Leu	Val	Thr	Arg	Pro	Arg	Asn	Leu	Ser	Arg	Ile	Pro	Asp	Asn	Val
		130					135					140			
Ser	Ala	Asp	Val	Ala	Ala	Ala	Ser	Thr	Asp	Ala	Val	Leu	Thr	Pro	Tyr
					150					155					160
His	Ala	Ile	Lys	Met	Ala	Gln	Val	Ser	Pro	Thr	Ser	Asn	Ile	Leu	Leu
				165					170					175	
Ile	Gly	Ala	Gly	Gly	Leu	Gly	Gly	Asn	Ala	Ile	Gln	Val	Ala	Lys	Ala
			180					185					190		
Phe	Gly	Ala	Lys	Val	Thr	Val	Leu	Asp	Lys	Lys	Lys	Glu	Ala	Arg	Asp
		195					200					205			
Gln	Ala	Arg	Lys	Leu	Gly	Ala	Asp	Ala	Val	Tyr	Glu	Thr	Leu	Pro	Glu
		210				215					220				
Ser	Ile	Ser	Pro	Gly	Ser	Phe	Ser	Ala	Cys	Phe	Asp	Phe	Val	Ser	Val
					230					235					240
Gln	Ala	Thr	Phe	Asp	Val	Cys	Gln	Lys	Tyr	Val	Glu	Pro	Lys	Gly	Val
				245					250					255	
Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Ser	Phe	Asn	Leu	Gly
			260					265					270		
Asp	Leu	Ala	Leu	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr
		275					280					285			
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
		290				295					300				
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
					310					315					320
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
				325					330					335	

<210> 73
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 73

atgtcgatecc	cgtcttctca	gtatggtttc	gtattttaaca	aacagtctgg	tctgaaactg	60
cgcaacgatc	tgccagtaca	caagccgaaa	gctgggtcaac	tgctgctgag	agtagatgca	120
gtaggtctgt	gccactctga	tctgcacgtt	atctacgaag	gcctggactg	cggtgacaac	180
tacgttatgg	gtcacgaaat	cgctgggtacc	gttgctgctg	ttggtgatga	cgttatcaac	240
tacaaaagtag	gtgaccgtgt	agcttgtggt	gggtccgaacg	gttgccggtgg	ttgcaaatac	300
tgccgtgggtg	ctatcgacaa	cgtttgcaaa	aacgcttttcg	gtgactgggt	cggtctgggt	360
tatgatgggtg	gctatcaaca	atacctgctg	gtaactcgcc	cgcgtaacct	gtctcgtatc	420
ccggataacg	tatctgctga	tgttgctgct	gcttctaccg	acgctgttct	gactccgtac	480
cacgctatca	aaatggctca	ggtttctccg	acctctaaca	tcttgctgat	cggtgctgggt	540
ggtctgggtg	gtaacgctat	ccagggttgct	aaagcattcg	gtgctaaagt	taccgttctg	600
gacaaaaaaa	aagaagctcg	tgaccaggct	aaaaaactgg	gtgctgacgc	tgtttacgaa	660
accctgccgg	aatctatctc	tccgggttct	ttctctgctt	gcttcgactt	cgtttctggt	720
caggctacct	tcgacgtttg	ccagaaatac	ggtgaaccga	aaggtgttat	catgccgggt	780
ggtctgggtg	ctccgaacct	gtcttttaac	ctgggtgacc	tggtctctgcg	tgaaatccgt	840
atcctgggtt	ctttctgggg	taccaccaac	gacctggacg	acgttctgaa	actggtttct	900
gaaggtaaag	ttaaaccggt	tgtacgttct	gctaaactga	aagaactgcc	ggaatacatc	960
gaaaaactgc	gtaacaacgc	ttacgaaggt	cgtgttggtt	tcaaccgta	a	1011

<210> 74
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 74
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Arg Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80
 Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
 85 90 95
 Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
 100 105 110
 Phe Gly Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr
 115 120 125
 Leu Leu Val Thr Arg Pro Arg Asn Leu Ser Arg Ile Pro Asp Asn Val
 130 135 140
 Ser Ala Asp Val Ala Ala Ala Ser Thr Asp Ala Val Leu Thr Pro Tyr
 145 150 155 160
 His Ala Ile Lys Met Ala Gln Val Ser Pro Thr Ser Asn Ile Leu Leu
 165 170 175
 Ile Gly Ala Gly Gly Leu Gly Gly Asn Ala Ile Gln Val Ala Lys Ala
 180 185 190
 Phe Gly Ala Lys Val Thr Val Leu Asp Lys Lys Lys Glu Ala Arg Asp
 195 200 205
 Gln Ala Lys Lys Leu Gly Ala Asp Ala Val Tyr Glu Thr Leu Pro Glu
 210 215 220
 Ser Ile Ser Pro Gly Ser Phe Ser Ala Cys Phe Asp Phe Val Ser Val
 225 230 235 240
 Gln Ala Thr Phe Asp Val Cys Gln Lys Tyr Val Glu Pro Lys Gly Val
 245 250 255
 Ile Met Pro Val Gly Leu Gly Ala Pro Asn Leu Ser Phe Asn Leu Gly
 260 265 270
 Asp Leu Ala Leu Arg Glu Ile Arg Ile Leu Gly Ser Phe Trp Gly Thr
 275 280 285
 Thr Asn Asp Leu Asp Asp Val Leu Lys Leu Val Ser Glu Gly Lys Val
 290 295 300
 Lys Pro Val Val Arg Ser Ala Lys Leu Lys Glu Leu Pro Glu Tyr Ile
 305 310 315 320
 Glu Lys Leu Arg Asn Asn Ala Tyr Glu Gly Arg Val Val Phe Asn Pro
 325 330 335

<210> 75
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 75

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atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
cgcaacgata tgccagtaca caagccgaaa gctgggtcaac tgctgctgag agtagatgca 120
gtaggctctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttgggtgatga cgttatcaac 240
tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
tgccgtgggtg ctatcgacaa cgtttgcaaa aacgcctttcg gtgactgggt cggtctgggt 360
tatgacgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tggtgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
ggctctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaa aagaagctcg tgaccaggct agaaaactgg gtgctgacgc tgtttacgaa 660
accctgcccg aatctatctc tccgcgttct ttctctgctt gcttcgactt cgtttctggt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
ggctctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaacgggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011
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<210> 76

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 76

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

Gln	Ala	Arg	Lys	Leu	Gly	Ala	Asp	Ala	Val	Tyr	Glu	Thr	Leu	Pro	Glu
210						215					220				
Ser	Ile	Ser	Pro	Arg	Ser	Phe	Ser	Ala	Cys	Phe	Asp	Phe	Val	Ser	Val
225					230					235				240	
Gln	Ala	Thr	Phe	Asp	Val	Cys	Gln	Lys	Tyr	Val	Glu	Pro	Lys	Gly	Val
				245					250					255	
Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Ser	Phe	Asn	Leu	Gly
			260					265					270		
Asp	Leu	Ala	Leu	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr
		275					280					285			
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
	290					295					300				
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305					310					315				320	
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
			325						330					335	

<210> 77
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 77
 atgtcgatcc cgtcttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcgggtg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgcttttc gtgactgggt cggtctgggt 360
 tatgacgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct agaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgcgttct ttctctgctt gcttcgactt cgtttctgtt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaacccgta a 1011

<210> 78
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 78
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly

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

<210> 79
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 79
 atgtcgatcc cgtcttctca gtatggtttc gtattttaaca aacagtcttg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480

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cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
ggctctgggtg gtaacgctat ccagggttgct aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgcgttct ttctctgctt gcttcgactt cgtttctgtt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccgggt 780
ggctctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

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<210> 80
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-NADH-102 variant

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

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Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305					310					315					320
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
				325					330					335	

<210> 81
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 81
 atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgag agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 taaaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgacgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatgggtca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgcgttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 82
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 82
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Arg Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
 35 40 45
 His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
 50 55 60
 His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
 65 70 75 80
 Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
 85 90 95
 Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
 100 105 110
 Phe Gly Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr

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

<220>
<223> KRED-NADH-102 variant

<210> 84

<211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

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

<210> 85
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 85

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atgtctatcc cgtctttctca gtatgggttc gtattttaaca aacagtcttg tctgaaactg 60
cgcaacgata tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
gtaggctctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggcgatgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaacgggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011
```

<210> 86

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 86

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

210		215		220
Ser Ile Ser Pro Gly	Ser Phe Ser Ala Cys Phe	Asp Phe Val Ser Val		
225	230	235	240	
Gln Ala Thr Phe Asp	Val Cys Gln Lys Tyr Val	Glu Pro Lys Gly Val		
	245	250	255	
Ile Met Pro Val Gly	Leu Gly Ala Pro Asn Leu	Ser Phe Asn Leu Gly		
	260	265	270	
Asp Leu Ala Met Arg	Glu Ile Arg Ile Leu Gly	Ser Phe Trp Gly Thr		
	275	280	285	
Thr Asn Asp Leu Asp	Asp Val Leu Lys Leu Val	Ser Glu Gly Lys Val		
	290	295	300	
Lys Pro Val Val Arg	Ser Ala Lys Leu Lys Glu	Leu Pro Glu Tyr Ile		
305	310	315	320	
Glu Lys Leu Arg Asn	Asn Ala Tyr Glu Gly Arg	Val Val Phe Asn Pro		
	325	330	335	

<210> 87
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 87
 atgtctatcc cgtcttctca gtatggtttc gtatttaaca aacagtctgg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg tggtgacaac 180
 tacggttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttaccaac 240
 tacaaaatccg gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgcttttc gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tgaacatgcg tgaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 88
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 88
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30

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

<210> 89
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 89
 atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtcttg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gccttgactg tggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaatccg gtgaccgtgt agcttggtgt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cagcgtatca aaatggctca ggtttctccg acctctaaca tctgctgat cggtgctgggt 540

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ggctctgggtg gtaacgctat ccagggttgct aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgcccg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctgtt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
ggctctgggtg ctccgaacct gtcttttaac ctgggtgacc tgaacatgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaacccgta a 1011

```

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<210> 90
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-NADH-102 variant

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

```

305		310		315		320
Glu Lys Leu Arg Asn Asn Ala Tyr Glu Gly Arg Val Val Phe Asn Pro						
		325		330		335

<210> 91
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 91
 atgtctatcc cgtcttctca gtatggtttc gtatttaaca aacagtctgg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaatccg gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggcgatgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011

<210> 92
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

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

Leu	Leu	Val	Thr	Arg	Pro	Arg	Asn	Leu	Ser	Arg	Ile	Pro	Asp	Asn	Val
130						135					140				
Ser	Ala	Asp	Val	Ala	Ala	Ala	Ser	Thr	Asp	Ala	Val	Leu	Thr	Pro	Tyr
145					150					155					160
His	Ala	Ile	Lys	Met	Ala	Gln	Val	Ser	Pro	Thr	Ser	Asn	Ile	Leu	Leu
				165					170					175	
Ile	Gly	Ala	Gly	Gly	Leu	Gly	Gly	Asn	Ala	Ile	Gln	Val	Ala	Lys	Ala
			180					185					190		
Phe	Gly	Ala	Lys	Val	Thr	Val	Leu	Asp	Lys	Lys	Lys	Glu	Ala	Arg	Asp
		195					200					205			
Gln	Ala	Lys	Lys	Leu	Gly	Ala	Asp	Ala	Val	Tyr	Glu	Thr	Leu	Pro	Glu
	210					215					220				
Ser	Ile	Ser	Pro	Gly	Ser	Phe	Ser	Ala	Cys	Phe	Asp	Phe	Val	Ser	Val
225					230					235					240
Gln	Ala	Thr	Phe	Asp	Val	Cys	Gln	Lys	Tyr	Val	Glu	Pro	Lys	Gly	Val
				245					250					255	
Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Ser	Phe	Asn	Leu	Gly
			260					265					270		
Asp	Leu	Ala	Met	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr
		275					280						285		
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
	290					295					300				
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305					310					315					320
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
				325					330					335	

<210> 93
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 93
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 cgcaacgatc tgccagtaca caagccgaaa gctggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccattctga tctgcacggt atctacgaag gcctggactg tggtgacaac 180
 tacgttatgg gtcacgaaat cgctggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactggtt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccgggt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tgaatatgcg tgaaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011

<210> 94
 <211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 94

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

<210> 95

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

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<400> 95
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cgcaacgata tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
gtaggctctgt gccactctga tctgcacggt atctacgaag gctttgacgc ggggtgacaac 180
tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttgggtgatga cgttatcaac 240
tacaaagttg gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tgttgcgtgt gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cgggtgctgg 540
gggtctgggtg gtaacgctat ccagggtgtt aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctgtt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
gggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggcgatgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaacgggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011

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<210> 96
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-NADH-102 variant

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<400> 96
Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
1          5          10          15
Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
20          25          30
Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
35          40          45
His Val Ile Tyr Glu Gly Phe Asp Ala Gly Asp Asn Tyr Val Met Gly
50          55          60
His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
65          70          75          80
Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
85          90          95
Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
100         105         110
Phe Gly Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr
115         120         125
Leu Leu Val Thr Arg Pro Arg Asn Leu Ser Arg Ile Pro Asp Asn Val
130         135         140
Ser Ala Asp Val Ala Ala Ser Thr Asp Ala Val Leu Thr Pro Tyr
145         150         155         160
His Ala Ile Lys Met Ala Gln Val Ser Pro Thr Ser Asn Ile Leu Leu
165         170         175
Ile Gly Ala Gly Gly Leu Gly Gly Asn Ala Ile Gln Val Ala Lys Ala
180         185         190
Phe Gly Ala Lys Val Thr Val Leu Asp Lys Lys Lys Glu Ala Arg Asp
195         200         205
Gln Ala Lys Lys Leu Gly Ala Asp Ala Val Tyr Glu Thr Leu Pro Glu
210         215         220

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Ser	Ile	Ser	Pro	Gly	Ser	Phe	Ser	Ala	Cys	Phe	Asp	Phe	Val	Ser	Val
225					230					235				240	
Gln	Ala	Thr	Phe	Asp	Val	Cys	Gln	Lys	Tyr	Val	Glu	Pro	Lys	Gly	Val
				245					250					255	
Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Ser	Phe	Asn	Leu	Gly
			260					265					270		
Asp	Leu	Ala	Met	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr
		275					280					285			
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
	290					295					300				
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305					310					315					320
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
			325						330					335	

<210> 97
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 97
 atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacgtt atctacgaag gcctggactg cggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
 tgccgtgggtg gcatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgggtgacc tggctctgctg tgaatccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
 gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 98
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 98
 Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
 1 5 10 15
 Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
 20 25 30
 Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu


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gacaaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctgtt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
ggctctggcg ctccgaacct gtcttttaac ctgggtgacc tggctctgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

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<210> 100

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 100

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

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Glu Lys Leu Arg Asn Asn Ala Tyr Glu Gly Arg Val Val Phe Asn Pro
325 330 335

<210> 101
<211> 1011
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED-NADH-102 variant

<400> 101
atgtctatcc cgtcttctca gtatggtttc gtatttaaca aacagtctgg tctgaaactg 60
cgcaacgatc tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
gtaggctctgt gccattctga tctgcacggt atctacgaag gcctggactt aggtgacaac 180
tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttgggtgatga cgttatcaac 240
tacaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcggtgg ttgcaaatac 300
tgccgtgggtg gcatcgacaa cgtttgcaaa aacgctttcc atgactgggt cggtctgggt 360
tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatgggtca ggtttctccg acctctaaca tcctgctgat cggtgctgggt 540
ggctctgggtg gtaacgctat ccagggttgct aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgcgttct ttctctgctt gcttcgactt cgtttctggt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
ggctctgggcg ctccgaacct gtcttttaac ctgggtgacc tggcgttgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttctgaa actggtttct 900
gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

<210> 102
<211> 336
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED-NADH-102 variant

<400> 102
Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
1 5 10 15
Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
20 25 30
Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
35 40 45
His Val Ile Tyr Glu Gly Leu Asp Leu Gly Asp Asn Tyr Val Met Gly
50 55 60
His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
65 70 75 80
Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
85 90 95
Gly Cys Lys Tyr Cys Arg Gly Gly Ile Asp Asn Val Cys Lys Asn Ala
100 105 110
Phe His Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr
115 120 125
Leu Leu Val Thr Arg Pro Arg Asn Leu Ser Arg Ile Pro Asp Asn Val

130		135		140											
Ser	Ala	Asp	Val	Ala	Ala	Ala	Ser	Thr	Asp	Ala	Val	Leu	Thr	Pro	Tyr
145				150						155					160
His	Ala	Ile	Lys	Met	Ala	Gln	Val	Ser	Pro	Thr	Ser	Asn	Ile	Leu	Leu
				165						170				175	
Ile	Gly	Ala	Gly	Gly	Leu	Gly	Gly	Asn	Ala	Ile	Gln	Val	Ala	Lys	Ala
			180					185					190		
Phe	Gly	Ala	Lys	Val	Thr	Val	Leu	Asp	Lys	Lys	Lys	Glu	Ala	Arg	Asp
		195					200					205			
Gln	Ala	Lys	Lys	Leu	Gly	Ala	Asp	Ala	Val	Tyr	Glu	Thr	Leu	Pro	Glu
	210					215					220				
Ser	Ile	Ser	Pro	Arg	Ser	Phe	Ser	Ala	Cys	Phe	Asp	Phe	Val	Ser	Val
225				230						235				240	
Gln	Ala	Thr	Phe	Asp	Val	Cys	Gln	Lys	Tyr	Val	Glu	Pro	Lys	Gly	Val
			245					250						255	
Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Ser	Phe	Asn	Leu	Gly
		260						265					270		
Asp	Leu	Ala	Leu	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr
	275					280						285			
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
	290				295						300				
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305				310					315					320	
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
			325					330					335		

<210> 103
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 103
 atgtctatcc cgtcttctca gtatggtttc gtattttaaca aacagtctgg tctgaaactg 60
 cgcaacgatac tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
 gtaggtctgt gccactctga tctgcacggt atctcagaag gcctggattt gggtgacaac 180
 tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttggtgatga cgttatcaac 240
 tacaaagtag gtgaccgtgt agcttgtggt ggtccgaacg gttgcgggtg ttgcaaatac 300
 tgccgtgggtg ctatcgacaa cgtttgcaaa aacgcttttc gtgactgggt cggtctgggt 360
 tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
 ccggataacg tatctgctga tgttgctgct gcttctaccg acgctgttct gactccgtac 480
 cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cggtgctggg 540
 ggtctgggtg gtaacgctat ccagggtgct aaagcattcg gtgctaaagt taccgttctg 600
 gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
 accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
 caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
 ggtctgggtg ctccgaacct gtcttttaac ctgcatgacc ttgctctgctg tgaacaccgt 840
 atcctgggtt ctttctgggg taccaccaac gacctggacg acgtttttta actggtttct 900
 gaaggtaaaag ttaaaccggt tgtacgatct gctaaactga aagaactgcc ggaatacatc 960
 gaaaaactgc gtaacaacgc ttacgaaggt cgtgttgttt tcaaccgta a 1011

<210> 104
 <211> 336
 <212> PRT

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 104

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

<210> 105

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

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<400> 105
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cgcaacgatac tgccagtaca caagccgaaa gctgggtcaac tgctgctgaa agtagatgca 120
gtagggtctgt gccactctga tctgcacggt atcgatgaag gcctggattt gggtgacaac 180
tacgttatgg gtcacgaaat cgctgggtacc gttgctgctg ttgggtgatga cgttatcaac 240
tacaaagtag gtgaccgtgt agcttgtgtt ggtccgaacg gttgcgggtg ttgcaaatac 300
tgccgtgggtg ctatcgacaa cgtttgcaaa aacgctttcg gtgactgggt cggtctgggt 360
tatgatgggtg gctatcaaca atacctgctg gtaactcgcc cgcgtaacct gtctcgtatc 420
ccggataacg tatctgctga tggtgctgct gcttctaccg acgctgttct gactccgtac 480
cacgctatca aaatggctca ggtttctccg acctctaaca tcctgctgat cgggtgctgg 540
gggtctgggtg gtaacgctat ccagggttgc aaagcattcg gtgctaaagt taccgttctg 600
gacaaaaaaa aagaagctcg tgaccaggct aaaaaactgg gtgctgacgc tgtttacgaa 660
accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctggt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aagggtgttat catgccggtt 780
gggtctgggtg ctccgaacct gtcttttaac ctgcatgacc ttgctctgcg tgaaatacgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttttgaa actggtttct 900
gaaggtaaag ttaaacgggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

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<210> 106
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-NADH-102 variant

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<400> 106
Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
1          5          10          15
Gly Leu Lys Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
20          25          30
Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
35          40          45
His Val Ile Asp Glu Gly Leu Asp Leu Gly Asp Asn Tyr Val Met Gly
50          55          60
His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
65          70          75          80
Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
85          90          95
Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
100         105         110
Phe Gly Asp Trp Phe Gly Leu Gly Tyr Asp Gly Gly Tyr Gln Gln Tyr
115         120         125
Leu Leu Val Thr Arg Pro Arg Asn Leu Ser Arg Ile Pro Asp Asn Val
130         135         140
Ser Ala Asp Val Ala Ala Ser Thr Asp Ala Val Leu Thr Pro Tyr
145         150         155         160
His Ala Ile Lys Met Ala Gln Val Ser Pro Thr Ser Asn Ile Leu Leu
165         170         175
Ile Gly Ala Gly Gly Leu Gly Gly Asn Ala Ile Gln Val Ala Lys Ala
180         185         190
Phe Gly Ala Lys Val Thr Val Leu Asp Lys Lys Lys Glu Ala Arg Asp
195         200         205
Gln Ala Lys Lys Leu Gly Ala Asp Ala Val Tyr Glu Thr Leu Pro Glu
210         215         220
Ser Ile Ser Pro Gly Ser Phe Ser Ala Cys Phe Asp Phe Val Ser Val

```

225		230		235		240									
Gln	Ala	Thr	Phe	Asp	Val	Cys	Gln	Lys	Tyr	Val	Glu	Pro	Lys	Gly	Val
				245					250					255	
Ile	Met	Pro	Val	Gly	Leu	Gly	Ala	Pro	Asn	Leu	Ser	Phe	Asn	Leu	His
				260					265					270	
Asp	Leu	Ala	Leu	Arg	Glu	Ile	Arg	Ile	Leu	Gly	Ser	Phe	Trp	Gly	Thr
				275					280					285	
Thr	Asn	Asp	Leu	Asp	Asp	Val	Leu	Lys	Leu	Val	Ser	Glu	Gly	Lys	Val
				290					295					300	
Lys	Pro	Val	Val	Arg	Ser	Ala	Lys	Leu	Lys	Glu	Leu	Pro	Glu	Tyr	Ile
305						310				315					320
Glu	Lys	Leu	Arg	Asn	Asn	Ala	Tyr	Glu	Gly	Arg	Val	Val	Phe	Asn	Pro
				325					330					335	

<210> 107
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 107

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cgcaacgatc	tgccagtaca	caagccgaaa	gctgggtcaac	tgctgctgaa	agtagatgca	120
gtaggctctgt	gccactctga	tctgcacgtt	atctcagaag	gcctggattt	gggtgacaac	180
tacgttatgg	gtcacgaaat	cgctgggtacc	gttgctgctg	ttggtgatga	cgttatcaac	240
tacaaagtag	gtgaccgtgt	agcttgtgtt	gggtccgaacg	gttgcggtgg	ttgcaaatac	300
tgccgtgggtg	ctatcgacaa	cgtttgcaaa	aacgcttttcg	gtgactgggt	cggtctgggt	360
tatgatgggtg	gctatcaaca	atacctgctg	gtaactcgcc	cgcgtaacct	gtctcgtatc	420
ccggataacg	tatctgctga	tgttgctgct	gcttctaccg	acgctgttct	gactccgtac	480
cacgctatca	aaatggctca	ggtttctccg	acctctaaca	tcctgctgat	cggtgctgggt	540
gggtctgggtg	gtaacgctat	ccagggttgc	aaagcattcg	gtgctaaagt	taccgttctg	600
gacaaaaaaa	aagaagctcg	tgaccaggct	aaaaaactgg	gtgctgacgc	tgtttacgaa	660
accctgccgg	aatctatctc	tccgggttct	ttctctgctt	gcttcgactt	cgtttctggt	720
caggctacct	tcgacgtttg	ccagaaatac	ggtgaaccga	aagggtgttat	catgccgggt	780
gggtctgggtg	ctccgaacct	gtcttttaac	ctgcatgacg	ttgctctgcg	tgaacaccgt	840
atcctgggtt	ctttctgggg	taccaccaac	gacctggacg	acgttttcaa	actggtttct	900
gaaggtaaag	ttaaaccggt	tgtacgatct	gctaaactga	aagaactgcc	ggaatacatc	960
gaaaaactgc	gtaacaacgc	ttacgaaggt	cgtgttggtt	tcaacccgta	a	1011

<210> 108
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-NADH-102 variant

<400> 108

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

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

<210> 109

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 109

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gtaggctctg	gccactctga	tctgcacgtt	atctcagaag	gcctggattt	gggtgacaac	180
tacgttatgg	gtcacgaaat	cgctgggtacc	ggtgctgctg	ttggtgatga	cggtatcaac	240
tacaaagtag	gtgaccgtgt	agcttgtggt	ggtccgaacg	ggtgcgggtg	ttgcaaatac	300
tgccgtgggt	ctatcgacaa	cgtttgcaca	aacgctttcg	gtgactgggt	cggtctgggt	360
tatgatgggt	gctatcaaca	atacctgctg	gtaactcgcc	cgcgtaacct	gtctcgtatc	420
ccggataacg	tatctgctga	tggtgctgct	gcttctaccg	acgctgttct	gactccgtac	480
cacgctatca	aaatggctca	ggtttctccg	acctctaaca	tctgctgat	cggtgctgggt	540
ggctctgggt	gtaacgctat	ccaggttgct	aaagcattcg	gtgctaaagt	taccgttctg	600
gacaaaaaaa	aagaagctcg	tgaccaggct	aaaaaactgg	gtgctgacgc	tgtttacgaa	660

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accctgccgg aatctatctc tccgggttct ttctctgctt gcttcgactt cgtttctgtt 720
caggctacct tcgacgtttg ccagaaatac gttgaaccga aaggtgttat catgccggtt 780
ggctctgggtg ctccgaacct gtcttttaac ctgcatgacc ttgctctgcg tgaaatccgt 840
atcctgggtt ctttctgggg taccaccaac gacctggacg acgttttcaa actggtttct 900
gaaggtaaag ttaaaccggt tgtacgttct gctaaactga aagaactgcc ggaatacatc 960
gaaaaactgc gtaacaacgc ttacgaaggt cgtgttggtt tcaaccgta a 1011

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<210> 110

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED-NADH-102 variant

<400> 110

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

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<210> 111
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 111
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 aacggttttcg ttggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttgtttcctt ctccaacaaa 300
 tacgacgaag ttgttaccac ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
 gctaccccgt ccgttaaaccg ttctggttctg acctcctcca ccgtttccgc tctgattccg 420
 aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
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 aagaccgaag ctgaactggc tgcattggaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacactatt ggcactattt tcgatccgga aactcagtc 660
 ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctgggtac tttcgattgg 840
 aacaccggtt tggctacctt ccgtaaactg taccctgcca aaaccttccc ggctgacttc 900
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
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 gaaaccgctt aa 1032

<210> 112
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 112
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 1 5 10 15
 Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
 20 25 30
 Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
 35 40 45
 Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
 50 55 60
 Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
 65 70 75 80
 Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Val Ser
 85 90 95
 Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Thr
 100 105 110
 Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
 115 120 125
 Val Leu Thr Ser Ser Thr Val Ser Ala Leu Ile Pro Lys Pro Asn Val

130		135		140
Glu Gly Ile Tyr Leu Asp	Glu Lys Ser Trp Asn	Leu Glu Ser Ile Asp		
145	150	155	160	
Lys Ala Lys Thr Leu Pro	Glu Ser Asp Pro Gln	Lys Ser Leu Trp Val		
	165	170	175	
Tyr Ala Ala Ser Lys Thr	Glu Ala Glu Leu Ala	Ala Trp Lys Phe Met		
	180	185	190	
Asp Glu Asn Lys Pro His	Phe Thr Leu Asn Ala	Val Leu Pro Asn Tyr		
	195	200	205	
Thr Ile Gly Thr Ile Phe	Asp Pro Glu Thr Gln	Ser Gly Ser Thr Ser		
	210	215	220	
Gly Trp Met Met Ser Leu	Phe Asn Gly Glu Val	Ser Pro Ala Leu Ala		
225	230	235	240	
Leu Met Pro Pro Gln Tyr	Tyr Val Ser Ala Val	Asp Ile Gly Leu Leu		
	245	250	255	
His Leu Gly Cys Leu Val	Leu Pro Gln Ile Glu	Arg Arg Arg Val Tyr		
	260	265	270	
Gly Thr Ala Gly Thr Phe	Asp Trp Asn Thr Val	Leu Ala Thr Phe Arg		
	275	280	285	
Lys Leu Tyr Pro Ser Lys	Thr Phe Pro Ala Asp	Phe Pro Asp Gln Gly		
	290	295	300	
Gln Asp Leu Ser Lys Phe	Asp Thr Ala Pro Ser	Leu Glu Ile Leu Lys		
305	310	315	320	
Ser Leu Gly Arg Pro Gly	Trp Arg Ser Ile Glu	Glu Glu Ser Ile Lys	Asp	
	325	330	335	
Leu Val Gly Ser Glu Thr	Ala			
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<210> 113
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 113
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 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggttgga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
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 tacgacgaag ttgttaccct ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
 gctaccccg tccgttaaaccg ttctgttctg acctcctcca ccgtttcggc tctgattccg 420
 aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgaccg cagaaatccc tgtgggtata cgctgcatcc 540
 aagaccgaag ctgaactggc tgcattggaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacactatt ggcactattt tcgatccgga aactcagggc 660
 ggttccacct ccggttggat gatgtccctg tttacaggcg aggtttcccc ggctctggct 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctggggttg 780
 ctggttctgc cacaatcgca acgtcgtcgt gtttacggta cggctgggtac tttcgattgg 840
 aacaccgttc tggctacctt ccgtaaaactg taccggtcca aaaccttccc ggctgacttc 900
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc gggcgctgga aattctgaaa 960
 tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
 gaaaccgctt aa 1032

<210> 114
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 114
 Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
 1 5 10 15
 Val Thr Gly Ala Asn Gly Phe Ile Gly Ser His Val Val Glu Gln Leu
 20 25 30
 Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
 35 40 45
 Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
 50 55 60
 Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
 65 70 75 80
 Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Val Ser
 85 90 95
 Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Gly Thr
 100 105 110
 Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
 115 120 125
 Val Leu Thr Ser Ser Thr Val Ser Ala Leu Ile Pro Lys Pro Asn Val
 130 135 140
 Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
 145 150 155 160
 Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
 165 170 175
 Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
 180 185 190
 Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Asn Tyr
 195 200 205
 Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Gly Gly Ser Thr Ser
 210 215 220
 Gly Trp Met Met Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala
 225 230 235 240
 Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu
 245 250 255
 His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr
 260 265 270
 Gly Thr Ala Gly Thr Phe Asp Trp Asn Thr Val Leu Ala Thr Phe Arg
 275 280 285
 Lys Leu Tyr Pro Ser Lys Thr Phe Pro Ala Asp Phe Pro Asp Gln Gly
 290 295 300
 Gln Asp Leu Ser Lys Phe Asp Thr Ala Arg Ala Leu Glu Ile Leu Lys
 305 310 315 320
 Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp
 325 330 335
 Leu Val Gly Ser Glu Thr Ala
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<210> 115
 <211> 1032
 <212> DNA

<213> Artificial Sequence

<220>

<223> KRED-101 variant

<400> 115

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ccgggtcggt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttatgacgaa 240
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ctgaacgctg tactgccaaa ctacactatt ggcactattt tcgatccgga aactcagggc 660
ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cgtgggtgca 780
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aacaccgttc tggctacctt ccgtaaactg taccctgcca aaaccttccc ggctgacttc 900
ccagatcaag gtcaggacct gtctaaattc gacaccgctc gggcgctgga aattctgaaa 960
tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct gggtgggtcc 1020
gaaaccgctt aa 1032
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<210> 116

<211> 343

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED-101 variant

<400> 116

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Val Thr Gly Ala Asn Gly Phe Ile Gly Ser His Val Val Glu Gln Leu
20        25        30
Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
35        40        45
Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
50        55        60
Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
65        70        75        80
Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Val Ser
85        90        95
Phe Ser Asn Lys Tyr Asp Glu Val Val Pro Pro Ala Ile Gly Gly Thr
100       105       110
Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
115       120       125
Val Leu Thr Ser Ser Thr Val Ala Ala Leu Ile Pro Lys Pro Asn Val
130       135       140
Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
145       150       155       160
Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
165       170       175
Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
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<223> KRED-101 variant

<400> 118

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

<210> 119

<211> 1032

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED-101 variant

<400> 119

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ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttgtttcctt ctccaacaaa 300
tacgacgaag ttgttaccct ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
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aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc acacttcact 600
ctgaacgctg tactgccaaa ctacactatt ggcactatct tcgatccgga aactcagtcc 660
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ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccgaaga acttctgaaa 960
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gaaaccgctt aa 1032

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<210> 120
<211> 343
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-101 variant

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

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225					230					235				240
Leu	Met	Pro	Pro	Gln	Tyr	Tyr	Val	Ser	Ala	Val	Asp	Ile	Gly	Leu
				245					250					255
His	Leu	Gly	Cys	Leu	Val	Leu	Pro	Gln	Ile	Glu	Arg	Arg	Arg	Val
			260					265					270	
Gly	Thr	Ala	Gly	Thr	Phe	Asp	Trp	Asn	Thr	Val	Leu	Ala	Thr	Phe
		275					280					285		
Lys	Leu	Tyr	Pro	Ser	Lys	Thr	Phe	Pro	Ala	Asp	Phe	Pro	Asp	Gln
	290					295					300			
Gln	Asp	Leu	Ser	Lys	Phe	Asp	Thr	Ala	Pro	Ser	Glu	Glu	Leu	Lys
305					310					315				320
Ser	Leu	Gly	Arg	Pro	Gly	Trp	Arg	Ser	Ile	Glu	Glu	Ser	Ile	Lys
			325					330						335
Leu	Val	Gly	Ser	Glu	Thr	Ala								
			340											

<210> 121
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

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 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttgtttcctt ctccaacaaa 300
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 gctaccccggt ccgttaaaccg ttctgttctg acctcctcca ccgtttccgc tctgattccg 420
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 aagaccgaag ctgaactggc tgcattggaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacaccatt ggcactattt tcgatccgga aactcagtcc 660
 ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
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 aacaccgttc tggctacctt ccgtaaaactg taccctgcca aaaccttccc ggctgacttc 900
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 gaaaccgctt aa 1032

<210> 122
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 122
 Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
 1 5 10 15
 Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu

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

<210> 123
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 123
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 aacggtttcg ttggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttgtttcctt ctccaacaaa 300
 tacgacgaag ttgttaccac ggctatcggt ggtacctga acgctctgcg tgctgctgct 360

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gctaccccgt ccgttaaacg tttcgttctg acctcctcca ccgtttccgc tctgattccg 420
aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
aaagctaaaa ccctgccgga atccgaccg cagaaatccc tgtgggtata cgctgcatcc 540
aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc acacttcact 600
ctgaacgctg tactgccagg gtacactatt ggcactatth tcgatccgga aactcagtcc 660
ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctggtac tttcgattgg 840
aacaccgttc tggctacctt ccgtaaacgt taccggtcca aaaccttccc ggctgacttc 900
ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
gaaaccgctt aa 1032

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<210> 124
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 124

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

	275					280						285							
Lys	Leu	Tyr	Pro	Ser	Lys	Thr	Phe	Pro	Ala	Asp	Phe	Pro	Asp	Gln	Gly				
	290					295					300								
Gln	Asp	Leu	Ser	Lys	Phe	Asp	Thr	Ala	Pro	Ser	Leu	Glu	Ile	Leu	Lys				
305					310					315					320				
Ser	Leu	Gly	Arg	Pro	Gly	Trp	Arg	Ser	Ile	Glu	Glu	Ser	Ile	Lys	Asp				
				325					330					335					
Leu	Val	Gly	Ser	Glu	Thr	Ala													
			340																

<210> 125
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 125

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ggtac	cgctc	gttcc	gcttc	caaact	gggt	aacct	gcaga	aacgt	ttggga	cgcta	aaatac	180
ccggg	tcgta	aaccc	gc	tggtg	ttgaa	gacat	gctga	aacag	gggtgc	ttacg	acgaa	240
ggtat	caaag	gtgct	gctgg	tggtg	ctcac	atcgt	ctccg	ttgtt	tcctt	ctcca	acaaa	300
tacga	cgaag	ttggt	taacc	ggcta	tcggt	ggta	ccttga	acgct	ctgcg	tgctg	ctgct	360
gctac	cccg	ttaa	acg	tttcg	ttctg	acctc	ctcca	ccgtt	tcgcg	tctga	ttccg	420
aaacc	gaacg	ttga	aggtat	ctacc	tggac	gaaaa	atcct	ggaac	cctgga	atcca	tcgac	480
aaagc	taaaa	ccctg	ccgga	atccg	acccg	cagaa	atccc	tgtgg	gtata	cgctg	catcc	540
aagac	cgaag	ctga	actggc	tgcat	ggaaa	tttat	ggatg	agaac	aagcc	acact	tcact	600
ctga	acgctg	tactg	ccagg	gtaca	ctatt	ggc	actattt	tcgat	ccgga	aactc	agtc	660
ggtt	ccacct	ccggt	ttgat	gatgt	ccctg	ttta	acggcg	agg	tttccc	ggct	ctgg	720
ctgat	gccac	cgcag	tacta	cgttt	ccgct	g	ttgatattg	gcctg	ctgca	cctgg	ggttg	780
ctggt	ttctgc	cacaa	atcga	acgtc	gtcgt	gttt	acggta	cggct	ggtac	tttcg	attgg	840
aacac	cggtt	tggt	acctt	ccgta	aaactg	tacc	cgcca	aaac	cttccc	ggct	gacttc	900
ccgat	caag	gtcag	gacct	gtcta	aattc	gacac	cgctc	cg	tcctgga	aatt	ctgaaa	960
tctct	gggtc	gccc	aggttg	gcgtt	ccatc	gaaga	aatcca	tcaa	agacct	ggtt	ggttc	1020
gaaac	cgctt	aa										1032

<210> 126
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 126

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

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

<210> 127
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 127
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 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacgttggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
 gttatcaaaag gtgctgctgg tgttgctcac atcgcttccg ttgtttcctt ctccaacaaa 300
 tacgacgaag ttgttaccct ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
 gctaccccggt ccgttaaaccg tttcgttctg acctcctcca ctttttccgc tctgattccg 420
 aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgaccg cagaaatccc tgtgggtata cgctgcatcc 540
 aagaccgaag ctgaactggc tgcatggaaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacactatt ggcactattt tcgatccgga aactcagtcc 660
 ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720

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ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctggggttc 780
ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctggtac tttcgattgg 840
aacaccgttc tggctacctt ccgtaaactg taccgcgtcca aaaccttccc ggctgacttc 900
ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattttgaaa 960
tctctgggtc gcccagggtg gcgttccatc gaagaatcca tcaaagacct gggttggttc 1020
gaaaccgctt aa 1032

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<210> 128
<211> 343
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-101 variant

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<400> 128
Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
1      5      10      15
Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
      20      25      30
Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
      35      40      45
Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
      50      55      60
Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
65      70      75      80
Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Val Ser
      85      90      95
Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Gly Thr
      100      105      110
Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
      115      120      125
Val Leu Thr Ser Ser Thr Phe Ser Ala Leu Ile Pro Lys Pro Asn Val
      130      135      140
Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
145      150      155      160
Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
      165      170      175
Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
      180      185      190
Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Asn Tyr
      195      200      205
Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Ser Gly Ser Thr Ser
      210      215      220
Gly Trp Met Met Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala
225      230      235      240
Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu
      245      250      255
His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr
      260      265      270
Gly Thr Ala Gly Thr Phe Asp Trp Asn Thr Val Leu Ala Thr Phe Arg
      275      280      285
Lys Leu Tyr Pro Ser Lys Thr Phe Pro Ala Asp Phe Pro Asp Gln Gly
      290      295      300
Gln Asp Leu Ser Lys Phe Asp Thr Ala Pro Ser Leu Glu Ile Leu Lys
305      310      315      320
Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp

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325
 Leu Val Gly Ser Glu Thr Ala
 340

330

335

<210> 129
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 129
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 aacggttttcg ttggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttgtttcctt ctccaacaaa 300
 tacgacgaag ttgttaccac ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
 gctaccccgt ccgttaaaccg tttcggttctg acctcctcca ctttttccgc tctgattccg 420
 aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaataa ccctgccgga atccgaccgc cagaaatccc tgtgggtata cgctgcatcc 540
 aagaccgaag ctgaactggc tgcattggaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacactatt ggcactatct tcgatccgga aactcagtcc 660
 ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctgggtac tttcgattgg 840
 aacaccggtc tggctacctt ccgtaaactg taccgcgtcc aaaccttccc ggctgacttc 900
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
 tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
 gaaaccgctt aa 1032

<210> 130
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

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

<210> 132
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 132
 Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
 1 5 10 15
 Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
 20 25 30
 Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
 35 40 45
 Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
 50 55 60
 Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
 65 70 75 80
 Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Val Ser
 85 90 95
 Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Gly Thr
 100 105 110
 Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
 115 120 125
 Val Leu Thr Ser Ser Thr Val Ser Ala Leu Val Pro Lys Pro Asn Val
 130 135 140
 Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
 145 150 155 160
 Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
 165 170 175
 Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
 180 185 190
 Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Ser Tyr
 195 200 205
 Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Ser Gly Ser Thr Ser
 210 215 220
 Gly Trp Met Met Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala
 225 230 235 240
 Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu
 245 250 255
 His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr
 260 265 270
 Gly Thr Ala Gly Thr Phe Asp Trp Asn Thr Val Leu Ala Thr Phe Arg
 275 280 285
 Lys Leu Tyr Pro Ser Lys Thr Phe Pro Ala Asp Phe Pro Asp Gln Gly
 290 295 300
 Gln Asp Leu Ser Lys Phe Asp Thr Ala Pro Ser Leu Glu Ile Leu Lys
 305 310 315 320
 Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp
 325 330 335
 Leu Val Gly Ser Glu Thr Ala
 340

<210> 133

<211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 133
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 aacggttttcg ttgggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tggtgttgaa gacatgctga aacaggggtgc ttacgacgaa 240
 gttatcaaag gtgctgctgg tggtgctcac atcgcttccg ttacatcctt ctccaacaaa 300
 tacgacgaag ttgttaccct ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
 gctaccccggt ccgttaaaccg tttcgttctg acctcctcca ccggttccgc tctgattccg 420
 aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgacctg cagaaatccc tgtgggtata cgctgcatcc 540
 aagaccgaag ctgaactggc tgcattggaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccagg gtacactatt ggcactattt tcgatccgga aactcagtcc 660
 ggttccacct ccggttggtat gatgtccctg tttaacggcg aggtttcccc ggccctggct 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
 ctgggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctgggtac tttcgattgg 840
 aacaccgttc tggctacctt ccgtaaacctg taccgcgtcca aaaccttccc ggctgacttc 900
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
 tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
 gaaaccgctt aa 1032

<210> 134
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 134
 Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
 1 5 10 15
 Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
 20 25 30
 Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
 35 40 45
 Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
 50 55 60
 Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
 65 70 75 80
 Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Thr Ser
 85 90 95
 Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Thr
 100 105 110
 Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
 115 120 125
 Val Leu Thr Ser Ser Thr Val Ser Ala Leu Ile Pro Lys Pro Asn Val
 130 135 140
 Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
 145 150 155 160
 Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val

				165					170				175				
Tyr	Ala	Ala	Ser	Lys	Thr	Glu	Ala	Glu	Leu	Ala	Ala	Trp	Lys	Phe	Met		
			180					185					190				
Asp	Glu	Asn	Lys	Pro	His	Phe	Thr	Leu	Asn	Ala	Val	Leu	Pro	Gly	Tyr		
		195					200					205					
Thr	Ile	Gly	Thr	Ile	Phe	Asp	Pro	Glu	Thr	Gln	Ser	Gly	Ser	Thr	Ser		
	210					215					220						
Gly	Trp	Met	Met	Ser	Leu	Phe	Asn	Gly	Glu	Val	Ser	Pro	Ala	Leu	Ala		
225					230					235				240			
Leu	Met	Pro	Pro	Gln	Tyr	Tyr	Val	Ser	Ala	Val	Asp	Ile	Gly	Leu	Leu		
				245					250					255			
His	Leu	Gly	Cys	Leu	Val	Leu	Pro	Gln	Ile	Glu	Arg	Arg	Arg	Val	Tyr		
			260					265					270				
Gly	Thr	Ala	Gly	Thr	Phe	Asp	Trp	Asn	Thr	Val	Leu	Ala	Thr	Phe	Arg		
	275						280					285					
Lys	Leu	Tyr	Pro	Ser	Lys	Thr	Phe	Pro	Ala	Asp	Phe	Pro	Asp	Gln	Gly		
	290					295					300						
Gln	Asp	Leu	Ser	Lys	Phe	Asp	Thr	Ala	Pro	Ser	Leu	Glu	Ile	Leu	Lys		
305					310					315					320		
Ser	Leu	Gly	Arg	Pro	Gly	Trp	Arg	Ser	Ile	Glu	Glu	Ser	Ile	Lys	Asp		
				325					330					335			
Leu	Val	Gly	Ser	Glu	Thr	Ala											
				340													

<210> 135
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 135
 atggcaaaga tcgataacgc agttctgccg gaagggttccc tggttcttggg taccgggtgct 60
 aacggtttca ttggtttccca cgttggttgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggttgaa gacatgctga aacaggggtg ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttacatcctt ctccaacaaa 300
 tacgacgaag ttgttaccct ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
 gctaccccggt ccgttaaaccg ttctgttctg acctcctcca ccgtttccgc tctgattccg 420
 aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgaccgg cagaaatccc tgtgggtata cgctgcatcc 540
 aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccagg atacactatt ggcactatct tcgatccgga aactcagtcc 660
 ggttccacct ccggttggat gacgtccctg tttaacggcg aggtttcccc ggccctgggt 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctgggtac tttcgattgg 840
 aacaccggtc tggctacctt ccgtaaaactg taccctgcca aaaccttccc ggctgacttc 900
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
 tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
 gaaaccgctt aa 1032

<210> 136
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>

<223> KRED-101 variant

<400> 136

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

<210> 137

<211> 1032

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED-101 variant

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<400> 137
atggcaaaga tcgataacgc agttctgccg gaagggttccc tggttctggt taccggtgct 60
aacggttttcg ttggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttacatcctt ctccaacaaa 300
tacgacgaag ttggtacccc ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
gctaccccgt ccgttaaaccg tttcgttctg acctcctcca ccttttccgc tctgggtccg 420
aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
aaagctaaaa ccctgccgga atccgacccg cagaaatccc tgtgggtata cgctgcgtcc 540
aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc acacttcact 600
ctgaacgctg tactgccaaa ctacactatt ggcactatct tcgatccgga aactcagtcc 660
ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctgggtac tttcgattgg 840
aacaccgttc tggctacctt ccgtaaactg taccctgcca aaaccttccc ggctgacttc 900
ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
gaaaccgctt aa 1032

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<210> 138
<211> 343
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-101 variant

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<400> 138
Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
1      5      10      15
Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
20     25     30
Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
35     40     45
Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
50     55     60
Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
65     70     75     80
Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Thr Ser
85     90     95
Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Thr
100    105    110
Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
115    120    125
Val Leu Thr Ser Ser Thr Phe Ser Ala Leu Val Pro Lys Pro Asn Val
130    135    140
Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
145    150    155    160
Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
165    170    175
Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
180    185    190
Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Asn Tyr
195    200    205
Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Ser Gly Ser Thr Ser

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210		215		220
Gly Trp Met Met Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala				
225		230		235
Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu				240
		245		250
His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr				255
		260		265
Gly Thr Ala Gly Thr Phe Asp Trp Asn Thr Val Leu Ala Thr Phe Arg				270
		275		280
Lys Leu Tyr Pro Ser Lys Thr Phe Pro Ala Asp Phe Pro Asp Gln Gly				285
		290		295
Gln Asp Leu Ser Lys Phe Asp Thr Ala Pro Ser Leu Glu Ile Leu Lys				300
305		310		315
Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp				320
		325		330
Leu Val Gly Ser Glu Thr Ala				335
		340		

<210> 139
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 139
 atggcataca tcgataacgc agttctgccg gaagggttccc tggttctggt taccggtgct 60
 aacggtttcg ttggttccca cgttggtgaa cagctgctgg aacacggtta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttacatcctt ctccaacaaa 300
 tacgacgaag ttgttaccct ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
 gctaccccggt ccgttaaaccg ttctgttctg acctcctcca ccgtttccgc tctgattccg 420
 aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgaccgc cagaaatccc tgtgggtata cgctgcatcc 540
 aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccagg gtacactatt ggcactatct tcgatccgga aactcagtcc 660
 ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggccctggct 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctggtac tttcgattgg 840
 aacaccggtt tggctacctt ccgtaaactg taccctgcca aaaccttccc ggctgacttc 900
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
 tctctgggtc gccagggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
 gaaaccgctt aa 1032

<210> 140
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 140
 Met Ala Tyr Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu

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

<210> 141
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 141
 atggcataca tcgataacgc agttctgccg gaagggttccc tggttctggt taccggtgct 60
 aacggtttcg ttggttccca cgttgttgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacgttggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttgttgaa gacatgctga aacagggtgc ttacgacgaa 240

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gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttacatcctt ctccaacaaa 300
tacgacgaag ttgttaccct ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
gctaccccggt ccgttaaacg tttcgttctg acctcctcca ccgtttccgc tctgattccg 420
aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
aaagctaaaa ccctgccgga atccgaccg cagaaatccc tgtgggtata cgctgcatcc 540
aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc acacttcact 600
ctgaacgctg tactgccagg atacactatt ggcactatth tcgatccgga aactcagtcc 660
ggttccacct ccggttggat gacgtccctg tttaacggcg aggtttcccc ggccctggct 720
ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctggtac tttcgattgg 840
aacaccgttc tggctacctt ccgtaaaactg taccgtcca aaaccttccc ggctgacttc 900
ccagatcaag gtcaggacct gtctaaattc gacaccgctc ggtccctgga aattctgaaa 960
tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
gaaaccgctt aa 1032

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<210> 142
<211> 343
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-101 variant

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<400> 142
Met Ala Tyr Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
1      5      10      15
Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
20     25     30
Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
35     40     45
Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
50     55     60
Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
65     70     75     80
Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Thr Ser
85     90     95
Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Gly Thr
100    105    110
Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
115    120    125
Val Leu Thr Ser Ser Thr Val Ser Ala Leu Ile Pro Lys Pro Asn Val
130    135    140
Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
145    150    155    160
Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
165    170    175
Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
180    185    190
Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Gly Tyr
195    200    205
Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Ser Gly Ser Thr Ser
210    215    220
Gly Trp Met Thr Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala
225    230    235    240
Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu
245    250    255
His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr

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

<210> 145
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 145
 atgggctaaaa tcgataacgc agttctgccg gaagggttccc tggttcttgggt taccggtgct 60
 aacggtttcg ttggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacgttggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
 gttatcaaaag gtgctgctgg tgttgctcac atcgcttccg ttgtttcctt ctccaacaaa 300
 tacgacgaag ttgttaccoc ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
 gctaccccggt ccgttaaaccg tttcgttctg acctcctcca ccgtttccgc tctgattccg 420
 aagccgaacg ttgaaggtat ctacctggac gaaaagtcct ggaacctgga atccgttgac 480
 aaagctaaaa ccctgccgga atccgaccgc cagaaatccc tgtgggtata cgctgcatcc 540
 aagaccgaag ctgaactggc tgcatggaaa tttatggatg agaacaagcc acacttcact 600

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ctgaacgctg tactgccagg gtacactatt ggcactatatt tcgatccgga aactcagtcc 660
ggttccacct ccggttggat gctgtccctg tttaacggcg aggtttcgcc ggctctggct 720
ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctggtac tttcgattgg 840
aacaccgttc tggctacctt ccgtaaactg taccgcgtcca aaaccttccc ggctgacttc 900
ccagatcaag gtcaggacct gtctcaattc gacaccgctc cgtccctgga aattctgaaa 960
tctctgggtc gcccgaggttg gcgttcctt gaagaatcca tcaaagacct ggttggttcc 1020
gaaaccgctt aa 1032

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<210> 146
<211> 343
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-101 variant

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<400> 146
Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
1      5      10      15
Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
      20      25      30
Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
      35      40      45
Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
      50      55      60
Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
      65      70      75      80
Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Val Ser
      85      90      95
Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Gly Thr
      100      105      110
Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
      115      120      125
Val Leu Thr Ser Ser Thr Val Ser Ala Leu Ile Pro Lys Pro Asn Val
      130      135      140
Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Val Asp
      145      150      155      160
Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
      165      170      175
Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
      180      185      190
Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Gly Tyr
      195      200      205
Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Ser Gly Ser Thr Ser
      210      215      220
Gly Trp Met Leu Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala
      225      230      235      240
Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu
      245      250      255
His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr
      260      265      270
Gly Thr Ala Gly Thr Phe Asp Trp Asn Thr Val Leu Ala Thr Phe Arg
      275      280      285
Lys Leu Tyr Pro Ser Lys Thr Phe Pro Ala Asp Phe Pro Asp Gln Gly
      290      295      300
Gln Asp Leu Ser Gln Phe Asp Thr Ala Pro Ser Leu Glu Ile Leu Lys

```

305		310		315		320									
Ser	Leu	Gly	Arg	Pro	Gly	Trp	Arg	Ser	Leu	Glu	Glu	Ser	Ile	Lys	Asp
		325				330								335	
Leu	Val	Gly	Ser	Glu	Thr	Ala									
		340													

<210> 147
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 147
 atggcaaaga tcgataacgc agttctgccg gaagggtccc tggttctggt taccggtgct 60
 aacggtttca ttggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgtgc gttccgctga aaaaaatgct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgt ggaagttcca gacatgctga aacaggggtgc ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac gttgcttccg taacatcctt ctccaacaaa 300
 tacgacgaag ttgttacccc ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
 gctaccccgt ccgttaaaccg ttctggtctg acctcctcca ccttttccgc tctggttccg 420
 aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgacccg cagaaatccc tgtgggtata cgctgcgctc 540
 aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacactatt ggcactatct tcgatccgga aaccagggtc 660
 ggggtccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctgggt 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctgggtac tttcgattgg 840
 aacaccgttc tggctacctt ccgtaaatcgt taccctgcca aaaccttccc ggctgacttc 900
 ccgatcaag gtcaggacct gtctaaattc gacaccgtc cgtccctgga aattctgaaa 960
 tctctgggtc gcccagggtt gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
 gaaaccgct 1029

<210> 148
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 148
 Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
 1 5 10 15
 Val Thr Gly Ala Asn Gly Phe Ile Gly Ser His Val Val Glu Gln Leu
 20 25 30
 Leu Glu His Gly Tyr Lys Val Arg Gly Thr Val Arg Ser Ala Glu Lys
 35 40 45
 Asn Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
 50 55 60
 Glu Thr Val Glu Val Pro Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
 65 70 75 80
 Val Ile Lys Gly Ala Ala Gly Val Ala His Val Ala Ser Val Thr Ser
 85 90 95
 Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Gly Thr

tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct gggtggttcc 1020
gaaaccgct 1029

<210> 150
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED-101 variant

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

<210> 151
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 151
 atggcaaaga tcgataacgc agttctgccg gaagggttccc tggttctggt taccggtgct 60
 aacggttttcg ttggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tggtgttgaa gacatgctta agcaagggtc ttttgacgaa 240
 gttatcaaag gtgctgctgg tggtgctcac atcgcttccg ttacatcctt ttccaacaaa 300
 tacgacgagg ttgttaccgg tgcgatcggg ggtacctga acgctctgcg tgctgctgct 360
 gctaccccgt ccgttaaaccg tttcgttctg acctcctcca ccttttccgc tctgggtccg 420
 aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgaccgc cagaaatccc tgtgggtata cgctgcgtcc 540
 aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacactatt ggcactatct ttgatccgga aactcagtcc 660
 ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctgggtac tttcgattgg 840
 aacaccggtt tggctacctt ccgtaaactg taccgcgtcca aaaccttccc ggctgacttc 900
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
 tctctgggtc gcccgaggtt gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
 gaaaccgct 1029

<210> 152
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 152
 Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
 1 5 10 15
 Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
 20 25 30
 Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
 35 40 45
 Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
 50 55 60
 Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Phe Asp Glu
 65 70 75 80
 Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Thr Ser
 85 90 95
 Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Gly Ala Ile Gly Thr
 100 105 110
 Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
 115 120 125
 Val Leu Thr Ser Ser Thr Phe Ser Ala Leu Val Pro Lys Pro Asn Val
 130 135 140
 Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp

145		150		155		160									
Lys	Ala	Lys	Thr	Leu	Pro	Glu	Ser	Asp	Pro	Gln	Lys	Ser	Leu	Trp	Val
		165		170		175									
Tyr	Ala	Ala	Ser	Lys	Thr	Glu	Ala	Glu	Leu	Ala	Ala	Trp	Lys	Phe	Met
		180		185		190									
Asp	Glu	Asn	Lys	Pro	His	Phe	Thr	Leu	Asn	Ala	Val	Leu	Pro	Asn	Tyr
		195		200		205									
Thr	Ile	Gly	Thr	Ile	Phe	Asp	Pro	Glu	Thr	Gln	Ser	Gly	Ser	Thr	Ser
		210		215		220									
Gly	Trp	Met	Met	Ser	Leu	Phe	Asn	Gly	Glu	Val	Ser	Pro	Ala	Leu	Ala
225				230		235									240
Leu	Met	Pro	Pro	Gln	Tyr	Tyr	Val	Ser	Ala	Val	Asp	Ile	Gly	Leu	Leu
				245		250									255
His	Leu	Gly	Cys	Leu	Val	Leu	Pro	Gln	Ile	Glu	Arg	Arg	Arg	Val	Tyr
			260			265									
Gly	Thr	Ala	Gly	Thr	Phe	Asp	Trp	Asn	Thr	Val	Leu	Ala	Thr	Phe	Arg
		275				280									
Lys	Leu	Tyr	Pro	Ser	Lys	Thr	Phe	Pro	Ala	Asp	Phe	Pro	Asp	Gln	Gly
		290				295									
Gln	Asp	Leu	Ser	Lys	Phe	Asp	Thr	Ala	Pro	Ser	Leu	Glu	Ile	Leu	Lys
305				310		315									320
Ser	Leu	Gly	Arg	Pro	Gly	Trp	Arg	Ser	Ile	Glu	Glu	Ser	Ile	Lys	Asp
				325		330									335
Leu	Val	Gly	Ser	Glu	Thr	Ala									
			340												

<210> 153
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 153

atggcaaaga	tcgataacgc	agttctgccg	gaagggttccc	tggttctggt	taccggtgct	60
aacggtttcg	ttggttccca	cgttggtgaa	cagctgctgg	aacacggtta	caaagttcgt	120
ggtaccgctc	gttccgcttc	caaactggct	aacctgcaga	aacggttgga	cgctaaatac	180
ccgggtcgtt	tcgaaaccgc	tgttggtgaa	gacatgcttg	cagaaggtgc	ttttgacgaa	240
gttatcaaag	gtgctgctgg	tgttgctcac	atcgcttccg	ttacatcctt	ctccaacaaa	300
tacgacgagg	ttgttaccct	cgtgatcggt	ggtaccttga	acgctctgcg	tgctgctgct	360
gctaccccg	ccgttaaacg	tttcgttctg	acctcctcca	ccttttccgc	tctggttccg	420
aaaccgaacg	ttgaagggtat	ctacctggac	gaaaaatcct	ggaacctgga	atccatcgac	480
aaagctaaaa	ccctgccgga	atccgaccgc	cagaaatccc	tgtgggtata	cgctgcgtcc	540
aagaccgaag	ctgaactggc	tgcatggaaa	tttatggatg	agaacaagcc	acacttcact	600
ctgaacgctg	tactgccaaa	ctacactatt	ggcactat	tcgatccgga	aactcagtcc	660
ggttccacct	cggttggtat	gatgtccctg	tttaacggcg	aggtttcccc	ggctctggct	720
ctgatgccac	cgcaatacta	cgtttccgct	ggtgatattg	gcctgctgca	cctgggttgc	780
ctggttctgc	cacaaatcga	acgtcgtcgt	gtttacggta	cggctggtac	tttcgattgg	840
aacaccgttc	tggttacctt	ccgtaaactg	taccgcgtcc	aaaccttccc	ggctgacttc	900
ccagatcaag	gtcaggacct	gtctaaattc	gacaccgctc	cgtccctgga	aattctgaaa	960
tctctgggtc	gcccagggtg	gcgttccatc	gaagaatcca	tcaaagacct	ggttggttcc	1020
gaaaccgct						1029

<210> 154
 <211> 343

<212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 154
 Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
 1 5 10 15
 Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
 20 25 30
 Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
 35 40 45
 Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
 50 55 60
 Glu Thr Ala Val Val Glu Asp Met Leu Ala Glu Gly Ala Phe Asp Glu
 65 70 75 80
 Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Thr Ser
 85 90 95
 Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Val Ile Gly Gly Thr
 100 105 110
 Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
 115 120 125
 Val Leu Thr Ser Ser Thr Phe Ser Ala Leu Val Pro Lys Pro Asn Val
 130 135 140
 Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
 145 150 155 160
 Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
 165 170 175
 Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
 180 185 190
 Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Asn Tyr
 195 200 205
 Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Ser Gly Ser Thr Ser
 210 215 220
 Gly Trp Met Met Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala
 225 230 235 240
 Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu
 245 250 255
 His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr
 260 265 270
 Gly Thr Ala Gly Thr Phe Asp Trp Asn Thr Val Leu Ala Thr Phe Arg
 275 280 285
 Lys Leu Tyr Pro Ser Lys Thr Phe Pro Ala Asp Phe Pro Asp Gln Gly
 290 295 300
 Gln Asp Leu Ser Lys Phe Asp Thr Ala Pro Ser Leu Glu Ile Leu Lys
 305 310 315 320
 Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp
 325 330 335
 Leu Val Gly Ser Glu Thr Ala
 340

<210> 155
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>

<223> KRED-101 variant

<400> 155

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atggcaaaga tcgataacgc agttctgccg gaaggttccc tggttctggt taccggtgct 60
aacggtttcg ttggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctta aggaagggtgc ttttgacgaa 240
gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttacatcctt ctcccccaaa 300
tacgacgagg ttggtacccc cgtgatcggt ggtaccttga acgctctgcg tgctgctgct 360
gctaccccgt ccgttaaaccg tttcgttctg acctcctcca ccttttccgc tctggttccg 420
aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
aaagctaaaa ccctgccgga atccgaccgc cagaaatccc tgtgggtata cgctgcgtcc 540
aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc acacttcact 600
ctgaacgctg tactgccaaa ctacactatt ggcactatct tttctccgga aactcagtcc 660
ggttccaccg cgggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctggtac tttcgattgg 840
aacaccgttc tggctacctt ccgtaaaactg taccgcgtcca aaaccttccc ggctgacttc 900
ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct gggttggttc 1020
gaaaccgct                                     1029
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<210> 156

<211> 343

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED-101 variant

<400> 156

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Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
1          5          10          15
Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
20          25          30
Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
35          40          45
Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
50          55          60
Glu Thr Ala Val Val Glu Asp Met Leu Lys Glu Gly Ala Phe Asp Glu
65          70          75          80
Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Thr Ser
85          90          95
Phe Ser Pro Lys Tyr Asp Glu Val Val Thr Pro Val Ile Gly Gly Thr
100          105          110
Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
115          120          125
Val Leu Thr Ser Ser Thr Phe Ser Ala Leu Val Pro Lys Pro Asn Val
130          135          140
Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
145          150          155          160
Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
165          170          175
Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
180          185          190
Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Asn Tyr
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<400> 158

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Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
1      5      10      15
Val Thr Ser Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
20     25     30
Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
35     40     45
Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
50     55     60
Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
65     70     75     80
Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Thr Ser
85     90     95
Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Gly Thr
100    105    110
Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
115    120    125
Val Leu Thr Ser Ser Thr Phe Ser Ala Leu Val Pro Lys Pro Asn Val
130    135    140
Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
145    150    155    160
Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
165    170    175
Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
180    185    190
Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Asn Tyr
195    200    205
Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Ser Gly Ser Thr Ser
210    215    220
Gly Trp Met Met Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala
225    230    235    240
Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu
245    250    255
His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr
260    265    270
Gly Thr Ala Gly Thr Phe Asp Trp Asn Thr Val Leu Ala Thr Phe Arg
275    280    285
Lys Leu Tyr Pro Ser Lys Thr Phe Pro Ala Asp Phe Pro Asp Gln Gly
290    295    300
Gln Asp Leu Ser Lys Phe Asp Thr Ala Pro Ser Leu Glu Ile Leu Lys
305    310    315    320
Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp
325    330    335
Leu Val Gly Ser Glu Thr Ala
340
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<210> 159

<211> 1029

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED-101 variant

<400> 159

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atggcaaaga tcgataacgc agttctgccg gaagggttccc tggttctggt taccggtgct 60
aacggtttcg ttggttccca cgttggtgaa cagctgctgg aacacggtta caaagttcgt 120
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ggtagcgcgtc gttccgcttc caaactggct aacctgcaga aacgttggga cgctaaatac 180
ccgggtcggtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
ggtatcaaag gtgctgctgg tgttgctcac atcgcttccg tttgttcctt ctccaacaaa 300
tacgacgaag ttgttaccct ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
gctaccccggt ccgttaaaccg tttcgttctg acctcctcca ccttttccgc tctggttccg 420
aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
aaagctaaaa ccctgccgga atccgaccgc cagaaatccc tgtgggtata cgctgcgtcc 540
aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc acacttcact 600
ctgaacgctg tactgcaaaa ctacactatt ggcactatct tcgatccgga aactcagtcc 660
ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
ctgggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctgggtac tttcgattgg 840
aacaccgttc tggctacctt ccgtaaacgt taccgcgtcc aaaccttccc ggctgacttc 900
ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
gaaaccgct                                     1029

```

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<210> 160
<211> 343
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-101 variant

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

```

				245					250					255			
His	Leu	Gly	Cys	Leu	Val	Leu	Pro	Gln	Ile	Glu	Arg	Arg	Arg	Val	Tyr		
			260					265					270				
Gly	Thr	Ala	Gly	Thr	Phe	Asp	Trp	Asn	Thr	Val	Leu	Ala	Thr	Phe	Arg		
		275					280					285					
Lys	Leu	Tyr	Pro	Ser	Lys	Thr	Phe	Pro	Ala	Asp	Phe	Pro	Asp	Gln	Gly		
	290					295					300						
Gln	Asp	Leu	Ser	Lys	Phe	Asp	Thr	Ala	Pro	Ser	Leu	Glu	Ile	Leu	Lys		
305					310					315					320		
Ser	Leu	Gly	Arg	Pro	Gly	Trp	Arg	Ser	Ile	Glu	Glu	Ser	Ile	Lys	Asp		
			325					330						335			
Leu	Val	Gly	Ser	Glu	Thr	Ala											
			340														

<210> 161
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 161
 atggcacaaga tcgataacgc agttctgccg gaagggttccc tggttctggt taccggtgct 60
 aacggttttcg ttggttccca cgttggtgaa cagctgctgg aacacggtta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtg ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttacaggggt ctccaacaaa 300
 tacgacgaag ttgttaccct ggctatcggt ggtaccttga acgctctgct tgctgctgct 360
 gctaccccggt ccgttaaacc tttcggttct acctcctcca ccttttccgc tctggttccg 420
 aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgaccgc cagaaatccc tgtgggtata cgctgcgtcc 540
 aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacactatt ggcactattt tcgatccgga aactcagtcc 660
 ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctgggt 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctggtac tttcgattgg 840
 aacaccgttc tggctacctt ccgtaaactg taccctgcca aaaccttccc ggctgacttc 900
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
 tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
 gaaaccgct 1029

<210> 162
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 162
 Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
 1 5 10 15
 Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
 20 25 30
 Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys


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aaagctaaaa ccctgccgga atccgacccg cagaaatccc tgtgggtata cgctgcgtcc 540
aagaccgaag ctgaactggc tgcattggaaa tttatggatg agaacaagcc acacttcact 600
ctgaacgctg tactgccaaa ctacactatt ggcactatgt tcgatccgga aactcagtcc 660
ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
ctgatgccac cgcagtacta cgtttcgcgt gttgatattg gcctgctgca cctgggttgc 780
ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctggtac tttcgattgg 840
aacaccgttc tggctacctt ccgtaaaactg taccgcgtcca aaaccttccc ggctgacttc 900
ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
tctctgggtc gcccgaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
gaaaccgct                                     1029

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<210> 164
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 164

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

290		295		300
Gln Asp Leu Ser Lys Phe Asp Thr Ala Pro Ser Leu Glu Ile Leu Lys				
305		310		315
Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp				
		325		330
Leu Val Gly Ser Glu Thr Ala				
		340		

<210> 165
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 165
 atggcaaaga tcgataacgc agttctgccg gaagggttccc tggttctggt taccggtgct 60
 aacggtttcg ttggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gaccagctga aacaggggtgc ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttacatcctt ctccaacaaa 300
 tacgacgaag ttgttacccc ggctatcggt ggtaccttga acgctctgcg tgctgctgct 360
 gctaccccgt ccgttaaaccg ttctggtctg acctcctcca ccttttccgc tctggttccg 420
 aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgacccg cagaaatccc tgtgggtata cgctgctgcc 540
 aagaccgaag ctgaactggc tgcattggaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacactatt ggcactatct tcgatccgga aactcagtcc 660
 gggtccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctggtac tttcgattgg 840
 aacaccgttc tggctacctt ccgtaaactg taccctgcca aaaccttccc ggctgacttc 900
 ccgatcaag gtcaggacct gtctaaattc gacaccgtc cgtccctgga aattctgaaa 960
 tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
 gaaaccgct 1029

<210> 166
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

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

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

<210> 167
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 167
 atggcaaaga tcgataacgc agttctgccg gaaggttccc tggttctggt taccggtgct 60
 aacggtttcg ttggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacgttggga cgctaaatac 180
 ccgggtcgtt tcgaaacctg ggttggtgaa gacatgctga aacaggggtg ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttacatcctt ctccaacaaa 300
 tacgacgaag ttgttaccct ggctatcggt ggtaccttga acgctctgct tgctgctgct 360
 gctaccccggt ccgttaaaccg tttcgttctg acctcctcca ccttttccgc tctgggttccg 420
 aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgaccg cagaaatccc tgtgggtata cgctgctgcc 540
 aagaccgaag ctgaactggc tgcatggaaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacactatt ggcactatct tcgatccgga aactcagtcc 660
 ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctggggtgc 780
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctggtac tttcgattgg 840

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aacaccgttc tggctacctt ccgtaaactg tacccgtcca aaaccttccc ggctgacttc 900
ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
tctctgggtc gcccagggtg gcgttccatc gaagaatcca tcaaagacct gggtgggttc 1020
gaaaccgct                                     1029

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<210> 168
<211> 343
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRED-101 variant

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<400> 168
Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
1      5      10      15
Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
20     25     30
Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
35     40     45
Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
50     55     60
Glu Thr Trp Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
65     70     75     80
Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Thr Ser
85     90     95
Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Gly Thr
100    105    110
Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
115    120    125
Val Leu Thr Ser Ser Thr Phe Ser Ala Leu Val Pro Lys Pro Asn Val
130    135    140
Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
145    150    155    160
Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
165    170    175
Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
180    185    190
Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Asn Tyr
195    200    205
Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Ser Gly Ser Thr Ser
210    215    220
Gly Trp Met Met Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala
225    230    235    240
Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu
245    250    255
His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr
260    265    270
Gly Thr Ala Gly Thr Phe Asp Trp Asn Thr Val Leu Ala Thr Phe Arg
275    280    285
Lys Leu Tyr Pro Ser Lys Thr Phe Pro Ala Asp Phe Pro Asp Gln Gly
290    295    300
Gln Asp Leu Ser Lys Phe Asp Thr Ala Pro Ser Leu Glu Ile Leu Lys
305    310    315    320
Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp
325    330    335
Leu Val Gly Ser Glu Thr Ala

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<210> 169
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

<400> 169
 atggcaaaga tcgataacgc agttctgccg gaagggttccc tggttctggt taccggtgct 60
 aacggttttcg ttggttccca cgttggtgaa cagctgctgg aacacgggta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttacatcctt ctccaacaaa 300
 tacgacgaag ttgttaccct ggctatcggt ggtaccttgg ttgctctgcg tgctgctgct 360
 gctaccccggt ccgttaaaccg ttctggttctg acctcctcca ccttttccgc tctggttccg 420
 aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgacctg cagaaatccc tgtgggtata cgctgctgcc 540
 aagaccgaag ctgaactggc tgcattggaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacactatt ggcactatct tcgatccgga aactcagtcc 660
 ggttccacct ccggttggat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
 ctgggttctgc cacaaatcga acgtcgtcgt gtttacggta cggctgggtac tttcgattgg 840
 aacaccggtt tggctacctt ccgtaaactg taccctgcca aaaccttccc ggctgacttc 900
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
 tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
 gaaaccgct 1029

<210> 170
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED-101 variant

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

130		135		140
Glu Gly Ile Tyr Leu Asp	Glu Lys Ser Trp Asn	Leu Glu Ser Ile Asp		
145	150	155	160	
Lys Ala Lys Thr Leu Pro	Glu Ser Asp Pro Gln	Lys Ser Leu Trp Val		
	165	170	175	
Tyr Ala Ala Ser Lys Thr	Glu Ala Glu Leu Ala	Ala Trp Lys Phe Met		
	180	185	190	
Asp Glu Asn Lys Pro His	Phe Thr Leu Asn Ala	Val Leu Pro Asn Tyr		
	195	200	205	
Thr Ile Gly Thr Ile Phe	Asp Pro Glu Thr Gln	Ser Gly Ser Thr Ser		
	210	215	220	
Gly Trp Met Met Ser Leu	Phe Asn Gly Glu Val	Ser Pro Ala Leu Ala		
225	230	235	240	
Leu Met Pro Pro Gln Tyr	Tyr Val Ser Ala Val	Asp Ile Gly Leu Leu		
	245	250	255	
His Leu Gly Cys Leu Val	Leu Pro Gln Ile Glu	Arg Arg Arg Val Tyr		
	260	265	270	
Gly Thr Ala Gly Thr Phe	Asp Trp Asn Thr Val	Leu Ala Thr Phe Arg		
	275	280	285	
Lys Leu Tyr Pro Ser Lys	Thr Phe Pro Ala Asp	Phe Pro Asp Gln Gly		
	290	295	300	
Gln Asp Leu Ser Lys Phe	Asp Thr Ala Pro Ser	Leu Glu Ile Leu Lys		
305	310	315	320	
Ser Leu Gly Arg Pro Gly	Trp Arg Ser Ile Glu	Glu Glu Ser Ile Lys	Asp	
	325	330	335	
Leu Val Gly Ser Glu Thr	Ala			
	340			

<210> 171
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 171

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ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cgccgctgtc	gcgatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgcccctga	gctgcgtgta	atcggtctgc	cgctcaaggg	cttcgacaat	240
ttcgatgtgg	acgcctgtac	tgcccgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acggtcccga	ctgccgagct	ggcgatcgga	ctggcgggtg	ggctggggcg	gcatctgcgg	360
gcagcagatg	cgttcgtccg	ctctggcaag	ttccggggct	ggcaaccacg	gttctacggc	420
acggggctgg	ataacgctac	ggtcggcttc	cttggcatgg	gcgccatcgg	actggccatg	480
gctgatcgct	tgcagggatg	gggcgcgacc	ctgcagtacc	acgcgcggaa	ggctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	caggtggcgt	gcagcgaact	cttcgccagc	600
tcggacttca	tcctgctggc	gcttcccttg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtacg	gccgggcgct	ctgcttgtaa	acccctgtcg	tggtctcggt	720
gtggatgaag	ccgccgtgct	cgcggcgctt	gagcgaaggc	agctcggcgg	gtatgcggcg	780
gatgtattcg	aaatggaaga	ctgggctcgc	gcggaccggc	cgcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttcact	ccgcacatag	ggtcggcagt	gcgcgcggtg	900
cgcctggaga	ttgaacgttg	tgcagcgcag	aacatcctcc	aggcattggc	aggtgagcgc	960
ccaatcaacg	ctgtgaaccg	tctgcccgaag	gccgagcctg	ccgcatgttg	a	1011

<210> 172

<211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 172
 Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
 1 5 10 15
 Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
 20 25 30
 Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Arg Asp Ala Gln Ala
 35 40 45
 Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
 50 55 60
 Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
 65 70 75 80
 Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
 85 90 95
 Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
 100 105 110
 Val Gly Leu Gly Arg His Leu Arg Ala Ala Asp Ala Phe Val Arg Ser
 115 120 125
 Gly Lys Phe Arg Gly Trp Gln Pro Arg Phe Tyr Gly Thr Gly Leu Asp
 130 135 140
 Asn Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Leu Ala Met
 145 150 155 160
 Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ala Arg
 165 170 175
 Lys Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
 180 185 190
 Ala Cys Ser Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
 195 200 205
 Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala
 210 215 220
 Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val
 225 230 235 240
 Val Asp Glu Ala Ala Val Leu Ala Ala Leu Glu Arg Gly Gln Leu Gly
 245 250 255
 Gly Tyr Ala Ala Asp Val Phe Glu Met Glu Asp Trp Ala Arg Ala Asp
 260 265 270
 Arg Pro Gln Gln Ile Asp Pro Ala Leu Leu Ala His Pro Asn Thr Leu
 275 280 285
 Phe Thr Pro His Ile Gly Ser Ala Val Arg Ala Val Arg Leu Glu Ile
 290 295 300
 Glu Arg Cys Ala Ala Gln Asn Ile Leu Gln Ala Leu Ala Gly Glu Arg
 305 310 315 320
 Pro Ile Asn Ala Val Asn Arg Leu Pro Lys Ala Glu Pro Ala Ala Cys
 325 330 335

<210> 173
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 173

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atgctgccga aactcgttat aactcacaaa gtacacgaag agatcctgca actgctggcg 60
ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
cgccgctgtc gcgatgctca ggcgatgatg gcgttcatgc ccgatcgggt cgatgcagac 180
tttcttcaag cctgccctga gctgctgtga atcggcgctg cgctcaaggg ctttgacaat 240
ttcgatgtgg acgcctgtac tgcccgcggg gtctggctga ccttcgtgcc tgatctgttg 300
acgggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatctgcgg 360
gcagcagatg cgttcgtccg ctctggcaag ttccggggct ggcaaccaca gttctacggc 420
acgggggctgg ataacgctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc acgcgcggaa ggctctggat 540
acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtagc gccgggcgct ctgcttggtta acccctgtcg tggctcggta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaaggc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttctact ccgcacatag ggtcggcagt gcgcgcgggtg 900
cgcctggaaa ttgaacgttg cgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
ccaatcaacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011
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<210> 174

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 174

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

210		215		220
Leu Val Arg Pro Gly Ala	Leu Leu Val Asn Pro	Cys Arg Gly Ser Val		
225	230	235	240	
Val Asp Glu Ala Ala Val	Leu Ala Ala Leu Glu	Arg Gly Gln Leu Gly		
	245	250	255	
Gly Tyr Ala Ala Asp Val	Phe Glu Met Glu Asp	Trp Ala Arg Ala Asp		
	260	265	270	
Arg Pro Gln Gln Ile Asp	Pro Ala Leu Leu Ala	His Pro Asn Thr Leu		
	275	280	285	
Phe Thr Pro His Ile Gly	Ser Ala Val Arg Ala	Val Arg Leu Glu Ile		
	290	295	300	
Glu Arg Cys Ala Ala Gln	Asn Ile Leu Gln Ala	Leu Ala Gly Glu Arg		
305	310	315	320	
Pro Ile Asn Ala Val Asn	Arg Leu Pro Lys Ala	Glu Pro Ala Ala Cys		
	325	330	335	

<210> 175
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 175
 atgctgccga aactcgttat aactcacaaa gtacacgaag agatcctgca actgctggcg 60
 ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
 cgccgctgtc gcgatgctca ggcgatgatg gcgttcatgc ccgatcgggt cgatgcagac 180
 tttcttcaag cctgcccctga gctgcgtgta atcggcgctg cgctcaaggg ctatgacaat 240
 ttcgatgtgg acgcctgtac tgcccgcggg gtctggctga ccttcgtgcc tgatctgttg 300
 acgggtcccga ctgccgagct ggccatcggg ctggcggttg ggctggggcg gcatctgcgg 360
 gcagcagatg cgttcgtccg ctctggcaag ttccggggct ggcaaccacg gttctacggc 420
 acggggctgg ataacgctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
 gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc acgcgcggaa ggctctggat 540
 acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
 tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
 gagctgcttg ccctcgtagc gccgggcgct ctgcttatta acccctgtcg tggctcggtg 720
 gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
 gatgtattcg aaatggaaga ctgggctcgc gcggaccggc gcgagcagat cgatcctgcg 840
 ctgctcgcgc atccgaatac gctgttact ccgcacatag ggtcggcagt gcgcgcgggtg 900
 cgcctggaga ttgaacgttg cgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
 ccaatcgacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

<210> 176
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 176
 Met Leu Pro Lys Leu Val Ile Thr His Lys Val His Glu Glu Ile Leu
 1 5 10 15
 Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
 20 25 30

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

<210> 177

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 177

atgctgccga	aactcgttat	aactcacaga	gtacacgaag	agatcctgca	actgctggcg	60
ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cgccgctgtc	gcgatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgccttga	gctgcgtgta	atcggctgtg	cgctcaaggg	ctttgacaat	240
ttcgatgtgg	acgcctgtac	tgcccgcggg	gtctggctga	ccttcgtgcc	tgatctggtg	300
acgggtcccga	ctgccgagct	ggccatcgga	ctggcggtgg	ggctggggcg	gcatctgcgg	360
gcagcagatg	cgttcgtccg	ctctggcaag	ttccggggct	ggcaaccaca	gttctacggc	420
acggggctgg	ataacgctac	ggtcggcttc	cttggcatgg	gcgccatcgg	actggccatg	480
gctgatcgct	tgacgggatg	gggcgcgacc	ctgcagtacc	acgcgcggaa	ggctctggat	540

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acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
tcggacttca tcttgctggc gcttccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtacg gccgggcgct ctgcttatta acccctgtcg tggctcggtg 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttctc cgcacatag ggtcggcagt gcgcgcggtg 900
cgcctggcaa ttgaacgttg cgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
ccaatcgacg ctgtgaaccg tctgccaag gccgagcctg ccgcatgttg a 1011

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<210> 178

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 178

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

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305		310		315		320									
Pro	Ile	Asp	Ala	Val	Asn	Arg	Leu	Pro	Lys	Ala	Glu	Pro	Ala	Ala	Cys
		325		330		335									

<210> 179
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 179

atgctgccga	aactcgttat	aactcacaaa	gtacacgaag	agatcctgca	actgctggcg	60
ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cgccgctgtc	gcgatgctca	ggcgatgatg	gcgttcacgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgccctga	gctgcgtgta	atcggcgctg	cgctcaaggg	ctatgacaat	240
ttcgatgtgg	acgcctgtac	tgcccgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acgggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatctgcgg	360
gcagcagatg	cgttcgctccg	ctctggcaag	ttccggggct	ggcaaccaca	gttctacggc	420
acgggggctgg	ataacgctac	ggtcggcttc	cttggcatgg	gcgccatcgg	actggccatg	480
gctgatcgct	tgcaggggatg	gggcgcgacc	ctgcagtacc	acgcgcggaa	ggctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	caggtggcgt	gcagcgaact	cttcgccagc	600
tccgacttca	tcctgctggc	gcttcccttg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtaacg	gccgggcgct	ctgcttgtaa	acccctgtcg	tggtctcggtg	720
gtggatgaag	ccgccgtgct	cgcggcgctt	gagcgaggcc	agctcggcgg	gtatgcggcg	780
gatgtattcg	aaatggaaga	ctgggctcgc	gcggaccggc	cgcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttcact	ccgcacatag	ggtcggcagt	gcgcgcggtg	900
cgcctggaga	ttgaacgttg	tgcagcgcag	aacatcctcc	aggcattggc	aggtgagcgc	960
ccaatcgacg	ctgcgaaccg	tctgcccga	gccgagcctg	ccgcatgttg	a	1011

<210> 180
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 180

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

Gly	Lys	Phe	Arg	Gly	Trp	Gln	Pro	Gln	Phe	Tyr	Gly	Thr	Gly	Leu	Asp
	130					135					140				
Asn	Ala	Thr	Val	Gly	Phe	Leu	Gly	Met	Gly	Ala	Ile	Gly	Leu	Ala	Met
145					150					155					160
Ala	Asp	Arg	Leu	Gln	Gly	Trp	Gly	Ala	Thr	Leu	Gln	Tyr	His	Ala	Arg
				165					170					175	
Lys	Ala	Leu	Asp	Thr	Gln	Thr	Glu	Gln	Arg	Leu	Gly	Leu	Arg	Gln	Val
			180					185					190		
Ala	Cys	Ser	Glu	Leu	Phe	Ala	Ser	Ser	Asp	Phe	Ile	Leu	Leu	Ala	Leu
	195						200				205				
Pro	Leu	Asn	Ala	Asp	Thr	Leu	His	Leu	Val	Asn	Ala	Glu	Leu	Leu	Ala
210						215					220				
Leu	Val	Arg	Pro	Gly	Ala	Leu	Leu	Val	Asn	Pro	Cys	Arg	Gly	Ser	Val
225					230					235					240
Val	Asp	Glu	Ala	Ala	Val	Leu	Ala	Ala	Leu	Glu	Arg	Gly	Gln	Leu	Gly
				245					250					255	
Gly	Tyr	Ala	Ala	Asp	Val	Phe	Glu	Met	Glu	Asp	Trp	Ala	Arg	Ala	Asp
			260					265					270		
Arg	Pro	Gln	Gln	Ile	Asp	Pro	Ala	Leu	Leu	Ala	His	Pro	Asn	Thr	Leu
		275					280					285			
Phe	Thr	Pro	His	Ile	Gly	Ser	Ala	Val	Arg	Ala	Val	Arg	Leu	Glu	Ile
	290					295					300				
Glu	Arg	Cys	Ala	Ala	Gln	Asn	Ile	Leu	Gln	Ala	Leu	Ala	Gly	Glu	Arg
305					310					315					320
Pro	Ile	Asp	Ala	Ala	Asn	Arg	Leu	Pro	Lys	Ala	Glu	Pro	Ala	Ala	Cys
				325					330					335	

<210> 181
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 181
 atgctgccga aactcgttat aactcaccga gtacacgaag agatcctgca actgctggcg 60
 ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
 cggcgctgtg cagatgctca ggcgatgatg gcgttcatgc ccgatcgggt cgatgcagac 180
 tttcttcaag cctgcccctga gctgctgtga atcggtgcg cgctcaaggg cttcgacaat 240
 ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga cttcgtgcc tgatctgttg 300
 acggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatctgcgg 360
 gcagcagatg cgttcgtccg ctctggcaag ttccagggtt ggcaaccacg gttctacggc 420
 acggggctgg atggagctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
 gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc acgcgcggaa ggctctggat 540
 acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
 tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
 gagctgcttg ccctcgtacg gccgggcgct ctgcttgtaa accctgtcgt tggctcggtg 720
 gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
 gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
 ctgctcgcgc atccgaatac gctgttact ccgcacatag ggtcggcagt gcgcgcggtg 900
 cgcctggaga ttgaacgttg tgcagcgag aacatcctcc aggcattggc aggtgagcgc 960
 ccaattaacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

<210> 182
 <211> 336

<212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 182
 Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
 1 5 10 15
 Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
 20 25 30
 Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
 35 40 45
 Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
 50 55 60
 Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
 65 70 75 80
 Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
 85 90 95
 Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
 100 105 110
 Val Gly Leu Gly Arg His Leu Arg Ala Ala Asp Ala Phe Val Arg Ser
 115 120 125
 Gly Lys Phe Gln Gly Trp Gln Pro Arg Phe Tyr Gly Thr Gly Leu Asp
 130 135 140
 Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Leu Ala Met
 145 150 155 160
 Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ala Arg
 165 170 175
 Lys Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
 180 185 190
 Ala Cys Ser Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
 195 200 205
 Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala
 210 215 220
 Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val
 225 230 235 240
 Val Asp Glu Ala Ala Val Leu Ala Ala Leu Glu Arg Gly Gln Leu Gly
 245 250 255
 Gly Tyr Ala Ala Asp Val Phe Glu Met Glu Asp Trp Ala Arg Ala Asp
 260 265 270
 Arg Pro Gln Gln Ile Asp Pro Ala Leu Leu Ala His Pro Asn Thr Leu
 275 280 285
 Phe Thr Pro His Ile Gly Ser Ala Val Arg Ala Val Arg Leu Glu Ile
 290 295 300
 Glu Arg Cys Ala Ala Gln Asn Ile Leu Gln Ala Leu Ala Gly Glu Arg
 305 310 315 320
 Pro Ile Asn Ala Val Asn Arg Leu Pro Lys Ala Glu Pro Ala Ala Cys
 325 330 335

<210> 183
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

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<400> 183
atgctgccga aactcgttat aactcaccga gtacacgatg agatcctgca actgctggcg 60
ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
gcacgctgtc gggatgctca ggcgatgatg gcgttcatgc ccgatcgggt cgatgcagat 180
tttcttgctg cctgccctga gctgcgtgta atcggtctgc cgctcaaggg cttcgacaat 240
ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga ccttcgtgcc tgatctgttg 300
acgggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatctgcgg 360
gcagcagatg cgttcgtccg ctctggcaag ttccagggct ggcaaccacg gttctacggc 420
acgggggctgg ataacgctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc acgcgcggaa ggctctggat 540
acacaaaccg agcaacggct cggcctgcgc caggtgtcgt gcgaagaact cttcgccagc 600
tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtacg gccgggcgct ctgcttgtaa acccctgtcg tggctcggta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttctact ccgcacatag ggtcggcagt gcgcgcggtg 900
cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
ccaatcaacg ctgtgaaccg tctgccaag gccgagcctg ccgcatgttg a 1011

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<210> 184
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> PDH-101 variant

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```

<400> 184
Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Asp Glu Ile Leu
1          5          10          15
Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
20          25          30
Thr Leu Thr Arg Glu Glu Ile Leu Ala Arg Cys Arg Asp Ala Gln Ala
35          40          45
Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Ala Ala
50          55          60
Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
65          70          75          80
Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
85          90          95
Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
100         105         110
Val Gly Leu Gly Arg His Leu Arg Ala Ala Asp Ala Phe Val Arg Ser
115         120         125
Gly Lys Phe Gln Gly Trp Gln Pro Arg Phe Tyr Gly Thr Gly Leu Asp
130         135         140
Asn Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Leu Ala Met
145         150         155         160
Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ala Arg
165         170         175
Lys Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
180         185         190
Ser Cys Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
195         200         205
Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala
210         215         220

```

Leu	Val	Arg	Pro	Gly	Ala	Leu	Leu	Val	Asn	Pro	Cys	Arg	Gly	Ser	Val
225					230					235					240
Val	Asp	Glu	Ala	Ala	Val	Leu	Ala	Ala	Leu	Glu	Arg	Gly	Gln	Leu	Gly
				245					250					255	
Gly	Tyr	Ala	Ala	Asp	Val	Phe	Glu	Met	Glu	Asp	Trp	Ala	Arg	Ala	Asp
			260				265					270			
Arg	Pro	Gln	Gln	Ile	Asp	Pro	Ala	Leu	Leu	Ala	His	Pro	Asn	Thr	Leu
		275				280					285				
Phe	Thr	Pro	His	Ile	Gly	Ser	Ala	Val	Arg	Ala	Val	Arg	Leu	Glu	Ile
	290				295				300						
Glu	Arg	Cys	Ala	Ala	Gln	Asn	Ile	Leu	Gln	Ala	Leu	Ala	Gly	Glu	Arg
305				310					315					320	
Pro	Ile	Asn	Ala	Val	Asn	Arg	Leu	Pro	Lys	Ala	Glu	Pro	Ala	Ala	Cys
			325					330					335		

<210> 185
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 185
 atgctgccga aactcgttat aactcaccga gtacacgaag agatcctgca actgctggcg 60
 ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
 gcacgctgtg cagatgctca ggcatgatg gcggtcatgc ccgatcgggt cgatgcagat 180
 tttcttcagg cctgcccctga gctgcgtgta atcggtctgc cgctcaaggg cttcgacaat 240
 ttcgatgtgg acgcctgtac tcggcgcggg gtctggctga ccttcgtgcc tgatctgttg 300
 acgggtcccga ctgccgagct ggcatcgga ctggcggttg ggctggggcg gcatctgcgg 360
 gcagcagatg cgttcgctccg ctctggcaag ttccggggct ggcaaccacg gttctacggc 420
 acggggctgg ataacgctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
 gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc acgcgcggaa ggctctggat 540
 acacaaaccg agcaacggct cggcctgcgc caggtgtcgt gcgaagaact cttcgccagc 600
 tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
 gagctgcttg ccctcgtagc gccgggcgct ctgcttgtaa acccctgtcg tggctcggta 720
 gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
 gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
 ctgctcgcgc atccgaatac gctgttact ccgcacatag ggtcggcagt gcgcgcgggtg 900
 cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
 ccaatcaacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

<210> 186
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 186
 Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
 1 5 10 15
 Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
 20 25 30
 Thr Leu Thr Arg Glu Glu Ile Leu Ala Arg Cys Ala Asp Ala Gln Ala


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tcggacttca tcttgctggc gcttccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtacg gccgggcgct ctgcttgtaa acccctgtcg tggctcggta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggttga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttctact ccgcacatag ggtcggcagt gcgcgcggtg 900
cgcctggaga ttgaacggtg tgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
ccaatcaacg ctgtgaaccg tctgccaag gccgagcctg ccgcatgttg a 1011

```

<210> 188
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 188

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

Pro Ile Asn Ala Val Asn Arg Leu Pro Lys Ala Glu Pro Ala Ala Cys
325 330 335

<210> 189
<211> 1011
<212> DNA
<213> Artificial Sequence

<220>
<223> PDH-101 variant

<400> 189
atgctgccga aactcgttat aactcaccga gtacacgaag agatcctgca actgctggcg 60
ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
cgccgctgtc gcgatgctca ggcgatgatg gcgttcacgc ccgatcgggt cgatgcagac 180
tttcttcaag cctgccctga gctgctgtga atcggtgctg cgctcaaggg cttcgacaat 240
ttcgatgtgg acgcctgtac tgcccgcggg gtctggctga ccttcgtgcc tgatctgttg 300
acggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatctgcgg 360
gcagcagatg cgttcgctccg ctctggcaag ttccggggct ggcaaccacg gttctacggc 420
acggggctgg ataacgctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
gctgatcgct tgcaggggatg gggcgcgacc ctgcagtacc acgcgcggaa ggctctggat 540
acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtaacg gccgggagct ctgcttgtaa acccctgtcg tggctcggta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatgtggga ctgggctcgc gcggaccggc gcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttact ccgcacatag ggtcggcagt gcgcgcggtg 900
cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
ccaatcaacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

<210> 190
<211> 336
<212> PRT
<213> Artificial Sequence

<220>
<223> PDH-101 variant

<400> 190
Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
1 5 10 15
Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
20 25 30
Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Arg Asp Ala Gln Ala
35 40 45
Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
50 55 60
Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
65 70 75 80
Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
85 90 95
Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
100 105 110
Val Gly Leu Gly Arg His Leu Arg Ala Ala Asp Ala Phe Val Arg Ser
115 120 125
Gly Lys Phe Arg Gly Trp Gln Pro Arg Phe Tyr Gly Thr Gly Leu Asp

130		135		140
Asn Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Leu Ala Met				
145		150		155
Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ala Arg				
	165		170	175
Lys Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val				
	180		185	190
Ala Cys Ser Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu				
	195		200	205
Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala				
	210		215	220
Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val				
225		230		235
Val Asp Glu Ala Ala Val Leu Ala Ala Leu Glu Arg Gly Gln Leu Gly				
	245		250	255
Gly Tyr Ala Ala Asp Val Phe Glu Met Trp Asp Trp Ala Arg Ala Asp				
	260		265	270
Arg Pro Gln Gln Ile Asp Pro Ala Leu Leu Ala His Pro Asn Thr Leu				
	275		280	285
Phe Thr Pro His Ile Gly Ser Ala Val Arg Ala Val Arg Leu Glu Ile				
	290		295	300
Glu Arg Cys Ala Ala Gln Asn Ile Leu Gln Ala Leu Ala Gly Glu Arg				
305		310		315
Pro Ile Asn Ala Val Asn Arg Leu Pro Lys Ala Glu Pro Ala Ala Cys				
	325		330	335

<210> 191
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 191

atgctgccga	aactcgttat	aactcaccga	gtacacgaag	agatcctgca	actgctggcg	60
ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cgccgctgtc	gcgatgctca	ggcgatgatg	gcggttcacgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgcccctga	gctgcgtgta	atcggtcgcg	cgctcaagg	cttcgacaat	240
ttcgatgtgg	acgcctgtac	tgcccgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acgggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatctgcgg	360
gcagcagatg	cgttcgtccg	ctctggcaag	ttccggggct	ggcaaccacg	gttctacggc	420
acggggctgg	ataacgctac	ggtcggcttc	cttggcatgg	gcgccatcgg	actggccatg	480
gctgatcgct	tgcagggatg	gggcgcgacc	ctgcagtacc	acgcgcggaa	ggctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	caggtggcgt	gcagcgaact	cttcgccagc	600
tcggacttca	tcttgcctggc	gcttcccttg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtacg	gccgggcgct	ctgcttgtaa	acccctgtcg	tggctcggta	720
gtggatgaag	ccgccgtgct	cgcggcgctt	gagcgaggcc	agctcggcgg	gtatgcggcg	780
gatgtattcg	aaatgtctga	ctgggctcgc	gcggaccggc	cgcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttctac	ccgcacatag	ggtcggcagt	gcgcgcggtg	900
cgcctggaga	ttgaacgttg	tgcagcgcag	aacatcctcc	aggcattggc	aggtgagcgc	960
ccaatcaacg	ctgtgaaccg	tctgcccgaag	gccgagcctg	ccgcatgttg	a	1011

<210> 192
 <211> 336
 <212> PRT

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 192

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

<210> 193

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

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<400> 193
atgctgccga aactcgttat aactcaccga gtacacgaag agatcctgca actgctggcg 60
ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
cggcgctgtg cagatgctca ggcgatgatg gcgttcatgc ccgatcgggt cgatgcagac 180
tttcttcaag cctgccctga gctgctgtga atcggtctgc cgctcaaggg cttcgacaat 240
ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga ccttcgtgcc tgatctgttg 300
acgggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatctgcgg 360
gcagcagatg cgttcgtccg ctctggcaag ttccagggtt ggcaggacca gttctacggc 420
acgggggctgg atggagctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc acgcgcggaa ggctctggat 540
acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtacg gccgggctgt ctgcttggtt acccctgtcg tggctcggta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttctact ccgcacctg ggtcggcagt gcgcgcgggtg 900
cgcctggaga ttgaacgttg tgcggcgag aacatcctcc aggcattggc aggtgagcgc 960
ccaattaacg ctgtgaaccg tctgccaag gccgagcctg ccgcatgttg a 1011

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<210> 194
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> PDH-101 variant

```

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<400> 194
Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
1          5          10          15
Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
20          25          30
Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
35          40          45
Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
50          55          60
Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
65          70          75          80
Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
85          90          95
Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
100         105         110
Val Gly Leu Gly Arg His Leu Arg Ala Ala Asp Ala Phe Val Arg Ser
115         120         125
Gly Lys Phe Gln Gly Trp Gln Asp Gln Phe Tyr Gly Thr Gly Leu Asp
130         135         140
Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Leu Ala Met
145         150         155         160
Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ala Arg
165         170         175
Lys Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
180         185         190
Ala Cys Ser Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
195         200         205
Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala
210         215         220
Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val

```

225		230		235		240									
Val	Asp	Glu	Ala	Ala	Val	Leu	Ala	Ala	Leu	Glu	Arg	Gly	Gln	Leu	Gly
		245		250		255									
Gly	Tyr	Ala	Ala	Asp	Val	Phe	Glu	Met	Glu	Asp	Trp	Ala	Arg	Ala	Asp
		260		265		270									
Arg	Pro	Gln	Gln	Ile	Asp	Pro	Ala	Leu	Leu	Ala	His	Pro	Asn	Thr	Leu
		275		280		285									
Phe	Thr	Pro	His	Leu	Gly	Ser	Ala	Val	Arg	Ala	Val	Arg	Leu	Glu	Ile
		290		295		300									
Glu	Arg	Cys	Ala	Ala	Gln	Asn	Ile	Leu	Gln	Ala	Leu	Ala	Gly	Glu	Arg
305				310		315									
Pro	Ile	Asn	Ala	Val	Asn	Arg	Leu	Pro	Lys	Ala	Glu	Pro	Ala	Ala	Cys
		325		330		335									

<210> 195
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 195
 atgctgccga aactcgttat aactcaccga gtacacgaag agatcctgca actgctggcg 60
 ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
 cggcgctgtg cagatgctca ggcatgatg gcggtcatgc ccgatcgggt cgatgcagac 180
 tttcttcaag cctgcccctga gctgcgtgta atcggtgctg cgctcaaggg cttcgacaat 240
 ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga ccttcgtgcc tgatctgttg 300
 acgggtcccga ctgccgagct ggcatcgga ctggcggtgg ggctggggcg gcatctgcgg 360
 gcagcagatg cgttcgctccg ctctggcaag ttccagggtt ggcatccaat tttctacggc 420
 acgggggctgg atggagctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
 gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc acgcgcggaa ggctctggat 540
 acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
 tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
 gagctgcttg ccctcgctacg gccgggcgct ctgcttatta acccctgtcg tggctcggta 720
 gtggatgaag ccgcctgtgt cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
 gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
 ctgctcgcgc atccgaatac gctgttctact ccgcacatag ggtcggcagt gcgcgcgggtg 900
 cgcctggaga ttgaacgttg tgtggcgcag aacatcctcc aggcattggc aggtgagcgc 960
 ccaattgacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

<210> 196
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 196
 Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
 1 5 10 15
 Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
 20 25 30
 Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
 35 40 45

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

<210> 197

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 197

atgctgccga	aactcgttat	aactcaccga	gtacacgaag	agatcctgca	actgctggcg	60
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cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgcccctga	gctgcggtga	atcggctgcg	cgctcaaggg	cttcgacaat	240
ttcgatgtgg	acgcctgtac	tgcacgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acgggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcattctgcg	360
gcagcagatg	cgttcgtccg	ctctggcaag	ttccagggtc	gggctgacat	tttctacggc	420
acggggctgg	atggagctac	ggtcggcttc	cttggcatgg	gcgccatcgg	actggccatg	480
gctgatcgct	tgacgggatg	gggcgcgacc	ctgcagtacc	acgcgcggaa	ggctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	cagggtggcg	gcagcgaact	cttcgccagc	600
tcggacttca	tctgtctggc	gcttcccttg	aatgccgata	ccttgcatct	ggtcaacgcc	660

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gagctgcttg ccctcgtacg gccgggcgct ctgcttggtta acccctgtcg tggctcggta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttcact ccgcaccttg ggtcggcagt gcgcgcggtg 900
cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
ccaattaacg ctgtgaaccg tctgcccacg gccgagcctg ccgcatgttg a 1011

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<210> 198
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> PDH-101 variant

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<400> 198
Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
1      5      10      15
Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
20      25      30
Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
35      40      45
Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
50      55      60
Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
65      70      75      80
Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
85      90      95
Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
100     105     110
Val Gly Leu Gly Arg His Leu Arg Ala Ala Asp Ala Phe Val Arg Ser
115     120     125
Gly Lys Phe Gln Gly Trp Ala Asp Ile Phe Tyr Gly Thr Gly Leu Asp
130     135     140
Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Leu Ala Met
145     150     155     160
Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ala Arg
165     170     175
Lys Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
180     185     190
Ala Cys Ser Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
195     200     205
Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala
210     215     220
Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val
225     230     235     240
Val Asp Glu Ala Ala Val Leu Ala Ala Leu Glu Arg Gly Gln Leu Gly
245     250     255
Gly Tyr Ala Ala Asp Val Phe Glu Met Glu Asp Trp Ala Arg Ala Asp
260     265     270
Arg Pro Gln Gln Ile Asp Pro Ala Leu Leu Ala His Pro Asn Thr Leu
275     280     285
Phe Thr Pro His Leu Gly Ser Ala Val Arg Ala Val Arg Leu Glu Ile
290     295     300
Glu Arg Cys Ala Ala Gln Asn Ile Leu Gln Ala Leu Ala Gly Glu Arg
305     310     315     320
Pro Ile Asn Ala Val Asn Arg Leu Pro Lys Ala Glu Pro Ala Ala Cys

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<210> 199
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 199
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 ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
 cggcgctgtg cagatgctca ggcgatgatg gcgttcacgc ccgatcgggt cgatgcagac 180
 tttcttcaag cctgccctga gctgctgtga atcggctgtg cgctcaaggg cttcgacaat 240
 ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga ccttcgtgcc tgatctgttg 300
 acggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatctgcgg 360
 gcagcagatg cgttcgtccg ctctggcaag ttccagggtt ggcagccaat tttctacggc 420
 acggggctgg atggagctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
 gctgatcgct tgcaggggatg gggcgcgacc ctgcagtacc acgcgcggaa ggctctggat 540
 acacaaaccg agcaacgggt cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
 tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
 gagctgcttg ccctcgtaacg gccgggagct ctgcttgtaa acccctgtcg tggctctgta 720
 gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
 gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
 ctgctcgcgc atccgaatac gctgttact cgcacacttg ggtcggcagt gcgcgcggtg 900
 cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
 ccaattgacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

<210> 200
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

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

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

<210> 201
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 201

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ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgcccctga	gctgcgtgta	atcggtcgcg	cgctcaaggg	cttcgacaat	240
ttcgatgtgg	acgcctgtac	tgcacgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acgggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcattctgcg	360
gcagcagatg	cgttcgtccg	ctctggcaag	ttccagggtc	ggcaaccacg	gttctacggc	420
acggggctgg	atggagctac	ggtcggcttc	cttggcatgg	gcgccatcgg	actggccatg	480
gctgatcgct	tgcagggatg	gggcgcgacc	ctgcagtacc	acgcgcggaa	ggctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	caggtggcgt	gcgaggaact	cttcgccagc	600
tcggacttca	tcttgcctgg	gcttcccttg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtacg	gccgggcgct	ctgcttggtt	acccctgtcg	tggtcggta	720
gtggatgaag	ccgccgtgct	cgcggcgctt	gagcgaggcc	agctcggcgg	gtatgcggcg	780
gatgtattcg	aaatggaaga	ctgggctcgc	gcggaccggc	gcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttcaat	ccgcaccttg	ggtcggcagt	gcgcgcggtg	900
cgcctggaga	ttgaacgttg	tgcagcgcag	aacatcctcc	aggcattggc	aggtgagcgc	960
ccaattgacg	ctgtgaaccg	tctgcccgaag	gccgagcctg	ccgcatgttg	a	1011

<210> 202
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 202

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

<210> 203

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 203

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cggcgctgtg cagatgctca ggcgatgatg gcgttcatgc ccgatcgggt cgatgcagac 180
tttcttcaag cctgccctga gctgcgtgta atcggctgcg cgctcaaggg cttcgacaat 240
ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga ccttcgtgcc tgatctgttg 300
acgggtcccga ctgccgagct ggcgatcgga ctggcgctcg ggctggggcg gcatctgcgg 360
gcagcagatg cgttcgtccg ctctggcaag ttccagggtt ggcaaccacg gttctacggc 420
acgggggctgg atggagctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc acgcgcggaa ggctctggat 540
acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
tcggacttca tcctgctggc gcttccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtagc gccgggcgct ctgcttgtaa acccctgtcg tggctcggtg 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttctact ccgcacatag ggtcggcagt gcgcgcgggtg 900
cgcctggaga ttgaacgctt tgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
ccaattaacg ctgtgaaccg tctgccaag gccgagcctg ccgcatgttg a 1011

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<210> 204
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 204

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

Val	Asp	Glu	Ala	Ala	Val	Leu	Ala	Ala	Leu	Glu	Arg	Gly	Gln	Leu	Gly
				245					250					255	
Gly	Tyr	Ala	Ala	Asp	Val	Phe	Glu	Met	Glu	Asp	Trp	Ala	Arg	Ala	Asp
			260					265					270		
Arg	Pro	Gln	Gln	Ile	Asp	Pro	Ala	Leu	Leu	Ala	His	Pro	Asn	Thr	Leu
			275				280					285			
Phe	Thr	Pro	His	Ile	Gly	Ser	Ala	Val	Arg	Ala	Val	Arg	Leu	Glu	Ile
	290					295					300				
Glu	Arg	Cys	Ala	Ala	Gln	Asn	Ile	Leu	Gln	Ala	Leu	Ala	Gly	Glu	Arg
305					310					315				320	
Pro	Ile	Asn	Ala	Val	Asn	Arg	Leu	Pro	Lys	Ala	Glu	Pro	Ala	Ala	Cys
				325					330					335	

<210> 205
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 205

atgctgccga	aactcgttat	aactcacaga	gtacacgaag	agatcctgca	aatgctggcg	60
ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgcccctga	gctgcgtgta	atcggtctgtg	cgctcaaggg	cttcgacaat	240
ttcgatgtgg	acgcctgtac	tgcacgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acgggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatttccgg	360
gcagcagatg	aattcgctccg	ctctggcaag	ttccagggct	ggcagccaat	tttctacggc	420
acgggggctgg	atggagcaac	ggtcggcttc	cttggcatgg	gcgccatcgg	actcgccatg	480
gctgatcgct	tgcagggatg	ggcgcgaccc	ctgcagtacc	acgcgcggaa	ggctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	caggtggcgt	gcagcgaact	cttcgccagc	600
tcggacttca	tcctgctggc	gcttcccttg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtagc	gccgggcgct	ctgcttgtaa	acccctgtcg	tggctctgta	720
gtggatgaag	ccgcctgtgt	cgcggcgctt	gagcgaggcc	agctcggcgg	gtatgcggcg	780
gatgtattcg	aaatggaaga	ctgggctcgc	gcggaccggc	cgcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttcaat	ccgcaccttg	ggcgggcagt	gcgcgcgggtg	900
cgcctggaga	ttgaacgttg	tgcagcgcag	aacatcctcc	aggcattggc	aggtgagcgc	960
ccaattgacg	ctgtgaaccg	tctgcccgaag	gccgagccca	aggcccgcgtg	a	1011

<210> 206
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 206

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

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

<210> 207

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 207

atgctgccga	aactcgttat	aactcacaga	gtacacgaag	agatcctgca	actgctggcg	60
ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgccttga	gctgctgtga	atcggtgtg	cgctcaagg	cttcgacaat	240
ttcgatgtgg	acgcctgtac	tgcacgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acgggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatttcggg	360
gcagcagatg	cattcgtccg	ctctggcaag	ttccagggt	ggcagccaat	tttctacggc	420
acggggctgg	atggagcaac	ggtcggcttc	cttggcatgg	gcgccatcgg	aaaagccatg	480
gctgatcgct	tgacgggatg	gggcgcgacc	ctgcagtacc	actcgcggac	agctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	cagggtggcgt	gcagcgaact	cttcgccagc	600
tcggacttca	tcctgctggc	gcttcccttg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtacg	gccggggcgt	ctgcttgtaa	accctgtctg	tggctctgta	720

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gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttcact ccgcaccttg ggtcggcagt gcgcgcggtg 900
cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattgcg aggtgagcgc 960
ccaattgacg ctgtgaaccg tctgcccacg gccgagcctg ccgcatgttg a 1011

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<210> 208
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> PDH-101 variant

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<400> 208
Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
1      5      10      15
Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
20      25      30
Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
35      40      45
Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
50      55      60
Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
65      70      75      80
Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
85      90      95
Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
100     105     110
Val Gly Leu Gly Arg His Phe Arg Ala Ala Asp Ala Phe Val Arg Ser
115     120     125
Gly Lys Phe Gln Gly Trp Gln Pro Ile Phe Tyr Gly Thr Gly Leu Asp
130     135     140
Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Lys Ala Met
145     150     155     160
Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ser Arg
165     170     175
Thr Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
180     185     190
Ala Cys Ser Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
195     200     205
Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala
210     215     220
Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val
225     230     235     240
Val Asp Glu Ala Ala Val Leu Ala Ala Leu Glu Arg Gly Gln Leu Gly
245     250     255
Gly Tyr Ala Ala Asp Val Phe Glu Met Glu Asp Trp Ala Arg Ala Asp
260     265     270
Arg Pro Gln Gln Ile Asp Pro Ala Leu Leu Ala His Pro Asn Thr Leu
275     280     285
Phe Thr Pro His Leu Gly Ser Ala Val Arg Ala Val Arg Leu Glu Ile
290     295     300
Glu Arg Cys Ala Ala Gln Asn Ile Leu Gln Ala Leu Arg Gly Glu Arg
305     310     315     320
Pro Ile Asp Ala Val Asn Arg Leu Pro Lys Ala Glu Pro Ala Ala Cys
325     330     335

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<210> 209
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 209
 atgctgccga aactcgttat aactcacaga gtacacgaag agatcctgca aatgctggcg 60
 ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
 cggcgctgtg cagatgctca ggcgatgatg gcgttcacgc ccgatcgggt cgatgcagac 180
 tttcttcaag cctgccctga gctgctgtga atcggtgtg cgctcaaggg cttcgacaat 240
 ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga ccttcgtgcc tgatctgttg 300
 acggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatttccgg 360
 gcagcagatg aattcgtccg ctctggcaag ttccagggct ggcagccaat tttctacggc 420
 acggggctgg atggagcaac ggtcggcttc cttggcatgg gcgccatcgg aaaagccatg 480
 gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc acgcgcggac agctctggat 540
 acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
 tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
 gagctgcttg ccctcgctacg gccgggcgct ctgcttgtaa acccctgtcg tggctctgta 720
 gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
 gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
 ctgctcgcgc atccgaatac gctgttcaat ccgcaccttg ggtcggcagt gcgcgcggtg 900
 cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
 ccaattgacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

<210> 210
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 210
 Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
 1 5 10 15
 Gln Met Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
 20 25 30
 Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
 35 40 45
 Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
 50 55 60
 Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
 65 70 75 80
 Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
 85 90 95
 Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
 100 105 110
 Val Gly Leu Gly Arg His Phe Arg Ala Ala Asp Glu Phe Val Arg Ser
 115 120 125
 Gly Lys Phe Gln Gly Trp Gln Pro Ile Phe Tyr Gly Thr Gly Leu Asp
 130 135 140
 Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Lys Ala Met

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

<210> 211
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 211

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ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgccctga	gctgctgtga	atcggtctgt	cgctcaagg	cttcgacaat	240
ttcgatgtgg	acgcctgtac	tgacgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatttcccg	360
gcagcagatg	aattcgctccg	ctctggcaag	ttccagggt	ggcagccaat	tttctacggc	420
acggggctgg	atggagcaac	ggtcggcttc	cttggcatgg	gcgccatcgg	aaaagccatg	480
gctgatcgct	tgacgggatg	ggcgcgacc	ctgcagtacc	actcgcggac	agctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	caggtggcgt	gcagtgaact	cttcgccagc	600
tcggacttca	tcttctgtgg	gcttcccttg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtacg	gccgggcgct	ctgcttgtaa	acccctgtcg	tggctctgta	720
gtggatgaag	ccgccgtgct	cgcggcgctt	gagcgaggcc	agctcggcgg	gtatgcggcg	780
gatgtattcg	aaatggaaga	ctgggctcgc	gcggaccggc	gcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttact	ccgcaccttg	ggtcggcagt	gcgcgcggtg	900
cgcctggaga	ttgaacgttg	tgacgcgcag	aacatcctcc	aggcattgcg	aggtgagcgc	960
ccaattgacg	ctgtgaaccg	tctgcccgaag	gccgagcctg	ccgcatgttg	a	1011

<210> 212
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 212

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

<210> 213

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 213

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ccacattgcg agctgataac caaccagacc gactcgacgc tgacgcgcga ggaaattctg 120
cggcgctgtg cagatgctca ggcgatgatg gcgttcatgc ccgatcgggt cgatgcagac 180
tttcttcaag cctgccctga gctgaaagta atcggctgtg cgctcaaggg cttcgacaat 240
ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga cttcgtgcc tgatctgttg 300
acgggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatctggtt 360
gcagcagatg cgttcgtccg ctctggcaag ttccagggct ggagccaat tttctacggc 420
acggggctgg atggagctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc acaccggaa ggctctggat 540
acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcgaggaact cttcgccagc 600
tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtacg gccgggcgct ctgcttgta acccctgtcg tggctctgta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttact ccgcacctg ggtcggcagt gcgcgcggtg 900
cgcctggaga ttgaacgttg tgcagcgag aacatcctcc aggcattggc aggtgagcgc 960
ccaattgacg ctgtgaaccg tctgccaag gccgagcctg ccgcatgttg a 1011

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<210> 214
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> PDH-101 variant

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<400> 214
Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
1      5      10      15
Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
20     25     30
Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
35     40     45
Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
50     55     60
Cys Pro Glu Leu Lys Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
65     70     75     80
Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
85     90     95
Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
100    105    110
Val Gly Leu Gly Arg His Leu Val Ala Ala Asp Ala Phe Val Arg Ser
115    120    125
Gly Lys Phe Gln Gly Trp Gln Pro Ile Phe Tyr Gly Thr Gly Leu Asp
130    135    140
Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Leu Ala Met
145    150    155    160
Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Thr Arg
165    170    175
Lys Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
180    185    190
Ala Cys Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
195    200    205
Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala
210    215    220
Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val
225    230    235    240
Val Asp Glu Ala Ala Val Leu Ala Ala Leu Glu Arg Gly Gln Leu Gly

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				245						250					255				
Gly	Tyr	Ala	Ala	Asp	Val	Phe	Glu	Met	Glu	Asp	Trp	Ala	Arg	Ala	Asp				
			260					265						270					
Arg	Pro	Gln	Gln	Ile	Asp	Pro	Ala	Leu	Leu	Ala	His	Pro	Asn	Thr	Leu				
		275					280					285							
Phe	Thr	Pro	His	Leu	Gly	Ser	Ala	Val	Arg	Ala	Val	Arg	Leu	Glu	Ile				
	290					295					300								
Glu	Arg	Cys	Ala	Ala	Gln	Asn	Ile	Leu	Gln	Ala	Leu	Ala	Gly	Glu	Arg				
305					310					315					320				
Pro	Ile	Asp	Ala	Val	Asn	Arg	Leu	Pro	Lys	Ala	Glu	Pro	Ala	Ala	Cys				
				325					330					335					

<210> 215
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 215
 atgctgccga aactcgttat aactcacaga gtacacgaag agatcctgca actgctggcg 60
 ccacattgcg agctgataac caaccagacc gacgtcacgc tgacgcgcga ggaaattctg 120
 cggcgctgtg cagatgctca ggcgatgatg gcggttcacgc ccgatcgggt cgatgcagac 180
 tttcttcaag cctgcccctga gctgagagta atcggctgtg cgctcaaggg cttcgacaat 240
 ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga ccttcgtgcc tgatctgttg 300
 acgggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcattctgcgc 360
 gcagcagatg cgttcgctccg ctctggcaag ttccagggct ggagccaat tttctacggc 420
 acgggggctgg atggagctac ggtcggcttc cttggcatgg gcgccatcgg actggccatg 480
 gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc acgcccggaa ggctctggat 540
 acacaaactg agcaaacctt cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
 tcggacttca tcttgcctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
 gagctgcttg ccctcgctacg tccgggcgct ctgcttatta acccctgtcg tggctctgta 720
 gtggatgaag ccgcctgtgt cgcggcgctt gagcgcaggc agctcggcgg gtatgcggcg 780
 gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
 ctgctcgcgc atccgaatac gctgttact cgcacacttg ggtcggcagt gcgcgcgggtg 900
 cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattggc aggtgagcgc 960
 ccaattgacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcaagctg a 1011

<210> 216
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 216
 Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
 1 5 10 15
 Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Val
 20 25 30
 Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
 35 40 45
 Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
 50 55 60

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

<210> 217

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 217

atgctgccga	aactcgttat	aactcacaga	gtacacgaag	agatcctgca	actgctggcg	60
ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgccttga	gctgcgtgta	atcggtctgt	cgctcaagg	ctatgacaat	240
ttcgatgtgg	acgcctgtac	tgcacgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acgggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatttccgg	360
gcagcagatg	cattcgtccg	ctctggcaag	ttccagggt	ggcagccaat	tttctacggc	420
acggggctgg	atggagcaac	ggtcggcatt	ctgggcatgg	gcgccatcgg	aaaagccatg	480
gctgatcgct	tgacgggatg	gggcgcgacc	ctgcagtacc	actcgcggac	agctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	cagggtggcgt	gcagcgaact	cttagccagc	600
tcggacttca	tcctgctggc	gcttccttgg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtacg	gccgggcgct	ctgcttgtaa	acccctgtcg	tggctctgta	720
gtggatgaag	ccgccgtgct	cgcggcgctt	gagcgcaggcc	agctcggcg	gtatgcggcg	780

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gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttctact ccgcaccttg ggtcggcagt gcgcgcggtg 900
cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattgcg aggtgagcgc 960
ccaattgacg ctgtgaacag cccgcccgaag gccgagcctg ccgcatgttg a 1011

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<210> 218
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 218

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

<210> 219
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 219
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 ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
 cggcgctgtg cagatgctca ggcgatgatg gcgttcacgc ccgatcgggt cgatgcagac 180
 tttcttcaag cctgccctga gctgctgtga atcggtctgt cgctcaaggg cttcgacaat 240
 ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga cctttgtgcc tgatctgttg 300
 acgggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatttccgg 360
 gcagcagatg cattcgctccg ctctggcaag ttccagggct ggcagccaat tttctacggc 420
 acgggggctgg atggagcaac ggtcggcttc cttggcatgg gcgccatcgg aaaagccatg 480
 gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc actcgcgggac agctctggat 540
 acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
 tcggacttca tcctgctggc gcttcccttg gcggcccaga ccctgcatct ggtcaacgcc 660
 gagctgcttg ccctcgctacg gccggggcgt ctgcttgtaa acccctgtcg tggctctgta 720
 gtggatgaag ccgcctgtgt cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
 gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
 ctgctcgcgc atccgaatac gctgttact cgcacacttg ggtcggcagt gcgcgcggtg 900
 cgcctggaga ttgaacgttg tgcagcgag aacatcctcc aggcattgcg aggtgagcgc 960
 ccacaagacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

<210> 220
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

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

Ala	Asp	Arg	Leu	Gln	Gly	Trp	Gly	Ala	Thr	Leu	Gln	Tyr	His	Ser	Arg	
				165					170					175		
Thr	Ala	Leu	Asp	Thr	Gln	Thr	Glu	Gln	Arg	Leu	Gly	Leu	Arg	Gln	Val	
			180					185					190			
Ala	Cys	Ser	Glu	Leu	Phe	Ala	Ser	Ser	Asp	Phe	Ile	Leu	Leu	Ala	Leu	
	195						200					205				
Pro	Leu	Ala	Ala	Gln	Thr	Leu	His	Leu	Val	Asn	Ala	Glu	Leu	Leu	Ala	
	210					215					220					
Leu	Val	Arg	Pro	Gly	Ala	Leu	Leu	Val	Asn	Pro	Cys	Arg	Gly	Ser	Val	
225					230				235						240	
Val	Asp	Glu	Ala	Ala	Val	Leu	Ala	Ala	Leu	Glu	Arg	Gly	Gln	Leu	Gly	
			245					250						255		
Gly	Tyr	Ala	Ala	Asp	Val	Phe	Glu	Met	Glu	Asp	Trp	Ala	Arg	Ala	Asp	
			260					265					270			
Arg	Pro	Gln	Gln	Ile	Asp	Pro	Ala	Leu	Leu	Ala	His	Pro	Asn	Thr	Leu	
	275					280						285				
Phe	Thr	Pro	His	Leu	Gly	Ser	Ala	Val	Arg	Ala	Val	Arg	Leu	Glu	Ile	
	290				295						300					
Glu	Arg	Cys	Ala	Ala	Gln	Asn	Ile	Leu	Gln	Ala	Leu	Arg	Gly	Glu	Arg	
305					310				315						320	
Pro	Gln	Asp	Ala	Val	Asn	Arg	Leu	Pro	Lys	Ala	Glu	Pro	Ala	Ala	Cys	
			325					330						335		

<210> 221
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 221

atgctgccga	aactcgttat	aactcacaga	gtacacgaag	agatcctgca	actgctggcg	60
ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgccctga	gctgcgtgta	atcggtctgt	cgctcaaggg	cttcgacaat	240
ttcgatgtgg	acgcctgtac	tgacgcggg	gtctggctga	cctttgtgcc	tgatctgttg	300
acggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatttcccg	360
gcagcagatg	cattcgctccg	ctctggcaag	ttccagggct	ggcagccaat	tttctacggc	420
acggggctgg	atggagcaac	ggtcggcttc	cttggcatgg	gcgccatcgg	aaaagccatg	480
gctgatcgct	tgacgggatg	gggcgcgacc	ctgcagtacc	actcgcggac	ccctctggat	540
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tcggacttca	tcctgctggc	gcttcccttg	gcggcccaga	ccctgcatct	ggtcaacgcc	660
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gatgtattcg	aaatggaaga	ctgggctcgc	gcggaccggc	cgacgcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttcaat	ccgcaccttg	ggtcggcagt	gcgcgcggtg	900
cgcctggaga	ttgaacgttg	tgacgcgcag	aacatcctcc	aggcattgcg	aggtgagcgc	960
ccacaagacg	ctgtgaaccg	tctgcccgaag	gccgagcccg	ccgcatgttg	a	1011

<210> 222
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 222

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

<210> 223

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 223

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ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120

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cggcgctgtg cagatgctca ggcgatgatg gcgttcatgc ccgatcgggt cgatgcagac 180
tttcttcaag cctgccctga gctgcgtgta atcggctgtg cgctcaaggg cttcgacaat 240
ttcgaatgtg acgcctgtac tgcacgcggg gtctggctga ccattgtgcc tgatctgttg 300
acgggtcccga ctgccgagct ggcgatcggg ctggcggtgg ggctggggcg gcatttccgg 360
gcagcagatg cattcgtccg ctctggcaag ttccagggct ggcagccaat tttctacggc 420
acgggggctgg atggagcaac ggtcggcttc cttggcatgg gcgccatcgg aaaagccatg 480
gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc actcgcggac agctctggat 540
acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
tcggacttca tcctgctggc gcttcccttg gcggcccaga ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtacg gccgggcgct ctgcttgtaa acccctgtcg tggctctgta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttact cgcaccttg ggtcggcagt gcgcgcggtg 900
cgcctggaga ttgaacgttg tgcagcgag aacatcctcc aggcattgcg aggtgagcgc 960
ccaatggacg ctgtgaaccg tctgcccag gccgagcctg ccgcatgttg a 1011

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<210> 224
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 224

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

Gly	Tyr	Ala	Ala	Asp	Val	Phe	Glu	Met	Glu	Asp	Trp	Ala	Arg	Ala	Asp
			260					265					270		
Arg	Pro	Gln	Gln	Ile	Asp	Pro	Ala	Leu	Leu	Ala	His	Pro	Asn	Thr	Leu
		275					280					285			
Phe	Thr	Pro	His	Leu	Gly	Ser	Ala	Val	Arg	Ala	Val	Arg	Leu	Glu	Ile
	290					295					300				
Glu	Arg	Cys	Ala	Ala	Gln	Asn	Ile	Leu	Gln	Ala	Leu	Arg	Gly	Glu	Arg
305					310					315				320	
Pro	Met	Asp	Ala	Val	Asn	Arg	Leu	Pro	Lys	Ala	Glu	Pro	Ala	Ala	Cys
				325					330					335	

<210> 225
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 225

atgctgccga	aactcgttat	aactcacaga	gtacacgaag	agatcctgca	actgctggcg	60
ccacattgcg	agctgataac	caaccagacc	gacgtcacgc	tgacgcgcga	ggaaattctg	120
cggcgctgtg	cagatgctca	ggcgatgatg	gcggttcacg	ccgatcgggt	cgatatggac	180
tttcttcaag	cctgccctga	gctgagagta	atcggtctgt	cgctcaaggg	cttcgacaat	240
ttcgatgtgg	acgcctgtac	tgacgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acgggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	acatttccgg	360
gcagcagatg	aattcgctccg	ctctggcaag	ttccagggct	ggcagccaat	tttctacggc	420
acgggggctgg	atggagcaac	ggtcggcttc	cttggcattg	gcgccatcgg	aaaagccatg	480
gctgatcgct	tgacgggatg	gggcgcgacc	ctgcagtacc	actcgcggag	cgctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	catgtggcgt	gcagcgaact	cttcgcccagc	600
tcggacttca	tcttgcctgg	gcttcccttg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgctacg	gccgggcgct	ctgcttgtaa	acccctgtcg	tggtctctgta	720
gtggatgaag	ccgcctgtgt	cgcggcgctt	gagcgcaggc	agctcggcgg	gtatgcggcg	780
gatgtattcg	aaatggaaga	ctgggctcgc	gcggaccggc	cgcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttctac	ccgcaccttg	ggtcggcagt	gcgcgcgggtg	900
cgcctggaga	ttgaacgttg	tgacgcgcag	aacatcctcc	aggcattgcg	aggtgagcgc	960
ccaattgacg	ctgtgaacga	tctgcccgaag	gccgagcctg	ccgcattggtg	a	1011

<210> 226
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 226

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

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

<210> 227
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 227
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 ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
 cggcgctgtg cagatgctca ggcgatgatg gcgttcatgc ccgatcgggt cgatgcagac 180
 tttcttcaag cctgccctga gctgcgtgta atcggtctgt cgctcaaggg cttcgacaat 240
 ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga cttcgtgcc tgatctgttg 300
 acggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatttccgg 360
 gcagcagatg cattcgtccg ctctggcaag ttccagggtt ggcagccaat tttctacggc 420
 acggggctgg atggagcaac ggtcggcttc cttggcatgg gcgccatcgg aaaagccatg 480
 gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc actcgcggac agctctggat 540
 acacaaaccg agcaacggct cggcctgcgc cagggtggcgt gcagcgaact cttcgccagc 600
 tcggacttca tcctgctggc gcttccttg aatgccgata ccccgcatct ggtcaacgcc 660
 gagctgcttg ccctcgtacg gccgggcgct ctgcttgtaa acccctgtcg tggctctgta 720
 gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
 gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840

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ctgctcgcgc atccgaatac gctgttcact ccgcaccttg ggtcggcagt gcgcgcgggtg 900
cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattgcg aggtgagcgc 960
ccaattgacg ctgtgaaccg tctgcccacg gccgagcctg ccgcattgttg a 1011

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<210> 228
<211> 336
<212> PRT
<213> Artificial Sequence

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<220>
<223> PDH-101 variant

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```

<400> 228
Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
1      5      10      15
Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
20      25      30
Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
35      40      45
Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
50      55      60
Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
65      70      75      80
Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
85      90      95
Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
100     105     110
Val Gly Leu Gly Arg His Phe Arg Ala Ala Asp Ala Phe Val Arg Ser
115     120     125
Gly Lys Phe Gln Gly Trp Gln Pro Ile Phe Tyr Gly Thr Gly Leu Asp
130     135     140
Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Lys Ala Met
145     150     155     160
Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ser Arg
165     170     175
Thr Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
180     185     190
Ala Cys Ser Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
195     200     205
Pro Leu Asn Ala Asp Thr Pro His Leu Val Asn Ala Glu Leu Leu Ala
210     215     220
Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val
225     230     235     240
Val Asp Glu Ala Ala Val Leu Ala Ala Leu Glu Arg Gly Gln Leu Gly
245     250     255
Gly Tyr Ala Ala Asp Val Phe Glu Met Glu Asp Trp Ala Arg Ala Asp
260     265     270
Arg Pro Gln Gln Ile Asp Pro Ala Leu Leu Ala His Pro Asn Thr Leu
275     280     285
Phe Thr Pro His Leu Gly Ser Ala Val Arg Ala Val Arg Leu Glu Ile
290     295     300
Glu Arg Cys Ala Ala Gln Asn Ile Leu Gln Ala Leu Arg Gly Glu Arg
305     310     315     320
Pro Ile Asp Ala Val Asn Arg Leu Pro Lys Ala Glu Pro Ala Ala Cys
325     330     335

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<210> 229
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 229
 atgctgccga aactcgttat aactcacaga gtacacgaag agatcctgca actgctggcg 60
 ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
 cggcgctgtg cagatgctca ggcatgatg gcgttcatgc ccgatcgggt cgatgcagac 180
 tttcttcaag cctgccctga gctgctgtga atcggtgtg cgctcaaggg cttcgacaat 240
 ttcatgtgtg acgcctgtac tgcacgcggg gtctggctga cttcgtgcc tgatctgttg 300
 acggtcccga ctgccgagct ggcatcgga ctggcggtgg ggctggggcg gcatttccgg 360
 gcagcagatg cattcgctccg ctctggcaag ttccagggtt ggagccaat tttctacggc 420
 acggggctgg atggagcaac ggtcggcttc cttggcatgg gcgccatcgg aaaagccatg 480
 gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc actcgcggac agctctggat 540
 acacaaaccg agcaacggct cggcctgcgc cagggtggcgt gcagcgaact cttcgccagc 600
 tcggacttca tcctgaatgc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
 gagctgcttg ccctcgtagc gccggggcgt ctgcttgtaa acccctgtcg tggctctgta 720
 gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
 gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
 ctgctcgcgc atccgaatac gctgttact ccgcacctg ggtcggcagt gcgcgcggtg 900
 cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattgcg aggtgagcgc 960
 ccaattgacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

<210> 230
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 230
 Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
 1 5 10 15
 Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
 20 25 30
 Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
 35 40 45
 Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
 50 55 60
 Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
 65 70 75 80
 Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
 85 90 95
 Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
 100 105 110
 Val Gly Leu Gly Arg His Phe Arg Ala Ala Asp Ala Phe Val Arg Ser
 115 120 125
 Gly Lys Phe Gln Gly Trp Gln Pro Ile Phe Tyr Gly Thr Gly Leu Asp
 130 135 140
 Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Lys Ala Met
 145 150 155 160
 Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ser Arg

<400> 232

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Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
1      5      10      15
Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
20      25      30
Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
35      40      45
Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
50      55      60
Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
65      70      75      80
Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
85      90      95
Pro Asp Leu Leu Thr Val Pro Phe Ala Glu Leu Ala Ile Gly Leu Ala
100     105     110
Val Gly Leu Gly Arg His Phe Arg Ala Ala Asp Ala Phe Val Arg Ser
115     120     125
Gly Lys Phe Gln Gly Trp Gln Pro Ile Phe Tyr Gly Thr Gly Leu Asp
130     135     140
Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Lys Ala Met
145     150     155     160
Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ser Arg
165     170     175
Thr Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
180     185     190
Ala Cys Ser Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
195     200     205
Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala
210     215     220
Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val
225     230     235     240
Val Asp Glu Ala Ala Val Leu Ala Ala Leu Glu Arg Gly Gln Leu Gly
245     250     255
Gly Tyr Ala Ala Asp Val Phe Glu Met Glu Asp Trp Ala Arg Ala Asp
260     265     270
Arg Pro Gln Gln Ile Asp Pro Ala Leu Leu Ala His Pro Asn Thr Leu
275     280     285
Phe Thr Pro His Leu Gly Ser Ala Val Arg Ala Val Arg Leu Glu Ile
290     295     300
Glu Arg Cys Ala Ala Gln Asn Ile Leu Gln Ala Leu Arg Gly Glu Arg
305     310     315     320
Pro Ile Asp Ala Val Asn Arg Leu Pro Lys Ala Glu Pro Ala Ala Cys
325     330     335
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<210> 233

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 233

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atgctgccga aactcggttat aactcacaga gtacacgaag agatcctgca actgctggcg 60
ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
cggcgctgtg cagatgctca ggcgatgatg gcgttcacgc ccgatcgggt cgatgcagac 180
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tttcttcaag cctgccctga gctgctgtga atcggctgtg cgctcaaggg cttcgacaat 240
ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga ccttcgtgcc tgatctgttg 300
acgggtcccgc ttgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatttccgg 360
gcagcagatg cattcgtccg ctctggcaag ttccagggct ggcagccaat tttctacggc 420
acgggggctgg atggagcaac ggtcggcttc cttggcatgg gcgccatcgg aaaagccatg 480
gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc actcgcggac agctctggat 540
acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtacg gccgggcgct ctgcttgtaa acccctgtcg tggctctgta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttctact ccgcaccttg ggtcggcagt gcgcgcggtg 900
cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattgcg aggtgagcgc 960
ccaattgacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

```

<210> 234

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 234

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

```

			260					265					270				
Arg	Pro	Gln	Gln	Ile	Asp	Pro	Ala	Leu	Leu	Ala	His	Pro	Asn	Thr	Leu		
		275					280					285					
Phe	Thr	Pro	His	Leu	Gly	Ser	Ala	Val	Arg	Ala	Val	Arg	Leu	Glu	Ile		
	290					295					300						
Glu	Arg	Cys	Ala	Ala	Gln	Asn	Ile	Leu	Gln	Ala	Leu	Arg	Gly	Glu	Arg		
305					310					315					320		
Pro	Ile	Asp	Ala	Val	Asn	Arg	Leu	Pro	Lys	Ala	Glu	Pro	Ala	Ala	Cys		
			325						330					335			

<210> 235
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 235

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ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
cggcgctgtg cagatgctca ggcatgatg gcgttcacgc ccgatcgggt cgatgcagac 180
tttcttcaag cctgccctga gctgctgtga atcggctgtg cgctcaaggg cttcgacaat 240
ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga ccttcgtgcc tgatctgttg 300
acgggtcccga ctgccgagct ggcatcgga ctggcggtgg ggctggggcg gcatttccgg 360
gcagcagatg cattcgctccg ctctggcaag ttccagggct ggcatccaat tttctacggc 420
acgggggctgg atggagcaac ggtcggcttc cttggcatgg gcgccatcgg aaaagccatg 480
gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc actcgcggac agctctggat 540
acacaaaccg agcaacggct cggcctgcgc cagggtggcgt gcagcgaact cttcgccagc 600
tcggacttca tcctgctggc gcttccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtagc gccggcgct ctgcttgtaa acccctgtcg tggctctgta 720
gtggatgaag ccgcctgtgt cgcgcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatgtctga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttact ccgcacctg ggtcggcagt gcgcgcgggtg 900
cgcttgagga ttgaacgttg tgcagcgcag aacatcctcc aggcattgcg aggtgagcgc 960
ccaattgacg ctgtgaaccg tctgcccagg gccgagcctg ccgcatgttg a 1011
  
```

<210> 236
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 236

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

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

<210> 237
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 237

atgctgccga	aactcgttat	aactcacaga	gtacacgaag	agatcctgca	actgctggcg	60
ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgcccctga	gctgcgtgta	atcggtgtg	cgctcaagg	cttcgacaat	240
ttcgatgtgg	acgcctgtac	tgcacgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acgggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatttcggg	360
gcagcagatg	cattcgtccg	ctctggcaag	ttccagggt	ggcagccaat	tttctacggc	420
acggggctgg	atggagcaac	ggtcggcttc	cttggcatgg	gcgccatcgg	aaaagccatg	480
gctgatcgct	tgacgggatg	gggcgcgacc	ctgcagtacc	actcgcggac	agctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	caggtggcgt	gcagcgaact	cttcgccagc	600
tcggacttca	tcctgctggc	gcttccttg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtacg	gccgggcgct	ctgcttgtaa	acccctgtcg	tggctctgta	720
gtggatgaag	ccgcctgtgct	cgcggcgctt	gagcgaaggc	agctcggcgg	gtatgcggcg	780
gaccccttcg	aaatggaaga	ctgggctcgc	gcggaccggc	cgcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttact	ccgcaccttg	ggtcggcagt	gcgcgcgggtg	900

cgcttgaga ttgaacgttg tgcagcgcag aacatcctcc aggcattgcg aggtgagcgc 960
 ccaattgacg ctgtgaaccg tctgcccacg gccgagcctg ccgcatgttg a 1011

<210> 238
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 238
 Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
 1 5 10 15
 Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
 20 25 30
 Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
 35 40 45
 Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
 50 55 60
 Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
 65 70 75 80
 Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
 85 90 95
 Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
 100 105 110
 Val Gly Leu Gly Arg His Phe Arg Ala Ala Asp Ala Phe Val Arg Ser
 115 120 125
 Gly Lys Phe Gln Gly Trp Gln Pro Ile Phe Tyr Gly Thr Gly Leu Asp
 130 135 140
 Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Lys Ala Met
 145 150 155 160
 Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ser Arg
 165 170 175
 Thr Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
 180 185 190
 Ala Cys Ser Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
 195 200 205
 Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala
 210 215 220
 Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val
 225 230 235 240
 Val Asp Glu Ala Ala Val Leu Ala Ala Leu Glu Arg Gly Gln Leu Gly
 245 250 255
 Gly Tyr Ala Ala Asp Pro Phe Glu Met Glu Asp Trp Ala Arg Ala Asp
 260 265 270
 Arg Pro Gln Gln Ile Asp Pro Ala Leu Leu Ala His Pro Asn Thr Leu
 275 280 285
 Phe Thr Pro His Leu Gly Ser Ala Val Arg Ala Val Arg Leu Glu Ile
 290 295 300
 Glu Arg Cys Ala Ala Gln Asn Ile Leu Gln Ala Leu Arg Gly Glu Arg
 305 310 315 320
 Pro Ile Asp Ala Val Asn Arg Leu Pro Lys Ala Glu Pro Ala Ala Cys
 325 330 335

<210> 239

<211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 239
 atgctgccga aactcgttat aactcacaga gtacacgaag agatcctgca actgctggcg 60
 ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
 cggcgctgtg cagatgctca ggcgatgatg gcgttcacgc ccgatcgggt cgatgcagac 180
 tttcttcaag cctgccctga gctgctgtga atcggctgtg cgctcaaggg cttcgacaat 240
 ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga ccttcgtgcc tgatctgttg 300
 acgggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatttccgg 360
 gcagcagatg cattcgctccg ctctggcaag ttccagggct ggcagccaat tttctacggc 420
 acgggggctgg atggagcaac ggtcggcttc cttggcatgg gcgccatcgg aaaagccatg 480
 gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc actcgcggac agctctggat 540
 acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
 tcggacttca tcctgctggc gcttccttg aatgccgata ccctgcatct ggtcaacgcc 660
 gagctgcttg ccctcgtagc gccggggcgt ctgcttgtaa acccctgtcg tggctctgta 720
 gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
 gatgatattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
 ctgctcgcgc atccgaatac gctgttact ccgcacctg ggtcggcagt gcgcgcggtg 900
 cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattgcg aggtgagcgc 960
 ccaattgacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

<210> 240
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

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

Thr	Ala	Leu	Asp	Thr	Gln	Thr	Glu	Gln	Arg	Leu	Gly	Leu	Arg	Gln	Val
			180					185					190		
Ala	Cys	Ser	Glu	Leu	Phe	Ala	Ser	Ser	Asp	Phe	Ile	Leu	Leu	Ala	Leu
		195					200					205			
Pro	Leu	Asn	Ala	Asp	Thr	Leu	His	Leu	Val	Asn	Ala	Glu	Leu	Leu	Ala
	210					215					220				
Leu	Val	Arg	Pro	Gly	Ala	Leu	Leu	Val	Asn	Pro	Cys	Arg	Gly	Ser	Val
225					230					235					240
Val	Asp	Glu	Ala	Ala	Val	Leu	Ala	Ala	Leu	Glu	Arg	Gly	Gln	Leu	Gly
			245					250						255	
Gly	Tyr	Ala	Ala	Asp	Asp	Phe	Glu	Met	Glu	Asp	Trp	Ala	Arg	Ala	Asp
		260					265					270			
Arg	Pro	Gln	Gln	Ile	Asp	Pro	Ala	Leu	Leu	Ala	His	Pro	Asn	Thr	Leu
	275					280						285			
Phe	Thr	Pro	His	Leu	Gly	Ser	Ala	Val	Arg	Ala	Val	Arg	Leu	Glu	Ile
	290				295					300					
Glu	Arg	Cys	Ala	Ala	Gln	Asn	Ile	Leu	Gln	Ala	Leu	Arg	Gly	Glu	Arg
305					310					315					320
Pro	Ile	Asp	Ala	Val	Asn	Arg	Leu	Pro	Lys	Ala	Glu	Pro	Ala	Ala	Cys
			325					330						335	

<210> 241
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 241

atgctgccga	aactcgttat	aactcacaga	gtacacgaag	agatcctgca	actgctggcg	60
ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgccctga	gctgctgtga	atcggtctgt	cgctcaagg	cttcgacaat	240
ttcgatgcgg	acgcctgtac	tgcacgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acgggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatttccgg	360
gcagcagatg	cattcgctccg	ctctggcaag	ttccagggct	ggcagccaat	tttctacggc	420
acggggctgg	atggagcaac	ggtcggcttc	cttggcatgg	gcgccatcgg	aaaagccatg	480
gctgatcgct	tgcagggatg	ggcgcgac	ctgcagtacc	actcgcgga	agctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	caggtggcgt	gcagcgaact	cttcgccagc	600
tcggacttca	tctgtctggc	gcttcccttg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtaac	gccgggcgct	ctgcttgtaa	acccctgtcg	tggtctctgta	720
gtggatgaag	ccgccgtgct	cgcggcgctt	gagcgaggcc	agctcggcgg	gtatgcggcg	780
gatgtattcg	aaatggcgga	ctgggctcgc	gcggaccggc	cgcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttact	ccgcaccttg	ggtcggcagt	gcgcgcggtg	900
cgcctggaga	ttgaacgttg	tgcagcgcag	aacatcctcc	aggcattgcg	aggtgagcgc	960
ccaattgacg	ctgtgaaccg	tctgcccgaag	gccgagcctg	ccgcatgttg	a	1011

<210> 242
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 242

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Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
1      5      10      15
Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
20      25      30
Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
35      40      45
Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
50      55      60
Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
65      70      75      80
Phe Asp Ala Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
85      90      95
Pro Asp Leu Leu Thr Val Pro Thr Ala Glu Leu Ala Ile Gly Leu Ala
100     105     110
Val Gly Leu Gly Arg His Phe Arg Ala Ala Asp Ala Phe Val Arg Ser
115     120     125
Gly Lys Phe Gln Gly Trp Gln Pro Ile Phe Tyr Gly Thr Gly Leu Asp
130     135     140
Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Lys Ala Met
145     150     155     160
Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ser Arg
165     170     175
Thr Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
180     185     190
Ala Cys Ser Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
195     200     205
Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala
210     215     220
Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val
225     230     235     240
Val Asp Glu Ala Ala Val Leu Ala Ala Leu Glu Arg Gly Gln Leu Gly
245     250     255
Gly Tyr Ala Ala Asp Val Phe Glu Met Ala Asp Trp Ala Arg Ala Asp
260     265     270
Arg Pro Gln Gln Ile Asp Pro Ala Leu Leu Ala His Pro Asn Thr Leu
275     280     285
Phe Thr Pro His Leu Gly Ser Ala Val Arg Ala Val Arg Leu Glu Ile
290     295     300
Glu Arg Cys Ala Ala Gln Asn Ile Leu Gln Ala Leu Arg Gly Glu Arg
305     310     315     320
Pro Ile Asp Ala Val Asn Arg Leu Pro Lys Ala Glu Pro Ala Ala Cys
325     330     335
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<210> 243

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 243

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atgctgccga aactcgttat aactcacaga gtacacgaag agatcctgca actgctggcg 60
ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
cggcgctgtg cagatgctca ggcgatgatg gcgttcatgc ccgatcgggt cgatgcagac 180
tttcttcaag cctgccctga gctgcgtgta atcggctgtg cgctcaaggg cttcgacaat 240
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ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga ccttcgtgcc tgatctgttg 300
acgggtcccga ctgccgagct ggcgatcgga ctggcgggtg ggctggggcg gcatttccgg 360
gcagcagatg cattcgtccg ctctggcaag ttccagggct ggcagccaat tttctacggc 420
acgggggctgg atggagcaac ggtcggcttc cttggcatgg gcgccatcgg aaaagccatg 480
gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc actcgcggac agctctggat 540
acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtacg gccgggcgct ctgcttgtaa acccctgtcg tggctctgta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttcaat ccgcaccttg ggtcggcagt gcgcgcggtg 900
cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattgcg aggtgagcgc 960
ccaattaatg cggatgaaccg tctgcccgaag gccgagcctg ccgcatgttg a 1011

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<210> 244

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 244

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

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Arg	Pro	Gln	Gln	Ile	Asp	Pro	Ala	Leu	Leu	Ala	His	Pro	Asn	Thr	Leu
		275					280					285			
Phe	Thr	Pro	His	Leu	Gly	Ser	Ala	Val	Arg	Ala	Val	Arg	Leu	Glu	Ile
		290				295					300				
Glu	Arg	Cys	Ala	Ala	Gln	Asn	Ile	Leu	Gln	Ala	Leu	Arg	Gly	Glu	Arg
305					310					315					320
Pro	Ile	Asn	Ala	Val	Asn	Arg	Leu	Pro	Lys	Ala	Glu	Pro	Ala	Ala	Cys
				325					330					335	

<210> 245
 <211> 1008
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 245

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ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcacgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgccctga	gctgctgtga	atcggtctgt	cgctcaaggg	cttcgacaat	240
ttcgatgcgg	acgcctgtac	tgacgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acggtcccgt	tggccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatttccgg	360
gcagcagatg	cattcgctccg	ctctggcaag	ttccagggct	ggcagccaat	tttctacggc	420
acggggctgg	atggagcaac	ggcggcttc	cttggcacatg	gcgccatcgg	aaaagccatg	480
gctgatcgct	tgacgggatg	ggcgcgac	ctgcagtacc	actcgcgga	agctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	caggtggcgt	gcagcgaact	cttcgccagc	600
tcggacttca	tcctgaatgc	gcttcccttg	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgctacg	gccgggcgt	ctgcttgtaa	acccctgtcg	tggtctctgta	720
gtggatgaag	ccgcctgtgt	cgcgcgctt	gagcgaggcc	agctcggcgg	gtatgcggcg	780
gatgtgttcg	aaatggagga	ctgggctcgc	gcggaccggc	cgcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttact	ccgcaccttg	ggtcggcagt	gcgcgcgggtg	900
cgcttgagga	ttgaacgttg	tgacgcgcag	aacatcctcc	aggcatttgcg	aggtgagcgc	960
ccaattgacg	ctgtgaaccg	tctgcccga	gccgagcctg	ccgcatgt		1008

<210> 246
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 246

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

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

<210> 247
 <211> 1008
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 247

atgctgccga	aactcgttat	aactcacaga	gtacacgaag	agatcctgca	actgctggcg	60
ccacattgcg	agctgataac	caaccagacc	gacagcacgc	tgacgcgcga	ggaaattctg	120
cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgcccctga	gctgcgtgta	atcggtgtga	ccctcaaggg	cttcgacaat	240
ttcgatgcgg	acgcctgtac	tgcacgcggg	gtctggctga	ccttcgtgcc	tgatctgttg	300
acggtcccga	ctgccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatttcctg	360
gcagcagatg	cattcgtccg	ctctggcaag	ttccagggtc	ggcagccaat	tttctacggc	420
acggggctgg	atggagcaac	ggtcggcttc	cttggcatgg	gcgccatcgg	aaaagccatg	480
gctgatcgct	tgacgggatg	gggcgcgacc	ctgcagtacc	actcgcggac	agctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	caggtggcgt	gcagcgaact	cttcgccagc	600
tcggacttca	tcctgaatgc	gcttccttgc	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtacg	gccgggcgct	ctgcttgtaa	acccctgtcg	tggctctgta	720
gtggatgaag	ccgcctgtgt	cgcggcgctt	gagcgaggcc	agctcggcgg	gtatgcggcg	780
gatgtgttcg	aaatggagga	ctgggctcgc	gcggaccggc	cgcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttcaat	ccgcaccttg	ggtcggcagt	gcgcgcggtg	900
cgcctggaga	ttgaacgttg	tgcagcgcag	aacatcctcc	aggcattgcg	aggtgagcgc	960

ccaattgacg ctgtgaaccg tctgcccgaag gccgagcctg ccgcatgt

1008

<210> 248

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 248

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

<210> 249

<211> 1008

<212> DNA
<213> Artificial Sequence

<220>
<223> PDH-101 variant

<400> 249
atgctgccga aactcgttat aactcacaga gtacacgaag agatcctgca actgctggcg 60
ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
cggcgctgtg cagatgctca ggcgatgatg gcgttcacgc ccgatcgggt cgatgcagac 180
tttcttcaag cctgccctga gctgctgtga atcggctgtg cgctcaaggg cttcgacaat 240
ttcgaatgtg acgcctgtac tgcacgcggg gtctggctga cttcgtgcc tgatctgttg 300
acgggtcccgt tggccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatttccgg 360
gcagcagatg cattcgctccg ctctggcaag ttccagggct ggcagccaat tttctacggc 420
acgggggctgg atggagcaac ggtcggcttc cttggcatgg gcgccatcgg aaaagccatg 480
gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc actcgcggac agctctggat 540
acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtagc gccgggcgct ctgcttgtaa acccctgtcg tggctctgta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatctgttcg aaatggagga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttact ccgcacctg ggtcggcagt gcgcgcggtg 900
cgcctggaga ttgaacgttg tgcagcgag aacatcctcc aggcattgcg aggtgagcgc 960
ccaattgacg ctgtgaaccg tctgccaag gccgagcctg ccgcatgt 1008

<210> 250
<211> 336
<212> PRT
<213> Artificial Sequence

<220>
<223> PDH-101 variant

<400> 250
Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
1 5 10 15
Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
20 25 30
Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
35 40 45
Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
50 55 60
Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
65 70 75 80
Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
85 90 95
Pro Asp Leu Leu Thr Val Pro Leu Ala Glu Leu Ala Ile Gly Leu Ala
100 105 110
Val Gly Leu Gly Arg His Phe Arg Ala Ala Asp Ala Phe Val Arg Ser
115 120 125
Gly Lys Phe Gln Gly Trp Gln Pro Ile Phe Tyr Gly Thr Gly Leu Asp
130 135 140
Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Lys Ala Met
145 150 155 160
Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ser Arg
165 170 175
Thr Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val

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

<210> 253

<211> 1008

<212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 253

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atgctgccga aactcgttat aactcacaga gtacacgaag agatcctgca actgctggcg 60
ccacattgcg agctgataac caaccagacc gacagcacgc tgacgcgcga ggaaattctg 120
cggcgctgtg cagatgctca ggcgatgatg gcgttcacgc ccgatcgggt cgatgcagac 180
tttcttcaag cctgccctga gctgcgtgta atcggtgtg cgctcaaggg cttcgacaat 240
ttcgatgtgg acgcctgtac tgcacgcggg gtctggctga cttcgtgcc tgatctgttg 300

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acggtcccga ctgccgagct ggcgatcgga ctggcggtgg ggctggggcg gcatttccgg 360
gcagcagatg cattcgtccg ctctggcaag ttccagggct ggcagccaat tttctacggc 420
acggggctgg atggagcaac ggtcggcttc cttggcatgg gcgccatcgg aaaagccatg 480
gctgatcgct tgcagggatg gggcgcgacc ctgcagtacc actcgcggac agctctggat 540
acacaaaccg agcaacggct cggcctgcgc caggtggcgt gcagcgaact cttcgccagc 600
tcggacttca tcctgctggc gcttcccttg aatgccgata ccctgcatct ggtcaacgcc 660
gagctgcttg ccctcgtacg gccgggcgct ctgcttgtaa acccctgtcg tggctctgta 720
gtggatgaag ccgccgtgct cgcggcgctt gagcgaggcc agctcggcgg gtatgcggcg 780
gatgtattcg aaatggaaga ctgggctcgc gcggaccggc cgcagcagat cgatcctgcg 840
ctgctcgcgc atccgaatac gctgttcaact ccgcaccttg ggcgggcagt gcgcgcggtg 900
cgcctggaga ttgaacgttg tgcagcgcag aacatcctcc aggcattgcg aggtgagcgc 960
ccaattgacg ctgtgaaccg tctgccaag gccgagcctg ccgcatgt 1008

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<210> 254

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 254

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

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

<210> 257
 <211> 1008
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 257

atgctgccga	aactcgttat	aactcacaga	gtacacgaag	agatcctgca	actgctggcg	60
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cggcgctgtg	cagatgctca	ggcgatgatg	gcgttcatgc	ccgatcgggt	cgatgcagac	180
tttcttcaag	cctgccctga	gctgcgtgta	atcggtctgt	cgctcaaggg	cttcgacaat	240
ttcgatgtgg	acgcctgtac	tgcacgcggg	gtctggctga	ccttcgtgcc	tgatctggtg	300
acggtcccga	tggccgagct	ggcgatcgga	ctggcggtgg	ggctggggcg	gcatttcctg	360
gcagcagatg	cattcgtccg	ctctggcaag	ttccagggct	ggcagccaat	tttctacggc	420
acggggctgg	atggagcaac	ggtcggcttc	cttggcatgg	gcgccatcgg	aaaagccatg	480
gctgatcgct	tgacgggatg	ggcgcgaccc	ctgcagtacc	actcgcggac	agctctggat	540
acacaaaccg	agcaacggct	cggcctgcgc	caggtggcgt	gcagcgaact	cttcgccagc	600
tcggacttca	tcctgctggc	gcttccttgc	aatgccgata	ccctgcatct	ggtcaacgcc	660
gagctgcttg	ccctcgtacg	gccgggcgct	ctgcttgtaa	acccctgtcg	tggtctctgta	720
gtggatgaag	ccgcccgtgct	cgcggcgctt	gagcgaaggc	agctcggcgg	gtatgcggcg	780
gatgtattcg	aaatggaaga	ctgggctcgc	gcggaccggc	cgcagcagat	cgatcctgcg	840
ctgctcgcgc	atccgaatac	gctgttcaat	ccgcaccttg	ggtcggcagt	gcgcgcgggtg	900
cgcctggaga	ttgaacgttg	tgcagcgcag	aacatcctcc	aggcattgcg	aggtgagcgc	960
ccaattgacg	ctgtgaaccg	tctgcccgaag	gccgagcctg	ccgcatgt		1008

<210> 258
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDH-101 variant

<400> 258
 Met Leu Pro Lys Leu Val Ile Thr His Arg Val His Glu Glu Ile Leu
 1 5 10 15
 Gln Leu Leu Ala Pro His Cys Glu Leu Ile Thr Asn Gln Thr Asp Ser
 20 25 30
 Thr Leu Thr Arg Glu Glu Ile Leu Arg Arg Cys Ala Asp Ala Gln Ala
 35 40 45
 Met Met Ala Phe Met Pro Asp Arg Val Asp Ala Asp Phe Leu Gln Ala
 50 55 60
 Cys Pro Glu Leu Arg Val Ile Gly Cys Ala Leu Lys Gly Phe Asp Asn
 65 70 75 80
 Phe Asp Val Asp Ala Cys Thr Ala Arg Gly Val Trp Leu Thr Phe Val
 85 90 95
 Pro Asp Leu Leu Thr Val Pro Met Ala Glu Leu Ala Ile Gly Leu Ala
 100 105 110
 Val Gly Leu Gly Arg His Phe Arg Ala Ala Asp Ala Phe Val Arg Ser
 115 120 125
 Gly Lys Phe Gln Gly Trp Gln Pro Ile Phe Tyr Gly Thr Gly Leu Asp
 130 135 140
 Gly Ala Thr Val Gly Phe Leu Gly Met Gly Ala Ile Gly Lys Ala Met
 145 150 155 160
 Ala Asp Arg Leu Gln Gly Trp Gly Ala Thr Leu Gln Tyr His Ser Arg
 165 170 175
 Thr Ala Leu Asp Thr Gln Thr Glu Gln Arg Leu Gly Leu Arg Gln Val
 180 185 190
 Ala Cys Ser Glu Leu Phe Ala Ser Ser Asp Phe Ile Leu Leu Ala Leu
 195 200 205
 Pro Leu Asn Ala Asp Thr Leu His Leu Val Asn Ala Glu Leu Leu Ala
 210 215 220
 Leu Val Arg Pro Gly Ala Leu Leu Val Asn Pro Cys Arg Gly Ser Val
 225 230 235 240
 Val Asp Glu Ala Ala Val Leu Ala Ala Leu Glu Arg Gly Gln Leu Gly
 245 250 255
 Gly Tyr Ala Ala Asp Val Phe Glu Met Glu Asp Trp Ala Arg Ala Asp
 260 265 270
 Arg Pro Gln Gln Ile Asp Pro Ala Leu Leu Ala His Pro Asn Thr Leu
 275 280 285
 Phe Thr Pro His Leu Gly Ser Ala Val Arg Ala Val Arg Leu Glu Ile
 290 295 300
 Glu Arg Cys Ala Ala Gln Asn Ile Leu Gln Ala Leu Arg Gly Glu Arg
 305 310 315 320
 Pro Ile Asp Ala Val Asn Arg Leu Pro Lys Ala Glu Pro Ala Ala Cys
 325 330 335

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 <212> DNA

<213> Artificial Sequence

<220>

<223> PDH-101 variant

<400> 259

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<213> Artificial Sequence

<220>

<223> PDH-101 variant

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