

SEQUENCE LISTING

<110> WUHAN NEUROPHTH BIOLOGICAL TECHNOLOGY LIMITED COMPANY

<120> COMPOSITIONS AND METHODS FOR TREATING LEBER'S HEREDITARY OPTIC NEUROPATHY

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<151> 2018-09-04

<150> PCT/CN2018/113799
<151> 2018-11-02

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<151> 2018-10-22

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<212> DNA

<213> Artificial Sequence

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<220>

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<400> 40

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<211> 2460

<212> DNA

<213> Artificial Sequence

<220>

<223> opt_COX10-opt_ND1-3'UTR

<400> 41

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 <212> DNA

<213> Artificial Sequence

<220>

<223> opt_COX10-opt_ND1-3'UTR*

<400> 42

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<212> DNA

<213> Artificial Sequence

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<223> opt_COX10*-ND4-3'UTR

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<211> 2089

<212> DNA

<213> Artificial Sequence

<220>

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<210> 45

<211> 2889

<212> DNA

<213> Artificial Sequence

<220>

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<400> 45

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<211> 2889

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<211> 2089

<212> DNA

<213> Artificial Sequence

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<400> 48

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<210> 49

<211> 2034

<212> DNA

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<220>
 <223> OPA1-ND1-3'UTR

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<220>
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<213> Artificial Sequence

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<223> beta-actin-S primer

<400> 85

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<210> 86

<211> 19
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<220>
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<400> 86
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<210> 87
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ND4-S primer

<400> 87
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<210> 88
 <211> 19
 <212> DNA
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<220>
 <223> ND4-A primer

<400> 88
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<210> 89
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<220>
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<210> 90
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<220>
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 <223> ND4-A primer

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 <223> opt-ND4-S primer

<400> 109
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<210> 110
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 <213> Artificial Sequence

<220>
 <223> opt-ND4-A primer

<400> 110
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<210> 111
 <211> 376
 <212> DNA
 <213> Homo sapiens

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gctccccgct tagccacagg agtgactgtg gttgtggtgg gggggttcctt aaaataactt 180

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agtgactgtt ctgtga	376

<210> 112
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 <212> DNA
 <213> Homo sapiens

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<210> 113
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 <213> Homo sapiens

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aggttgcttt accagctgtt tactttcttt ttgttgttgt tttgagacaa ggtttcgctc	300
tgccaccctg gctggagtgc agtggcgtga tcttggtcga cggcaacctc tgcctcctgg	360
ggctcaagca attatcccac ctcagcctcc tgagcagctg ggactacagg tgcattgccac	420
aacacctggc tgatatttgt attttttgta gagacaggat tttgccaagt tgcccaggct	480
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tcatagtatt tcttccattt ccagcagctg attagaagtc caggatcatg tgaagtcagg	720
cagggtcaca gttcctgatg gcacattatg gacagagaat tccattttgt tttctaacc	780

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<210> 114
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 <212> DNA
 <213> Homo sapiens

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aaaaaataga ttcaaagtgt ttatcctctc tctgaaacgc ttcctataac tcgagtttat	300
aggggaagaa aaagctattg tttaacaatta tatcaccatt aaggcaactg ctacaccctg	360
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<210> 115

<211> 1465

<212> DNA

<213> Homo sapiens

<400> 115

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tcagtgatca cttgacagtt tttttttttt ttaaataatta cccaaaatgc tccccaaata	180
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<210> 116
 <211> 288
 <212> DNA
 <213> Homo sapiens

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tgcaaacatt aatgtgaaat aaattgaatt taatgttgaa tactttcagg cattcactta	180
ataaagacac tgtaagcac tgttatgctc agtcatacac gcgaaaggta caatgtcttt	240
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<210> 117
 <211> 83
 <212> DNA
 <213> Homo sapiens

<400> 117 cccaccaccc tggcctgctg tcctgcgtct atccatgtgg aatgctggac aataaagcga	60
gtgctgcca ccctccagct gcc	83

<210> 118
 <211> 66
 <212> DNA
 <213> Homo sapiens

<400> 118 tttatattga actgtaaata tgtcactaga gaaataaaat atggacttcc aatctacgta	60
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66

<210> 119
 <211> 214
 <212> DNA
 <213> Homo sapiens

<400> 119
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 atttcataaa caacttaatg ttctgaataa tttcttacta aacattttgt tattgggcaa 180
 gtgattgaaa atagtaaag ctttgtgtga ttga 214

<210> 120
 <211> 286
 <212> DNA
 <213> Homo sapiens

<400> 120
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 aattaacaaa tactttggac agtaagtctt tctcagttct taatgataat gcagggcact 180
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<210> 121
 <211> 721
 <212> DNA
 <213> Homo sapiens

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 gtagtgccag aaagagagaa ccaagcttgt ctttaaagtt actgatcaca ggacgttgct 300
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<210> 122
 <211> 163
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 <213> Homo sapiens

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catggattca agtcctggct ccgcctcttc catcaggacc act	163

<210> 123
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 <212> DNA
 <213> Homo sapiens

<400> 123	
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<210> 124
 <211> 65
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 <213> Rattus norvegicus

<400> 124	
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<210> 125
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<213> Homo sapiens

<400> 125

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ccaagtgatc ttccattca cagagttagt aaacctctgt actacatgct g 231

<210> 126

<211> 28

<212> PRT

<213> Homo sapiens

<400> 126

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<210> 127

<211> 29

<212> PRT

<213> Homo sapiens

<400> 127

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1 5 10 15

Ser Ala Ala Pro Val Arg Arg Ala Arg Ile His Ser Leu
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<210> 128

<211> 10

<212> PRT

<213> Homo sapiens

<400> 128

Met Trp Arg Leu Arg Arg Ala Ala Val Ala
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<210> 129
 <211> 28
 <212> PRT
 <213> Homo sapiens

<400> 129

Met Ala Ala Ser Pro His Thr Leu Ser Ser Arg Leu Leu Thr Gly Cys
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Val Gly Gly Ser Val Trp Tyr Leu Glu Arg Arg Thr
 20 25

<210> 130
 <211> 122
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 130

Met Ala Phe Lys Ser Phe Ile Tyr Ser Lys Gly Tyr His Arg Ser Ala
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Ala Gln Lys Lys Thr Ala Thr Ser Phe Phe Asp Ser Ser Tyr Gln Tyr
 20 25 30

Leu Arg Gln Asn Gln Gly Leu Val Asn Ser Asp Pro Val Leu His Ala
 35 40 45

Ser His Leu His Pro His Pro Val Val Val Ala Asn Val Asn Tyr Asn
 50 55 60

Asn Val Asp Asp Ile Leu His Pro His Asp Leu Asp Ser Ser Ile Asn
 65 70 75 80

Asn Thr Asn Asn Pro Leu Thr His Glu Glu Leu Leu Tyr Asn Gln Asn
 85 90 95

Val Ser Leu Arg Ser Leu Lys Gln Gln Gln Ser Thr Asn Tyr Val Asn
 100 105 110

Asn Asn Asn Asn Asn Gln His Arg Tyr Tyr

115

120

<210> 131
 <211> 174
 <212> PRT
 <213> Larimichthys crocea
 <400> 131

Met Arg Lys Arg Ser Leu Arg Cys His Leu Trp Ser Ala Asn Ala Ser
 1 5 10 15

Leu Ser Pro Arg Lys Asp Glu Val Thr Ser Arg Lys Glu Ser Glu Asn
 20 25 30

Leu Val Lys Gly Lys Lys Asn Lys Lys Ser His Leu His Leu Leu Leu
 35 40 45

Phe Thr Ala Ser Lys Ile Gly Thr Asp Ser Val Phe Asp Val Gln Lys
 50 55 60

Ser Lys Glu Cys Cys Lys Glu Leu Gly Leu Leu Phe Thr Ser Leu Ile
 65 70 75 80

His Ser Ile Gly Ser Phe Pro Phe Asp Glu Glu Pro Lys Ala Ala Ala
 85 90 95

Val Phe Leu Pro Gly Ser Leu Pro Gln Leu Thr Val Leu Val Leu Ala
 100 105 110

Pro Gly Ser Gly Ser Cys Pro Thr Gly Lys Ser Thr Pro His Leu Ala
 115 120 125

Ala Ser Gly Arg Asn Ala Glu Leu Leu Arg Pro Gln Asn Ser Met Ile
 130 135 140

Val Arg Gln Phe Thr Cys Arg Gly Thr Ile Ser Ser His Leu Cys Ala
 145 150 155 160

His Leu Arg Lys Pro His Asp Ser Arg Asn Met Ala Arg Pro
 165 170

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<210> 132
 <211> 56
 <212> PRT
 <213> Trypanosoma brucei

<400> 132

Met Leu Arg Arg Thr Ser Phe Asn Phe Thr Gly Arg Ala Met Ile Ser
 1 5 10 15

Arg Gly Ser Pro Glu Trp Ser His Arg Leu Asp Leu Lys Lys Gly Lys
 20 25 30

Lys Thr Thr Met Met His Lys Leu Gly Thr Ser Lys Pro Asn Asn Ala
 35 40 45

Leu Gln Tyr Ala Gln Met Thr Leu
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<210> 133
 <211> 46
 <212> PRT
 <213> Neurospora crassa

<400> 133

Met Ile Ser Arg Ser Ala Leu Ser Arg Gly Ser Gln Leu Ala Leu Arg
 1 5 10 15

Arg Pro Ala Ala Ala Lys Thr Ala Gln Arg Gly Phe Ala Ala Ala Ala
 20 25 30

Ala Ser Pro Ala Ala Ser Tyr Glu Pro Thr Thr Ile Ala Gly
 35 40 45

<210> 134
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 134

Met Pro Glu Leu Ile Leu Tyr Val Ala Ile Thr Leu Ser Val Ala Glu

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Pro	Gly	His	Ala
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Cys	Ala	Glu	Pro
			30
Ser	Phe	Arg	Ser
Ser	Arg	Cys	Ser
	35		
Ala	Pro	Leu	Cys
			40
Leu	Leu	Cys	Ser
			45
Gly	Ser	Ser	Ser
Pro	Ala	Thr	Ala
	50		
Pro	His	Pro	Leu
			55
Lys	Met	Phe	Ala
			60
Cys	Ser	Lys	Phe
Val	Ser	Thr	Pro
	65		
Ser	Leu	Val	Lys
			70
Ser	Thr	Ser	Gln
			75
Leu	Leu	Ser	Arg
			80
Pro	Leu	Ser	Ala
			85
Val	Val	Leu	Lys
			90
Arg	Pro	Glu	Ile
			95
Leu	Thr	Asp	Glu
Ser	Leu	Ser	Ser
	100		
Leu	Ala	Val	Ser
			105
Cys	Pro	Leu	Thr
			110
Ser	Leu	Val	Ser
Ser	Arg	Ser	Phe
	115		
Gln	Thr	Ser	Ala
			120
Ile	Ser	Arg	Asp
			125
Ile	Asp	Thr	Ala
<210>	135		
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<213>	Homo sapiens		
<400>	135		
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Thr	Ala	Arg	Ala
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Ala	Ala	Ala	Pro
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	20		
Ser	Ser	Cys	Gly
			25
Arg	Arg	Gly	Val
			30
His	Gln	Arg	Ala
Leu	Pro	Pro	Leu
	35		
Gly	His	Gly	Trp
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Val	Gly	Gly	Leu
			45
Gly	Leu	Gly	Leu
Gly	Leu	Ala	Leu
	50		
Gly	Val	Lys	Leu
			55
Ala	Gly	Gly	Leu
			60
Arg	Gly	Ala	Ala

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Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu Ala Ser Pro Leu Ala
65 70 75 80

Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro Trp Ser Pro Gln Thr Pro
85 90 95

Ala Pro Pro Cys Ser Arg Cys Phe Ala Arg Ala Ile Glu Ser Ser Arg
100 105 110

Asp Leu Leu
115

<210> 136
<211> 140
<212> PRT
<213> Schizosaccharomyces pombe

<400> 136

Met Thr Val Leu Ala Pro Leu Arg Arg Leu His Thr Arg Ala Ala Phe
1 5 10 15

Ser Ser Tyr Gly Arg Glu Ile Ala Leu Gln Lys Arg Phe Leu Asn Leu
20 25 30

Asn Ser Cys Ser Ala Val Arg Arg Tyr Gly Thr Gly Phe Ser Asn Asn
35 40 45

Leu Arg Ile Lys Lys Leu Lys Asn Ala Phe Gly Val Val Arg Ala Asn
50 55 60

Ser Thr Lys Ser Thr Ser Thr Val Thr Thr Ala Ser Pro Ile Lys Tyr
65 70 75 80

Asp Ser Ser Phe Val Gly Lys Thr Gly Gly Glu Ile Phe His Asp Met
85 90 95

Met Leu Lys His Asn Val Lys His Val Phe Gly Tyr Pro Gly Gly Ala
100 105 110

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Ile Leu Pro Val Phe Asp Ala Ile Tyr Arg Ser Pro His Phe Glu Phe
115 120 125

Ile Leu Pro Arg His Glu Gln Ala Ala Gly His Ala
130 135 140

<210> 137
<211> 125
<212> PRT
<213> Glycine max

<400> 137

Met Ile Leu Cys Pro Leu Glu Ala Phe Ile Val Gln His Ile Leu Thr
1 5 10 15

Ile Ser Val Met Gly Leu Leu Ser Cys Phe Arg Ser Thr Val Leu Arg
20 25 30

Lys Cys Ser Lys Gly Ser Ser Gly Met Ser Arg Phe Leu Tyr Thr Asn
35 40 45

Asn Phe Gln Arg Asn Leu Ile Ser Ser Gly Gly Asn Glu Ser Tyr Tyr
50 55 60

Gly Tyr Phe Asn Arg Arg Ser Tyr Thr Ser Leu Tyr Met Gly Thr Gly
65 70 75 80

Thr Val Gly Gly Ile Thr Ser Ala Arg Ile Arg Val Pro Asn Val Gly
85 90 95

Cys Glu Gly Phe Met Cys Ser Ser His Leu Ser Ile Thr Gln Arg Asn
100 105 110

Ser Arg Leu Ile His Ser Thr Ser Lys Ile Val Pro Asn
115 120 125

<210> 138
<211> 107
<212> PRT
<213> Chlamydomonas reinhardtii

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<400> 138

Met Ala Leu Gln Gln Ala Ala Pro Arg Val Phe Gly Leu Leu Gly Arg
1 5 10 15

Ala Pro Val Ala Leu Gly Gln Ser Gly Ile Leu Thr Gly Ser Ser Gly
20 25 30

Phe Lys Asn Gln Gly Phe Asn Gly Ser Leu Gln Ser Val Glu Asn His
35 40 45

Val Tyr Ala Gln Ala Phe Ser Thr Ser Ser Gln Glu Glu Gln Ala Ala
50 55 60

Pro Ser Ile Gln Gly Ala Ser Gly Met Lys Leu Pro Gly Met Ala Gly
65 70 75 80

Ser Met Leu Leu Gly Lys Ser Arg Ser Gly Leu Arg Thr Gly Ser Met
85 90 95

Val Pro Phe Ala Ala Gln Gln Ala Met Asn Met
100 105

<210> 139

<211> 87

<212> PRT

<213> Homo sapiens

<400> 139

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1 5 10 15

Leu Val Lys His Ser Ser Gly Ile Lys Gly Ser Leu Pro Leu Gln Lys
20 25 30

Leu His Leu Val Ser Arg Ser Ile Tyr His Ser His His Pro Thr Leu
35 40 45

Lys Leu Gln Arg Pro Gln Leu Arg Thr Ser Phe Gln Gln Phe Ser Ser
50 55 60

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Leu Thr Asn Leu Pro Leu Arg Lys Leu Lys Phe Ser Pro Ile Lys Tyr
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Gly Tyr Gln Pro Arg Arg Asn
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<210> 140
<211> 56
<212> PRT
<213> Homo sapiens

<400> 140

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Arg Ala Leu Leu Leu Arg Thr Pro Val Val Arg Pro Ala His Ile Ser
20 25 30

Ala Phe Leu Gln Asp Arg Pro Ile Pro Glu Trp Cys Gly Val Gln His
35 40 45

Ile His Leu Ser Pro Ser His His
50 55

<210> 141
<211> 162
<212> PRT
<213> Homo sapiens

<400> 141

Met Ala Ala Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val
1 5 10 15

Lys Leu Thr Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile
20 25 30

Gly Gly Glu Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val
35 40 45

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Glu Gln Ile Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His
50 55 60

Glu Glu Tyr Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His
65 70 75 80

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

Ser Ala Pro Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser
100 105 110

Glu Gly Pro Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala
115 120 125

Gly Phe Pro Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg
130 135 140

Leu Phe Ala Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg
145 150 155 160

Arg Phe

<210> 142
<211> 117
<212> PRT
<213> Oryza sativa

<400> 142

Met Ala Leu Leu Leu Arg His Ser Pro Lys Leu Arg Arg Ala His Ala
1 5 10 15

Ile Leu Gly Cys Glu Arg Gly Thr Val Val Arg His Phe Ser Ser Ser
20 25 30

Thr Cys Ser Ser Leu Val Lys Glu Asp Thr Val Ser Ser Ser Asn Leu
35 40 45

His Pro Glu Tyr Ala Lys Lys Ile Gly Gly Ser Asp Phe Ser His Asp

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55

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Arg Gln Ser Gly Lys Glu Leu Gln Asn Phe Lys Val Ser Pro Gln Glu
65 70 75 80

Ala Ser Arg Ala Ser Asn Phe Met Arg Ala Ser Lys Tyr Gly Met Pro
85 90 95

Ile Thr Ala Asn Gly Val His Ser Leu Phe Ser Cys Gly Gln Val Val
100 105 110

Pro Ser Arg Cys Phe
115

<210> 143
<211> 66
<212> PRT
<213> Neurospora crassa

<400> 143

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1 5 10 15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
20 25 30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr
35 40 45

Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys
50 55 60

Arg Ala
65

<210> 144
<211> 44
<212> PRT
<213> Homo sapiens

<400> 144

207420009W00-seq1

Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val
1 5 10 15

Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile
20 25 30

Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu
35 40

<210> 145
<211> 68
<212> PRT
<213> Homo sapiens

<400> 145

Met Ala Ser Arg Val Leu Ser Ala Tyr Val Ser Arg Leu Pro Ala Ala
1 5 10 15

Phe Ala Pro Leu Pro Arg Val Arg Met Leu Ala Val Ala Arg Pro Leu
20 25 30

Ser Thr Ala Leu Cys Ser Ala Gly Thr Gln Thr Arg Leu Gly Thr Leu
35 40 45

Gln Pro Ala Leu Val Leu Ala Gln Val Pro Gly Arg Val Thr Gln Leu
50 55 60

Cys Arg Gln Tyr
65

<210> 146
<211> 67
<212> PRT
<213> Homo sapiens

<400> 146

Met Phe Ala Cys Ala Lys Leu Ala Cys Thr Pro Ser Leu Ile Arg Ala
1 5 10 15

Gly Ser Arg Val Ala Tyr Arg Pro Ile Ser Ala Ser Val Leu Ser Arg

207420009W00-seq1

20

25

30

Pro Glu Ala Ser Arg Thr Gly Glu Gly Ser Thr Val Phe Asn Gly Ala
35 40 45

Gln Asn Gly Val Ser Gln Leu Ile Gln Arg Glu Phe Gln Thr Ser Ala
50 55 60

Ile Ser Arg
65

<210> 147
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> crATP6_hsADCK3

<400> 147

Met Ala Leu Gln Gln Ala Ala Pro Arg Val Phe Gly Leu Leu Gly Arg
1 5 10 15

Ala Pro Val Ala Leu Gly Gln Ser Gly Ile Leu Thr Gly Ser Ser Gly
20 25 30

Phe Lys Asn Gln Gly Phe Asn Gly Ser Leu Gln Ser Val Glu Asn His
35 40 45

Val Tyr Ala Gln Ala Phe Ser Thr Ser Ser Gln Glu Glu Gln Ala Ala
50 55 60

Pro Ser Ile Gln Gly Ala Ser Gly Met Lys Leu Pro Gly Met Ala Gly
65 70 75 80

Ser Met Leu Leu Gly Lys Ser Arg Ser Gly Leu Arg Thr Gly Ser Met
85 90 95

Val Pro Phe Ala Ala Gln Gln Ala Met Asn Met Gly Gly Met Ala Ala
100 105 110

207420009W00-seq1

Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val Lys Leu Thr
115 120 125

Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile Gly Gly Glu
130 135 140

Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val Glu Gln Ile
145 150 155 160

Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His Glu Glu Tyr
165 170 175

Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His Phe Ser Val
180 185 190

Pro His Ala Ala Gly Ala Ser Thr Asp Phe Ser Ser Ala Ser Ala Pro
195 200 205

Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser Glu Gly Pro
210 215 220

Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala Gly Phe Pro
225 230 235 240

Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg Leu Phe Ala
245 250 255

Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg Arg Phe Gly
260 265 270

Gly

<210> 148
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> ncATP9_ncATP9

207420009W00-seq1

<400> 148

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1 5 10 15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
20 25 30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr
35 40 45

Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys
50 55 60

Arg Ala Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln
65 70 75 80

Met Ala Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln
85 90 95

Val Ser Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys
100 105 110

Arg Thr Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe
115 120 125

Gln Lys Arg Ala
130

<210> 149

<211> 119

<212> PRT

<213> Zea mays

<400> 149

Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg Gly Arg
1 5 10 15

Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser Ser Leu
20 25 30

207420009W00-seq1

Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn Pro His
35 40 45

Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro Leu Pro
50 55 60

Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly Leu Leu
65 70 75 80

Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser Ser Ser
85 90 95

Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys Trp Ile
100 105 110

Pro Glu Ala Ala Arg Pro Tyr
115

<210> 150
<211> 391
<212> PRT
<213> Artificial Sequence

<220>
<223> ncATP9_zmLOC100282174_spilv1_ncATP9

<400> 150

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1 5 10 15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
20 25 30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr
35 40 45

Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys
50 55 60

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Arg Ala Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg
65 70 75 80

Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser
85 90 95

Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn
100 105 110

Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro
115 120 125

Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly
130 135 140

Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser
145 150 155 160

Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys
165 170 175

Trp Ile Pro Glu Ala Ala Arg Pro Tyr Met Thr Val Leu Ala Pro Leu
180 185 190

Arg Arg Leu His Thr Arg Ala Ala Phe Ser Ser Tyr Gly Arg Glu Ile
195 200 205

Ala Leu Gln Lys Arg Phe Leu Asn Leu Asn Ser Cys Ser Ala Val Arg
210 215 220

Arg Tyr Gly Thr Gly Phe Ser Asn Asn Leu Arg Ile Lys Lys Leu Lys
225 230 235 240

Asn Ala Phe Gly Val Val Arg Ala Asn Ser Thr Lys Ser Thr Ser Thr
245 250 255

Val Thr Thr Ala Ser Pro Ile Lys Tyr Asp Ser Ser Phe Val Gly Lys
260 265 270

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Thr Gly Gly Glu Ile Phe His Asp Met Met Leu Lys His Asn Val Lys
275 280 285

His Val Phe Gly Tyr Pro Gly Gly Ala Ile Leu Pro Val Phe Asp Ala
290 295 300

Ile Tyr Arg Ser Pro His Phe Glu Phe Ile Leu Pro Arg His Glu Gln
305 310 315 320

Ala Ala Gly His Ala Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu
325 330 335

Ala Ser Gln Met Ala Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg
340 345 350

Val Ala Gln Val Ser Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln
355 360 365

Thr Leu Lys Arg Thr Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg
370 375 380

Gln Ala Phe Gln Lys Arg Ala
385 390

<210> 151
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> zmlOC100282174_hsADCK3_crATP6 _hsATP5G3

<400> 151

Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg Gly Arg
1 5 10 15

Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser Ser Leu
20 25 30

Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn Pro His
35 40 45

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Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro Leu Pro
50 55 60

Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly Leu Leu
65 70 75 80

Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser Ser Ser
85 90 95

Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys Trp Ile
100 105 110

Pro Glu Ala Ala Arg Pro Tyr Met Ala Ala Ile Leu Gly Asp Thr Ile
115 120 125

Met Val Ala Lys Gly Leu Val Lys Leu Thr Gln Ala Ala Val Glu Thr
130 135 140

His Leu Gln His Leu Gly Ile Gly Gly Glu Leu Ile Met Ala Ala Arg
145 150 155 160

Ala Leu Gln Ser Thr Ala Val Glu Gln Ile Gly Met Phe Leu Gly Lys
165 170 175

Val Gln Gly Gln Asp Lys His Glu Glu Tyr Phe Ala Glu Asn Phe Gly
180 185 190

Gly Pro Glu Gly Glu Phe His Phe Ser Val Pro His Ala Ala Gly Ala
195 200 205

Ser Thr Asp Phe Ser Ser Ala Ser Ala Pro Asp Gln Ser Ala Pro Pro
210 215 220

Ser Leu Gly His Ala His Ser Glu Gly Pro Ala Pro Ala Tyr Val Ala
225 230 235 240

Ser Gly Pro Phe Arg Glu Ala Gly Phe Pro Gly Gln Ala Ser Ser Pro
245 250 255

207420009W00-seq1

Leu Gly Arg Ala Asn Gly Arg Leu Phe Ala Asn Pro Arg Asp Ser Phe
260 265 270

Ser Ala Met Gly Phe Gln Arg Arg Phe Met Ala Leu Gln Gln Ala Ala
275 280 285

Pro Arg Val Phe Gly Leu Leu Gly Arg Ala Pro Val Ala Leu Gly Gln
290 295 300

Ser Gly Ile Leu Thr Gly Ser Ser Gly Phe Lys Asn Gln Gly Phe Asn
305 310 315 320

Gly Ser Leu Gln Ser Val Glu Asn His Val Tyr Ala Gln Ala Phe Ser
325 330 335

Thr Ser Ser Gln Glu Glu Gln Ala Ala Pro Ser Ile Gln Gly Ala Ser
340 345 350

Gly Met Lys Leu Pro Gly Met Ala Gly Ser Met Leu Leu Gly Lys Ser
355 360 365

Arg Ser Gly Leu Arg Thr Gly Ser Met Val Pro Phe Ala Ala Gln Gln
370 375 380

Ala Met Asn Met Met Phe Ala Cys Ala Lys Leu Ala Cys Thr Pro Ser
385 390 395 400

Leu Ile Arg Ala Gly Ser Arg Val Ala Tyr Arg Pro Ile Ser Ala Ser
405 410 415

Val Leu Ser Arg Pro Glu Ala Ser Arg Thr Gly Glu Gly Ser Thr Val
420 425 430

Phe Asn Gly Ala Gln Asn Gly Val Ser Gln Leu Ile Gln Arg Glu Phe
435 440 445

Gln Thr Ser Ala Ile Ser Arg
450 455

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<210> 152
 <211> 348
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> zmlOC100282174_hsADCK3_hsATP5G3

<400> 152

Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg Gly Arg
 1 5 10 15

Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser Ser Leu
 20 25 30

Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn Pro His
 35 40 45

Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro Leu Pro
 50 55 60

Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly Leu Leu
 65 70 75 80

Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser Ser Ser
 85 90 95

Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys Trp Ile
 100 105 110

Pro Glu Ala Ala Arg Pro Tyr Met Ala Ala Ile Leu Gly Asp Thr Ile
 115 120 125

Met Val Ala Lys Gly Leu Val Lys Leu Thr Gln Ala Ala Val Glu Thr
 130 135 140

His Leu Gln His Leu Gly Ile Gly Gly Glu Leu Ile Met Ala Ala Arg
 145 150 155 160

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Ala Leu Gln Ser Thr Ala Val Glu Gln Ile Gly Met Phe Leu Gly Lys
165 170 175

Val Gln Gly Gln Asp Lys His Glu Glu Tyr Phe Ala Glu Asn Phe Gly
180 185 190

Gly Pro Glu Gly Glu Phe His Phe Ser Val Pro His Ala Ala Gly Ala
195 200 205

Ser Thr Asp Phe Ser Ser Ala Ser Ala Pro Asp Gln Ser Ala Pro Pro
210 215 220

Ser Leu Gly His Ala His Ser Glu Gly Pro Ala Pro Ala Tyr Val Ala
225 230 235 240

Ser Gly Pro Phe Arg Glu Ala Gly Phe Pro Gly Gln Ala Ser Ser Pro
245 250 255

Leu Gly Arg Ala Asn Gly Arg Leu Phe Ala Asn Pro Arg Asp Ser Phe
260 265 270

Ser Ala Met Gly Phe Gln Arg Arg Phe Met Phe Ala Cys Ala Lys Leu
275 280 285

Ala Cys Thr Pro Ser Leu Ile Arg Ala Gly Ser Arg Val Ala Tyr Arg
290 295 300

Pro Ile Ser Ala Ser Val Leu Ser Arg Pro Glu Ala Ser Arg Thr Gly
305 310 315 320

Glu Gly Ser Thr Val Phe Asn Gly Ala Gln Asn Gly Val Ser Gln Leu
325 330 335

Ile Gln Arg Glu Phe Gln Thr Ser Ala Ile Ser Arg
340 345

<210> 153
<211> 185
<212> PRT
<213> Artificial Sequence

207420009W00-seq1

<220>

<223> ncATP9_zmLOC100282174

<400> 153

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1 5 10 15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
20 25 30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr
35 40 45

Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys
50 55 60

Arg Ala Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg
65 70 75 80

Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser
85 90 95

Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn
100 105 110

Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro
115 120 125

Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly
130 135 140

Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser
145 150 155 160

Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys
165 170 175

Trp Ile Pro Glu Ala Ala Arg Pro Tyr
180 185

<210> 154
 <211> 455
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hsADCK3_zmLOC100282174_crATP6 _hsATP5G3

<400> 154

Met Ala Ala Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val
 1 5 10 15

Lys Leu Thr Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile
 20 25 30

Gly Gly Glu Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val
 35 40 45

Glu Gln Ile Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His
 50 55 60

Glu Glu Tyr Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His
 65 70 75 80

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

Ser Ala Pro Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser
 100 105 110

Glu Gly Pro Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala
 115 120 125

Gly Phe Pro Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg
 130 135 140

Leu Phe Ala Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg
 145 150 155 160

207420009W00-seq1

Arg Phe Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg
165 170 175

Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser
180 185 190

Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn
195 200 205

Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro
210 215 220

Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly
225 230 235 240

Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser
245 250 255

Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys
260 265 270

Trp Ile Pro Glu Ala Ala Arg Pro Tyr Met Ala Leu Gln Gln Ala Ala
275 280 285

Pro Arg Val Phe Gly Leu Leu Gly Arg Ala Pro Val Ala Leu Gly Gln
290 295 300

Ser Gly Ile Leu Thr Gly Ser Ser Gly Phe Lys Asn Gln Gly Phe Asn
305 310 315 320

Gly Ser Leu Gln Ser Val Glu Asn His Val Tyr Ala Gln Ala Phe Ser
325 330 335

Thr Ser Ser Gln Glu Glu Gln Ala Ala Pro Ser Ile Gln Gly Ala Ser
340 345 350

Gly Met Lys Leu Pro Gly Met Ala Gly Ser Met Leu Leu Gly Lys Ser
355 360 365

207420009W00-seq1

Arg Ser Gly Leu Arg Thr Gly Ser Met Val Pro Phe Ala Ala Gln Gln
370 375 380

Ala Met Asn Met Met Phe Ala Cys Ala Lys Leu Ala Cys Thr Pro Ser
385 390 395 400

Leu Ile Arg Ala Gly Ser Arg Val Ala Tyr Arg Pro Ile Ser Ala Ser
405 410 415

Val Leu Ser Arg Pro Glu Ala Ser Arg Thr Gly Glu Gly Ser Thr Val
420 425 430

Phe Asn Gly Ala Gln Asn Gly Val Ser Gln Leu Ile Gln Arg Glu Phe
435 440 445

Gln Thr Ser Ala Ile Ser Arg
450 455

<210> 155
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> crATP6 _hsADCK3_zmLOC100282174_hsATP5G3

<400> 155

Met Ala Leu Gln Gln Ala Ala Pro Arg Val Phe Gly Leu Leu Gly Arg
1 5 10 15

Ala Pro Val Ala Leu Gly Gln Ser Gly Ile Leu Thr Gly Ser Ser Gly
20 25 30

Phe Lys Asn Gln Gly Phe Asn Gly Ser Leu Gln Ser Val Glu Asn His
35 40 45

Val Tyr Ala Gln Ala Phe Ser Thr Ser Ser Gln Glu Glu Gln Ala Ala
50 55 60

Pro Ser Ile Gln Gly Ala Ser Gly Met Lys Leu Pro Gly Met Ala Gly
65 70 75 80

207420009W00-seq1

Ser Met Leu Leu Gly Lys Ser Arg Ser Gly Leu Arg Thr Gly Ser Met
85 90 95

Val Pro Phe Ala Ala Gln Gln Ala Met Asn Met Met Ala Ala Ile Leu
100 105 110

Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val Lys Leu Thr Gln Ala
115 120 125

Ala Val Glu Thr His Leu Gln His Leu Gly Ile Gly Gly Glu Leu Ile
130 135 140

Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val Glu Gln Ile Gly Met
145 150 155 160

Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His Glu Glu Tyr Phe Ala
165 170 175

Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His Phe Ser Val Pro His
180 185 190

Ala Ala Gly Ala Ser Thr Asp Phe Ser Ser Ala Ser Ala Pro Asp Gln
195 200 205

Ser Ala Pro Pro Ser Leu Gly His Ala His Ser Glu Gly Pro Ala Pro
210 215 220

Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala Gly Phe Pro Gly Gln
225 230 235 240

Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg Leu Phe Ala Asn Pro
245 250 255

Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg Arg Phe Met Ala Leu
260 265 270

Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg Gly Arg Gly Ala Leu
275 280 285

207420009W00-seq1

Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser Ser Leu Ser Pro Arg
290 295 300

Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn Pro His Ala Asp Arg
305 310 315 320

Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro Leu Pro Ala Ser Ala
325 330 335

Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly Leu Leu Pro Arg His
340 345 350

Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser Ser Ser Ser Arg Pro
355 360 365

Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys Trp Ile Pro Glu Ala
370 375 380

Ala Arg Pro Tyr Met Phe Ala Cys Ala Lys Leu Ala Cys Thr Pro Ser
385 390 395 400

Leu Ile Arg Ala Gly Ser Arg Val Ala Tyr Arg Pro Ile Ser Ala Ser
405 410 415

Val Leu Ser Arg Pro Glu Ala Ser Arg Thr Gly Glu Gly Ser Thr Val
420 425 430

Phe Asn Gly Ala Gln Asn Gly Val Ser Gln Leu Ile Gln Arg Glu Phe
435 440 445

Gln Thr Ser Ala Ile Ser Arg
450 455

<210> 156
<211> 285
<212> PRT
<213> Artificial Sequence

<220>

<223> hsADCK3_zmLOC100282174

<400> 156

Met Ala Ala Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val
 1 5 10 15

Lys Leu Thr Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile
 20 25 30

Gly Gly Glu Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val
 35 40 45

Glu Gln Ile Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His
 50 55 60

Glu Glu Tyr Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His
 65 70 75 80

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

Ser Ala Pro Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser
 100 105 110

Glu Gly Pro Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala
 115 120 125

Gly Phe Pro Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg
 130 135 140

Leu Phe Ala Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg
 145 150 155 160

Arg Phe Gly Gly Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg
 165 170 175

Arg Arg Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu
 180 185 190

207420009W00-seq1

Leu Ser Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro
195 200 205

Asn Asn Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys
210 215 220

Pro Pro Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala
225 230 235 240

Arg Gly Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr
245 250 255

Ser Ser Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val
260 265 270

Asp Lys Trp Ile Pro Glu Ala Ala Arg Pro Tyr Gly Gly
275 280 285

<210> 157
<211> 394
<212> PRT
<213> Artificial Sequence

<220>
<223> hsADCK3_zmLOC100282174_crATP6

<400> 157

Met Ala Ala Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val
1 5 10 15

Lys Leu Thr Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile
20 25 30

Gly Gly Glu Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val
35 40 45

Glu Gln Ile Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His
50 55 60

Glu Glu Tyr Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His
65 70 75 80

207420009W00-seq1

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

Ser Ala Pro Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser
100 105 110

Glu Gly Pro Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala
115 120 125

Gly Phe Pro Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg
130 135 140

Leu Phe Ala Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg
145 150 155 160

Arg Phe Gly Gly Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg
165 170 175

Arg Arg Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu
180 185 190

Leu Ser Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro
195 200 205

Asn Asn Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys
210 215 220

Pro Pro Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala
225 230 235 240

Arg Gly Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr
245 250 255

Ser Ser Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val
260 265 270

Asp Lys Trp Ile Pro Glu Ala Ala Arg Pro Tyr Gly Gly Met Ala Leu
275 280 285

207420009W00-seq1

Gln Gln Ala Ala Pro Arg Val Phe Gly Leu Leu Gly Arg Ala Pro Val
290 295 300

Ala Leu Gly Gln Ser Gly Ile Leu Thr Gly Ser Ser Gly Phe Lys Asn
305 310 315 320

Gln Gly Phe Asn Gly Ser Leu Gln Ser Val Glu Asn His Val Tyr Ala
325 330 335

Gln Ala Phe Ser Thr Ser Ser Gln Glu Glu Gln Ala Ala Pro Ser Ile
340 345 350

Gln Gly Ala Ser Gly Met Lys Leu Pro Gly Met Ala Gly Ser Met Leu
355 360 365

Leu Gly Lys Ser Arg Ser Gly Leu Arg Thr Gly Ser Met Val Pro Phe
370 375 380

Ala Ala Gln Gln Ala Met Asn Met Gly Gly
385 390

<210> 158
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> ncATP9_zmLOC100282174_spilv1_GNFP_ncATP9

<400> 158

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1 5 10 15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
20 25 30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr
35 40 45

207420009W00-seq1

Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys
50 55 60

Arg Ala Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg
65 70 75 80

Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser
85 90 95

Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn
100 105 110

Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro
115 120 125

Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly
130 135 140

Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser
145 150 155 160

Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys
165 170 175

Trp Ile Pro Glu Ala Ala Arg Pro Tyr Met Thr Val Leu Ala Pro Leu
180 185 190

Arg Arg Leu His Thr Arg Ala Ala Phe Ser Ser Tyr Gly Arg Glu Ile
195 200 205

Ala Leu Gln Lys Arg Phe Leu Asn Leu Asn Ser Cys Ser Ala Val Arg
210 215 220

Arg Tyr Gly Thr Gly Phe Ser Asn Asn Leu Arg Ile Lys Lys Leu Lys
225 230 235 240

Asn Ala Phe Gly Val Val Arg Ala Asn Ser Thr Lys Ser Thr Ser Thr
245 250 255

207420009W00-seq1

Val Thr Thr Ala Ser Pro Ile Lys Tyr Asp Ser Ser Phe Val Gly Lys
 260 265 270

Thr Gly Gly Glu Ile Phe His Asp Met Met Leu Lys His Asn Val Lys
 275 280 285

His Val Phe Gly Tyr Pro Gly Gly Ala Ile Leu Pro Val Phe Asp Ala
 290 295 300

Ile Tyr Arg Ser Pro His Phe Glu Phe Ile Leu Pro Arg His Glu Gln
 305 310 315 320

Ala Ala Gly His Ala Val Ser Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 325 330 335

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 340 345 350

Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg
 355 360 365

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro
 370 375 380

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 385 390 395 400

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 405 410 415

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 420 425 430

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 435 440 445

Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His
 450 455 460

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Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
465 470 475 480

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
485 490 495

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Met Ala Ser Thr
500 505 510

Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala Ala Ser Ala Lys
515 520 525

Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser Lys Arg Thr Ile
530 535 540

Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr Gln Met Thr Ser
545 550 555 560

Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys Arg Ala
565 570

<210> 159
<211> 810
<212> PRT
<213> Artificial Sequence

<220>
<223> ncATP9_zmLOC100282174_spilv1_lcSirt5_osP0644B06.24-2_hsATP5G2_ncA
TP9

<400> 159

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1 5 10 15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
20 25 30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr
35 40 45

Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys

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50

55

60

Arg Ala Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg
65 70 75 80

Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser
85 90 95

Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn
100 105 110

Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro
115 120 125

Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly
130 135 140

Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser
145 150 155 160

Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys
165 170 175

Trp Ile Pro Glu Ala Ala Arg Pro Tyr Met Thr Val Leu Ala Pro Leu
180 185 190

Arg Arg Leu His Thr Arg Ala Ala Phe Ser Ser Tyr Gly Arg Glu Ile
195 200 205

Ala Leu Gln Lys Arg Phe Leu Asn Leu Asn Ser Cys Ser Ala Val Arg
210 215 220

Arg Tyr Gly Thr Gly Phe Ser Asn Asn Leu Arg Ile Lys Lys Leu Lys
225 230 235 240

Asn Ala Phe Gly Val Val Arg Ala Asn Ser Thr Lys Ser Thr Ser Thr
245 250 255

Val Thr Thr Ala Ser Pro Ile Lys Tyr Asp Ser Ser Phe Val Gly Lys

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260

265

270

Thr Gly Gly Glu Ile Phe His Asp Met Met Leu Lys His Asn Val Lys
 275 280 285

His Val Phe Gly Tyr Pro Gly Gly Ala Ile Leu Pro Val Phe Asp Ala
 290 295 300

Ile Tyr Arg Ser Pro His Phe Glu Phe Ile Leu Pro Arg His Glu Gln
 305 310 315 320

Ala Ala Gly His Ala Met Arg Lys Arg Ser Leu Arg Cys His Leu Trp
 325 330 335

Ser Ala Asn Ala Ser Leu Ser Pro Arg Lys Asp Glu Val Thr Ser Arg
 340 345 350

Lys Glu Ser Glu Asn Leu Val Lys Gly Lys Lys Asn Lys Lys Ser His
 355 360 365

Leu His Leu Leu Leu Phe Thr Ala Ser Lys Ile Gly Thr Asp Ser Val
 370 375 380

Phe Asp Val Gln Lys Ser Lys Glu Cys Cys Lys Glu Leu Gly Leu Leu
 385 390 395 400

Phe Thr Ser Leu Ile His Ser Ile Gly Ser Phe Pro Phe Asp Glu Glu
 405 410 415

Pro Lys Ala Ala Ala Val Phe Leu Pro Gly Ser Leu Pro Gln Leu Thr
 420 425 430

Val Leu Val Leu Ala Pro Gly Ser Gly Ser Cys Pro Thr Gly Lys Ser
 435 440 445

Thr Pro His Leu Ala Ala Ser Gly Arg Asn Ala Glu Leu Leu Arg Pro
 450 455 460

Gln Asn Ser Met Ile Val Arg Gln Phe Thr Cys Arg Gly Thr Ile Ser

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465		470		475		480									
Ser	His	Leu	Cys	Ala	His	Leu	Arg	Lys	Pro	His	Asp	Ser	Arg	Asn	Met
				485					490					495	
Ala	Arg	Pro	Met	Ala	Leu	Leu	Leu	Arg	His	Ser	Pro	Lys	Leu	Arg	Arg
			500					505					510		
Ala	His	Ala	Ile	Leu	Gly	Cys	Glu	Arg	Gly	Thr	Val	Val	Arg	His	Phe
		515					520					525			
Ser	Ser	Ser	Thr	Cys	Ser	Ser	Leu	Val	Lys	Glu	Asp	Thr	Val	Ser	Ser
	530					535					540				
Ser	Asn	Leu	His	Pro	Glu	Tyr	Ala	Lys	Lys	Ile	Gly	Gly	Ser	Asp	Phe
545					550					555					560
Ser	His	Asp	Arg	Gln	Ser	Gly	Lys	Glu	Leu	Gln	Asn	Phe	Lys	Val	Ser
				565					570					575	
Pro	Gln	Glu	Ala	Ser	Arg	Ala	Ser	Asn	Phe	Met	Arg	Ala	Ser	Lys	Tyr
			580					585					590		
Gly	Met	Pro	Ile	Thr	Ala	Asn	Gly	Val	His	Ser	Leu	Phe	Ser	Cys	Gly
		595					600					605			
Gln	Val	Val	Pro	Ser	Arg	Cys	Phe	Met	Pro	Glu	Leu	Ile	Leu	Tyr	Val
	610					615					620				
Ala	Ile	Thr	Leu	Ser	Val	Ala	Glu	Arg	Leu	Val	Gly	Pro	Gly	His	Ala
625					630					635					640
Cys	Ala	Glu	Pro	Ser	Phe	Arg	Ser	Ser	Arg	Cys	Ser	Ala	Pro	Leu	Cys
				645					650					655	
Leu	Leu	Cys	Ser	Gly	Ser	Ser	Ser	Pro	Ala	Thr	Ala	Pro	His	Pro	Leu
			660					665					670		
Lys	Met	Phe	Ala	Cys	Ser	Lys	Phe	Val	Ser	Thr	Pro	Ser	Leu	Val	Lys

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675

680

685

Ser Thr Ser Gln Leu Leu Ser Arg Pro Leu Ser Ala Val Val Leu Lys
690 695 700

Arg Pro Glu Ile Leu Thr Asp Glu Ser Leu Ser Ser Leu Ala Val Ser
705 710 715 720

Cys Pro Leu Thr Ser Leu Val Ser Ser Arg Ser Phe Gln Thr Ser Ala
725 730 735

Ile Ser Arg Asp Ile Asp Thr Ala Met Ala Ser Thr Arg Val Leu Ala
740 745 750

Ser Arg Leu Ala Ser Gln Met Ala Ala Ser Ala Lys Val Ala Arg Pro
755 760 765

Ala Val Arg Val Ala Gln Val Ser Lys Arg Thr Ile Gln Thr Gly Ser
770 775 780

Pro Leu Gln Thr Leu Lys Arg Thr Gln Met Thr Ser Ile Val Asn Ala
785 790 795 800

Thr Thr Arg Gln Ala Phe Gln Lys Arg Ala
805 810

<210> 160
<211> 459
<212> PRT
<213> Homo sapiens

<400> 160

Met Leu Lys Leu Ile Val Pro Thr Ile Met Leu Leu Pro Leu Thr Trp
1 5 10 15

Leu Ser Lys Lys His Met Ile Trp Ile Asn Thr Thr Thr His Ser Leu
20 25 30

Ile Ile Ser Ile Ile Pro Leu Leu Phe Phe Asn Gln Ile Asn Asn Asn
35 40 45

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Leu Phe Ser Cys Ser Pro Thr Phe Ser Ser Asp Pro Leu Thr Thr Pro
50 55 60

Leu Leu Met Leu Thr Thr Trp Leu Leu Pro Leu Thr Ile Met Ala Ser
65 70 75 80

Gln Arg His Leu Ser Ser Glu Pro Leu Ser Arg Lys Lys Leu Tyr Leu
85 90 95

Ser Met Leu Ile Ser Leu Gln Ile Ser Leu Ile Met Thr Phe Thr Ala
100 105 110

Thr Glu Leu Ile Met Phe Tyr Ile Phe Phe Glu Thr Thr Leu Ile Pro
115 120 125

Thr Leu Ala Ile Ile Thr Arg Trp Gly Asn Gln Pro Glu Arg Leu Asn
130 135 140

Ala Gly Thr Tyr Phe Leu Phe Tyr Thr Leu Val Gly Ser Leu Pro Leu
145 150 155 160

Leu Ile Ala Leu Ile Tyr Thr His Asn Thr Leu Gly Ser Leu Asn Ile
165 170 175

Leu Leu Leu Thr Leu Thr Ala Gln Glu Leu Ser Asn Ser Trp Ala Asn
180 185 190

Asn Leu Met Trp Leu Ala Tyr Thr Met Ala Phe Met Val Lys Met Pro
195 200 205

Leu Tyr Gly Leu His Leu Trp Leu Pro Lys Ala His Val Glu Ala Pro
210 215 220

Ile Ala Gly Ser Met Val Leu Ala Ala Val Leu Leu Lys Leu Gly Gly
225 230 235 240

Tyr Gly Met Met Arg Leu Thr Leu Ile Leu Asn Pro Leu Thr Lys His
245 250 255

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Met Ala Tyr Pro Phe Leu Val Leu Ser Leu Trp Gly Met Ile Met Thr
260 265 270

Ser Ser Ile Cys Leu Arg Gln Thr Asp Leu Lys Ser Leu Ile Ala Tyr
275 280 285

Ser Ser Ile Ser His Met Ala Leu Val Val Thr Ala Ile Leu Ile Gln
290 295 300

Thr Pro Trp Ser Phe Thr Gly Ala Val Ile Leu Met Ile Ala His Gly
305 310 315 320

Leu Thr Ser Ser Leu Leu Phe Cys Leu Ala Asn Ser Asn Tyr Glu Arg
325 330 335

Thr His Ser Arg Ile Met Ile Leu Ser Gln Gly Leu Gln Thr Leu Leu
340 345 350

Pro Leu Met Ala Phe Trp Trp Leu Leu Ala Ser Leu Ala Asn Leu Ala
355 360 365

Leu Pro Pro Thr Ile Asn Leu Leu Gly Glu Leu Ser Val Leu Val Thr
370 375 380

Thr Phe Ser Trp Ser Asn Ile Thr Leu Leu Leu Thr Gly Leu Asn Met
385 390 395 400

Leu Val Thr Ala Leu Tyr Ser Leu Tyr Met Phe Thr Thr Thr Gln Trp
405 410 415

Gly Ser Leu Thr His His Ile Asn Asn Met Lys Pro Ser Phe Thr Arg
420 425 430

Glu Asn Thr Leu Met Phe Met His Leu Ser Pro Ile Leu Leu Leu Ser
435 440 445

Leu Asn Pro Asp Ile Ile Thr Gly Phe Ser Ser
450 455

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<210> 161
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 161

Met Met Tyr Ala Leu Phe Leu Leu Ser Val Gly Leu Val Met Gly Phe
 1 5 10 15

Val Gly Phe Ser Ser Lys Pro Ser Pro Ile Tyr Gly Gly Leu Val Leu
 20 25 30

Ile Val Ser Gly Val Val Gly Cys Val Ile Ile Leu Asn Phe Gly Gly
 35 40 45

Gly Tyr Met Gly Leu Met Val Phe Leu Ile Tyr Leu Gly Gly Met Met
 50 55 60

Val Val Phe Gly Tyr Thr Thr Ala Met Ala Ile Glu Glu Tyr Pro Glu
 65 70 75 80

Ala Trp Gly Ser Gly Val Glu Val Leu Val Ser Val Leu Val Gly Leu
 85 90 95

Ala Met Glu Val Gly Leu Val Leu Trp Val Lys Glu Tyr Asp Gly Val
 100 105 110

Val Val Val Val Asn Phe Asn Ser Val Gly Ser Trp Met Ile Tyr Glu
 115 120 125

Gly Glu Gly Ser Gly Leu Ile Arg Glu Asp Pro Ile Gly Ala Gly Ala
 130 135 140

Leu Tyr Asp Tyr Gly Arg Trp Leu Val Val Val Thr Gly Trp Thr Leu
 145 150 155 160

Phe Val Gly Val Tyr Ile Val Ile Glu Ile Ala Arg Gly Asn
 165 170

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<210> 162
 <211> 316
 <212> PRT
 <213> Homo sapiens

<400> 162

Met Ala Asn Leu Leu Leu Ile Val Pro Ile Leu Ile Ala Met Ala
 1 5 10 15

Phe Leu Met Leu Thr Glu Arg Lys Ile Leu Gly Tyr Met Gln Leu Arg
 20 25 30

Lys Gly Pro Asn Val Val Gly Pro Tyr Gly Leu Leu Gln Pro Phe Ala
 35 40 45

Asp Ala Ile Lys Leu Phe Thr Lys Glu Pro Leu Lys Pro Ala Thr Ser
 50 55 60

Thr Ile Thr Leu Tyr Ile Thr Ala Pro Thr Leu Ala Leu Thr Ile Ala
 65 70 75 80

Leu Leu Leu Trp Thr Pro Leu Pro Met Pro Asn Pro Leu Val Asn Leu
 85 90 95

Asn Leu Gly Leu Leu Phe Ile Leu Ala Thr Ser Ser Leu Ala Val Tyr
 100 105 110

Ser Ile Leu Trp Ser Gly Trp Ala Ser Asn Ser Asn Tyr Ala Leu Ile
 115 120 125

Gly Ala Leu Arg Ala Val Ala Gln Thr Ile Ser Tyr Glu Val Thr Leu
 130 135 140

Ala Ile Ile Leu Leu Ser Thr Leu Leu Met Ser Gly Ser Phe Asn Leu
 145 150 155 160

Ser Thr Leu Ile Thr Thr Gln Glu His Leu Trp Leu Leu Leu Pro Ser
 165 170 175

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Trp Pro Leu Ala Met Met Trp Phe Ile Ser Thr Leu Ala Glu Thr Asn
180 185 190

Arg Thr Pro Phe Asp Leu Ala Glu Gly Glu Ser Glu Leu Val Ser Gly
195 200 205

Phe Asn Ile Glu Tyr Ala Ala Gly Pro Phe Ala Leu Phe Phe Met Ala
210 215 220

Glu Tyr Thr Asn Ile Ile Met Met Asn Thr Leu Thr Thr Thr Ile Phe
225 230 235 240

Leu Gly Thr Thr Tyr Asp Ala Leu Ser Pro Glu Leu Tyr Thr Thr Tyr
245 250 255

Phe Val Thr Lys Thr Leu Leu Leu Thr Ser Leu Phe Leu Trp Ile Arg
260 265 270

Thr Ala Tyr Pro Arg Phe Arg Tyr Asp Gln Leu Met His Leu Leu Trp
275 280 285

Lys Asn Phe Leu Pro Leu Thr Leu Ala Leu Leu Met Trp Tyr Val Ser
290 295 300

Met Pro Ile Thr Ile Ser Ser Ile Pro Pro Gln Thr
305 310 315

<210> 163
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> GFP forward primer

<400> 163
acaagttcag cgtgtccg

18

<210> 164
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
 <223> GFP reverse primer

 <400> 164
 ctcgttgggg tctttgct 18

 <210> 165
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> ND4-F primer

 <400> 165
 atctccgcac actctctcct ca 22

 <210> 166
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> ND4-R primer

 <400> 166
 taggttggtg ttgatttggt t 21

 <210> 167
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> B-actin F2 primer

 <400> 167
 cctagaagca tttgcggt 18

 <210> 168
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> B-actin R2 primer

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<400> 168
gagctacgag ctgcctga

18