

SEQUENCE LISTING

<110> Unilever N. V.
<120> Screening Methods

<130> T3190

<160> 60

<170> SeqWin99

<210> 1
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> SNP region

<220>
<221> variation
<222> 5
<223> /replace = "Thr"

<400> 1
Asp Val Ala Gly Ala Thr Phe Met Ala Ala Gly
1 5 10

<210> 2
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Myc tag

<400> 2
Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5

<210> 3
<211> 1617
<212> DNA
<213> Homo Sapiens

<400> 3
cctcacatga tccagtttaa tcctcctctt ctcccttcct gaagctgcac gctgcagtaa 60
gagcacagca gaaatgcaga caaaaggggg ccaaacatgg gcgagaaggg ctctgttgct 120
cggcacctcg tgggccactg cacatctgcc tctctcaggg acctccctgc cccaacgtct 180
cccaagggcc acaggaaata gcacccaatg tgttatttct ccatcatcgg agtttcccgga 240
agggtttttc acgagacagg agcgagaga tggaggcatc ataatctatt tcttaattat 300
cgtttacatg ttcatggcca tatctattgt ctgtgatgaa tacttcctac cctccctgga 360
aatcatcagt gaatcccttg gattgtctca ggatgttgca ggcacaactt tcatggcagc 420
gggcagttca gtcctgaat tagttactgc tttcctaggt gtatttatca caaagggaga 480
tattggcatt agcaccatcc ttggatctgc aattttataat ctccttggca tctgtgctgc 540
ctgtggtttg ctatctaata cgggtctcaac actatcatgt tggcccctat tcagagactg 600
tgcagcgtac acaattagtg cagcagcagt tcttggtata atatatgaca accaagttta 660
ctggtatgaa ggggctttac tgcttttgat atatggattg tatgttttgg tgctgtgttt 720
tgacattaaa attaaccaat atattataaa gaaatgcagt ccttgctgcg cctgtcttgc 780

caaagctatg	gagagaagtg	aacaacagcc	actgatgggc	tgggaagatg	aaggtcaacc	840
attcattcgt	cggcaatcaa	gaactgatag	tgggaatattt	tatgaagatt	ctggctactc	900
tcagctctct	ataagtttac	atggccttag	tcaggtttct	gaagatccac	caagtgtttt	960
caacatgcct	gaagcagact	taaaaagaat	tttttgggta	ttatcccttc	ctattattac	1020
attacttttt	ctaaccacac	cagattgtag	aaaaaagttt	tggaaaaact	acttttgtgat	1080
aacctttttc	atgtctgcaa	tatggatatc	cgcattttaca	tatatcctgg	tttggatggg	1140
cacaataact	ggggaaacac	tagaaattcc	cgatacagta	atgggcctta	ctttatttagc	1200
agcaggaaca	agcataccag	acacaattgc	aagtgtgttg	gttgcaagaa	aagggaaagg	1260
agatatggct	atgtctaaca	tcgtgggatc	caatgtgttt	gatatgttgt	gccttggtat	1320
tccatggttt	attaaaaactg	cattttataaa	tggatcagct	cctgcagaag	taaacagcag	1380
aggactaact	tacataacca	tctctctcaa	cattttcaatt	atTTTTcctt	tttttagcagt	1440
tcacttcaat	ggctggaaac	tagacagaaa	gttgggaata	gtctgcctat	tatcatactt	1500
ggggcttgct	acattatcag	ttctatatga	acttggaatt	attggaaata	ataaaataag	1560
gggctgtgga	ggttgatatt	attaatagtg	ttatgcagaa	aatatgaatg	gcaggga	1617

<210> 4
 <211> 500
 <212> PRT
 <213> Homo Sapiens

<400> 4
 Met Gln Thr Lys Gly Gly Gln Thr Trp Ala Arg Arg Ala Leu Leu Leu
 1 5 10 15

Gly Ile Leu Trp Ala Thr Ala His Leu Pro Leu Ser Gly Thr Ser Leu
 20 25 30

Pro Gln Arg Leu Pro Arg Ala Thr Gly Asn Ser Thr Gln Cys Val Ile
 35 40 45

Ser Pro Ser Ser Glu Phe Pro Glu Gly Phe Phe Thr Arg Gln Glu Arg
 50 55 60

Arg Asp Gly Gly Ile Ile Ile Tyr Phe Leu Ile Ile Val Tyr Met Phe
 65 70 75 80

Met Ala Ile Ser Ile Val Cys Asp Glu Tyr Phe Leu Pro Ser Leu Glu
 85 90 95

Ile Ile Ser Glu Ser Leu Gly Leu Ser Gln Asp Val Ala Gly Thr Thr
 100 105 110

Phe Met Ala Ala Gly Ser Ser Ala Pro Glu Leu Val Thr Ala Phe Leu
 115 120 125

Gly Val Phe Ile Thr Lys Gly Asp Ile Gly Ile Ser Thr Ile Leu Gly
 130 135 140

Ser Ala Ile Tyr Asn Leu Leu Gly Ile Cys Ala Ala Cys Gly Leu Leu
 145 150 155 160

Ser Asn Thr Val Ser Thr Leu Ser Cys Trp Pro Leu Phe Arg Asp Cys
 165 170 175

Ala Ala Tyr Thr Ile Ser Ala Ala Ala Val Leu Gly Ile Ile Tyr Asp
 180 185 190

Asn Gln Val Tyr Trp Tyr Glu Gly Ala Leu Leu Leu Leu Ile Tyr Gly
 195 200 205

Leu Tyr Val Leu Val Leu Cys Phe Asp Ile Lys Ile Asn Gln Tyr Ile

210					215					220					
Ile	Lys	Lys	Cys	Ser	Pro	Cys	Cys	Ala	Cys	Leu	Ala	Lys	Ala	Met	Glu
225					230					235					240
Arg	Ser	Glu	Gln	Gln	Pro	Leu	Met	Gly	Trp	Glu	Asp	Glu	Gly	Gln	Pro
				245					250					255	
Phe	Ile	Arg	Arg	Gln	Ser	Arg	Thr	Asp	Ser	Gly	Ile	Phe	Tyr	Glu	Asp
			260					265					270		
Ser	Gly	Tyr	Ser	Gln	Leu	Ser	Ile	Ser	Leu	His	Gly	Leu	Ser	Gln	Val
		275					280					285			
Ser	Glu	Asp	Pro	Pro	Ser	Val	Phe	Asn	Met	Pro	Glu	Ala	Asp	Leu	Lys
	290					295					300				
Arg	Ile	Phe	Trp	Val	Leu	Ser	Leu	Pro	Ile	Ile	Thr	Leu	Leu	Phe	Leu
305					310					315					320
Thr	Thr	Pro	Asp	Cys	Arg	Lys	Lys	Phe	Trp	Lys	Asn	Tyr	Phe	Val	Ile
				325					330					335	
Thr	Phe	Phe	Met	Ser	Ala	Ile	Trp	Ile	Ser	Ala	Phe	Thr	Tyr	Ile	Leu
			340					345					350		
Val	Trp	Met	Val	Thr	Ile	Thr	Gly	Glu	Thr	Leu	Glu	Ile	Pro	Asp	Thr
		355					360					365			
Val	Met	Gly	Leu	Thr	Leu	Leu	Ala	Ala	Gly	Thr	Ser	Ile	Pro	Asp	Thr
	370					375					380				
Ile	Ala	Ser	Val	Leu	Val	Ala	Arg	Lys	Gly	Lys	Gly	Asp	Met	Ala	Met
385					390					395					400
Ser	Asn	Ile	Val	Gly	Ser	Asn	Val	Phe	Asp	Met	Leu	Cys	Leu	Gly	Ile
				405					410					415	
Pro	Trp	Phe	Ile	Lys	Thr	Ala	Phe	Ile	Asn	Gly	Ser	Ala	Pro	Ala	Glu
			420					425					430		
Val	Asn	Ser	Arg	Gly	Leu	Thr	Tyr	Ile	Thr	Ile	Ser	Leu	Asn	Ile	Ser
		435					440					445			
Ile	Ile	Phe	Leu	Phe	Leu	Ala	Val	His	Phe	Asn	Gly	Trp	Lys	Leu	Asp
	450					455					460				
Arg	Lys	Leu	Gly	Ile	Val	Cys	Leu	Leu	Ser	Tyr	Leu	Gly	Leu	Ala	Thr
465					470					475					480
Leu	Ser	Val	Leu	Tyr	Glu	Leu	Gly	Ile	Ile	Gly	Asn	Asn	Lys	Ile	Arg
				485					490					495	
Gly	Cys	Gly	Gly												
			500												

<210> 5
 <211> 46
 <212> PRT
 <213> Homo Sapiens

<400> 5
 Ile Val Cys Asp Asp Phe Phe Val Pro Ser Leu Glu Lys Ile Cys Glu
 1 5 10 15

Arg Leu His Leu Ser Glu Asp Val Ala Gly Ala Thr Phe Met Ala Ala
 20 25 30

Gly Ser Ser Thr Pro Glu Leu Phe Ala Ser Val Ile Gly Val
 35 40 45

<210> 6
 <211> 46
 <212> PRT
 <213> Homo Sapiens

<400> 6
 Ile Val Cys Asp Asp Phe Phe Xaa Pro Ser Leu Glu Lys Ile Cys Glu
 1 5 10 15

Arg Leu His Leu Ser Glu Asp Val Ala Gly Ala Thr Phe Met Ala Ala
 20 25 30

Gly Ser Ser Ala Pro Glu Leu Phe Thr Ser Val Ile Gly Val
 35 40 45

<210> 7
 <211> 46
 <212> PRT
 <213> Homo Sapiens

<400> 7
 Ile Val Cys Asp Glu Tyr Phe Leu Pro Ser Leu Glu Ile Ile Ser Glu
 1 5 10 15

Ser Leu Gly Leu Ser Gln Asp Val Ala Gly Thr Thr Phe Met Ala Ala
 20 25 30

Gly Ser Ser Ala Pro Glu Leu Val Thr Ala Phe Leu Gly Val
 35 40 45

<210> 8
 <211> 46
 <212> PRT
 <213> Homo Sapiens

<400> 8
 Ile Val Cys Asp Glu Phe Phe Val Pro Ser Leu Thr Val Ile Thr Glu
 1 5 10 15

Lys Leu Gly Ile Ser Asp Asp Val Ala Gly Ala Thr Phe Met Ala Ala
 20 25 30

Gly Gly Ser Ala Pro Glu Leu Phe Thr Ser Leu Ile Gly Val
 35 40 45

<210> 9
 <211> 46
 <212> PRT
 <213> Homo Sapiens

<400> 9

Ile Val Cys Asp Glu Tyr Phe Val Pro Ala Leu Gly Val Ile Thr Asp
 1 5 10 15

Lys Leu Gln Ile Ser Glu Asp Val Ala Gly Ala Thr Phe Met Ala Ala
 20 25 30

Gly Gly Ser Ala Pro Glu Leu Phe Thr Ser Leu Ile Gly Val
 35 40 45

<210> 10
 <211> 300
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pIE1/153A (V4-) polylinker

<400> 10
 ctaattcaag aggtgcgacg aagaagttgc cgcgttggtg gtagacggta tcgataagct 60
 tgatatcgaa ttctgcagc cctgtaatac gactcactat agggcgaatt gggtagcggg 120
 cccccctcg aggtcgacgg tatcgataag cttgatatcg aattcctgca gcccggggga 180
 tccactagtt ctagagcggc cgccaccgcg gtggagctcc agcttttggt cccttttagtg 240
 agggttcgag aagtcttacg aacttcccga cggtcaggtc atcaccatcg gaaacgaaag 300

<210> 11
 <211> 300
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pIE1/153A (V4+) polylinker

<400> 11
 ctaattcaag aggtgcgacg aagaagttgc cgcgttggtg gtagacggta tcgataagct 60
 tgatatcgaa ttctgcagc ccaaccctca ctaaaggga caaaagctgg agctccaccg 120
 cggtggcggc cgctctagaa ctagtggatc ccccgggctg caggaattcg atatcaagct 180
 tatcgatacc gtcgacctcg agggggggcc cggtagccaa ttgcacctat agtgagtcgt 240
 attagacgag aagtcttacg aacttcccga cggtcaggtc atcaccatcg gaaacgaaag 300

<210> 12
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Actin 1 primer

<400> 12
 gacgaagaag ttgccgcggt gg 22

<210> 13
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Actin 3 primer

<400> 13
 cgatggatgat gacctgaccg tc 22

<210> 14
<211> 1547
<212> DNA
<213> Artificial Sequence

<220>
<223> myc tagged human nckx5

<400> 14
ctcgagatgc agacaaaagg gggccaaaca tgggcgagaa gggctctgtt gctcggcatc 60
ctgtgggcca ctgcacatct gcctctctca gggacctccc tgccccaacg tctcccaagg 120
gccacaggaa atagcaccca atgtgttatt tctccatcat cggaacagaa gctcatctca 180
gaagaggatc tgggaattccc cgaagggttt ttcacgagac aggagcgcag agatggaggc 240
atcataatct atttcctaata tatcgtttac atgttcatgg ccatatctat tgtctgtgat 300
gaataacttc taccctccct ggaaatcatc agtgaatccc ttggattgtc tcaggatgtt 360
gcaggcgcaa ctttcatggc agcgggcagt tcagctcctg aattagttac tgctttccta 420
ggtgtattta tcacaaaggg agatattggc attagcacca tccttggatc tgcaatttat 480
aatctccttg gcatctgtgc tgctgtggt ttgctatcta atacggtctc aacactatca 540
tgttggcccc tattcagaga ctgtgcagcg tacacaatta gtgcagcagc agttcttggg 600
ataatatatg acaaccaagt ttactggtat gaaggggctt tactgctttt gatatatgga 660
ttgtatgttt tgggtgctgtg ttttgacatt aaaattaacc aatatattat aaagaaatgc 720
agtccttgct gcgcctgtct tgccaaagct atggagagaa gtgaacaaca gccactgatg 780
ggctgggaag atgaaggtca accattcatt cgtcggcaat caagaactga tagtgggaata 840
ttttatgaag attctggcta ctctcagctc tctataagtt tacatggcct tagtcagggt 900
tctgaagatc caccaagtgt tttcaacatg cctgaagcag acttaaaaag aatttttttg 960
gtattatccc ttcctattat tacattactt tttctaacca caccagattg tagaaaaaag 1020
ttttggaaaa actactttgt gataaccttt ttcattgtct caatatggat atccgcattt 1080
acatatatcc tggtttggat ggtcaccaatt acaggggaaa cactagaaat tcccgatata 1140
gtaatgggcc ttactttatt agcagcagga acaagcatat cagacacaat tgcaagtgtg 1200
ttggttgcaa gaaaagggaaggagatatg gctatgtcta acatcgtggg atccaatgtg 1260
tttgatatgt tgtgccttgg tattccatgg tttattaaaa ctgcatttat aaatggatca 1320
gctcctgcag aagtaaacag cagaggacta acttacataa ccatctctct caacatttca 1380
attatttttc ttttttttagc agttcacttc aatggctgga aactagacag aaagttggga 1440
atagtctgcc tattatcata cttggggctt gctacattat cagttctata tgaacttgga 1500
attattggaa ataataaaat aaggggctgt ggaggttgag cggccgc 1547

<210> 15
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> myc tagged human nckx5

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

					85						90						95	
Cys	Asp	Glu	Tyr	Phe	Leu	Pro	Ser	Leu	Glu	Ile	Ile	Ser	Glu	Ser	Leu			
					100						105						110	
Gly	Leu	Ser	Gln	Asp	Val	Ala	Gly	Ala	Thr	Phe	Met	Ala	Ala	Gly	Ser			
					115						120						125	
Ser	Ala	Pro	Glu	Leu	Val	Thr	Ala	Phe	Leu	Gly	Val	Phe	Ile	Thr	Lys			
					130						135						140	
Gly	Asp	Ile	Gly	Ile	Ser	Thr	Ile	Leu	Gly	Ser	Ala	Ile	Tyr	Asn	Leu			
145						150						155						160
Leu	Gly	Ile	Cys	Ala	Ala	Cys	Gly	Leu	Leu	Ser	Asn	Thr	Val	Ser	Thr			
					165						170						175	
Leu	Ser	Cys	Trp	Pro	Leu	Phe	Arg	Asp	Cys	Ala	Ala	Tyr	Thr	Ile	Ser			
					180						185						190	
Ala	Ala	Ala	Val	Leu	Gly	Ile	Ile	Tyr	Asp	Asn	Gln	Val	Tyr	Trp	Tyr			
					195						200						205	
Glu	Gly	Ala	Leu	Leu	Leu	Leu	Ile	Tyr	Gly	Leu	Tyr	Val	Leu	Val	Leu			
					210						215						220	
Cys	Phe	Asp	Ile	Lys	Ile	Asn	Gln	Tyr	Ile	Ile	Lys	Lys	Cys	Ser	Pro			
225						230						235						240
Cys	Cys	Ala	Cys	Leu	Ala	Lys	Ala	Met	Glu	Arg	Ser	Glu	Gln	Gln	Pro			
					245						250						255	
Leu	Met	Gly	Trp	Glu	Asp	Glu	Gly	Gln	Pro	Phe	Ile	Arg	Arg	Gln	Ser			
					260						265						270	
Arg	Thr	Asp	Ser	Gly	Ile	Phe	Tyr	Glu	Asp	Ser	Gly	Tyr	Ser	Gln	Leu			
					275						280						285	
Ser	Ile	Ser	Leu	His	Gly	Leu	Ser	Gln	Val	Ser	Glu	Asp	Pro	Pro	Ser			
					290						295						300	
Val	Phe	Asn	Met	Pro	Glu	Ala	Asp	Leu	Lys	Arg	Ile	Phe	Trp	Val	Leu			
305						310						315						320
Ser	Leu	Pro	Ile	Ile	Thr	Leu	Leu	Phe	Leu	Thr	Thr	Pro	Asp	Cys	Arg			
					325						330						335	
Lys	Lys	Phe	Trp	Lys	Asn	Tyr	Phe	Val	Ile	Thr	Phe	Phe	Met	Ser	Ala			
					340						345						350	
Ile	Trp	Ile	Ser	Ala	Phe	Thr	Tyr	Ile	Leu	Val	Trp	Met	Val	Thr	Ile			
					355						360						365	
Thr	Gly	Glu	Thr	Leu	Glu	Ile	Pro	Asp	Thr	Val	Met	Gly	Leu	Thr	Leu			
					370						375						380	
Leu	Ala	Ala	Gly	Thr	Ser	Ile	Pro	Asp	Thr	Ile	Ala	Ser	Val	Leu	Val			
385						390						395						400
Ala	Arg	Lys	Gly	Lys	Gly	Asp	Met	Ala	Met	Ser	Asn	Ile	Val	Gly	Ser			
					405						410						415	

Asn Val Phe Asp Met Leu Cys Leu Gly Ile Pro Trp Phe Ile Lys Thr
 420 425 430

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

Thr Tyr Ile Thr Ile Ser Leu Asn Ile Ser Ile Ile Phe Leu Phe Leu
 450 455 460

Ala Val His Phe Asn Gly Trp Lys Leu Asp Arg Lys Leu Gly Ile Val
 465 470 475 480

Cys Leu Leu Ser Tyr Leu Gly Leu Ala Thr Leu Ser Val Leu Tyr Glu
 485 490 495

Leu Gly Ile Ile Gly Asn Asn Lys Ile Arg Gly Cys Gly Gly
 500 505 510

<210> 16
 <211> 1577
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> myc and id4 tagged human nckx5

<400> 16
 ctcgagatgc agacaaaagg gggccaaaca tgggcgagaa gggctctgtt gctcggcatc 60
 ctgtgggcca ctgcacatct gcctctctca gggacctccc tgccccaacg tctcccaagg 120
 gccacaggaa atagcaccca atgtgttatt tctccatcat cggaacagaa gctcatctca 180
 gaagaggatc tggaattccc cgaagggttt ttcacgagac aggagcgcag agatggaggc 240
 atcataatct atttccta atctgtttac atgttcatgg ccataatctat tgtctgtgat 300
 gaatacttcc taccctccct ggaaatcatc agtgaatccc ttggattgtc tcaggatgtt 360
 gcaggcgcaa ctttcatggc agcgggcagt tcagctcctg aattagttac tgctttccta 420
 ggtgtattta tcacaaaggg agatattggc attagcacca tccttggatc tgcaatttat 480
 aatctccttg gcatctgtgc tgcctgtggg ttgctatcta atacggtctc aacactatca 540
 tgttggcccc tattcagaga ctgtgcagcg tacacaatta gtgcagcagc agttcttggg 600
 ataatatatg acaaccaagt ttactggtat gaaggggctt tactgctttt gatatatgga 660
 ttgtatgttt tgggtgctgtg ttttgacatt aaaattaacc aatatattat aaagaaatgc 720
 agtccttgct gcgcctgtct tgccaaagct atggagagaa gtgaacaaca gccactgatg 780
 ggctgggaag atgaaggtca accattcatt cgtcggcaat caagaactga tagtgggaata 840
 ttttatgaag attctggcta ctctcagctc tctataagtt tacatggcct tagtcagggt 900
 tctgaagatc caccaagtgt tttcaacatg cctgaagcag acttaaaaag aatttttttg 960
 gtattatccc ttcctattat tacattactt tttctaacca caccagattg tagaaaaaag 1020
 ttttgaaaaa actactttgt gataaccttt ttcattgtct caatatggat atccgcattt 1080
 acatatatcc tggtttggat ggtcacaatt acaggggaaa cactagaaat tcccgatata 1140
 gtaatgggcc ttactttatt agcagcagga acaagcatac cagacacaat tgcaagtgtg 1200
 ttggttgcaa gaaaagggaagg agagatatg gctatgtcta acatcgtggg atccaatgtg 1260
 tttgatattg tgtgccttgg tattccatgg tttattaaaa ctgcatttat aaatggatca 1320
 gtcctgcag aagtaaacag cagaggacta acttacataa ccatctctct caacatttca 1380
 attatttttc ttttttttagc agttcacttc aatggctgga aactagacag aaagttggga 1440
 atagtctgcc tattatcata cttggggctt gctacattat cagttctata tgaacttgga 1500
 attattggaa ataataaaat aaggggctgt ggaggtacag agacatccca ggctgcacca 1560
 gcatagttag cggccgc 1577

<210> 17
 <211> 519
 <212> PRT
 <213> Artificial Sequence

<220>

<223> myc and id4 tagged human nckx5

<400> 17

Met Gln Thr Lys Gly Gly Gln Thr Trp Ala Arg Arg Ala Leu Leu Leu
1 5 10 15

Gly Ile Leu Trp Ala Thr Ala His Leu Pro Leu Ser Gly Thr Ser Leu
20 25 30

Pro Gln Arg Leu Pro Arg Ala Thr Gly Asn Ser Thr Gln Cys Val Ile
35 40 45

Ser Pro Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Glu Phe
50 55 60

Pro Glu Gly Phe Phe Thr Arg Gln Glu Arg Arg Asp Gly Gly Ile Ile
65 70 75 80

Ile Tyr Phe Leu Ile Ile Val Tyr Met Phe Met Ala Ile Ser Ile Val
85 90 95

Cys Asp Glu Tyr Phe Leu Pro Ser Leu Glu Ile Ile Ser Glu Ser Leu
100 105 110

Gly Leu Ser Gln Asp Val Ala Gly Ala Thr Phe Met Ala Ala Gly Ser
115 120 125

Ser Ala Pro Glu Leu Val Thr Ala Phe Leu Gly Val Phe Ile Thr Lys
130 135 140

Gly Asp Ile Gly Ile Ser Thr Ile Leu Gly Ser Ala Ile Tyr Asn Leu
145 150 155 160

Leu Gly Ile Cys Ala Ala Cys Gly Leu Leu Ser Asn Thr Val Ser Thr
165 170 175

Leu Ser Cys Trp Pro Leu Phe Arg Asp Cys Ala Ala Tyr Thr Ile Ser
180 185 190

Ala Ala Ala Val Leu Gly Ile Ile Tyr Asp Asn Gln Val Tyr Trp Tyr
195 200 205

Glu Gly Ala Leu Leu Leu Leu Ile Tyr Gly Leu Tyr Val Leu Val Leu
210 215 220

Cys Phe Asp Ile Lys Ile Asn Gln Tyr Ile Ile Lys Lys Cys Ser Pro
225 230 235 240

Cys Cys Ala Cys Leu Ala Lys Ala Met Glu Arg Ser Glu Gln Gln Pro
245 250 255

Leu Met Gly Trp Glu Asp Glu Gly Gln Pro Phe Ile Arg Arg Gln Ser
260 265 270

Arg Thr Asp Ser Gly Ile Phe Tyr Glu Asp Ser Gly Tyr Ser Gln Leu
275 280 285

Ser Ile Ser Leu His Gly Leu Ser Gln Val Ser Glu Asp Pro Pro Ser
290 295 300

Val Phe Asn Met Pro Glu Ala Asp Leu Lys Arg Ile Phe Trp Val Leu
305 310 315 320

Ser Leu Pro Ile Ile Thr Leu Leu Phe Leu Thr Thr Pro Asp Cys Arg
325 330 335

Lys Lys Phe Trp Lys Asn Tyr Phe Val Ile Thr Phe Phe Met Ser Ala
340 345 350

Ile Trp Ile Ser Ala Phe Thr Tyr Ile Leu Val Trp Met Val Thr Ile
355 360 365

Thr Gly Glu Thr Leu Glu Ile Pro Asp Thr Val Met Gly Leu Thr Leu
370 375 380

Leu Ala Ala Gly Thr Ser Ile Pro Asp Thr Ile Ala Ser Val Leu Val
385 390 395 400

Ala Arg Lys Gly Lys Gly Asp Met Ala Met Ser Asn Ile Val Gly Ser
405 410 415

Asn Val Phe Asp Met Leu Cys Leu Gly Ile Pro Trp Phe Ile Lys Thr
420 425 430

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

Thr Tyr Ile Thr Ile Ser Leu Asn Ile Ser Ile Ile Phe Leu Phe Leu
450 455 460

Ala Val His Phe Asn Gly Trp Lys Leu Asp Arg Lys Leu Gly Ile Val
465 470 475 480

Cys Leu Leu Ser Tyr Leu Gly Leu Ala Thr Leu Ser Val Leu Tyr Glu
485 490 495

Leu Gly Ile Ile Gly Asn Asn Lys Ile Arg Gly Cys Gly Gly Thr Glu
500 505 510

Thr Ser Gln Val Ala Pro Ala
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gtcttaggcc ttttcatggg tctggtagcc attagcactg tctcattttc aatcagtgcc 180
ttttctgaga cagatacaca gagcacagga gaggccagtg ttgtaagtgg ccctagggta 240
gcacagggtt accatgaaca aaagctgatc agcgaagaag atctgggtta ccatcagaga 300
actctcttag atttaaatga caagattctg gattatactc cacagccacc tcttttctaag 360
gaaggcgagt ctgagaatag tacagatcac gcccaagaat tccccgaagg gtttttcacg 420
agacaggagc gcagagatgg aggcatacata atctattttc taattatcgt ttacatgttc 480
atggccatat ctattgtctg tgatgaatac ttctaccct ccttggaat catcagtga 540
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cctgaattag ttactgcttt cctaggtgta tttatcacaa agggagatat tggcattagc 660
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aaccaatata ttataaagaa atgcagtcct tgctgcgcct gtcttgccaa agctatggag 960
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caatcaagaa ctgatagtgg aatattttat gaagattctg gctactctca gctctctata 1080
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20 25 30

Lys Leu Lys Leu Ile Arg Val Leu Gly Leu Phe Met Gly Leu Val Ala
35 40 45

Ile Ser Thr Val Ser Phe Ser Ile Ser Ala Phe Ser Glu Thr Asp Thr
50 55 60

Gln Ser Thr Gly Glu Ala Ser Val Val Ser Gly Pro Arg Val Ala Gln
65 70 75 80

Gly Tyr His Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Tyr His
85 90 95

Gln Arg Thr Leu Leu Asp Leu Asn Asp Lys Ile Leu Asp Tyr Thr Pro
100 105 110

Gln Pro Pro Leu Ser Lys Glu Gly Glu Ser Glu Asn Ser Thr Asp His
115 120 125

Ala Gln Glu Phe Pro Glu Gly Phe Phe Thr Arg Gln Glu Arg Arg Asp
130 135 140

Gly Gly Ile Ile Ile Tyr Phe Leu Ile Ile Val Tyr Met Phe Met Ala
145 150 155 160

Ile Ser Ile Val Cys Asp Glu Tyr Phe Leu Pro Ser Leu Glu Ile Ile

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Ala	Ala	Gly	Ser	Ser	Ala	Pro	Glu	Leu	Val	Thr	Ala	Phe	Leu	Gly	Val				
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Phe	Ile	Thr	Lys	Gly	Asp	Ile	Gly	Ile	Ser	Thr	Ile	Leu	Gly	Ser	Ala				
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Phe	Trp	Val	Leu	Ser	Leu	Pro	Ile	Ile	Thr	Leu	Leu	Phe	Leu	Thr	Thr				
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				405					410					415					
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Ser	Val	Leu	Val	Ala	Arg	Lys	Gly	Lys	Gly	Asp	Met	Ala	Met	Ser	Asn				
465					470					475					480				
Ile	Val	Gly	Ser	Asn	Val	Phe	Asp	Met	Leu	Cys	Leu	Gly	Ile	Pro	Trp				
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Phe Ile Lys Thr Ala Phe Ile Asn Gly Ser Ala Pro Ala Glu Val Asn
500 505 510

Ser Arg Gly Leu Thr Tyr Ile Thr Ile Ser Leu Asn Ile Ser Ile Ile
515 520 525

Phe Leu Phe Leu Ala Val His Phe Asn Gly Trp Lys Leu Asp Arg Lys
530 535 540

Leu Gly Ile Val Cys Leu Leu Ser Tyr Leu Gly Leu Ala Thr Leu Ser
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Val Leu Tyr Glu Leu Gly Ile Ile Gly Asn Asn Lys Ile Arg Gly Cys
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gcacagggtt accatgaaca aaagctgata agcgaagaag atctgggtta ccatcagaga 300
actctcttag atttaaataa caagattctg gattatactc cacagccacc tctttctaag 360
gaaggcgagt ctgagaatag tacagatcac gcccaagaat tccccgaagg gtttttcacg 420
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cctgaattag ttactgcttt cctaggtgta tttatcacaa agggagatat tggcattagc 660
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Lys Leu Lys Leu Ile Arg Val Leu Gly Leu Phe Met Gly Leu Val Ala
35 40 45

Ile Ser Thr Val Ser Phe Ser Ile Ser Ala Phe Ser Glu Thr Asp Thr
50 55 60

Gln Ser Thr Gly Glu Ala Ser Val Val Ser Gly Pro Arg Val Ala Gln
65 70 75 80

Gly Tyr His Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Tyr His
85 90 95

Gln Arg Thr Leu Leu Asp Leu Asn Asp Lys Ile Leu Asp Tyr Thr Pro
100 105 110

Gln Pro Pro Leu Ser Lys Glu Gly Glu Ser Glu Asn Ser Thr Asp His
115 120 125

Ala Gln Glu Phe Pro Glu Gly Phe Phe Thr Arg Gln Glu Arg Arg Asp
130 135 140

Gly Gly Ile Ile Ile Tyr Phe Leu Ile Ile Val Tyr Met Phe Met Ala
145 150 155 160

Ile Ser Ile Val Cys Asp Glu Tyr Phe Leu Pro Ser Leu Glu Ile Ile
165 170 175

Ser Glu Ser Leu Gly Leu Ser Gln Asp Val Ala Gly Ala Thr Phe Met
180 185 190

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

Phe Ile Thr Lys Gly Asp Ile Gly Ile Ser Thr Ile Leu Gly Ser Ala
210 215 220

Ile Tyr Asn Leu Leu Gly Ile Cys Ala Ala Cys Gly Leu Leu Ser Asn
225 230 235 240

Thr Val Ser Thr Leu Ser Cys Trp Pro Leu Phe Arg Asp Cys Ala Ala
245 250 255

Tyr Thr Ile Ser Ala Ala Ala Val Leu Gly Ile Ile Tyr Asp Asn Gln
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