Supporting Information

Okuda and Tokuda 10.1073/pnas.0900896106

SI Text

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Construction of *E. coli* KTA2(DE3) and KT60. KTA2 (JE5506 $\Delta lolA::kan$) harboring pKT011 (*lolA* temperature-sensitive replicon) was constructed like KT6 (JE5506 $\Delta lolB::kan$ pKT021)

 Tanaka K, Narita S, Matsuyama S, Tokuda H (2001) Deletion of *lolB*, encoding an outer membrane lipoprotein, is lethal for *Escherichia coli* and causes accumulation of lipoprotein localization intermediates in the periplasm. *J Bacteriol* 183:6538–6542. (1), and then lysogenized with lambda DE3, using a kit (Novagen) to construct KTA2(DE3). KT60 (JE5506 $\Delta lolB::kan$) is a strain that was derived from KT6 by curing pKT021 and always harbored a plasmid carrying a functional LolB derivative.

 Osborn MJ, Munson R (1974) Separation of the inner (cytoplasmic) and outer membranes of gram-negative bacteria. *Methods Enzymol* 62:642–653.



Fig. 51. LolA and mLolB derivatives containing pBPA are functional. (*A*) KTA2(DE3) cells harboring pKT011, which was constructed by inserting the *lolA* gene into pMAN997 (1) carrying a temperature-sensitive replicon, were transformed with pS51-Xamber and pSup-BpaRS-6TRN(D286R). (*B*) KT60(DE3) cells harboring pNAS021, which was constructed by inserting the *spc* gene into *bla* of pKT021 carrying a temperature-sensitive replicon and *lolB*, were transformed with pS524-Xamber and pSup-BpaRS-6TRN(D286R). (*B*) KT60(DE3) cells harboring pNAS021, which was constructed by inserting the *spc* gene into *bla* of pKT021 carrying a temperature-sensitive replicon and *lolB*, were transformed with pS524-Xamber and pSup-BpaRS-6TRN(D286R). The cells were grown on LB broth containing 10 μ M IPTG with (closed symbols) or without (open symbols) 1 mM pBPA at 42 °C to delete the temperature-sensitive plasmids for the indicated times by inoculating portions of the cultures into fresh medium. The results obtained with LolA derivatives (*A*) having amber mutations at Q33 (squares) and E144 (triangles), and those with mLolB derivatives (*B*) having amber mutations at I40 (squares) and E138 (triangles) are shown. Essentially the same pBPA-dependent growth was obtained with other derivatives except LolA derivatives having amber could not grow, and the latter, lacking only three residues, grew in the presence and absence of pBPA. As a control, growth with wild-type LolA (*A*) and mLolB (*B*) is also shown (circles).



Fig. 52. Expression of amber mutants of LoIA and mLoIB in the presence and absence of pBPA. BL21(DE3) cells harboring pSup-BpaRS-6TRN(D286R) and pSS1-Xamber encoding a LoIA derivative (*A*), which had amber mutations in place of the indicated residues, or pSS24-Xamber encoding a mLoIB derivative (*B*), which had amber mutations in place of the indicated residues, were grown at 37 °C on LB broth with or without 1 mM pBPA. The expression of LoIA-FLAG and mLoIB-His₆ derivatives was induced by the addition of 10 μ M IPTG for 2 h at the mid-log phase of growth and analyzed by SDS/PAGE and immunoblotting with anti-LoIA and anti-LoIB antibidies, respectively. Two bands were detected with derivatives having an amber mutation in the C-terminal region. Faster migrating bands represent truncated derivatives, whose translation was terminated at the amber codon and thereby they lacked FLAG-tag (*A*) or His₆-tag (*B*), too. Slower migrating bands represent derivatives having pBPA incorporated into the amber codon.



Fig. S3. Confirmation of cross-linked products generated from LolA and mLolB. Cells expressing wild-type (WT) LolA-FLAG or the LolA-FLAG derivative having pBPA in place of Q33 and mLolB-His₆ were UV-irradiated and converted into spheroplasts, as reported (2). Periplasmic fractions were obtained as spheroplast supernatants and adsorbed to a TALON affinity column. The column was then washed with 50 mM Tris-HCl (pH 7.5) containing 300 mM NaCl supplemented with imidazole. Each fraction was analyzed by SDS/PAGE and immunoblotting with anti-LolA and -LolB antibodies. i, input sample; u, unbound fraction; w, washing fraction; e1, eluate with 50 mM imidazole; e2, eluate with 100 mM imidzole.



Fig. 54. Charge distribution in LolA and mLolB molecules. The LolA (A) and mLolB (B) molecules are each shown as a ribbon model. Positive and negative residues are shown as red and yellow stick models, respectively. The structural information on LolA (11WL) and mLolB (11WM) was obtained from the RCSB protein data bank (http://pdb.protein.osaka-u.ac.jp/pdb/), and visualized with PyMOL ver.0.98 (http://pymol.sourceforge.net/index.php).

LolC: ILGLMPQAIL SSEHGSLNPQ QLPETAVKLD GVNRVAPITT GDVVLQSARS VAVGVMLGID CSVTTPKGPG KSPDSPOWRO HOODVRNLNO YOTRGAFAYI SDOOKVYAR- -FFWOOTGOD LolB: LolC: PAQKDPLTPY LVNVKQTDLE PGKYNVILGE QLASQLGVNR GDQIRVMVPS ASQFTPMG--RYRLLLTNP L---GSTELE ---LNAQPG- --NVQLVDNK GQRYTADDAE EMIGKLTGMP LolB: LolC: IPSORLFNVI GTFAANSEVD GYEMLVNIED ASRLMRYPAG NITGWRLWLD EPLKVDSLSO IPLNSLRQWI -----LGLP GDATDYKLDD QYRL--SEIT YSQNGKNWKV VYGGYDTKTQ LolB: LolC: QKLPEGSKWQ DWRDRKGELF QAVRMEK LolB: PAMPANMELT DGGQR-IKLK MDNWIVK

Fig. S5. Sequence alignment of LolB and the periplasmic region of LolC. The sequence of the I59-K264 region of LolC was compared with the sequence of LolB using GENETYX ver. 6 (GENETYX). These sequences were found to be 18.8% identical. Identical residues are indicated in red.

Table S1. Construction of pSS24 encoding mLolB-His₆

Primer Sequence (5'-3')
pSS24-F CATGCCATGGCCTCCGTTACCACGCCCAAAGGTCCT

pSS24-F CATGCCATGGCCTCCGTTACCACGCCCAAAGGTCCT pSS24-R CCGCTCGAGTTTCACTATCCAGTTATCCATTTT

Bold letters indicate restriction sites. F, forward; R, reverse.

PNAS PNAS

Table S2. Amber mutants of LolA

PNAS PNAS

Mutated		
residue	Primer	Sequence (5'-3')
F20	F	AGCTTCCACGCCAGC TAG ACACAAAAAGTGACT
120	R	AGTCACTTTTTGTGT CTA GCTGGCGTGGAAGCT
V24	F	ΑGCTTCACACAAAAA TAG ACTGACGGTAGCGGC
V 2-7	R	GCCGCTACCGTCAGTCTAGTCTAGTCGAGGCTAGCGGCC
Q33	F	
	R	
W40	F	GGTCAGGGCGATCTG TAG GTGAAACGTCCAAAC
	R	GTTTGGACGTTTCACCTACAGATCGCCCTGACC
R/13	F	GATCTGTGGGTGAAA TAG CCAAACTTATTCAAC
145	R	GTIGAATAAGTTIGG CTA TTICACCCACAGATC
D55	5	
033	Г	
1 50	г. Г	
L59	г	
KCA	ĸ	
K64	F	
	к	AIAGAACCACAGIGICIAAACCGICAGAAACCAG
W67	F	GACGGIAAAACACIGTAGIICIAIAACCCGIIC
	R	GAACGGGTTATAGAACTACAGTGTTTTACCGTC
F72	F	TGGTTCTATAACCCG TAG GTTGAGCAAGCTACG
	R	CGTAGCTTGCTCAAC CTA CGGGTTATAGAACCA
F90	F	ACCGGTAATACGCCG TAG ATGCTGATTGCCCGC
	R	GCGGGCAATCAGCAT CTA CGGCGTATTACCGGT
193	F	ACGCCGTTTATGCTG TAG GCCCGCAACCAGTCC
	R	GGACTGGTTGCGGGC CTA CAGCATAAACGGCGT
S99	F	GCCCGCAACCAGTCC TAG GACTGGCAGCAGTAC
	R	GTACTGCTGCCAGTC CTA GGACTGGTTGCGGGC
V114	F	AATGGCGATGACTTT TAG CTGACGCCGAAAGCC
	R	GGCTTTCGGCGTCAG CTA AAAGTCATCGCCATT
K118	F	TTTGTCCTGACGCCG TAG GCCAGCAATGGCAAT
	R	ATTGCCATTGCTGGC CTA CGGCGTCAGGACAAA
F127	F	GGCAATCTGAAGCAG TAG ACCATTAACGTGGGA
	R	TCCCACGTTAATGGT CTA CTGCTTCAGATTGCC
R133	F	ACCATTAACGTGGGA TAG GATGGCACAATCCAT
	R	ATGGATTGTGCCATC CTA TCCCACGTTAATGGT
E144	F	CAGTTTAGCGCGGTG TAG CAGGACGATCAGCGC
	R	GCGCTGATCGTCCTG CTA CACCGCGCTAAACTG
R149	F	GAGCAGGACGATCAG TAG AGCAGTTATCAACTG
	R	CAGTTGATAACTGCT CTA CTGATCGTCCTGCTC
K155	F	AGCAGTTATCAACTG TAG TCCCAGCAAAATGGG
	R	CCCATTTTGCTGGGACTACAGTTGATAACTGCT
A165	F	GGGGCTGTGGATGCA TAG AAATTTACCTTCACC
,,,,,,,	R	GGTGAAGGTAAATTT CTA TGCATCCACAGCCCC
Q173	F	
	R	
T176	F	
	R	
0180	r.	
Q180	г р	
	ĸ	GICCICGAGCITACGCIAATCATCIACCGIGAC

The amber codon replaced the codons in bold letters. F, forward; R, reverse.

Table S3. Amber mutants of mLolB

PNAS PNAS

S12FAAAGGTCCTGGCAAATAGCCGGATTCGCCACAARTTGTGGCGAATCCGGCTATTGCCAAGAGACGTCGCCACTTQ22FCAATGCGCCGCGCGCGTTGCTAATGCTGACGCCATTGQ32FAATGTCAATCAGTATTAGCACGCGCGCGCGCGCGCGCGCG	Mutated residue	Primer	Sequence (5′-3′)
312 F AAAGUTCET GUADATA RECOGGATA COGGENERTITIS CCAGGACCTTT Q22 F CAATGGCGATCCGGCTTTGCTATGCTGAGGCGCAGTT Q32 F AATGTCAGTATTAGACTCGCGGGGGCGCAGTT Q32 F AATGTCAGTATTAGACTCGCGGGGGCGCGGTT Q32 F AATGTAATCAGGATTAGACTCGCGGGGGGGGGGGGGGGG	c12	E	
Q22FCAATGGCGATCAGCATTAGCAAGACGTGCGCAATQ32FAATCTTAATCAGTATTAGCAAGACGTGCGCCAATGQ32FAATCTTAATCAGTATTAGCATGCGCGGCGCGCGGCGCGTTGQ32FCACGCGCCGCGAGTCTAATACTGATTAAGATTG35FCAGTATCAGACTCGCTAGTAATACTGATTAAGATTG35FCGCGGCGCTTCGCTTAGATTTCTGACCAACAARAATATAAGCGAACGCCTAGCGAGTCTGATACTGY39FCGCGGCGTTCGCTTAGATTTCTGACCAACAAAAARTTGTTGGTCAGAAATCTAAGCGAACGCGCCGCGI40FGGCGCGTTCGCTTATATTCTTAGCCAACAAAAAARTTTTGTTGGTCAGAACTAATAGCGAACGCGCCCD42FTTCGCTCAACAAAATGTAGCACAAAAAAGTGTACRGTACACTTTTGTTGCTAAGAATATAAGCGAAK45FATTTCTGACCAACAAAAATGTACGCCCGCGTTTTCRAAAGCGGGCGTACACCTATTGTTGGTCAGAAATV46FTCTGACCAACAAAAAATGTAGCGCCGCGCGTTTTCRGAAAAAGCGGGCGTACACTATTTGTTGGTCAGAAATV46FTCTGACCAACAAAAATGGCGACAACCGGCCAGARGTGCCCCAGCAAAAACTAGGCGTACACTTTTGW52FTACCGCCGCTTTGCTAGAAACCGGCCAGAACGGAARCTGGCCCGATTGCTGCTGTAGAAAACCGGGCCAARCTGGCCCAATGGGTTCTAGAACACCATAAAGGCGGCAAACRCGGCTGCACGTGAACCTGTAGGCTGAATGCTCAACCGRGGTAACGTGCAGTTAAGGTAACGGCCCAGTGCGN76FACCGTGAACGTCGAGTTAGGCTAACGGCTGAACCGCGTAACCRGGTGAACGTGCAGTTAGCTAACGGCCAAGGCGAAACCGGTRGGTGACGTGCAGTTAGCTAACGGCCCAGGTGGATTACCN76FACGGTGACGTGCAGTTGGTTAGGCCAAGGCGGTAACCRCGGCGGCGTTGCTGAGAGCATAAAAGGCGGCGTAACC<	312	F D	
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D42FTITGGTTATATTICTTAGCAACAAAAAGTGTACD42FTITGGTTATATTICTTAGCAACAAAAAAGTGTACRGTACACTTTTTGTGCTAAGAATATAAAGCGAAK45FATTTCTGACCAACAACAATAGGTGTACGCCCGCTTTRAAAGCGGGCGTACACCTATTGTTGGTCAGAAATV46FTCTGACCAACAAAAATAGTACGCCCGCTTTTCRGAAAAAGCGGACGTACACTATTTTGTGGTCAGAAATV46FTCTGACCAACAAAAATAGTACGCCCGCGTTTTCR49FCAAAAAGTGTACGCCTAGTTTTTGTGGTCAGAAAR49FCAAAAAGTGTACGCCTAGTTTTTGTGGCAGCAGARTTGCTGCCAGAAAAACTAGGCGACACCTTGGCAGCAARCTGGCCGGTTTGCTGCTAGAAAAACCGGCGCAGARCTGGCCGGTTTGCTGCTAGAAAAACCGGCGCCAGRCTGGCCCCAATGGGTTCTAGAACACCATTGGGCAGCRGCTGCCCCAATGGGTTCAGAGCAGAGAGGTAE74FGGCAGCACGGAACTGTAGCTGAAGCAGAACAACAACGGGCARCGGTTGAGCATTCAGGTACAGTTCCGTGCCN76FACGGTGACGTGAGCTGAAGGCTCAACCGGGTAACRGTTACCCGGTTGAGCTACAGCTCCAGTTCCGTV85FGGTAACGTGCAGTTAGTCTAGAATAAAGGTCAGCGTRACGCTGAACTTATTGCCTATAACTGCACGTTACCD86FAACGTGAACATAAAGGTCAGTAGATAACCGCCGATGACRGTCATCGGCCGATAACTAGCACGGCGGTATGCCACGTGAGGCGAAAAACTGGACGGRCCGCTCAACAGCTTGAGATTACCTACAGCCGGGGGTAACCACGCGGGCAAAAACTGGACGGGGTAACCACGCGGGGTAACCACGCGTGAGGTAACCACCGGTGGTAACCACCGGTGGTAACCACCGGTGGTAACCACCGTCGGTGAGGN144FACCATAAAACAACCTTCAGACTAAGATAAAAGGTAAATGGATAAAAGRCTTCCACCGACGGTGGTAACCACCGGTGGTAACAAGTAAAAGGGTGATAAAARCCAGAAAAACTGGATAACTGGCAAAAATGGATAAAAGGATAAATG	140	F D	
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K45FATTTCTGACCAATAGGTGTACGCCCGCTTTRAAAGCGGGCGTACAATAGGTGTACGCCCGCTTTTCRGAAAAAGCGGGCGTACACTATTGTTGGTCAGAAATV46FTCTGACCAACAAAAATAGTACGCCGCTTTTCRGAAAAAGCGGGCGTACTATTTTTGTTGGTCAGAR49FCAAAAAGTGTACGCCTAGTTTTTCTGGCAGCAARTTGCTGCCAGAAAAACTAGGCGTACACTTTTGW52FTACGCCGGTTTGCTGCTAGAAAAACCGGCGGCGTAT65FTACCGCCGGTTTGCTGCTCTAGAAAAAGCGGGCGGTAT65FTACCGCCGGTTGCTCTAGAAAAAGCGGGCGGTAE74FGGCAGCACGGAACTGTAGCTCAAGTCCAGCGGGCGTARCGGTTGAGCACGGACGTAGCTCCAGGTCCCAGCTGCCN76FACGGGACTGGAGCTGTAGGCTCAACCGGTAACRGTAACGTGCAGTTATGGACAATAAAGGTCAGGRCTGACCTTTATTGTCCTATAACTGCACGTTACCD86FAACGTGCAGTTATAGGACAATAAAGGTCAGCGTRRGTCATCGGCGGTATACTACTGCACGTTAACTGCACGTTR91FGACAATAAAAGTCACTGTAGAGTGAGTATACCGCCGATGACRRCCGCTCAACAGCTTGTAGCAGTGAGATTTAGGCGGGGE138FCAGTACCGCCTGAGCTAGAGTACTGACGCGGGAACTGN144FATTACCTACAGCCAGTAGGGGGTATACTACGGCGGTAATGGTN144FACCATAAAACAACCTTCAGGCTGTAAGGTAATW148FCAGAATGGCAAAAACTGGAAGACACCCCTGAGGTGTATGGCAAAAACTGGAAGGRTTTAACTTGATGGCCTAACAACCTTCCAGTTQ174FCTCACCGACGGTGGTCAATGGATAACGAGCTGAGAGAAAACTGGAGGRRTTTAACTTGATGGCCAAAAACTGGATAAACTGGRCCAGACGGCGGCGCACAAAAACTGGATAAACTGGGTGAGAAAATGGATAAACTGGRRCCAGACGGCGTGACAAAAACTGGATAAACTGGGTGAGAAAATGGATAAACTGGG	D42	D	GTACACTITITETTECTCCTAACAAAAAAAAAAAAAAAAAA
N+3FATTREGACCAACAATAGGTGTACGCCCGCTTTRAAAGCGGGCGTACACCTATTGTTGTGGTCAGAAATV46FTCTGACCAACAAAATAGTACGCCCGCTTTTTCRGAAAAAGCGGCGGCGTACTACTTTTTGTGGTCAGAR49FCAAAAAGTGTACGCCTAGTTTTTCTGGCAGCACAARTTGCTGCCAGAAAAACTAGGCGTACACTTTTGW52FTACGCCCGGTTTGCTGCTAGAAAAAGCGGGCGTAT65FTACCGTCTGCTGCTCTAGAAAAAGCGGGCGGARGCTGCCCAATGGGTTCTAGAACCAGAACGGGCGGAE74FGGCAGCACGGAACTGTAGCTGAAGCTCAACCGGRCGGTTGAGCATTCAGCTACAGTTCCGTGCCN76FACGGTGAGCATTGAGCCTACAGCTCCAGTTCCGTV85FGGTAACGTGCAGTTATAGGACAATAAAGGTCAGRCTGACCTTTATTGTCCTATAACTGCACGTTACCD86FAACGTGCAGTTAAGTCAACTGCACGTTACGCGCGATGACRGTCACCGCGCTAACGTGCAGTTATACGCCGCGATGACRGTCATCGGCGGTATACTACTGCACGTTACGCGGTR91FGACAATAAAGGTCAGTAGTATACCGCCGATGACRCCGCTCAACAGCTTGTAGCAGTGAGACTTTATGTCR115FCCGCTCAACAGCTTGTAGGAAAAACTGGACGGE138FCAGTACCGCCTGAGCTAGATTACCTACAGGCGGTACTGN144FATTACCTACAGCCAGTAGGGCAAAAACCTGGAAGARCTTCCAGGAAGGTTGTTTAGGGTGAGGTAATGGTN148FCACATAAACAACCTTCAGTTTAGGCGCATCAAGTAAAAARCTTCACGGCAGCAGCAGCAGCAGCAAAACCTGCAGTGAGR175FACCGACGGTGCAATAACAGCCTTCAGTTAAAAAARTTTTAACTTGATCGACCACCGTCGGGTAAAAATGGAAAAATGGR175F </td <td>V/F</td> <td></td> <td></td>	V/F		
V46FTCTGACCAACAAAATAGTACGCCCGGTTTTTCRGAAAAAGCGGGCGTACTACTATTTTTGTTGGTCAGAR49FCAAAAAGTGTACGCCTAGTTTTTCTGGCAGCAARTTGCTGCCAGAAAAACTAGGCGTACACTTTTGW52FTACGCCCGGTTTGCTGCTAGAAAAAGCGGGCGGARCTGGCCGGTTTGCTGCTAGAAAAAGCGGGCGGCAGRCTGGCCGGTTGCTCTAGAAAAAGCGGGCGGCAGRGCTGCCCAATGGGTTCTAGAACCCATTGGGCAGCRGCTGCCCAATGGGTTCTAGAACACCGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	K4J	F D	
V40FICIGACCAACAAAAATAGTAGGCCCCCCCCCTGTTTTTCRGAAAAAGCGGGCGTACTATTTTTGTGGCAGCAAR49FCAAAAAGTGGCAGCTAGTTTTTCTGGCAGCAGAARTTGCTGCCAGAAAAAACTAGGCGTACCACTTTTGW52FTACGCCCGCTTTTCTAGCAGCAAACCGGCCAGRCTGGCCGGTTTGCTGCTAGAAAAAGCGGGCGCAAT65FTACCGTCGCCAATGGGTTCTAGAACCCATTGGGCAGCARGCTGCCCAATGGGTTCTAGAACCCAGTAGCTGAACGGCAGCAGACGGTAE74FGGCAGCACGGAACTGTAGCTGAAGCTGCAACCGRCGGTTGAGCATTCAGCTACAGTCACAGGCTGCAACCGN76FACGGACTGGAGCTGTAGGCCCAACAGGTAACRGTAACCGGCGAGTTATAGGACAATAAAGGTCAGRGTAACGTGCAGTTATGGACCATACCGGTAACCD86FAACGTGCAGTTAGTCTAGAATAAAGGTCAGCGTRACGCTGAACTGTAGCAGTAGACCGCGATGACRGTCATCGGCGGTATACTACTGCACCGTGTAGCGGGTATACTACCGCCGATGACRGTCATCGGCGGTATACTACTGCACGTGTGAGCGGE138FCCGCTCAACAGCTGGTAGGCGAAAAACTGGAAGGRCTGCCGTAGGTAATCTAGCTCAGGCGGTACTGN144FATTACCTACAGCCAGTAGGGCAAAAACTGGAAAGRCTTCCAGTTTTGCCCTCACTGGCTGTAGGTAATGGTY152FAACTGGAAGGTTGTTTAGGGCAAAAACCGTCCAGTTQ174FCCCACCGCCGGCGCACAACAACCCTCCAGTTAAAARTTTTAACTTGATCGACCACCGTCGGGTAAAAATGGAAAATGGAAAARTTTTAACTTGATCGACACACCGTCGGTGAGR175FACCGACGGTCAATAGAGAAAAGGATAAAAAGGATAAATGGRCCAGTTATCCATTATGACCACCGTCGGGTL178FGTCAACGCATCAAGTAGAGAAAACTGGAAAAA	1/46		
R49FCAAAAAGCGGGGGTACGCTAGTITTTGTGGCAGCAAR49FCAAAAAGCGGGCTAGGTTTTGTGGGCAGCAARTTGCTGCCCAGAAAAACTAGGCGTACACTTTTGW52FTACGCCCGGTTTTGCTGGCAGAAAAAGCGGGCGAGARCTGGCCGGTTTGCTGCTGCTAGAAAAAGCGGGCGGAAT65FTACCGTCTGCTGCTCTAGAACCCATTGGGCAGCRGCTGCCCAATGGGTTCTAGAACCCATTGGGCAGCGAACGGTAE74FGGCAGCACGGAACTGTAGGCTGAAGGCTCAACCGGRCGGTTGAGCATTCAGCTACAGTTCCGTGCCN76FACGGAACTGGAGCTGTAGGCTCAACCGGGTAACCRGTTACCCGGTTGAGCCTACAGCTCCAGTTCCGTV85FGGTAACGTGCAGTTATAGGACAATAAAGGTCAGGRCTGACCTTTATTGTCCTATAAGCACAGTATACCD86FAACGTGCAGTTAGTATAGGACAATAAAGGTCAGCGTR91FGACAATAAAGGTCAGTAGTATACCGCCGATGACRGTCATCGGCGGTATACTACTGACGTGGAGTTTATGTCR115FCCGCTCAACAGCTTGTAGCAGTGGAATTTAGGTR114FATTACCTACAGCCAGGAGCTAGAAAACTGGAAGGRCTGGCTGTAAGGCAAAAACTAGAGGTGATGGAAATW148FCAGAATGGCAAAAACTAGAAGGTTGTTAGACACCRGGTGTCATAACCACCCTTAAGGTAATGGAAAARTTTTAACTTGATGGCGCAAAAACTGGTAAAQ174FCTCACCGACGGTGGTTAGGCCAACAACCTTCCAGTTR175FACCGACGGAGCACAAGACTAGAAAACGGGTGGTTAAAAAACTGGGTAGARCATTTTAACTTGATCTAATGACCACCGCTGGGTL178FGGTCAACGCATCAAGTAGAAAATGGATAACTGGRCCAGTTATCCATTTGACCACGGTTGACGCTTGACGCTGGGTL178FGGTCAACGCATCAAGTAGAAAATGGATAACTGG	V40	F D	
N45FCAAAAAGIGTACGCCTAGTTITICTGCAGCAGAAARTTGCTGCCGCCCCAGAAAAACTAGGCGTACACTTTTGW52FTACGCCCGCTTTGCTGCTAGAAAAAGCGGCGCAGRCTGGCCGGTTTGCTGCTAGAAAAAGCGGCGCGTAT65FTACCGTCTGCTGCTGCTAGAAAAAGCGGCAGCAGAE74FGGCAGCACGGAACTGTAGGCTGAAGCCCAACCGGRCGGTTGAGCATTCAGCTACAGTTCCGTGCTGCCN76FACGGAACTGGAGCTGTAGGCTCAACCGGGTAACRGTTACCCGGTTGAGCCTACAGCTCCAGTTCCGTV85FGGTAACGTGCAGTTATAGGACAATAAAGGTCAGGRCTGACCTTTATTGTCTAGAATAAAGGTCAGCGTN86FAACGTGCAGTTAGTCTAGAATAAAGGTCAGCGTR91FGACAATAAAGGTCAGTAGTATACCGCCGAGTACCRGTCATCGGCGGTAACTGACAGTGAGACTATGACGCGGGR115FCCGCTCAACAGCTTGTAGCAGTGGATTTAGGTR115FCCGCTCAACAGCCTGAGCTAGAGTGAGCAGGGGB138FCAGTACCGCCTGAGCTAGGAAAAACTGGAAGGRCTTCCAGTTTTTGCCCTACGGCGGTAACTGN144FATTACCTACAGCCAGTAGGGCAAAAACTGGAAGRCTTCCAGTTTTTGCCCTACTGGCTGTAGGTAATW148FCAGAATGGCAAAAACTAGAAGGTTGTTTATGGTR152FAACTGGAAGGTGGTTAGGGCAAAAACTGGAAGRCTTCCAGTTTTTGCCCTACTGGCTGTAGGTAATW148FCAGAATGGCAAAAACTAGAACAACCTTCCAGTTQ174FCTCACCGACGGTGGTTAGGCCATCAAGTTAAAAAARTTTTAACTTGATCGATCAGTAGAAAATGGATAAAAAGGTAAAATGGATRACTTTTAACTTGATCAATGAACAACCTCCCGTCGGTL178FGGTCAACGCATCAAGTAGAAAATGGATAACAGGTTAAACTGGGRCCAGTTATCCATTGACACCACCGTCGGTTAACGGCTGACACGGTGGTTAACCGGCTG	P/0	r.	
W52FTACGCCCCGCTTTTTCTAGCAGCAAACCGGCCAGW52FTACGCCCGCTTTTGCTGCTAGAAAAAGCGGCAGCAGT65FTACCGTCTGCTGCTGCTAGAAAAAGCGGCAGCAGT65FTACCGTCTGCTGCTCTAGAACCCATTGGGCAGCRGCTGCCCAATGGGTTCTAGAACCCATTGGGCAGCAGCAGACGGTAE74FGGCAGCACGGAACTGTAGCTGAAGTCCGAGCGGCAACCGRCCGGTTGAGCCTTACAGCTCCAGTGCCGN76FACGGAACTGGAGCCTACAGCTCCAGTTCCGTV85FGGTAACGTGCAGTTATAGGACAATAAAGGTCAGRCTGACCTTTATTGTCCTATAACTGCACGTTACCD86FAACGTGCAGTTAGTCTAGAATAAAGGTCAGCGTRACGCTGACCTTTATTGTCAGAATAAAGGTCAGCGTR91FGACAATAAAGGTCAGTAGTATACCGCCGATGACRGTCATCGGCGGTATACTACTGACAGTGGATTTTAGGTR115FCCGCTCAACAGCTTGTAGCAGTGGATTTTAGGTR114FATTACCTACAGCCAGTAGGGCAAAAACTGGAAGN144FATTACCTACAGCCAGTAGGGCAAAAACTGGAAGRCTTGCATGGAGGTAATTAGGTCTAGAAGGTTGTTTATGGTN148FCAGAATGGCAAAAACTAGAAGGTTGTTTATGGTN148FCAGAATGGCAAAAACTAGAAGGTTGTTATGGTN144FATTACCTACAGCCAGTAGGGGCAAAAACTGGAAGRCTTCCAGTGGTGAGGTAATGAACACCTTCCAGTTGTGN148FCAGAATGGAAGGTTGTTTAGGGTGGTTATGACACCRGGTGTCATAACCACCCTCAAACAACCTTCCAGTTQ174FCTCACCGACGGTGAACAACACCCTCAAGTTAAAAAAAGRCTTTTAACTTGATGAACAACAACAACCACCGTCGGTGAGR175FACCGACGGTCAATCAAGTCAAGATAAAAAGGATAAACTGGRCCAGTTATCCATCAAGAAAACGGATAAAACGGTGGTTAAACACGGTGGTL178FGGTC	N49	F D	
W32FTACGCCCGCTTTTCTAGAACCAAAAGCGGGCCGTARCTGGCCGGTTTGCTGCTAGAAAAAGCGGGGGGCAGCRGCTGCCCAATGGGTTCTAGAACCCATTGGGCAGCE74FGGCAGCACGGAACTGTAGCTGAATGCTCAACCGRCGGTTGAGCATTCAGCTACAGTTCCGTGCTGACCN76FACGGAACTGGAGCTGTAGGCTCAACCGGGTAACRGTTACCGGTTGAGCCTACAGCTCCAGTTCCGTV85FGGTAACGTGCAGTTATAGGACAATAAAGGTCAGGRCTGACCTTTATTGTCCTATAACTGCACGTTACCD86FAACGTGCAGTTAATGCTAGACTAACTGCACGTTR91FGACAATAAAGGTCAGCTGTAGACTAACTGCACGTTR115FCCGCTCAACAGCTTGTAGCAGTGGATTTTAGGTRACCTAAAATCCACTGCTACAGCGGGATACTGN144FATTACCTACAGCCAGTAGGCAAAAACTGGAAGGRCTTCCAGTTTTTGCCCTACAGGCGGTACTGN144FACTGAAAGGTGATATTAGGTAGCAGTGGTGAGGAAATW148FCAGAATGGCAAAAACCTTGAGAGGGGAAAAACTGGAAGRCCTTCCAGGCGGTGTTGTTGGGGTGATGGTAATW148FCAGAATGGCAAAAACCTTCTGGCTGTAGGTAATW148FCAGAATGGCAAAAACCACCCTAAACAACCTTCCAGTTQ174FCTCACCGACGGTGGTTAGCCCCCACAGTTAAAAAGGR175FACCGACGGTGGTCAATAGATCAAGTTAAAAATGRCATTTTAACTTGATCAATGAAAATGGATAACTGGRCCAGTTATCCATTTCTAGTTGACCACCGTCGGTL178FGGTCACACCATCAAGTAAAATGGATAACTGGRCCAGTTATCCATTTCTAGTTGACCCCGTGGTTGACC		к с	
T65FTACCGTCTGCTGCTGCTGCTAGAACAAAAGGGGGGGAGCT65FTACCGTCTGCTGCTGCTGAGAACCCATTGGGCAGCRGCTGCCCAATGGGTTCTAGAAGCCAACGGGCAGCE74FGGCAGCAGGAACTGTAGGCTGAAGCTGCAACCGRCGGTTGAGCATTCAGCTACAGTTCCGTGCCCN76FACGGAACTGGAGCTGTAGGCTCAACCGGGTAACRGTTACCCGGTTGAGCCTACAGCTCCAGTTCCGTV85FGGTAACGTGCAGTTATAGGACAATAAAGGTCAGRCTGACCTTTATTGTCCTATAACTGCACGTTACCD86FAACGTGCAGTTAGTCTAGACTAACTGCACGTTR91FGACAATAAAGGTCAGTAGTATACCGCCGATGACRGTCATCGGCGGTATACTACTGACCTTTATTGTCR115FCCGCTCAACAGCTTGTAGCAGTGGATTTTAGGTRACCTAAAATCCACTGCTACAAGCTGTGAGCGGE138FCAGTACCGCCTGAGCTAGATTACCTACAGCCAGRCTTGCCTGTAGGTAATCTAGGTCAGGCGGAAATW148FCAGAATGGCAAAAACCTGGAAGGGGAAAAACTGGAAGRCTTCCAGTTTTTGCCCTACAGGCGGTAATW148FCAGAATGGCAAAAACCTTCTGGCTGTAGGTAATW148FCAGAATGGCAAAAACCTTCTGGCTGTAGGTAATW148FCAGAATGGCAAAAACCTTCTAGAGTGAAAACCAGCTRGGTGTCATAACCACCCTAAACAACCTTCCAGTTQ174FCTCACCGACGGTGGTTAGCGCATCAAGTTAAAAATGRCATTTTAACTTGATGGCCTAACCACCGTCGGTGAGR175FACCGACGGTGGTCAATAGATCAAGTTAAAAATGRCATTTTAACTTGATCATTGACCACCGTCGGTL178FGGTCAACGCATCAAGTAAAATGGATAACTGGRCCAGTTATCCATTTCCATTGATGACCACCGTCGGTTGACCRCCAGTTATCCATTTCCATTTCACTTGATGACCCCCGATCAAGTTAACCACC	VV52	Г	
163FIACCGICIAGAGACCCATIGAGAACCCATIGAGAACCCAGCAGAACGGTARGCTGCCCAATGGGTTCTAGAGACGCAGCAGAACGGTAE74FGGCAGCAGGAACTGTAGCTGAAGCTGCAACCGRCGGTTGAGCATTCAGCTACAGCTGCAGCTGCACCGN76FACGGAACTGGAGCTGTAGGCTCAACCGGGTAACRGTTACCCGGTTGAGCCTACAGCTCCAGTTCCGTV85FGGTAACGTGCAGTTATAGGACAATAAAGGTCAGGRCTGACCTTTATTGTCCTATAACTGCACGTTACCD86FAACGTGCAGTTAGTCTAGACTAACTGCACGTTR91FGACAATAAAGGTCAGTAGTATACCGCCGATGACRGTCATCGGCGGTATACTACTGACCTTTATTGTCR115FCCGCTCAACAGCTTGTAGCAGTGGATTTTAGGTRACCTAAAATCCACTGCTACAAGCTGTTGAGCGGE138FCAGTACCGCCTGAGCTAGATTACCTACAGCCAGRCTTGCCTGTAGGTAATCTAGCTCAGGCGGTACTGN144FATTACCTACAGCCAGTAGGGCGAAAAACTGGAAGRCCTTCCAGTTTTTGCCCTACTGGCTGTAGGTAATW148FCAGAATGGCAAAAACCTTCTAGAGCAGTTGTTATGGTRACCTAAAACAACCTTCTAGAGCGGTGATATGGCATCAGRCCTTCCAGGCGGGTGTTGTGGCGTAAGAAACTGGAAAAW148FCAGAATGGCAAAAACCTTCTGGCTGTAGGTAATW148FCAGAATGGCAAAAACCTTCTAGTTTTATGGTRACCGTAAACCACCCTCAAGCACCATCAAGTTAAAAARTTTTAACTTGATGCGCTAACCACCGTCAGGTGAGR175FACCGACGGTGGTCAATAGAACAACGAGTTAAAAATGRCATTTTAACTTGATCATTGACCACCGTCGGTL178FGGTCAACGCATCAAGTAGAAAATGGATAACTGGRCCAGTTATCCATTTCTACTTGATGACCACCGTCGGTL178FGGTCAACGCATCAATTTCACTTGATGACCCC	TEE		
E74FGGCAGCACGGAACTGTAGCTGAAGCAGACAGACAGACAGA	105	F D	
L14FGGCAGCAGCAGCAACTGTAGCTGAACCGGCTAACCGRCGGTTGAGCATTCAGCTGAGCTGAAGCTCAACCGGGTAACCRGTTACCCGGTTGAGCCTACAGGCTCAACGGGTAACRGTTACCCGGTTGAGCCTACAGGCTCAACGGTCAGV85FGGTAACGTGCAGTTATGGACCAATAAAGGTCAGRCTGACCTTTATTGTCCTATAACTGCACGTTACCD86FAACGTGCAGTTAGTCTAGAATAAAGGTCAGCGTR91FGACAATAAAGGTCAGTAGCGCGATGACRGTCATCGGCGGTATACTAGCGCGCGATGACR115FCCGCTCAACAGCTTGTAGCAGGGGATTACTGACCGCGGTGAGRACCTAAAATCCACTGCTACAAGCTGTTGAGCGGE138FCAGTACCGCCTGAGCTAGATTACCTACAGCCAGRCTGGCTGTAGGTAATCTAGCTCAGGCGGATCTGN144FATTACCTACAGCCAGTAGGCGAAAAACTGGAAGRCTTCCAGTTTTGCCCTACTGGCTGTAGGTAATW148FCAGAATGGCAAAAACTAGAAGGTTGTTTAGGTRACCATAAACAACCTTCTAGTTTTGCCATTCTGY152FAACTGGAAGGTTGTTTAGGGTGGTTATGACACCRGGTGTCATAACCACCCTTAACAACCTTCCAGTTQ174FCTCCACGACGGTGGTTAGGCGCATCAAGTTAAAAR175FACCGACGGTGGTCAATGACACCCCTGAGTGAGR175FACCGACGGTGGTCAATGACAACGTTCAAGTTAAAAATGR178FGGTCAACGCATCAAGTAAAATGGATAACTGGTL178FGGTCAACGCATCAAGTAAATGGATAACTGGRCCAGTTATCCATTTCTACTTGATGCGTTGACCRCCAGTTATCCATTTCTACTTGATGCGCTTGACC	E7/		GECAGEAATGGGTTCTAGAGEAGEAGACGGTA
N76FACGGAACTGGAGCTGTAGGCTCAACGGGCTAACN76FACGGAACTGGAGCTGTAGGCTCAACGGGCACGGGTAACRGTTACCCGGTTGAGCCTACAGGCTCCAGTTGCGTV85FGGTAACGTGCAGTTATGGACCAATAAAGGTCAGRCTGACCTTTATTGTCCTATAACTGCACGTTACCD86FAACGTGCAGTTAGTCTAGAATAAAGGTCAGCGTR91FGACAATAAAGGTCAGTAGTCAACTGCACGTTR91FGACAATAAAGGTCAGTATACCGCCGATGACRGTCATCGGCGGTATACTACTGACCTTTATTGTCR115FCCGCTCAACAGCTTGTAGCAGTGGGATTTAGGTRACCTAAAATCCACTGCTACAAGCTGTTGAGCGGE138FCAGTACCGCCTGAGCTAGATTACCTACAGCCAGRCTGGCTGTAGGTAATCTAGCTCAGGCGGTACTGN144FATTACCTACAGCCAGTAGGCGAAAAACTGGAAGRCTTCCAGTTTTGCCCTACTGGCTGTAGGTAATW148FCAGAATGGCAAAAACTAGAAGGTTGTTTATGGTRACCATAAACAACCTTCTAGTTTTGCCATTCTGY152FAACTGGAAGGTTGTTTAGGGTGGTTATGACACCRGGTGTCATAACCACCCTTAACAACCTTCCAGTTQ174FCTCACCGACGGTGGTTAGGCAACAACTTCAAGTTAAAAR175FACCGACGGTGGTCAATAGAACACCTCCAGTTAAAAAACAGGTTAAAAAAGGR175FACCGACGGTGGTCAATGAAAAATGGATAAATGGATAACTGGRCCATTTTTAACTTGATCTATTGACCACCGTCGGTL178FGGTCAACGCATCAAGTAAAATGGATAACTGGRCCAGTTATCCATTTCTACTTGATGACCCC	L/4	P	CECTTEACEATTEACECTAC
N76FACGGAACTGGAGCTGTAGGCTCAAGGCTCAACGGGTACAGRGTTACCCGGTTGAGCCTACAGGCTCCAGTTCGTV85FGGTAACGTGCAGTTATGGACCAATAAAGGTCAGRCTGACCTTTATTGTCCTATAACTGCACGTTACCD86FAACGTGCAGTTAGTCTAGAATAAAGGTCAGCGTR91FGACAATAAAGGTCAGTAGTATACCGCCGATGACR115FCCGCTCAACAGCTTGTAGCAGTGGACTTTATGTCR115FCCGCTCAACAGCTTGTAGCAGTGGATTTAGGTRACCTAAAATCCACTGCTACAAGCTGTTGAGCGGE138FCAGTACCGCCTGAGCTAGATTACCTACAGCCAGRCTGGCTGTAGGTAATCTAGGTCGAGGGGACTGN144FATTACCTACAGCCAGTAGGCGAAAAACTGGAAGRCTTCCAGTTTTGCCCTACTGGCTGTAGGTAATW148FCAGAATGGCAAAAACTAGAAGGTTGTTTAGGTRACCATAAACAACCTTCTAGTTTTGCCATTCTGY152FAACTGGAAGGTTGTTTAGGGTGGTTATGACACCRGGTGTCATAACCACCCTTAACAACCATCCAGTTAGACACCRGGTGTCATAACCACCCTTAACAACCATCCAGTTAAAAR175FACCGACGGTGGTCAATAGAACAACGTTCAAGTTAAAAAGGR175FACCGACGCTGACAAGAAAATGGATAAATGGATAACTGGRCCATTTTTAACTTGATCTATTGACCACCGTCGGTL178FGGTCAACGCATCAAGTAAAATGGATAACTGGRCCAGTTATCCATTTCTACTTGATGCGCTTGACC	N76	E	
V85FGGTAACCGTGCAGTTATAGAGCCAGTATACAGGTCAGV85FGGTAACCGTGCAGTTATTGTACAGCCACATAAAGGTCAGRCTGACCTTTATTGTCCTATAACTGCACGTTACCD86FAACGTGCAGTTAGTCTAGAATAAAGGTCAGCGTR91FGACAATAAAGGTCAGTAGTATACCGCCGATGACR115FCCGCTCAACAGCTTGTAGCAGTGGATTTATGTCR115FCCGCTCAACAGCTTGTAGCAGTGGAGTTTAGGTR115FCCGCTCAACAGCTTGTAGCAGTGGGATTTAGGTRACCTAAAATCCACTGCTACAAGCTGTTGAGCGGE138FCAGTACCGCCTGAGCTAGATTACCTACAGCCAGRCTGGCTGTAGGTAATCTAGCTCAGGCGGACTGN144FATTACCTACAGCCAGTAGGCGAAAAACTGGAAGRCTTCCAGTTTTGCCCTACTGGCTGTAGGTAATW148FCAGAATGGCAAAAACTAGAAGGTTGTTTATGGTRACCATAAACAACCTTCTAGTTTTGCCATTCTGY152FAACTGGAAGGTTGTTTAGGGTGGTTATGACACCRGGTGTCATAACCACCCTTAACAACCATCCAGTTAGACACCRGGTGTCATAACCACCCTAAACAACCTTCCAGTTQ174FCTCACCGACGGTGGTCAATGACCACCGTCGGTGAGR175FACCGACGGTGGTCAATAGAATCAAGTTAAAAATGR178FGGTCAACGCATCAAGTAAAATGGATAACTGGRCCAGTTATCCATTTCAACTAGAAAATGGATAACTGGRCCAGTTATCCATTTCTACTTGATGGCGTTAACGGTTGACC	1170	R	GTTACCCGGTTGAGCCCTACCGGTTCCGT
RCTGACCTTTATTGTCCTATAACTGCACGTTACCD86FAACGTGCAGTTAGTCTAGAATAAAGGTCAGCGTRACGCTGACCTTTATTGTCAGACTAACTGCACGTTR91FGACAATAAAGGTCAGTAGTATACCGCCGATGACRGTCATCGGCGGTATACTACTGACCTTTATTGTCR115FCCGCTCAACAGCTTGTAGCAGGGGATTACTGAGCGGE138FCAGTACCGCCTGAGCTAGACTGCTACAGCCAGRCTGGCTGTAGGTAATCTACGTCAGGCGGTACTGN144FATTACCTACAGCCAGTAGGCAAAAACTGGAAGRCTTCCAGTTTTGCCCTACAGGCGGTAATW148FCAGAATGGCAAAAACTAGAAGGTTGTTATGGTRACCATAAACAACCTTCTAGTTTTGCCATTCTGY152FAACTGGAAGGTTGTTTAGGGTGGTTATGACACCRGGTGTCATAACCACCCTAAACAACCTTCCAGTTQ174FCTCCACGACGGTGGTCAATGACCACCGTGAGGTAATQ174FACCGACGGTGGTCAATAGACACCACCGTCGGTGAGR175FACCGACGGTGGTCAATAGAACAACCTTCAAGTTAAAAAR178FGGTCAACGCATCAAGTAAAAATGGATAACTGGTL178FGGTCAACGCATCAAGTAAAATGGATAACTGGRCCAGTTATCCATTTCTACTTGATGCGTTGACC	1/85	F	GTAACGTGCAGTTA TAG GACAATAAAGGTCAG
D86FAACGTGCAGTTAGTCTAGAATAAAGGTCAGCGTD86FAACGTGCAGTTAGTCTAGAATAAAGGTCAGCGTTR91FGACAATAAAGGTCAGTAGTATACCGCCGATGACRGTCATCGGCGGTATACTACTGACCTTTATTGTCR115FCCGCTCAACAGCTTGTAGCAGTGGATTTAGGTRACCTAAAAATCCACTGCTACAAGCTGTTGAGCGGE138FCAGTACCGCCTGAGCTAGATTACCTACAGCCAGRCTGGCTGTAGGTAATCTAGCTCAGGCGGTACTGN144FATTACCTACAGCCAGTAGGCAAAAACTGGAAGRCTTCCAGTTTTGCCCTACTGGCTGTAGGTAATW148FCAGAATGGCAAAAACTAGAAGGTTGTTATGGTRACCATAAACAACCTTCTAGTTTTGCCATTCTGY152FAACTGGAAGGTTGTTTAGGGTGGTTATGACACCRGGTGTCATAACCACCCTAAACAACCTTCCAGTTQ174FCTCCACGACGGTGGTCAATGACCACCGTCGGTGAGR175FACCGACGGTGGTCAATAGAACACCACCGTCGGTGAGR175FACCGACGGTGGTCAATAGAAACTAGAAAATGAAAAATGR178FGGTCAACGCATCAAGTAAAAATGGATAAATGGATAACTGGRCCATTTTAACTTGATCTATTGACCACCGTCGGTL178FGGTCAAACGCATCAAGTAAAATGGATAACTGGRCCAGTTATCCATTTCTACTTGATGCGCTTGACC	005	R	
BitAACGTIGACTITIATICTAGAATIAAACGTCACGTTR91FGACAATAAAGGTCAGTAGACTGAACTGCACGTTR91FGACAATAAAGGTCAGTAGTATACCGCCGATGACRGTCATCGGCGGTATACTACTGACCTTTATTGTCR115FCCGCTCAACAGCTTGTAGCAGTGGATTTAGGTRACCTAAAATCCACTGCTAGCAGGCGATTACCTACAGCCAGE138FCAGTACCGCCTGAGCTAGATTACCTACAGCCAGRCTGGCTGTAGGTAATCTAGCTCAGGCGGTACTGN144FATTACCTACAGCCAGTAGGCAAAAACTGGAAGRCTTCCAGTTTTGCCCTACTGGCTGTAGGTAATW148FCAGAATGGCAAAAACTAGAAGGTTGTTATGGTRACCATAAACAACCTTCTAGTTTTGCCATTCTGY152FAACTGGAAGGTTGTTTAGGGTGGTTATGACACCRGGTGTCATAACCACCCTAAACAACCTTCCAGTTQ174FCTCACCGACGGTGGTCAATGGCAACAAGTTAAAAAR175FACCGACGGTGGTCAATAGATCAAGTTAAAAATGR178FGGTCAACGCATCAAGTAAAAATGGATAACTGGATL178FGGTCAACGCATCAAGTAGAAAATGGATAACTGGRCCAGTTATCCATTTCTACTTGATGCGCTTGACC	D86	F	
R91FGACAATAAAAGGTCAGTAGTATACCGACGATGACR91FGACAATAAAAGGTCAGTAGTATACCGACGCGATGACRGTCATCGGCGGTATACTACTGACCTTTATTGTCR115FCCGCTCAACAGCTTGTAGCAGTGGATTTAGGTRACCTAAAATCCACTGCTACAAGCTGTTGAGCGGE138FCAGTACCGCCTGAGCTAGATTACCTACAGCCAGRCTGGCTGTAGGTAATCTAGCTCAGGCGGTACTGN144FATTACCTACAGCCAGTAGGCAAAAACTGGAAGRCTTCCAGTTTTGCCCTACTGGCTGTAGGTAATW148FCAGAATGGCAAAAACTAGAAGGTTGTTATGGTRACCATAAACAACCTTCTAGTTTTGCCATTCTGY152FAACTGGAAGGTTGTTTAGGGTGGTTATGACACCRGGTGTCATAACCACCCTAAACAACCTTCCAGTTQ174FCTCACCGACGGTGGTCAATGGCCAACAAGTTAAAAAR175FACCGACGGTGGTCAATAGATCAAGTTAAAAATGR178FGGTCACACGCATCAAGTAGAAAATGGATAACTGGRCCATTTTAACTTGATCTATTGACCACCGTCGGTL178FGGTCACACGATCAAGTAAAATGGATAACTGGRCCAGTTATCCATTTCTACTTGATGCGTTGACC	200	R	
R GTCATCGGCGGTATACTACTGACCCTTATTGTC R115 F CCGCTCAACAGCTTGTAGCAGTGGACTTTAGGT R ACCTAAAATCCACTGCTACAGACTGTGAGCGG E138 F CAGTACCGCCTGAGCTAGATTACCTACAGCCAG R CTGGCTGTAGGTAATCTAGGTCAGGCGGAACTG N144 F ATTACCTACAGCCAGTAGGCGAAAAACTGGAAG R CTTCCAGTTTTGCCCTACTGGCTGAGGTAAT W148 F CAGAATGGCAAAAACTAGAAGGTTGTTATGGT R ACCATAAACAACCTTCTAGTTTTGCCATTCTG Y152 F AACTGGAAGGTTGTTAGGGTGATTAGACACC R GGTGTCATAACCACCCTAAACAACCTTCCAGTT Q174 F CTCACCGACGGTGGTCAATGACAACGTTCAAGTTAAAAA R175 F ACCGACGGTGGTCAATAGATCAAGTTAAAAATG R175 F ACCGACGGTGGTCAATGACACCGTCGGTGAG R175 F GGTCACACGCATCAAGTAAAATGGATAACTGGT L178 F GGTCACACCATCAAGTAGAAAATGGATAACTGGG	R91	F	GACAATAAAGGTCAG TAG TATACCGCCGATGAC
R115FCCGCTCAACAGCTTGTAGCAGTGGATTTAGGTR115FCCGCTCAACAGCTTGTAGCAGTGGATTTAGGTRACCTAAAATCCACTGCTACAGAGCTGTTGAGCGGE138FCAGTACCGCCTGAGCTAGATTACCTACAGCCAGRCTGGCTGTAGGTAATCTAGCTCAGGCGGTACTGN144FATTACCTACAGCCAGTAGGCAAAAACTGGAAGRCTTCCAGTTTTGCCCTACTGGCTGTAGGTAATW148FCAGAATGGCAAAAACTAGAAGGTTGTTATGGTRACCATAAACAACCTTCTAGTTTTGCCATTCTGY152FAACTGGAAGGTTGTTTAGGGTGGTTATGACACCRGGTGTCATAACCACCCTAAACAACCTTCCAGTTQ174FCTCACCGACGGTGGTCAATGGCAATCAAGTTAAAAAR175FACCGACGGTGGTCAATGACCACCGTCGGTGAGR175FGGTCAACGCATCAAGTTAAAAATGRCATTTTTAACTTGATGCCAATGAAAATGGATAACTGGTL178FGGTCACACGCATCAAGTAGAAAATGGATAACTGGRCCAGTTATCCATTTCTACTTGATGCGTTGACC	NOT	R	GTCATCGGCGGTATACTACTGACCTTTATTGTC
R ACCTAAAATCCACTGCTACAAGCTGTTGAGCGG E138 F CAGTACCGCCTGAGCTAGATTACCTACAGCCAG R CTGGCTGTAGGTAATCTAGCTCAGGCGGTACTG N144 F ATTACCTACAGCCAGTAGGCAAAAACTGGAAG R CTTCCAGTTTTGCCCTACTGGCTGTAGGTAAT W148 F CAGAATGGCAAAAACTAGAAGGTTGTTATGGT R ACCATAAACAACCTTCTAGTTTTGCCATTCTG Y152 F AACTGGAAGGTTGTTTAGGGTGGTTATGACACC R GGTGTCATAACCACCCTAAACAACCTTCCAGTT Q174 F CTCACCGACGGTGGTCAATGACCACCGTCGGTGAG R175 F ACCGACGGTGGTCAATAGATCAAGTTAAAAATG R178 F GGTCACACGCATCAAGTAAAATGGATAACTGGT L178 F GGTCACACCATTTTCTACTTGATGCGCTTAACTGG	R115	F	CCGCTCAACAGCTTG TAG CAGTGGATTTTAGGT
E138 F CAGTACCGCCTGAGCTAGATTACCTACAGCCAG R CTGGCTGTAGGTAATCTAGCTCAGGCGGTACTG N144 F ATTACCTACAGCCAGTAGGCAAAAACTGGAAG R CTTCCAGTTTTGCCCTACGGCGGTACTGGCTGAGGTAAT W148 F CAGAATGGCAAAAACTAGAAGGTTGTTATGGT Y152 F AACTGGAAGGTTGTTTAGGGTGGTTATGACACC R GGTGTCATAACCACCCTAACAGCGTCAGTTAGACACC Q174 F CTCACCGACGGTGGTTAGGCAACACCTTCAGTTAAAAA R175 F ACCGACGTGGTCAATGACCACCGTCGGTGAG R175 F ACCGACGGTGGTCAATGACCACCGTCGGT L178 F GGTCACACGCATCAAGTAAAATGGATAACTGG R CCAGTTATCCATTTTCTACTTGATGCGTTAACCGCGTGGCGT	NT15	R	ΔΟΥΤΑΔΑΔΑΤΟ ΔΟΥΤ Α ΟΔΑΘΥΤΟΥΤΑΔΟΥΤΑ
R CTGGCTGTAGGTAATCTAGCTCAGGCGGTACTG N144 F ATTACCTACAGCCAGTAGGCGAACTGGAAG R CTTCCAGTTTTGCCCTACTGGCTGAGGTAAT W148 F CAGAATGGCAAAAACTAGAAGGTTGTTATGGT R ACCATAAACAACCTTCTAGTTTTTGCCATTCTG Y152 F AACTGGAAGGTTGTTTAGGGTGGTTATGACACC R GGTGTCATAACCACCCTCAAACAACCTTCCAGTT Q174 F CTCACCGACGGTGGTTAGCGCATCAAGTTAAAA R175 F ACCGACGGTGGTCAATGACCACCGTCGGTGAG R175 F ACCGACGGTGGTCAATGACCACCGTCGGT L178 F GGTCACACCATCAAGTAGAAAATGGATAACTGG R CCAGTTATCCATTTTCTACTTGATGCGTTGACC	F138	F	
N144 F ATTACCTACAGCCAGTAGGGCAAAAACTGGAAG R CTTCCAGTTTTGCCCTACTGGCTGAGGTAAT W148 F CAGAATGGCAAAAACTAGAAGGTTGTTATGGT R ACCATAAACAACCTTCTAGTTTTTGCCATTCTG Y152 F AACTGGAAGGTTGTTTAGGTGGTTATGACACC R GGTGTCATAACCACCCTCAAACAACCTTCCAGTT Q174 F CTCACCGACGGTGGTTAGCGCATCAAGTTAAAAA R TTTTAACTTGATGCGCTAACACCGTCGGTGAG R175 F ACCGACGGTGGTCAATGACCACCGTCGGT R CATTTTTAACTTGATCAATTGACCACCGTCGGT L178 F GGTCAACGCATCAAGTAGAAAATGGATAACTGG R CCAGTTATCCATTTTCTACTTGATGCGTTGACC	2150	R	
R CTTCCAGTTTTTGCCCTACTGGCTGAGGTAAT W148 F CAGAATGGCAAAAAACTAGAAGGTTGTTATGGT R ACCATAAACAACCTTCTAGTTTTTGCCATTCTG Y152 F AACTGGAAGGTTGTTTAGGTGGTGATGGCAACACC R GGTGTCATAACCACCCTCAACGGTGGTTATGACACC Q174 F CTCACCGACGGTGGTTAGCGCATCAAGTTAAAAA R TTTTAACTTGATGCGCTAACCACCGTCGGTGAG R175 F ACCGGCGTGGTCAATGACCACCGTCGGT R CATTTTTAACTTGATGCGCTAATGACCACCGTCGGT L178 F GGTCACACGATCAAGTAGAAAATGGATAACTGG R CCAGTTATCCATTTTCTACTTGATGCGTTGACC	N144	F	
W148 F CAGAATGGCAAAAACTAGAAGGTTGTTATGGT W148 F CAGAATGGCAAAAACTAGAAAGTTGGCTGTTATGGT R ACCATAAACAACCTTCTAGTTTTTGCCATTCTG Y152 F AACTGGAAGGTTGTTTAGGTGGTTATGACACC R GGTGTCATAACCACCCTAAACAACCTTCCAGTT Q174 F CTCACCGACGGTGGTTAGCGCATCAAGTTAAAAA R TTTTAACTTGATGCGCTAACCACCGTCGGTGAG R175 F ACCGACGGTGGTCAATAGATCAAGTTAAAAATG R CATTTTTAACTTGATCTATTGACCACCGTCGGT L178 F GGTCAACGCATCAAGTAGAAAATGGATAACTGG R CCAGTTATCCATTTTCTACTTGATGCGTTGACC	111-7-7	R	CTTCCAGTITITGCCCTACTGGCTGTAGGTAAT
R ACCATAAACAACCTTCTAGTTTTGCCATTCTG Y152 F AACTGGAAGGTTGTTTAGGGTGGTTATGACACC R GGTGTCATAACCACCCTAAACAACCTTCCAGTT Q174 F CTCACCGACGGTGGTTAGCGCATCAAGTTAAAAA R TTTTAACTTGATGCGCTAACCACCGTCGGTGAG R175 F ACCGACGGTGGTCAATGACCACCGTCGGTGAG R CATTTTTAACTTGATCCACTTATTGACCACCGTCGGT L178 F GGTCAACGCATCAAGTAAAAATGGATAACTGG R CCAGTTATCCATTTTCTACTTGATGCGTTGACC	W/148	F	
Y152 F AACTGGAAGGTTGTTTAGGGTGGTTATGACACC R GGTGTCATAACCACCCTAAGCACCACCAGTT Q174 F CTCACCGACGGTGGTTAGCGCATCAAGTTAAAA R TTTTAACTTGATGCGCTAACCACCGTCGGTGAG R175 F ACCGACGGTGGTCAATGACCACCGTCGGTGAG R CATTITTAACTTGATGCCCTAATGACCACCGTCGGTG L178 F GGTCAACGCATCAAGTAGAAAATGGATAACTGG R CCAGTTATCCATTTTCTACTTGATGCGTTGACC	1140	R	ΔCCΔTΔΔΔCΔΔCCTT CTΔ GTTTTTGCCΔTTCTG
R GGTGTCATAACCACCCTAAACAACCATCCAGTT Q174 F CTCACCGACGGTGGTTAGCGCATCAAGTTAAAA R TTTTAACTTGATGCGCTAACCACCGTCGGTGAG R175 F ACCGACGGTGGTCAATAGATCAAGTTAAAAATG R CATTTTTAACTTGATGCCTATGACCACCGTCGGT L178 F GGTCAACGCATCAAGTAGAAAATGGATAACTGG R CCAGTTATCCATTTTCTACTTGATGCGTTGACC	Y152	F	AACTGGAAGGTTGTT AG GGTGGTTATGACACC
Q174 F CTCACCGACGGTGGTTAGCGCATCAAGTTAAAA R TTTTAACTTGATGCG CTA GCGCATCAAGTTAAAAA R ACCGACGGTGGTCAA TA GATCAAGTTAAAAATG R CATTTTTAACTTGATCAAGTTGACCACCGTCGGT L178 F GGTCAACGCATCAAG TA GAAAATGGATAACTGG R CCAGTTATCCATTTT CTA CTTGATGCGTTGACC	1152	R	GGTGTCATAACCACC CTA AACAACCTTCCAGTT
R TTTTAACTTGATGCGCTAACCACCGTCGGTGAG R175 F ACCGACGGTGGTCAATAGATCAAGTTAAAAATG R CATTTTTAACTTGATCTATTGACCACCGTCGGT L178 F GGTCAACGCATCAAGTAGAAAATGGATAACTGG R CCAGTTATCCATTTTCTACTTGATGCGTTGACC	0174	F	
R175 F ACCGACGGTGGTCAA TAG ATCAAGTTAAAAATG R CATTTTTAACTTGAT CTA TTGACCACCGTCGGT L178 F GGTCAACGCATCAAG TAG AAAATGGATAACTGG R CCAGTTATCCATTTT CTA CTTGATGCGTTGACC	Y117	R	TTTTAACTTGATGCG CTA ACCACCGTCGGTGAG
R CATTTTTAACTTGATCTAATGACACCGTCGGT L178 F GGTCAACGCATCAAGTAGAAAATGGATAACTGG R CCAGTTATCCATTTTCTACTTGATGCGTTGACC	R175	F	ΑΓΓΓΑΔΓΑΓΤΟΑΤΑΔΑΛΑΤΟ
L178 F GGTCAACGCATCAAG TAG AAAATGGATAACTGG R CCAGTTATCCATTTT CTA CTTGATGCGTTGACC		R	
R CCAGTTATCCATTTT CTA CTTGATGCGTTGACC	L178	F	GGTCAACGCATCAAGTAGAAAATGGATAACTGG
		R	CCAGTTATCCATTTT CTA CTTGATGCGTTGACC

The amber codon replaced the codons in bold letters. F, forward; R, reverse.