

1. WP\_103592558.1 hypothetical protein [Bacillus thuringiensis]
2. WP\_001196891.1 hypothetical protein [Bacillus thuringiensis]
3. WP\_043936493.1 MULTISPECIES: hypothetical protein [unclassified Bacillus (in: Bacteria)]
4. WP\_214931495.1 hypothetical protein [Bacillus sp. ISL-8]
5. WP\_098223856.1 hypothetical protein [Bacillus thuringiensis]
6. WP\_198130194.1 hypothetical protein [Bacillus thuringiensis]
7. WP\_150159506.1 hypothetical protein [Bacillus cereus]
8. WP\_001196890.1 MULTISPECIES: hypothetical protein [Bacillaceae]
9. WP\_151619209.1 hypothetical protein [Bacillus cereus]
10. WP\_087876301.1 hypothetical protein [Bacillus thuringiensis]
11. WP\_242555206.1 hypothetical protein [Bacillus cereus]
12. WP\_118415087.1 hypothetical protein [Bacillus thuringiensis]
13. WP\_153599337.1 hypothetical protein [Bacillus thuringiensis]
14. WP\_093290892.1 hypothetical protein [Thermoactinomycetes sp. DSM 45892]
15. WP\_090719323.1 hypothetical protein [Nitrosomonas sp. Nm166]
16. WP\_090657007.1 hypothetical protein [Nitrosomonas marina]
17. WP\_090629228.1 hypothetical protein [Nitrosomonas marina]
18. WP\_090698829.1 hypothetical protein [Nitrosomonas aestuarii]
19. MCB1985445.1 hypothetical protein [Nitrosomonas sp.]
20. MCO6429124.1 hypothetical protein [Nitrosomonas communis]
21. SER17553.1 hypothetical protein SAMN05421690\_10118 [Nitrosomonas sp. Nm51]
22. WP\_143058755.1 hypothetical protein [Nitrosomonas marina]
23. WP\_143057368.1 hypothetical protein [Nitrosomonas sp. Nm51]
24. MCP5243701.1 hypothetical protein [Burkholderiales bacterium]
25. WP\_090698296.1 hypothetical protein [Nitrosomonas aestuarii]
26. WP\_090634528.1 hypothetical protein [Nitrosomonas marina]
27. WP\_090331542.1 hypothetical protein [Nitrosomonas sp. Nm51]
28. MCB1948730.1 hypothetical protein [Nitrosomonas sp.]
29. MBV6516776.1 hypothetical protein [Planctomycetes bacterium]
30. NUO17800.1 hypothetical protein [Planctomycetaceae bacterium]
31. MCC6151602.1 hypothetical protein [Planctomycetes bacterium]
32. MCC6149736.1 hypothetical protein [Planctomycetes bacterium]
33. MBP9893028.1 hypothetical protein [Planctomycetes bacterium]
34. MCA8919643.1 hypothetical protein [Planctomycetes bacterium]
35. MCQ3948913.1 hypothetical protein [Planctomycetes bacterium]
36. WP\_254705115.1 hypothetical protein [Bacillus thuringiensis]
37. MCC7510907.1 hypothetical protein [Planctomycetes bacterium]
38. KAA0216165.1 hypothetical protein EDM80\_04610 [bacterium]
39. WP\_199019276.1 hypothetical protein [Paenibacillus roseus]
40. MBK8207208.1 hypothetical protein [Planctomycetes bacterium]
41. WP\_199019274.1 hypothetical protein [Paenibacillus roseus]
42. MCC7507738.1 hypothetical protein [Planctomycetes bacterium]
43. MCC7508108.1 hypothetical protein [Planctomycetes bacterium]
44. MBK8206537.1 hypothetical protein [Planctomycetes bacterium]
45. MBP9891346.1 hypothetical protein [Planctomycetes bacterium]
46. MBK8206605.1 hypothetical protein [Planctomycetes bacterium]
47. MBE7490899.1 hypothetical protein [Planctomycetes bacterium]
48. MBK8207622.1 hypothetical protein [Planctomycetes bacterium]
49. MBK8205278.1 hypothetical protein [Planctomycetes bacterium]
50. MCC7509103.1 hypothetical protein [Planctomycetes bacterium]
51. MCB9934236.1 hypothetical protein [Planctomycetes bacterium]
52. KAA0210941.1 hypothetical protein EDM80\_12875 [bacterium]
53. MCC6742171.1 hypothetical protein [Planctomycetia bacterium]
54. MCB9894499.1 hypothetical protein [Planctomycetes bacterium]
55. MCC6742172.1 hypothetical protein [Planctomycetia bacterium]
56. MCQ3951076.1 hypothetical protein [Planctomycetes bacterium]
57. MCC6687398.1 hypothetical protein [Fimbriimonadaceae bacterium]
58. MCB9935966.1 hypothetical protein [Planctomycetes bacterium]
59. NUN50366.1 hypothetical protein [Candidatus Brocadiae bacterium]
60. MBX3458745.1 hypothetical protein [Planctomycetes bacterium]
61. MCE9583168.1 hypothetical protein [Planctomycetes bacterium]
62. MCC7510851.1 hypothetical protein [Planctomycetes bacterium]
63. MBP9891054.1 hypothetical protein [Planctomycetes bacterium]
64. MCE9583169.1 phage major capsid protein [Planctomycetes bacterium]
65. NUN50365.1 hypothetical protein [Candidatus Brocadiae bacterium]
66. MCA8918287.1 hypothetical protein [Planctomycetes bacterium]
67. MBX3461049.1 hypothetical protein [Planctomycetes bacterium]
68. KAF0245036.1 hypothetical protein FD180\_1973 [Planctomycetes bacterium]
69. MCC6738530.1 hypothetical protein [Planctomycetia bacterium]
70. MCC6149762.1 hypothetical protein [Planctomycetes bacterium]
71. MCQ3949629.1 hypothetical protein [Planctomycetes bacterium]
72. NUO16364.1 hypothetical protein [Planctomycetaceae bacterium]
73. CAG0962046.1 hypothetical protein PLCT2\_00815 [Planctomycetaceae bacterium]
74. WP\_002731357.1 hypothetical protein [Magnetospirillum molischianum]
75. MBX3459031.1 hypothetical protein [Planctomycetes bacterium]
76. MCQ3948721.1 hypothetical protein [Planctomycetes bacterium]
77. MCB9933912.1 hypothetical protein [Planctomycetes bacterium]
78. MBO6507501.1 phage major capsid protein [Roseibium sp.]

79. KAA0209033.1 hypothetical protein EDM80\_15205, partial [bacterium]  
80. WP\_238616883.1 phage major capsid protein [Ectothiorhodospira shaposhnikovii]  
81. NQZ53225.1 phage major capsid protein [Piscirickettsiaceae bacterium]  
82. WP\_199153549.1 hypothetical protein [Chromobacterium sp. ASV23]  
83. TDW20413.1 hypothetical protein EV128\_12543 [Rhizobium azibense]  
84. WP\_221103340.1 phage major capsid protein [Rhizobium bangladeshense]  
85. WP\_221122355.1 phage major capsid protein [Rhizobium lentis]  
86. QIG69072.1 major capsid protein [Rhizobium phage RHph\_N1\_10]  
87. MBP9891731.1 hypothetical protein [Planctomycetes bacterium]  
88. MCA8917006.1 hypothetical protein [Planctomycetes bacterium]  
89. QIG75611.1 major capsid protein [Rhizobium phage RHph\_Y2\_11]  
90. WP\_092498438.1 phage major capsid protein [Chelativorans sp. A52C2]  
91. MCB9936365.1 hypothetical protein [Planctomycetes bacterium]  
92. CAG0968390.1 hypothetical protein PLCT2\_01190 [Planctomycetaceae bacterium]  
93. MCC6150886.1 hypothetical protein [Planctomycetes bacterium]  
94. WP\_045991564.1 phage capsid protein [Halomonas sp. S2151]  
95. WP\_065784019.1 MULTISPECIES: phage capsid protein [unclassified Ensifer]  
96. WP\_144196640.1 phage major capsid protein [Cupriavidus campinensis]  
97. WP\_253399773.1 hypothetical protein [Methylorubrum extorquens]  
98. YP\_009620683.1 major capsid protein [Pseudomonas phage nickie]  
99. AMB48270.1 phage capsid protein [Methylobacterium sp. AMS5]  
100. UKL14918.1 major capsid protein [Pseudomonas phage hairong]  
101. WP\_026610715.1 hypothetical protein [Methylocaldum szegediense]  
102. MCC6152092.1 hypothetical protein [Planctomycetes bacterium]  
103. UIS24576.1 major capsid protein [Pseudomonas phage ZY21]  
104. WP\_247125312.1 phage major capsid protein [Acinetobacter baumannii]  
105. WP\_031986190.1 phage capsid protein [Acinetobacter baumannii]  
106. MBP4651980.1 phage major capsid protein [Acinetobacter baumannii]  
107. MCL2874769.1 phage major capsid protein [Betaproteobacteria bacterium]  
108. WP\_176966547.1 phage major capsid protein, partial [Acinetobacter baumannii]  
109. HAV4743116.1 phage major capsid protein [Acinetobacter baumannii]  
110. WP\_001130341.1 MULTISPECIES: hypothetical protein [Acinetobacter]  
111. WP\_224446258.1 hypothetical protein [Cupriavidus metallidurans]  
112. WP\_252429529.1 hypothetical protein, partial [Acinetobacter baumannii]  
113. MBQ0662298.1 phage major capsid protein [Acinetobacter baumannii]  
114. EIU0976857.1 phage major capsid protein [Acinetobacter baumannii]  
115. WP\_115292648.1 phage major capsid protein [Pseudomonas mendocina]  
116. DAP19794.1 TPA: MAG TPA: major capsid protein [Siphoviridae sp.]  
117. WP\_161289910.1 phage major capsid protein [Acinetobacter baumannii]  
118. WP\_001130337.1 hypothetical protein [Acinetobacter baumannii]  
119. DAM63278.1 TPA: MAG TPA: major capsid protein [Siphoviridae sp.]  
120. WP\_063664455.1 phage major capsid protein [Comamonas thiooxydans]  
121. WP\_252436504.1 phage major capsid protein, partial [Acinetobacter baumannii]  
122. WP\_104915983.1 phage major capsid protein [Acinetobacter baumannii]  
123. WP\_151708812.1 phage major capsid protein [Acinetobacter brisouii]  
124. WP\_031980863.1 phage capsid protein [Acinetobacter baumannii]  
125. WP\_023897583.1 hypothetical protein [Acinetobacter baumannii]  
126. HAV4899581.1 phage major capsid protein [Acinetobacter baumannii]  
127. WP\_042670060.1 phage capsid protein [Methylobacterium sp. B34]  
128. WP\_209651035.1 MULTISPECIES: hypothetical protein [Methylobacterium]  
129. WP\_124618513.1 phage major capsid protein [Burkholderia contaminans]  
130. WP\_059608968.1 hypothetical protein [Burkholderia anthina]  
131. WP\_059789217.1 hypothetical protein [Burkholderia sp. MSMB1072]  
132. EGY2841718.1 phage major capsid protein [Acinetobacter baumannii]  
133. MCK9569022.1 phage major capsid protein [Candidatus Pacearchaeota archaeon]  
134. WP\_059858205.1 hypothetical protein [Burkholderia cepacia]  
135. WP\_252414503.1 phage major capsid protein, partial [Acinetobacter baumannii]  
136. DAS20049.1 TPA: MAG TPA: major capsid protein [Siphoviridae sp.]  
137. WP\_093294920.1 phage major capsid protein [Sphingomonas sp. NFR04]  
138. WP\_102064968.1 phage major capsid protein [Ralstonia pickettii]  
139. WP\_247300523.1 hypothetical protein [Bradyrhizobium sp. 179]  
140. WP\_047884360.1 hypothetical protein [Photobacterium ganghwense]  
141. WP\_187057131.1 phage major capsid protein [Dyella telluris]  
142. WP\_155041137.1 phage major capsid protein [Paracoccus litorisediminis]  
143. WP\_207104130.1 phage major capsid protein [Photobacterium ganghwense]  
144. RWB95541.1 phage major capsid protein [Mesorhizobium sp.]  
145. WP\_150063515.1 phage major capsid protein [Roseospira marina]  
146. HIV77377.1 hypothetical protein [Candidatus Sphingomonas excrementigallinarum]  
147. WP\_097566451.1 phage major capsid protein [Cronobacter sakazakii]  
148. WP\_166500133.1 phage major capsid protein [Cronobacter sakazakii]  
149. WP\_216296239.1 phage major capsid protein [Cronobacter sakazakii]  
150. WP\_080953189.1 phage capsid protein [Cronobacter sakazakii]  
151. HAV7489798.1 phage major capsid protein [Escherichia coli]  
152. WP\_161580717.1 phage major capsid protein [Cronobacter muciljensii]  
153. RWI35418.1 phage major capsid protein [Mesorhizobium sp.]  
154. WP\_130097775.1 MULTISPECIES: phage major capsid protein [Citrobacter]  
155. EFG0346231.1 phage major capsid protein [Escherichia coli]  
156. WP\_029590302.1 MULTISPECIES: hypothetical protein [Cronobacter]  
157. WP\_085044976.1 phage capsid protein [Cronobacter sakazakii]  
158. WP\_052904762.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]

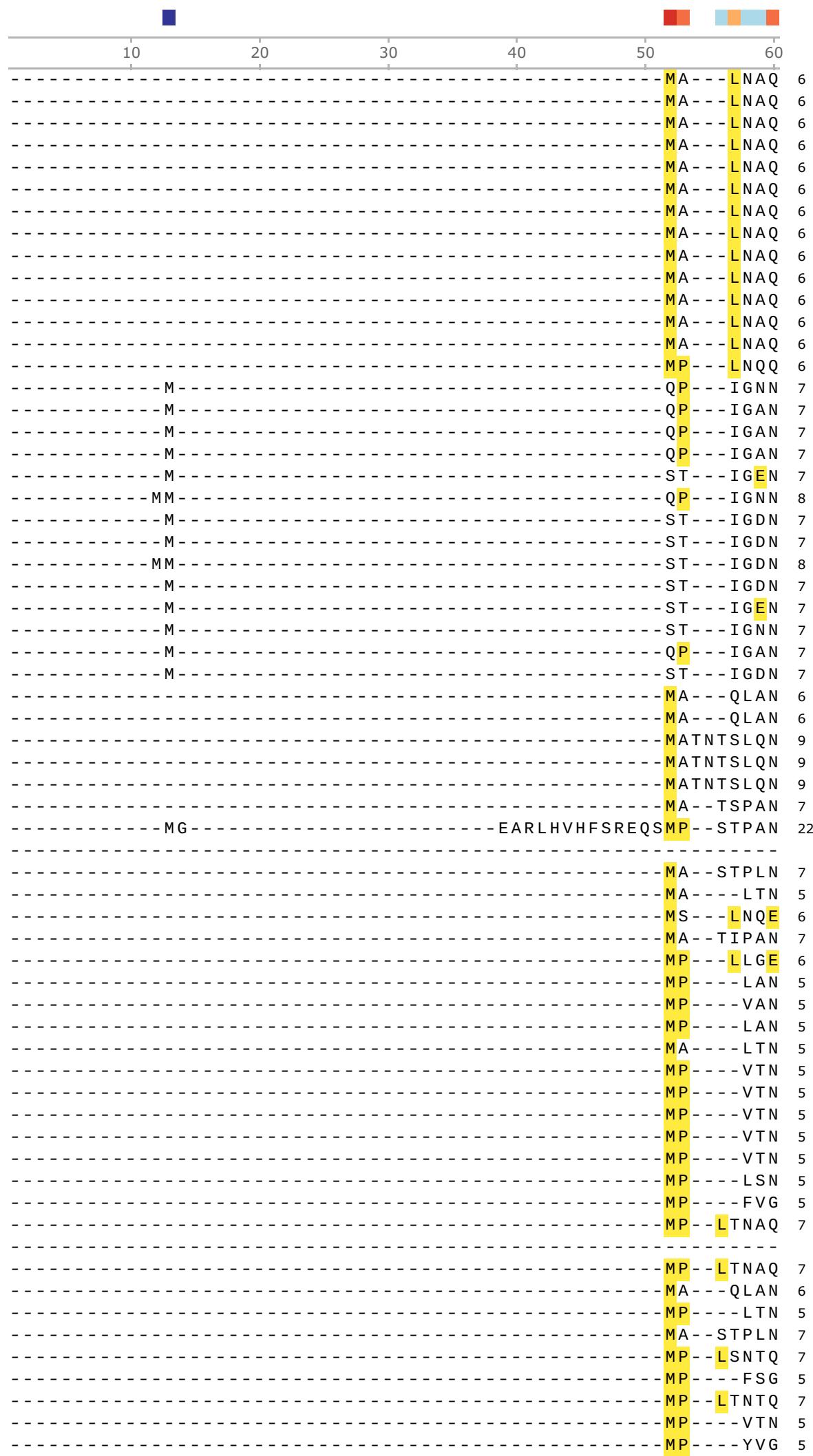
- 159.** WP\_014962239.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**160.** WP\_052904335.1 hypothetical protein [Escherichia coli]  
**161.** WP\_059296125.1 phage capsid protein, partial [Acinetobacter baumannii]  
**162.** MBE0438045.1 phage major capsid protein [Methylomicrobium sp.]  
**163.** WP\_052983289.1 hypothetical protein [Shigella sonnei]  
**164.** WP\_105875125.1 phage major capsid protein [Cronobacter malonaticus]  
**165.** WP\_080817813.1 phage capsid protein [Cronobacter sakazakii]  
**166.** WP\_029463964.1 MULTISPECIES: hypothetical protein [Cronobacter]  
**167.** WP\_209732192.1 phage major capsid protein [Cronobacter sakazakii]  
**168.** WP\_032969640.1 hypothetical protein [Cronobacter malonaticus]  
**169.** WP\_080781210.1 phage capsid protein [Cronobacter sakazakii]  
**170.** WP\_096095769.1 phage major capsid protein [Escherichia coli]  
**171.** WP\_076734789.1 phage capsid protein [Cronobacter sakazakii]  
**172.** EFF6507864.1 phage major capsid protein [Escherichia coli]  
**173.** HAL3311757.1 phage major capsid protein [Escherichia coli]  
**174.** UTU32364.1 phage major capsid protein [Escherichia coli]  
**175.** MCK2723972.1 phage major capsid protein [Escherichia coli]  
**176.** EGS6838749.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Agona]  
**177.** WP\_244079899.1 phage major capsid protein [Escherichia coli]  
**178.** EHC2975283.1 phage major capsid protein [Shigella sonnei]  
**179.** WP\_069127011.1 phage capsid protein [Klebsiella pneumoniae]  
**180.** EDZ1273658.1 phage major capsid protein [Salmonella enterica]  
**181.** WP\_193125375.1 phage major capsid protein [Escherichia coli]  
**182.** EJF8070929.1 phage major capsid protein [Escherichia coli]  
**183.** WP\_161620577.1 phage major capsid protein [Escherichia coli]  
**184.** EFJ2838014.1 phage major capsid protein [Escherichia coli]  
**185.** EJK5757188.1 phage major capsid protein [Escherichia coli]  
**186.** EIH9371074.1 phage major capsid protein [Escherichia coli]  
**187.** WP\_001130339.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**188.** MHX32748.1 phage major capsid protein [Escherichia coli]  
**189.** WP\_072644904.1 phage capsid protein [Escherichia coli]  
**190.** MBC7264957.1 phage major capsid protein [Chloroflexi bacterium]  
**191.** HBL6848639.1 phage major capsid protein [Escherichia coli]  
**192.** WP\_062120516.1 phage major capsid protein [Aureimonas sp. AU40]  
**193.** HAH5045117.1 phage major capsid protein [Escherichia coli]  
**194.** WP\_243540855.1 phage major capsid protein [Escherichia coli]  
**195.** WP\_112901748.1 phage major capsid protein [Escherichia coli]  
**196.** EIT7775743.1 phage major capsid protein [Escherichia coli]  
**197.** EFV7979351.1 phage major capsid protein [Shigella sonnei]  
**198.** WP\_042063131.1 hypothetical protein [Escherichia coli]  
**199.** EEZ8393064.1 phage major capsid protein [Escherichia coli]  
**200.** EY7369300.1 phage major capsid protein [Escherichia coli]  
**201.** EFG0309418.1 phage major capsid protein [Escherichia coli]  
**202.** WP\_182552267.1 phage major capsid protein [Phyllobacterium myrsinacearum]  
**203.** WP\_063091425.1 hypothetical protein [Escherichia coli]  
**204.** CAB4122113.1 hypothetical protein UFOVP26\_79 [uncultured Caudovirales phage]  
**205.** WP\_112043712.1 phage major capsid protein [Escherichia coli]  
**206.** HBB7811611.1 phage major capsid protein [Escherichia coli]  
**207.** WP\_001130338.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**208.** HAJ7535281.1 phage major capsid protein [Escherichia coli]  
**209.** WP\_096165287.1 phage major capsid protein [Escherichia coli]  
**210.** WP\_085457360.1 phage capsid protein [Escherichia coli]  
**211.** WP\_032328869.1 hypothetical protein [Escherichia coli]  
**212.** WP\_053904528.1 MULTISPECIES: hypothetical protein [Escherichia]  
**213.** MBB0544530.1 phage major capsid protein [Escherichia coli]  
**214.** EFK7891705.1 phage major capsid protein [Escherichia coli]  
**215.** EAB8604575.1 phage major capsid protein [Shigella sonnei]  
**216.** WP\_149556591.1 phage major capsid protein [Escherichia coli]  
**217.** WP\_149540218.1 phage major capsid protein [Escherichia albertii]  
**218.** EFH9124402.1 phage major capsid protein [Escherichia coli]  
**219.** WP\_052988632.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**220.** WP\_247150342.1 phage major capsid protein [Escherichia coli]  
**221.** WP\_094259633.1 phage major capsid protein [Escherichia coli]  
**222.** WP\_061158051.1 hypothetical protein [Escherichia coli]  
**223.** WP\_033803025.1 hypothetical protein [Escherichia coli]  
**224.** MBZ8365671.1 phage major capsid protein [Escherichia coli]  
**225.** WP\_203054096.1 phage major capsid protein [Escherichia coli]  
**226.** EFC1505940.1 phage major capsid protein [Escherichia coli]  
**227.** WP\_134894003.1 phage major capsid protein [Escherichia coli]  
**228.** WP\_251569595.1 hypothetical protein [Parasutterella sp. DSM 108034]  
**229.** HBU8289600.1 phage major capsid protein [Escherichia coli]  
**230.** WP\_160334835.1 phage major capsid protein [Parasutterella sp. NM82\_D38]  
**231.** HBH5230159.1 phage major capsid protein [Escherichia coli]  
**232.** WP\_106889102.1 phage major capsid protein [Escherichia coli]  
**233.** HAM5980914.1 phage major capsid protein [Escherichia coli]  
**234.** WP\_161623763.1 phage major capsid protein [Escherichia coli]  
**235.** EFF1057382.1 phage major capsid protein [Escherichia coli]  
**236.** EFZ7197477.1 phage major capsid protein [Shigella sonnei]  
**237.** WP\_231351989.1 phage major capsid protein [Escherichia coli]  
**238.** WP\_193119742.1 phage major capsid protein [Escherichia coli]

- 239.** WP\_252127766.1 phage major capsid protein [Thermomicrobium sp. CFH 73360]  
**240.** EFW0034188.1 phage major capsid protein [Shigella sonnei]  
**241.** EJE3861318.1 phage major capsid protein [Escherichia coli]  
**242.** WP\_085458157.1 MULTISPECIES: phage capsid protein [Escherichia]  
**243.** WP\_094337983.1 MULTISPECIES: phage major capsid protein [Escherichia]  
**244.** WP\_053886737.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**245.** MCN1174709.1 phage major capsid protein [Escherichia coli]  
**246.** WP\_152935148.1 phage major capsid protein [Escherichia coli]  
**247.** EFX2756071.1 phage major capsid protein [Shigella sonnei]  
**248.** EFC0466466.1 phage major capsid protein [Escherichia coli]  
**249.** MCN4038342.1 phage major capsid protein [Escherichia coli]  
**250.** EFD9355743.1 phage major capsid protein [Escherichia coli]  
**251.** WP\_097497792.1 phage major capsid protein [Escherichia coli]  
**252.** EFA9209962.1 phage major capsid protein [Escherichia coli]  
**253.** HBB1414416.1 phage major capsid protein [Escherichia coli]  
**254.** HAO7436534.1 phage major capsid protein [Escherichia coli]  
**255.** HAW3037422.1 phage major capsid protein [Escherichia coli]  
**256.** HAW1565627.1 phage major capsid protein [Escherichia coli]  
**257.** WP\_032187309.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**258.** EQQ2490861.1 phage major capsid protein [Escherichia coli]  
**259.** WP\_053900371.1 hypothetical protein [Escherichia coli]  
**260.** WP\_109949435.1 phage major capsid protein [Escherichia coli]  
**261.** HCC6220448.1 phage major capsid protein [Klebsiella pneumoniae]  
**262.** HAN9820645.1 phage major capsid protein [Escherichia coli]  
**263.** WP\_046622184.1 MULTISPECIES: hypothetical protein [Enterobacter cloacae complex]  
**264.** WP\_039264878.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**265.** WP\_113613520.1 phage major capsid protein [Klebsiella pneumoniae]  
**266.** EV7694734.1 phage major capsid protein [Escherichia coli]  
**267.** WP\_072124166.1 phage capsid protein [Klebsiella varicola]  
**268.** WP\_048292500.1 hypothetical protein [Klebsiella pneumoniae]  
**269.** WP\_247188155.1 phage major capsid protein [Escherichia coli]  
**270.** DAE04111.1 TPA: MAG TPA: major capsid protein [Siphoviridae sp. ctmpG14]  
**271.** WP\_001405040.1 hypothetical protein [Escherichia coli]  
**272.** WP\_065304476.1 phage capsid protein [Escherichia coli]  
**273.** HBZ3184842.1 phage major capsid protein [Klebsiella pneumoniae]  
**274.** WP\_119127007.1 phage major capsid protein [Klebsiella pneumoniae]  
**275.** EIM7866883.1 phage major capsid protein [Escherichia coli]  
**276.** WP\_001130340.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**277.** WP\_202979481.1 phage major capsid protein [Escherichia coli]  
**278.** HAT3636238.1 phage major capsid protein [Raoultella ornithinolytica]  
**279.** EFI9420290.1 phage major capsid protein [Escherichia coli]  
**280.** WP\_126646421.1 phage major capsid protein [Escherichia coli]  
**281.** WP\_252461054.1 phage major capsid protein, partial [Acinetobacter baumannii]  
**282.** WP\_221016063.1 phage major capsid protein [Klebsiella pneumoniae]  
**283.** EFK0326126.1 phage major capsid protein [Escherichia coli]  
**284.** HAJ7861025.1 phage major capsid protein [Escherichia coli]  
**285.** EHH5028748.1 phage major capsid protein [Escherichia coli]  
**286.** HAU5664456.1 phage major capsid protein [Citrobacter freundii]  
**287.** EAB6775759.1 phage major capsid protein [Escherichia coli]  
**288.** EBZ0832066.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Java]  
**289.** WP\_064343494.1 MULTISPECIES: hypothetical protein [Klebsiella]  
**290.** WP\_087507360.1 phage capsid protein [Escherichia coli]  
**291.** WP\_236525880.1 phage major capsid protein [Escherichia coli]  
**292.** WP\_096178288.1 phage major capsid protein [Escherichia coli]  
**293.** WP\_104074192.1 phage major capsid protein [Escherichia coli]  
**294.** HAL2790855.1 phage major capsid protein [Escherichia coli]  
**295.** HBR7729850.1 phage major capsid protein [Klebsiella pneumoniae]  
**296.** WP\_221012288.1 phage major capsid protein [Klebsiella pneumoniae]  
**297.** HBV4481339.1 phage major capsid protein [Klebsiella pneumoniae]  
**298.** EFF2501934.1 phage major capsid protein [Escherichia coli]  
**299.** EIW9109236.1 phage major capsid protein [Klebsiella pneumoniae]  
**300.** HAO3297438.1 phage major capsid protein [Escherichia coli]  
**301.** WP\_064165097.1 hypothetical protein [Klebsiella pneumoniae]  
**302.** QJJ61945.1 phage major capsid protein [Klebsiella pneumoniae]  
**303.** WP\_089075232.1 phage major capsid protein [Escherichia coli]  
**304.** WP\_097307300.1 phage major capsid protein [Escherichia coli]  
**305.** HBR4262047.1 phage major capsid protein [Klebsiella pneumoniae]  
**306.** WP\_004109857.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**307.** EEO4716749.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Tennessee]  
**308.** HBT8335443.1 phage major capsid protein [Klebsiella pneumoniae]  
**309.** EHK0743263.1 phage major capsid protein [Salmonella enterica]  
**310.** WP\_006812514.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**311.** WP\_054625182.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**312.** WP\_032217427.1 hypothetical protein [Escherichia coli]  
**313.** EET8203310.1 phage major capsid protein [Escherichia coli]  
**314.** WP\_045339225.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
**315.** EIH0829516.1 phage major capsid protein [Escherichia coli]  
**316.** CAF2811462.1 hypothetical protein AI2925V1\_5194 [Klebsiella pneumoniae]  
**317.** EJG5508613.1 phage major capsid protein [Salmonella enterica]  
**318.** WP\_194797343.1 phage major capsid protein [Klebsiella pneumoniae]

319. WP\_078207497.1 phage capsid protein [Escherichia coli]  
320. WP\_016607444.1 hypothetical protein [Yersinia pestis]  
321. WP\_204363305.1 phage major capsid protein [Klebsiella pneumoniae]  
322. EBK5293162.1 phage major capsid protein [Salmonella enterica]  
323. WP\_063929200.1 hypothetical protein [Enterobacter hormaechei]  
324. EEZ8608344.1 phage major capsid protein [Escherichia coli]  
325. WP\_096842503.1 phage major capsid protein [Escherichia coli]  
326. HBX2495344.1 phage major capsid protein [Klebsiella pneumoniae]  
327. WP\_065519942.1 phage capsid protein [Klebsiella pneumoniae]  
328. WP\_086910796.1 MULTISPECIES: phage capsid protein [Klebsiella]  
329. WP\_040110313.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
330. WP\_194304202.1 phage major capsid protein [Enterobacter hormaechei]  
331. WP\_116431201.1 phage major capsid protein [Klebsiella pneumoniae]  
332. WP\_001130336.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
333. WP\_250209263.1 phage major capsid protein [Enterobacter cloacae]  
334. WP\_023316010.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
335. ECB7446470.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Braenderup]  
336. HAM5174158.1 phage major capsid protein [Escherichia coli]  
337. EHR3333785.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Senftenberg]  
338. HBV3788408.1 phage major capsid protein [Klebsiella pneumoniae]  
339. EBS8359733.1 phage major capsid protein [Salmonella enterica]  
340. WP\_159115294.1 phage major capsid protein [Klebsiella pneumoniae]  
341. WP\_060458874.1 MULTISPECIES: hypothetical protein [Enterobacter cloacae complex]  
342. EET8285689.1 phage major capsid protein [Escherichia coli]  
343. WP\_002211784.1 MULTISPECIES: hypothetical protein [Gammaproteobacteria]  
344. WP\_072105584.1 phage capsid protein [Enterobacter cloacae]  
345. WP\_150006605.1 phage major capsid protein, partial [Klebsiella pneumoniae]  
346. WP\_175617232.1 phage major capsid protein [Escherichia coli]  
347. WP\_192856648.1 phage major capsid protein, partial [Escherichia coli]  
348. EHJ4216072.1 phage major capsid protein [Salmonella enterica]  
349. WP\_227899545.1 phage major capsid protein [Escherichia coli]  
350. HCD2326535.1 phage major capsid protein [Enterobacter hormaechei]  
351. WP\_086374674.1 phage capsid protein, partial [Acinetobacter baumannii]  
352. EDQ0380811.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Oslo]  
353. BDD45295.1 hypothetical protein 17 [bacterium]  
354. HBT7858040.1 phage major capsid protein [Klebsiella pneumoniae]  
355. WP\_060453932.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]  
356. EAA4173638.1 phage major capsid protein [Salmonella enterica subsp. enterica]  
357. HBQ8554378.1 phage major capsid protein [Klebsiella pneumoniae]  
358. WP\_247156820.1 phage major capsid protein [Escherichia coli]  
359. HBV0452233.1 phage major capsid protein [Escherichia coli]  
360. EDW0215574.1 phage major capsid protein [Salmonella enterica subsp. enterica]  
361. WP\_046083837.1 hypothetical protein [Escherichia fergusonii]  
362. EIW8542850.1 phage major capsid protein [Klebsiella pneumoniae]  
363. HAK0268282.1 phage major capsid protein [Salmonella enterica]  
364. EGK6915180.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Enteritidis]  
365. WP\_071692149.1 phage capsid protein [Citrobacter portucalensis]  
366. EBN2282108.1 phage major capsid protein [Salmonella enterica]  
367. EDQ3388105.1 phage major capsid protein [Salmonella enterica subsp. houtenae]  
368. ECT3984105.1 phage major capsid protein [Salmonella enterica subsp. houtenae serovar 53:z4,z23:-]  
369. EBV1651518.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Bareilly]  
370. WP\_042863544.1 hypothetical protein [Enterobacter hormaechei]  
371. WP\_048231968.1 MULTISPECIES: hypothetical protein [Citrobacter freundii complex]  
372. EEP8077587.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Braenderup]  
373. WP\_016587721.1 hypothetical protein [Yersinia pestis]  
374. HAX9983652.1 phage major capsid protein [Escherichia coli]  
375. WP\_075191900.1 MULTISPECIES: phage capsid protein [Cronobacter]  
376. HAY3994692.1 phage major capsid protein [Escherichia coli]  
377. MBO9360510.1 phage major capsid protein [Thermomicrombium sp.]  
378. HAD4280041.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Typhi str. CT18]  
379. HBY0825155.1 phage major capsid protein [Klebsiella pneumoniae]  
380. EBH6160155.1 phage major capsid protein [Salmonella enterica]  
381. WP\_023221754.1 hypothetical protein [Salmonella enterica]  
382. MCK5604243.1 phage major capsid protein [Candidatus Pacearchaeota archaeon]  
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384. ECQ3861573.1 phage major capsid protein [Salmonella enterica]  
385. EGQ6262282.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Enteritidis]  
386. WP\_114569653.1 phage major capsid protein [Escherichia coli]  
387. WP\_028449712.1 phage major capsid protein [Chitinibacter tainanensis]  
388. ECC6545565.1 phage major capsid protein [Salmonella enterica]  
389. MCM6396231.1 phage major capsid protein [Klebsiella pneumoniae]  
390. RPJ40005.1 phage major capsid protein [Planctomycetaceae bacterium]  
391. EAB0133809.1 phage major capsid protein [Salmonella enterica]  
392. HCH9832956.1 phage major capsid protein [Salmonella enterica]  
393. WP\_169724898.1 phage major capsid protein [Enterobacter hormaechei]  
394. ECG2845924.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Manhattan]  
395. EBX1374166.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Newport]  
396. HAX2345276.1 phage major capsid protein [Escherichia coli]  
397. UQM93941.1 major head protein [Stenotrophomonas phage vB\_Sm\_QDWS359]  
398. EEU2445140.1 phage major capsid protein [Escherichia coli]

- 399.** EBS5432372.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Alachua]  
**400.** EAX1817979.1 phage major capsid protein [Salmonella enterica]  
**401.** EBR9946236.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Krefeld]  
**402.** HBC0308464.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Napoli]  
**403.** HBZ3547779.1 phage major capsid protein [Klebsiella pneumoniae]  
**404.** MCB2982456.1 phage major capsid protein [Klebsiella pneumoniae]  
**405.** EER4805513.1 phage major capsid protein [Escherichia coli]  
**406.** EGO4917944.1 phage major capsid protein [Salmonella enterica]  
**407.** HBV9739600.1 phage major capsid protein [Klebsiella pneumoniae]  
**408.** HAD4904499.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Typhi str. CT18]  
**409.** EAB5862671.1 phage major capsid protein [Salmonella enterica subsp. enterica]  
**410.** WP\_079825253.1 phage capsid protein [Salmonella enterica]  
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**416.** ECD3753536.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Orion]  
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**426.** EFH0306860.1 phage major capsid protein [Escherichia coli]  
**427.** EFW4078867.1 phage major capsid protein [Shigella sonnei]  
**428.** EDU5118278.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Anatum]  
**429.** EV7166997.1 phage major capsid protein [Escherichia coli]  
**430.** HBE0118361.1 phage major capsid protein [Shigella sonnei]  
**431.** EAQ8609054.1 phage major capsid protein [Salmonella enterica]  
**432.** QXN72400.1 major capsid protein [Rhodobacter phage RcSimone-Hastad]  
**433.** EFO1692251.1 phage major capsid protein [Escherichia coli]  
**434.** MBD7755531.1 phage major capsid protein [Klebsiella pneumoniae]  
**435.** WP\_102003656.1 phage major capsid protein [Klebsiella pneumoniae]  
**436.** EEA1371212.1 phage major capsid protein [Salmonella enterica]  
**437.** MBA8354127.1 phage major capsid protein [Escherichia coli]  
**438.** EGI1978062.1 phage major capsid protein [Salmonella enterica]  
**439.** DAJ05229.1 TPA: MAG TPA: major capsid protein [Siphoviridae sp.]  
**440.** EJF9244945.1 phage major capsid protein [Escherichia coli]  
**441.** WP\_015922589.1 phage major capsid protein [Thermomicrobium roseum]  
**442.** WP\_181374643.1 phage major capsid protein [Pectobacterium carotovorum]  
**443.** HCH7946627.1 phage major capsid protein [Escherichia coli]  
**444.** WP\_223762983.1 phage major capsid protein [Corallococcus sp. AS-1-6]  
**445.** MBW2636049.1 phage major capsid protein [Deltaproteobacteria bacterium]  
**446.** EET1013303.1 phage major capsid protein [Escherichia coli]  
**447.** EIQ1087120.1 phage major capsid protein [Escherichia coli]  
**448.** MCM8749459.1 phage major capsid protein [Thermomicrobium CFH 74404]  
**449.** EJA7649394.1 phage major capsid protein [Escherichia coli]  
**450.** EIT1058465.1 phage major capsid protein [Escherichia coli]  
**451.** GBD19714.1 hypothetical protein HRbin28\_00148 [bacterium HR28]  
**452.** MBX5446219.1 phage major capsid protein [Sphaerobacter sp.]  
**453.** EJA5029925.1 phage major capsid protein [Salmonella enterica]  
**454.** YP\_009996955.1 major head protein [Xanthomonas phage Xoo-sp2]  
**455.** WP\_224020286.1 hypothetical protein [Burkholderia vietnamiensis]  
**456.** HBQ7547743.1 phage major capsid protein [Klebsiella pneumoniae]  
**457.** EFC1758968.1 phage major capsid protein [Escherichia coli]  
**458.** EDU4451998.1 phage major capsid protein [Salmonella enterica subsp. enterica serovar Anatum]  
**459.** WP\_153283238.1 phage major capsid protein [Variovorax paradoxus]  
**460.** HBB2595907.1 phage major capsid protein [Escherichia coli]  
**461.** YP\_009997022.1 hypothetical protein JTY56\_gp20 [Xanthomonas phage Bosa]  
**462.** EEZ6802210.1 phage major capsid protein [Escherichia coli]  
**463.** MBX3473679.1 hypothetical protein [Planctomyces bacterium]  
**464.** EFW0729459.1 phage major capsid protein [Shigella sonnei]  
**465.** EHL0287849.1 phage major capsid protein [Escherichia coli]  
**466.** EER8844980.1 phage major capsid protein [Escherichia coli]  
**467.** EFN9767071.1 phage major capsid protein [Escherichia coli]  
**468.** WP\_137447163.1 phage major capsid protein, partial [Escherichia coli]  
**469.** MCJ8600995.1 phage major capsid protein [Klebsiella pneumoniae]  
**470.** EFH8846498.1 phage major capsid protein [Escherichia coli]  
**471.** UAW07626.1 major head protein [Pseudomonas phage AIIMS-Plu-RaNi]  
**472.** WP\_152881049.1 phage major capsid protein [Duganella sp. FT27W]  
**473.** YP\_009196268.1 major head protein [Pseudomonas phage PaMx11]  
**474.** EIB9668287.1 phage major capsid protein [Escherichia coli]  
**475.** HBL5398680.1 phage major capsid protein [Escherichia coli]  
**476.** UIS24744.1 major head protein [Stenotrophomonas phage vB\_SmaS-AXL\_1]  
**477.** CAH1069075.1 Uncharacterised protein [Acinetobacter phage MD-2021a]  
**478.** WP\_163998672.1 phage major capsid protein [Pyxidicoccus caerfyrdinensis]

- 479.** URA07134.1 major capsid protein [Xanthomonas phage Mallos]  
**480.** YP\_009996845.1 major head protein [Pseudomonas phage Epa5]  
**481.** EFC2304030.1 phage major capsid protein [Escherichia coli]  
**482.** EHH4005454.1 phage major capsid protein [Escherichia coli]  
**483.** WP\_067370658.1 phage capsid protein [Morganella psychrotolerans]  
**484.** EHW0876436.1 phage major capsid protein [Escherichia coli]  
**485.** WP\_012870511.1 phage major capsid protein [Sphaerobacter thermophilus]  
**486.** WP\_136134600.1 phage major capsid protein [Providencia sp. MGF014]  
**487.** EDS1306404.1 phage major capsid protein [Salmonella enterica]  
**488.** WP\_099110294.1 phage major capsid protein [Xenorhabdus sp. KJ12.1]  
**489.** WP\_038234216.1 hypothetical protein [Xenorhabdus szentirmaii]  
**490.** UGL62843.1 major head protein [Xanthomonas phage MET13-T1]  
**491.** EIH9254667.1 phage major capsid protein [Escherichia coli]  
**492.** WP\_121762769.1 phage major capsid protein [Corallococcus sp. AB038B]  
**493.** EFH8389121.1 phage major capsid protein [Escherichia coli]  
**494.** WP\_038038123.1 phage major capsid protein [Thermorudis peleae]  
**495.** HBZ3723017.1 phage major capsid protein [Klebsiella pneumoniae]  
**496.** WP\_064173653.1 hypothetical protein, partial [Klebsiella pneumoniae]  
**497.** MCA1800049.1 phage major capsid protein [Actinomycetia bacterium]  
**498.** EFH8991876.1 phage major capsid protein [Escherichia coli]  
**499.** WP\_047963505.1 hypothetical protein [Xenorhabdus khoisanae]  
**500.** QNN97178.1 hypothetical protein [Xanthomonas phage Xp12]



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413		MP	LLREE	7
414		MP	LLREE	7
415		MP	LLREE	7
416		MP	LLREE	7
417		MP	LLREE	7
418		MP	LLRDE	7
419		MS	LLVEE	7
420		MP	LLREE	7
421		MP	LLREE	7
422		MP	LLREE	7
423		MP	LLREE	7
424		MP	LLREE	7
425		MP	LLREE	7
426		MP	LLREE	7
427		MP	LLREE	7
428		MP	LLREE	7
429		MP	LLREE	7
430		MP	LLREE	7
431		MP	LLREE	7
432	- M -	PS	VTLTE	8
433		MP	LLREE	7
434		MP	LLREE	7
435		MP	LLREE	7
436		MP	LLREE	7
437		MP	LLREE	7
438		MP	LLREE	7
439		MP	LLRAE	7
440		MP	LLREE	7
441		MA	LTKVE	7
442		MP	LLREE	7
443		MP	LLREE	7
444	- M -	PS	VILSE	8
445	- M -	AS	VTLAE	8
446		MP	LLREE	7
447		MP	LLREE	7
448			MTKVE	5
449		MP	LLREE	7
450		MP	LLREE	7
451		MA	LTKVE	7
452		MA	LTKVE	7
453		MP	LLREE	7
454	- M -	SS	VTLAE	8
455		MP	LLQAE	7
456		MP	LLREE	7
457		MP	LLREE	7
458		MP	LLREE	7
459		MP	LLKAT	7
460		MP	LLREE	7
461	- M -	AS	VTLAE	8
462		MP	LLREE	7
463			-	-
464		MP	LLREE	7
465		MP	LLREE	7

466		MP	LLREE	7
467		MP	LLREE	7
468		MP	LLREE	7
469		MP	LLREE	7
470		MP	LLREE	7
471	-M-	AS	VTLVE	8
472	-M-	MP	LLRTE	7
473	-M-	AS	VTLVE	8
474		MP	LLREE	7
475		MP	LLRDE	7
476	-M-	AS	VTLAE	8
477	-M-	AT	ITLAE	8
478	-M-	PS	NPLIE	8
479	-M-	AS	VTLTE	8
480	-M-	AS	VTLAE	8
481		MP	LLREE	7
482		MP	LLREE	7
483		MP	LLREE	7
484		MP	LLREE	7
485		MA	LTKVE	7
486		MP	LLREE	7
487		MP	LLREE	7
488		MP	LLREE	7
489		MP	LLREE	7
490	-M-	AS	VTLAE	8
491		MP	LLREE	7
492	-M-	PS	VILSE	8
493		MP	LLREE	7
494		MA	LTKLE	7
495		MP	LLREE	7
496		MP	LLREE	7
497	-M-	AS	VTLAE	8
498		MP	LLREE	7
499		MP	LLREE	7
500	-M-	AS	VTLAE	8

70 80 90 100 110 120

1	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEVFP <sub>85</sub> FHHVEGDSLRYVR	-TPELTP	-ASI	56
2	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEVFP <sub>85</sub> FHHVEGDSLRYVR	-TPELTP	-ASI	56
3	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEVFP <sub>85</sub> FHHVEGDSLRYVR	-TPALTP	-ASI	56
4	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEIFPFH <sub>85</sub> HVEGDSLRYVR	-TPELTP	-ASI	56
5	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEIFPFH <sub>85</sub> HVEGDSLRYVR	-TPELTP	-ASI	56
6	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEVFP <sub>85</sub> FHHVEGDSLRYVR	-TPELTP	-ASI	56
7	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEIFPFH <sub>85</sub> HVEGDSLRYVR	-TPELTP	-ASI	56
8	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEVFP <sub>85</sub> FHHVEGDSLRYVR	-TPELTP	-ASI	56
9	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEIFPFH <sub>85</sub> HVEGDSLRYVR	-TPELTP	-ASI	56
10	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEIFPFH <sub>85</sub> HVEGDSLRYVR	-TPELTP	-ASI	56
11	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEVFP <sub>85</sub> FHHVEGDSLRYVR	-TPELTP	-ASI	56
12	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEVFP <sub>85</sub> FHHVEGDSLRYVR	-TPELTP	-ASI	56
13	AQFLSILELTKG <sub>70</sub> LLENS <sub>75</sub> PKRLQH <sub>80</sub> LEIFPFH <sub>85</sub> HVEGDSLRYVR	-TPELTP	-ASI	56
14	VQFLSIDALALGLIENAPKRMQYLPFFPFYSIKGSALRYVR	-TPELVP	-AEI	56
15	ARLLSNDVLA <sub>70</sub> KWLIEDFPFRIQLSTAFPFLPVAGDALRYAT	-TGPLIP	-GIA	57
16	ARLLSND <sub>70</sub> ALAKWLIEDFPFRIQLSSIFPFIPVSGHSLRYAA	-TGALTP	-GNA	57
17	ARLLSND <sub>70</sub> ALAKWLVEDFPFRIQLSSIFPFIPVSGHSLRYAT	-TDALMP	-GNA	57
18	ARLLSND <sub>70</sub> ALAKWLIEDFPFRIQLSSIFPFIPVAGDSFRYAT	-TGLLN	-GST	57
19	ARLLSNDVQAKWLIEDFPFRIQLASVL <sub>70</sub> PLPVAGDALRYTT	-TPVLQP	-GVT	57
20	ARLLSNDVLA <sub>70</sub> KWLIEDFPFRIQLSTAFPFLPIAGDALRYAT	-TGPLTP	-GVT	58
21	ARLLSNDVQAKWLIEDFPFRIQLASVFP <sub>70</sub> FYPVAGDALRYTT	-TPVLQP	-GVT	57
22	ARLLSNDVQAKWLIEDFPFRIQLASVFPFCPVAGDALRYTT	-TPILQP	-GVM	57
23	ARLLSNDVQAKWLIEDFPFRIQLASVFP <sub>70</sub> FYPVAGDALRYTT	-TPVLQP	-GVT	58
24	ARLLSNDVQAKWLIEDFPFRIQLASALPF <sub>70</sub> FYPVAGDALRYTT	-TPVLQP	-GVT	57
25	ARLLSNDVQAKWLIEDFPFRIQLASVL <sub>70</sub> PLPVAGDALRYTT	-TSVLQP	-GVT	57
26	ARLLSNDVQAKWLIEDFPFRIQLASVFP <sub>70</sub> FYPVAGDALRYTT	-TPVLQP	-GVT	57

27	AQLLSNDVLAKWLIEDFPFRIQLSSIFPPLSVSGHSLRYAT-----TGPLIP----GAA	57
28	ARLLSNDVQAKWLIEDFPFRIQLASALPFYPVAGDALRYTT-----TPVLPQ----GVT	57
29	ADLLTLRDLWPWLVENFPWKIQIAHHWPFFMGIDGGFLRVAR-----TARFDQ----TDL	56
30	ADLLTLRDLWPWLVENFPWKIQIAHHWPFFMGIDGGFLRVARTARFDQTARFDQ----TDL	62
31	ADRLVLTDQWQWLIEENFPWKLQIARFWPFFMGIYGGFLRVPR-----TNQFDK----SEL	59
32	ADRLVLTDQWQWLIEENFPWKLQIARFWPFTGIHGGFLRVAR-----TNLIDK----SDL	59
33	ADRLVLTDQWQWLIEENFPWKLQIARFWPFFMGIHGGFLRVAR-----TNQISN----ADL	59
34	STNLTQDQLAKWLIEDAPYKIQIARVWPFMGIQGGKISYAR-----TAALESLANIDDM	61
35	AVNLTQEQLSKFLLETIEYKLQIMQIWPFMGVLGKLRAYER-----TNQLEAIADINNM	76
36	-----	
37	SINLTQDQLAKWLIEDMPYRIQIARIFFPFMGIQGGKISYAR-----TPALEAVADINDM	61
38	VSLLLQKLSQSWLIEENFPYKLQIPRAWKGIEGTQVSFAR-----TPAFNK----ASL	55
39	ANRLSTNHLLPGLQENAPKRLDILKALFLQITGNALAVVR-----TPALPD----ALA	56
40	SINLTQDQLAKWLIEDAPYKIQIARIWFPMGIQGGKISYAR-----IADLTTGFSFDTV	61
41	AQYLSTDELLPGLLENWSKEIPGLECFPFYEIRGNALTAVA-----TDALPD----AGT	56
42	VSRLLQLLRQAWLIEENPHKLQIPRAWVWKAIEGTQVAFAR-----TNRMDP----AEL	55
43	VERFMQLLRQSWLVENFPHKLQIPRRWIWHGIAGTRVAFPR-----TNRIDK----DNL	55
44	VSRLLQLLRQAWLIEENPHKLQIPRAWVWKAIEGTQVAFAR-----INRMDP----AEL	55
45	VSMLLQKLSQSWLIEENPHKLQIPRAWKGIEGTQVSFAR-----TPQLDK----ATL	55
46	ADLLSDDLALWLVENAPIKIPFFQAWSWQQVAGKSLIYPR-----TTALAP----ASV	55
47	ADLLADDLLALSLVENSPVKIPFFQAWIWIQEVAVGKSLTYAR-----TPL LAP----ATE	55
48	ADLLSDDLALWLVENAPIKIPFFQAWAWQQVAGKSLIYPR-----TTALAP----AGV	55
49	ADLLSDDLALWLVENAPIKIPFFQAWSWQQVAGKSLIYPR-----TTALAP----AGV	55
50	ADLLSDDLALWLVENAPIKIPFFQAWAWQQVAGKSLIYPR-----TTT LSP----AGV	55
51	AFLLGDSPVARWLVENSPVAIPFPLYAWQGVGDGQSLTYPR-----ATELTP----ASV	55
52	AANATTQQATRWLVENEPEIIQIHHFPSQAVQGGFLTYAR-----VPKLI E----ASP	55
53	AQLLSEEALLLAGLVENDPKRIQLARRLPFYAVGGDRLAVPRV-----TSGNLGT----AVW	59
54	-----MLSKFLLELEYKLQIARIWFPMGVVGGKLRAYER-----TDQLETVANIDSM	47
55	ALLLSNDAFIKGLIEAEPKRIQM SHIFPF FEIDGDKLTVPR-----TSANLGT----AIF	59
56	ADLLTRRDLWPWLVENFPWKIQIARHWPFMGI DGGFLRVAR-----TTRFDE----TDL	56
57	ASLLSENRRTRFIVENSPIKLQIARVWPWLGVGDGSGNM YAR-----KNAQLTP----TPV	56
58	AVDLTQEQLVKTVIEKIRYKVEIANFWPMRGVIGGKLRAYER-----TDQLSA-GDINAM	60
59	ASLLSDEQLLSNLVENEPKRIQFALRFPPFYAIIGGDR LTVP RV-----TAANLGT----AVW	59
60	ASGTANTIA TP HAVE NEPR LIQIHRRM ATKG VPGG TLVY PR-----VPALKP----ASV	55
61	ALLLSNDALFLQGLVENDPKRIQLMSNLLPFFEIDGDKLTIPRV-----TNANLGT----AIW	59
62	ADLLSDDLALWLVENAPIKIPFFQAWSWQQVAGKSLIYPR-----TTALAP----AVM	55
63	AQNAVNQIATPWLVENDPEIIQVHGHAWQGVPGGLLTYAR-----VPKLI A----ASA	55
64	ALLLSNDALLAGLVENDPKRIQLSRLLPFYALAGDRLTVPRV-----TNANLGT----ALW	59
65	ALLLSNDALFLQGLTENEPRRIQM SHVLEFFEIDGDKLTIPRV-----TSANLGT----AIF	59
66	AYMLGESPVARWLIE NSPINIAFYQAWAWQGVGDGQSLTYPR-----ATELSP----AAV	55
67	TQFLNSIPVARYAVERAPTRI QHMLWSFQGVAGRELLYAQ-----VPQLVA----SGQ	55
68	GLLLSNDFLVGRFIEDSPFVIQPAHFLPFFEVPGD SERWST-----TAAILP----ASA	57
69	GLLLSNDFLVGRFIEDSPFVIQPAHFLPFFEVPGD SERWST-----TVAIPP----ASP	73
70	AQALAEEKVAKWLLENWPVKLQFGLVC PITWVDGKSLKFNSLTD-PAGNPPIF-----AYP	61
71	AQALAEEKITKWLENWPVKLQFGLVC PITWVDGKSLKFNSLTD-AGGNPMPF-----AYP	112
72	AQALAEEKITKWLENWPVKLQFGLVC PITWVDGKSLKFNSLTD-AGGNPMPF-----AYP	107
73	AQALAEEKVTRWLLENWPVKLQFGLVC PITWVDGKSLKFNSLTD-PDGNPIPF-----AYP	61
74	AELLSQEQM ERGIEEIIDKDDLF A VLPFKQVVGKAYVYDR-----ELTLSE----GDF	57
75	ADLLADDLLALWLVENSPVKIPFYQAWIWIQEVAVGKSLTYAR-----TPL LAP----ATI	55
76	-----	
77	APDTANIQA AKWFVENEPRRIQI HGVMPVFGVNGGFLVYPR-----VPAIKP----AQV	55
78	AAKLSREQFERGVIEEIIDKDEL FALPFPMKVEGKTYDYVR-----EGTLSE----GDF	57
79	ADLLTLRDLWPWLVENFPWKIQIARHWPFMGIN GGFLRVAR-----TARFDE----TDL	56
80	AAKLSNNDLVAGVIEEVIDKDEL LAVLPFTETKGKAYVYNR-----ENFISE----AVF	57
81	AEKLSNNQLVSGVIEEIIDKDEL ALLPFM GVNGKAYVYNR-----ENTISE----GDF	57
82	AETLTNNDLVAGVIEEIIDTESL DMFAILPFVHTEGKAYVYNR-----EKT LAE----GVF	57
83	AAKLSQEDKARGVIEEIIDTESL FALMPFQHVNDKTFTYVR-----EGTLSE----GEF	57
84	AAKLSQEDKARGVIEEIIDTESL FALMPFQHVTDKTFTYVR-----EGTLSE----GEF	57
85	AAKLSQEDKARGVIEEIIDTESL FALMPFQHVTDKTFTYVR-----EGTLSE----GEF	57
86	AAKLSQEDKARGVIEEIIDDES LFALMPFQHVTDKTFTYVR-----EGTLSE----GEF	57
87	AENAGQNFLQPHIVETAPVPMQIARHMPVQFVN G RAKSF AVI-----GKLEP----GVA	55
88	-----M	1
89	ADKLSQEDKARGVIEEIIDTESL FALMPFQHVSDKTFTYVR-----EGTLSE----GEF	57
90	AAKLSQEQM ERG VIEEIIDTDEL FALIPPFM GVNGKAYVYNR-----EDTLSE----GEF	57
91	-----MKYAR-----SAVLAA----ATK	14
92	AENAGQNFLQPHIVETAPVPLQIARHMPVRYINGRALSFAVI-----DAMAA----GVA	55
93	AENAGSDFLQPHIVETAPVPLQIARHMPVRYVN GRAMSFAVI-----GKMQP----GIA	55

94	AAKLS EADLQRG IIEEI DKE DLL AVL PFP VRT DGK SYD YVR	- - - EKT LSE - - - AEF	57
95	AEKLS QED KARGV IEEI IDTESLF ALMPF QHV ND KTFTY VR	- - - EGTLSE - - - GEF	57
96	AERLS NNQL VAG IIEEI ERDDL FAIL PFT GING KAY VYN R	- - - ENTLAG - - - ASW	57
97	AAKLS VNQL LERGV IEEI IDV DEL FAL PPF M QVNG KAY DY IR	- - - ESTLSE - - - GDF	57
98	AEKLS QEEM LRGV IEEI IDR DDL ALL LPF ARTEG KALV Y IR	- - - ELTNSE - - - GSF	57
99	AEKLS SQDY LERGV IEEI IDQ DEM FAL VP FM VNG KAY DY VR	- - - EKELSE - - - GAF	57
100	AETLS QEDML RGV IEEI IH RDD LL ALL PFS RVDG KALV Y IR	- - - ELTNSE - - - GTF	57
101	AEKLS NNTL VQGIV EEL IDR DEL SLL PFE QVNS KAY VYN R	- - - EKT LSE - - - ADF	57
102	AQYLS RDAL AML WLET DPWR NE LA AVFP YM PID GPALK VAR	- - - QT KVAI - - - GSL	57
103	AEKLS QEEM LRGV IEEI IDR DDL ALL LPF ARTEG KALV Y IR	- - - ELTNSE - - - GSF	57
104	AAKLS NNQL VSGV VEEI IDK DEM FAFL PFP VGV KG KAY VYN R	- - - EKT LAD - - - ADF	57
105	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
106	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	55
107	AEKLS NNQL VSGV IDEI IF RDDM FAIL PFP MG VNG KAY VYN R	- - - ENTLGD - - - AEF	57
108	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
109	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
110	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
111	ADKLS NNQL LERGV IEEI EIER DEL FAL PFP M RVN SKAY VYN R	- - - ENGLSG - - - AAF	57
112	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	59
113	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
114	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
115	AETLS QEDM VRGV IEEI VH KDD LM AL MPF S RTD G KAY VY VR	- - - EKT NSE - - - GSF	57
116	AEKLS NNQL LRGV ITEI IDK DDM FAIL LPFT QVNG KAY VYN R	- - - EGELAD - - - GQW	57
117	AAKLS NNQL VSGV VEEI IDK DEM FAFL PFP VGV KG KAY VYN R	- - - EKT LAD - - - ADF	57
118	AAKLS NNQL VSGV VEEI IDK DEM FAFL PFP VGV KG KAY VYN R	- - - EKT LAD - - - ADF	57
119	AEKLS NNQL LRGV ITEI IDK DDM FAIL LPFT QVNG KAY VYN R	- - - EGELAD - - - GQW	57
120	AEKLS QDQV VQGIV EEEIFT NEM YNML PFT KV SG KAY LY KR	- - - EGTLAT - - - VDY	57
121	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
122	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
123	AEKLS NNTL VAGV IDEI ERDDL FS VLPF VAV NS KAY VYN R	- - - EAT LAD - - - ADF	57
124	AEKLS NNQL VQGV VEEI IDR DDL FAVL PFP VQV NG KAY VYN R	- - - EKT LGG - - - ANW	57
125	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
126	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
127	AAKLS VDQL ERG IIEEI VQ DDL FAL PFP VH VNG KAY DY IR	- - - EAT LSE - - - GSF	57
128	AAKLS VDQL ERG IIEEI VQ DDL FAL PFP VH VNG KAY DY IR	- - - EAT LSE - - - GAF	57
129	AEKLS NNQL VAGV IEEI EIER DEL FAL I PFIGING KAY VY DR	- - - ENSLPT - - - ADF	57
130	AEKLS NNQL VAGV IEEI EIER DEL FAL I PFIGING KAY VY DR	- - - ENTLPT - - - ADF	57
131	AEKLS NNQL VAGV IEEI EIER DEL FAL I PFIGING KAY VY DR	- - - ENTLPT - - - ADF	57
132	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
133	AAKLC QDEL VSGL IEN VIT VNP FYN IL PFD SID GN GL TY NR	- - - EDVLGD - - - VQV	58
134	AEKLS NNQL VAGV IEEI EIER DEL FAL I PFIGING KAY VY DR	- - - ENSLPT - - - ADF	57
135	AEKLS NNQL VQGV VEEI IDR DDL FAIL PFT QVNG KAY VYN R	- - - EKT LGG - - - ANW	57
136	AAKLS NNQL LEAGV ITEI YTR DDL FAVL PFP TRV NG KAY VYN R	- - - ENELAT - - - ADW	57
137	AEKLS NNVL EQGV IEEI IDND AMF AML PFP KRV VG KAY MY NR	- - - EKT LSE - - - GEF	57
138	AETLS NNQL VAGV IDQI IDR DDL FAIL LPF ERV NG KAY VYN R	- - - EDTLGG - - - ADW	57
139	ANKL SESL MERGV IEEI IDREAL FAL PFP KTV DG KAY LY HR	- - - ENTISE - - - GDF	57
140	AKKLS NNELE QGII EITI IDREEL FAVL PFP MKV NS KAY LY NR	- - - EKELSE - - - ASF	57
141	ADKLS NNDL VRGV IEEV IDR DDL FAVL PFP TRTD G KAY VYN R	- - - ENGV VE - - - AEF	57
142	AAKLS IE DRQR GV IEEI IK DD ALF ALL PFP VGT DEV SY VR	- - - EAT LAQ - - - GAF	57
143	AKKLS NNELE QGII EITI IDREEL FAVL PFP MKV NS KAY LY NR	- - - EKELSE - - - ASF	57
144	AEKLS QEDM ERGV IEEI IDK DEL FAL VP FM HVT DKT TY Y VR	- - - EGNLPS - - - AEF	57
145	AEKL SEE FM ERGV IEEI IDR DEL FQFL PFM GVD NKAY TY NR	- - - EGTLSE - - - GQF	57
146	AEKLS NNILE QGV IEEI IDND AMF ALL PFP K RIV G KAY VYN R	- - - EKSLSE - - - GAF	57
147	AEKLS NNELE QGV IETI IDR DDL FAVL PFP MKIDS KAY LY NR	- - - EAT LSE - - - ATF	57
148	AEKLS NNELE QGV IETI IDR DDL FAVL PFP MKIDS KAY LY NR	- - - EAT LSE - - - ATF	57
149	AEKLS NNELE QGV IETI IDR DDL FAVL PFP MKIDS KAY LY NR	- - - EAT LSE - - - ATF	57
150	AEKLS NNELE QGV IETI IDR DDL FAVL PFP MKIDS KAY LY NR	- - - EAT LSE - - - ATF	57
151	AEKLS NNELE QGV IETI IDR DDL FAIL LP FM KINS KAY LY NR	- - - EAT LSE - - - ATF	57
152	AEKLS NNELE QGV IETI IDR DDL FAVL PFP MKIDS KAY LY NR	- - - EAT LSE - - - ATF	57
153	AEKLS QEDM ERGV IEEI IDK DEL FAL VP FM HVT DKT TY Y VR	- - - EGNLPS - - - AEF	57
154	AEKLS NNELE QGV IETI IDR DDL FAVL PFP MKIDS KAY LY NR	- - - EAT LSE - - - ATF	57
155	AEKLS NNELE QGV IETI IDR DDL FAIL LP FM KINS KAY LY NR	- - - EAT LSE - - - ATF	57
156	AEKLS NNELE QGV IETI IDR DDL FAVL PFP MKIDS KAY LY NR	- - - EAT LSE - - - ATF	57
157	AEKLS NNELE QGV IETI IDR DDL FAIL LP FM KINS KAY LY NR	- - - EAT LSE - - - ATF	57
158	AEKLS NNELE QGV IETI IDR DDL FAIL LP FM KINS KAY LY NR	- - - EAT LSE - - - ATF	57
159	AEKLS NNELE QGV IETI IDR DDL FAIL LP FM KINS KAY LY NR	- - - EAT LSE - - - ATF	57
160	AEKLS NNELE QGV IETI IDR DDL FAIL LP FM KINS KAY LY NR	- - - EAT LSE - - - ATF	57

161	AAKLSNNQLVSGVVEEIIDKDEMFAFLPFVGVKGKAYVYNR-----EKT	LAD	-	ADF	57
162	AKKLSNNQLEIGVVEEIIDKEDLFSVLPPFMGINGKAYVYNR-----EKT	LSE	-	GDF	57
163	AEKLSNNELEQGVIEETIIDRDDLFSILPFMKINSKAYLYNR-----EAT	LSE	-	ATF	57
164	AEKLSNNELEQGVIEETIIDRDDLFAVLPPFMKIDS SKAYLYNR-----EAT	LSE	-	ATF	57
165	AEKLSNNELEQGVIEETIIDRDDLFAVLPPFMKIDS SKAYLYNR-----EAT	LSE	-	ATF	57
166	AEKLSNNELEQGVIEETIIDRDDLFAVLPPFMKIDS SKAYLYNR-----EAT	LSE	-	ATF	57
167	AEKLSNNELEQGVIEETIIDRDDLFAVLPPFMKIDS SKAYLYNR-----EAT	LSE	-	ATF	57
168	AEKLSNNELEQGVIEETIIDRDDLFAVLPPFMKIDS SKAYLYNR-----EAT	LSE	-	ATF	57
169	AEKLSNNELEQGVIEETIIDRDDLFAVLPPFMKIDS SKAYLYNR-----EAT	LSE	-	ATF	57
170	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
171	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKIDS SKAYLYNR-----EAT	LSE	-	ATF	57
172	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EAT	LSE	-	ATF	57
173	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
174	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
175	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
176	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKIDS SKAYLYNR-----EAT	LSE	-	ATF	57
177	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EAT	LSE	-	ATF	57
178	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EAT	LSE	-	ATF	57
179	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
180	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKIDS SKAYLYNR-----EAT	LSE	-	ATF	57
181	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
182	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
183	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
184	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
185	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EAT	LSE	-	ATF	57
186	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
187	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
188	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
189	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
190	AAKL TQDLL LRGVIEAIVKESAVFDYLPMFAITGSALKYNR-----EAT	LGD	-	AEF	57
191	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKIDS SKAYLYNR-----EAT	LSE	-	ATF	57
192	AEKLS EIDL VRGVIEEEIHKDEL FAILLPWVRTEGKS YDY VR-----ELT	ISE	-	GEF	57
193	AEKLSNNELEQGVIEETIIDRDDLFAIMPFFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
194	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
195	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
196	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
197	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
198	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
199	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
200	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
201	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
202	AAKLS QEDMERG IIEEI D R D E L F A L M P F L H V N D K V Y T Y NR-----EKELSS	-	-	ATF	57
203	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
204	AEKLSNNQLISGVIDQIITRDDLFAVLPPVGVN G KAYVYNR-----ENTLPS	-	-	ADF	57
205	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKITSKAYLYNR-----EKT	LSE	-	ATF	57
206	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
207	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
208	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
209	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
210	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
211	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKITSKAYLYNR-----EKT	LSE	-	ATF	57
212	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
213	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
214	AEKLSNNELEQGVIEETIIDRDDLFAILPFKINSKAYLYNR-----EAT	LSE	-	ATF	57
215	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
216	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
217	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
218	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
219	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
220	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
221	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
222	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
223	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKITSKAYLYNR-----EKT	LSE	-	ATF	57
224	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
225	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
226	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57
227	AEKLSNNELEQGVIEETIIDRDDLFAILPFMKINSKAYLYNR-----EKT	LSE	-	ATF	57





362	AEKLSNNELEQGVIETIIDRDDLFAVLPPFMKINSKAYLYNR-----	EKTLSE-----	ATF	57
363	AEKLSNNELEQGVIETIIDRDDLFAVLPPFMKINSKAYLYNR-----	EATLSE-----	ATF	57
364	AEKLSNNELEQGVIETIIDRDDLFAVLPPFMKINSKAYLYNR-----	EATLSE-----	ATF	57
365	AEKLSNNELEQGVIETIIDRDDLFAVLPPFMKINSKAYLYNR-----	EATLSE-----	ATF	57
366	AEKLSNNELEQGVIETIIDRDDLFAVLPPFMKINSKAYLYNR-----	EATLSE-----	ATF	57
367	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
368	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
369	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
370	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
371	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
372	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
373	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
374	AEKLSNNELEQGVIETIIDRDDLFAILPFMKITS SKAYLYNR-----	EATLSE-----	ATF	57
375	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
376	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EKTLSE-----	ATF	57
377	AAKL TDDMLLRGVVIETIVMESPVLQR LPFM EVVGTGLTYNR-----	EATLPA-----	ASF	57
378	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
379	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
380	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
381	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
382	SAKLAQDTLTIGLIESITVNHM FQLLPFEINGNALAYNR-----	ENALGD-----	VES	58
383	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS KAKAYLYNR-----	EATLSE-----	ATF	57
384	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS KAKAYLYNR-----	EATLSE-----	ATF	57
385	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS KAHLYNR-----	EATLSE-----	ATF	57
386	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS KAYLYNR-----	EKTLSE-----	ATF	57
387	ADRLSATSV ERGV VEEV IDRALFA LLPFHRIEGKAWVY NR-----	EGVLSE-----	GAF	57
388	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
389	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EKTLSE-----	ATF	57
390	AAKLCQDEL VSGLIENI ITVNPFYQVFPFD SIEGNGLTYNR-----	EDVLGD-----	VQV	58
391	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
392	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
393	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
394	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
395	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
396	AEKLSNNELEQGVIETIIDRDDLFAILPFMKVNNKAYLYNR-----	EATLSE-----	ATF	57
397	SAKLAQDEL VAGV IENVITVNELYELLPF D GIDGNALAYNR-----	ENALGD-----	VQM	58
398	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EKTLSE-----	ATF	57
399	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
400	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
401	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
402	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
403	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EKTLSE-----	ATF	57
404	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EKTLSE-----	ATF	57
405	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EKTLSE-----	ATF	57
406	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
407	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EKTLSE-----	ATF	57
408	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
409	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
410	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
411	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
412	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS KAKAYLYNR-----	EATLSE-----	ATF	57
413	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EKTLSE-----	ATF	57
414	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
415	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
416	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS KAKAYLYNR-----	EATLSE-----	ATF	57
417	AEKLSNNELEQGVIETIIDRDDLFAILPFMKVNNKAYLYNR-----	EATLSE-----	ATF	57
418	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
419	AAKLSIEDKQRGVIEEI IDR DELF ALVPFPVR AKDKV Y SVR-----	EGELPT-----	GDW	57
420	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
421	AEKLSNNELEQGVIETIIDRDDLFAILPFMKITS SKAYLYNR-----	EKTLSE-----	ATF	57
422	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
423	AEKLSNNELEQGVIETIIDRDDLFAILPFMKVNNKAYLYNR-----	EATLSE-----	ATF	57
424	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
425	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
426	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
427	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57
428	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS SKAYLYNR-----	EATLSE-----	ATF	57

429	AEKLSNNELEQGVIETIIDRDDLFAILPFMKITSKAYLYNR-----EKTlse-----ATF 57
430	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EATlse-----ATF 57
431	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDSKAYLYNR-----EATlse-----ATF 57
432	SAKLAQDELVAGVIENVITVNKMYQLLPFDGIDGNSLAYNR-----ENVLGD-----VQV 58
433	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
434	AEKLSNNELEQGVIETIIDRDDLFAVLPFMKINSKAYLYNC-----EKTlse-----ATF 57
435	AEKLSNNELEQGVIETIIDRDDLFAVLPFMKINSKAYLYNC-----EKTlse-----ATF 57
436	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDSKAYLYNR-----EATlse-----ATF 57
437	AERLSNNTEQGVIETIIDRDDLFAIMPFFKINSKAYLYNR-----EKTlse-----AEF 57
438	AEKLSNNELEQGVIETIVDRDDLFAILPFMKIDSKAYLYNR-----EATlse-----ATF 57
439	AERLSNNTLISGIITEIIDRDDLFSILPFVKVNSKAYVYNR-----ENTLAG-----ADW 57
440	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
441	AAKL TDDMLLRGVVIETIVMESPVLQR LPFMEVVGTGLTYNR-----EATLPA-----ATF 57
442	AEKLSNNTLEQGVIETIIDREDLFAVLPFMKVDSKAYLYNR-----EELSE-----ASF 57
443	AEKLSNNELEQGVIETIIDRDDLFAILPFFKVN SKAYLYNR-----EATlse-----AGF 57
444	AAKLSNNDLVAGIIENIVTVDRFFGVLPPFEPVEGPAAVYNR-----ENVLGD-----VQM 58
445	SAKLCQDVLIQGVIESIVTVDDFYWMLPPEGIDGNALSYNR-----ENALGD-----VES 58
446	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
447	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
448	AAKL TNDLLLRGVVIETIVKESSVLLMLPFMEVTGTALT YNR-----EATMPQ-----AQF 55
449	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
450	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
451	AAKL TDDLLLRGVVIETIVMESPVLQR LPFMEVVGTGLTYNR-----EGTLPA-----TDF 57
452	AAKL TNDMLLRGVVIETIVMESSVLTMLPFMNVTGTALT YNR-----EKTMPA-----AKF 57
453	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS KAYLYNR-----EATlse-----ATF 57
454	SAKLAQDELVAGVIENVITVNELYELLPFDGIDGNALAYNR-----ENVLGD-----VQM 58
455	AEKLSNNQLVAGVIEEIIERDELFALIPFIGINGKAYVYDR-----ENSLPT-----ADF 57
456	AEKLSNNELEQGVIETIIDRDDLFAVLPFMKINSKAYLYNR-----EKTlse-----ATF 57
457	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
458	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS KAYLYNR-----EATlse-----ATF 57
459	AEMLSQNDVVVGIIIEITVNELFGLLPFVKTEGKAYVYHR-----ENTLPS-----VSY 57
460	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
461	SAKLAQDELVAGVIENVITVNEIFEQLPFDGIDGNALAYNR-----ENVLGD-----VQM 58
462	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
463	-----
464	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EATlse-----ATF 57
465	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
466	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
467	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
468	AEKLSNNELEQGVIETIIDRDDLFAILPFMKITSKAYLYNR-----EKTlse-----ATF 57
469	AEKLSNNELEQGVIETIIDHEDLFAVLPFHKINSKAYLYNR-----EATlse-----AQF 57
470	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
471	SAKLAALDLVAGVIENVITVNRMYEMIPFDGIAGNALAYNR-----ENVLGD-----VQV 58
472	AERLSANQMVQGVIEEIIERDDLFSILPFVQTEGKAYLYNR-----EKTIGG-----ADW 57
473	SAKLAALDLVAGVIENVITVNRMYEMIPFDGIAGNALAYNR-----ENVLGD-----VQV 58
474	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
475	AEKLSNNELEQGVIETIIDRDDLFAILPFMKITSKAYLYNR-----EATlse-----ATF 57
476	SAKLAQDELVAGVIENVITVNEIFEQLPFDGIDGNALAYNR-----ENVLGD-----VQM 58
477	SAKLSQNLLYAGIIESIVEVNPFPEILPFQEIEGNALSYNR-----EKTLD-----IQF 58
478	AAKLSQDDLVSGIIANIIVTVDRFFGVLPPFEPVEGPAAVYNR-----ENVLGD-----VQM 58
479	SAKLAQDELVAGVIENVITVNEMFDLLLPFDGIDGNALAYNR-----ENVLGD-----VQV 58
480	SAKLAALDELVAGVIENVITVNRMFEVIPFDGIGSGNALAYNR-----ENVLGN-----VQV 58
481	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
482	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
483	AEKLSNNTLEQGVIETIIDREDLFAVLPFMKVDSKAYLYNR-----EELSE-----AEF 57
484	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
485	AAKL TNDMLLRGVVIETIVMESSVLTLLPFMNVTGTALT YNR-----EKTMPA-----AQF 57
486	AEKLSNNTLEQGVIETIIDREDLFAVLPFMKVDSKAYLYNR-----EELSE-----AAF 57
487	AEKLSNNELEQGVIETIIDRDDLFAILPFMKIDS KAYLYNR-----EATlse-----ATF 57
488	AEKLSNNTLEQGVIETIIDREDLFAVLPFMKVDSKAYLYNR-----EELSE-----AQF 57
489	AEKLSNNTLEQGVIETIIDREDLFAVLPFMKVDSKAYLYNR-----EELSE-----ATF 57
490	SAKLAQDELVAGVIENVITVNEIFEQLPFDGIDGNALAYNR-----ENVLGD-----VQM 58
491	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
492	AAKLSNNDLVAGIVENIVTVDRFFGVLPPFEPVEGPAAVYNR-----ENVLGD-----VQM 58
493	AEKLSNNELEQGVIETIIDRDDLFAILPFMKINSKAYLYNR-----EKTlse-----ATF 57
494	AAKL TNDLLLRGVVETIVRESSVALLPFTEVGTALT YVR-----EATLPA-----ASW 57
495	AEKLSNNELEQGVIETIIDRDDLFAVLPFMKINSKAYLYNR-----EKTlse-----ATF 57

496	AEKLSNNELEQGVIETIIDRDDLFAVLPPFMKINSKAYLYNR-----EKTLS-----ATF	57
497	SAKLSQDLLLSGVIESIVDVNPPIYEVFPFMGIEGNSLAYNR-----ENVLG-----VQF	58
498	AEKLSNNELEQGVIETIIDRDDLFAILPFMVKDSKAYLYNR-----EKTLS-----ATF	57
499	AEKLSNNTLEQGVIETIIDREDLFAVLPPFMVKDSKAYLYNR-----ESELSE-----AQF	57
500	SAKLAQDELVAGVIENVITVNEIFEQLPFDGIDGNALAYNR-----ENVLG-----VQM	58

130 140 150 160 170 180

1	IGFG-----DPIPDPNTTIPDEPI-TFPMSLATSFLVAYKGQDIY-S-YTNDLVKLEEHL	108
2	IGFG-----DPIPDPNTTIPDEPI-TFPMSLATSFLVAYKGQDIY-S-YTNDLVKLEEHL	108
3	IGFG-----DPIPDPNTTIPDEPI-TFPMSLATSFLVAYKGQDIY-S-YTNDLVKLEEHL	108
4	IGFG-----DPIPDPNTTIPDEPI-TFPMSLATSFLVAYKGQDIY-S-YTNDLVKLEEHL	108
5	IGFG-----DPIPDPNTTIPDEPI-TFPMSLATSFLVAYKGQDIY-S-YTNDLVKLEEHL	108
6	IGFG-----DPIPDPNTTIPDEPI-TFPMSLATSFLVAYKGQDIY-S-YTNDLVKLEEHL	108
7	IGFG-----DPIPDPNTTIPDEPI-TFPVSELATSFLVAYKGQDIY-S-YTNDLVKLEDHL	108
8	IGFG-----DPIPDPNTTIPDEPI-TFPVSELATSFLVAYKGQDIY-S-YTNDLVKLEEHL	108
9	IAFG-----DPIPDPNTTIPDEPI-TFPVSELATSFLVAYKGQDIY-S-YTNDLVKLEDHL	108
10	IGFG-----DPIPDPNTTIPDEPI-TFPMSLATSFLVAYKGQDIY-S-YTNDLVKLEEHL	108
11	IGFG-----DPIPDPNTTIPDEPI-TFPMSLATSFLVAYKGQDIY-S-YTNDLVKLEEHL	108
12	IGFG-----DPISDNTTIPDEPI-TFSMSELATSFLVAYKGQDIY-S-YTNDLVKLEEHL	108
13	IGFG-----VPIPDNTTIPDEPI-TFPMSLATSFLVAYKVQDIY-S-YTNDLVKLEEHL	108
14	IGFG-----DAIEDQTSLPEEPV-IFPMTEFATQFVVSYTGQDVY-S-DTNNLLQVEHDS	108
15	IGQC-----GTIAEDTKQPNDTNRIYRFAEIATQFRVCYKAQDIFSS-NVNDQVAVQMAL	111
16	IGQN-----SPIPEDTKQPNDPNRVRFAEIATHFRVSYKAQDIFSS-NANDQVAVQMAL	111
17	IGQN-----SPIPEDTKQPNDPNRVRFAEIATHFRVSYKAQDIFSS-NANDQVAVQMAL	111
18	LGQC-----DTISEDTKQPNDLNVRHRFAEIATHFRVSYKAQDIFSS-NVNDQVAVQMAL	111
19	IGFE-----EGILEDTKMPNDQKRAFAAEIATQFRVSYKAQDVFSS-NVNDQVSVQMAL	111
20	INQC-----DSIAADTKQPHDTNRIYRFAEIATQFRVCYKAQDIFSS-NVNDQAAVQMAL	112
21	IGFE-----EGIVEDTKMPNDASRVFSFAEIATQFRVSYKAQDIFSS-NVNDQVSVQMAL	111
22	IGFE-----EGIVEDTKMPNDPSRVFTFAEIATQFRVAYKAQDIFSS-NVNDQVSVQMAL	111
23	IGFE-----EGIVEDTKMPNDASRVFSFAEIATQFRVSYKAQDIFSS-NVNDQVSVQMAL	112
24	IGFE-----EGIVEDTKMPSDASRVFSFAEIATQFRVSYKAQDIFSS-NVNDQVSVQMAL	111
25	IGFE-----EGIMEDTKMPNDQKRNFTEFAEIATHFRVSYKAQDVFSS-NVNDQVSVQMAL	111
26	IGFE-----EGIVEDTKMPNDASRVFSFAEIATQFRVSYKAQDIFSS-NVNDQVSVQMAL	111
27	IGQN-----DTIPEDTKQPADPNRVRHRFAEIATHFRVSYKAQDIFSS-NVNDQVAVQMAL	111
28	IGFE-----EGIVEDTKMPSDASRVFSFAEIATQFRVSYKAQDIFSS-NVNDQVSVQMAL	111
29	ANLNS-EC-GPVTDRSQPTDPEVVFGLANIITRYSVCFDDQDKF-S-NPNNLDRTEYVL	112
30	ANLNS-EC-GPVTDRSQPTDPEVVFGLANIITRYSVCFDDQDKF-S-NPNNLDRTEYVL	118
31	ADFNS-SC-GQVTLHTDQP-DSTVTFGLANLITRYQVCFDDQDKF-E-IPNNLDETEYVL	114
32	ADFNS-SC-GQVTLHTDQP-DSTVTFGLANLITRYQVCFDDQDKF-E-IPNNLDETEYVL	114
33	ADFNS-SC-GQVTLHTDQP-DSTVTFGLANLITRYQVCFDDQDKF-E-IPNNLDETEYVL	114
34	ATILGDGATSGITVQTAADPDNPNTTFTLGELETTRYKIDYSSMDRF-K-VPNNLDAVESAL	119
35	ATILGDGTD--ITDKTANADTS-KTFTVGELATTRYKVDYNAQDRY-R-F-QSIDAVEAVL	130
36	-----MSELATSFLVAYKGQDIY-S-YTNDLVKLEEHL	31
37	ATILGEGGTSGIAVQTAADPAASNATFTLGELETTRYKIESSMDRF-K-YPNNLDAVESAL	119
38	ADLSTGTCSEVTERDSP-DSEAVFELVSLMTRYQICMADLDLV-R-YPEQLKQIEFEL	112
39	NGFG-----TVIPDQTSMPDPQI-LFVLKQLATSYQVAPEAQDVD-S-AINNQKEIQDDL	108
40	ADILGDGDTA-VTEQANDPDASNTTFTIGALATTRYFLDYASTDRF-K-YPNDFDAVESAL	118
41	IGYG-----SPLLDQTTIPNVPI-TYPFIDLATSFRISVKALDTCS-GTNNLVLIQIKL	108
42	AEISDGGCTTEVPERTDQP-DSEAIFELVLTIMTRFQICMADIDRI-R-DPELLKQVLGVL	112
43	ASVLT-GCSTEVTEHTDQP-DSEAVFELVTLTMTRYQICMADLDRI-Q-DPELLKQVYWEL	111
44	AEISAGGCDAVPERTDQP-DSEAIFELVTLITRFFQICMADIDRI-R-DPELLKQVLGVL	112
45	ADLSTGCDSEVSDRTDSP-SSEAIFELVSLMTRYQICMADLDLV-R-YPEQLKQIEFEL	112
46	MA----DC-ATVLEQLPDI--SQAEMTFLDYVTRWQACASDLDRY-R-NPQLLQAIMFAA	106
47	IT----AC-ANVPEQEAV--SQAGFEFVDFATRYAICASDLDRF-R-HPQLLQSVFYAI	106
48	MA----DC-TTVEEQLPDI--SQAEMTFLDYVTRWQACASDLDRY-R-NPQLLQAIMFAA	106
49	MA----DC-TTVEEQLPDI--SQAEMTFLDYVTRWQACASDLDRY-R-NPQLLQAIMFAA	106
50	MA----DC-ATVLEQLPDI--SQAEMTFLDYVTRWQACASDLDRY-R-NPQLLQDIMFAA	106
51	KS----DC-TEVTEALPTV--SQATFSLDFIARYAICGVLDdrv-Q-FPTQLDAARYAI	106
52	AG----AC-LPKDHSDDEA-TQAKFGFLEYATRLVICNADEDTL-R-VPNPPEEEVEL	106
53	-DTGG----TAISDTSAVPSDPDVTFPLKLVLVTSFKVNATAEYDM-S-NVNDQVEVQMV	112
54	AQILGDNTPA-ITDKTADADTS-VTFTVGELATSYLLDYTAQDRF-R-Y-QSIDAVESVL	102
55	-DAGG----TAVGDTPAVPTSPDVTYALKLLISAVKSNYTAQYTM-S-NVNDQEQVQISA	112
56	ANLNS-EC-GPVTDRSQPTDPEVVFGLANIITRYSVCFDDQDKF-S-SPNNLNDHTEYVL	112

57	NT ---- GC - SNVAETADTL -- ASITFPVVDFVVRKQICFTDADRY - H - LPNNPDEDEYL V	107
58	ATILADGAD -- ITDQTAGVDET - VTFTCGELASRYKIDYNAQDRW - R - Y - QSIDNALAII	114
59	- DEGG ---- SAISDTSAVPSSPNVTFPLKLVATSFKVNDTAEALM - S - SVNDQVETQSVA	112
60	VD ---- PC - QSADDISTSV -- TPARFGMVEYVARVPVCMAQDIF - Q - HPNDITDFNITL	106
61	- DAGG ---- TAVSDTPAVPTSPNATFSKL LISA AKTN YTAQYDM - S - NVNDQEGVQINA	112
62	MT ---- AC - GTVDEQLPDL -- SQAEMVFVVDYATTRYTICASDLDRY - R - NPLLLQAILFAV	106
63	AG ---- AC - LPIKDHSDEA -- TQVQFGMVEYATRVVICNAADEDTQ - R - GPNTPELNETVL	106
64	- DAGG ---- TALSDTPAVPNDPNVSFSLKLLATSFKVNYTAEYDM - S - NVNDQVEVQTVA	112
65	- DAGG ---- TAVSDTPAVPTSPNPTFSKL LISMVKTNQTAQYTM - S - NVNNQEVALAA	112
66	RN ---- DC - GEVIEQLPTV - SQAAFNLYDFIAHYSICSIDLDRV - Q - YPTQLDAAMFAI	106
67	VP ---- PC - DAVPDRSSVF -- SQATFGMTYLNTRVRVCHANQDTF - R - TPITPEAAEYPL	106
68	LPF ---- C - APIADQTT - VPVARSYSFGELET SRIVCYGTQDLQ - S - NVNDQSAVQLEM	108
69	LPF ---- C - GPIADQTT - VPAARSYSFGEVATSRIVCYGTQDLQ - S - NVNDQAAVQIEM	124
70	LGQ ---- CKDYTDQSFD - SWQERVFDGFAPATMYQSCESAIKYTS - SINDVIDAQYAK	114
71	LGQ ---- CEDYTDQSFD - SWQERVFSFGAPATMYQSCESAIKYTS - SINDVIDVQYAK	165
72	LGQ ---- CEDYTDQSFD - SWQERVFDGFAPATLYQSCESAIKYTS - SINDVIDVQYAK	160
73	LGQ ---- CEDYLDQSFD - SWQERVFDGFAPATLYQSCESAIKYTS - SINDVIDVQFAK	114
74	IDV - N ----- DDVPEGAA - TFEEVVCR LARLAGDV DVDFKFLDETM - S - DIN DQKATQIAS	108
75	FT ---- SC - AGVPEQEATV - SQAEFQFVDFATRYAICASDLDRF - R - NPQLLQTVLYAI	106
76	----- VTDRTSQPTDPEVVFGLANII TRY SVC FDDQDKF - S - NPNNLDRT EYVL	47
77	VA ---- PC - EPADDISTQV - TPARFGM VQYVARVPVCMAQAIY - R - HPTDIVDGVAL	106
78	LDP - Y ----- EDVPEGAA - TFDPVSTR LRLAGQVLLDKFLIKTQ - S - DVNDQLAEQISA	108
79	ANFNS - EC - GPVTDRTSQ PANPEVVFGLANII TRY SVC FDDQDKF - S - NPNNLDHAEYVL	112
80	LDP - N ----- EVVPEEAS - TFEEVVARLRLIGDV DVDFKFLNTTM - D - DTNNQKAIQIAQ	108
81	LDPVN ----- DTVNEEAS - TFTEV TANLRLVLAGDV DVDFKFLDATM - G - DHNSQKAIQIAQ	109
82	LDP - N ----- EAIPESGS - DFDEVTAKL KILAGDV DVDFKFLMETM - S - DVNSQLGLQLAA	108
83	LDA - Y ----- EAVPEGAA - TFDEVTTKLKVLAGDV D IDKFTA AVQ - S - NLNPQVAIQLAA	108
84	LDA - Y ----- EAVPEGAA - TFDEVTTKLKVLAGDV D IDKFTA AVQ - S - NLNPQIAIQLAA	108
85	LDA - Y ----- EAVPEGAA - TFDEVTTKLKVLAGDV D IDKFTA AVQ - S - NLNPQIAIQLAA	108
86	LDA - Y ----- EAVPEGAA - TFDEVTTKLKVLAGDV D IDKFTA AVQ - S - NLNPQIAIQLAA	108
87	LGA ----- CLDYTLQDYE - I - EQATYVY GELVSAF QTCS TTQD - ITG - GPNNLNNA LRKK	106
88	AQVLGDNTPA - IADKTADADTS - VTFVGELATSYLLDYTA KDRFSS - Y - QSIDNVESVL	57
89	LDA - Y ----- EAVPEGAA - TFDEVTTKLKVLAGDV D IDKFTA AVQ - S - NLNPQVAIQLAA	108
90	LDP - Y ----- EVVPEGAA - TFKEVMTKLRLAGDV D LDKFLITTQ - S - DTNDQLAQIAQ	108
91	VS ---- DC - SLVDEQVPTI - SEAEFALQEFITRYKICTFDLDSY - Q - FPNQLETVLYAL	65
92	LGA ----- CLDYTLQDYE - I - EQATYIY GELVSAF QTCS TTQD - ITG - GPNNLNNA LRKK	106
93	LGA ----- CLDYTLQDYE - I - EQATYIY GELVSAF QTCS TTQD - ITG - GPNNLNNA LRKK	106
94	LSP - Y ----- DPVPEGAA - TFDEVSTKLRLAGDV D IDKFTAETQ - S - DLNDQIAIQLQG	108
95	LDA - Y ----- EAVPEGAA - TFDEVTAKL KVLAGDV D IDKFTA AVQ - S - HLNPQIAIQLAA	108
96	LDP - N ----- DVVPEEAS - TFQEVVAKLRLAGHV D LDN FILETQ - S - DTNSQIVTQLAA	108
97	LDP - Y ----- EDIKEGAA - TFEEVQAKLRLAGHV D LDN FILETQ - S - DT HDQLAQIAQ	108
98	LDV - N ----- EVVPEGTS - DVEEVVTKLRLAGDV DVDFKFI DETM - S - DKNSQLALQIAM	108
99	LDP - Y ----- EDIPEGAA - TFDEVQAKLRLAGHV D LDN FILETQ - S - ETNPQLAIQLAA	108
100	LDV - N ----- EIVPEGAS - DVEEVVTKLRIIAGDV DVDNFLNETM - S - DTNSQLALQIAL	108
101	IDPVVT ----- DTVPEGAA - TFESVTETLKVLIGDV DVDNFL RETM - S - DTNNQFETQIAA	109
102	AQPL ----- DYNAAIADSTMAP - SANVTFPGVVASRYRIAYSALGRF - D - ANQDLDAVEAAL	112
103	LDV - N ----- EVVPEGTS - DVEEVVTKLRLAGDV DVDFKFI DETM - S - DKNSQLALQIAM	108
104	LDP - N ----- EEIKESAS - TFEEVTAKLRLAGDV D IDKFLDSTM - D - DTNNQMAIQVTQ	108
105	LDP - N ----- EVIEEEGS - TFDEVTAKLRLAGDV D IDKFLDSTM - G - DTNAQKAIQIKQ	108
106	LDP - N ----- EVIEEEGS - TFDEVTAHLRILAGDV DVDFKFLDSTM - G - DTNAQKAIQIKQ	106
107	LDP - N ----- DPITESAA - TFTEVVAKLRLILGVGDV DVDFKFLQATM - G - DTNDQMAIQIAK	108
108	LDP - N ----- EVIEEEGS - TFDEVTAHLRILAGDV DVDFKFLDSTM - G - DTNAQKAIQIKQ	108
109	LDP - N ----- EVIEEEGS - TFDEVTAHLRILAGDV DVDFKFLDSTM - G - DTNAQKAIQIKQ	108
110	LDP - N ----- EVIEEEGS - TFDEVTAHLRILAGDV DVDFKFLDSTM - G - DTNAQKAIQIKQ	108
111	LDP - N ----- EEPESAA - TFTPITVTLKIIAGDV DVDFKFIQATE - S - DTNDQKAVQIAA	108
112	LDP - N ----- EVIEEEGS - TFDEVTAHLRILAGDV DVDFKFLDSTM - G - DTNAQKAIQIKQ	110
113	LDP - N ----- EVIEEEGS - TFDEVTAHLRILAGDV DVDFKFLDSTM - G - DTNAQKAIQIKQ	108
114	LDP - N ----- EVIEEEGS - TFDEVTAHLRILAGDV DVDFKFLDSTM - G - DTNAQKAIQIKQ	108
115	LDV - N ----- EVVPEGAS - EVEEVVTKLRIIAGDV DVDFKFLNETM - S - DTNQQLAIQIAM	108
116	LDP - N ----- DEVPE SAS - KFVEVTTKLRLAGDV DVDFKFLASTM - G - DTNPQKALQIAA	108
117	LDP - N ----- EEIKESAS - TFEEVTAKLRLAGDV D IDKFLGSTM - D - DTNNQMAIQVTQ	108
118	LDP - N ----- EEIKESAS - TFEEVTAKLRLAGDV D IDKFLDSTM - D - DTNNQMAIQVTQ	108
119	LDP - N ----- DEVPE SAS - KFVEVTTKLRLAGDV DVDFKFLASTM - G - DTNPQKALQIAA	108
120	LDV - N ----- EVVPENAS - TFKEVTTKLRLILGVDF DVDFKFLMAETM - S - DTEDQLGVQIAL	108
121	LDP - N ----- EVIEEEGS - TFDEVTAHLRILAGDV DVDFKFLDSTM - G - DTNAQKAIQIKQ	108
122	LDP - N ----- EVIEEEGS - TFDEVTAHLRILAGDV DVDFKFLDSTM - G - DTNAQKAIQIKQ	108
123	LDP - N ----- DEITEGAS - TFTEVVAKLRLAGDV D IDKFLETTM - G - DTNSQM KI QISK	108

124	LDP-N---	EVIEEEGS-	TFDEVT AHLRILAGDV DVDFKFL DSTM-G-DTNAQKAIQIKQ	108
125	LDP-N---	EVIEEEGS-	TFDEVT AHLRILAGDV DVDFKFL DSTM-G-DTNAQKAIQIKQ	108
126	LDP-N---	EVIEEEGS-	TFDEVT AHLRILAGDV DVDFKFL DSTM-G-DTNAQKAIQIKQ	108
127	LDP-Y---	EDITEGAA-	TFEEVQAKLRLAGHVD LDNF VETQ-S-DTQDQLAVQLAA	108
128	LDP-Y---	EDITEGAA-	TFEEVQAKLRLAGHVD LDNF VETQ-S-DTQDQLAVQLAA	108
129	LSP-N---	DTVNEDAG-	TFDEVVSKLRLILAGDV DVDFKFL QETD-S-DTNDQRATQIAM	108
130	LSP-N---	DTVNEDAG-	TFDEVVSKLRLILAGDV DVDFKFL QETD-S-DTNDQRATQIAM	108
131	LSP-N---	DTVNEDAG-	TFDEVVSKLRLILAGDV DVDFKFL QETD-S-DTNDQRATQIAM	108
132	LDP-N---	EVIEEEGS-	TFDEVT AHLRILAGDV DVDFKFL DSTM-G-DTNAQKAIQIKQ	108
133	AGVGD---	TITAKNAT-	TFTSVTSVLTSILGDAEVNGLVQATQ-S-GETNQTAQQIAS	110
134	LSP-N---	DTVNEDAG-	TFDEVVSKLRLILAGDV DVDFKFL QETD-S-DTNDQRATQIAM	108
135	LDP-N---	EVIEEEGS-	TFDEVT AHLRILAGDV DVDFKFL DSTM-G-DTNAQKAIQIKQ	108
136	LDP-N---	DEIHESAS-	KFTEVTTNLRLILAGDV DVDFKFL MATM-G-DTNDQLALQLAQ	108
137	LDP-Y---	DTVPEGGA-	EFDEVVAKLRLILGDVDIDNFLDETM-S-DTNDQTATQIAA	108
138	LDP-N---	DPVNESAA-	TFTEVVAKLRLILAGDV DVDFKFL QSTM-G-DTNDQMAIQIAK	108
139	LDP-Y---	DPVPEGAA-	TFTEVTRRLRLILAGDV DMDFKFL STQ-S-DKNPQLAIQIAA	108
140	LDP-N---	DAVPEGAA-	KFSEHVAKLRIIAGDV DVDFKFIQTTM-S-DTSDQLATQVRL	108
141	LDP-N---	EEVPEGAA-	KFTEVTTALRVLAHDV DIDKFLASSE-S-DVNDQVALQIAA	108
142	VDP-Y---	EVLEESAS-	TFTSHSTKIRRFAGQV DIDNFMDEVQ-S-NLPNQTAIQLAS	108
143	LDP-N---	DAVPEGAA-	KFSEHVAKLRIIAGDV DVDFKFIQTTM-S-DTSDQLATQVRL	108
144	MDP-Y---	DDFEESAA-	TFTEVSTKLKILGGDILLDKFTTATQ-S-ALNDQVGIQLQK	108
145	LDP-Y---	DVVPEGAA-	TFEEVVTRRLRLILAGDV DLDKFL MSTM-S-DANPQLAIQLAA	108
146	LDP-Y---	DVVPEGGA-	DFDEVVVAKLRLILGDVDIDNFLDETM-S-DTNDQTATQIAA	108
147	IDV-N---	DTITEGAA-	TFTEHVAKLRLILAGDV DVDFKFL ATT M-S-DTNQQLAIQVRQ	108
148	IDV-N---	DTITEGAA-	TFTEHVAKLRLILAGDV DVDFKFL ATT M-S-DTNQQLAIQVRQ	108
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153	MDP-Y---	DDFEESAA-	TFQEVS TKLKILGGDILLDKFTTATQ-S-ALNDQVGIQLQK	108
154	IDV-N---	DTITEGAA-	TFTEHVAKLRLILAGDV DVDFKFL ATT M-S-DTNQQLAVQVRQ	108
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156	IDV-N---	DTITEGAA-	TFTEHVAKLRLILAGDV DVDFKFL ATT M-S-DTNQQLAIQVRQ	108
157	IDV-N---	DTITEGAA-	TFTEHVAKLRLILAGDV DVDFKFL ATT M-S-DTNQQLAIQVRQ	108
158	IDV-N---	DTIAEGAA-	TFSEHVAKLRLILAGDV DVDFKFL ATT M-S-DTNQQLAVQVRQ	108
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161	LDP-N---	EEIKESAA-	TFEEVTAKLRLILAGDV DIDKFL DSTM-D-DTNQQLAIQVTQ	108
162	LDP-S---	ETVNEGAA-	TFEEIVTRRLRLILGDVDV DKFM MQGTL-S-DHNNQKAIQIAQ	108
163	IDV-N---	DTIAEGAA-	TFSEHVAKLRLILAGDV DVDFKFL ATT M-S-DTNQQLAVQVRQ	108
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189	IDV-N---	DTIPEGAA-	TFEECVAKLRLILAGDV DVDFKFL ATT M-A-DTNQQLAIQVRQ	108
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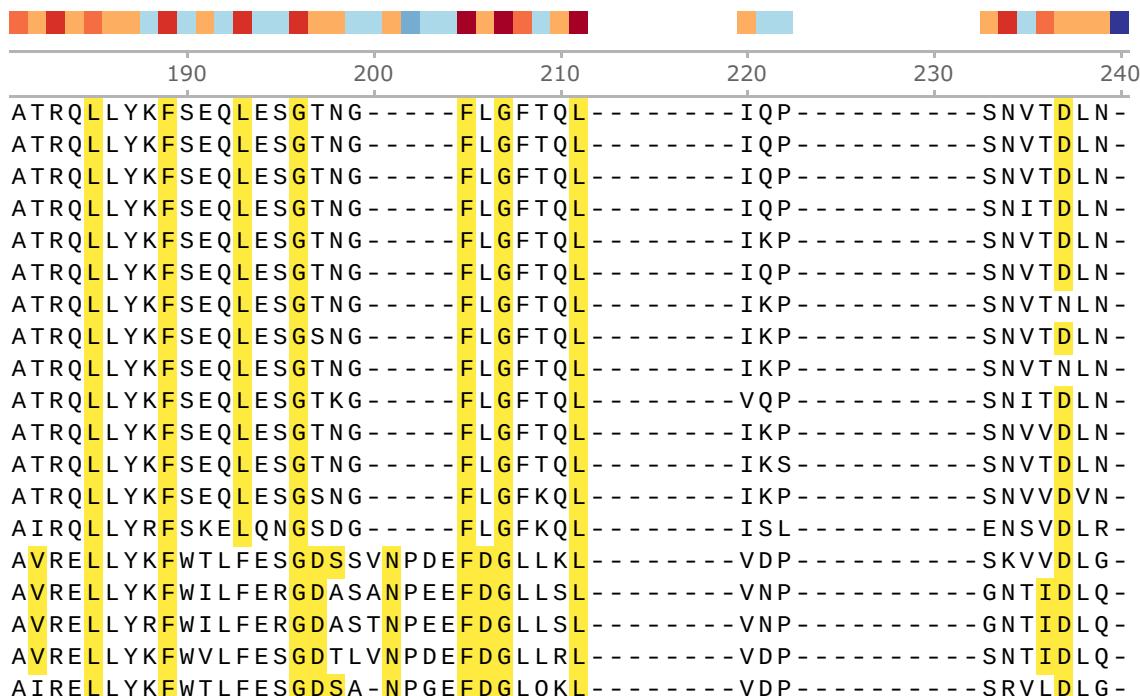
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192	LSA	-Y-----	EDVPEGAA	-TFDEV	STKCKVLAGQILLDNFTTESM	-S	DLN PQLG I QIRS	108
193	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
194	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
195	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
196	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
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198	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
199	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLSTTM	-A	DTNNQLAIQVRQ	108
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205	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
206	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLCLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
207	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
208	IDV	-N-----	DTIPEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
209	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
210	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
211	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
212	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
213	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
214	IDV	-N-----	DTIAEGAA	-TFSEH	VAKLRLILAGDVVDVKFLATTM	-S	DTNNQLAVQVRQ	108
215	IDV	-N-----	DTITEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
216	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
217	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
218	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
219	IDV	-N-----	DTITEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
220	IDV	-N-----	DTITEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
221	IDV	-N-----	DTIPEGAA	-TFEEC	I A K L R I L A G D V D V D K F L A T T M	-A	DTNNQLAIQVRQ	108
222	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
223	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
224	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
225	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
226	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
227	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
228	LDP	-N-----	EVVNESAS	-TFTEV	VAKLRLILIGD V DV D K F L Q T T Q	-S	DHNNQLAIQIAK	108
229	IDV	-N-----	DTITEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
230	LDP	-N-----	EVVNESAS	-TFTEV	VAKLRLILIGD V DV D K F L Q T T Q	-S	DHNNQLAIQIAK	108
231	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
232	IDV	-N-----	DTIAEGAA	-TFSEH	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
233	IDV	-N-----	DTITEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
234	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
235	IDV	-N-----	DTIPEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
236	IDV	-N-----	DTITEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
237	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
238	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
239	YDV	-G-----	DTWTESTP	-T FEQVT	T G L K I L G G D A D I D H F L L Q T Y	-R	D PNQLEAVVLQQ	108
240	IDV	-N-----	DTIAEGAA	-TFSEH	VAKLRLILAGDVVDVKFLATTM	-S	DTNNQLAVQVRQ	108
241	IDV	-N-----	DTITEGAA	-TFSEH	VAKLRLILAGDVVDVKFLATTM	-S	DTNNQLAIQVRQ	108
242	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
243	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
244	IDV	-N-----	DTITEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
245	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
246	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
247	IDV	-N-----	DTITEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
248	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
249	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
250	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
251	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S	DTNNQLAIQVRQ	108
252	IDV	-N-----	DTISEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
253	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
254	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
255	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A	DTNNQLAIQVRQ	108
256	IDV	-N-----	DTITEGAA	-TFSEH	VAKLRLILAGDVVDVKFLATTM	-S	DTNNQLAIQVRQ	108
257	IDV	-N-----	DTITEGAA	-TFSEH	VAKLRLILAGDVVDVKFLATTM	-S	DTNNQLAIQVRQ	108



325	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
326	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
327	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
328	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
329	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
330	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
331	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
332	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
333	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
334	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNSQLAIQVRQ	108
335	IDV	-N-----	DTIAEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
336	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
337	IDV	-N-----	DNITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
338	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
339	IDV	-N-----	DTIAEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
340	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
341	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
342	IDV	-N-----	DTIAEGAA	-TFSEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAVQVRQ	108
343	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
344	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
345	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
346	IDV	-N-----	DTITEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
347	IDV	-N-----	DTIPEGAA	-TFEEC	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
348	IDV	-N-----	DTISEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNSQLAIQVRQ	108
349	IDV	-N-----	DTITEGAA	-TFSEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
350	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
351	LDP	-N-----	EVIEEGS	-TFDEVTAHLRILAGDVVDVKFLDSTM	-G-	DTNAQKAIQIKQ	89	
352	IDV	-N-----	DTIAEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
353	AGVGT	-TITAKSPA	-TFTQVTSSLTSLLGDAEVNGLIQATR	-S-	NIQDQKAIQVAS		110	
354	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	105
355	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNSQLAIQVRQ	108
356	IDV	-N-----	DTIAEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
357	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
358	IDV	-N-----	DTITEGAA	-TFSEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
359	IDV	-N-----	DTITEGAA	-TLEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
360	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
361	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
362	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
363	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
364	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
365	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNSQLAIQVRQ	108
366	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
367	IDV	-N-----	DTISEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNSQLAIQVRQ	108
368	IDV	-N-----	DTIAEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNSQLAIQVRQ	108
369	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
370	IDV	-N-----	DTIIEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
371	IDV	-N-----	DTISEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
372	IDV	-N-----	DTIAEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
373	IDV	-N-----	DTITEGAA	-TFIEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
374	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
375	IDV	-N-----	DTIAEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
376	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
377	YEV	-G-----	DTWTESTP	-TFTQVTTGLKILGGDADIDHFLQTY	-R-	DPNELEAIVIQS		108
378	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
379	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
380	IDV	-N-----	DTISEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNSQLAIQVRQ	108
381	IDV	-N-----	DTISEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNSQLAIQVRQ	108
382	IGVGD	-TITAKAAA	-TFTQVTSLNTKIIGDAEVVDGLIQT	-S-	ADNDQTGVQIAS		110	
383	IDV	-N-----	DTIAEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
384	IDV	-N-----	DTISEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNSQLAIQVRQ	108
385	IDV	-N-----	DTITEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNNQLAIQVRQ	108
386	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
387	IDPYN	-N-----	DTVPEEAS	-TVTDVTVLKTLIGDVVDVKFSEATK	-S-	DTNDQKALQIAM		109
388	IDV	-N-----	DTIAEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNSQLAIQVRQ	108
389	IDV	-N-----	DTITEGAA	-TFEEK	VAKLRLILAGDVVDVKFLATTM	-A-	DTNNQLAIQVRQ	108
390	AGVGA	-TITAKAAT	-TFTSVTSVLTSILGDAEVNGLVQATQ	-S-	PDTDQTAQQIAS		110	
391	IDV	-N-----	DTISEGAA	-TFTEH	VAKLRLILAGDVVDVKFLATTM	-S-	DTNSQLAIQVRQ	108

392	IDV	-N-----	DTITTEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNNQLAIQVRQ	108
393	IDV	-N-----	DTITTEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNNQLAIQVRQ	108
394	IDV	-N-----	DTISEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
395	IDV	-N-----	DTIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
396	IDV	-N-----	ETIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
397	AGVGS	---	TITAKNP	-TFTQVTSTLTTIIGDAEVNGLIQATR	-SGDGNDQTAQVQVAS	111
398	IDV	-N-----	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
399	IDV	-N-----	DTIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNNQLAIQVRQ	108
400	IDV	-N-----	DTISEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
401	IDV	-N-----	DTISEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
402	IDV	-N-----	DTIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
403	IDV	-N-----	DTITTEGAA	-TFEEKVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
404	IDV	-N-----	DTITTEGAA	-TFEEKVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
405	IDV	-N-----	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
406	IDV	-N-----	DTIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVCQ	108
407	IDV	-N-----	DTITTEGAA	-TFEEKVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
408	IDV	-N-----	DTITTEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNNQLAIQVRQ	108
409	IDV	-N-----	DTISEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
410	IDV	-N-----	DTISEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
411	IDV	-N-----	DTIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
412	IDV	-N-----	DTISEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
413	IDV	-N-----	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
414	IDV	-N-----	DTIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
415	IDV	-N-----	DTIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
416	IDV	-N-----	DTISEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
417	IDV	-N-----	ETIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
418	IDV	-N-----	DTITTEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNNQLAIQVRQ	108
419	YDA	-Y-----	EDIEESAA	-KYVEVETKLKVLAGQVDIDNFTAETQ	-S-ELNDQVALQLAA	108
420	IDV	-N-----	DTIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
421	IDV	-N-----	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
422	IDV	-N-----	DTIAEGAA	-TFSEHVAKLRLILAGDVVDVKFLATTM	-S-DTNNQLAVQVRQ	108
423	IDV	-N-----	ETIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
424	IDV	-N-----	DTISEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
425	IDV	-N-----	DTIAEGAA	-TFSEHVAKLRLILAGDVVDVKFLATTM	-S-DTNNQLAVQVRQ	108
426	IDV	-N-----	DTIAEGAA	-TFSEHVAKLRLILAGDVVDVKFLATTM	-S-DTNNQLAVQVRQ	108
427	IDV	-N-----	DTIAEGAA	-TFSEHVAKLRLILAGDVVDVKFLATTM	-S-DTNNQLAVQVRQ	108
428	IDV	-N-----	DTISEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
429	IDV	-N-----	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
430	IDV	-N-----	DTIAEGAA	-TFSEHVAKLRLILAGDVVDVKFLATTM	-S-DTNNQLAVQVRQ	108
431	IDV	-N-----	DTISEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
432	ATVGD	---	TITAKNA	-TFTKVNNSNLTTIIGDAEVNGLIQATR	-S-ATTDQEATQIAS	110
433	IDV	-N-----	DTITTEGAA	-TFEEKVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
434	IDV	-N-----	DTITTEGAA	-TFEEKVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
435	IDV	-N-----	DTITTEGAA	-TFEEKVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
436	IDV	-N-----	DTIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
437	IDV	-N-----	DVVPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
438	IDV	-N-----	DTIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
439	LDP	-N-----	DTVQESAS	-TFTEVVAKLRLILIGDVVDVKFLQATM	-S-DHNNQLAIQIAK	108
440	IDV	-N-----	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
441	YEV	-G-----	DTWTESTP	-TFTQVTTGLKILGGDADIDHFLQQTY	-R-DPNELEAIVIQS	108
442	IDV	-N-----	DVIPEGAA	-KFTEHVAKLRLILAGDVVDVKFLASTM	-G-DTNSQLAIQIRA	108
443	IDV	-N-----	EVIPEGAA	-TFTEHTAKLRIIMAGDVVDVKFLATTM	-D-DTNSQLAIQVRQ	108
444	LGVGG	---	TITAKAAT	-TFTQVTPLKRIVGDAEVDNFVEATH	-S-DTTDQEAVQVAG	110
445	IGVGG	---	TITAKTAA	-TFTQINSNLTKIIGDAEVDNMIQATR	-S-SINDQTGQQIAS	110
446	IDV	-N-----	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
447	IDV	-N-----	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
448	YDV	-G-----	DTWAEATP	-TFTQVTVPRLILGGDADIDNFLQQTY	-A-NPNDLEAVVLES	106
449	IDV	-N-----	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLSTTM	-A-DTNNQLAIQVRQ	108
450	IDV	-N-----	DTITTEGAA	-TFEEKVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
451	YDV	-G-----	DTWTESTP	-TFEQVTTGLKILGGDADIDHFLQQTY	-R-DPNQLEAVVLQQ	108
452	YDV	-G-----	DTWEETATP	-EFTQVTVALKILGGDADVDNFLQQTY	-A-DPNDLEAVVIES	108
453	IDV	-N-----	DTIAEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108
454	AGVGS	---	TITAKAPA	-TFTQVTSTLTTIIGDAEVNGLIQATR	-SGDGNDQTAQVQVAS	111
455	LSP	-N-----	DTVNEDAG	-TFDEVVSKLRLILAGDVVDVKFLQETD	-S-DTNDQRATQIAM	108
456	IDV	-N-----	DTITTEGAA	-TFEEKVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
457	IDV	-N-----	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNNQLAIQVRQ	108
458	IDV	-N-----	DTISEGAA	-TFTTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAIQVRQ	108

459	LDP-N	DVVPESTG	-DFTEVVTKLRLILAGDVVDVKFLAETM	-S-DTENQLATQIGL	108
460	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAIQVRQ	108
461	AGVGS	-TITAKNPA	-TFTQVTSTLTTIIGDAEVNGLIQATR	-SGDGNDQTAQVQVAS	111
462	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAIQVRQ	108
463			-MASQDIF-R-HRNDLVDFSVTL		20
464	IDV-N	DTIAEGAA	-TFSEHVAKLRLILAGDVVDVKFLATTM	-S-DTNQNLAQVVRQ	108
465	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAIQVRQ	108
466	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAIQVRQ	108
467	IDV-N	DTITEGAA	-TFEEKVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAIQVRQ	108
468	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAIQVRQ	108
469	IDV-N	DVVPEGAA	-TFTEHVAKLRIIAGDVVDVKFLASTM	-G-DTNSQLAQVVRQ	108
470	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAIQVRQ	108
471	AGVDA	-TITAKAPA	-TFTKVTSELTTIIGDAEVNGLIQATR	-SSDGNDQTAQVQVAS	111
472	LDP-N	DPINESAA	-TFEEVVAKLRLILAGDVVDVKFLNQTM	-S-DTNSQMATTQIAK	108
473	AGVDA	-TITAKAPA	-TFTKVTSELTTIIGDAEVNGLIQATR	-SSDGNDQTAQVQVAS	111
474	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAIQVRQ	108
475	IDV-N	DTITEGAA	-TFTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNQNLAIQVRQ	108
476	AGVGS	-TITAKNPA	-TFTQVTSTLTTIIGDAEVNGLIQATR	-SGDGNDQTAQVQVAS	111
477	AGVGD	-TITAKNPA	-TFEQITSSLTTLIGDAEVNGLIQATR	-S-NINDQKTVQIMS	110
478	LGVGG	-TITAKAPT	-TFTQVTSAKLRIVGDAEVDNFVEATH	-S-DTDDQLAVQVAG	110
479	AGVGT	-TITAKNPA	-TFTHTVTSTLTTIIGDAEVNGLIQATR	-SGDGNDQTAQVQVAS	111
480	AGVDA	-TITAKAPA	-TFTKVTSELTTIIGDAEVNGLIQATR	-SSDGNDQTAQVQVAS	111
481	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAIQVRQ	108
482	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAIQVRQ	108
483	IDV-N	DVVPEGAA	-KFTEHVAKLRLILAGDVVDVKFLATTM	-A-DTNSQLAQIIRS	108
484	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAIQVRQ	108
485	YDV-G	-DTWQEATP	-EFTQVTVALKILGGDADVDNFLQQTY	-A-DPNDEALAVIES	108
486	IDV-N	DIVPEGAA	-KFTEHVAKLRLILAGDVVDVKFLATTM	-A-DTNSQLAQIIRA	108
487	IDV-N	DTISEGAA	-TFTEHVAKLRLILAGDVVDVKFLATTM	-S-DTNSQLAQVVRQ	108
488	IDV-N	DEVPEGAA	-KFSEHVAKLRLILAGDVVDVKFLASTM	-G-DTNSQMAIQIIRS	108
489	IDV-N	DVVPEGAA	-KFTEHVAKLRLIMAGDVVDVKFLATTM	-A-DTNSQLAQIIRA	108
490	AGVGS	-TITAKNPA	-TFTQVTSTLTTIIGDAEVNGLIQATR	-SGDGNDQTAQVQVAS	111
491	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAQVVRQ	108
492	LGVGS	-SITAKAAT	-TFTQVTSPKLRIVGDAEVDNFIEATH	-S-DTDDQLAVQVAG	110
493	IDV-N	DTITEGAA	-TFFEKVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAQVVRQ	108
494	YDV-G	-DTWSEATP	-TYTQVTASLKILGGDADVDFTLQQTY	-A-DPNDEALVLES	108
495	IDV-N	DTITEGAA	-TFFEKVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAQVVRQ	108
496	IDV-N	DTITEGAA	-TFFEKVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAQVVRQ	108
497	AGNDD	-TITAKSPA	-TFTRVSADLTIIIGDAEINGLIQATR	-S-NITDQKAVQIAS	110
498	IDV-N	DTIPEGAA	-TFEECVAKLRLILAGDVVDVKFLATTM	-A-DTNQNLAQVVRQ	108
499	IDV-N	DEVPEGAA	-KFTEHVAKLRLILAGDVVDVKFLSSTM	-G-DTNSQMAIQIIRS	108
500	AGVGS	-TITAKNPA	-TFTQVTSTLTTIIGDAEVNGLIQATR	-SGDGNDQTAQVQVAS	111



20	AVRELLYKFWMLFEGGDSATNPDEFDGLLKL-----VDP-----SKVVVDLE-	153
21	AIRELLYKFWTLFESGDSV-NAGEFDGLHKL-----ADP-----SRVLDLG-	151
22	AIRELLYKFWILFESGDSA-NAGEFDGLHKI-----VDP-----SRVLDLG-	151
23	AIRELLYKFWTLFESGDSV-NAGEFDGLHKL-----ADP-----SRVLDLG-	152
24	AIRELLYKFWTLFESGDSA-NTGEFDGLYKL-----VDP-----SRVLDLG-	151
25	AIRELLYKFWMLFESGDSA-NPGEFDGLQKL-----VDP-----SRILDLG-	151
26	AIRELLYKFWTLFESGDSA-NTGEFDGLHRL-----VDS-----SRVLDLG-	151
27	AVRELLYRFWILFERGDTSTNPEEFDGLLRL-----VNP-----DNTIDLQ-	152
28	AIRELLYKFWTLFESGDSA-NTGEFDGLYKL-----VDP-----SRVLDLG-	151
29	AVQRLVYRYFRQLGLGATGS--FNFPSLQDV-----VGT-----GQTIDMG-	151
30	AVQRLVYRYFRQLGLGATGS--FNFPSLQDV-----VGT-----GQTIDMG-	157
31	AQMRLVYRYFRRLGQAAAGT--FDFPTLQDV-----VGT-----GQTINMG-	153
32	AQMRLIYRYFRRLGQAAAGT--FDFPTLQDV-----VGT-----GQTIDMG-	153
33	AQMRLIYRYFRRLGQAAAGT--FDFPTLQDV-----VGT-----GQTIDMG-	153
34	AIRRLMMYMYFRKLDLGGGN-GDFPSLADM-----AVL-----GNVVTSA-	159
35	ACKRLMMYMYARKLDLNGGG-SGDFDSLSDM-----CAA-----GQKVAGG-	170
36	ATRQLLYKFSEQLESGSNG---FLGFTQL-----IKP-----SNVTDLN-	67
37	AIRRLTYMFYRKLDLATTGPN-GDFPSLSDM-----CAA-----GQRFNSA-	159
38	AKIRLLYRYFQRLGETTGAV--TTFPGLTGM-----VGT-----GQTIAMG-	151
39	ANRRLLYAFCRLLLEVGDTTANPNEFDGFLKL-----VNP-----ANVVDKA-	149
40	AIRRLMMYMYFRKLDLNGAGTKVGDFDLSLGE-----AT-----NITTA-	156
41	AIQRLLYKFFNLLEIGNPAINPNEFAGLKKL-----VDP-----FNVVNLLG-	149
42	ADMRLMYRYFQRLDEVGGI--SQFPGLQDM-----VGA-----GKTINMG-	151
43	AKIRLLYGYFRRLGAEATGGI--SQFPGLQDM-----VGA-----GKTINMA-	150
44	ADMRLMYRYFQRLGQATGGV--SQFPGLQDI-----VGA-----GKTINMG-	151
45	AKIRLLYRYFQRLGETGVV--TTFPSLTGM-----VGA-----GQTIAMG-	151
46	AKRRILYAYAQQLDSF--GS--AVGPGLPDL-----CAA-----SQLVDMG-	143
47	AKRRILYAYAARLGAAT-GN--PAQGGLRDL-----ADP-----ARVINLA-	144
48	AKRRILYAYAQQLDSF--GS--AVGPGLPDL-----CAA-----GQLVDMA-	143
49	AKRRILYAYAQQLDSF--GS--AVGPGLPDL-----CAA-----GQLVDMA-	143
50	AKRRILYAYAQQLDSF--GS--AVGPGLPDL-----CAA-----GQLVDMA-	143
51	AKRQVLYAYAQWIV-----NTATGLVTL-----CDA-----SRIVDMA-	139
52	AKIKLDYGYAAHLDVAT-GD--PVFGGLQDI-----VAP-----GNVINVG-	144
53	AVKRLYYKFWETFNTGDNsanPQEFDGLRRL-----VAS-----GQTVTARD	154
54	ACKRLMMYMYFRKLDLNGNTLSGDFDSLFDIANDVAPTMVG-----ANVVDMG-	151
55	AIRRM MYQFWATFNTGNEGANTPQEFDGLQQL-----VTG-----GQTITANA	154
56	AVQRLIYRYFRQLGLAATGS--FNFPSLQDV-----VGA-----GQTIDMG-	151
57	ALAEILIYGYFAWLD---GT--PGTGGLRDY-----IAA-----ARIVDMG-	142
58	ACTRLLLMSFRKLDKVNGGT-EGDYDSLSDYDM-----CDA-----NQIVAGG-	154
59	AIKRLYYKFWGTFTGNSSLNPEEFDGLRQL-----VSS-----GQTLTARD	154
60	AEVQN WYGFYARM DVL T-GN--PSLGGLPDL-----VAP-----SRTLNLG-	144
61	AIRRMLYQFWTTLNTGNEGTPNQEFDGLRQL-----VVA-----GQTITANA	154
62	AKRRILYSYAAQQLDSA--GV--LAAPGLPDL-----CAA-----GQLVDMG-	143
63	AEIKCDYGYYARMDTLT-GD--PVHGGLLDL-----VAP-----GNIINPG-	144
64	AVKRLYYKFWETFNTGDNsvNQEFFDGLRRL-----VVS-----GQTLTARD	154
65	AVRRMTYQFWTAFNTGNEGTPNQEFDGLRQL-----VVA-----GQTVTANG	154
66	AKRQILYAYAEHIV-----SPTIGLPAA-----CDS-----DRNVDMG-	139
67	MIRQLLYGFSERLDAAP-SP--ANPLALRNY-----IEP-----DRIVNLA-	144
68	ACRQLLYGFFRLLFIGN-PVNPGEFIGFDNI-----ITGA-----AFAGQIVDAL-	152
69	ATRQVLYGFFRLLFVGN-PANPGEFIGFDNI-----ITGA-----PFAGQIVDAL-	168
70	ACRQCMYEGFRLLESGISGND-GEFAGLRLSL-----VPA-----NMTVTVG-	154
71	ACRQCMYQGFRLLESGISGND-GEFAGLRLSL-----VPA-----NMTVTVG-	205
72	ACRQCMYQGFRLLESGISGND-GEFAGLRLSL-----VPA-----NMTVTVG-	200
73	ACRQCMYDGFRRLLENGIAGND-GEFAGLRLSL-----VPA-----NMTVTVG-	154
74	KAKALGRKFKRRTLATGDRSVNSKAFDGIAKL-----VAA-----GQTISAGT	150
75	AKRRILYSYAQRLGTAT-GN--PAQAGLRDL-----ADP-----ARVIDLA-	144
76	AVQRLVYRYFRQLGLGATGS--FNFPSLQDV-----VGT-----GQTIDMG-	86
77	GEIENWYGYYGRMDTAT-GD--PVFGGLLDL-----VAP-----GRIVNMG-	144
78	KAKAMGRKFRRTLAI GDGSNAKEFDGIASL-----TPA-----GQTLAAAT	150
79	AVQRLIYRYFRQLGLAATGS--FNFPSLQDV-----VGA-----GQTIDMG-	151
80	KAKGIARKFRRTLANGNASVNAKEFDGVHRL-----VTA-----NQTISAGT	150
81	KAKGLARKFRRTLAIGDNGTNAKEFDGVASL-----VTG-----GQTITAGA	151
82	KAKGMARQFHRTLAMGDS SKNRKEFDGLASL-----TPA-----AQTLVAGK	150
83	KAKGLGRKFKRTIVNGDSSVNAKSFDGIKKL-----TPA-----AQTLVAGA	150
84	KAKGLGRKFKRTIVNGDSSVNAKSFDGIKKL-----TPA-----AQTLIAGT	150
85	KAKGLGRKFKRTIVNGDSSVNAKSFDGIKKL-----TPA-----SQTLIAGT	150
86	KAKGLGRKFKRTIVNGDSSVNAKSFDGIKKL-----TPS-----AQTLIAGT	150

87	AERRLQQLFWELIDTGVAGS--GSFLGLSGL-----LPA-----GQKVVG--	145
88	ACKRLMYMYFRKLDLVNGNTLSGDFDSLFDIAGDV---NSG-----SQIIDMS-	102
89	KAKALGRKFRTIVNGDSSVNAKSFDGVKKL-----TPA-----SQTLIAGT	150
90	KSKALGRKFRRALVQGDSSVNAKEFDGIRAL-----TPA-----AQTLVAGA	150
91	AKRRLLYAYATFIAD---S--NQSGSLVGI-----CDA-----ARVVNMA-	100
92	AERRLQQLFWELIDTGVSGS--GSFLGLSGL-----LPA-----GQRVVVG-	145
93	AERRLQQLFWELIDTGVAGS--GRFLGLAGL-----LPA-----GQRVVVG-	145
94	KAKGIGTRKFRRSLAQGDSSVNAKEFDGIDRL-----VYN-----DQVIVGG-	149
95	KAKGLGRKFRTIVNGDSAVNPKSFDGIKKL-----TPA-----AQTLVAGT	150
96	KAKGVAREFHRTLMLGDSATNAKEFDGLPKL-----VSG-----SQTLISAGA	150
97	KAKGIGRQFRRTLVNGDSSVNRKEFDGVKKL-----VPA-----KQTLIAGK	150
98	KAKGMARTFRRAVVQGNSTDPKSFDGIEKL-----VADT-----GNFFEAGL	151
99	KAKALGRQFRRRTLVNGDSAVNRKEFDGIKKL-----VPA-----KQTLVAGL	150
100	KAKGMATTFRRALVVG DSTVNPKQFDGLEKL-----VTDT-----GNFIEAGV	151
101	KAKGMARKFRRTLAIGDATSNPKEFNGVAKL-----VTA-----GQTITAGT	151
102	AVRNCMNGFFYLLILADAAGG-TGSPPTLVSL-----CTGT-----SQMNDFN-	153
103	KAKGMARTFRRAVVQGDSTVDNKSFDGIEKL-----VKDT-----GNFFEAGV	151
104	KAKGVGRKFHKTLATGDASVNPKEFDGIAKL-----VTE-----EQTISAGP	150
105	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
106	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	148
107	KAKSLAMTFHKTLAQGDASANPKAFDGLPKM-----VTP-----TQTVVG-	149
108	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
109	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
110	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
111	KSKALNRLFKQTLVSGDATANPKQFDGLSKL-----VTA-----GQTMDAAP	150
112	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	152
113	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
114	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
115	KAKGLATTFRRALIQGDSAVNPKSFDGLNKL-----VNDT-----GNYFEAGP	151
116	KAKGMSRQYRAALVEGDSTTNAKQFDGLKKL-----VTT-----TQTLDAK-	149
117	KAKGVGRKFHKTLATGDASVNPKEFDGIAKL-----VTE-----EQTISAGP	150
118	KAKGVGRKFHKTLATGDASVNPKEFDGIAKL-----VTE-----EQTISAGP	150
119	KAKGMSRQYRAALVEGDSATNAKQFDGLKKL-----VTT-----AQTLDAK-	149
120	KAKSMARAFQKSVVNGDSSVNEKEFDGLKAL-----VTA-----EQTIEAGV	150
121	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
122	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
123	KAKGVGRKFHQTLATGDATA NTKA FDGLPKL-----VDA-----SQTTITAGD	150
124	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
125	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
126	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
127	KAKALGMQFRRTLVNGDSTKNRKEFDGVKML-----VPA-----KQTLIAGA	150
128	KAKALGMQFRRTLVNGDTTKNRKEFDGVKAL-----VPA-----KQTLIAGA	150
129	KAKAVGRIFKKTIAQGNASKNPKEFDGLPQL-----VTS-----AMTLDADT	150
130	KAKAVGRIFKKTIAQGNAAKNPKEFDGLPQL-----VTS-----AMTLDADT	150
131	KAKAVGRIFKKTIAQGNAAKNPKEFDGLPQL-----VTS-----AMTLDADA	150
132	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
133	TKT T ASRKYQDMLINGTGAGN--EFLGLLL-----VPS-----AQKVPTGA	150
134	KAKAVGRIFKKTIAQGNASKNPKEFDGLPQL-----VTS-----AMTLDADT	150
135	KAKGVAREFHRTLARGDSKTNAKEFDGFDFKL-----VTS-----TQIVDAGA	150
136	KAKAVGREFRKVLAEGDHDTNAKQFDGISKL-----VTT-----TQKIDAG-	149
137	KAKGMARKFQRTLATGNSTDPKSFDGISEL-----CAD-----NQVLPTSG	150
138	KAKAVAREFHRTLAKG NATANPKEFDGLPQL-----AAAA-----PNSQQVVAGA	153
139	KAKALTRKLKR TLVNGNNNAVNAKEFDGLKVL-----TPA-----EQTLIAGT	150
140	KVKGLARSFKRALVLGDETSNSKSF DGLGRL-----TAS-----DQIIDAA-	149
141	KAKGLRTKFQKTLINGDRSVHSKEFDGIAAI-----SNG-----LGSSQVQVVA	153
142	KAKGMSLQFRSELVNGDTAVNAKSFDGLRK-----TPA-----GQTLGAGT	150
143	KVKGLARSFKRALVLGDETSNSKSF DGLGRL-----TAS-----EQIIDAA-	149
144	KAKAINRTFRNLT VNGDSAVNAKA FDGVKKL-----TPA-----GQTLVAGA	150
145	KAKALGRALRRTIINGDNSVNAKEFDGLKKL-----MPA-----NQTLVAGN	150
146	KAKGMSRKFQRTLATGNSTDPKSFDGIAEL-----CAD-----NQVISADG	150
147	KVKGLARA FRRNLILGDSTTNSKA FDGIPKL-----MHK-----DQKV DIA-	149
148	KVKGLARA FRRNLILGDSTTNSKA FDGIPKL-----MHN-----DQKIDIA-	149
149	KVKGLARA FRRNLILGDSTTNSKA FDGIPKL-----MHK-----DQKV DIA-	149
150	KVKGLARA FRRNLILGDSTTNSKA FDGIPKL-----MHD-----DQKIDIA-	149
151	KVKGLARA FRRNLILGNSETNTKA FDGIPRL-----MHK-----DQKIDIA-	149
152	KVKGLARA FRRNLILGDSTTNSKA FDGIPKL-----MHD-----DQKIDIA-	149
153	KAKAINRTFRNLT VNGDSAVNAKA FDGVKKL-----TPA-----GQTLVAGA	150

154	KVKGLARAFRRNLILGDSTTNTKAFDGIPKL-----	MID-----	DQKIDIA-	149
155	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQNIDIA-	149
156	KVKGLARAFRRNLILGDSTTNSKAFDGIPKL-----	MHD-----	DQKIDIA-	149
157	KVKGLARAFRRNLILGDSTTNSKAFDGIPKL-----	MHD-----	DQKIDIA-	149
158	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-	149
159	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-	149
160	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQNIDIA-	149
161	KAKGVGRKFHKTLATGDASVNPKEFDGIAKL-----	VTE-----	EQTISAGP	150
162	KAKGLARKFKRTLVVGDATSSPKEFDGLGKI-----	AEA-----	ITAGDASRTVVAGT	156
163	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-	149
164	KVKGLARAFRRNLILGDSTTNSKAFDGIPKL-----	MHD-----	DQKIDIA-	149
165	KVKGLARAFRRNLILGDSSANSKAFDGIPKL-----	MHN-----	DQKIDIA-	149
166	KVKGLARAFRRNLILGDSTTNSKAFDGIPKL-----	MHD-----	DQKIDIA-	149
167	KVKGLARAFRRNLILGDSTTNSKAFDGIPKL-----	MHK-----	DQNVDIA-	149
168	KVKGLARAFRRNLILGDSTTNSKAFDGIPKL-----	MHN-----	DQKIDIA-	149
169	KVKGLARAFRRNLILGDSTTNSKAFDGIPKL-----	MHK-----	DQNVDIA-	149
170	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	IHA-----	DQKIDIA-	149
171	KVKGLARAFRRNLILGDSTANSKAFDGIPKL-----	MHN-----	DQKIDIA-	149
172	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQNIDIA-	149
173	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
174	KVKGLARAFRRNLIVGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
175	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
176	KVKGLARAFRRNLILGDSTTNSKAFDGIPKL-----	MHK-----	DQKVIA-	149
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178	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-	149
179	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
180	KVKGLARAFRRNLILGDSTTNSKAFDGIPKL-----	MHK-----	DQNVDIA-	149
181	KVKGLARAFRRNLIVGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
182	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
183	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
184	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
185	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-	149
186	KVKGLARAFRRNLIVGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
187	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
188	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
189	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
190	KAKAVAHKFMETFYVGDTAEDENAFDGLAKL-----	VDA-----	GQEVSMT	150
191	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-	149
192	KAKGLGIKFRTTLVNGDSSQNKKSFBDGIKTL-----	TPA-----	GQTLVAGA	150
193	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
194	KVKGLARAFRRNLILGDSSSTNNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
195	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
196	KVKGLARAFRRNLILGDSISNNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
197	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
198	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
199	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
200	KVKGLARAFRRNLIVGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
201	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
202	KAKSINRVFRNAIVNGSDDVNAKSFDGIKKL-----	TPA-----	SQTLVAGA	150
203	KVKGLARAFRRNLIVGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
204	KAKALAYAFQQTVATGDSGSNAKQFDGLAVL-----	NDN-----	TNQVVSAGT	151
205	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
206	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
207	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
208	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
209	KVKGLARAFRRNLILGDSSSNKAFDGITRL-----	MHA-----	DQKIDIA-	149
210	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
211	KVKGLARAFRRNLILGDSSSTNNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
212	KVKGLARAFRRNLILGDSSSTNNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
213	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
214	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-	149
215	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
216	KVKGLARAFRRNLIVGDSTTNNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
217	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
218	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
219	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHA-----	DQKIDIA-	149
220	KVKGLARAFRRNLILGDSSSNKAFDGIPRL-----	MHT-----	DQKIDIA-	149

221	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
222	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHE-----DQKIDIA - 149
223	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
224	KVKGLARAFRRNLIVGDSTTNNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
225	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
226	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
227	KVKGLARAFRRNLILGD <sup>S</sup> TNNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
228	KAKGMGREFSKVLIQGDSAVNAKQFDGVAKL-----VTS-----DQTIDGK - 149
229	KVKGLARAFRRNLILGDSSNTNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
230	KAKGMGREFSKVLIQGDSAVNAKQFDGVAKL-----VTS-----DQTIDGK - 149
231	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
232	KVKGLARAFRRNLILGNSETNTKAFDGI <sup>P</sup> RL-----MHK-----DQKIDIA - 149
233	KVKGLARAFRRNLILGDSSNTKAFDGI <sup>P</sup> RL-----MHT-----DQKIDIA - 149
234	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
235	KVKGLARAFRRNLIVGDSTTNNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
236	KVKGLARAFRRNLILGDSSNTKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
237	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
238	KVKGLARAFRRNLIVGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
239	KAKAVAHAFLQAFYRGNSVNPQFDGLRKL-----VPA-----SQTIQPGP 150
240	KVKGLARAFRRNLILGNSETNTKAFDGI <sup>P</sup> RL-----MHK-----DQKIDIA - 149
241	KVKGLARAFRRNLILGDSSNTKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIE - 149
242	KVKGLARAFRRNLILGDSSNTNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
243	KVKGLARAFRRNLIVGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
244	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
245	KVKGLARAFRRNLILGDSSNTNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
246	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
247	KVKGLARAFRRNLILGDSSNTKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
248	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
249	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
250	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
251	KVKGLARAFRRNLILGDSSNSKA <sup>F</sup> DGI <sup>P</sup> RL-----MHE-----DQKIDIA - 149
252	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
253	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
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255	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
256	KVKGLARAFRRNLILGN <sup>S</sup> NTKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIE - 149
257	KVKGLARAFRRNLILGD <sup>S</sup> NTKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIE - 149
258	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
259	KVKGLARAFRRNLILGDSSNTNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
260	KVKGLARAFRRNLIVGDSTTNNKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIA - 149
261	KVKGLARAFRRNLIVGD <sup>S</sup> NTNKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIS - 149
262	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
263	KVKGLARAFRRNLILGN <sup>T</sup> NTKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIA - 149
264	KVKGLARAFRRNLILGD <sup>S</sup> NTNKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIA - 149
265	KVKGLARAFRRNLIVGD <sup>S</sup> ITNNKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIS - 149
266	KVKGLARAFRRNLILGDSSNTNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
267	KVKGLARAFRRNLIVGDSTTNNKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIS - 149
268	KVKGLARAFRRNLIVGD <sup>S</sup> TTNNKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIS - 149
269	KVKGLARAFRRNLILGD <sup>S</sup> NTKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIE - 149
270	KAKGMGREFSKVLIQGN <sup>S</sup> TTNAKQFDGIAKL-----VTS-----DQTIDGK - 149
271	KVKGLARAFRRNLILGDSSNTNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
272	KVKGLARAFRRNLIVGD <sup>S</sup> TTNNKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIS - 149
273	KVKGLARAFRRNLIVGD <sup>S</sup> TTNSKA <sup>F</sup> DGI <sup>P</sup> KL-----MHD-----DQKIDIS - 149
274	KVKGLARAFRRNLIVGD <sup>S</sup> TTNNKAFDGI <sup>P</sup> KL-----MHD-----DQMIDIS - 149
275	KVKGLARAFRRNLILGDSSNSKA <sup>F</sup> DGI <sup>P</sup> RL-----MHT-----DQKIDIA - 149
276	KVKGLARAFRRNLIVGD <sup>S</sup> TTNNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
277	KVKGLARAFRRNLILGDSSNTKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
278	KVKGLARAFRRNLIVGD <sup>S</sup> TTNNKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIS - 149
279	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
280	KVKGLARAFRRNLIVGD <sup>S</sup> TTDNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
281	KAKGVAREFHRTLARGDSKTNAKEFDGF <sup>D</sup> KL-----VTS-----TQIVDAGA 150
282	KVKGLARAFRRNLIVGD <sup>S</sup> TTNNKAFDGI <sup>P</sup> KL-----MHD-----DQKIDIS - 149
283	KVKGLARAFRRNLILGD <sup>S</sup> TTNNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
284	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
285	KVKGLARAFRRNLILGDSSNTNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149
286	KVKGLARAFRRNLILGD <sup>S</sup> STNNKSFDGI <sup>P</sup> KL-----MHD-----DQKIDIE - 149
287	KVKGLARAFRRNLILGDSSSNKAFDGI <sup>P</sup> RL-----MHA-----DQKIDIA - 149

288	KVKGLARAFRRNLILGDSSTNKAFDGIPKL-----MHD-----DQKIDIE- 149
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291	KVKGLARAFRRNLILGDSSTNKAFDGIPRL-----MHA-----DQKIDIA- 149
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301	KVKGLARAFRRNLIVGDSTTNNKAFDGIPKL-----MHD-----DQKIDIS- 149
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319	KVKGLARAFRRNLIVGDSTTNNKAFDGIPKL-----MHD-----DQKIDIS- 149
320	KVKGLARAFCRNLILGDSTTNTKAFDGIPKL-----MHD-----DQKIDIE- 149
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349	KVKGLARAFRRNLILGDSSSTNTKAFDGIPKL-----MHD-----DQKIDIE- 149
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351	KAKGVAREFHRTLARGDSKTNAKEFDGFDKL-----VTS-----TQIVDAGA 131
352	KVKGLARAFRRNLILGNSTENNNKAFDGIPKL-----MHD-----DQKIDIE- 149
353	KAKSVGRQYQDTMINGDGTSE--TFQGLLSSL-----VAA-----GQTITGDT 150
354	KVKGLARAFRRNLIVGDSTTNNKAFDGIPKL-----MHD-----DQKIDIS- 146

355	KVKGLARAFRRNLILGNSTENTKAFDGIPKL-----MHN-----DQKIDIA - 149
356	KVKGLARAFRRNLILGDSSTNTKAFDGIPKL-----MHD-----DQKIDIE - 149
357	KVKGLARAFRRNLIVGDSTTNNKAFDGIPKL-----MHD-----DQKIDIS - 149
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361	KVKGLARAFRRNLILGDSNNKAFDGIPRL-----MHA-----DQKIDIA - 149
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388	KVKGLARAFRRNLILGNSTENTKAFDGIPKL-----MHN-----DQKIDIA - 149
389	KVKGLARAFRRNLIVGDSTTNNKAFDGIPKL-----MHD-----DQKIDIS - 149
390	KTKTASRKYQDMLINGTGAGD--EFLGLLLG-----VPV-----AQKVATGA 150
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392	KVKGLARAFRRNLILGDSSTNTKAFDGIPKL-----MHD-----DQKIDIE - 149
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396	KVKGMARAFRRNLLILGNSETNNKAFDGIPRL-----MHE-----DQKIDIA - 149
397	KAKSCGRKYQDQMVNQDGTGN--NMTGMFGL-----VAA-----GQTITANN 151
398	KVKGLARAFRRNLILGDSNNKAFDGIPRL-----MHA-----DQKIDIA - 149
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403	KVKGLARAFRRNLIVGDSTTNNKAFDGIPKL-----MHD-----DQKIDIS - 149
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418	KVKGLARAFRRNLILGDSSTNNKAFDGIPKL-----MHD-----DQKIDIE - 149
419	KAKGLGRKFRMNLVTGDTSVNSKQFDGVRKL-----VTA-----DQTLDAGV 150
420	KVKGLARAFRRNIILGNSTENTKAFDGIPKL-----MHN-----DQKIDIA - 149
421	KVKGLARAFRRNLILGDSSTNNKAFDGIPRL-----MHA-----DQKIDIA - 149

422	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQNIDIA-----	149
423	KVKGMARAFRRNLILGNSEANNKAFDGIPRL-----	MHE-----	DQKIDIA-----	149
424	KVKGLARAFRRNLILGNSTENTKAFDGIPKL-----	MHN-----	DQKIDIA-----	149
425	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-----	149
426	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-----	149
427	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-----	149
428	KVKGLARAFRRNLILGNSTENTKAFDGIPKL-----	MHN-----	DQKIDIA-----	149
429	KVKGLARAFRRNLILGDSSTNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
430	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-----	149
431	KVKGLARAFRRNLILGNSTANNKAFDGIPKL-----	MHN-----	DQKIDIA-----	149
432	KAKSAGRQYQTMLATGDTGN--TFAGLPTL-----	VDA-----	SQKVVTGT-----	150
433	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
434	KVKGLARAFRRNLILGDSTTNNKAFDGIPKL-----	MHD-----	DQKIDIS-----	149
435	KVKGLARAFRRNLIVGDSTTNNKAFDGIPKL-----	MHD-----	DQKIDIS-----	149
436	KVKGLARAFRRNIILGNSTENTKAFDGIPKL-----	MHN-----	DQKIDIA-----	149
437	KVKGLARAFRRNLILGDGANSKSFDGIPLL-----	MHA-----	DQKIDIA-----	149
438	KVKGLARAFRRNIILGNSTENTKAFDGIPKL-----	MHN-----	DQKIDIA-----	149
439	KAKGMGREFSKVLIQGNSTTNAKQFDGIAKL-----	VTS-----	DQTIDGK-----	149
440	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
441	KAKAVAHAFLATFYTGDAASADPKQFDGLRRL-----	VPA-----	SQTFQPGP-----	150
442	KVKGLARSFRRSLILGDSTTNAKSFDGIPKL-----	IHA-----	DQKI-IA-----	148
443	KVKGLARAFRRNLILGDSSNTKAFDGIPKL-----	MHD-----	DQKIDIE-----	149
444	KAKAVGRKYSSLLINGTGANE--EFVGLLGL-----	VSS-----	GQTLTAGT-----	150
445	KAKSAGRNYRNQLINGSGAAD--EFNGMINL-----	CAT-----	SQKVDTGN-----	150
446	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
447	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
448	RAKAVAYAFTESFFIGDSTANPKSFDGLRKL-----	VPA-----	AQTISPGA-----	148
449	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
450	KVKGLARAFRRNLIVGDSTTNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
451	KAKAVAHAFLNAYRGDSAVENTPKQFDGLRKL-----	VPA-----	SQTIQPGP-----	150
452	RAKAVAHLFSDTFFNGDSTANPKAFDGLAKL-----	VPP-----	SQTLLEPGP-----	150
453	KVKGLARAFRRNIILGNSTENTKAFDGIPKL-----	MHN-----	DQKIDIA-----	149
454	KAKSCGRKYQDQMVMNGDGTAN--NMTGLFGL-----	VAA-----	GQTITANN-----	151
455	KAKAVGRIFKKTVAQGNATANPKEFDGLPQL-----	VTS-----	PMTLAAGA-----	150
456	KVKGLARAFRRNLIVGDSTTNNKAFDGIPKL-----	MHD-----	DQKIDIS-----	149
457	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
458	KVKGLARAFRRNLILGNSTENTKAFDGIPKL-----	MHN-----	DQKIDIA-----	149
459	KAKALARTFQDSVVNGDNVARPKEFDGLKAL-----	TTA-----	AQTITAGA-----	150
460	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
461	KAKSAGRQYQSQMVNGDGTGN--NMAGLFGL-----	VAG-----	SQTTITANN-----	151
462	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
463	GEIQTWYGYGRMDVLT-GN--PVFGGLPDL-----	VAP-----	ARTINMG-----	58
464	KVKGLARAFRRNLILGNSETNTKAFDGIPRL-----	MHK-----	DQKIDIA-----	149
465	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
466	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
467	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
468	KVKGLARAFRRNLILGDSTTNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
469	KVKGLARAFRRNLILGDESVDAKAFNGIPKL-----	MVP-----	DQSI-VA-----	148
470	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHE-----	DQKIDIA-----	149
471	KAKSCGRKFQDMLINGTGAN--QFEGLINL-----	VAA-----	GQTLNDGT-----	151
472	KAKTVAREFHRALATGDSVNSKVFDFGLPRL-----	LKQAQDFAA TAGGSQIVSAGT-----	160	
473	KAKSCGRKFQDMLINGTGAN--QFEGLINL-----	VAA-----	GQTLNDGT-----	151
474	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
475	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHE-----	DQKIDIA-----	149
476	KAKSAGRQYQSQMVNGDGTGN--NMAGLFGL-----	VAG-----	SQTTITANN-----	151
477	KAKSLGRKFQDSLINGDGTGN--SFQGLASL-----	ASA-----	SQIIDVGT-----	150
478	KAKAVGRKYANLLNLTGANE--EFEGLLTL-----	ASA-----	GQTLIAGA-----	150
479	KAKSAGRKYQDQLINGDGTGN--TFTGLLGL-----	AAA-----	GQTIGANN-----	151
480	KAKSCGRKYQDMLINGTGAN--EFEGIINL-----	CAE-----	GQKVATGD-----	151
481	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
482	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
483	KVKGLARAFRRNLILGDSATNTKSFDFGIPKL-----	IHK-----	DQKI-IA-----	148
484	KVKGLARAFRRNLILGDSSNNKAFDGIPRL-----	MHA-----	DQKIDIA-----	149
485	RAKAVAHLFSDTFFNGDSTANPKAFDGLATL-----	VPA-----	SQTLLEPGP-----	150
486	KVKGLARAFRRSLILGNADENAKSFDGIPRL-----	IHK-----	DQKI-VA-----	148
487	KVKGLARAFRRNLILGNSTENTKAFDGIPKL-----	MHN-----	DQKIDIA-----	149
488	KVKGLARAFRRNLILGDSSANAKTFDGIPKL-----	IHN-----	DQKI-IA-----	148

489	KVKGLARAFRRLNLLGDSVTNAKSF D G I P K L - - - - - I H N - - - - - D Q K I - V A - 148
490	KAKSAGRQYQNQMVNNGDGTGN--NVAGLFSL-----VAA-----SQTITANN 151
491	KVKGLARAFRRLNLLGDSSSNKA F D G I P R L - - - - - M H A - - - - - D Q K I D I A - 149
492	KAKAVGRKYSNLLINGTAND--EFVGLLGL-----ASS-----G Q T L T A G A 150
493	KVKGLARAFRRLNIVGDSTTNKA F D G I P K L - - - - - M H D - - - - - D Q K I D I S - 149
494	RAKAVAHAFSDAFYNGDSAANPKQFDGLKKL-----VSA-----A Q T I A P G A 150
495	KVKGLARAFRRLNIVGDSTTNKA F D G I P K L - - - - - M H D - - - - - D Q K I D I S - 149
496	KVKGLARAFRRLNIVGDSTTNKA F D G I P K L - - - - - M H D - - - - - D Q K I D I S - 149
497	KAKSIGRQFQTTMVTGDGS GN --TFEGLMSL-----VAS-----T Q S F E V G T 150
498	KVKGLARAFRRLNLLGDSSSNKA F D G I P R L - - - - - M H A - - - - - D Q K I D I A - 149
499	KVKGLARAFRRLNLLGDSSSNAKTFDGIPKL-----I H N - - - - - D Q K I - I A - 148
500	KAKSAGRQYQNQMVNNGDGTGN--NVAGLFSL-----VAG-----SQTITANN 151



250 260 270 280 290 300

1	-----G N I - - - L K L E D L D R A K G Q I R V K E G E S G V I F T N Q S G Y E Q I R K A Y Y N R - - - N Q I P - - - 191
2	-----G N T - - - L K L E D L D H A K G Q I R V K E G E S G V I F T N Q S G Y E Q I R K A Y Y N R - - - N Q I P - - - 191
3	-----G N T - - - L K L E D L D R A K G Q I R V K E G E S G V I F T N Q S G Y E Q I R K A Y Y N R - - - N Q I P - - - 191
4	-----G N T - - - L K L E D L D R A K G Q I R V K E G E S G V I F T N Q S G Y E Q I R K A Y Y N R - - - N Q I P - - - 191
5	-----G N T - - - L K L E D L D R A K G Q I R V K E G E S G V I F T N Q S G Y E Q I R K A Y Y N R - - - N Q I P - - - 191
6	-----G N T - - - L K L E D L D R A K G Q I R V K E G E S G V I F T N Q S G Y E Q I R R A Y Y N R - - - N Q I P - - - 191
7	-----G N T - - - L K L E D L D R A K G Q I R V K E G E S G V I F T N Q S G Y E Q I R K A Y Y N R - - - N Q I P - - - 191
8	-----G N T - - - L K L E D L D R A K G Q I R V K E G E S G V I F T N Q S G Y E Q I R K A Y Y N R - - - D Q I P - - - 191
9	-----G N T - - - L K L E D L D R A K G Q I R V K E G E S G V I F T N Q S G Y E Q I R K A Y Y N R - - - N Q I P - - - 191
10	-----G N T - - - L K L E D L D R A K G Q I R V K E G E S G V I F T N Q S G Y E Q I R K A Y Y N R - - - N Q I P - - - 191
11	-----G N I - - - L N L E D L D R A K G Q I R V K E G E S G V I F T N Q P G Y E Q I R K A Y Y N R - - - D Q I P - - - 191
12	-----G N T - - - L K L E D L D R A K G Q I R V K E G E S G V I F T N Q P G Y E Q I R K A Y Y N R - - - N Q I P - - - 191
13	-----G N I - - - L R L E D L D R A K G Q I R V K E G E Y G V I F T N Q S G Y E Q I R K A Y Y N R - - - N Q I P - - - 191
14	-----G A T - - - L T L E D L D R A K G K I R I R N G E S G I I T N E P G Y R L I R K A Y Y N R - - - N I L P - - - 191
15	-----G R E - - - L T L E D M D S A K E M V R T N D G R H T V I F T S S I G K R A I H A A Y W N R - - - A V A P E Y 201
16	-----G R P - - - L T L E D L D R A K E L V R A N D G R C V V I F T S S I G K R A I N A S H Y V R - - - G L R P D S 201
17	-----G R P - - - L T L E D L D R T K E L V R A N D G R C V V I F T S S I G K R A I N A S H Y V R - - - G L R P D S 201
18	-----G R A - - - L T L E D L D R A R E R V R A N D G R C V V I F T S S I G K R A I N A S H Y V R - - - G F K P D S 201
19	-----F K P - - - L T L E V L E Q G K E L V R T N D G R G T V V F T N S I G K R A I H A A H W T R - - - G L T P Q Y 200
20	-----G R E - - - L T L E D M D R A K E M V R T N D G R C I V I F T S T I G K R A I H A A Y W N R - - - G V A P E Y 202
21	-----F Q P - - - L T L E V L E Q G K E L V R T N D G R G T V L F T N S T G K R A I H A A H W T R - - - G L T P Q Y 200
22	-----F Q P - - - L T L E T L E Q G K E L V R T N D G R G T V L F T N S I G K R A I H A A H W T R - - - G L T P Q Y 200
23	-----F Q P - - - L T L E V L E Q G K E L V R T N D G R G T V L F T N S T G K R A I H A A H W T R - - - G L T P Q Y 201
24	-----F Q P - - - L T L E V L E Q G K E L V R T N D G R G T V L F T N S T G K R A I H A A H W T R - - - G L T P Q Y 200
25	-----F R P - - - L T L E V L E Q G K E L V R T N D G R G T V V F T N S I G K R A I H A A H W T R - - - G L T P Q Y 200
26	-----F N P - - - L T L E A L E Q G K E L V R T N D G R G T V L F T N S I G K R A I H A A H W T R - - - G L T P Q Y 200
27	-----G R A - - - L T L E D L D S A K E L V R A N D G R C I V I F T S S I G K R A I N A S H Y V R - - - G L R P A S 201
28	-----F Q P - - - L T L E V L E Q G K E L V R T N D G R G A V L F T N S T G K R A I H A A H W T R - - - G L T P Q Y 200
29	-----G A A - - - L T F A A L D Q A Y H L I S E N N G R P N A I M S N S R A L R T Y R N L F V A T - - - H G I E P P T 201
30	-----G A A - - - L T F A A L D Q A Y H L I S E N N G R P N A I M S N S R A L R T Y R N L F V A T - - - H G I E P P T 207
31	-----A V N - - - L T F A A L D Q A Y N L V T E N E G R P N A I M S N S R A L R T Y Q N L F V A T - - - H G I L P P T 203
32	-----G V A - - - L T F A A L D Q T Y N L V T E N E G R P N A I M S N S R A L R T Y Q N L F V A T - - - H G I L P P T 203
33	-----G V A - - - L T F A A L D Q A Y N L V T E N E G R P N A I M S N S R A L R T Y Q N L F A T T - - - Y G I L P P T 203
34	-----G A S L D T A G Q M E E L Q Q T Y N L V T A N N G R P T A I M C N S R A L R Y I V S T F Y G L - - - G A N L E Y 212
35	-----S A A - - - P T L A K L Q E T Y H L V A A N A G M A N C I M C N T R G S R A I I K A Y N D V - - - G M H P L Y 219
36	-----G N T - - - L K L E D L D R A K G Q I R V K E G E S G V I F T N Q S G Y E Q I R K A Y Y N R - - - D Q I P - - - 114
37	-----A A P - N A A R I D E L Q K A Y S L I T S N N G R P N A I M C N S R A Y R W I M A A Y F G V - - - G A N P E Y 211
38	-----G A A - - - L T F A A M D Q A Y N L I K S N Q G R P T A I M C N S R A Q R T F A N L Y F G A - - - G A G E P P M 201
39	-----G A T - - - L T L K D L D I A K G N V R A N N G A P I I I T T N Q H G Y E A I R T A H Y D A - - - G I T P E I 198
40	-----T N T - D K Y T K L R S L Q E A Y F K I T A N N G R P N A I M C N S A A M R W I I N A Y Y L A - - - G M N P E V 208
41	-----G T P - - - L T L E A V D R A K G Y I R T S E M K N K I I - - - T N T T G Y I L Y R E A V H N A - - - G I S F S - 196
42	-----G A A - - - L T F A A L D Q A Y H L I D S N Q G R A N A I M S N S R A L R T F R N L Y F G D - - - G G G E P K D 201
43	-----G A A - - - L T F A A V D Q A Y H L I E S N Q G R P N A I M S N S R A L R T F R S L Y F G A - - - G G G E P K E 200
44	-----G A A - - - L T F A A L D Q A Y H L I E S N Q G R A N A I M S N S R A L R T F R N L Y F G D - - - G G G E P K D 201
45	-----G A A - - - L T F A A L D Q A Y N L I R S N Q G R P S A I M S N S R A Q R T F A S L Y F G A - - - G G G E P P M 201
46	-----G G A - - - L T L D C L D D A Y E R I T A G T G R P T L I M S H S R S L R T Y R K L C R D A - - - G F K A E R 192
47	-----G G A - - - L T L P C L D D A Y E R I T A G T G R P T L I M S H S R S L R T Y R N L C R V A - - - G F K P E R 193
48	-----G G A - - - L T L D C L D D A Y E R I T A G T G R P T L I M S H S R S L R T Y R K L C R D S - - - G L V P E R 192
49	-----G G A - - - L T L D C L D D A Y E R I T A G T G R P T L I M S H S R S L R T Y R K L C R D A - - - G F K A E R 192

50 -----GGA----LT<sub>L</sub>AC<sub>L</sub>DDAYERITAGTGRPTLIMSH<sub>S</sub>RSLRTYR<sub>K</sub>LCRDA--GFKPER 192  
 51 -----AGA----LT<sub>L</sub>DC<sub>L</sub>DDAYERVVAGTGRPTLIMSSKRLRTYR<sub>S</sub>LCRAA--GFKPER 188  
 52 -----GAP----LSFPCLEATFGKV<sub>T</sub>NNNRP<sub>S</sub>VIMSNLRSRESYRN<sub>L</sub>CWAA--GIEPPM 193  
 53 -----GAGGV--PALREL<sub>D</sub>QLVGKITTNGGRPHVLYTSRKGAEAIRRAHYRA--SVTP-E 204  
 54 -----SAS----PSLAKLQETYHLVVAGGAEANC<sub>M</sub>CNSRASRAIIAYNAA--GMHPQR 200  
 55 -----GAGGV--PTLAEFDNLLDVKSADGRATVLYSCRTGFDAWKKAHYNL--NSVPTE 205  
 56 -----GAA----LTFAALDQAFHLISENNGRPNAIMSNSRALRTYRN<sub>L</sub>FVAT-HGIEPPT 201  
 57 -----GGA----LT<sub>F</sub>PCLN<sub>L</sub>AYNFVVSNNRPTVIVSSSRELRTYEQLCRDN--GFAPPQ 191  
 58 -----SVA----PTLDLLQQTWHLVTAGNARANC<sub>M</sub>CNNRASRAIIKAYNDQ--GMHPT<sub>E</sub> 203  
 59 -----GAGGI--PSLREL<sub>D</sub>QLVGKITANGGRPHVLYTSRKGAESIRR<sub>A</sub>YYRA--GITP-E 204  
 60 -----GGL----LT<sub>F</sub>ACLEEAHDLVTANQGKPTVIMSNARS<sub>L</sub>RSYRN<sub>L</sub>CWNA--GIKPPE 193  
 61 -----GAGGQ--PTLAEFDQLMALVKSADGRPTVLYSSRKGFDSWKKAHYAL--STVPAE 205  
 62 -----GLG----LT<sub>L</sub>DC<sub>L</sub>DDAYERITAGTGRPTLIMSH<sub>S</sub>RSLRTYR<sub>K</sub>LCRDA--GFKAER 192  
 63 -----GAP----LSFPCLEAAF<sub>D</sub>KITGNNNRPSFIMSNLASRAS<sub>S</sub>YRN<sub>L</sub>CWAT--GIKPPE 193  
 64 -----GAGGI--PALREL<sub>D</sub>QLIGKITTNGGRPHVFYTSRKGAEAIRRAYRE--QVTP-E 204  
 65 -----GAGGV--PTLAEFDQLIGKV<sub>K</sub>ASDG<sub>H</sub>P<sub>T</sub>VLYTSRK<sub>G</sub>LEALKKAHYNL--NSVPSE 205  
 66 -----LSS----LT<sub>L</sub>DC<sub>L</sub>DDAYS<sub>R</sub>VTAGTGRPTLIMSS<sub>T</sub>KGLRTYR<sub>S</sub>LCRAA--GIPQER 188  
 67 -----GGA----LN<sub>F</sub>HCLGDAWHRV<sub>D</sub>ANDGRPTMISATPALATYELLCRMS--GFEPPK 193  
 68 -----GLA----LTTRLLDRAQR<sub>R</sub>PKSGDNFDGYICTSAQGYIEIRQAFLAS--GTL<sub>P</sub>QE 201  
 69 -----GLA----LTTRLLDRAQR<sub>R</sub>IKAGDNFEGMIWTSQAQGYIEIRQAFLAS--GTL<sub>P</sub>QE 217  
 70 -----GVP----TLQQFDDAFFSVVDNEGYPNAIMGRTGSLKRYLNLMRAA--NQDIVY 202  
 71 -----GVP----TLQQFDDAFFKVVDNEGYPNAV<sub>M</sub>GRTGSLKRF<sub>L</sub>NLMRAA--NQDIVY 253  
 72 -----GVP----TLQQFDDAFFKVVDNEGYPNAV<sub>M</sub>GRTGSLKRF<sub>L</sub>NLMRAA--NQDIVF 248  
 73 -----GVP----TLQQFDDAFFR<sub>V</sub>V<sub>D</sub>NEGYP<sub>S</sub>VIMGRTGSLKRF<sub>L</sub>NLMRAA--NQDIKY 202  
 74 -----N-GNA--LSFSMLDELLDAV<sub>P</sub>Y--GA-DAIIMR<sub>S</sub>GT<sub>V</sub>RAYRALLRAT-GAT<sub>G</sub>P<sub>T</sub>E 198  
 75 -----GGA----LTLPCLDEAYERVAAGTGRPTLIMSH<sub>S</sub>RSLRTYRN<sub>L</sub>CRAA--GLKPER 193  
 76 -----GAA----LTFAALDQAYHLISENNGRPNAIMSNSRALRTYRN<sub>L</sub>FVAT-HGIEPPT 136  
 77 -----AAP----LSFPCLSRAYHLVAANNKPTVIMSNARS<sub>S</sub>YENL<sub>C</sub>R<sub>L</sub>N--GQNLEY 193  
 78 -----N-GAA--VTCEMLDELKD<sub>T</sub>VLN--GA-DVLMMR<sub>R</sub>QGT<sub>T</sub>WRAIR<sub>S</sub>ILRN<sub>M</sub>-GGNDASH 198  
 79 -----GAA----LTFAALDQAFHLISENNGRPNAIMSNSRALRTYRN<sub>L</sub>FVAT-HGIEPPT 201  
 80 -----N-GNA--LTLSMLDELLDAV<sub>P</sub>N--GA-DVLMMR<sub>R</sub>SGT<sub>I</sub>RAYRALLRAS-GGLEPAH 198  
 81 -----N-GAP--ITLTMLDELLDAV<sub>P</sub>N--GA-DAIIMR<sub>S</sub>GT<sub>L</sub>RAYRALLRAM-GGTL<sub>P</sub>ES 199  
 82 -----D-GAA--LTLSMLDELCD<sub>A</sub>IPN--GA-DVLVMSRGAI<sub>R</sub>AYRTLLRAT-YGTDAM<sub>V</sub> 198  
 83 -----N-GAA--VSAEMLDELLDAV<sub>K</sub>L--GA-DVLMMR<sub>R</sub>GT<sub>T</sub>WRAIR<sub>A</sub>IMRSF-GGNTGDM 198  
 84 -----N-GAA--VSAEMLDELLDAV<sub>K</sub>L--GA-DVLMMR<sub>R</sub>GT<sub>T</sub>WRAIR<sub>A</sub>IMRSF-GGNTGDM 198  
 85 -----N-GAA--VSAEMLDELLDAV<sub>K</sub>L--GA-DVLMMR<sub>R</sub>GT<sub>T</sub>WRAIR<sub>A</sub>IMRSF-GGNTGDM 198  
 86 -----N-GAA--VSAEMLDELLDAV<sub>K</sub>L--GA-DVLMMR<sub>R</sub>GT<sub>T</sub>WRAIR<sub>A</sub>IMRSF-GGNTGDM 198  
 87 -----GVP----TLQQFDEALS<sub>L</sub>V<sub>V</sub>DNEAHPTAIMSNWGALKRYLALLRAA--GLK<sub>P</sub>D<sub>L</sub> 193  
 88 -----SAA----PTLAKLQETYHLVVAGGAEANC<sub>M</sub>CNSRASRAIIAYNAA--GLHPNR 151  
 89 -----N-GAA--ISAEMLDELLDAV<sub>K</sub>L--GA-DVLMMR<sub>R</sub>GT<sub>T</sub>WRAIR<sub>A</sub>IMRSF-GGNTGDM 198  
 90 -----N-GSA--VNFGMLDELKD<sub>A</sub>VKN--GA-DVLMMR<sub>R</sub>QGT<sub>T</sub>WRAV<sub>R</sub>ALLRAA-GGNEAAT 198  
 91 -----GAA----LT<sub>L</sub>DC<sub>L</sub>DDAYERVTAGTGRPTLIMSH<sub>S</sub>RSLRTYR<sub>S</sub>LCRAA--GI-YQR 148  
 92 -----GVP----TLAQFDQAYSLVVDNEAHPTAIMSNWGALKRYL<sub>D</sub>LLR<sub>A</sub>A--GLK<sub>P</sub>D<sub>L</sub> 193  
 93 -----GVP----TLAQFD<sub>R</sub>ALS<sub>L</sub>V<sub>V</sub>DNEAHPTAIMSNWGALKRYL<sub>D</sub>LLR<sub>T</sub>A--GLK<sub>P</sub>D<sub>L</sub> 193  
 94 -----GNA--MSFTMLDELLDAV<sub>P</sub>N--GA-DAIFMTSAHIR<sub>A</sub>RLRAM<sub>L</sub>RAT-GGLEPAH 196  
 95 -----N-GAA--VSAEMLDELLDAV<sub>K</sub>L--GA-DVLMMR<sub>R</sub>GT<sub>T</sub>WRAIR<sub>A</sub>IMRSF-GGNTGDM 198  
 96 -----N-GGS--LT<sub>L</sub>AM<sub>L</sub>DELCD<sub>A</sub>V<sub>P</sub>K--GA-DVLMMR<sub>R</sub>GT<sub>I</sub>RAYRN<sub>L</sub>RAT-SGTDAM<sub>V</sub> 198  
 97 -----D-GAA--VSFTMLDELRDVVK<sub>N</sub>--GC-DVLMMR<sub>R</sub>GT<sub>T</sub>WRSIKALLRAM-GGNDAGT 198  
 98 -----N-GAA--ISLSMLDELIDKLEG--RRPDALM<sub>M</sub>MRTGT<sub>L</sub>RALKALWRLA-GGNTGGM 200  
 99 -----N-GSA--VTFTMLDELRAV<sub>K</sub>N--GC-DVLMMR<sub>R</sub>GT<sub>T</sub>WRAIKQ<sub>L</sub>RAM-GGNDATT 198  
 100 -----N-GGA--VSLAILDELVD<sub>K</sub>LTG--KKPDAFVMRS<sub>G</sub>TLRALKALWRAA-GGNTGNM 200  
 101 -----N-GAA--LTLSMLDELLDAV<sub>P</sub>Y--GA-DVIMMR<sub>R</sub>AGTLRAHR<sub>R</sub>ALLRSL-GGTSVDN 199  
 102 -----GAA--LALADYDTYYFKVSA--GRCNAIVNSA<sub>S</sub>QVIRYL<sub>L</sub>TMRAA--GLT<sub>P</sub>EF 200  
 103 -----N-GGA--ISLSMLDELIDK<sub>L</sub>DG--RRPDALM<sub>M</sub>MRTGT<sub>L</sub>RALKALWRLA-GGNTGGM 200  
 104 -----D-GGA--ITLALLDELLDK<sub>V</sub>PH--GA-DCLVM<sub>M</sub>R<sub>R</sub>GT<sub>I</sub>RAYRN<sub>L</sub>LR<sub>T</sub>-SGTDAM<sub>V</sub> 198  
 105 -----D-GNP--LT<sub>L</sub>TM<sub>L</sub>DELCD<sub>A</sub>V<sub>P</sub>N--GA-DVIVM<sub>M</sub>R<sub>R</sub>GT<sub>I</sub>RAYRALLRAT-YGTDAM<sub>V</sub> 198  
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 107 -----GQA--LTLSMLDELCD<sub>T</sub>VPH--GA-DALVM<sub>M</sub>R<sub>R</sub>GT<sub>I</sub>R<sub>A</sub>V<sub>R</sub>G<sub>L</sub>LRAT-YGTDAM<sub>V</sub> 196  
 108 -----D-GNP--LT<sub>L</sub>TM<sub>L</sub>DELCD<sub>A</sub>V<sub>P</sub>N--GA-DVIVM<sub>M</sub>R<sub>R</sub>GT<sub>I</sub>RAYRALLRAT-YGTDAM<sub>V</sub> 198  
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 111 -----N-GGA--LTLSMLDQLYD<sub>M</sub>V<sub>L</sub>T--GA-DAFFMR<sub>R</sub>AGT<sub>I</sub>RAYRALVRAT-GGT<sub>D</sub>AT<sub>Q</sub> 198  
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 115 -----N-GSA--LSLAALDELIDMVNG--RPDALM<sub>M</sub>MR<sub>P</sub>GT<sub>F</sub>RALKTLWRAA-GGNTGGM 199  
 116 -----GSA----LTFSMLDELVD<sub>A</sub>V<sub>P</sub>L--KP-DCLIMR<sub>S</sub>GT<sub>V</sub>RAYL<sub>Q</sub>LLRAT-SGT<sub>N</sub>APL 196

117	----D-GGA-----ITLALLDELLDKVPH--	GA-DCLVMRRGTTIRAYRNLLRVT-SGTDAM	198
118	----D-GGG-----ITLALLDELLDKVPH--	GA-DCLVMRRGTTIRAYRNLLRVT-SGTDAM	198
119	-----NAA-----LTFSMLDELVDAVPL--	KP-DCLIMRSGYRAYLQLLRAT-SGTNAPL	196
120	----D-GGA-----LTLSALDHLDVDSVPN--	GGPDFLMMRSGTTRRAYVAQLRAA-GGNTGAM	199
121	----D-GNP-----LTLTMLDELCAAVPN--	GA-DVIVMRRGTTIRAYRALLRAT-YGTDAM	198
122	----D-GNP-----LTLTMLDELCAAVPN--	GA-DVIVMRRGTTIRAYRALLRAT-YGTDAM	198
123	----N-GGA-----LTLAKLDELCDLVPN--	GA-DVIVMRRGTTIRAFRSLLRAT-YGTDAM	198
124	----D-GNP-----LTLTMLDELCAAVPN--	GA-DVIVMRRGTTIRAYRALLRAT-YGTDAM	198
125	----D-GNP-----LTLTMLDELCAAVPN--	GA-DVIVMRRGTTIRAYRALLRAT-YGTDAM	198
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127	----D-GAA-----VSFTMLDELRAVIG--	GA-DVLMMRKGTVRAIKALLRAM-GGNDAGT	198
128	----D-GAA-----VSFTMLDELRAVIG--	GA-DVLMMRKGTVRSIKALLRAM-GGNDAGT	198
129	----N-GAP-----LTLSMMDELADAVIN--	GA-DAFVMRPGTIRAYRALLYAT-GGVQPM	198
130	----N-GAP-----LTLSMMDELADAVIN--	GA-DAFVMRPGTIRAYRALLYAT-GGIQPM	198
131	----N-GAS-----LTLSMMDELADAVIN--	GA-DAFVMRPGTIRAYRALLYAT-GGIQPM	198
132	----D-GNP-----LTLTMLDELCAAVPN--	GA-DVIVMRRGTTIRAYRALLRAT-YGTDAM	198
133	----T-GMN-----LSFGVLDLTMHLVVSKDGQVDYMLMPARTIRAYKALLRAL-GGA <del>G</del> VNE		201
134	----N-GAP-----LTLSMMDELADAVIN--	GA-DAFVMRPGTIRAYRALLYAT-GGIQPM	198
135	----D-GNP-----LTLTMLDELCAAVPN--	GA-DVIVMRRGTTIRAYRALLRAT-YGTDAM	198
136	----SNA-----LTFSMLDELLDAIPL--	GA-DCLIMMRSGTYRAYLNLLRAT-SGTNAPL	196
137	----D-GEA-----LTFERLDQLLRMLVPL--	GA-DALVMRGHTHDAILAMLRLNL-GGTPND	198
138	----N-GGA-----LTLSMLDELCAAVPN--	GA-DVIVMRRGTTIRAFRGLLRAT-YGTDAM	201
139	----N-GAA-----VTFSMLDELRAVLL--	GA-DCFMMRQGTWRAIKALLRGF-NGNTAET	198
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141	----N-GSA-----LTLSMLDELVDMVPN--	GA-DCLVMRSGTVRAYRALLRAA-GGTPSE	201
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143	----GAA-----MNWSMLDEVVDAVNAL-	GC-DAIMMRSEHKRAYLQLLRVT-GGLQPSE	197
144	----N-GAA-----ISPSMLDELKDAVKY--	GA-DVLMMRQGTWRAIRALREIMRQF-GGNTGDM	198
145	----D-GGA-----VSLMALDELLDAVSL--	GA-DCLIMMREGTVRAIRALLRAT-GGITPEY	198
146	----D-GEA-----LTFERLDQLLRAVPL--	GA-DALVMRGHTHDAILAMLRLNL-GGTPDH	198
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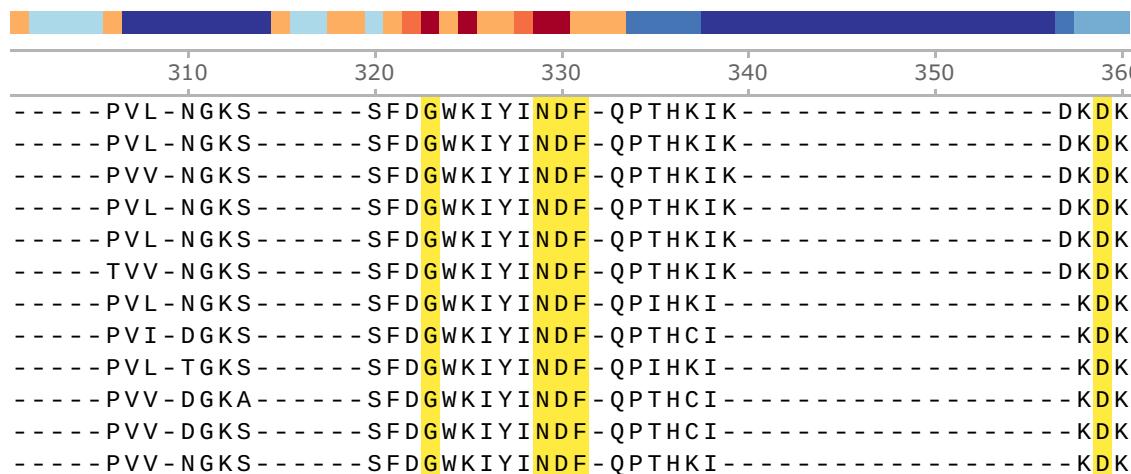




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320	- - - - -	GAS	- - - - -	MTFSMFDELVDAVKDL	- GA	- DCIMMRSEHLRAYRALLRTV	- - SLGPSE	196
321	- - - - -	GAS	- - - - -	MTFSMFDELVDAVKDL	- GA	- DCIMMRSEHLRAYRALLRTV	- - NVGPSE	196
322	- - - - -	GAS	- - - - -	MTFSMFDELIDAVKDL	- GA	- DCIMMRSEHLRAYRALLRTV	- - SLGPSE	196
323	- - - - -	GAS	- - - - -	MTFSMFDELVDAVKDL	- GA	- DCIMMCSEHLRAYRALLRTV	- - SLGPSE	196
324	- - - - -	GAS	- - - - -	MTFSMFDELVDAVKDL	- GA	- DCIMMRSEHLRAYRALLRTV	- - NVGPSE	196
325	- - - - -	GAS	- - - - -	MTFSMFDELVDAVKDL	- GA	- DCIMMRSEHLRAYRALLRTV	- - NVGPSE	196
326	- - - - -	GAS	- - - - -	MTFSMFDELVDAVKDL	- GA	- DCIMMRSEHLRAYRALLRTV	- - NVGPSE	196
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328	- - - - GSS	- - - - -	- - - - -	MTFSMFDELVDAVKDL	- GA	- DCIMMRSEHLRAYRALLRTV	- - NVGPSE	196
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346	- - - - -	GAS	- - - - -	MTFSMFDELVDAVKDL	- GA	- DCIMMRSEHLRAYRALLRTV	- - NVGPSE	196
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348	- - - - KAS	- - - - -	- - - - -	MTFSMFDELVDAIKDL	- GA	- DCIMMRSEHLRAYRALLRTV	- - NVGPSE	196
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351	- - D - GNP	- - - - -	- L T L T M L D E L C D A V P N	- - - - -	- GA	- DVIVMRRGTIRAYRALLRTA	- - YGTDAM	179
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384	- - - - - KAS	- - - - -	- MTFSMFDELVDAIKDL	- GA	- DCIMMRSEHLRAYRALLRTV	- - NVGPSE	196	

385	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--SLGPSE	196
386	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
387	GPTNN	LTFSM <sub>1</sub> LDLVDRVPN	GA	DAIMMHSSTLRYYRALCRAQ	-NGTDAQ	200
388	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
389	DAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
390	T-GKN	LGFE <sub>1</sub> LDLTLHLLVVSKDQGV	DYMLFPARTIRSFKALLRGL	GGASVNE	201	
391	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
392	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--SLGPSE	196
393	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--SLGPSE	196
394	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
395	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
396	AAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
397	GAAN-GAV	LSFEDLDALIDLVTDKGQV	DYLMMHGRTRKYLALLRSL	GGTSPAD	205	
398	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
399	NAS	ITFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
400	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
401	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
402	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
403	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
404	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
405	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
406	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
407	SAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
408	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--SLGPSE	196
409	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
410	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
411	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
412	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
413	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
414	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
415	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
416	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
417	AAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
418	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--SLGPSE	196
419	D-GNP	ISYAALDELKDMVKL	GA	DVFMMRSGTWRAIRELNRIH	-GGNTAET	198
420	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
421	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
422	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
423	AAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
424	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
425	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
426	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
427	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
428	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
429	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
430	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
431	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
432	N-GGA	LSFAFLDELLDLVVDKDGNV	DYITMH <sub>1</sub> SRTI <sub>1</sub> RSYKALIRAL	GGVTADD	201	
433	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
434	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
435	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
436	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
437	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--SVPSE	196
438	KAS	MTFSMFDELVDAIKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
439	ASA	LNFAMLDELLDKVPN	GA	DVLVMNRPTIRAYRQILRAT	-SGTDAVM	196
440	GVS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
441	N-GGS	LTLELLDQLV <sub>1</sub> VKP	GKP <sub>1</sub> DALLMSKRTRKLSQLRRQS	GT <sub>1</sub> VLES <sub>1</sub> D	199	
442	NSA	MTFSMLDELVDAVKDL	GA	DAIMMRSEH <sub>1</sub> RAYRALLRTV	--NVGPQE	195
443	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--SLGPSE	196
444	N-GAD	VSFSLLDELLDAVKA <sub>1</sub> KDGKVDFLMMHART <sub>1</sub> RSVKTLLRGQ	-SGAGIIE	201		
445	N-GGA	LSFEWL <sub>1</sub> DNLLDLVVSKDGDV	DY <sub>1</sub> LIMHART <sub>1</sub> R <sub>1</sub> RSYK <sub>1</sub> L <sub>1</sub> R <sub>1</sub> AL	-GGVPME	201	
446	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
447	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
448	N-GGS	LTLDLM <sub>1</sub> DQLIDL <sub>1</sub> V <sub>1</sub> KP	GKP <sub>1</sub> DALLMSKRTRKLSALRRAS	-GNLLET <sub>1</sub> D	197	
449	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
450	GAS	MTFSMFDELVDAVKDL	GA	DCIMMRSEHLRAYRALLRTV	--NVGPSE	196
451	N-GGS	LTLELLEQLIDL <sub>1</sub> V <sub>1</sub> KP	GKP <sub>1</sub> DALLMAKRTRKLAQLRRSS	-GSV <sub>1</sub> LETE	199	

452 ---D-GGA---LTLDLMDELIDLVRP--GRP D ALL MHKTRRKLSQLRRTS-GNLLETD 199  
 453 -----KAS---MTFSMFDELVDAIKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 454 GAAN-GAA---LSFEDLDALIDLVTDKDGQVDYLMMHGRTRRKYLALLRSL-GGTSPAD 205  
 455 ---N-GAA---LTLSMMDELADQVIN--GA-DAFIMRP GTIRAYRALLYAS-GGIQPAM 198  
 456 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 457 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 458 -----KAS---MTFSMFDELVDAIKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 459 ---N-GAA---MTLGMLDQLIDAVPN--GA-DFLMMRSGT RRAYTALVRAA-GGNTASM 198  
 460 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 461 GAAN-GAG---LSFEDLDALIDLVTDKDGQVDYLMMHSRTRRKYLALLRAL-GGTSPGD 205  
 462 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 463 -----GAP---LSFPCLSKAWHLVKANNGKPTVIMS NARSLESYENLCRLS-GQNVEY 107  
 464 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 465 -----GVS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 466 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 467 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 468 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 469 -----GAA---ITFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTM-NAGPAE 195  
 470 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 471 ---N-GAA---LSFEKLDELMDTVTDKDGEVDYLTMHARSLRSFNALLRGL-GGASIGD 202  
 472 ---N-GNP---LTLTMMDELCDAVPN--GA-DVLVMRRGTIRAYRALLRAT-YG TDAVM 208  
 473 ---N-GAA---LSFEKLDELMDTVTDKDGEVDYLTMHARSLRSFNALLRGL-GGASIGD 202  
 474 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 475 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 476 GAAN-GAA---LSFEDLDALIDLVTDKDGQVDYLMMHSRTRRKYLALLRAL-GGTSPGD 205  
 477 ---N-GSA---LQFELLDELIDSVKDKDGQVDYI LASARTIRSYYALLRGL-GGATIGD 201  
 478 ---N-GAT---LSFELLDELLDRVTAKDGVDFLMMHGR TIRSLKALLRAQ-GGA GIVE 201  
 479 GAAN-GAA---LSFEDLDALIDLVTDKDGQVDYIMMHGRTRRKYLALLRAL-GGTSPGD 205  
 480 ---N-GSA---LSFEILDELMDLVVDKDQVDYLTMHARTLSYNALLRSL-GGASIGD 202  
 481 -----GVS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 482 -----GVS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 483 -----DSA---MTFSMLDELVDAVKDL-GA-DAIMMRSEHRLRAYRALLRTV--N VGPQE 195  
 484 -----GVS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 485 ---D-GGA---LTLDLMDELIDLVRP--GRP D ALL MHKTRRKLSQLRRTS-GNLLETD 199  
 486 -----DSA---MTFSMLDELVDAVKDL-GA-DAIMMRSEHRLRAYRALLRTV--N VGPQE 195  
 487 -----KAS---MTFSMFDELVDAIKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 488 -----DSA---MTFSMLDELVDAVKDL-GA-DAIMMRSEHRLRAYRALLRTV--N VGPTE 195  
 489 -----DSA---MTFSMLDELVDAVKDL-GA-DAIMMRSEHRLRAYRALLRTV--N VGPQE 195  
 490 GAAN-GAG---LSFEDLDALIDLVTDKDGQVDYLMMHSRTRRKYLALLRAL-GGTSPGD 205  
 491 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 492 ---N-GGA---LSFEMLDELLDAVKAKDGKVDFLMMHGR TIRSLKSLLRGQ-GGAGIVE 201  
 493 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 494 -----N-GGS---LTLDLMDQLIDLVPK--GRP D ALL MSKRSRRKLSALR RAS-GNLLETD 199  
 495 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 496 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 497 --DN-GAN---LSFDQLDQLIDLVPKDKDGQVDYMMMPARTIRSFYALLRQL-GGATIND 202  
 498 -----GAS---MTFSMFDELVDAVKDL-GA-DCIMMRSEHRLRAYRALLRTV--N VGPSE 196  
 499 -----DSA---MTFSMLDELVDAVKDL-GA-DAIMMRSEHRLRAYRALLRTV--N VGPTE 195  
 500 GAAN-GAG---LSFEDLDALIDLVTDKDGQVDYLMMHSRTRRKYLALLRAL-GGTSPGD 205



13	-----PVI-DGKS-----SFDGWKIYINDE-QPTHCI-----	KDK	219
14	-----PEV-NGHT-----VFDGWLIVYINDM-QPLNCN-----	DSE	219
15	EEMTFPGP-DGSSRMQQVLFKFDGAPVYINDLNQIYACDGSKPKDYLIPPEKALNLDGFDP	S 260	
16	EEMEFTCP-DGTTKFEHVLKFDGAPVYINDLNQVYECGHNVGAISPENVLENGMEPP	260	
17	EEMEFACP-DGTTKFEHVLKFDGAPVYINDLNQVYECGHNVGAISPENVLENGMEPP	260	
18	EEMEFTSP-DGTAKFEQVLKFDGAPVYINDLNQIYECNDNNNTGTPIPSEKISRNLNDNEPP	260	
19	TDMIFPCP-RNENQVERVLTVDGAPVYVNDLNQNLGSPDNPAGESVHENPGEGL--NSD	257	
20	EEMAFFPSP-DGSSKMQQVLFKFDGAPVYINDLNQIYACDGSKPKLIPPPKALNLDGFDP	261	
21	TDMIFPCP-RNENQAEQVLTFDGAPVYVNDLNQNLGGSPDAPDGEPVNPENPLAPD--SAG	257	
22	TDMIFPCP-RNENQMERVLTFDGAPVYINDLNQNFSGSPDNPSGELVHENPQILG--SPG	257	
23	TDMIFPCP-RNENQAEQVLTFDGAPVYVNDLNQNLGGSPDAPDGEPVNPENPLAPD--SAG	258	
24	TDMIFSCP-YNENQAEQVLTFDGAPVYVNDLNQNLGRSPDTPDGESIVENPLAFG--SAG	257	
25	TDMIFPCP-RNENHTERVLTVDGAPVYVNDLNQNLGSPPDAPDGEPVNPENPLAPD--SAG	257	
26	TDMIFPCP-RNENQGERVLTVDGAPVYVNDLNQNLGSPPDTPDGEPVNPENPLASD--STG	257	
27	EEMEFTCP-DGTTKFEHVLKFDGAPVYINDLNQIFECSHNQVGAIPPERVLA LNGTEPP	260	
28	TDMIFSCP-YNENQAEQVLTFDGAPVYVNDLNQNLGRSPDTPDGESIVENPLAFG--SAG	257	
29	VTETWTDVKGRVSAP-ITCFNGTPWYINDLIDDDQAG-----	237	
30	VTETWTDVKGRVSAP-ITCFNGTPWYINDLIDDDQAG-----	243	
31	VKVARPDPIKGMLLEE-IAAFNGTPWYINDLIDDDQAS-----	239	
32	VKVARPDPIKGMLLEE-IAAFNGTPWYINDLIDDDQAS-----	239	
33	VKVRPTDPIKGIVLEE-IASFNGTPWFINDLIDDDQAN-----	239	
34	VDAEWTDPTKGTVRVPQI-AINGTPVYVNDMIATVEDPGP-----PAT	254	
35	TEMDFDPAQGRTVKRLVPSINGAPILINDMVAT-DG-----S	256	
36	-----PVI-DGKS-----SFDGWKIYINDE-QPTHCI-----KDK	142	
37	VPYEWTDPPIKGRLTVQVA-SINGTPIFINDMIAT-EDSDP-----E	250	
38	VMDTWFDPIRGEITAG-ITSFKGTPWYINDLIDDDLP-----	237	
39	VEFI-PLQ-DGPA--QKVMYDGCPILINDA-QPEHVLGGNP-----	235	
40	VETEWGDPLKGTMRAPQI-AINGTPVYINDWIAT-----DT	243	
41	-----NFEDWPICLND--QQPTCSACGVD-----	218	
42	VLDTWMDPVLGEVTAP-ITAFNGTPWYINDLIDDEAG-----	237	
43	VMDTWSDPIHGQITAP-ITAFNGTPWYINDLIDDDQAG-----	236	
44	VPASWMDPVLGEVTAP-ITAFNGTPWYINDLIDDDQAG-----	237	
45	VMDTWFDPIRGQVSAG-ITSFKGTPWYINDLIDDDLP-----	237	
46	APFRWYNPASRRMEDGSVDAFNGTPWLANDLCNAAGAP-----G	231	
47	VPFRWYNPAIGGMQECSVDALNGTPWLANDMLGS-----	227	
48	VPFMLYDPASRRMEDDAVDAFNGTPWLANDLCNADGL-----	229	
49	APFRWYNPASRRMEDGSVDAFNGTPWLANDLCNAAGTP-----G	231	
50	VPFMLYNPASRRMEDDTVDAFNGTPWLANDLCNAAGI-----	229	
51	EPWTWYHPDKRMRMGPSVDSFNNGTPWLVNDFINKSGLD-----	226	
52	VPWTWYDPFKG-WQQGKVTSFHGPWLVNTKMNAGLLP-----	230	
53	TIEMRIEDADGSTRVMPVLAWDGIPVVLVDDQVPSDET-----SNNY	245	
54	VEMEWIDPLTGKKRQWMNAINGAPILINDMIET-DE-----G	237	
55	FEVMELPAPGGGTRMVKVPCWDGIPWVIDDNPANEQP-----GGTS	247	
56	VMETWTDVKQGRMSAP-ITCFNGTPWYINDLIDDDQAG-----	237	
57	MPWQWYNPSLGRMEESLVTQFNGTPWLINGCMAGEASPK-----P	231	
58	VEMPFDPISGGGVKMRVPAINGTPILVNDLIET-TSP-----G	241	
59	MKATTSEDVDGSRREIPGLAFTDGIPIVVVDDLPVNEG-----SGSQ	245	
60	VQWRWYCPATRMWHDDWISAFRGVPWVINQEMNPGLLP-----	231	
61	YEMMEIPVAGGGSRMIKVPCWGDGVWPVVIDDNVPNDEQP-----SGTN	247	
62	AAFKWYNPASRRMEDGSVDAFNGTPWLANDLCNADGT-----	229	
63	MPWRWYDPLRG-WQVGKVTTFHGPWLVNTKMNAGLLA-----	230	
64	TVLMQVEDADGASRTVSAALAFDGIPIVVVDDQVPNNET-----SNSY	245	
65	YMDWEVPRPGGGTRVRTLWCWEGGPVIVDDSPNDEQP-----GGTS	247	
66	SPWTWYYPAKGSSGPGSVDSFNNGTPWLVNDFINKDGHD-----	226	
67	VDFMWYDPVRRRMTPKVTAFTNGTPWLVNDRMEGKTNPA-----A	233	
68	VAVVVPDG-NGGLKTVTMMHVNGWLVMWTFVPIEQFQ-----GSTV	242	
69	VSVAVPDG-NGGLKTISMHMHVNGWLVSWTDFVPIEQFQ-----GSTV	258	
70	AEIEVPDPRTGTR-LARVPSIHGPWYINDAMEVPPEGE-----	240	
71	ADIEVPDPRTGTR-IARVPSIHGPWYINDAMEVPPEGE-----	291	
72	ADIEVPDPRTGTR-IARVPSIHGPWYINDAMEVPPEGE-----	286	
73	VEIDADPDLTGT-KQWVPSIHGPWYINDAMEVPPEGE-----	240	
74	VMIENF-----GRPMCLCHNGVPIIVNDFLPLNEVQ-----GSSS	232	
75	VPYRWYNPTVGGMQECSVDAFNGTPWLANDMLGS-----	227	
76	VTETWTDVKGRVSAP-ITCFNGTPWYINDLIDDDQAG-----	172	
77	VPWRWYCPATGRWKDGVVPSFNGTPWVINDEMNPVGQP-----	231	
78	ITVENF-----G-TVRAYDGTGPVIINDFLPGDEVQ-----GTEN	231	
79	VTETWTDVKGRVSAP-ITCFNG-----	223	

80	VMMENF-----	GRPMLTHNGVPIIVNDFLPSNEVQ-----	GSSS	232
81	IMIENF-----	GRAVPGHNGIPPIIVNDFLPIDEVQ-----	GTET	233
82	QQLENF-----	GRPMLTHNGIPILMNEFLPKNEVQ-----	GASS	232
83	IQIPNF-----	GKPVPAYDGPVVIINDFMTADEVQ-----	GSAN	232
84	IQIPNF-----	GKPVPAYDGPVVIINDFLTADEVM-----	GSAN	232
85	IQIPNF-----	GKPVPAYDGPVVIINDFLTADEVM-----	GSAN	232
86	IMIPNF-----	GKPVPAYDGPVVIINDFLTADEVM-----	GSAN	232
87	VETHWADPVKGVV	-RGKVISMYGTPWYINAAMTRPEGT-----		231
88	VEMEWVDPLTGGKKRQWMNAINGAPILINDMIET-DG-----		S	188
89	IQIPNF-----	GKPVPAYDGPVVIINDFLTADEVM-----	GSAN	232
90	MMIKNF-----	GQAVPCYDGKPVIIINDFLPADEVQ-----	GTAD	232
91	VPWRWYDPAR GRMVEGSVDAFN GTPWLANDFVN-AGAD-----		P	186
92	VDAPWADPIRGVA	-LGKVVSMYGTPWYINGAMNTTRPEGT-----		231
93	VETQWADPIRGVV	-PGKVVSVYGTPWYINGAMTRPEGT-----		231
94	IMMENF-----	GRPMLTHNGVPILVNDFLNVAQ-D-----	GEGK	229
95	IQIANF-----	GKPVPAYDGPVVIINDFITADEVQ-----	GSAN	232
96	QMLDNF-----	GRPMLTHNGVPIIMNEFSPGTEDQ-----	GTAT	232
97	IIVKDF-----	GKALPAFDGTPVIIINDFMTADEVQ-----	GTNE	232
98	LQIENF-----	GM-MPAHDGIPIIIINDFIPVK-AQ-----	GTAA	232
99	IMIPNF-----	GRPIPAPFDGTPVIIINDYMNADETQ-----	GTAE	232
100	LQLDNF-----	GV-IPAHDGVPPIIINDFIPVK-AQ-----	GTNA	232
101	VVQGEY-----	G-PIPAHNGVPIIVNDFLPADEVQ-----	GNSS	232
102	IECVKEDPILGPV RVKQL	-CLYGTPWYICDLIQARTVNS-----	Q	239
103	LQLDNY-----	GQ-IPAHDGIPPIIINDFIPVK-AQ-----	GTAA	232
104	QMVENF-----	GRPMLTHNGVPIVNMNEFLPADEVM-----	GTNT	232
105	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
106	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	230
107	QQGLNFD-----	GRPVLTHNGIPPIIMNEYLDGNENG-----	N	228
108	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
109	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
110	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
111	VMIKDF-----	GM-VMAHNGTPLLRNDLPGNETL-----	GTGN	231
112	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	234
113	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
114	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
115	LQIDNF-----	GLSVP AHDGIPPIIINEFIPGNVAQ-----	GSTA	233
116	VMLKNF-----	GHPMLTHNGVPIIVNDYIKVDE-----	GDES	228
117	QMVENF-----	GRPM LAHNGVPIVNMNEFLPADEVM-----	GTNT	232
118	QMVENF-----	GRPMLTHNGVPIVNMNEFLPADEVM-----	GTNT	232
119	VMLKNF-----	GHPMLTHNGVPIIVNDYIKVDE-----	GDES	228
120	IQHPNF-----	DVPVLAHNGCPIIINDFMPGDELM-----	GSNS	233
121	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
122	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
123	QQLENF-----	GRPMLTHNGIPPIIMNEFLAADEAQ-----	GTAT	232
124	QQLSNF-----	GRPMLTHNGIPPIIMNEWIAGDEVK-----	GTNQ	232
125	QQLSNF-----	GRPMLTHNGIPPIIMNEWIAGDEVK-----	GTNQ	232
126	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
127	IIVKDF-----	GKLP AFDGTPVIIINDYIGADEVQ-----	GAST	232
128	IIVKDF-----	GKALPAFDGTPVIIINDYITADEVQ-----	GAST	232
129	VEIPNF-----	GQAVLAHNGIPILRNDWLANDET M-----	GTNA	232
130	VEIPNF-----	GQAVLAHNGIPILRNDWLANDET M-----	GTNA	232
131	VEIPNF-----	GQAVLAHNGIPILRNDWLANDET M-----	GTNA	232
132	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
133	VMEMPN-----	GARVIA YEGVPIFRNDYIPTNQTK-----	GGYA	235
134	VEIPNF-----	GQAVLAHNGIPILRNDWLANDET M-----	GSNA	232
135	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
136	VMMENF-----	GRPMLTHNGTPPIIVNDFI-AKT-----	GDAG	227
137	VTLPGT-----	GISVPAYRRTPPIIINDFLPGDELH-----	GTKS	232
138	QQLENF-----	GRPMLTHNGIPIPVIMNEFLAADEAQ-----	GSAN	235
139	IMLPNF-----	GHPVPAIDGMPVIIINDFIPANEVT-----	GSSS	232
140	VMLPQF-----	GKVMLTHNGVPIIVNDFLPVTD-----	GE GT	229
141	LILPNF-----	GRPMLCHNGMPIIVNDYI-GTEAQ-----	GSAD	234
142	TMIENF-----	GHPVKAYDGPVVIINDFLPANEVQ-----	GTAN	232
143	VMLPQF-----	GKVMLTHNGVPIIVNDFLPVTD-----	GE GT	229
144	IMIPNF-----	GHPVKAYDGPVVIINDFLTANEVQ-----	GSAT	232
145	IMLENF-----	GQSIPAYNGKPVIIINNYITADETQ-----	GAGD	232
146	VTLPGT-----	GINVPAYRRTPPIIINDFLPGDEVH-----	AAGT	232

147	IMMENF-----	S R P M L C H N G V P F I V N D F I P K -----	NEG D	226
148	IMMENF-----	G R P M L C H N G V P F I V N D F I P K -----	NEG D	226
149	IMMENF-----	G R P M L C H N G V P F I V N D F I P K -----	NEG D	226
150	I M I E N F -----	G R P M L C H N G V P F I V N D F I P K -----	N D D N	226
151	IMMENF-----	G R P M L C H N G I P F I V N D F I P K N G V K V T E D S E Q -----	K T E G Q E	239
152	IMMENF-----	G R P M L C H N G V P F I V N D F I P K -----	N D D N	226
153	I M I P N F -----	G H P V K A Y D G T P V I I N D F I L T A D E V Q -----	G S A T	232
154	IMMENF-----	G R P M L C H N G V P F I I N D F I P K -----	T E E N	226
155	IMMENF-----	G R P M L C H N G I P F I V N D F I P K N G V K V T E Y S E Q -----	K T E G Q E	239
156	I M I E N F -----	G R P M L C H N G V P F I V N D F I P K -----	N D D N	226
157	I M I E N F -----	G R P M L C H N G V P F I V N D F I P K -----	N D D N	226
158	IMMENF-----	G R P M L C H N G I P F I V N D F I P K N G V K V T E D S E Q -----	K T E G Q E	239
159	IMMENF-----	G R P M L C H N G I P F I V N D F I P K N G V K V T E G S E Q -----	K T E G Q E	239
160	IMMENF-----	G R P M L C H N G I P F I V N D F I P K N G V K V T E D S E Q -----	K T E G Q E	239
161	Q M V E N F -----	G R P M L T H N G V P I V M N E F L P A D E V M -----	G T N T	232
162	V M M P A F -----	G R P M L T H N G V P I L I N D F I P L N E T T -----	G T S N	239
163	IMMENF-----	G R P M L C H N G I P F I V N D F I P K N G V K V T E G S E Q -----	K T E G Q E	239
164	I M I E N F -----	G R P M L C H N G V P F I V N D F I P K -----	N D D N	226
165	IMMENF-----	G R P M L C H N G V P F I V N D F I P K -----	N D D S	226
166	IMMENF-----	G R P M L C H N G V P F I V N D F I P K -----	N D D N	226
167	IMMENF-----	G R P M L C H N G V P F I V N D F I P K -----	N D G D	226
168	IMMENF-----	G R P M L C H N G V P F I V N D F I P K -----	N D D S	226
169	I M M E D F -----	G R P M L C H N G V P F I V N D F I P K -----	N D G D	226
170	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
171	IMMENF-----	G R P M L C H N G V P F I V N D F I P K -----	N D D S	226
172	IMMENF-----	G R P M L C H N G I P F I V N D F I P K N G V K V T G D S E Q -----	K T E G Q E	239
173	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
174	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
175	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
176	IMMENF-----	G R P M L C H N G V P F I V N D F I P K -----	N D G D	226
177	IMMENF-----	G R P M L C H N G I P F I V N D F I P K N G V K V T E D S E Q -----	K T E G Q E	239
178	IMMENF-----	G R P M L C H N G I P F I V N D F I P K N G V K V T E D S E Q -----	K T E G Q E	239
179	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
180	IMMENF-----	G R P M L C H N G V P F I V N D F I P K -----	N D D S	226
181	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D A	224
182	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
183	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D A	224
184	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
185	IMMENF-----	G R P M L C H N G I P F I V N D F I P K N G V K V T E D S E Q -----	K T E G Q E	239
186	IMMENF-----	G R P M L C H N G V P F I V N D F I P -----	T D S	224
187	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
188	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D A	224
189	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
190	V - N A F -----	G R R I E T Y D G I P I A A D D F I L N T E T Q -----	G T S S	231
191	IMMENF-----	G R P M L C H N G I P F I V N D F I P K N G V K I S E E P E K -----	K T E G Q E	239
192	M M I E N F -----	G - M V P A I D G M P V I I N D F I R A D E V Q -----	G T N D	231
193	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
194	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
195	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
196	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
197	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
198	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D A	224
199	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
200	IMMENF-----	G R P M L C H N G V P F I V N D F I P -----	T D S	224
201	IMMENF-----	D R P M L C H N G V P F I I N D F I P -----	T D A	224
202	I T I K D F -----	G - T V K A Y D G T P V I I N D F I L T D N E V Q -----	G T A N	231
203	IMMENF-----	G R P M L C H N G V P F I V N D F I P -----	T D A	224
204	Q Q L E N F -----	G R P M L T H N G I P V I M N E W L P A N E T Q -----	G T S V	233
205	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
206	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
207	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D A	224
208	IMMENF-----	G R P M L C H N G V P F I V N D F I P -----	T D A	224
209	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
210	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D A	224
211	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D S	224
212	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D A	224
213	IMMENF-----	G R P M L C H N G V P F I I N D F I P -----	T D A	224

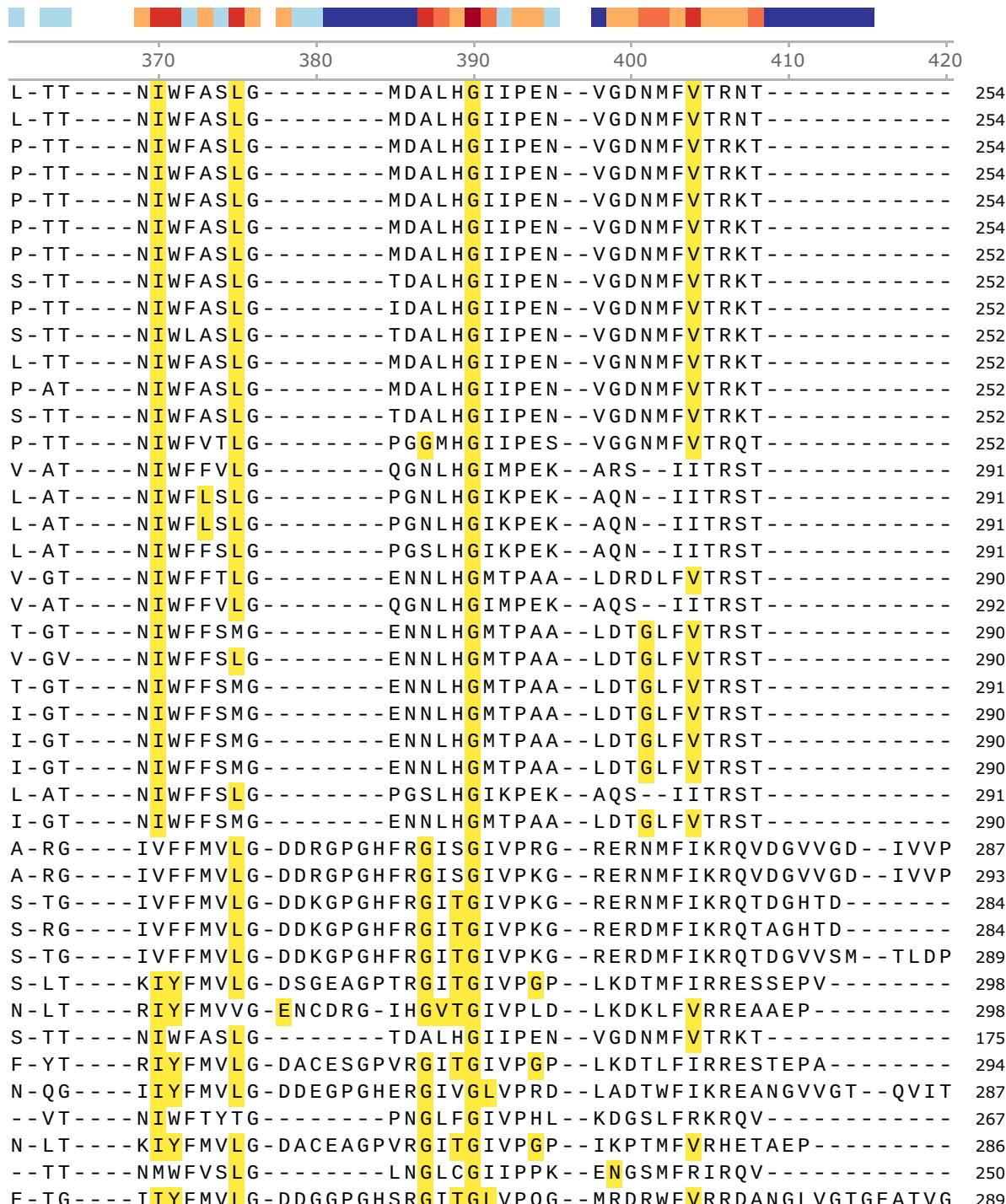
214	IMMENF-----	GRPMLCHNGIPFIVNDFIPKNGVKVTEGSEQ-----	KTEGQE	239
215	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
216	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
217	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
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222	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
223	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
224	IMMENF-----	GRSMLCHNGVPFIVNDFIP-----	TDA	224
225	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
226	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
227	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
228	QMLPAF-----	GHPMLVHQGMPILMNEFIPMGED-----	G-----	226
229	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
230	QMLPAF-----	GHPMLVHQGMPILMNEFIPMGED-----	G-----	226
231	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TGA	224
232	IMMENF-----	GRPMLCHNGIPFIVNDFIPKNGVKVTEDSEQ-----	KTEGQE	239
233	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
234	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
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236	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
237	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
238	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDS	224
239	I--DQF-----	GQRIVTYDGIPVLVDDFVPDDETL-----	GSGT	231
240	IMMENF-----	GRPMLCHNGIPFIVNDFIPKNGVKVTEDSEQ-----	KTEGQE	239
241	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
242	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
243	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
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245	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
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261	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	VADS	225
262	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
263	IMLENF-----	GRPMLCHNGIPFIINDFIPK-----	TEEN	226
264	IMMENF-----	GRPMLCHNGVPFIINDFIPK-----	NEDN	226
265	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VSDS	225
266	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
267	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	225
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269	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
270	QMLPAF-----	GHHMLVHQGMPILMNEFIPMETD-----	G-----	226
271	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
272	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
273	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	225
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275	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
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277	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
278	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	VADS	225
279	IMMENF-----	GRPMLCHNGVPFIINDFTP-----	TDA	224
280	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224

281	QQLSNF-----	GRPMLTHNGIPPIIMNDWIAGDEVK-----	GTNS	232
282	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	225
283	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
284	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
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286	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDS	224
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301	IMIENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	225
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304	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VVDS	225
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307	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	ADA	224
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316	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	225
317	IMMENF-----	GRPMLCHNGVPFIINDFIPK-----	NEDN	226
318	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	225
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340	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	225
341	IMMENF-----	GRPMLCHNGIPFIVNDFIP-----	TDA	224
342	IMMENF-----	GRPMLCHNGIPFIVNDFIPKNGVKVTEDSEQ-----	KTEGQE	239
343	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
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346	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
347	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224

348	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	NEDG	226
349	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
350	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDS	224
351	QQLSNF-----	GRPMLTHNGIPIIMNDWIAGDEVK-----	GTNS	213
352	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
353	VITLPD-----	GSQIPAYRNIPIFRNDYIPTDQTK-----	GATS	236
354	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	222
355	IMMENF-----	GRPMLCHNGVPFIINDFIPK-----	SEDN	226
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367	IMLENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
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369	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
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375	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	ADA	224
376	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
377	V--DQF-----	GQRVLFYDGIPVVLVDDFVPDNETL-----	GTGT	231
378	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
379	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDS	224
380	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
381	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
382	VFELPS-----	GKNVPAYSIGIPLRNWDWIPINQTK-----	GSGT	235
383	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	SEDG	226
384	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	SEDG	226
385	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
386	IMMENF-----	GRPMLCHNDVPFIVNDFIP-----	TDA	224
387	IMIPNF-----	GLALPAHNGVPPIIINDFMPTTENV-----	GGTA	234
388	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
389	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	225
390	VVEMPN-----	GTRIMAYEGVPIFRNDYIIPVNQAK-----	GGQA	235
391	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
392	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	TDA	224
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394	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
395	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
396	IMIENF-----	GRPMLCHNGIPIFIVNDFIPKNGVTI-EGSEE-----	KAEGTE	238
397	VYTMAS-----	GRQVPAYRGIPPLFRNDWIPINQTQ-----	GSAT	239
398	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
399	IMMENF-----	GRPMLCHNGVPFIINDFIPK-----	DTAN	226
400	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
401	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
402	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
403	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	225
404	IMMENF-----	GRPMLCHNDVPFIVNDFIP-----	VADS	225
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406	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDS	226
407	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	VADS	225
408	IMMENF-----	GRPMLCHNGVPFIVNDFIS-----	TDA	224
409	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
410	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
411	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDS	226
412	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	TEDG	226
413	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
414	IMMENF-----	GRPMLCHNGIPIFIINDFIPK-----	SEDG	226

415	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	TEDG	226
416	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	TEDG	226
417	IMIENF-----	GRPMLCHNGIPFIVNDFIPKNGVTI-EGSEE-----	KAEGTE	238
418	IMMENF-----	GRPMLCHNGVPFIVNDFIL-----	TDA	224
419	MMVKNF-----	GMPIKCYDGTTPVIINDFIPADEKQ-----	GSAT	232
420	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	SEDG	226
421	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
422	IMMENF-----	GRPMLCHNGIPFIVNDFIPKNGVKVTEDSEQ-----	KTEGQE	239
423	IMIENF-----	GRPMLCHNGIPFIVNDFIPKNGVTI-EGSEE-----	KAEGTE	238
424	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	TEDG	226
425	IMMENF-----	GRPMLCHNGIPFIVNDFIPKNGVKVTEDSEQ-----	KTEGQE	239
426	IMMENF-----	GRPMLCHNGIPFIVNDFIPKNGVKVTEDSEQ-----	KTEGQE	239
427	IMMENF-----	GRPMLCHNGIPFIVNDFIPKNGVKVTEDSEQ-----	KTEGQE	239
428	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	TEDG	226
429	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
430	IMMENF-----	GRPMLCHNGIPFIVNDFIPKNGVKVTEDSEQ-----	KTEGQE	239
431	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	TEDD	226
432	VYQMPS-----	GETVIAYSGVPIFRNDYLATNQVK-----	GSGS	235
433	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
434	IMIENF-----	GRPMLCHNGVPFIINDFIP-----	VADS	225
435	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	VADS	225
436	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	SEGG	226
437	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	NEG	224
438	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	SEDG	226
439	QMLPAF-----	GHHMLVHQGMPILMNEFIPMAD-D-----	G-----	226
440	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
441	V--DQF-----	QRVLFYDGIPVLVDDFVPDNEL-----	GTGT	231
442	IMIENF-----	GRPMLTHNGVPFIINDFIPKTG-----	EAKS	227
443	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
444	TLLPS-----	GEETLVYEGVPIFRNDWVPTNQTQ-----	GSST	235
445	VFTLPS-----	GKEMLAYSGVPIFRNDYIPVNQTK-----	GTGS	235
446	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
447	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
448	V--DQF-----	GRRALFYDGIPILVDDFIPDNEL-----	GTGT	229
449	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
450	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
451	V--DQF-----	GQRIVTYDGIPVLVDDFVPEDETL-----	GTGN	231
452	V--DAF-----	GRRALFYDGIPIIIVDDFIPIDETL-----	GAGS	231
453	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	SEDG	226
454	VYTMAS-----	GRQVPAYRGIPPLFRNDWIPINQTQ-----	GSAS	239
455	VEIPNF-----	GQPVLAHNGIPILRNDWLNSNSETM-----	GSNS	232
456	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	VADS	225
457	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
458	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	TEDG	226
459	IQHKNF-----	DNPVLAHNGTPIIVNDFLPATEAK-----	GTGT	232
460	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
461	VYVMAS-----	GRSVPAYRGIPIFRNDWIPINQTQ-----	GTSA	239
462	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
463	MPWRWYCPAKRHWDGKVPSFNGTPWVINDEMNPVGVL-----	-----	145	
464	IMMENF-----	GRPMLCHNGIPFIVNDFIPKNGVKVTEDSEQ-----	KTEGQE	239
465	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
466	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
467	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
468	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
469	VMVENF-----	GRPMLTHNGVPFIINDFIPVAD-----	NGGT	227
470	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
471	VVTLPS-----	GAEVPAYRGVPIFRNDFIPVNQTV-----	GTST	236
472	QMMENF-----	GRPMLTHNGIPPIIMNEFLSGAEVK-----	GTSI	242
473	VVTLPS-----	GAEVPAYRGVPIFRNDFIPVNQTV-----	GTST	236
474	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
475	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
476	VYTMAS-----	GRTVPAYRGIPIFRNDWIPINQTQ-----	GTSA	239
477	VVTLPS-----	GRQVPAYRGVPIFRNDYIATNQTK-----	GTAT	235
478	TLELPS-----	GEEVLEYEGVPVFRNDWMPTNQTQ-----	GTST	235
479	IYTMPS-----	GRQVPAYRGIPIFRNDWIPINQTQ-----	GTSV	239
480	VVTLPS-----	GAEVPAYRGVPIFRNDYIPTNQTK-----	GTGT	236
481	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224

482	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
483	IMIENF-----	GRPMLTHNGIPFLVNDFIPVAG-----	DGNA	227
484	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
485	V--DAF-----	GRRALFYDGIPPIIVDDFIPIDETL-----	GAGS	231
486	IMIENF-----	GRPMLTHNGVPFIVNDFIPVVG-----	DAKA	227
487	IMMENF-----	GRPMLCHNGIPFIINDFIPK-----	TEDG	226
488	IMIENF-----	GRPMLTHNGVPFLVNDFIPKTG-----	DTKA	227
489	IMIENF-----	GRPMLTHNGVPFIVNDFIPVVG-----	DTKA	227
490	VYTMAS-----	GRTVPAYRGIPIFRNNDWIPITQTQ-----	GTAT	239
491	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDS	224
492	TLKLPS-----	GEEVLEYEGVPVFRNDWMPTNQTQ-----	GSST	235
493	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VVDS	225
494	V--DAF-----	GRRALFYDGIPILVDDFISDSETL-----	GSGT	231
495	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	225
496	IMMENF-----	GRPMLCHNGVPFIVNDFIP-----	VADS	225
497	VLELPS-----	GRRVPVYRDIPIFRNDFIPTDQTV-----	GTSD	236
498	IMMENF-----	GRPMLCHNGVPFIINDFIP-----	TDA	224
499	IMIENF-----	GRPMLTHNGVPFLVNDFIPKTG-----	DTKA	227
500	VYTMAS-----	GRTVPAYRGIPIFRNNDWIPITQTQ-----	GTAT	239



43	E-TG---I IYFMVLG-DDGGPGHYRGITGLVPKK--LEHGWGVKRESNGVSGTGEALVT	288
44	E-TG---I IYFMVLG-DDGGPGHYRGITGLVPQG--FENRWFVRRDANGLVTGEATVG	289
45	D-QG---I IYFMVLG-DDEGPGHHERGIVGLVPHD--LSDTWFIKREANGVIQTIT	287
46	G-VE---RTYFMVVG-DDGKSGPTRGVTVGIVPAH--LGSEMFIKRTVPALV-----	275
47	T-PE---RTYFMVVG-DDGNAGPTRGVTVGIVPAH--LGRNMFIKRTVPAIISVE-----	274
48	G-TE---RTYFMVVG-DDGKAGPTRGVTVGIVPAN--LGREMFIKRTVPALV-----	273
49	G-VE---RTYFMVVG-DDGKAGPTRGVTVGIVPAH--LGREMFIKRTVPALV-----	275
50	G-TE---RTYFMVVG-DDGKAGPTRGVTVGIVPAH--MGREMFIKRTVPALL-----	273
51	--GE---YIYFMVTG-DDGGKG PTRGVTVGILPRQ--QMSNPFNKRVVQGIYNPD-----	272
52	V-DR---RIYFMVMG-DDGGPGHTRGITCIRPAD--LMNRRYIKRAVNGVPDF-----	276
53	T-----SIYALV LG-RE-----GIYGVIPEG--FQGRMIRANRA-----	276
54	N-LT---RIYMMVVG-EVCDRQ-IHGVTGIVPKD--LENKLFIRREAAEP-----	279
55	T-----SVYALV LG-QE-----GLHGIVPAG--TKNSMFRVARS-----	278
56	T-RG---IVFFMVLG-DDKGPGHFRG-----	258
57	S-NQ---RIYFMVLG-DDGGE GTTRGVTVGIVPQH--LISWP FVKRVTVNGTHFD-----	278
58	N-LT---RIYMMV MG-EDCERQ-IYGVTVGIPKD--LEGKLFIRRESAEP-----	283
59	T-----SIYALV VG-RE-----GLYGVIPRG--FGGRMFRIQAG-----	276
60	A-DR---RIYFMVLG-DDDGKG PTRGLTRMVPAG--MEYNP FILRMTNGVPDF-----	277
61	T-----SVYALV LG-QD-----GLHGIVPQG--TKDSMFRVART-----	278
62	G-TE---RTYFMVVG-DDGKASPTRGVTVGIVPAH--LGSEMFIKRTVPALLPGP-----	276
63	P-DR---RIYFIVMG-DDGGKG PTRGLT GIPAD--MMNR PYVKRAVNGVPDF-----	276
64	T-----SIYALV LG-RE-----GIYGVI PRG--SEGRMIQAARV-----	276
65	T-----SVYALALG-RE-----GLHGIVPRG--TRESMFRVSKS-----	278
66	--GE---YIFFMVTG-DDGGQG PTRGVTVGITPRQ--QVGRMF NKR TVQGIFAPD-----	272
67	G-AQ---RIYFMVLG-DDGSSG PTRGVTVGIVPQE--LLHSMFVVKRVVPAAYNIE-----	280
68	T-----KIWFVKFG-----RRHIHGIVPASG-GRRSMFKIRS-----	273
69	T-----KIWFVKLG-----RRHIHGIVPASS-GTRSMFKVRS-----	289
70	-----NVYFMVMG-DNGHHTPGHGLQLIMPQV--RRGDMFVKRHIPITPSND-----	284
71	-----NVYFMVMG-DNGHHTPGHGLQLILPQV--RRGDMFVKRHIPITPSND-----	335
72	-----NVYFMVMG-DNGHHTPGHGLQLILPQV--RRGDMFVKRHIPITPSND-----	330
73	-----NVYFMVLG-DNGHHTPGHGLQLIMPA--RRGDMFVKRHIPITPTAD-----	284
74	T-TC---SIYAA RFN-EAD-----GLHG IYGGG--SAGIRIEDIG-----	265
75	T-PE---RTYFMVVG-DDGGAGPTRGVSS--PRH-----	254
76	A-RG---IVFFMVLG-DDRGPGHFRG ISGIVPRG--RERNMFIKRQVDGVVGD--IVVP	222
77	A-DR---RIWFMVLG-DDGGKG PTRGLTRIVPAG--MERSPFILRMTNGVPDF-----	277
78	N-SC---SIYAMRLN-TAD-----GFHGIYGGD--SAGLVFEDLG-----	264
79	-----	223
80	A-TA---SIYAMRLN-EVD-----GLHG IYGGG--NAGFVVEDIG-----	265
81	A-AT---SIYAMRLN-EVD-----GLHAIYGGG--SAGIVVVEDIG-----	266
82	A-TG---SIYAVRLN-EVD-----GLHG IYGGG--NAGFSVDEDIG-----	265
83	A-TC---SIYALRLN-EAD-----GFHGIYGGG--SAGIQFEEIG-----	265
84	E-TC---SIYALRLN-EAD-----GFHGIYGGG--SAGIQFEEIG-----	265
85	A-TC---SIYALRLN-EAD-----GFHGIYGGG--SAGIQFEEIG-----	265
86	A-TC---SIYALRLN-EAD-----GFHGIYGGG--SAGIQFEEIG-----	265
87	-----NIYFMVLG-DNGEARPGHGLTMIMP AE--RMGNPYVEREWPMLKTDG-----	275
88	N-LT---RIYMMVVG-EVCDRQ-IHGVTGIVPKD--LENKYFIRREAH E-----	230
89	A-TC---SVYALRLN-EAD-----GFHGIYGGP--SAGIQFEEIG-----	265
90	A-TC---SIYALRLN-ETD-----GFHGIYGGP--NAGIQVESIG-----	265
91	T-EE---RTFFMVMG-DDGGQG PTRGVTVGIVPAA--QGRNLFNRRRIEGVFAAD-----	233
92	-----NIYFMVLG-DNGEARPGHGLTMIMP AE--RRGNPYVEREWPMLKTDG-----	275
93	-----NIYFMVLG-DNGEARPGHGLTMIMP AE--RRGNPYIEREWPMLKTDG-----	275
94	R-TA---PIFAARLN-ETD-----GLHG IYGGG--SAGVRMEEIG-----	262
95	E-TT---SIYALRLN-EAD-----GFHGIYGGP--SAGIQFEDIG-----	265
96	D-TC---SVYALRLN-ELD-----GLHG IYGGG--NAGIVVENLG-----	265
97	T-TC---SIYALRLN-EVD-----GIHGLYGGG--SAGLRVEEIG-----	265
98	N-TC---SVYALRLN-EVD-----GLHGLYGGG--SAGIRVEDIG-----	265
99	N-TC---SIYALRLN-EAD-----GFHGIYGGG--SAGLRVEEIG-----	265
100	N-TT---SIYAVRLN-EVD-----GLHGLYGGG--SAGVRVEDIG-----	265
101	A-CC---SIYAMRLN-VAD-----GLHGLYGGP--ELGIRIEDVG-----	265
102	T-VS---NIYMMVLGANNKDPQGPFGTVGIIPKQNVQPDTMFRMRESNIVY-----	286
103	N-TC---SVYALRLN-EVD-----GLHGLYGGG--SAGIRVEDIG-----	265
104	K-TC---SIYAIRAN-EVD-----GLHG IYGGG--PAGIVVENIG-----	265
105	K-TT---SIYAVRLN-EVD-----GLHGLYGGG--NAGIVVVEDIG-----	265
106	K-TT---SIYAVRLN-EVD-----GLHGLYGGG--NAGIVVVEDIG-----	263
107	--TC---SVYAVRMN-ELD-----GLHG IYGGD--NAGIVVENIG-----	260
108	K-TT---SIYAVRLN-EVD-----GLHGLYGGG--NAGIVVVEDIG-----	265
109	K-TT---SIYAVRLN-EVD-----GLHGLYGGG--NAGIVVVEDIG-----	265

110	K-TT----	SIYAVRLN-EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	265
111	N-LC----	SVYAAARFN-ESD-----	GLHAIYGGD-----	NAGIVVEDIG-----	264
112	K-TT----	SIYAVRLN-EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	267
113	K-TT----	SIYAVRLN-EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	265
114	K-TT----	SIYAVRLN-EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	265
115	N-TC----	SVYALRLN-EVD-----	GVHGLFGGE-----	SAGIRIEDIG-----	266
116	SKSC---	YIYAARFN-EVD-----	GVHGLFGGP-----	NAGMVVEDIG-----	262
117	K-TC----	SIYAIRAN-EVD-----	GLHGIYGGG-----	PAGIVVENIG-----	265
118	K-TC----	SIYAIRAN-EVD-----	GLHGIYGGG-----	PAGIVVENIG-----	265
119	SKSC---	YIYAARFN-EVD-----	GVHGLFGGP-----	NAGMVVEDIG-----	262
120	S-TC----	SVYAVRAN-ELD-----	GLHGLYGGA-----	SAGIRVETIG-----	266
121	K-TT----	SIYAVRLN-EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	265
122	K-TT----	SIYAGRLN-EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	265
123	A-TC----	SVYALRLN-EAD-----	GLHGLYGG-----	SAGIVVENLG-----	265
124	N-TT----	SIYAVRLN-EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	265
125	N-TT----	SIYAVRLN-EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	265
126	K-TT----	SIYAVRLN-EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	265
127	A-ST----	SIYALRLN-EVD-----	GVHGLYGGA-----	TAGLRVEEIG-----	265
128	A-ST----	SIYALRLN-EVD-----	GIHGLYGGA-----	TAGLRVEEIG-----	265
129	K-TC----	SIYAVRLN-ELD-----	GMHGLWGGK-----	DAGIRVEDVG-----	265
130	K-TC----	SIYAVRLN-ELD-----	GMHGLWGGK-----	DAGIRVEDVG-----	265
131	K-TC----	SIYAVRLN-ELD-----	GMHGLWGGK-----	DAGIRVEDVG-----	265
132	K-TT----	SIYAVRLN-EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	265
133	N-CT----	TIFAGCID-DGSR---	KVGLTGLTARN-----	AYGLEVEQVG-----	271
134	K-TC----	SVYAIRLN-ELD-----	GMHGLWGGK-----	DAGIRVEDVG-----	265
135	K-TT----	SIYAVRLN-EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	265
136	SEVC---	PIYAMRLN-EVD-----	GLHGLYGGN-----	NAGIVVENIG-----	261
137	K-SC----	SIYAVRFN-EAD-----	GMHGFIFGGP-----	TAGFRVQSIG-----	265
138	A-TT----	SVYALRLN-ELD-----	GLHGIYGGS-----	DAGIVVENIG-----	268
139	V-TT----	SIYALRLN-EVD-----	GFHGIVGGE-----	AAGLKVEEIG-----	265
140	K-KA---	PIYALHLS-EEN-----	GVTGLYGGD-----	NAGIVVESIG-----	262
141	A-TT----	SVYALRLN-EDD-----	GLHGLHGGE-----	AAGIRLEALG-----	267
142	E-TC----	SIYALRLN-EAD-----	GLHGIYGGH-----	SAGVRMEEIG-----	265
143	K-KA---	PIYALHLS-EEN-----	GVTGLYGGD-----	NAGIVVESIG-----	262
144	A-TC----	SIYALRLN-EAD-----	GFHGIYGGA-----	NAGVQLEDIG-----	265
145	D-LT----	SIYALRLN-ETD-----	GFHMLYGG-----	SAGIVVENVG-----	265
146	K-TA---	SIYAVRFN-EAD-----	GMHGFIFGGP-----	QAGLRVSHVG-----	265
147	D-SA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
148	D-SA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
149	D-SA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
150	T-TA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
151	G-TA---	NIYCLHLS-EEN-----	GLTGLYGGD-----	NAGIVVENIG-----	272
152	T-TA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
153	A-TC----	SIYALRLN-EAD-----	GFHGIYGGA-----	NAGVQLEDIG-----	265
154	D-AA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
155	G-TA---	NIYCLHLS-EEN-----	GLTGLYGGD-----	NAGIVVENIG-----	272
156	T-TA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NGIVVENIG-----	259
157	T-SA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
158	G-TA---	NIYCLHLS-EEN-----	GLTGLYGGD-----	NAGIVVENIG-----	272
159	G-TA---	NIYCLHLS-EEN-----	GLTGLYGGD-----	NAGIVVENIG-----	272
160	G-TA---	NIYCLHLS-EEN-----	GLTGLYGGD-----	NAGIVVENIG-----	272
161	K-TC----	SIYAIRAN-EVD-----	GLHGIYGGG-----	PAGIVVENIG-----	265
162	V-TT----	SVYALRLN-EYD-----	GLHGLYGGG-----	TAGVVVEDIG-----	272
163	G-TA---	NIYCLHLS-EEN-----	GLTGLYGGD-----	NAGIVVENIG-----	272
164	T-AA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
165	T-GA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
166	T-AA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
167	D-SA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
168	T-GA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
169	D-SA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
170	G-KA---	SIYCLHLS-EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
171	T-GA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
172	G-TA---	NIYCLHLS-EEN-----	GLTGLYGGD-----	NAGIVVENIG-----	272
173	S-KA---	SIYCLHLS-EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
174	G-KA---	SIYCLHLS-EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
175	G-KA---	SIYCLHLS-EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
176	D-SA---	NIYCLHLS-EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259

177	G-TA	-	-	NIYCLHLS	EEN	-	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
178	G-TA	-	-	NIYCLHLS	EEN	-	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
179	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
180	T-GA	-	-	NIYCLHLS	EEN	-	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
181	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
182	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVESIG	-	-	257
183	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
184	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
185	G-TA	-	-	NIYCLHLS	EEN	-	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
186	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
187	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
188	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
189	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
190	D-CT	-	-	SIWFIQFG-MMR	-	-	-	GVIGLE	-	-	NGGIVHEDVG	-	261
191	G-TA	-	-	NIYCLHLS	EEN	-	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
192	K-TT	-	-	SIYALRLN	EAD	-	-	GFHGLWAGA	-	QAGIRYEHLG	-	-	264
193	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
194	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
195	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
196	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
197	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
198	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
199	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
200	G-KA	-	-	SIYCLHMS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
201	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
202	E-TC	-	-	SIYALRLN	ETD	-	-	GFHGIYGGP	-	TAGVQFEDIG	-	-	264
203	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
204	GNTC	-	-	SVYAARLN	EVD	-	-	GLHGLYGGD	-	NAGLVVENIG	-	-	267
205	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
206	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
207	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
208	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
209	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
210	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
211	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
212	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
213	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
214	G-TA	-	-	NIYCLHLS	EEN	-	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
215	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
216	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
217	G-KA	-	-	SIYCLHLS	EES	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
218	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
219	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
220	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
221	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
222	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
223	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
224	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
225	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGE	-	NAGIVVENIG	-	-	257
226	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
227	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
228	--TC	-	-	PIYAIRAN	ELD	-	-	GLHGLFGGD	-	NAGIVVENIG	L	-	258
229	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
230	--TC	-	-	QIYAIRAN	ELD	-	-	GLHGLFGGD	-	NAGIVVENIG	L	-	258
231	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
232	G-TA	-	-	NIYCLHLS	EEN	-	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
233	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
234	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
235	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
236	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
237	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
238	G-KA	-	-	SIYCLHMS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
239	N-LS	-	-	SIYAVKFG-PS	-	-	-	GLMGLE	-	-	NGGITVEEVG	-	260
240	G-TA	-	-	NIYCLHLS	EEN	-	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
241	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGE	-	NAGIVVENIG	-	-	257
242	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
243	G-KA	-	-	SIYCLHLS	EEN	-	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257



311	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
312	T-KA---	DIYCLHLS	EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	258
313	G-KA---	SIYCLHLS	EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
314	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
315	G-KA---	SIYCLHLS	EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
316	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
317	T-AA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
318	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
319	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
320	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
321	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
322	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
323	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
324	G-KA---	SIYCLHLS	EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
325	G-KA---	SIYCLHLS	EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
326	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
327	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
328	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
329	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
330	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
331	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
332	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
333	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
334	T-AA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
335	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
336	G-KA---	SIYCLHLS	EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
337	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
338	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
339	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
340	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
341	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
342	G-TA---	NIYCLHLS	EEN-----	GLTGLYGGD-----	NAGIVVENIG-----	272
343	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
344	G-KA---	SIYCLHMS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
345	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
346	G-KA---	SIYCLHLS	EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
347	G-KA---	SIYCLHLS	EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
348	S-AA---	DIYGLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
349	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
350	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
351	K-TT---	SIYAVRLN	EVD-----	GLHGLYGGG-----	NAGIVVEDIG-----	246
352	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
353	T-CT---	SVVAGTLD	DGSM-----	QSGIAGLTAMD-----	ASGIQVEEVG-----	272
354	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	255
355	T-AA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
356	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
357	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
358	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
359	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
360	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
361	D-AA---	DIYCLHLS	EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	259
362	T-KA---	DIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	258
363	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
364	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
365	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
366	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
367	A-AA---	DIYGLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
368	A-AA---	DIYGLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	259
369	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
370	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
371	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
372	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
373	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
374	G-KA---	SIYCLHLS	EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
375	G-KA---	SIYCLHLS	EEN-----	GVTGLYGG-----	NAGIVVENIG-----	257
376	G-KA---	SIYCLHLS	EEN-----	GVTGLYGGD-----	NAGIVVENIG-----	257
377	G-LS---	SIYAVKWG	-PS-----	GLMGLE-----	NGGIVVEEVG-----	260

378	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	257
379	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	257
380	S-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
381	S-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
382	A-CT	-	TIFAGVFD	DGDM	-	KTGLLGLTAAN	-	AYGMHVVVDVG	-	-	271
383	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
384	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
385	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	257
386	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
387	L-TGGSFRSVYAMRLN	-	EAD	-	-	GLFGVYGGG	-	EAAGFTVEDIG	-	-	272
388	S-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
389	T-KA	-	DIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	258
390	N-CT	-	TILAGVLD	DGSR	-	KVGVTGLTAKN	-	AYGLAVEPVG	-	-	271
391	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
392	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	257
393	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	257
394	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
395	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
396	G-TA	-	NIYCLHLS	EEN	-	GLTGLYGGE	-	NAGIVVENIG	-	-	271
397	N-AT	-	SVFAGTFD	DGSR	-	THGIAGLTAER	-	QAGMHIKYVG	-	-	275
398	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
399	S-TA	-	DIFCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
400	T-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
401	S-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
402	S-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
403	T-KA	-	DIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	258
404	T-KA	-	DIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	258
405	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
406	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
407	T-KA	-	DIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	258
408	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	257
409	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
410	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
411	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
412	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
413	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
414	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
415	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
416	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
417	G-TA	-	NIYCLHLS	EEN	-	GLTGLYGGE	-	NAGIVVENIG	-	-	271
418	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	257
419	A-TT	-	SVYALRLN	EID	-	GFHGLYGGN	-	AAGIRIDL	-	-	265
420	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
421	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
422	G-TA	-	NIYCLHLS	EEN	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
423	G-TA	-	NIYCLHLS	EEN	-	GLTGLYGGE	-	NAGIVVENIG	-	-	271
424	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
425	G-TA	-	NIYCLHLS	EEN	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
426	G-TA	-	NIYCLHLS	EEN	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
427	G-TA	-	NIYCLHLS	EEN	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
428	S-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
429	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
430	G-TA	-	NIYCLHLS	EEN	-	GLTGLYGGD	-	NAGIVVENIG	-	-	272
431	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
432	A-QT	-	TIFAGTLD	DGSR	-	THGIAGLTAAN	-	DAGIVIEDVG	-	-	271
433	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
434	T-KA	-	DIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	258
435	T-KA	-	DIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	258
436	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
437	G-KA	-	SIYGLHMS	EEN	-	GLTGLYGGD	-	NAGIVVENIG	-	-	257
438	A-AA	-	DIYGLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	259
439	--TC	-	QIFALRAN	ELD	-	GLHGLYGG	-	NAGIVVENIG	-	-	258
440	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGD	-	NAGIVVENIG	-	-	257
441	G-LS	-	SIYAVKWG	-PS	-	GLMGLE	-	NGGIVVEEVG	-	-	260
442	Q-KA	-	DIYCLHMS	EEN	-	GLTGLYGGD	-	TAGIVVVEDIG	-	-	260
443	G-KA	-	SIYCLHLS	EEN	-	GVTGLYGGE	-	NAGIVVENIG	-	-	257
444	T-CT	-	SIAGCLD	DGSR	-	KVGIAGLHAKK	-	AMGIQVKALG	-	-	271

445	A-QT----TVFAGVFD-DGDR---KT	GLAGLTATN---	AFGLHVVERVG		271
446	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
447	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
448	N-LS---SIYAVKFG-SA-----	GVMGLE-----	NGGIQVVRVG		258
449	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
450	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
451	N-LS---SIYAVKFG-PS-----	GLMGLE-----	NGGITVEEVG		260
452	N-LS---SIYAVKFG-PS-----	GVMGIE-----	NGGIQIEAIG		260
453	A-AA---DIYGLHLS-EEN-----	GVTGLYGGE--	NAGIVVENIG		259
454	N-AT---SVFAGTFD-DGSR---TH	GIAGLTAER--	QAGMHKIVVG		275
455	S-TC---SIYAVRLN-ELD-----	GFHGLWGGK--	DAGIRVEDVG		265
456	T-KA---DIYCLHLS-EEN-----	GVTGLYGGE--	NAGIVVENIG		258
457	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
458	A-AA---DIYGLHLS-EEN-----	GVTGLYGGE--	NAGIVVENIG		259
459	N-LA---SVYAVRAN-ELD-----	GFHGLYGGD--	AAGVRVREAIG		265
460	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
461	N-AT---SVFAGTFD-DGSR---TH	GIAGLTAER--	QAGMHVKYVG		275
462	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
463	A-NR---RIWFMLVLDGGKGPTRLS	RIVPAG-----	MERRPFVVRMTNGVPDF		191
464	G-TA---NIYCLHLS-EEN-----	GLTGLYGGD--	NAGIVVENIG		272
465	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
466	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
467	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
468	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
469	K-SA---SIYCLHMS-EEN-----	GLTGLYGGD--	NAGIVVVEDIG		260
470	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
471	N-CT---TVFAGTFD-DGSR---TH	GIAGLTAEE--	AAGIQIEDVG		272
472	A-TA---SVYALRLN-EQD-----	GLHGLYGGD--	NAGIVVENIG		275
473	N-CT---TVFAGTFD-DGSR---TH	GIAGLTAEE--	AAGIQIEDVG		272
474	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
475	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
476	N-AT---SVFAGTFD-DGSR---TH	GIAGLTAER--	QAGMHVKYVG		275
477	N-TT---TLFAGTLD-DGSGLKHG	IAGLTAAG--	EAGIRVTEIG		271
478	N-CT---SIIAGCLD-DGSQ---RV	GIAGLHAKK--	AMGIQVKDIG		271
479	N-AT---SVFAGTFD-DGSR---TH	GIAGLTAAT--	EAGVKIKYVG		275
480	N-TT---SIFAGTLD-DGSR---TH	GLAGLTAEE--	AAGIRVEDVG		272
481	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
482	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
483	K-KS---DIFCLHMS-EEN-----	GLTGLYGGE--	NAGIVVVEDIG		260
484	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
485	N-LS---SIYAVKFG-PS-----	GVMGIE-----	NGGIQIEAIG		260
486	K-KS---DIYCLHMS-EEN-----	GLTGLYGGD--	TAGIVVVEDIG		260
487	A-AA---DIYGLHLS-EEN-----	GVTGLYGGE--	NAGIVVENIG		259
488	Q-KA---DIYCLHLS-EEN-----	GLTGLYGGD--	NAGIVVVEDIG		260
489	K-KA---DIYCLHLS-EEN-----	GLTGLYGGD--	NAGIVVESIG		260
490	N-AT---SVFAGTFD-DGSR---TH	GIAGLTAEK--	QAGMHVKYVG		275
491	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
492	T-ST---SIVAGCLD-DGSQ---RV	GIAGLHAKK--	AMGIQVKNIG		271
493	T-KA---DIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		258
494	G-LS---SIYAVKFG-PA-----	GLMGLE-----	HGGIQVERVG		260
495	T-KA---DIYCLHLS-EEN-----	GVTGLYGGE--	NAGIVVENIG		258
496	T-KA---DIYCLHLS-EEN-----	GVTGLYGGE--	NAGIVVENIG		258
497	N-CT---TVFAGTFD-DGSGLMHG	VSGITPTM--	NAGMSVTEIG		272
498	G-KA---SIYCLHLS-EEN-----	GVTGLYGGD--	NAGIVVENIG		257
499	Q-KA---DIYCLHLS-EEN-----	GLTGLYGGD--	NAGIVVVEDIG		260
500	N-AT---SVFAGTFD-DGSR---TH	GIAGLTAEK--	QAGMHVKYVG		275



430 440 450 460 470 480

1	-----IRTEGSEIVV-----	HKTWPVGLALGSQAALSSLKNVAI		288
2	-----IRTEGSEIVV-----	HKTWPVGLALGSQAALSSLKNVAI		288
3	-----LRTEGSEIVV-----	HKTWPVGLALGSQAALASVKNVAI		288
4	-----IRTEGSEIVV-----	HKTWPVGLALGSQAALASVKNVAI		288
5	-----VRTEGSEIVV-----	HKTWPVGLALGSQAALASVKNVAI		288

6 -----IRTEGSEIVV-----HKTWPVGLALGSQAALASVKNVAI--- 288  
 7 -----IRTEGSEIVV-----HKTWPVGLALGSQAALASLKNVAI--- 286  
 8 -----VRTEGSEIVV-----HKTWPVGLALGSQAALASVKNVAI--- 286  
 9 -----IRTEGSEIVV-----HKTWPVGLALGSQAALASLKNVAI--- 286  
 10 -----VRTEGSEIVV-----HKTWPVGLALGSQAALASVKNVAI--- 286  
 11 -----IRTEGSEIIL----HKTWPVGLALGSQAALASVNNVAI--- 286  
 12 -----LRTEGSEIVV----HKTWPVGLALGSQAALASVKNVAI--- 286  
 13 -----VRTEGSEIVV----HKTWPVGLALGSQAALASVKNVAIQ--- 287  
 14 -----SQADQSQTVV----SVTWPVGLALGSQGALSGILNVGIN--- 287  
 15 -----IQADASTLVY----HLTMPVGIALGSACALAVIKNATIPK 327  
 16 -----ILADASTLVY----HLSMPAGIALGSSAALS VIRNATIPV 327  
 17 -----ILADASTLVY----HLSMPAGIALGSSAALS VIRNATIPV 327  
 18 -----ILADASTLVY----HLAMPVGIALGSAAALS VIKNV TIPK 327  
 19 -----MLPDGSTLVY----HVTMPVSIALGSASSLAVIKNVAIPS 326  
 20 -----ILADASTLVY----HMMMPVGIALGSACALSVIKNATIPR 328  
 21 -----MLPDGSTLVY----HV TMPASIALGSASSLAVIKNAVIPA 326  
 22 -----MLPDGSTLVY----HV TMPASIALGSASSLAVIKNAVIPA 326  
 23 -----MLPDGSTLVY----HV TMPASIALGSASSLAVIKNAVIPA 327  
 24 -----MLPDGSTLVY----HV TMPASIALGSVSSLAVIKNAVIPA 326  
 25 -----MLPDGSTLVY----HV TMPASIALGSASSLAVIKNALIPA 326  
 26 -----MLPDGSTLVY----HV TMPASIALGSASSLAVIKNAVIPA 326  
 27 -----ILADASTLVY----HLAMPVGIALGSSAALS VIRHATIPG 327  
 28 -----MLPDGSTLVY----HV TMPASIALGSVSSLAVIKNAVIPA 326  
 29 SQQVLVPDVPTTITVNGATITPSLNAVTTN----WV SWPCGMAMGAQGSLSILKGFL-V 342  
 30 SQQVLVPDVPTTITVNGATITPSLNAVTTN----WV SWPCGMAMGAQGSLSILKGFL-V 348  
 31 -----EVPEAP-----YLKAITNT----WV SWPCGMAMGAQGSLSILKGFL-V 323  
 32 -----EVPEAP-----YLKAITNT----WV SWPCGMAMGAQGSLSILKGFL-V 323  
 33 -----VTVPEVPTTIQPTG----SVTVNAITDT----WV SMP CGLAVGAQGSLSILKGFL-V 338  
 34 -----AASSTSQINV----DYTFPVATA MGSSGALAILEGVD--V 332  
 35 -----SAATTSRINV----TYTFPVATA MGQTQGALAILENVL--V 332  
 36 -----VRTEGSEIVV----HKTWPVGLALGSQAALASVKNVAI--- 209  
 37 -----SAHSTS LINV----DYTFPVIAIMGSSGALSILDQVD--V 328  
 38 -----APDPGKPF----TVQLPTLPTL-DT----WV SWP TGVA MGSQGSLSILSGFAL-V 332  
 39 -----TMPDGSETVG----QIFLPIGLALATESALAGITNIA--- 300  
 40 -----STSTKSRICV----TYTFPVATAVGS SGA LS VLEGV D--V 320  
 41 -----YDPDNGTIIV----FVTWPVSI SLATKAALSAVVNIAITP 286  
 42 -----LDIPSPVFIGSVLAPVTIPLPTV-DT----WV SWP TGVA MGSQGSLSILRGFP L-V 340  
 43 -----LDIPSPVFIGTAEGAVTVPLPTV-DT----WASWPTGIAMGSQGSLSILKGFL-V 339  
 44 -----LDIASVPFIGSVQAPVTIPLPTV-DT----WV SWP TGVA MGSQGSLSILKGFL-V 340  
 45 -----VPDPGNPI----TVQLPTLPTL-DT----WV SWP TGIA MGSQGSLSIRAYP--KI-P 330  
 46 -----TIDGP GEDT----FVTMPAGIAVGSQGALSIIQNYTT-V 309  
 47 -----AESQPGEET----WV TMPAGLA LGSQGALSIIENYTI-I 309  
 48 -----TIDGP GEDT----FVTMPAGIAVGSQGALSIIQNYTT-A 307  
 49 -----TIDGP GEDT----FVTMPAGIAVGSQGALSIIQNYTT-V 309  
 50 -----PNDGP GEDT----FVTMPAGIAVGSQGALSIIQNYTT-A 307  
 51 -----AGGPGSPGMQPGIDV----WV SMPAGVAVGSQGALSIIRNFTT-V 312  
 52 -----ANGEVNMRNV----WL TMPAGLA MGSQGSLSILTNFEN-V 312  
 53 -----LVDGKGQDCW----VAYWPVGVALESQGGVARLQQVG--- 309  
 54 -----SGATSSQM RV----TYTFPVATA MGTSALAVLKNVV--V 313  
 55 -----LVDGKAQDNL----TVHWAVGLALASDQAIARLKQVAK-A 313  
 56 -----258  
 57 -----VGQ----TLPVRDM----WV SFPSGLAIGSQGAI SMIQNFEPLV 314  
 58 -----SAATT SRMNV----TYTYPTATA MG CASALAI LENVL--V 317  
 59 -----DVGKGQRSW----VV SWP VSVALESQSGVARLQKV G--- 309  
 60 -----ANQTVNMTKDI----WL TMPAGLA LGSQGALSMLTNFEH-V 313  
 61 -----LIDGKAQDTN----TLYWAVGLALAAEQAVARLQKV S--- 311  
 62 -----I----QPDAGPGEDT----FVTMPAGIAVGSQGALSIIQNYTT-V 312  
 63 -----ANAEVNMRNI----WL TMPAGLA LGSQGCLSI LTNFAN-V 312  
 64 -----LIDGKGQDGW----IAYWPVGVALESQAGVARLQQVG--- 309  
 65 -----LVDGKAQDQQ----IVSWAVGLALASEQAIARLEKV AS-S 313  
 66 -----GGG-GQPAMLPGVDV----WV STPAGYAVGSQGALSIIRNFTP-V 311  
 67 -----AGI----GDPIAADDV----FLGPWVGTAVGSPAAISLLQNFSI-A 317  
 68 -----TLSQSGSGI RY----DVVFPAISVP AVSDIAVISNV LV-- 307  
 69 -----TLSQSGSGTRY----DVVFPAISVP AVPAVTDIAVISNV LV-- 323  
 70 -----PSADAGTLSSRNAVSVI WPMGIAYGSAGAVSRLANITP-L 323  
 71 -----RGADTGTLASRHAVSVI WPMGIAYGSAGAVSRLANITP-L 374  
 72 -----RGADTGTLASRHAVSVI WPMGIAYGSAGAVSRLANITP-L 369

73 -----RLADAGTLSSRQAISCIWPMGIAYGSGAVSRLANITP-L 323  
 74 -----TVQTKDASRT-----RLKWYAAALALKSTKSLARIKGVTN-S 300  
 75 -----HQGSG----- 259  
 76 SQQVLVPDVPTTITVNGATITPSLNAVTTN----WWSWPCGMAMGAQGSLSILKGFGL-V 277  
 77 -----ANQTVNMT----- 285  
 78 -----THATKDAMSF-----RMKWYVGOTALKATHAVARLKGITN-I 299  
 79 ----- 223  
 80 -----TVQNKDAATTRT-----RVKWCGLALKSTRSLARVRGVTN-V 300  
 81 -----TVQNKDAATTRT-----RLKWCCTALKSTKSLARIQGIQN-I 301  
 82 -----TVQNKDAQRF-----RMKWYVGOTALKSTKSLARLKGVTT-V 300  
 83 -----TVQNKDASRY-----RVKWCAGTALKATHSVARLKKGILN-I 300  
 84 -----TIQNKDASRY-----RVKWCAGTALKATHSVARLKKGILN-I 300  
 85 -----TIQNKDASRY-----RVKWCAGTALKATHSVARLKKGILN-I 300  
 86 -----TIQNKDASRY-----RVKWCAGTALKATHSVARLKKGILN-I 300  
 87 -----SLTPTSTITR-----ALHWPVGYALGSMGAVSMLENITP-L 310  
 88 -----SGATTTSQTRV-----TYTFPVATAMGTGSALAILKNVV--V 264  
 89 -----TIQNKDASRY-----RVKWCAGTALKATHSVARLKKGILN-I 300  
 90 -----TIQNKDAVRY-----RVKWCAGTALKATHSVARLKGVTN-V 300  
 91 -----AGA-GAPDMLPGVDT-----WVSMPAGLALGSQGALSIIENYTT-V 272  
 92 -----SLTPTSTITR-----ALHWPVGYALGSMGAVSMLENITP-L 310  
 93 -----SLMPTSTITR-----ALHWPVGYALGSMGAVSMLENITP-L 310  
 94 -----TVQNKDAIRY-----RVKWCAGLALKSTKSLAKVADVAM-G 297  
 95 -----TIQNKDASRY-----RVKWCAGTALKATHSVARLKKGILN-I 300  
 96 -----TVQNKDATRI-----RMKWYTGLALKSTKSLARLKGVTN-I 300  
 97 -----KLQGKDAQRW-----RLKWCCTALKATHSVARLKGVTN-V 300  
 98 -----TVQNKDAATTRT-----RLKWCGLALKSTKSLAAVKGITN-V 300  
 99 -----KLEGKDAQRW-----RLKWCAGTVLRATHSVARLKGITN-V 300  
 100 -----TVQNKDAATTRT-----RLKWCAGLALKSTHSLAAIKGITN-V 300  
 101 -----LVQNKDARRT-----RLKWCGLALKSTKSLARIKGITN-I 300  
 102 -----EGASGASELNV-----DYIFTAGVALGQEMALSIMRNARE-- 321  
 103 -----TVQNKDAATTRT-----RLKWCGLALKSTKSLAAVKGITN-V 300  
 104 -----TVQNKDATRI-----RLKWCAGLALKSTKSLARLKGVTN-I 300  
 105 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAAIRGVTN-I 300  
 106 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAAIRGVTN-I 298  
 107 -----TVQNKDATRI-----RLKWCAGLALKSTRSIAIRLGITN-I 295  
 108 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAAIRGVVT--- 298  
 109 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAAIRGVTN-- 299  
 110 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAAIRGVTN-I 300  
 111 -----TVQNKDAATTRT-----RLKWCAGLALKSTRSIAIRLGITN-I 299  
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 114 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAAIRGVV--- 297  
 115 -----TVQNKDAATTRT-----RLKWCAGLALKSTRSIAIRGVTN-V 301  
 116 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAALKGVPN-I 297  
 117 -----TVQNKDATRI-----RLKWCAGLALKSTRSIAIRLGITN-I 300  
 118 -----TVQNKDATRI-----RLKWCAGLALKSTRSIAIRGVTN-I 300  
 119 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAALKGVPN-I 297  
 120 -----TVQNKDAIRT-----RLKWCAGLALKSTRSIALLAGVTN-V 301  
 121 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAAIRG---- 296  
 122 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAAIRGVTN-I 300  
 123 -----TVQNKDATRI-----RLKWCAGLALKSTRSIAIRLGITN-I 300  
 124 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAAIRGVTN-I 300  
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 126 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAAIR---- 295  
 127 -----KLEGKDAQRW-----RLKWCCTALKRTTSVARLKGVTN-I 300  
 128 -----KLEGKDAQRW-----RLKWCCTALKRTTSVARLKGVTN-I 300  
 129 -----TVQNKDADRI-----RVKWCCTALKSTRSLARLRGVTN-I 300  
 130 -----TVQNKDADRI-----RVKWCCTALKSTRSLARLRGVTN-I 300  
 131 -----TVQNKDADRI-----RVKWCCTALKSTRSLARLRGVTN-I 300  
 132 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAIRG---- 291  
 133 -----VHQTKDERIW-----RVKWCAGLALFSQLGVASADGIRD-- 305  
 134 -----TVQNKDADRI-----RVKWCCTALKSTRSLARLRGVTN-I 300  
 135 -----TVQNKDAATTRT-----RIKWYCGLALKSTRSIAIRG---- 289  
 136 -----TVQNKDAIRT-----RLKWCAGLALKSTRSIAALTNVPN-V 296  
 137 -----TVQNKDVERY-----RMKWYCGTALKSTRSLARLKGITN-I 300  
 138 -----TVQNKDATRI-----RLKWCAGLALKSTRSIAIRLGITN-I 303  
 139 -----TIQNKDAVRY-----RVKWCAGTALKATHSVARLAGITN-I 300

140	-	TVQNKDAVRT	-	RVKWCGLANKHDYAIARIDNVKF--	296
141	-	TVQNKDAWRY	-	RLKWYVGLALKSTRSMARLKGITN-V	302
142	-	TLEDKDATTRY	-	RLKWYAGLVLKATHGVARLKGLTN-I	300
143	-	TVQNKDAVRT	-	RVKWCGLANKHDYAIARIDNVKF--	296
144	-	THHTKDARKW	-	RVKWYAGTALKATHSVARLKGLTN-I	300
145	-	TVQNKDAERW	-	RVKWYVGSAKATHSVARLRAISN-V	300
146	-	TVQNKDVERY	-	RMKWYVGTALKSTKSLARLKGLTN-I	300
147	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
148	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
149	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
150	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
151	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAALNNVKI--	306
152	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
153	-	THHTKDARKW	-	RVKWYAGTALKATHSVARLKGLTN-I	300
154	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
155	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALNNVKI--	306
156	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
157	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
158	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALNNVKI--	306
159	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALNNVKI--	306
160	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALNNVKI--	306
161	-	TVQNKDATRI	-	RLKWYVGLVLKSTK-----	289
162	-	TVQTKDSSRT	-	RLKWCGLALKSTKSMARLKGLTN-V	307
163	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALNNVKI--	306
164	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
165	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
166	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
167	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
168	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
169	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
170	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
171	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
172	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALNNVKI--	306
173	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
174	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
175	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
176	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
177	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAATLNNSVKI--	306
178	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALNNV-----	304
179	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
180	-	TVQNKDATRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	293
181	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
182	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
183	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
184	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--Q	292
185	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAATLNNSVKI--	306
186	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
187	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
188	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
189	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
190	-	PMETKDARRH	-	RIKWCGLALFRKAALARLKGRP-L	296
191	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALNNVKI--	306
192	-	TSHVKDADLH	-	RLKWCCTALKATHALARLKGVTN-I	299
193	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
194	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
195	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
196	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
197	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
198	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
199	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
200	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
201	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
202	-	THATKDAHKW	-	RLKWYAGTALKATHSVARLKGLIN-I	299
203	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
204	-	TVQNKDATRI	-	RLKWYAGLALKSTKSLARLKGVTN-I	302
205	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291
206	-	TVQNKDAVRT	-	RVKWCSSLANKHDKAIAAALTNVKI--	291

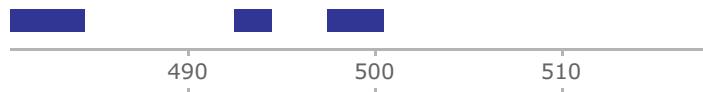
207 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
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213 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKV--- 291  
214 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALNNVKI--- 306  
215 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
216 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
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228 -----TVQNKDAIRT-----RLKWCGLALKSTKSLACLKNVQI-G 293  
229 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
230 -----TVQNKDAIRT-----RLKWCGLALKSTKSLACLKNVQI-G 293  
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239 -----ALETKNARRW-----RVRWYVGLALFSTVAVAQLQGITAN 295  
240 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALNN---- 303  
241 -----TVQNKDATRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
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251 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
252 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
253 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
254 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVK--- 290  
255 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
256 -----TVQNKDATRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
257 -----TVQNKDATRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
258 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
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263 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAAALKNVKI--- 293  
264 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 293  
265 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 292  
266 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVK--- 290  
267 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 292  
268 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 292  
269 -----TVQNKDATRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
270 -----TVQNKDAIRT-----RLKWCGLALKSTKSLACLKNVQI-G 293  
271 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
272 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 291  
273 -----TVQNKDAVRT-----RVKWYCSLANKHDKAIAALTNVKI--- 292

274		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
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278		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
279		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	291
280		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	291
281		TVQNKDATRT	RIKWYCG-	282
282		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
283		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	291
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285		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNV	289
286		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
287		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
288		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
289		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
290		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	291
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298		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNV	289
299		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
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301		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
302		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
303		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
304		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
305		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
306		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
307		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
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309		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
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313		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	291
314		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
315		TVQNKDAVRT	RVKWCSLANKHDKAIAALT <span style="background-color: yellow;">DVKI</span>	291
316		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
317		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	293
318		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
319		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
320		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
321		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
322		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
323		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
324		TVQNKDAVRT	RVKWCSLANKHDKAIAALT <span style="background-color: yellow;">TN</span>	288
325		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	291
326		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
327		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
328		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
329		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
330		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
331		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
332		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
333		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
334		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	293
335		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
336		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNV	289
337		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
338		TVQNKDAVRT	RVKWCSLANKHDKAIAALTNVKI	292
339		TVQNKDATRT	RVKWCSLANKHDKAIAALTNVKI	291
340		TVQNKDAVRT	RVKWCSLANKHDKAIAALT <span style="background-color: yellow;">NVKR</span>	292

341	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
342	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	-	-	-	-	-	-	301											
343	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
344	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
345	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
346	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
347	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	-	-	-	-	288											
348	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
349	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
350	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	290										
351	-	TVQNKDA	T	R	RIKWC	G	L	A	L	K	S	T	R	S	I	A	I	R	G	V	T	N	-	I	281											
352	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
353	-	T	S	E	T	K	D	E	T	I	T	-	R	V	K	W	C	G	L	A	F	S	E	K	G	L	A	A	L	T	G	I	T	N	-	306
354	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	287										
355	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
356	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
357	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	290										
358	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
359	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	292										
360	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
361	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
362	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	292										
363	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	T	-	-	291										
364	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
365	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
366	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
367	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
368	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
369	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
370	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
371	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
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373	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
374	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
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376	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
377	-	A	E	L	E	T	N	A	R	R	W	R	Y	C	G	L	A	F	S	T	V	A	V	R	L	Q	G	I	A	-	N	295				
378	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
379	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
380	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
381	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
382	-	E	A	E	A	K	D	E	H	I	W	-	R	V	K	W	C	G	L	A	F	S	E	G	L	S	A	A	E	G	I	L	N	-	305	
383	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
384	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
385	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
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387	-	TVQNKDA	T	R	RLKWC	N	L	A	L	K	S	T	K	S	L	R	L	Y	G	V	S	N	-	-	306											
388	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
389	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	292										
390	-	V	H	Q	S	K	D	E	R	I	W	-	R	V	K	W	C	G	L	A	F	S	Q	L	G	I	A	A	D	G	I	R	N	-	305	
391	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
392	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	K	V	K	I	-	-	291										
393	-	TVQNKDA	T	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	291										
394	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
395	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
396	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	305										
397	-	E	K	E	D	A	D	E	S	I	T	-	R	I	S	W	Y	C	G	L	A	F	S	E	K	G	L	A	V	L	K	G	V	P	-	310
398	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	287										
399	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
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405	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	286										
406	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	293										
407	-	TVQNKDA	V	R	TVKWC	S	L	A	N	K	H	D	K	A	I	A	A	L	T	N	V	K	I	-	-	290										

408	- - - - -	TVQNKDA TRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	291
409	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	293
410	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	293
411	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	293
412	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	293
413	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AALT - - - - -	287
414	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	293
415	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	293
416	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	293
417	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL ANVKI - - -	305
418	- - - - -	TVQNKDA TRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	291
419	- - - - -	LLEKRDARRW	- RLRWY CGA ALKATHSLARLKGVTN - V	300
420	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHN KAI AAL TNVKI - - -	293
421	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AALT - - - - -	287
422	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD - - - - -	295
423	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL ANVKI - - -	305
424	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	293
425	- - - - -	TVQNKDA VRT	- - - RVKWC SLANK - - - - -	293
426	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD - - - - -	295
427	- - - - -	TVQNKDA VRT	- - - RVKWC SLA - - - - -	291
428	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNV - - -	291
429	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL - - - -	286
430	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI - - - - -	298
431	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	293
432	- - - - -	IHQSKDEHIT	- - - RVKWC CGL ALF S L K GLAA ADGITN - - -	305
433	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL - - - - -	286
434	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	292
435	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	292
436	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	293
437	- - - - -	TVQNKDA TRT	- - - RVKWC VSLANKHD KAI ASL N NVKI - - -	291
438	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	293
439	- - - - -	TVQNKDA IRT	- - - RLKWC CGL ALK ST K S L A CLK NVQI - G	293
440	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI AALT - - - - -	287
441	- - - - -	ALETKNARRW	- - - RVRWY CGL ALF S T V A V A R L Q G I A A - N	295
442	- - - - -	TVQNKD STRT	- - - RVKWC SLANKHD KAI S A L T G V A L - - -	294
443	- - - - -	TVQNKDA TRT	- - - RVKWC SLANKHD KAI AAL TNVKI - - -	291
444	- - - - -	ESESKDESIT	- - - RVKF Y CGL ACY S D L A L A V V K G I S N - - -	305
445	- - - - -	ISETKD E T I W	- - - RVKWC CGL ALF S E L G L A A A E G I T N - - -	305
446	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI A - - - - -	284
447	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI A - - - - -	285
448	- - - - -	DLETKDASRW	- - - RVKWC VSLAV F S E L G V A R L Q G I T A - N	293
449	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI A - - - - -	284
450	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI A A L - - - - -	286
451	- - - - -	ALETKNARRW	- - - RVRWY VGL ALF S T V A V A R L Q G I T A - N	295
452	- - - - -	ELETKDASRH	- - - RIKWC VAGL ALF S E L G V A R L R G I E G - A	295
453	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI A A L T K V K I - - -	293
454	- - - - -	EKEADESIT	- - - RISWY CGL ALF S E K G L A V L K G V I P - G	310
455	- - - - -	TVQNKDA DRI	- - - RVKWC CGT A L K S T R S L A R L Q G I T N - I	300
456	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI A A L T - - - - -	288
457	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI A - - - - -	282
458	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI A A L T N - - - - -	290
459	- - - - -	TVQNKDA TRT	- - - RLKWC V G A A L K S T K S V A R L E A V T N - V	300
460	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI - - - - -	283
461	- - - - -	EKEADESIT	- - - RISWY CGL ALF S E K G L A V L K G V T P - G	310
462	- - - - -	TVQNKDA VRT	- - - RVKWC SLANK - - - - -	278
463	- - - - -	VNQTVNMT KDI	- - - W V S M P A G L A L G S Q A A L S L L T N F E H - V	227
464	- - - - -	TVQNKDA VRT	- - - RVKWC S L - - - - -	290
465	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD KAI A A - - - - -	285
466	- - - - -	TVQNKDA VRT	- - - RVKWC SLA - - - - -	276
467	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD - - - - -	280
468	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD K - - - - -	281
469	- - - - -	TVQNKDA TRT	- - - RVKWC G L A N K H E K A I A A L T D V Q L - - -	294
470	- - - - -	TVQNKDA VRT	- - - RVKWC SLANKHD K A - - - - -	282
471	- - - - -	ASETKD NY IT	- - - RVKWC CGL ALF S E K G L A A L P G V T N - - -	306
472	- - - - -	TVQNKDA TRI	- - - RLKWC V T S L A L K S T R S I A A L Q G V T N - I	310
473	- - - - -	ASETKD NY IT	- - - RVKWC CGL ALF S E K G L A A L P G V T N - - -	306
474	- - - - -	TVQNKDA VRT	- - - RVKWC SLA - - - - -	276

475	-TVQNKDAVRT-	-RVKWC SLANKHDKA-	-	282
476	-EKEDADESIT-	-RISWYCGLALFSEKGLAVLKGVTP-G	-	310
477	-ESETKDETIT-	-RVKMYCGLANFSQLGLYAMPGITN-	-	305
478	-ESETKDESIT-	-RVKFYCGLAVYSDLALAVAQGVKN-	-	305
479	-EKEDADESIT-	-RITWYCGLALFSEKGLAVLEGVTP-	-	309
480	-PAEDKDNYIT-	-RVKWC GLALFSEKGLAMADGITN-	-	306
481	-TVQNKDAVRT-	-RVKWC SLANK-	-	278
482	-TVQNKDAVRT-	-RVKWC SLA-	-	276
483	-TVQNKDSTRT-	-RVKWC SLANKHDKA LAALTGVAL-	-	294
484	-TVQNKDAVRT-	-RVKWC SLAN-	-	277
485	-ELETKDASRH-	-RIKWYAGLALFSELGVARLRGIEG-A	-	295
486	-TVQNKDSTRT-	-RVKWC SLANKHDKA ISALTGVAL-	-	294
487	-TVQNKDAVRT-	-RVKWC SLANKHDKAIAAL-	-	288
488	-TVQNKDATRT-	-RVKWC SLANKHDKAIAALTGVAL-	-	294
489	-TVQNKDATRT-	-RVKWC SLANKHDKAISALTGVAL-	-	294
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491	-TVQNKDAVRT-	-RVKWC CSL-	-	275
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493	-TVQNKDAVRT-	-RVKWC SLANK-	-	279
494	-ALETKDATRW-	-RVKWYVGLALASDLGVARLQGITAN	-	295
495	-TVQNKDAVRT-	-RVKWC SLA-	-	277
496	-TVQNKDAVRT-	-RVKWC SLAN-	-	278
497	-ESETKDNTIT-	-RVKMYTGMALFSELGLAAAMTGVTN-	-	306
498	-TVQNKDAVRT-	-RVKWC CSL-	-	275
499	-TVQNKDATRT-	-RVKWC SLANKHNKAIAALTGVAL-	-	294
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15	GDGY	-SSKRKG-	337
16	CGK	-	330
17	CGK	-	330
18	CR	-	329
19	SRIPL	-INFENHGA-	339
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21	QRSPL	-IDFDIIRGA-	339
22	HRSPL	-IDFDIIRGA-	339
23	QRSPL	-IDFDIIRGA-	340
24	HRSPL	-IDFDIIRGA-	339
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27	CR	-	329
28	HRSPL	-IDFDIIRGA-	339
29	ANLT	-TT-	348
30	ANLT	-TT-	354
31	ADLP	-TT-	329
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33	ANLA	-AT-	344
34	VDFA	-	336
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37	AAYT	-----	332
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40	SNVA	-----	324
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42	ADLP	- TT -----	346
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44	ADLP	- TT -----	346
45	AHL	-----	333
46	GSCG	- GG -----	315
47	GPCV	- PDPA -----	317
48	ASCG	- GG -----	313
49	ASCG	- GGGG -----	317
50	ASCG	- GGT -----	314
51	ADC G	- GG -----	318
52	GECA	- GIVP -----	320
53		-----	309
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56		-----	258
57	EDCN	- GAE LAMEAGATSAKS KSKRSK	339
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60	GECA	- GG PPPA -----	323
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62	ASCG	- GGGG -----	320
63	GECT	- GIVP -----	320
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66	SDCS	- VG -----	317
67	GPCP	- TITPA -----	326
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74	GGQ	- DQSGTGKPTLV -----	314
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76	ANLT	- TT -----	283
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439	AKPTTGGS - GGTQGSTGGN -	312
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**Compare to:** the consensus

Amino acids that match the reference are marked with yellow highlighting.

**Created:** 4 Aug 2022

**Last Modified:** 4 Aug 2022

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Feature

Location

Size

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Type

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