Amino Acid Conservation Scores

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- POS: The position of the AA in the SEQRES derived sequence.

- SEQ: The SEQRES derived sequence in one letter code.

- 3LATOM: The ATOM derived sequence in three letter code, including the AA's positions as they appear in the PDB file and the chain identifier.

- SCORE: The normalized conservation scores.

- COLOR: The color scale representing the conservation scores (9 - conserved, 1 - variable).

- CONFIDENCE INTERVAL: When using the bayesian method for calculating rates, a confidence interval is assigned to each of the inferred evolutionary conservation scores.

- CONFIDENCE INTERVAL COLORS: When using the bayesian method for calculating rates. The color scale representing the lower and upper bounds of the confidence interval.

- MSA DATA: The number of aligned sequences having an amino acid (non-gapped) from the overall number of sequences at each position.

- RESIDUE VARIETY: The residues variety at each position of the multiple sequence alignment.

POS SEQ 3LATOM SCORE COLOR CONFIDENCE INTERVAL CONFIDENCE INTERVAL COLORS MSA DATA RESIDUE VARIETY

(normalized)

1 R ARG1:A -1.256 9 -1.295,-1.237 9,9 81/150 R,K

2 K LYS2:A -0.270 6 -0.447,-0.129 7,5 106/150 Q,M,T,I,N,P,R,V,A,K,E,S

3 P PRO3:A 0.655 3 0.163, 0.857 4,2 122/150 L,S,A,K,N,R,P,F,I,Y,T,Q,M

4 I ILE4:A -0.075 5 -0.353, 0.006 6,5 132/150 C,W,H,V,L,I,F,M,T,Y

5 I ILE5:A -0.571 7 -0.747,-0.532 8,7 136/150 F,I,L,V,A,M

6 A ALA6:A -0.871 8 -0.962,-0.807 8,8 139/150 I,F,M,V,A,G,S

7 G GLY7:A -0.829 8 -0.962,-0.747 8,8 140/150 T,S,G,A

8 N ASN8:A -1.274 9 -1.306,-1.259 9,9 140/150 S,N

9 W TRP9:A -1.202 9 -1.278,-1.154 9,9 140/150 W,F

10 K LYS10:A -1.297 9 -1.310,-1.295 9,9 140/150 K

11 M MET11:A -1.132 9 -1.184,-1.086 9,9 143/150 C,I,L,M

12 H HIS12:A -0.947 8 -1.048,-0.914 9,8 143/150 Y,H,C,N,F

13 K LYS13:A -0.162 6 -0.353, 0.006 6,5 143/150 H,V,K,L,G,C,M,Q,Y,T,I,F,R,P,N

14 T THR14:A 0.007 5 -0.247, 0.163 6,4 143/150 T,Q,M,N,R,I,D,E,S,G,L,V,A,H

15 L LEU15:A 1.151 1 0.572, 1.246 3,1 143/150 K,H,S,X,Q,F,N,P,R,V,A,W,L,C,M,Y,I

16 A ALA16:A 1.010 2 0.572, 1.246 3,1 144/150 Q,T,D,F,R,P,N,H,K,S,I,V,A,G,L,E

17 E GLU17:A -0.218 6 -0.447,-0.129 7,5 144/150 W,A,V,L,G,E,I,M,K,S,D,F,R,N,Q,T

18 A ALA18:A -0.293 6 -0.447,-0.247 7,6 144/150 F,I,N,M,T,C,V,A,G,L,S

19 V VAL19:A 2.947 1 1.246, 3.502 1,1 142/150 I,M,C,A,V,E,G,L,D,N,R,P,Q,T,K,S

20 Q GLN20:A 1.076 1 0.572, 1.246 3,1 142/150 I,M,G,E,A,V,R,P,N,D,T,Q,X,S,H,K

21 F PHE21:A 0.035 5 -0.247, 0.163 6,4 143/150 F,I,R,M,Y,T,V,A,W,H,S,L

22 V VAL22:A 0.627 3 0.163, 0.857 4,2 125/150 M,T,I,F,N,A,V,L,S,C

23 E GLU23:A 1.204 1 0.572, 1.246 3,1 144/150 T,Y,Q,N,R,D,E,S,G,V,K,A,H

24 D ASP24:A 0.519 3 0.163, 0.572 4,3 144/150 V,A,E,L,G,I,M,Y,K,S,F,D,N,P,R,Q,T

25 V VAL25:A 0.007 5 -0.247, 0.163 6,4 144/150 F,I,V,M,W,L

26 K LYS26:A 0.951 2 0.572, 1.246 3,1 143/150 I,D,N,R,M,Q,T,C,K,A,V,E,S,G,L

27 G GLY27:A 1.848 1 1.246, 1.855 1,1 143/150 F,D,N,R,P,Q,T,K,H,S,I,M,Y,A,V,W,E,L,G

28 H HIS28:A 1.432 1 0.857, 1.855 2,1 142/150 M,I,G,L,E,A,V,C,T,Q,R,N,D,F,S,H,K

29 V VAL29:A 2.168 1 1.246, 1.855 1,1 141/150 M,Y,I,W,A,V,L,G,E,Q,T,D,F,P,N,H,K,S

30 P PRO30:A 3.397 1 1.855, 3.502 1,1 140/150 I,M,V,A,W,E,L,G,F,D,N,R,P,Q,T,K,H,S

31 P PRO31:A 1.650 1 0.857, 1.855 2,1 134/150 E,G,V,A,C,M,S,K,H,T,Q,N,P,R,F,D

32 A ALA32:A 2.625 1 1.246, 3.502 1,1 95/150 W,V,A,G,L,E,M,Y,I,H,K,S,Q,T,D,F,P,R,N

33 D ASP33:A 1.912 1 1.246, 1.855 1,1 144/150 M,I,V,A,L,G,E,C,Q,T,D,P,R,N,H,K,S,X

34 E GLU34:A 1.854 1 1.246, 1.855 1,1 145/150 D,P,R,N,Q,T,H,K,S,I,M,Y,W,V,A,G,E

35 V VAL35:A 0.550 3 0.163, 0.572 4,3 146/150 C,L,S,G,V,A,W,H,P,R,D,I,T,M,Q

36 I ILE36:A 0.233 4 0.006, 0.347 5,4 146/150 I,D,N,R,Q,T,V,A,K,E,S,L

37 S SER37:A -0.141 5 -0.353, 0.006 6,5 147/150 I,F,R,P,T,C,K,A,V,G,S,L

38 V VAL38:A 0.037 5 -0.247, 0.163 6,4 148/150 P,F,I,Y,T,M,L,G,V,K,A,W

39 V VAL39:A -0.221 6 -0.447,-0.129 7,5 149/150 C,I,F,L,V

40 C CYS40:A 0.143 5 -0.129, 0.347 5,4 149/150 C,V,A,S,G,L,I,F,M,T

41 A ALA41:A -0.620 7 -0.807,-0.532 8,7 149/150 C,P,V,A,T,G,L

42 P PRO42:A -0.765 8 -0.914,-0.681 8,7 149/150 A,V,S,Q,T,I,D,P

43 F PHE43:A 0.029 5 -0.247, 0.163 6,4 149/150 M,Y,T,F,D,P,V,A,S,L,G

44 L LEU44:A -0.164 6 -0.353, 0.006 6,5 149/150 A,V,S,L,M,T,I,P

45 F PHE45:A -0.160 6 -0.353, 0.006 6,5 149/150 I,D,F,N,Q,M,T,Y,C,H,A,V,S,G,L

46 L LEU46:A -0.362 6 -0.532,-0.247 7,6 149/150 F,I,A,V,E,L,G

47 D ASP47:A 1.004 2 0.572, 1.246 3,1 149/150 P,R,N,D,F,T,Q,S,H,K,Y,M,G,L,E,W,V,A

48 R ARG48:A 0.911 2 0.572, 1.246 3,1 149/150 Y,M,I,E,G,L,V,A,C,T,Q,N,P,R,F,D,S,K,H

49 L LEU49:A 0.128 5 -0.129, 0.347 5,4 148/150 T,M,N,I,F,S,L,G,V,A,C,X

50 V VAL50:A 0.817 2 0.347, 0.857 4,2 148/150 K,H,S,F,N,R,Q,T,C,A,V,E,L,G,I,Y

51 Q GLN51:A 1.100 1 0.572, 1.246 3,1 145/150 X,H,K,V,A,G,S,L,E,D,R,N,Q,T

52 A ALA52:A 1.462 1 0.857, 1.855 2,1 145/150 I,Y,M,C,G,L,E,A,V,P,R,N,D,F,T,Q,S,H,K

53 A ALA53:A 0.712 3 0.347, 0.857 4,2 139/150 F,I,R,T,Y,X,K,V,A,H,S,L,G

54 D ASP54:A 1.495 1 0.857, 1.855 2,1 127/150 Q,T,D,R,P,N,H,K,S,X,M,V,A,L,G,E

55 G GLY55:A 1.407 1 0.857, 1.855 2,1 140/150 N,P,R,D,T,Q,E,L,S,G,A,V

56 T THR56:A -0.032 5 -0.247, 0.006 6,5 140/150 Y,L,G,E,A,C,T,Q,P,R,N,D,F,S,H,K

57 D ASP57:A 1.383 1 0.857, 1.855 2,1 142/150 S,K,H,T,Q,N,P,R,F,D,E,G,L,A,Y,M

58 L LEU58:A -0.020 5 -0.247, 0.163 6,4 149/150 M,F,I,L,S,V,A,W

59 K LYS59:A 1.560 1 0.857, 1.855 2,1 149/150 I,Y,M,C,E,G,L,V,A,N,R,P,F,D,T,Q,S,K,H

60 I ILE60:A 0.567 3 0.163, 0.857 4,2 149/150 F,I,T,Y,M,C,L,K,A,V,W

61 G GLY61:A -0.423 6 -0.610,-0.353 7,6 149/150 V,A,G,S,C

62 A ALA62:A -0.654 7 -0.807,-0.610 8,7 149/150 G,S,V,A,P,I,F

63 Q GLN63:A -1.234 9 -1.278,-1.212 9,9 149/150 E,Q

64 T THR64:A -0.988 8 -1.086,-0.962 9,8 149/150 S,E,T,D,N

65 M MET65:A 0.293 4 0.006, 0.347 5,4 148/150 S,G,L,A,V,C,X,M,R,I,F

66 H HIS66:A -0.224 6 -0.447,-0.129 7,5 149/150 C,G,S,E,H,W,A,R,N,D,F,Y

67 F PHE67:A 1.516 1 0.857, 1.855 2,1 149/150 L,E,W,A,V,C,Y,I,S,H,K,T,Q,R,P,N,D,F

68 A ALA68:A 0.232 4 0.006, 0.347 5,4 149/150 Q,T,F,D,N,K,H,S,Y,I,V,A,W,E,G,L,C

69 D ASP69:A 0.939 2 0.572, 1.246 3,1 149/150 T,Q,N,R,P,D,E,G,L,S,K,V,A,H

70 Q GLN70:A 0.281 4 0.006, 0.347 5,4 148/150 R,N,D,F,T,Q,S,H,K,I,M,C,G,E,A,V

71 G GLY71:A -1.249 9 -1.295,-1.237 9,9 150/150 E,G

72 A ALA72:A -1.232 9 -1.278,-1.212 9,9 150/150 P,S,K,A

73 Y TYR73:A -0.024 5 -0.247, 0.163 6,4 150/150 F,C,R,W,H,Y,S

74 T THR74:A -1.298 9 -1.310,-1.295 9,9 150/150 T

75 G GLY75:A -1.249 9 -1.295,-1.237 9,9 150/150 S,G

76 E GLU76:A -1.138 9 -1.212,-1.121 9,9 150/150 D,C,A,K,E

77 V VAL77:A -0.331 6 -0.532,-0.247 7,6 150/150 T,L,A,V,I

78 S SER78:A -1.118 9 -1.184,-1.086 9,9 150/150 S,G,T,A,P,C,D

79 P PRO79:A -0.128 5 -0.353, 0.006 6,5 150/150 A,V,S,G,M,T,I,P

80 V VAL80:A 1.879 1 1.246, 1.855 1,1 149/150 A,V,E,G,L,M,K,H,S,Q,T,F,D,N,R,P

81 M MET81:A -0.956 8 -1.048,-0.914 9,8 149/150 Q,M,I,F,S,L,V,A,X

82 L LEU82:A -0.600 7 -0.747,-0.532 8,7 150/150 T,L,V,A,M,I

83 K LYS83:A 0.530 3 0.163, 0.572 4,3 150/150 L,G,E,V,A,C,Y,M,I,S,H,K,T,Q,R,N

84 D ASP84:A -0.346 6 -0.532,-0.247 7,6 149/150 N,R,D,Q,X,E,G,S,K,A,V

85 L LEU85:A 0.719 3 0.347, 0.857 4,2 150/150 Y,T,M,I,F,L,S,A,V,C

86 G GLY86:A -0.342 6 -0.532,-0.247 7,6 146/150 Q,N,R,F,D,S,G,A,K,H,C

87 V VAL87:A 0.291 4 0.006, 0.347 5,4 150/150 G,L,S,A,V,C,T,R,F,I

88 T THR88:A 1.676 1 0.857, 1.855 2,1 150/150 D,N,R,P,Q,T,Y,A,K,H,E,S,G

89 Y TYR89:A 0.089 5 -0.129, 0.163 5,4 150/150 N,F,I,Y,T,M,C,L,S,A,W,H

90 V VAL90:A -0.866 8 -0.962,-0.807 8,8 149/150 X,C,V,A,S,L,I,T

91 I ILE91:A -0.630 7 -0.747,-0.532 8,7 150/150 M,A,V,L,E,T,I

92 L LEU92:A -0.110 5 -0.353, 0.006 6,5 150/150 L,T,M,A,V,I

93 G GLY93:A -1.284 9 -1.310,-1.278 9,9 150/150 G

94 H HIS94:A -1.297 9 -1.310,-1.295 9,9 150/150 H

95 S SER95:A -1.261 9 -1.295,-1.237 9,9 150/150 A,S,Y

96 E GLU96:A -1.299 9 -1.310,-1.295 9,9 149/150 E,X

97 R ARG97:A -1.279 9 -1.306,-1.259 9,9 149/150 Q,X,R

98 R ARG98:A -1.279 9 -1.306,-1.259 9,9 149/150 K,R

99 Q GLN99:A 0.186 4 -0.129, 0.347 5,4 149/150 T,Q,M,R,I,E,L,G,S,K,V,A,H

100 M MET100:A 0.614 3 0.163, 0.857 4,2 149/150 N,I,D,F,Y,Q,M,G,L,E,H,V,K,A

101 F PHE101:A -0.608 7 -0.747,-0.532 8,7 149/150 A,H,L,F,I,M,Q,Y

102 A ALA102:A 1.180 1 0.572, 1.246 3,1 150/150 Q,Y,F,R,N,H,K,A,L,S,G,E,C

103 E GLU103:A -1.240 9 -1.278,-1.212 9,9 150/150 E,D

104 T THR104:A 0.092 5 -0.129, 0.163 5,4 150/150 C,A,K,S,L,G,D,N,P,Q,T

105 D ASP105:A -0.673 7 -0.807,-0.610 8,7 150/150 P,N,D,G,S,L,E,H,V

106 E GLU106:A 0.385 4 0.006, 0.572 5,3 149/150 V,A,G,L,E,I,Y,X,H,K,S,D,P,R,N,Q,T

107 T THR107:A 1.323 1 0.857, 1.246 2,1 150/150 M,I,V,A,W,E,L,G,Q,T,F,D,N,R,H,S

108 V VAL108:A -0.578 7 -0.747,-0.532 8,7 150/150 S,L,T,V,A,C,I

109 N ASN109:A -0.194 6 -0.353,-0.129 6,5 150/150 D,R,N,M,Q,W,H,V,K,A,L,G,S,E

110 K LYS110:A 0.367 4 0.006, 0.572 5,3 150/150 V,A,K,E,G,L,S,Q,T,F,D,N,R

111 K LYS111:A -1.217 9 -1.259,-1.184 9,9 149/150 R,X,K

112 V VAL112:A 0.168 4 -0.129, 0.347 5,4 150/150 C,A,V,L,F,I,M,T

113 L LEU113:A 1.164 1 0.572, 1.246 3,1 150/150 K,A,V,H,E,S,G,L,D,I,N,R,M,Q,T

114 A ALA114:A -0.210 6 -0.447,-0.129 7,5 150/150 H,K,S,Q,T,F,R,P,N,A,V,G,L,C,Y,I

115 A ALA115:A -0.790 8 -0.914,-0.747 8,8 150/150 T,I,G,L,S,V,A,C

116 F PHE116:A 0.536 3 0.163, 0.572 4,3 150/150 K,A,V,H,W,E,G,L,F,I,R,Q,Y,T

117 T THR117:A 1.279 1 0.857, 1.246 2,1 150/150 V,A,K,H,E,S,L,G,D,N,R,Q,T

118 R ARG118:A 0.497 3 0.163, 0.572 4,3 150/150 Q,Y,T,F,I,D,N,R,A,K,H,E,L,G,S

119 G GLY119:A 0.228 4 -0.129, 0.347 5,4 150/150 R,N,D,Q,G,S,E,K,V,A

120 L LEU120:A -0.564 7 -0.747,-0.447 8,7 150/150 L,M,Q,V,I,F

121 I ILE121:A 0.656 3 0.347, 0.857 4,2 150/150 M,I,V,A,G,L,E,Q,T,D,F,R,P,N,H,K,S

122 P PRO122:A -0.554 7 -0.747,-0.447 8,7 150/150 A,V,T,I,C,P

123 I ILE123:A -0.820 8 -0.914,-0.747 8,8 150/150 M,V,L,I

124 I ILE124:A 0.100 5 -0.129, 0.163 5,4 150/150 F,I,Y,L,A,V,M

125 C CYS125:A -1.212 9 -1.278,-1.184 9,9 150/150 C,L,A

126 C CYS126:A -0.451 7 -0.610,-0.353 7,6 150/150 L,V,C,F,I

127 G GLY127:A -1.284 9 -1.310,-1.278 9,9 150/150 G

128 E GLU128:A -1.286 9 -1.306,-1.278 9,9 150/150 E,D

129 S SER129:A -0.337 6 -0.532,-0.247 7,6 150/150 T,Q,M,P,N,D,L,G,S,E,H,A,V,K

130 L LEU130:A -0.331 6 -0.532,-0.247 7,6 149/150 K,A,E,L,S,Q,I,R

131 E GLU131:A 0.047 5 -0.247, 0.163 6,4 150/150 H,K,V,A,L,G,S,E,Q,T,I,D,F,P,N

132 E GLU132:A -0.662 7 -0.807,-0.610 8,7 149/150 X,H,A,V,E,D,I,R,Q,T

133 R ARG133:A -0.955 8 -1.048,-0.914 9,8 149/150 L,Y,H,Q,K,R,N

134 E GLU134:A -0.370 6 -0.532,-0.247 7,6 149/150 L,S,E,K,A,P,R,N,D,Q

135 A ALA135:A 0.317 4 0.006, 0.347 5,4 149/150 A,K,E,S,G,Q,T,I,D,N,R

136 G GLY136:A -0.152 6 -0.447, 0.006 7,5 149/150 H,A,K,G,E,D,N,Q

137 Q GLN137:A 1.057 1 0.572, 1.246 3,1 150/150 Q,T,I,D,F,R,N,V,K,A,L,G,S,E

138 T THR138:A -0.603 7 -0.747,-0.532 8,7 150/150 L,G,S,V,A,H,C,T,Y,Q,P,F

139 N ASN139:A 0.538 3 0.163, 0.572 4,3 150/150 K,S,Q,T,D,F,R,N,W,V,A,L,E,M,Y,I

140 A ALA140:A 0.868 2 0.347, 0.857 4,2 149/150 E,S,G,K,V,A,W,X,T,Q,N,P,R,D

141 V VAL141:A -0.554 7 -0.681,-0.447 7,7 150/150 Y,T,F,I,K,A,V,W,H,L

142 V VAL142:A -0.172 6 -0.353,-0.129 6,5 150/150 I,N,P,T,C,A,V,L

143 A ALA143:A 2.590 1 1.246, 3.502 1,1 150/150 S,K,H,T,Q,N,R,F,D,E,L,G,V,A,C,Y,M,I

144 S SER144:A 1.143 1 0.572, 1.246 3,1 150/150 Y,T,Q,M,R,N,D,S,G,E,W,H,K,V,A

145 Q GLN145:A -1.300 9 -1.310,-1.295 9,9 150/150 Q

146 V VAL146:A 0.251 4 0.006, 0.347 5,4 150/150 I,F,T,M,C,L,A,V

147 E GLU147:A 1.256 1 0.857, 1.246 2,1 150/150 Q,T,F,D,N,R,K,H,S,M,I,V,A,E,L,G,C

148 K LYS148:A 0.765 2 0.347, 0.857 4,2 150/150 P,R,N,D,T,Q,S,H,K,I,M,C,L,G,E,W,V,A

149 A ALA149:A -0.107 5 -0.353, 0.006 6,5 147/150 C,L,G,S,V,A,R,D,I,F,Y,M

150 L LEU150:A -0.244 6 -0.447,-0.129 7,5 150/150 L,S,V,K,A,C,Y,Q,M,I,F

151 A ALA151:A 1.342 1 0.857, 1.855 2,1 150/150 V,K,A,H,E,G,S,Q,T,F,D,I,N,R,P

152 G GLY152:A 1.262 1 0.857, 1.246 2,1 148/150 Q,T,D,F,R,N,H,K,S,Y,I,V,A,L,G,E

153 L LEU153:A 1.020 1 0.572, 1.246 3,1 129/150 C,H,W,A,V,L,G,S,I,F,R,Q

154 T THR154:A 0.588 3 0.163, 0.857 4,2 123/150 M,Q,T,D,I,P,R,N,H,A,K,L,S,G,E

155 P PRO155:A 1.271 1 0.572, 1.246 3,1 126/150 K,H,S,Q,T,D,N,P,V,A,W,E,L,G,C,I

156 E GLU156:A 0.749 2 0.347, 0.857 4,2 127/150 K,H,S,F,D,N,R,P,Q,T,V,A,E,L,G,Y

157 Q GLN157:A 0.801 2 0.347, 0.857 4,2 146/150 T,Q,N,R,P,F,D,S,K,H,Y,E,G,L,V,A,C

158 V VAL158:A 0.826 2 0.347, 0.857 4,2 146/150 I,Y,M,E,L,G,V,A,W,P,R,F,T,Q,S,H

159 K LYS159:A 1.280 1 0.857, 1.246 2,1 150/150 Q,T,D,F,P,R,N,H,V,K,A,L,G,S,E

160 Q GLN160:A 0.945 2 0.572, 1.246 3,1 150/150 H,W,A,V,K,L,G,S,E,Q,T,D,R,P,N

161 A ALA161:A 0.994 2 0.572, 1.246 3,1 150/150 C,S,G,L,W,V,A,D,I,F,Y,T,M

162 V VAL162:A -0.364 6 -0.532,-0.247 7,6 150/150 C,A,V,E,S,L,I,T

163 I ILE163:A -0.380 6 -0.532,-0.247 7,6 150/150 L,V,P,F,I

164 A ALA164:A -1.283 9 -1.306,-1.278 9,9 150/150 A,M

165 Y TYR165:A -1.292 9 -1.310,-1.278 9,9 150/150 Y

166 E GLU166:A -1.299 9 -1.310,-1.295 9,9 150/150 E

167 P PRO167:A -1.289 9 -1.310,-1.278 9,9 150/150 P

168 I ILE168:A -0.826 8 -0.962,-0.747 8,8 150/150 I,R,V,L

169 W TRP169:A -1.283 9 -1.310,-1.278 9,9 150/150 W

170 A ALA170:A -1.283 9 -1.306,-1.278 9,9 150/150 S,A

171 I ILE171:A -1.285 9 -1.306,-1.278 9,9 148/150 I,V

172 G GLY172:A -1.284 9 -1.310,-1.278 9,9 148/150 G

173 T THR173:A -1.114 9 -1.184,-1.086 9,9 148/150 T,Q,D,E,S,V,A,K,C

174 G GLY174:A -1.169 9 -1.237,-1.121 9,9 148/150 P,K,G

175 K LYS175:A 0.218 4 0.006, 0.347 5,4 148/150 T,M,Q,R,N,D,I,L,E,H,V,K

176 S SER176:A -0.581 7 -0.747,-0.532 8,7 148/150 T,N,P,F,I,S,A,V

177 S SER177:A -1.062 9 -1.154,-1.006 9,8 148/150 C,P,T,S,A

178 T THR178:A -0.471 7 -0.610,-0.353 7,6 148/150 A,K,L,G,S,E,D,R,M,T

179 P PRO179:A 0.412 4 0.006, 0.572 5,3 148/150 T,M,P,N,D,F,L,S,G,E,A,V,K

180 E GLU180:A 0.192 4 -0.129, 0.347 5,4 148/150 Q,P,R,N,D,G,S,E,H,A,K

181 D ASP181:A -0.651 7 -0.807,-0.610 8,7 148/150 Y,M,Q,F,D,I,E,G,V,A

182 A ALA182:A -1.027 9 -1.121,-0.962 9,8 148/150 I,L,A,V

183 N ASN183:A -0.567 7 -0.681,-0.532 7,7 148/150 D,R,N,Q,T,C,H,K,A,V,L,G,S,E

184 S SER184:A -0.330 6 -0.532,-0.247 7,6 148/150 N,R,I,D,T,Q,E,S,K,A,H

185 V VAL185:A -0.245 6 -0.447,-0.129 7,5 148/150 A,V,L,S,G,I,R,M,Q,T

186 C CYS186:A -0.879 8 -1.006,-0.807 8,8 148/150 M,Q,T,I,N,R,V,A,H,S,C

187 G GLY187:A 0.872 2 0.347, 1.246 4,1 148/150 S,K,H,T,Q,N,R,F,D,E,L,G,A,V,C,I

188 H HIS188:A 0.945 2 0.572, 1.246 3,1 148/150 S,H,K,R,N,D,F,T,Q,G,L,E,W,A,V,I,Y,M

189 I ILE189:A -0.865 8 -0.962,-0.807 8,8 147/150 I,M,A,V,L

190 R ARG190:A -1.201 9 -1.259,-1.184 9,9 147/150 H,A,K,R

191 S SER191:A 1.601 1 0.857, 1.855 2,1 147/150 K,V,A,H,E,G,S,L,D,N,R,Q,T

192 V VAL192:A 1.786 1 1.246, 1.855 1,1 147/150 H,K,S,Q,T,F,R,N,W,V,A,L,G,E,C,M,Y,I

193 V VAL193:A -0.045 5 -0.247, 0.006 6,5 146/150 V,A,M,L,F,I

194 S SER194:A 0.848 2 0.347, 0.857 4,2 146/150 Q,T,Y,I,D,N,R,V,K,A,H,E,G,S

195 R ARG195:A 1.108 1 0.572, 1.246 3,1 146/150 V,K,A,H,E,G,S,I,D,N,R,Q,M,T

196 L LEU196:A 1.280 1 0.857, 1.246 2,1 141/150 G,L,E,W,A,V,I,Y,M,S,H,K,R,N,D,F,T,Q

197 F PHE197:A 0.430 4 0.006, 0.572 5,3 113/150 I,F,M,T,Y,C,W,H,V,A,S,L,E

198 G GLY198:A 0.413 4 0.006, 0.572 5,3 129/150 K,A,S,G,E,Q,T,D,N

199 P PRO199:A 1.862 1 1.246, 1.855 1,1 132/150 T,Q,P,R,N,I,D,F,S,G,E,V,K,A

200 E GLU200:A 0.918 2 0.572, 1.246 3,1 113/150 T,Q,N,R,P,D,E,G,S,K,A

201 A ALA201:A 1.037 1 0.572, 1.246 3,1 143/150 T,Q,N,R,P,F,D,S,K,H,M,I,E,L,G,A,V,W,C

202 A ALA202:A -0.838 8 -0.962,-0.747 8,8 144/150 L,G,S,A,K,V,P,Q

203 E GLU203:A 1.402 1 0.857, 1.855 2,1 144/150 R,P,N,D,T,Q,M,S,G,E,H,K,V,A

204 A ALA204:A 1.761 1 1.246, 1.855 1,1 146/150 K,H,S,Q,T,D,N,P,R,V,A,E,G,C,Y,I

205 I ILE205:A 0.695 3 0.347, 0.857 4,2 145/150 T,M,Q,P,I,L,S,A,V,C

206 R ARG206:A -0.219 6 -0.447,-0.129 7,5 146/150 S,L,H,K,A,V,C,T,Q,R,P,I

207 I ILE207:A -0.868 8 -0.962,-0.807 8,8 146/150 V,L,I,C

208 Q GLN208:A -0.727 8 -0.862,-0.681 8,7 146/150 L,Q,M,V,I

209 Y TYR209:A -1.292 9 -1.310,-1.278 9,9 146/150 Y

210 G GLY210:A -1.284 9 -1.310,-1.278 9,9 146/150 G

211 G GLY211:A -1.284 9 -1.310,-1.278 9,9 146/150 G

212 S SER212:A -1.300 9 -1.310,-1.295 9,9 146/150 S

213 V VAL213:A -0.945 8 -1.048,-0.914 9,8 146/150 V,A,M,L,I,C

214 K LYS214:A -0.620 7 -0.747,-0.532 8,7 146/150 N,D,T,S,K

215 P PRO215:A 0.136 5 -0.129, 0.347 5,4 146/150 D,P,A,K,V,L,S,G,E

216 D ASP216:A 1.598 1 0.857, 1.855 2,1 146/150 Q,T,D,N,K,A,E,G,S

217 N ASN217:A -1.208 9 -1.259,-1.184 9,9 146/150 I,N,L,T

218 I ILE218:A -0.663 7 -0.807,-0.610 8,7 146/150 I,C,V,A,S,L,T

219 R ARG219:A 0.966 2 0.572, 1.246 3,1 146/150 I,E,G,L,V,A,N,R,P,F,D,T,Q,S,K,H

220 D ASP220:A -0.106 5 -0.353, 0.006 6,5 145/150 G,S,E,A,V,R,P,N,D,Q,M

221 F PHE221:A -0.684 7 -0.807,-0.610 8,7 145/150 Q,L,Y,I,F

222 L LEU222:A -0.201 6 -0.447,-0.129 7,5 144/150 G,S,L,V,A,H,M,F,I

223 A ALA223:A 0.093 5 -0.129, 0.163 5,4 144/150 N,R,D,T,Q,X,E,L,S,G,K,A,H

224 Q GLN224:A -0.073 5 -0.247, 0.006 6,5 145/150 N,R,I,Y,T,M,Q,C,E,L,V,A,K

225 Q GLN225:A 1.158 1 0.572, 1.246 3,1 143/150 N,P,R,D,T,Q,E,S,G,L,K,A,V,H

226 Q GLN226:A -0.563 7 -0.747,-0.447 8,7 144/150 Q,D,I,N,H,E,G,S

227 I ILE227:A -0.775 8 -0.914,-0.681 8,7 144/150 I,L,Y,V

228 D ASP228:A -1.019 9 -1.121,-0.962 9,8 144/150 A,Q,G,S,D,N

229 G GLY229:A -1.284 9 -1.310,-1.278 9,9 144/150 G

230 P PRO230:A -0.602 7 -0.747,-0.532 8,7 144/150 F,P,A,V,G,L

231 L LEU231:A -1.238 9 -1.295,-1.212 9,9 144/150 L,G,F

232 V VAL232:A -0.985 8 -1.086,-0.914 9,8 144/150 V,A,I

233 G GLY233:A -1.207 9 -1.278,-1.184 9,9 144/150 G,T,E

234 G GLY234:A -1.144 9 -1.237,-1.086 9,9 144/150 R,G,S

235 A ALA235:A -1.231 9 -1.278,-1.212 9,9 144/150 F,S,A,V

236 S SER236:A -1.133 9 -1.184,-1.086 9,9 144/150 A,S,G,C

237 L LEU237:A -1.240 9 -1.295,-1.212 9,9 144/150 W,L,I

238 E GLU238:A 0.023 5 -0.247, 0.163 6,4 144/150 V,K,S,L,E,Q,T,D,I,R,N

239 P PRO239:A -0.329 6 -0.532,-0.247 7,6 132/150 S,L,G,A,V,X,T,P,F

240 A ALA240:A 0.995 2 0.572, 1.246 3,1 144/150 V,K,A,H,E,S,G,Q,T,D,I,N,R,P

241 S SER241:A -0.229 6 -0.447,-0.129 7,5 140/150 D,N,Q,T,V,A,K,H,E,G,S

242 F PHE242:A -1.266 9 -1.306,-1.259 9,9 142/150 F,Y

243 L LEU243:A 0.931 2 0.572, 1.246 3,1 140/150 S,H,K,D,F,T,Q,C,G,L,E,A,V,I,Y,M

244 Q GLN244:A 0.986 2 0.572, 1.246 3,1 138/150 T,Q,N,R,P,D,I,E,S,G,L,A,V,K

245 L LEU245:A -1.074 9 -1.154,-1.048 9,9 138/150 I,F,L,M,V

246 V VAL246:A 0.075 5 -0.129, 0.163 5,4 127/150 L,A,V,C,I

247 E GLU247:A 0.783 2 0.347, 0.857 4,2 107/150 Q,T,D,I,N,R,A,K,H,E,G,L,S

248 A ALA248:A -0.747 8 -0.914,-0.681 8,7 77/150 I,F,R,N,Q,T,A,S,G,L

249 G GLY249:A 0.541 3 0.006, 0.857 5,2 32/150 S,G,Y,E,Q,W,A

250 R ARG250:A 1.285 1 0.347, 1.855 4,1 17/150 K,A,E,S,G,D,N,R,Q

251 H HIS251:A -0.640 7 -1.006,-0.447 8,7 9/150 R,N,H

252 E - -0.806 8\* -1.237,-0.610 9,7 3/150 E

\*Below the confidence cut-off - The calculations for this site were performed on less than 6 non-gaped homologue sequences,

or the confidence interval for the estimated score is equal to- or larger than- 4 color grades.