# Amino Acid Conservation Scores

- 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 (normalized) | COLOR | CONFIDENCE INTERVAL | CONFIDENCE INTERVAL COLORS | MSA DATA | RESIDUE VARIETY |
|---|---|---|---|---|---|---|---|---|
| 1 | M | MET1:F | -1.190 | 9 | -1.321,-1.131 | 9,9 | 115/150 | M,V,L |
| 2 | E | GLU2:F | -1.259 | 9 | -1.377,-1.225 | 9,9 | 136/150 | K,D,E |
| 3 | F | PHE3:F | -0.309 | 6 | -0.601,-0.135 | 7,5 | 136/150 | L,Y,F |
| 4 | Q | GLN4:F | -1.319 | 9 | -1.414,-1.272 | 9,9 | 136/150 | H,Q |
| 5 | A | ALA5:F | -1.131 | 9 | -1.272,-1.085 | 9,9 | 136/150 | G,A,P,V |
| 6 | V | VAL6:F | -1.001 | 8 | -1.131,-0.939 | 9,8 | 136/150 | I,V |
| 7 | V | VAL7:F | -0.570 | 7 | -0.779,-0.465 | 8,7 | 136/150 | I,L,V,M |
| 8 | M | MET8:F | -0.791 | 8 | -0.939,-0.663 | 8,7 | 136/150 | L,M,F |
| 9 | A | ALA9:F | -1.359 | 9 | -1.414,-1.377 | 9,9 | 136/150 | A |
| 10 | V | VAL10:F | -0.685 | 7 | -0.887,-0.601 | 8,7 | 136/150 | Y,V,G,A |
| 11 | G | GLY11:F | -1.192 | 9 | -1.321,-1.131 | 9,9 | 136/150 | C,A,G |
| 12 | G | GLY12:F | -0.023 | 5 | -0.312, 0.198 | 6,4 | 136/150 | I,V,Q,T,A,S,K,R,G,P,E |
| 13 | G | - | -1.267 | 9 | -1.377,-1.225 | 9,9 | 136/150 | G,S |
| 14 | S | - | -1.345 | 9 | -1.414,-1.321 | 9,9 | 136/150 | T,S |
| 15 | R | - | -1.221 | 9 | -1.321,-1.178 | 9,9 | 136/150 | P,R,H,K |
| 16 | M | - | -1.160 | 9 | -1.272,-1.085 | 9,9 | 138/150 | L,I,M,F |
| 17 | T | - | -0.319 | 6 | -0.535,-0.135 | 7,5 | 138/150 | E,F,P,G,R,Y,M,H,L,S,N,A,T,V |
| 18 | D | - | -0.876 | 8 | -1.037,-0.779 | 8,8 | 138/150 | E,D,P |
| 19 | L | - | -0.795 | 8 | -0.988,-0.663 | 8,7 | 138/150 | M,I,V,L |
| 20 | T | - | -1.161 | 9 | -1.272,-1.085 | 9,9 | 138/150 | A,I,S,T,M |
| 21 | S | - | -0.146 | 5 | -0.392,-0.036 | 6,5 | 138/150 | D,A,N,T,Q,E,F,P,Y,S,H,C |
| 22 | S | - | -0.284 | 6 | -0.535,-0.135 | 7,5 | 136/150 | C,S,K,R,G,T,D,A,N |
| 23 | I | - | 0.092 | 5 | -0.228, 0.340 | 6,4 | 138/150 | Q,V,I,T,N,L,C,S,K,R,Y,M |
| 24 | P | - | -0.745 | 7 | -0.939,-0.601 | 8,7 | 138/150 | Y,C,H,P,A,G |

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  25       K              -      -1.345           9     -1.414,-1.321                    9,9
138/150 K
  26       P       PRO26:F       -0.281           6     -0.535,-0.135                    7,5
138/150 A,P,C,S,Y
  27       L       LEU27:F       -0.943           8     -1.131,-0.834                    9,8
138/150 F,A,I,L,V,M
  28       L       LEU28:F       -1.200           9     -1.321,-1.131                    9,9
138/150 M,L,V
  29       P       PRO29:F       -0.840           8     -1.037,-0.722                    8,7
138/150 P,L,S,Q,H,T,M
  30       V       VAL30:F       -0.770           8     -0.939,-0.663                    8,7
138/150 I,V,A
  31       G       GLY31:F       -0.842           8     -1.037,-0.722                    8,7
138/150 A,G,C,H
  32       N       ASN32:F       -1.298           9     -1.377,-1.272                    9,9
138/150 R,N,G
  33       K       LYS33:F        0.919           2      0.503, 1.265                    3,1
138/150 I,V,R,Y,M,H,L,K,E,F
  34       P       PRO34:F       -1.333           9     -1.414,-1.321                    9,9
138/150 P
  35       L       LEU35:F       -0.557           7     -0.779,-0.392                    8,6
138/150 M,I,V,L
  36       I       ILE36:F       -0.374           6     -0.601,-0.228                    7,6
137/150 M,I,V,L,X
  37       W       TRP37:F       -0.326           6     -0.663,-0.135                    7,5
140/150 W,F,Y,M,I
  38       Y       TYR38:F       -0.960           8     -1.131,-0.834                    9,8
138/150 H,C,Y,F
  39       P       PRO39:F       -0.592           7     -0.834,-0.465                    8,7
138/150 P,V,S,L,T
  40       L       LEU40:F       -0.416           6     -0.663,-0.228                    7,6
137/150 P,I,L,V
  41       N       ASN41:F       -0.636           7     -0.834,-0.535                    8,7
137/150 Y,R,H,S,K,D,A,N,Q,V
  42       L       LEU42:F        0.316           4     -0.036, 0.503                    5,3
137/150 N,T,Q,I,W,M,S,L,K
  43       L       LEU43:F       -1.056           8     -1.225,-0.988                    9,8
138/150 F,M,L,C
  44       E       GLU44:F       -0.746           7     -0.939,-0.663                    8,7
138/150 D,E,V,L,Q,K
  45       R       ARG45:F       -0.003           5     -0.312, 0.198                    6,4
138/150 E,G,R,K,H,S,N,T,Q
  46       V       VAL46:F       -0.029           5     -0.312, 0.076                    6,5
138/150 N,A,V,I,T,F,E,S,L,M
  47       G       GLY47:F       -1.191           9     -1.321,-1.131                    9,9
138/150 W,N,G
  48       F       PHE48:F       -1.121           9     -1.272,-1.037                    9,8
138/150 F,V,I
  49       E       GLU49:F        0.029           5     -0.228, 0.198                    6,4
139/150 E,G,R,K,H,L,S,N,A,D,T,Q
  50       E       GLU50:F       -0.562           7     -0.779,-0.465                    8,7
139/150 E,G,D,R,K,S,Q
  51       V       VAL51:F       -0.508           7     -0.722,-0.392                    7,6
139/150 I,C,V,T,M,A,F
  52       I       ILE52:F       -1.061           9     -1.178,-0.988                    9,8
138/150 T,M,L,I,K,X,F
  53       V       VAL53:F       -0.625           7     -0.834,-0.535                    8,7
139/150 V,L,I
  54       V       VAL54:F        0.046           5     -0.228, 0.198                    6,4
139/150 I,L,V
  55       T       THR55:F       -1.018           8     -1.131,-0.939                    9,8
139/150 A,T,C,I,V,Q
  56       T       THR56:F       -0.099           5     -0.392, 0.076                    6,5
139/150 A,N,D,Q,V,T,P,F,C,H,S,L,Y,R
  57       R              -       0.239           4     -0.135, 0.503                    5,3
139/150 D,A,N,T,Q,E,M,R,S,K
  58       D              -       0.058           5     -0.228, 0.198                    6,4
139/150 E,H,S,L,C,M,Y,N,A,D,Q,I,T
  59       V              -       0.773           2      0.340, 0.940                    4,2
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139/150 Y,M,K,S,C,E,F,G,T,I,V,Q,A,D
  60       Q              -       0.526            3      0.198, 0.697                    4,3
139/150 A,N,T,Q,V,E,G,R,C,L,S,H,K
  61       K       LYS61:F        0.499            3      0.076, 0.697                    5,3
139/150 T,Q,D,N,A,R,L,H,S,K,E,G,P
  62       A       ALA62:F        1.394            1      0.940, 1.759                    2,1
139/150 E,K,H,L,S,C,M,R,A,N,D,V,Q,T
  63       L       LEU63:F       -0.109            5     -0.392, 0.076                    6,5
139/150 T,V,Q,I,F,M,S,L
  64       C       CYS64:F        1.261            1      0.697, 1.759                    3,1
136/150 Q,V,T,D,N,A,H,S,R,G,W,I,C,L,K,Y,F,E
  65       A       ALA65:F        2.150            1      1.265, 3.048                    1,1
137/150 T,Q,V,D,A,N,R,H,S,G,P,I,M,L,K,E,F
  66       E       GLU66:F        0.630            3      0.198, 0.940                    4,2
111/150 L,C,S,K,E,T,I,V,Q,D,A
  67       F       PHE67:F        0.275            4     -0.135, 0.503                    5,3
108/150 R,M,S,L,P,F,V,I,Q,N,A
  68       K       LYS68:F        0.476            3      0.076, 0.697                    5,3
139/150 R,K,S,L,E,G,Q,N,D
  69       M       MET69:F        0.677            3      0.198, 0.940                    4,2
140/150 A,N,Q,I,V,T,F,P,G,C,L,S,R,M
  70       K       LYS70:F        0.213            4     -0.135, 0.340                    5,4
140/150 K,S,L,R,P,G,E,I,Q,T,N,D
  71       M       MET71:F        0.392            4      0.076, 0.503                    5,3
140/150 M,V,L,S,I
  72       K       LYS72:F        0.026            5     -0.312, 0.198                    6,4
139/150 E,X,R,K,S,H,N,A,D,T,I
  73       P       PRO73:F        0.519            3      0.076, 0.697                    5,3
140/150 I,V,T,A,L,M,F,P
  74       D       ASP74:F       -0.325            6     -0.535,-0.135                    7,5
140/150 N,D,E,K,S,L,H
  75       I       ILE75:F        0.340            4     -0.036, 0.503                    5,3
140/150 I,V,T,F,W,L,M,Y
  76       V       VAL76:F       -0.762            8     -0.939,-0.663                    8,7
139/150 I,V,T,A,K,Y,F,E
  77       C       CYS77:F        0.980            2      0.503, 1.265                    3,1
139/150 I,T,A,S,C,K,Y,M,G,P,E
  78       I       ILE78:F       -0.538            7     -0.722,-0.392                    7,6
139/150 N,F,L,V,I
  79       P       PRO79:F        0.327            4     -0.036, 0.503                    5,3
139/150 N,A,T,Q,E,P,R,L,S,K
  80       D       ASP80:F        0.066            5     -0.228, 0.198                    6,4
139/150 Y,R,S,L,K,E,G,P,F,T,Q,V,D,A,N
  81       D       ASP81:F        0.525            3      0.198, 0.697                    4,3
135/150 G,E,S,K,D,A,N,Q,V
  82       A       ALA82:F        0.486            3      0.076, 0.697                    5,3
139/150 G,E,K,S,L,M,N,A,D,Q,V,I,T
  83       D       ASP83:F       -0.835            8     -0.988,-0.722                    8,7
139/150 K,S,Y,A,D,E
  84       M       MET84:F        0.572            3      0.198, 0.940                    4,2
138/150 P,G,W,R,D,V,Q,T,F,E,K,C,L,Y,M,I
  85       G       GLY85:F       -1.200            9     -1.321,-1.131                    9,9
139/150 S,G,D
  86       T       THR86:F       -1.340            9     -1.414,-1.321                    9,9
139/150 T,E
  87       A       ALA87:F       -1.088            9     -1.225,-1.037                    9,8
139/150 L,V,S,C,G,A
  88       D       ASP88:F       -1.042            8     -1.178,-0.988                    9,8
139/150 E,N,G,D
  89       S       SER89:F       -0.953            8     -1.085,-0.887                    9,8
139/150 T,S,V,A
  90       L       LEU90:F       -0.946            8     -1.131,-0.834                    9,8
140/150 L,V,I,E
  91       R       ARG91:F       -1.225            9     -1.321,-1.178                    9,9
140/150 C,H,R
  92       Y       TYR92:F        1.462            1      0.940, 1.759                    2,1
140/150 N,Q,I,T,F,E,L,S,H,Y,R
  93       I       ILE93:F       -0.888            8     -1.037,-0.779                    8,8
141/150 Y,L,V,I
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  94       Y       TYR94:F       0.335          4     -0.036, 0.503                  5,3
141/150 Q,N,A,R,Y,H,S,K,E
  95       P       PRO95:F       0.431          4      0.076, 0.697                  5,3
141/150 D,N,A,Q,T,G,P,E,S,K,R
  96       K       LYS96:F      -0.564          7     -0.779,-0.392                  8,6
142/150 F,P,L,K,Y,R,D,A,Q,V
  97       L       LEU97:F      -0.866          8     -1.037,-0.779                  8,8
142/150 L,V,I,P,F,A
  98       K       LYS98:F      -0.199          6     -0.465,-0.036                  7,5
144/150 S,L,H,K,Y,R,E,Q,I,T
  99       T       THR99:F      -0.367          6     -0.601,-0.228                  7,6
146/150 P,G,K,S,Y,R,N,A,Q,V,T
 100       D      ASP100:F      -1.227          9     -1.321,-1.178                  9,9
146/150 R,L,N,D
 101       V      VAL101:F       0.191          4     -0.135, 0.340                  5,4
146/150 M,V,I,L,F
 102       L      LEU102:F      -0.255          6     -0.535,-0.036                  7,5
146/150 M,I,V,L,F
 103       V      VAL103:F      -0.856          8     -0.988,-0.779                  8,8
146/150 L,I,V
 104       L      LEU104:F       0.213          4     -0.135, 0.340                  5,4
146/150 A,L,I,V,T,M
 105       S      SER105:F      -1.214          9     -1.321,-1.178                  9,9
146/150 G,P,S,Q,T
 106       C      CYS106:F      -0.960          8     -1.131,-0.834                  9,8
146/150 C,S,A,G
 107       D      ASP107:F      -1.353          9     -1.414,-1.321                  9,9
146/150 D
 108       L      LEU108:F      -0.802          8     -0.988,-0.663                  8,7
146/150 L,I,V,K,M
 109       I      ILE109:F      -0.959          8     -1.085,-0.887                  9,8
146/150 T,L,V,I
 110       T      THR110:F      -0.704          7     -0.887,-0.601                  8,7
146/150 A,T,C,V,L,S
 111       D      ASP111:F      -0.788          8     -0.939,-0.663                  8,7
146/150 E,G,D,N,T,S
 112       V      VAL112:F       0.258          4     -0.036, 0.503                  5,3
146/150 F,A,T,M,I,L,V
 113       A      ALA113:F       0.060          5     -0.228, 0.198                  6,4
147/150 C,S,L,K,P,E,V,Q,D,A,N
 114       L      LEU114:F      -0.954          8     -1.131,-0.834                  9,8
147/150 F,V,L,I,Q
 115       H      HIS115:F      -0.674          7     -0.834,-0.535                  8,7
146/150 L,S,C,H,Y,R,G,E,Q,N
 116       E      GLU116:F       0.596          3      0.198, 0.940                  4,2
146/150 Q,N,A,D,R,Y,K,H,L,E,P,G
 117       V      VAL117:F      -0.596          7     -0.779,-0.465                  8,7
146/150 M,H,L,S,F,T,I,V,A
 118       V      VAL118:F      -0.716          7     -0.887,-0.601                  8,7
146/150 F,A,I,L,V,T
 119       D      ASP119:F      -0.938          8     -1.085,-0.834                  9,8
146/150 T,N,D,E
 120       L      LEU120:F       0.061          5     -0.228, 0.198                  6,4
146/150 A,D,V,I,T,H,S,L,M
 121       F      PHE121:F      -0.700          7     -0.887,-0.601                  8,7
146/150 Y,H,L,F
 122       R      ARG122:F      -1.275          9     -1.377,-1.225                  9,9
146/150 R,K,Q
 123       A      ALA123:F      -0.130          5     -0.392, 0.076                  6,5
146/150 N,A,I,Q,V,T,K,S,L,C,M
 124       Y      TYR124:F      -0.468          7     -0.663,-0.312                  7,6
146/150 Y,R,Q,H,L,N
 125       D      ASP125:F      -0.425          6     -0.663,-0.312                  7,6
146/150 Q,S,R,N,D,E
 126       A      ALA126:F      -0.971          8     -1.131,-0.887                  9,8
146/150 P,A,S,V
 127       S      SER127:F      -0.522          7     -0.722,-0.392                  7,6
146/150 A,G,M,T,S
 128       L      LEU128:F       0.789          2      0.340, 0.940                  4,2
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146/150 M,I,L,V,A,F
 129 A ALA129:F -0.416 6 -0.601,-0.312 7,6
146/150 A,L,C,S,V,T
 130 M MET130:F -0.512 7 -0.722,-0.392 7,6
147/150 S,V,I,M,T,A
 131 L LEU131:F -0.806 8 -0.988,-0.663 8,7
146/150 F,M,V,L
 132 M MET132:F -0.712 7 -0.887,-0.601 8,7
146/150 L,Y,M,A,F
 133 R ARG133:F -0.153 6 -0.392,-0.036 6,5
146/150 K,H,L,C,S,R,Y,M,F,W,V,Q,A
 134 K LYS134:F 0.744 3 0.340, 0.940 4,2
146/150 K,H,S,R,P,E,V,Q,T,N,A,D
 135 G - 1.423 1 0.940, 1.759 2,1
145/150 I,F,X,L,C,M,D,A,N,Q,V,T,G,P,S,R
 136 Q - 1.016 2 0.503, 1.265 3,1
146/150 Q,V,T,D,A,N,H,S,P,I,C,L,K,Y,M,F,E
 137 D - 1.224 1 0.697, 1.759 3,1
146/150 A,N,D,Q,E,P,M,R,K,L,S
 138 S - 1.228 1 0.697, 1.759 3,1
146/150 G,P,F,E,C,L,S,D,N,A,V,Q,I,T
 139 I - 1.416 1 0.940, 1.759 2,1
146/150 F,E,L,K,Y,M,I,G,P,H,S,R,D,N,A,V,Q,T
 140 E - 0.631 3 0.198, 0.940 4,2
147/150 K,S,L,M,R,F,G,E,V,I,T,A,N,D
 141 P - 1.077 1 0.503, 1.265 3,1
147/150 A,N,V,Q,T,P,G,S,R,I,F,E,K,L,Y,M
 142 V - -0.145 5 -0.392,-0.036 6,5
147/150 I,V,T,A,N,L,M,P,G
 143 P - -1.094 9 -1.225,-1.037 9,8
145/150 L,T,N,A,P
 144 G - -0.913 8 -1.085,-0.779 9,8
145/150 K,C,V,N,A,G
 145 Q - 0.225 4 -0.135, 0.503 5,3
145/150 Y,R,K,L,S,H,P,G,T,Q,V,I,A,N
 146 K - -1.043 8 -1.178,-0.939 9,8
145/150 Q,K,T,Y,R
 147 G - -0.276 6 -0.535,-0.135 7,5
145/150 T,V,Q,N,A,K,S,H,P,G
 148 K - -0.965 8 -1.131,-0.887 9,8
145/150 D,N,I,E,G,F,R,K
 149 K - 0.440 4 0.076, 0.697 5,3
143/150 I,Q,A,N,S,C,H,K,Y,R,G,F,P
 150 K - -0.534 7 -0.722,-0.392 7,6
144/150 P,A,N,R,Q,H,K
 151 A - 2.183 1 1.265, 3.048 1,1
101/150 Q,T,A,N,L,H,S,G,P,E
 152 V - 0.374 4 -0.036, 0.697 5,3
111/150 V,Q,I,T,A,S,L,G,P,E
 153 E - 0.412 4 0.076, 0.697 5,3
149/150 I,L,K,M,F,E,Q,V,T,D,N,H,S,R,G,P
 154 Q - -0.880 8 -1.037,-0.779 8,8
149/150 H,S,V,Q,D,N,E
 155 R ARG155:F -0.526 7 -0.722,-0.392 7,6
149/150 T,I,Q,G,R,K,C,L,H
 156 D ASP156:F -1.137 9 -1.272,-1.085 9,9
149/150 H,D,P,E
 157 F PHE157:F -0.255 6 -0.535,-0.036 7,5
149/150 F,Y,V,I,L
 158 I ILE158:F -0.411 6 -0.601,-0.312 7,6
149/150 T,M,L,V,I,F
 159 G GLY159:F -0.864 8 -1.037,-0.722 8,7
150/150 G,A,M,S
 160 V VAL160:F -0.598 7 -0.779,-0.465 8,7
150/150 F,Y,M,V,I,L
 161 D ASP161:F -0.665 7 -0.834,-0.535 8,7
150/150 N,D,E,C,H,S,T
 162 S SER162:F 2.091 1 1.265, 3.048 1,1
150/150 R,H,S,W,G,P,T,Q,V,D,N,A,L,K,E,I

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 163       T      THR163:F       0.829          2      0.340, 0.940                    4,2
150/150 T,Q,V,A,N,D,R,M,K,S,C,H,E,G
 164       G      GLY164:F      -0.294          6     -0.535,-0.135                    7,5
148/150 D,N,T,Q,E,G,F,R,H,L,C,S,K
 165       K      LYS165:F       0.224          4     -0.135, 0.340                    5,4
150/150 N,D,T,Q,E,P,F,G,R,K,S
 166       R      ARG166:F      -1.053          8     -1.178,-0.988                    9,8
150/150 K,Q,H,R
 167       L      LEU167:F      -0.498          7     -0.722,-0.312                    7,6
149/150 I,V,L,M
 168       L      LEU168:F      -0.419          6     -0.663,-0.228                    7,6
149/150 L,C,I,V,M
 169       F      PHE169:F       0.042          5     -0.312, 0.198                    6,4
149/150 F,Q,I,L,Y,M
 170       M      MET170:F      -0.184          6     -0.465,-0.036                    7,5
149/150 H,L,S,C,M,F,I,V,T,A
 171       A      ALA171:F      -0.682          7     -0.834,-0.601                    8,7
150/150 A,N,D,V,Q,T,G,L,S,R
 172       N      ASN172:F      -0.963          8     -1.085,-0.887                    9,8
150/150 A,P,N,H,S,K,M
 173       E      GLU173:F      -0.941          8     -1.085,-0.834                    9,8
150/150 E,A,D,G,I,V,Q
 174       A      ALA174:F      -1.113          9     -1.225,-1.037                    9,8
149/150 V,S,K,G,D,A,E
 175       D      ASP175:F      -1.275          9     -1.377,-1.225                    9,9
149/150 L,D,P
 176       L      LEU176:F      -0.239          6     -0.535,-0.036                    7,5
149/150 V,I,Q,A,Y,H,L,F
 177       D      ASP177:F      -0.363          6     -0.601,-0.228                    7,6
148/150 S,E,G,D,A
 178       E      GLU178:F      -0.007          5     -0.312, 0.198                    6,4
148/150 Q,V,D,N,A,S,F,E
 179       E      GLU179:F       0.272          4     -0.036, 0.503                    5,3
148/150 Y,M,S,L,E,G,F,P,T,V,I,D,N,A
 180       L      LEU180:F      -0.367          6     -0.601,-0.228                    7,6
148/150 X,F,M,Y,V,I,L
 181       V      VAL181:F       0.536          3      0.198, 0.697                    4,3
149/150 P,G,E,K,L,S,N,A,I,V,T
 182       I      ILE182:F       0.692          3      0.340, 0.940                    4,2
148/150 F,M,Q,L,V,I
 183       K      LYS183:F      -0.068          5     -0.312, 0.076                    6,5
147/150 N,P,R,K,H,S,Q
 184       G      GLY184:F       0.152          4     -0.135, 0.340                    5,4
147/150 G,R,M,K,S,L,H,N,A,Q,V
 185       S      SER185:F      -0.501          7     -0.722,-0.392                    7,6
147/150 A,D,T,P,F,G,K,S,Y,R
 186       I      ILE186:F       0.541          3      0.198, 0.697                    4,3
148/150 F,P,V,L,I,M,T
 187       L      LEU187:F       0.058          5     -0.228, 0.198                    6,4
148/150 M,I,V,L,F,A,G
 188       Q      GLN188:F       0.477          3      0.076, 0.697                    5,3
149/150 T,I,Q,N,Y,M,R,S,C,H,K,E
 189       K      LYS189:F      -0.179          6     -0.465,-0.036                    7,5
149/150 E,R,K,H,N,D,Q,I
 190       H      HIS190:F       0.187          4     -0.135, 0.340                    5,4
150/150 N,A,F,Y,C,H
 191       P      PRO191:F      -0.589          7     -0.779,-0.465                    8,7
150/150 S,L,T,P,A,G
 192       R      ARG192:F       0.775          2      0.340, 0.940                    4,2
150/150 N,I,Q,V,F,C,H,S,L,K,Y,M,R
 193       I      ILE193:F      -0.262          6     -0.535,-0.135                    7,5
150/150 F,M,R,L,I,V
 194       R      ARG194:F       0.361          4      0.076, 0.503                    5,3
150/150 Q,I,T,N,K,L,S,C,H,R,F,G,E
 195       F      PHE195:F      -0.072          5     -0.312, 0.076                    6,5
150/150 F,M,L,V,I
 196       H      HIS196:F       0.405          4      0.076, 0.697                    5,3
150/150 L,H,C,K,R,Y,G,F,E,Q,V,N
 197       T      THR197:F      -0.801          8     -0.939,-0.722                    8,7
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|---|---|---|---|---|---|---|
| 150/150 W,G,M,C,S,K,N,A,T | | | | | | |
| 198 | G | GLY198:F | 0.383 | 4 | 0.076, 0.503 | 5,3 |
| 150/150 S,K,R,G,E,Q,T,D,A,N | | | | | | |
| 199 | L | LEU199:F | -0.992 | 8 | -1.178,-0.887 | 9,8 |
| 150/150 F,V,L,Y,M | | | | | | |
| 200 | V | VAL200:F | 0.428 | 4 | 0.076, 0.697 | 5,3 |
| 149/150 N,A,T,V,Q,I,X,E,M,H,S,L | | | | | | |
| 201 | D | ASP201:F | -1.322 | 9 | -1.414,-1.272 | 9,9 |
| 150/150 E,D | | | | | | |
| 202 | A | ALA202:F | -0.602 | 7 | -0.779,-0.465 | 8,7 |
| 150/150 G,A,S,V,C,T | | | | | | |
| 203 | H | HIS203:F | -1.329 | 9 | -1.414,-1.321 | 9,9 |
| 150/150 T,H | | | | | | |
| 204 | L | LEU204:F | -0.192 | 6 | -0.465,-0.036 | 7,5 |
| 150/150 A,T,V,I,W,F,M,L | | | | | | |
| 205 | Y | TYR205:F | -1.258 | 9 | -1.377,-1.225 | 9,9 |
| 150/150 F,Y | | | | | | |
| 206 | C | CYS206:F | -0.274 | 6 | -0.535,-0.135 | 7,5 |
| 150/150 V,L,C,I,F,G | | | | | | |
| 207 | L | LEU207:F | -0.026 | 5 | -0.312, 0.198 | 6,4 |
| 150/150 F,C,V,I,L,M | | | | | | |
| 208 | K | LYS208:F | -0.677 | 7 | -0.887,-0.535 | 8,7 |
| 149/150 K,S,Q,R,N,E | | | | | | |
| 209 | K | LYS209:F | -0.775 | 8 | -0.939,-0.663 | 8,7 |
| 149/150 R,H,S,K | | | | | | |
| 210 | Y | TYR210:F | 0.123 | 5 | -0.228, 0.340 | 6,4 |
| 150/150 Y,S,C,E,W,P,A,D | | | | | | |
| 211 | I | ILE211:F | -0.640 | 7 | -0.834,-0.535 | 8,7 |
| 150/150 L,V,C,I,T,M | | | | | | |
| 212 | V | VAL212:F | 0.415 | 4 | 0.076, 0.697 | 5,3 |
| 150/150 M,C,V,L,I,F | | | | | | |
| 213 | D | ASP213:F | -0.821 | 8 | -0.988,-0.722 | 8,7 |
| 150/150 D,P,N,E,H,Q,K | | | | | | |
| 214 | F | PHE214:F | -0.120 | 5 | -0.392, 0.076 | 6,5 |
| 150/150 H,L,Y,F | | | | | | |
| 215 | L | LEU215:F | -0.792 | 8 | -0.988,-0.663 | 8,7 |
| 150/150 I,V,L,A,P | | | | | | |
| 216 | M | MET216:F | 1.321 | 1 | 0.697, 1.759 | 3,1 |
| 150/150 A,D,T,V,I,Q,E,P,G,M,K,C,S,L | | | | | | |
| 217 | E | GLU217:F | 1.347 | 1 | 0.697, 1.759 | 3,1 |
| 150/150 D,A,N,T,V,Q,E,G,F,Y,M,C,S,H,K | | | | | | |
| 218 | N | ASN218:F | -0.552 | 7 | -0.722,-0.465 | 7,7 |
| 150/150 T,Q,N,D,R,Y,K,H,S,E,P,G | | | | | | |
| 219 | G | GLY219:F | 0.922 | 2 | 0.503, 1.265 | 3,1 |
| 150/150 R,S,K,E,G,P,T,Q,V,N,A | | | | | | |
| 220 | S | SER220:F | -0.248 | 6 | -0.465,-0.135 | 7,5 |
| 150/150 K,S,H,C,M,F,G,T,N,A | | | | | | |
| 221 | I | ILE221:F | -0.151 | 5 | -0.392,-0.036 | 6,5 |
| 150/150 I,V,F,S,L,R,Y,M | | | | | | |
| 222 | T | THR222:F | -0.571 | 7 | -0.779,-0.465 | 8,7 |
| 149/150 S,C,L,M,G,E,T,A,N | | | | | | |
| 223 | S | SER223:F | -0.918 | 8 | -1.085,-0.834 | 9,8 |
| 150/150 S,Y,M,T,N | | | | | | |
| 224 | I | ILE224:F | -0.158 | 6 | -0.392,-0.036 | 6,5 |
| 150/150 I,L,V,F | | | | | | |
| 225 | R | ARG225:F | -1.166 | 9 | -1.272,-1.085 | 9,9 |
| 150/150 K,R | | | | | | |
| 226 | S | SER226:F | -0.891 | 8 | -1.085,-0.779 | 9,8 |
| 150/150 R,T,S,G | | | | | | |
| 227 | E | GLU227:F | -1.313 | 9 | -1.414,-1.272 | 9,9 |
| 150/150 D,E | | | | | | |
| 228 | L | LEU228:F | -0.716 | 7 | -0.939,-0.601 | 8,7 |
| 150/150 V,L,T,M,A,F | | | | | | |
| 229 | I | ILE229:F | -0.229 | 6 | -0.465,-0.036 | 7,5 |
| 150/150 V,L,I,F | | | | | | |
| 230 | P | PRO230:F | -1.284 | 9 | -1.414,-1.225 | 9,9 |
| 150/150 S,P | | | | | | |
| 231 | Y | TYR231:F | 0.711 | 3 | 0.340, 0.940 | 4,2 |
| 150/150 A,I,F,Y,S,L,C,H,K | | | | | | |

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 232       L      LEU232:F      -0.734           7     -0.939,-0.601                    8,7
150/150 I,V,L,T,F,A
 233       V      VAL233:F      -1.074           9     -1.225,-0.988                    9,8
150/150 I,V
 234       R      ARG234:F      -0.364           6     -0.601,-0.228                    7,6
150/150 K,H,S,R,Q,T,A,N
 235       K      LYS235:F      -1.158           9     -1.272,-1.085                    9,9
150/150 K,R,E
 236       Q              -     -1.353           9     -1.414,-1.321                    9,9
150/150 Q
 237       F              -     -0.586           7     -0.834,-0.465                    8,7
150/150 F,L,S,H,K,Y,M
 238       S              -     -0.587           7     -0.779,-0.465                    8,7
150/150 A,Q,I,T,L,S,K,Y,R
 239       S              -      0.557           3      0.198, 0.697                    4,3
150/150 A,T,Q,I,V,E,R,L,H,C,S,K
 240       A              -      2.051           1      1.265, 3.048                    1,1
148/150 R,H,S,P,T,V,Q,N,A,D,M,K,L,E,F,I
 241       S      SER241:F       2.647           1      1.265, 3.048                    1,1
148/150 P,C,H,L,S,K,M,R,N,A,Q,I,V,T
 242       S      SER242:F       2.498           1      1.265, 3.048                    1,1
150/150 I,K,L,C,F,T,Q,V,A,N,D,R,H,S,P,G
 243       Q      GLN243:F       3.033           1      1.759, 3.048                    1,1
149/150 R,H,S,G,P,T,Q,V,D,N,A,Y,C,L,K,E,F,I
 244       Q              -      2.431           1      1.265, 3.048                    1,1
117/150 D,A,N,Q,V,T,P,E,S,L,H,K,Y,R
 245       G              -      3.048           1      1.759, 3.048                    1,1
132/150 D,N,A,Q,V,T,G,P,W,H,S,R,I,E,L,K,M
 246       Q              -      3.026           1      1.759, 3.048                    1,1
140/150 A,N,D,V,Q,T,P,G,S,R,I,E,K,C,L,M,Y
 247       E              -      2.711           1      1.759, 3.048                    1,1
140/150 M,K,H,S,L,E,P,G,T,I,Q,A,N,D
 248       E              -      1.318           1      0.697, 1.759                    3,1
143/150 T,I,Q,A,N,D,M,K,H,L,S,E,P
 249       K              -      3.026           1      1.759, 3.048                    1,1
144/150 F,E,K,C,L,M,I,P,G,S,H,R,A,N,D,Q,V,T
 250       E              -      0.487           3      0.076, 0.697                    5,3
143/150 R,H,S,K,E,G,T,D,A,N
 251       E              -      1.902           1      1.265, 1.759                    1,1
143/150 A,N,T,Q,V,P,G,R,S,H,I,E,F,M,K,L
 252       D              -      0.885           2      0.503, 1.265                    3,1
144/150 T,I,N,A,D,M,K,S,L,E,G
 253       L              -      1.529           1      0.940, 1.759                    2,1
144/150 F,E,C,L,K,M,I,P,S,H,R,D,N,V,Q,T
 254       K              -      0.797           2      0.340, 0.940                    4,2
141/150 D,N,A,T,I,V,E,G,F,P,M,R,S,L,K
 255       K              -      1.798           1      0.940, 3.048                    2,1
90/150  T,Q,V,D,M,R,L,K,G
 256       K              -      1.616           1      0.940, 1.759                    2,1
138/150 K,L,S,R,P,G,E,V,I,Q,T,N,A,D
 257       E              -      2.974           1      1.759, 3.048                    1,1
142/150 I,E,F,Y,M,L,K,D,N,A,T,Q,V,G,S,H
 258       L              -      3.045           1      1.759, 3.048                    1,1
142/150 T,V,Q,D,N,A,R,H,L,C,S,K,E,G,P
 259       K              -      2.898           1      1.759, 3.048                    1,1
142/150 D,A,N,T,Q,V,G,P,H,S,I,E,F,M,L,K
 260       S      SER260:F       1.207           1      0.697, 1.265                    3,1
143/150 N,D,Q,V,I,T,F,P,G,E,K,C,S,R
 261       L      LEU261:F       2.967           1      1.759, 3.048                    1,1
143/150 S,H,R,P,G,V,Q,T,A,N,D,K,L,M,E,I
 262       D      ASP262:F      -0.627           7     -0.834,-0.535                    8,7
147/150 E,G,D,K,Q,L,H
 263       I      ILE263:F      -0.420           6     -0.663,-0.312                    7,6
146/150 F,N,I,L,V
 264       Y      TYR264:F       2.297           1      1.265, 3.048                    1,1
146/150 V,I,Q,T,D,N,A,S,C,L,H,R,Y,F
 265       S      SER265:F       0.024           5     -0.228, 0.198                    6,4
147/150 F,G,E,K,S,H,R,A,N,D,I,Q,V,T
 266       F      PHE266:F       0.786           2      0.340, 0.940                    4,2
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149/150 T,I,A,M,Y,C,H,L,S,W,G,F,P
 267       I      ILE267:F       1.201           1      0.697, 1.265                    3,1
149/150 D,A,I,Q,V,T,G,F,P,E,C,S,L,K,M
 268       K             -       1.734           1      0.940, 1.759                    2,1
150/150 D,N,A,T,Q,V,W,G,P,R,S,H,I,E,M,L,C,K
 269       E             -       0.772           2      0.340, 0.940                    4,2
150/150 L,S,K,Y,R,G,F,P,E,V,Q,T,D,N,A
 270       A             -       0.871           2      0.503, 1.265                    3,1
150/150 D,N,A,T,V,E,G,F,L,H,S,K
 271       N             -       3.034           1      1.759, 3.048                    1,1
150/150 K,L,S,R,P,F,G,E,V,Q,T,A,N,D
 272       T             -       0.517           3      0.076, 0.697                    5,3
149/150 T,V,I,Q,D,N,A,M,Y,S,L,W,E,F,P
 273       L             -       0.900           2      0.503, 1.265                    3,1
149/150 I,Y,M,L,K,E,F,T,Q,V,D,A,N,R,H,S,P
 274       N             -       2.771           1      1.759, 3.048                    1,1
149/150 M,R,L,S,H,K,E,G,T,V,I,Q,D,A,N
 275       L             -       1.564           1      0.940, 1.759                    2,1
149/150 T,Q,V,A,D,R,S,W,P,I,M,Y,K,L,E,F
 276       A      ALA276:F       0.158           4     -0.135, 0.340                    5,4
148/150 L,S,Y,G,X,E,I,V,T,D,A
 277       P      PRO277:F       0.855           2      0.340, 1.265                    4,1
149/150 A,N,T,Q,E,F,P,Y,R,K,H,C,L,S
 278       Y      TYR278:F       1.343           1      0.697, 1.759                    3,1
150/150 Q,T,A,N,D,K,H,S,Y,R,P,F,G,E
 279       D      ASP279:F       0.304           4     -0.036, 0.503                    5,3
150/150 M,Y,R,L,H,K,T,D,N
 280       A      ALA280:F      -0.697           7     -0.887,-0.601                    8,7
150/150 Y,M,L,S,E,F,G,T,I,V,A
 281       C      CYS281:F      -0.059           5     -0.312, 0.076                    6,5
149/150 M,Y,L,S,C,W,F,P,T,I,V,A,N,D
 282       W      TRP282:F       0.539           3      0.076, 0.940                    5,2
144/150 W,F,Y,R,C,H,A,V
 283       N      ASN283:F      -0.545           7     -0.722,-0.392                    7,6
143/150 G,P,S,K,R,N,I,T
 284       A      ALA284:F      -0.119           5     -0.392, 0.076                    6,5
141/150 G,P,E,H,S,D,A,N,V,Q,I
 285       C      CYS285:F      -0.133           5     -0.392, 0.076                    6,5
143/150 S,C,H,L,K,M,Y,R,G,F,E,Q,T,D,N
 286       R      ARG286:F       1.581           1      0.940, 1.759                    2,1
139/150 M,L,C,K,E,F,I,R,S,H,W,G,T,V,Q,D,N,A
 287       G      GLY287:F      -0.211           6     -0.535,-0.036                    7,5
137/150 I,K,T,R,G,F,A
 288       D      ASP288:F      -0.548           7     -0.779,-0.392                    8,6
138/150 S,K,G,E,Q,T,D,A,N
 289       R      ARG289:F       0.227           4     -0.135, 0.503                    5,3
141/150 M,R,L,S,K,E,G,T,I,V,N,A
 290       W      TRP290:F       1.007           2      0.503, 1.265                    3,1
143/150 G,W,E,S,C,K,R,D,A,N,V,Q,I,T
 291       E      GLU291:F       0.356           4     -0.036, 0.503                    5,3
142/150 N,P,A,D,G,E,R
 292       D      ASP292:F       0.918           2      0.503, 1.265                    3,1
145/150 Y,M,R,K,S,C,P,G,T,I,V,A,N,D
 293       L             -       0.802           2      0.340, 0.940                    4,2
145/150 D,N,V,I,Q,T,G,F,E,S,C,L,Y
 294       S             -       0.126           5     -0.135, 0.340                    5,4
146/150 F,X,E,C,L,K,Y,I,P,H,S,R,D,A,N,Q,T
 295       R             -       1.209           1      0.697, 1.759                    3,1
149/150 E,G,M,R,K,H,S,N,D,T,Q,I
 296       S             -       0.096           5     -0.228, 0.340                    6,4
150/150 D,N,A,T,G,E,H,S,L,K,R
 297       Q             -       2.612           1      1.265, 3.048                    1,1
150/150 T,V,I,Q,A,N,R,M,S,L,K,E,G,P
 298       V             -      -0.432           6     -0.663,-0.312                    7,6
150/150 M,L,I,V
 299       R             -      -0.677           7     -0.887,-0.535                    8,7
150/150 V,T,N,K,S,H,R,E
 300       C             -      -1.249           9     -1.377,-1.178                    9,9
150/150 C,V
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 301       Y             -      -0.718           7     -0.939,-0.601                    8,7
150/150 L,H,Y,F
 302       V             -      -0.607           7     -0.779,-0.465                    8,7
150/150 S,C,L,G,T,I,V,A
 303       H             -      -0.263           6     -0.535,-0.135                    7,5
150/150 F,Y,I,C,L,H
 304       I             -      -0.218           6     -0.465,-0.036                    7,5
150/150 L,V,I,M,T,E
 305       M             -       0.084           5     -0.228, 0.198                    6,4
150/150 G,P,L,S,Y,M,D,A,I,V,Q,T
 306       K             -       1.529           1      0.940, 1.759                    2,1
147/150 N,D,T,Q,E,P,G,K,S
 307       E             -       1.204           1      0.697, 1.265                    3,1
150/150 E,G,S,H,K,D,N,A,T,Q
 308       G             -      -0.075           5     -0.392, 0.076                    6,5
150/150 Q,V,D,A,N,C,S,K,E,G
 309       L             -       1.202           1      0.697, 1.759                    3,1
150/150 M,Y,H,L,P,F,T,I,V,A
 310       C             -      -0.862           8     -1.037,-0.722                    8,7
150/150 C,I,L,A,F,G
 311       S             -       1.228           1      0.697, 1.759                    3,1
150/150 V,I,T,C,S,L,Y,M,F
 312       R             -      -1.184           9     -1.321,-1.131                    9,9
149/150 R,K,S,X,N
 313       V             -      -0.460           7     -0.663,-0.312                    7,6
150/150 A,T,I,L,V
 314       S             -      -1.162           9     -1.272,-1.085                    9,9
150/150 N,G,K,S
 315       T             -      -0.864           8     -1.037,-0.779                    8,8
150/150 T,S,H,N
 316       L             -       0.131           5     -0.228, 0.340                    6,4
150/150 M,V,I,L
 317       G             -       0.272           4     -0.036, 0.503                    5,3
150/150 A,N,V,Q,T,G,P,F,L,S,Y
 318       L             -       0.299           4     -0.036, 0.503                    5,3
150/150 S,H,L,M,G,E,Q,T,A,N,D
 319       Y             -      -1.258           9     -1.377,-1.225                    9,9
150/150 F,Y
 320       M             -      -0.134           5     -0.392, 0.076                    6,5
150/150 V,I,N,A,M,H,C,S
 321       E             -      -0.564           7     -0.779,-0.465                    8,7
150/150 D,A,E,F,R,C,L,S
 322       A             -      -0.583           7     -0.779,-0.465                    8,7
150/150 M,I,L,S,V,A
 323       N             -      -1.361           9     -1.414,-1.377                    9,9
150/150 N
 324       R             -      -0.763           8     -0.939,-0.663                    8,7
150/150 F,A,K,S,R,T
 325       Q             -      -0.088           5     -0.392, 0.076                    6,5
150/150 I,V,Q,N,M,R,Y,S,L,K,E
 326       V             -      -0.445           6     -0.663,-0.312                    7,6
148/150 M,V,L,I,A
 327       P             -       1.219           1      0.697, 1.759                    3,1
148/150 F,P,H,C,S,L,K,R,N,A,Q,V,I,T
 328       K             -      -0.222           6     -0.465,-0.036                    7,5
148/150 Q,D,A,R,S,H,K,E
 329       L             -       1.045           2      0.503, 1.265                    3,1
146/150 A,Q,V,I,F,P,W,E,L,S,H,K,R,M
 330       L             -       1.068           1      0.503, 1.265                    3,1
146/150 V,I,N,A,D,M,R,Y,K,C,S,L,W,F,P
 331       S             -       1.474           1      0.940, 1.759                    2,1
104/150 E,P,G,M,K,H,C,L,S,A,N,D,T,I,Q
 332       A             -       3.008           1      1.759, 3.048                    1,1
100/150 D,N,A,T,I,Q,V,E,G,R,H,C,L,S,K
 333       L             -       0.789           2      0.340, 0.940                    4,2
99/150  N,D,V,I,T,F,G,E,L,M
 334       C             -       1.565           1      0.940, 1.759                    2,1
94/150  I,E,F,M,Y,C,L,K,D,N,A,T,V,G,R,H,S
 335       P             -       2.479           1      1.265, 3.048                    1,1
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96/150  Q,I,D,A,N,C,H,S,L,K,R,G,P,E
 336       E              -       0.671           3      0.198, 0.940                    4,2
141/150 P,F,G,E,K,L,R,Y,N,D,Q,V,I
 337       E              -       0.755           3      0.340, 0.940                    4,2
143/150 K,S,L,M,Y,P,F,E,V,Q,I,T,D
 338       P              -       2.925           1      1.759, 3.048                    1,1
147/150 E,P,F,M,L,H,S,K,D,A,N,T,V,I,Q
 339       P              -       2.851           1      1.759, 3.048                    1,1
147/150 F,M,C,L,K,I,G,P,R,H,S,D,N,A,T,Q,V
 340       V              -       0.689           3      0.340, 0.940                    4,2
147/150 V,I,T,D,S,L,K,P,F
 341       H              -      -0.538           7     -0.722,-0.392                    7,6
147/150 P,Y,S,L,H,D,N,A,T,I
 342       S      SER342:F       0.974           2      0.503, 1.265                    3,1
147/150 C,S,M,R,P,G,E,V,Q,T,A,N
 343       S      SER343:F       0.367           4      0.076, 0.503                    5,3
144/150 N,A,T,W,E,G,M,R,C,S,L,K
 344       A      ALA344:F      -0.410           6     -0.601,-0.312                    7,6
144/150 T,V,I,A,N,D,C,S,L
 345       Q      GLN345:F       1.159           1      0.697, 1.265                    3,1
145/150 R,S,H,A,N,D,T,Q,V,E,F,Y,M,K,L,I
 346       I      ILE346:F       0.359           4     -0.036, 0.503                    5,3
145/150 K,H,L,S,E,F,G,T,V,I,A
 347       V      VAL347:F       1.307           1      0.697, 1.759                    3,1
143/150 D,N,A,V,Q,T,G,P,H,S,R,I,F,E,L,K,M
 348       S      SER348:F       0.740           3      0.340, 0.940                    4,2
148/150 T,V,Q,D,A,N,R,Y,S,K,E,G,P
 349       K      LYS349:F       0.010           5     -0.312, 0.198                    6,4
148/150 R,H,L,C,S,K,N,T,Q
 350       H      HIS350:F       0.351           4     -0.036, 0.503                    5,3
146/150 Q,V,T,A,N,D,K,L,S,C,H,Y,F,P,G
 351       L      LEU351:F       0.305           4     -0.036, 0.503                    5,3
147/150 M,K,L,S,F,P,T,Q,I,V,N
 352       V      VAL352:F      -0.237           6     -0.465,-0.135                    7,5
140/150 D,G,E,L,I,V,M
 353       G      GLY353:F      -0.772           8     -0.988,-0.663                    8,7
140/150 R,K,S,E,D,G
 354       V      VAL354:F       1.505           1      0.940, 1.759                    2,1
148/150 S,H,L,K,E,G,P,F,T,V,Q,D,A,N
 355       D      ASP355:F      -0.559           7     -0.779,-0.465                    8,7
148/150 T,D,N,R,S,L,E,G
 356       S      SER356:F      -0.483           7     -0.722,-0.312                    7,6
148/150 T,V,S,C
 357       L      LEU357:F       0.514           3      0.198, 0.697                    4,3
148/150 V,I,Q,A,M,R,Y,S,L,C,F
 358       I      ILE358:F      -0.706           7     -0.887,-0.601                    8,7
148/150 M,I,L,V
 359       G      GLY359:F      -0.749           7     -0.939,-0.601                    8,7
148/150 W,G,D,A
 360       P      PRO360:F       0.607           3      0.198, 0.940                    4,2
148/150 G,P,E,S,H,Y,D,A,N,T
 361       E      GLU361:F       1.926           1      1.265, 1.759                    1,1
148/150 R,H,S,G,T,V,Q,D,A,N,M,Y,L,K,E,F
 362       T      THR362:F      -0.063           5     -0.312, 0.076                    6,5
148/150 G,A,T,S,C,V
 363       Q      GLN363:F       1.057           2      0.503, 1.265                    3,1
148/150 E,F,R,K,S,H,L,N,T,I,V,Q
 364       I      ILE364:F       0.678           3      0.340, 0.940                    4,2
148/150 L,V,C,I
 365       G      GLY365:F       0.048           5     -0.228, 0.198                    6,4
148/150 T,D,N,A,C,H,S,M,G,E
 366       E      GLU366:F      -0.289           6     -0.535,-0.135                    7,5
148/150 E,G,K,S,A,N,D,Q
 367       K      LYS367:F      -0.647           7     -0.834,-0.535                    8,7
148/150 R,Q,K,E,N
 368       S      SER368:F      -0.429           6     -0.663,-0.312                    7,6
148/150 A,V,C,S,I,T
 369       S      SER369:F      -1.078           9     -1.178,-1.037                    9,8
148/150 G,A,F,T,S
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 370       I      ILE370:F      -0.410          6     -0.601,-0.312                  7,6
148/150 Y,L,V,I,F
 371       K      LYS371:F      -0.897          8     -1.085,-0.779                  9,8
148/150 Q,I,T,E,K,S,M,R
 372       R      ARG372:F       0.677          3      0.340, 0.940                  4,2
148/150 E,G,F,Y,R,H,C,S,K,N,A,T,Q,V
 373       S      SER373:F      -1.118          9     -1.225,-1.037                  9,8
148/150 A,T,C,S,I
 374       V      VAL374:F       0.113          5     -0.135, 0.340                  5,4
148/150 N,V,I,T,S,H,L,M,Y
 375       I      ILE375:F      -0.712          7     -0.887,-0.601                  8,7
147/150 I,L,V
 376       G      GLY376:F      -1.267          9     -1.377,-1.225                  9,9
147/150 N,G
 377       S      SER377:F       0.731          3      0.340, 0.940                  4,2
146/150 I,M,Y,L,K,X,E,T,V,Q,N,A,R,H,S,P
 378       S      SER378:F      -0.089          5     -0.312, 0.076                  6,5
147/150 F,G,K,H,S,M,R,Y,A,N,D,Q,V,T
 379       C      CYS379:F      -0.164          6     -0.465,-0.036                  7,5
147/150 T,S,V,C,I,A
 380       L      LEU380:F       2.085          1      1.265, 3.048                  1,1
147/150 I,F,E,L,C,K,M,D,N,A,Q,V,T,H,S,R
 381       I      ILE381:F      -0.383          6     -0.601,-0.228                  7,6
147/150 F,V,L,I,T
 382       K      LYS382:F       0.572          3      0.198, 0.697                  4,3
147/150 D,A,N,Q,E,G,Y,R,S,L,C,K
 383       D      ASP383:F      -0.176          6     -0.465,-0.036                  7,5
147/150 P,G,E,K,S,N,D,Q,T
 384       R      ARG384:F      -0.136          5     -0.392, 0.076                  6,5
147/150 N,L,H,K,R,G,F,W
 385       V      VAL385:F      -0.788          8     -0.939,-0.663                  8,7
147/150 A,T,S,V,C,L
 386       T      THR386:F      -0.715          7     -0.887,-0.601                  8,7
147/150 N,M,R,T,K,S,Q
 387       I      ILE387:F      -0.347          6     -0.535,-0.228                  7,6
147/150 T,I,L,V
 388       T      THR388:F       0.432          4      0.076, 0.697                  5,3
147/150 A,N,I,V,T,F,L,S,M
 389       N      ASN389:F      -0.534          7     -0.722,-0.392                  7,6
147/150 S,K,M,Y,R,G,Q,D,N
 390       C      CYS390:F      -0.695          7     -0.887,-0.601                  8,7
147/150 F,V,S,C
 391       L      LEU391:F      -0.470          7     -0.663,-0.312                  7,6
147/150 T,I,V,L
 392       L      LEU392:F      -0.524          7     -0.722,-0.392                  7,6
147/150 L,V,I,G
 393       M      MET393:F      -1.175          9     -1.272,-1.131                  9,9
147/150 L,V,M,T
 394       N      ASN394:F      -0.393          6     -0.601,-0.228                  7,6
147/150 S,H,L,E,G,Q,D,N,A
 395       S      SER395:F      -0.178          6     -0.392,-0.036                  6,5
147/150 E,G,F,Y,R,C,H,S,D,N,T
 396       V      VAL396:F      -1.106          9     -1.225,-1.037                  9,8
147/150 W,A,T,C,V,I
 397       T      THR397:F      -0.110          5     -0.392, 0.076                  6,5
147/150 E,K,S,H,L,R,N,A,V,I,T
 398       V      VAL398:F      -0.759          8     -0.939,-0.663                  8,7
147/150 I,L,V
 399       E      GLU399:F       0.547          3      0.198, 0.697                  4,3
146/150 E,G,R,M,S,L,C,K,D,N,A,Q
 400       E      GLU400:F      -0.431          6     -0.663,-0.312                  7,6
146/150 N,D,E,K,S,Q,Y
 401       G      GLY401:F      -0.460          7     -0.722,-0.312                  7,6
146/150 G,N,E,S,C,K,R
 402       S      SER402:F      -0.178          6     -0.465,-0.036                  7,5
142/150 T,V,Q,S,C,G
 403       N      ASN403:F       0.492          3      0.198, 0.697                  4,3
141/150 H,C,S,D,A,N,T,Q,I,V
 404       I      ILE404:F      -0.633          7     -0.834,-0.535                  8,7
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140/150 H,V,L,I
 405 Q GLN405:F 0.317 4 -0.036, 0.503 5,3
141/150 N,D,T,I,Q,V,E,R,K,S,H
 406 G GLY406:F -0.494 7 -0.722,-0.312 7,6
141/150 D,G,N,C,S,R
 407 S SER407:F -0.782 8 -0.939,-0.663 8,7
140/150 T,S,Q,C
 408 V VAL408:F -0.712 7 -0.887,-0.601 8,7
140/150 C,V,L,I
 409 I ILE409:F -0.296 6 -0.535,-0.135 7,5
140/150 Q,L,V,I
 410 C CYS410:F -0.855 8 -1.037,-0.722 8,7
140/150 S,C,H,M,G
 411 N ASN411:F 0.247 4 -0.036, 0.503 5,3
140/150 G,P,E,H,S,K,R,D,N,A,Q,T
 412 N ASN412:F 0.528 3 0.198, 0.697 4,3
140/150 K,H,C,S,R,F,G,E,Q,N,D
 413 A ALA413:F -0.535 7 -0.722,-0.392 7,6
140/150 P,A,T,C,V,S
 414 V VAL414:F 0.636 3 0.198, 0.940 4,2
140/150 I,V,T,F,E,W,L,S,H,R,Y
 415 I ILE415:F -0.535 7 -0.722,-0.392 7,6
140/150 L,V,I,M
 416 E GLU416:F 0.759 2 0.340, 0.940 4,2
140/150 A,N,Q,G,P,E,H,C,S,K,R
 417 K LYS417:F 0.127 5 -0.228, 0.340 6,4
140/150 E,P,R,K,H,L,S,A,N,D,T,V,Q
 418 G GLY418:F -0.062 5 -0.392, 0.076 6,5
140/150 R,K,S,Q,N,A,G
 419 A ALA419:F -0.259 6 -0.535,-0.135 7,5
140/150 T,V,C,I,S,A
 420 D ASP420:F -0.463 7 -0.663,-0.312 7,6
140/150 H,S,R,E,Q,T,D,N
 421 I ILE421:F -0.211 6 -0.465,-0.036 7,5
140/150 M,L,I,V
 422 K LYS422:F -0.836 8 -0.988,-0.722 8,7
140/150 E,Q,I,K,T,R
 423 D ASP423:F -0.692 7 -0.887,-0.601 8,7
140/150 Y,D,N,A
 424 C CYS424:F -1.024 8 -1.178,-0.939 9,8
139/150 C,S
 425 L LEU425:F -0.450 6 -0.663,-0.312 7,6
139/150 M,V,Q,I,L,F
 426 I ILE426:F -0.823 8 -0.988,-0.722 8,7
139/150 V,L,I
 427 G GLY427:F -1.052 8 -1.225,-0.939 9,8
139/150 T,S,A,G
 428 S SER428:F 0.374 4 0.076, 0.503 5,3
137/150 K,S,L,H,C,R,Y,P,G,E,Q,N,A,D
 429 G GLY429:F 1.045 2 0.503, 1.265 3,1
137/150 G,C,H,S,K,R,D,N,A,Q,T
 430 Q GLN430:F -0.537 7 -0.722,-0.392 7,6
139/150 Q,I,F,E,H,L,K,Y
 431 R ARG431:F 1.375 1 0.940, 1.759 2,1
139/150 R,K,S,L,H,C,E,W,T,V,Q,I,A,N,D
 432 I ILE432:F -0.184 6 -0.465,-0.036 7,5
139/150 F,I,V,L
 433 E GLU433:F 1.652 1 0.940, 1.759 2,1
138/150 D,A,N,I,Q,V,T,P,E,S,H,K,M
 434 A ALA434:F 0.506 3 0.076, 0.697 5,3
136/150 D,A,V,T,G,P,E,S,K
 435 K LYS435:F 0.676 3 0.198, 0.940 4,2
132/150 A,N,D,G,E,K,L,S,M,R
 436 A ALA436:F 0.856 2 0.340, 1.265 4,1
133/150 T,V,A,R,C,S,E,G
 437 K LYS437:F -0.415 6 -0.663,-0.228 7,6
129/150 Q,V,T,D,N,S,K,R,E
 438 R ARG438:F 0.169 4 -0.135, 0.340 5,4
125/150 E,F,Y,R,K,C,L,S,H

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|---|---|---|---|---|---|---|
| 439 | V | VAL439:F | 0.388 | 4 | 0.076, 0.503 | 5,3 |
| 123/150 | V,I,T,A,N,H,S,L,K,M,Y,R | | | | | |
| 440 | N | ASN440:F | -0.591 | 7 | -0.779,-0.465 | 8,7 |
| 122/150 | G,S,H,K,R,Y,D,N,Q,V | | | | | |
| 441 | E | GLU441:F | -0.773 | 8 | -0.939,-0.663 | 8,7 |
| 121/150 | Q,S,V,E,D,N | | | | | |
| 442 | V | VAL442:F | -0.459 | 7 | -0.663,-0.312 | 7,6 |
| 120/150 | N,A,T,I,V,F,M,L,S | | | | | |
| 443 | I | ILE443:F | -0.831 | 8 | -0.988,-0.722 | 8,7 |
| 120/150 | L,V,I,F | | | | | |
| 444 | V | VAL444:F | -0.535 | 7 | -0.722,-0.392 | 7,6 |
| 119/150 | M,L,S,G,T,V,I,Q,A | | | | | |
| 445 | G | - | -0.057 | 5 | -0.392, 0.198 | 6,4 |
| 117/150 | E,G,K,S,A,N,D,T,I,Q | | | | | |
| 446 | N | - | 1.837 | 1 | 0.940, 1.759 | 2,1 |
| 116/150 | S,L,R,M,P,G,E,V,I,T,A,N,D | | | | | |
| 447 | D | - | -0.290 | 6 | -0.535,-0.135 | 7,5 |
| 115/150 | E,A,N,D,Q,S | | | | | |
| 448 | Q | - | 0.000 | 5 | -0.312, 0.198 | 6,4 |
| 113/150 | G,Y,M,R,S,H,L,K,A,V,Q | | | | | |
| 449 | L | - | -0.833 | 8 | -1.037,-0.722 | 8,7 |
| 112/150 | F,L,M | | | | | |
| 450 | M | - | -0.943 | 8 | -1.085,-0.834 | 9,8 |
| 111/150 | M,L,I | | | | | |
| 451 | E | - | -1.089 | 9 | -1.225,-0.988 | 9,8 |
| 112/150 | D,E,Q,T | | | | | |
| 452 | I | - | -1.241 | 9 | -1.377,-1.178 | 9,9 |
| 107/150 | L,I,V | | | | | |

*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.