Phyre2

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Description	P0AGC7
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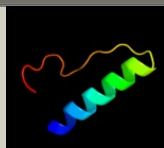
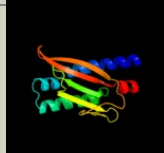
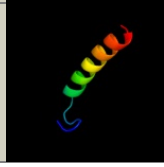
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2asxa1	Alignment		97.8	3	**Fold:**HAMP domain-like **Superfamily:**HAMP domain-like **Family:**HAMP domain
2	d3by8a1	Alignment		97.3	16	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
3	d1p0za_	Alignment		97.2	18	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
4	c3by9A_	Alignment		54.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the v. cholerae histidine kinase dctb2 sensor domain
5	c3pjvD_	Alignment		48.0	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd periplasmic domain
6	d2p7ja2	Alignment		43.0	15	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Ykul C-terminal domain-like
7	c3b42B_	Alignment		31.7	18	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**methyl-accepting chemotaxis protein, putative; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0935
8	c3b47A_	Alignment		28.8	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0582
9	c3e4pB_	Alignment		25.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**c4-dicarboxylate transport sensor protein dctb; **PDBTitle:** crystal structure of malonate occupied dctb
10	c2qhkA_	Alignment		25.5	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of methyl-accepting chemotaxis protein from vibrio2 parahaemolyticus rimd 2210633
11	c2kseA_	Alignment		20.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein qsec; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor qsec, center for structures of3 membrane proteins (csmp) target 4311c

12	d1u6ka1	Alignment		19.7	6	**Fold:**F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) **Superfamily:**F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) **Family:**F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD)
13	c3lnrA_	Alignment		18.0	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**aerotaxis transducer aer2; **PDBTitle:** crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
14	c3fosA_	Alignment		17.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of two-component sensor histidine kinase domain from2 bacillus subtilis subsp. subtilis str. 168
15	c3hd7A_	Alignment		10.5	10	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
16	d1sxja1	Alignment		6.3	0	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain

17	c1hp9A_	Alignment		5.7	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**kappa-hefutoxin 1; **PDBTitle:** kappa-hefutoxins: a novel class of potassium channel toxins2 from scorpion venom