Phyre^2

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Description	P64451
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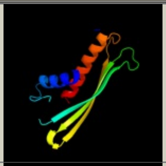
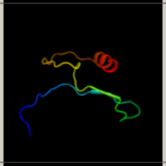
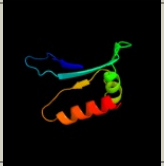
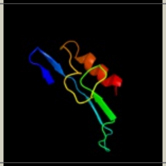
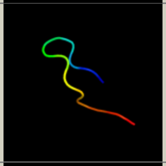
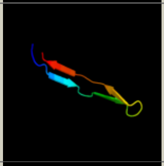
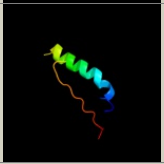
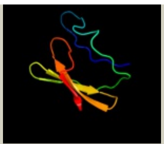
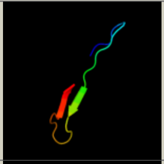
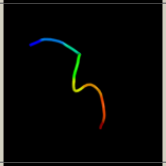
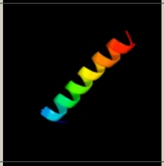
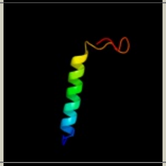
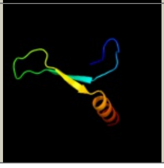
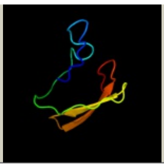
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2iqia1	Alignment		61.4	9	**Fold:**Anticodon-binding domain-like **Superfamily:**XCC0632-like **Family:**XCC0632-like
2	c2dzjA_	Alignment		49.8	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**synaptic glycoprotein sc2; **PDBTitle:** 2dzj/solution structure of the n-terminal ubiquitin-like2 domain in human synaptic glycoprotein sc2
3	d1pn2a1	Alignment		38.4	4	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
4	c3ly8A_	Alignment		20.7	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**transcriptional activator cadc; **PDBTitle:** crystal structure of mutant d471e of the periplasmic domain of cadc
5	d2hqsa2	Alignment		15.3	11	**Fold:**Anticodon-binding domain-like **Superfamily:**TolB, N-terminal domain **Family:**TolB, N-terminal domain
6	c3ov5A_	Alignment		14.9	29	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** atomic structure of the xanthomonas citri virb7 globular domain.
7	c3nqyA_	Alignment		12.4	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed complex of vibriolysin mcp-022 with a single point mutation e346a
8	d2axto1	Alignment		9.8	7	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**PsbO-like
9	d2bi0a1	Alignment		9.2	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
10	c2l4wA_	Alignment		8.5	27	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of the xanthomonas virb7
11	d1mwwa_	Alignment		8.0	6	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**Hypothetical protein HI1388.1
						PDB header:oxidoreductase

12	c1yiqA_	Alignment		7.9	19	**Chain:** A: **PDB Molecule:**quinohemoprotein alcohol dehydrogenase; **PDBTitle:** molecular cloning and structural analysis of2 quinohemoprotein alcohol dehydrogenase adhiig from3 pseudomonas putida hk5. compariison to the other4 quinohemoprotein alcohol dehydrogenase adhiib found in the5 same microorganism.
13	d2cy9a1	Alignment		6.6	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
14	c1ztoA_	Alignment		5.6	50	**PDB header:**potassium channel **Chain:** A: **PDB Molecule:**potassium channel protein rck4; **PDBTitle:** inactivation gate of potassium channel rck4, nmr, 82 structures
15	d1pu1a_	Alignment		5.5	19	**Fold:**Hypothetical protein MTH677 **Superfamily:**Hypothetical protein MTH677 **Family:**Hypothetical protein MTH677
16	d3e9va1	Alignment		5.4	9	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
17	c2rcel_	Alignment		5.4	10	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**protease degs; **PDBTitle:** dfp modified degs delta pdz

18	c1kb0A_	Alignment		5.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein alcohol dehydrogenase; **PDBTitle:** crystal structure of quinohemoprotein alcohol dehydrogenase from2 comamonas testosteroni