Phyre^2

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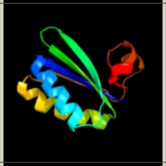
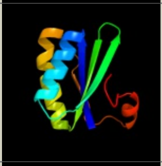
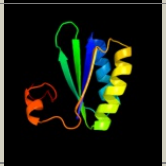
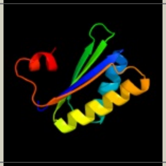
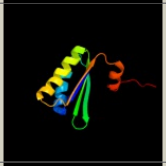
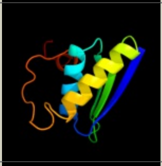
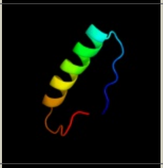
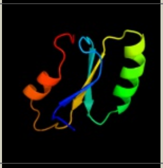
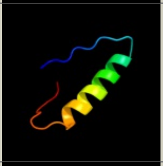
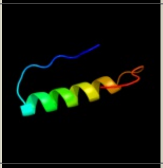
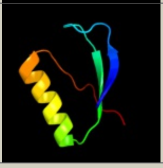
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3i6pF_	Alignment		100.0	100	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**ethanolamine utilization protein eutm; **PDBTitle:** ethanolamine utilization microcompartment shell subunit, eutm
2	c3ngkA_	Alignment		100.0	66	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**propanediol utilization protein pdua; **PDBTitle:** pdua from salmonella enterica typhimurium
3	d2a10a1	Alignment		100.0	38	**Fold:**Ferredoxin-like **Superfamily:**CcmK-like **Family:**CcmK-like
4	d2ewha1	Alignment		100.0	53	**Fold:**Ferredoxin-like **Superfamily:**CcmK-like **Family:**CcmK-like
5	d2a1ba1	Alignment		100.0	54	**Fold:**Ferredoxin-like **Superfamily:**CcmK-like **Family:**CcmK-like
6	c3n79A_	Alignment		100.0	38	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**pdut; **PDBTitle:** pdut c38s mutant from salmonella enterica typhimurium
7	c3nwgA_	Alignment		100.0	27	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**microcompartments protein; **PDBTitle:** the crystal structure of a microcomparments protein from2 desulfitobacterium hafniense dcb
8	c3io0A_	Alignment		99.8	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**etub protein; **PDBTitle:** crystal structure of etub from clostridium kluyveri
9	c3i82A_	Alignment		99.6	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ethanolamine utilization protein eutl; **PDBTitle:** ethanolamine utilization microcompartment shell subunit, eutl closed2 form
10	c3cgiD_	Alignment		99.0	24	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**propanediol utilization protein pduu; **PDBTitle:** crystal structure of the pduu shell protein from the pdu2 microcompartment
11	c3ia0c_	Alignment		99.0	25	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**ethanolamine utilization protein euts; **PDBTitle:** ethanolamine utilization microcompartment shell subunit,2 euts-g39v mutant

12	c3f56F_	Alignment		97.1	21	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**csos1d; **PDBTitle:** the structure of a previously undetected carboxysome shell2 protein: csos1d from prochlorococcus marinus med4
13	d2c42a3	Alignment		46.6	16	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
14	d1m5sa2	Alignment		15.7	27	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
15	c2c3yA_	Alignment		14.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
16	d1ftra2	Alignment		12.5	24	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
17	d2qrra1	Alignment		10.7	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
18	d1m5ha2	Alignment		10.3	30	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
19	d2ctma1	Alignment		10.2	10	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
20	d3dhxa1	Alignment		9.1	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
21	c1m5sC_	Alignment	not modelled	7.7	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**formylmethanofuran--tetrahydromethanopterin **PDBTitle:** formylmethanofuran:tetrahydromethanopterin2 fromyltransferase from methanosarcina barkeri
22	c2fhjD_	Alignment	not modelled	6.7	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**formylmethanofuran--tetrahydromethanopterin **PDBTitle:** crystal structure of formylmethanofuran:2 tetrahydromethanopterin formyltransferase in complex with3 its coenzymes
23	d2qn6b1	Alignment	not modelled	6.6	16	**Fold:**Ferredoxin-like **Superfamily:**eIF-2-alpha, C-terminal domain **Family:**eIF-2-alpha, C-terminal domain
24	d1qd1a1	Alignment	not modelled	6.3	16	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. **Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.
25	c1qd1A_	Alignment	not modelled	6.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**formiminotransferase-cyclodeaminase; **PDBTitle:** the crystal structure of the formiminotransferase domain of2 formiminotransferase-cyclodeaminase.
26	d1j9ba_	Alignment	not modelled	6.0	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
27	d1xhja_	Alignment	not modelled	6.0	26	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
						Fold: Chromosomal protein MC1

28	d1t23a_	Alignment	not modelled	5.9	50	**Superfamily:**Chromosomal protein MC1 **Family:**Chromosomal protein MC1
29	c2c1lA_	Alignment	not modelled	5.6	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease; **PDBTitle:** structure of the bfii restriction endonuclease
30	c1m5hF_	Alignment	not modelled	5.4	30	**PDB header:**transferase **Chain:** F: **PDB Molecule:**formylmethanofuran--tetrahydromethanopterin **PDBTitle:** formylmethanofuran:tetrahydromethanopterin2 formyltransferase from archaeoglobus fulgidus