Phyre2

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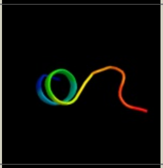
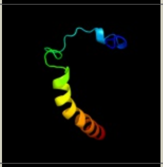
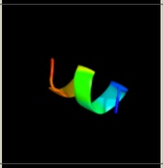
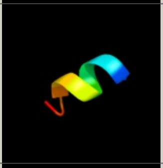
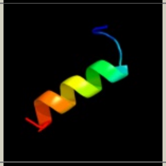
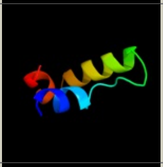
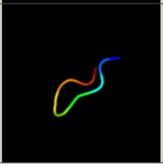
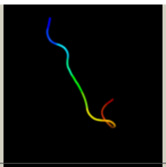
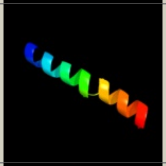
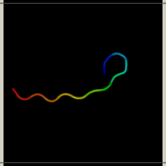
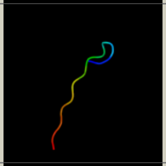
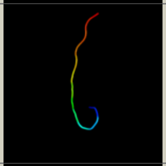
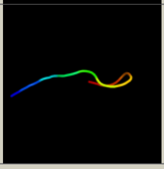
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y69Y_	Alignment		31.2	13	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**cytochrome c oxidase subunit 7c; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
2	c3pcsB_	Alignment		23.4	25	**PDB header:**protein transport/transferase **Chain:** B: **PDB Molecule:**espg; **PDBTitle:** structure of espg-pak2 autoinhibitory ialpha3 helix complex
3	c2k21A_	Alignment		20.2	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
4	d1rzhh2	Alignment		19.3	40	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
5	d1l9bh2	Alignment		18.4	40	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
6	d2rcrh2	Alignment		16.3	40	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
7	d3buxb2	Alignment		16.3	17	**Fold:**N-cbl like **Superfamily:**N-terminal domain of cbl (N-cbl) **Family:**N-terminal domain of cbl (N-cbl)
8	c4a18P_	Alignment		16.0	44	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**rpl38; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
9	c3b4sA_	Alignment		15.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein luxt; **PDBTitle:** crystal structure of a luxt domain from vibrio2 parahaemolyticus rimd 2210633
10	c3iz5n_	Alignment		13.3	44	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
11	c3izcn_	Alignment		12.4	22	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein rpl14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome

12	d1vcca_	Alignment		12.2	36	**Fold:**DNA topoisomerase I domain **Superfamily:**DNA topoisomerase I domain **Family:**Vaccinia DNA topoisomerase I, 9 kDa N-terminal fragment
13	c1q90L_	Alignment		10.4	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**cytochrome b6f complex subunit petl; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
14	d1q90l_	Alignment		10.4	30	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
15	d1v54l_	Alignment		9.5	13	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa) **Family:**Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa)
16	c2gw4C_	Alignment		8.7	38	**PDB header:**luminescent protein **Chain:** C: **PDB Molecule:**kaede; **PDBTitle:** crystal structure of stony coral fluorescent protein kaede, red form
17	c3lf4A_	Alignment		8.5	38	**PDB header:**fluorescent protein **Chain:** A: **PDB Molecule:**fluorescent timer precursor blue102; **PDBTitle:** crystal structure of fluorescent timer precursor blue102
18	d1r0va3	Alignment		7.1	43	**Fold:**MutS N-terminal domain-like **Superfamily:**tRNA-intron endonuclease N-terminal domain-like **Family:**tRNA-intron endonuclease N-terminal domain-like
19	c2a56A_	Alignment		7.0	38	**PDB header:**luminescent protein **Chain:** A: **PDB Molecule:**gfp-like non-fluorescent chromoprotein fp595 chain 1; **PDBTitle:** fluorescent protein asfp595, a143s, on-state, 5min irradiation
20	c3hzpA_	Alignment		6.8	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of ntf2-like protein of unknown function mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 natl2a at 1.40 a resolution
21	c1xrxD_	Alignment	not modelled	6.7	21	**PDB header:**replication inhibitor **Chain:** D: **PDB Molecule:**seqa protein; **PDBTitle:** crystal structure of a dna-binding protein
22	d1xrxa1	Alignment	not modelled	6.7	21	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**SeqA N-terminal domain-like
23	c3op0B_	Alignment	not modelled	6.4	22	**PDB header:**signaling protein/signaling protein regu **Chain:** B: **PDB Molecule:**signal transduction protein cbl-c; **PDBTitle:** crystal structure of cbl-c (cbl-3) tkb domain in complex with egfr2 py1069 peptide
24	c2cblA_	Alignment	not modelled	6.3	17	**PDB header:**complex (proto-oncogene/peptide) **Chain:** A: **PDB Molecule:**proto-oncogene cbl; **PDBTitle:** n-terminal domain of cbl in complex with its binding site2 on zap-70
25	c3bunB_	Alignment	not modelled	6.3	17	**PDB header:**ligase/signaling protein **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase cbl; **PDBTitle:** crystal structure of c-cbl-tkb domain complexed with its2 binding motif in sprouty4
26	c2yvxD_	Alignment	not modelled	5.9	7	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
27	d1ckva_	Alignment	not modelled	5.8	10	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein
28	c2npiB_	Alignment	not modelled	5.6	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protein clp1; **PDBTitle:** clp1-atp-pcf11 complex
						PDB header:protein binding **Chain:** B: **PDB Molecule:**pexrd2 family secreted rxlr effector

29	c3zrgB_	Alignment	not modelled	5.6	18	peptide, putative; **PDBTitle:** crystal structure of rxlr effector pexrd2 from phytophthora infestans
30	c3l32B_	Alignment	not modelled	5.6	44	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**phosphoprotein; **PDBTitle:** structure of the dimerisation domain of the rabies virus2 phosphoprotein
31	d1dvoa_	Alignment	not modelled	5.6	22	**Fold:**FinO-like **Superfamily:**FinO-like **Family:**FinO-like
32	c1fbvA_	Alignment	not modelled	5.6	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**signal transduction protein cbl; **PDBTitle:** structure of a cbl-ubch7 complex: ring domain function in2 ubiquitin-protein ligases
33	c2jo1A_	Alignment	not modelled	5.4	30	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
34	c3t2dA_	Alignment	not modelled	5.4	6	**PDB header:**lyase, hydrolase **Chain:** A: **PDB Molecule:**fructose-1,6-bisphosphate aldolase/phosphatase; **PDBTitle:** fructose-1,6-bisphosphate aldolase/phosphatase from thermoproteus2 neutrophilus, fbp-bound form
35	d2csba5	Alignment	not modelled	5.4	44	**Fold:**Topoisomerase V catalytic domain-like **Superfamily:**Topoisomerase V catalytic domain-like **Family:**Topoisomerase V catalytic domain-like
36	c3sjaG_	Alignment	not modelled	5.3	30	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**golgi to er traffic protein 1; **PDBTitle:** crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
37	c2jp3A_	Alignment	not modelled	5.1	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles