Phyre2

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Description	Q96A56
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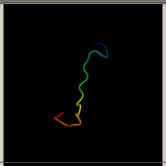
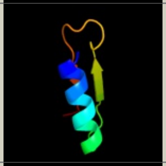
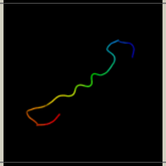
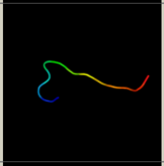
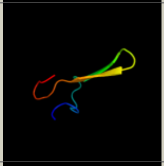
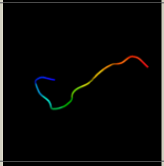
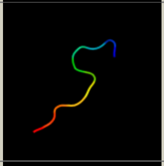
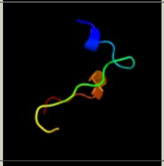
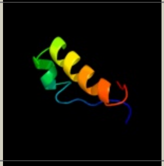
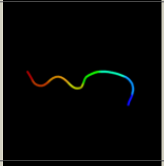
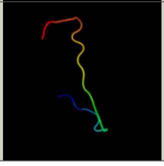
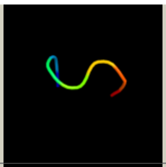
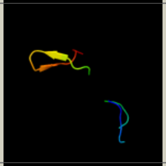
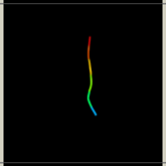
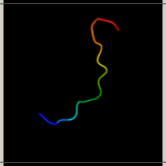
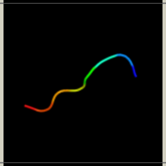
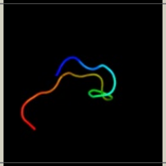
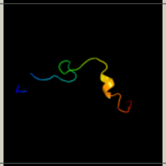
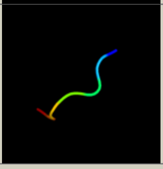
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3npeA_	Alignment		32.9	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**9-cis-epoxycarotenoid dioxygenase 1, chloroplastic; **PDBTitle:** structure of vp14 in complex with oxygen
2	d2id1a1	Alignment		27.8	22	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
3	c2biwC_	Alignment		26.7	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**apocarotenoid-cleaving oxygenase; **PDBTitle:** crystal structure of apocarotenoid cleavage oxygenase from2 synechocystis, native enzyme
4	c3upsA_	Alignment		26.4	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**iojap-like protein; **PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis
5	c3hxrA_	Alignment		26.3	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**nucleoporin nup120; **PDBTitle:** nucleoporin nup120 from s.cerevisiae (aa 1-757)
6	d2o5aa1	Alignment		26.2	38	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
7	c3fsnA_	Alignment		24.5	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**retinal pigment epithelium-specific 65 kda protein; **PDBTitle:** crystal structure of rpe65 at 2.14 angstrom resolution
8	d1oa8a_	Alignment		18.0	35	**Fold:**AXH domain **Superfamily:**AXH domain **Family:**AXH domain
9	c2yheD_	Alignment		16.7	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sec-alkyl sulfatase; **PDBTitle:** structure determination of the stereoselective inverting2 sec-alkylsulfatase pisa1 from pseudomonas sp.
10	d2cfua2	Alignment		13.6	63	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
11	d1k12a_	Alignment		13.4	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Fucose binding lectin

12	c3s63B_	Alignment		13.3	57	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**saposin-like protein; **PDBTitle:** saposin-like protein na-slp-1
13	c2i7fB_	Alignment		13.1	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin component of dioxygenase; **PDBTitle:** sphingomonas yanoikuyae b1 ferredoxin
14	d1p5dx4	Alignment		11.7	43	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
15	d1w66a1	Alignment		11.1	33	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
16	c2cfuA_	Alignment		10.9	63	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
17	c2jeuA_	Alignment		9.8	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein e2; **PDBTitle:** transcription activator structure reveals redox control of2 a replication initiation reaction
18	c3ce8A_	Alignment		9.7	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative pii-like nitrogen regulatory protein; **PDBTitle:** crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution
19	c3zv0D_	Alignment		9.2	29	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1p-cbf5p complex
20	c1sr4A_	Alignment		8.9	43	**PDB header:**toxin **Chain:** A: **PDB Molecule:**cytolethal distending toxin subunit a; **PDBTitle:** crystal structure of the haemophilus ducreyi cytolethal2 distending toxin
21	d1sr4a_	Alignment	not modelled	8.9	43	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like
22	d1aisb1	Alignment	not modelled	8.4	43	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
23	d3proc2	Alignment	not modelled	8.3	50	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
24	d1v5xa_	Alignment	not modelled	7.8	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
25	d1piia1	Alignment	not modelled	7.7	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
26	c2zpnB_	Alignment	not modelled	7.6	21	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy-related protein 8; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg8-2 atg19(412-415) complex
27	c2fugC_	Alignment	not modelled	7.3	44	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
28	d1d0qa_	Alignment	not modelled	7.2	50	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
29	d1ee8a2	Alignment	not modelled	7.0	25	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins

						Family:N-terminal domain of MutM-like DNA repair proteins
30	d1xzwa1	Alignment	not modelled	6.7	56	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Purple acid phosphatase, N-terminal domain **Family:**Purple acid phosphatase, N-terminal domain
31	d1usra_	Alignment	not modelled	6.7	29	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
32	c2c2xB_	Alignment	not modelled	6.3	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
33	c2eouA_	Alignment	not modelled	6.2	100	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 370-2 400) of human zinc finger protein 473
34	d1a4ia1	Alignment	not modelled	6.1	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
35	c3h7nD_	Alignment	not modelled	6.1	26	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**nucleoporin nup120; **PDBTitle:** structure of nup120
36	c2kqrA_	Alignment	not modelled	6.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the n-terminal domain (residues 1-111) of brugia2 malayi asparaginyl-trna synthetase
37	c3r8kB_	Alignment	not modelled	6.0	24	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul protein (hexagonal form)
38	c3cs5B_	Alignment	not modelled	6.0	57	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**phycobilisome degradation protein nbla; **PDBTitle:** nbla protein from synechococcus elongatus pcc 7942
39	d2gova1	Alignment	not modelled	5.9	12	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**SOUL heme-binding protein
40	c2gl1A_	Alignment	not modelled	5.8	83	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**pdf1; **PDBTitle:** nmr solution structure of vigna radiata defensin 2 (vrd2)
41	d2f2fa1	Alignment	not modelled	5.5	43	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like
42	d1sgva2	Alignment	not modelled	5.4	15	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
43	d1prtd_	Alignment	not modelled	5.4	40	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
44	d1oh1a_	Alignment	not modelled	5.4	22	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Staphostatin
45	c2qhsA_	Alignment	not modelled	5.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoyltransferase; **PDBTitle:** structural basis of octanoic acid recognition by lipoate-protein2 ligase b
46	c2qhvA_	Alignment	not modelled	5.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoyltransferase; **PDBTitle:** structural basis of octanoic acid recognition by lipoate-protein2 ligase b
47	d1v3ea_	Alignment	not modelled	5.3	29	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
48	d1nsja_	Alignment	not modelled	5.3	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
49	c3metB_	Alignment	not modelled	5.3	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**saga-associated factor 29 homolog; **PDBTitle:** crystal structure of sgf29 in complex with h3k4me2
50	d1k6ya1	Alignment	not modelled	5.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**N-terminal Zn binding domain of HIV integrase **Family:**N-terminal Zn binding domain of HIV integrase
51	d1ckaa_	Alignment	not modelled	5.1	9	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain