Phyre^2

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Description	Q8CFU8
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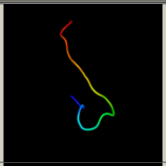
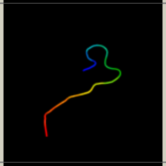
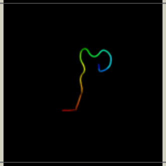
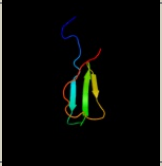
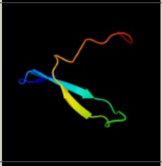
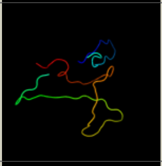
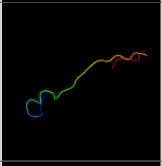
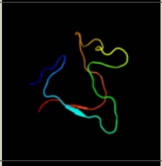
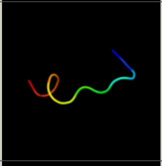
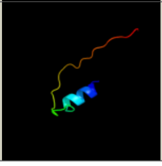
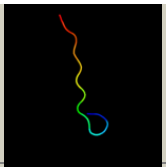
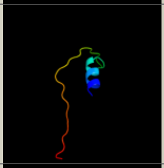
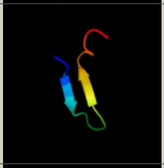
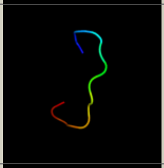
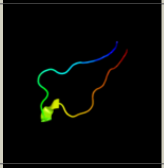
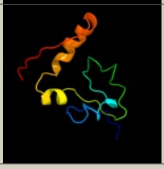
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2o5aa1	Alignment		43.7	47	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
2	c3upsA_	Alignment		42.7	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**iojap-like protein; **PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis
3	d2id1a1	Alignment		41.2	33	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
4	c2biwC_	Alignment		36.8	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**apocarotenoid-cleaving oxygenase; **PDBTitle:** crystal structure of apocarotenoid cleavage oxygenase from2 synechocystis, native enzyme
5	d1wfwa_	Alignment		32.8	18	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
6	c3qsqA_	Alignment		31.4	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid polyprotein; **PDBTitle:** crystal structure of the projection domain of the human astrovirus2 capsid protein
7	c3npeA_	Alignment		29.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**9-cis-epoxycarotenoid dioxygenase 1, chloroplastic; **PDBTitle:** structure of vp14 in complex with oxygen
8	c3fsnA_	Alignment		24.2	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**retinal pigment epithelium-specific 65 kda protein; **PDBTitle:** crystal structure of rpe65 at 2.14 angstrom resolution
9	c3m1hB_	Alignment		21.5	21	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**lysine specific cysteine protease; **PDBTitle:** crystal structure analysis of the k3 cleaved adhesin domain of lys-2 gingipain (kgp) from porphyromonas gingivalis w83
10	d1zcza1	Alignment		18.1	25	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
11	c3r8kB_	Alignment		17.3	12	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul protein (hexagonal form)

12	c3hxrA_	Alignment		16.4	23	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**nucleoporin nup120; **PDBTitle:** nucleoporin nup120 from s.cerevisiae (aa 1-757)
13	d2gova1	Alignment		14.8	3	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**SOUL heme-binding protein
14	d2cfua2	Alignment		14.3	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
15	c3fkaD_	Alignment		13.9	18	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized ntf-2 like protein; **PDBTitle:** crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
16	d1q1oa_	Alignment		13.5	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
17	c3alzB_	Alignment		13.5	23	**PDB header:**viral protein/membrane protein **Chain:** B: **PDB Molecule:**cdw150; **PDBTitle:** crystal structure of the measles virus hemagglutinin bound to its2 cellular receptor slam (form i)
18	c3dukD_	Alignment		13.4	12	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
19	c4eoyB_	Alignment		13.3	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**microtubule-associated protein 1 light chain 3; **PDBTitle:** plasmodium falciparum atg8 in complex with plasmodium falciparum atg32 peptide
20	c3kubA_	Alignment		13.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semi-aldehyde dehydrogenase complexed2 with glycerol and phosphate of mycobacterium tuberculosis h37rv
21	c2zpnB_	Alignment	not modelled	11.4	23	**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
22	c2yheD_	Alignment	not modelled	11.3	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sec-alkyl sulfatase; **PDBTitle:** structure determination of the stereoselective inverting2 sec-alkylsulfatase pisa1 from pseudomonas sp.
23	c2cfuA_	Alignment	not modelled	11.2	16	**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.
24	d1pqsa_	Alignment	not modelled	10.3	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
25	d1sgva2	Alignment	not modelled	10.3	27	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
26	c3n0kA_	Alignment	not modelled	10.0	19	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**serine protease inhibitor 1; **PDBTitle:** proteinase inhibitor from coprinopsis cinerea
27	c1xk5A_	Alignment	not modelled	9.7	30	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of the m3g-cap-binding domain of2 snurportin1 in complex with a m3gpppg-cap dinucleotide
28	c1zczA_	Alignment	not modelled	9.2	25	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase /

						imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
29	c1plpA_	Alignment	not modelled	9.1	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**phospholamban; **PDBTitle:** solution structure of the cytoplasmic domain of2 phospholamban
30	d3d32a1	Alignment	not modelled	8.9	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**GABARAP-like
31	d1oa8a_	Alignment	not modelled	8.9	26	**Fold:**AXH domain **Superfamily:**AXH domain **Family:**AXH domain
32	c3nrlB_	Alignment	not modelled	8.9	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rumgna_01417; **PDBTitle:** crystal structure of protein rumgna_01417 from ruminococcus gnavus,2 northeast structural genomics consortium target ugr76
33	c3s63B_	Alignment	not modelled	8.7	71	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**saposin-like protein; **PDBTitle:** saposin-like protein na-slp-1
34	c2gp4B_	Alignment	not modelled	8.5	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
35	d1p5dx4	Alignment	not modelled	8.2	29	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
36	c2istA_	Alignment	not modelled	8.2	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d; **PDBTitle:** crystal structure of rlud from e. coli
37	d2zjda1	Alignment	not modelled	8.1	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**GABARAP-like
38	d1k12a_	Alignment	not modelled	8.0	24	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Fucose binding lectin
39	c2gp4A_	Alignment	not modelled	7.6	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
40	c2qz9B_	Alignment	not modelled	7.4	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 ii from vibrio cholerae
41	c2i82D_	Alignment	not modelled	7.4	13	**PDB header:**lyase/rna **Chain:** D: **PDB Molecule:**ribosomal large subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure
42	c1qyuA_	Alignment	not modelled	7.3	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d; **PDBTitle:** structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud
43	d1eo6a_	Alignment	not modelled	6.3	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**GABARAP-like
44	c2gz3D_	Alignment	not modelled	6.3	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aspartate beta-semialdehyde dehydrogenase; **PDBTitle:** structure of aspartate semialdehyde dehydrogenase (asadh) from2 streptococcus pneumoniae complexed with nadp and aspartate-3 semialdehyde
45	c3vvwB_	Alignment	not modelled	6.2	16	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**microtubule-associated proteins 1a/1b light chain 3c; **PDBTitle:** ndp52 in complex with lc3c
46	d1wj6a_	Alignment	not modelled	6.0	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
47	c2kpmA_	Alignment	not modelled	5.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein from gene2 locus ne0665 of nitrosomonas europaea. northeast structural3 genomics target ner103a
48	c3am2A_	Alignment	not modelled	5.5	24	**PDB header:**toxin **Chain:** A: **PDB Molecule:**heat-labile enterotoxin b chain; **PDBTitle:** clostridium perfringens enterotoxin
49	c3mxuA_	Alignment	not modelled	5.3	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from bartonella2 henselae
50	d1ee8a2	Alignment	not modelled	5.2	32	**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
51	c2m65A_	Alignment	not modelled	5.2	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable dna dc->du-editing enzyme apobec-3a; **PDBTitle:** nmr structure of human restriction factor apobec3a
52	c3metB_	Alignment	not modelled	5.2	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**saga-associated factor 29 homolog; **PDBTitle:** crystal structure of sgf29 in complex with h3k4me2
53	d2gpia1	Alignment	not modelled	5.1	25	**Fold:**Shew3726-like **Superfamily:**Shew3726-like

						Family: Shew3726-like
54	c4esrB_	Alignment	not modelled	5.0	6	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**jouberin; **PDBTitle:** molecular and structural characterization of the sh3 domain of ahi-12 in regulation of cellular resistance of bcr-abl+ chronic myeloid3 leukemia cells to tyrosine kinase inhibitors