Phyre2

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Description	P60438
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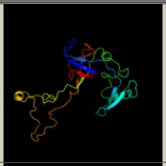
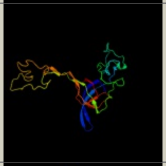
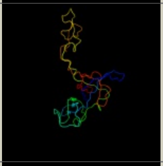
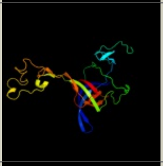
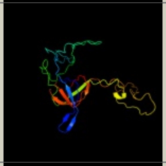
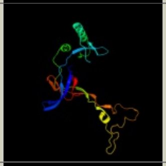
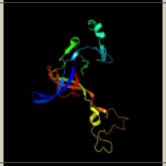
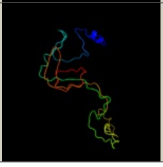
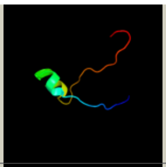
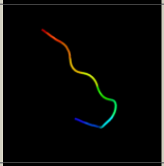
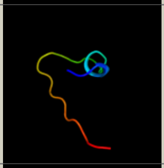
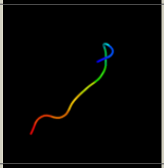
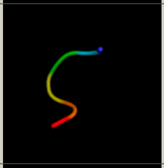
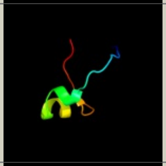
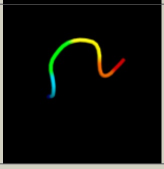
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gycb1	Alignment		100.0	100	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
2	d2zjrb1	Alignment		100.0	51	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
3	d2j01e1	Alignment		100.0	53	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
4	c2ftcC_	Alignment		100.0	31	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**mitochondrial 39s ribosomal protein l3; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
5	d1vqob1	Alignment		100.0	26	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
6	c3jywC_	Alignment		100.0	24	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**60s ribosomal protein l3; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
7	c2zkrb_	Alignment		100.0	23	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es4; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
8	c1s1iC_	Alignment		100.0	24	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**60s ribosomal protein l3; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
9	c3iz5C_	Alignment		100.0	23	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**60s ribosomal protein l3 (l3p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
10	c4a1aB_	Alignment		100.0	29	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein l3; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
11	c3bboF_	Alignment		100.0	46	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**ribosomal protein l3; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome

12	c1a8pA_	Alignment		29.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph\:ferredoxin oxidoreductase; **PDBTitle:** ferredoxin reductase from azotobacter vinelandii
13	d1qfja1	Alignment		23.6	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
14	c3iuwA_	Alignment		19.9	23	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**activating signal cointegrator; **PDBTitle:** crystal structure of activating signal cointegrator (np_814290.1) from2 enterococcus faecalis v583 at 1.58 a resolution
15	d1vqoq1	Alignment		19.2	44	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
16	d1fdra1	Alignment		18.8	10	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
17	c2bruC_	Alignment		17.2	33	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p) transhydrogenase subunit beta; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
18	d1a8pa1	Alignment		17.1	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
19	d1qcsa1	Alignment		16.3	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
20	d1d4oa_	Alignment		16.2	50	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
21	c2zkrq_	Alignment	not modelled	15.6	22	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 part ii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
22	d1pnoa_	Alignment	not modelled	15.4	50	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
23	c1pt9B_	Alignment	not modelled	15.0	50	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
24	c1v1cA_	Alignment	not modelled	14.6	10	**PDB header:**sh3-domain **Chain:** A: **PDB Molecule:**obscurin; **PDBTitle:** solution structure of the sh3 domain of obscurin
25	c1tvcA_	Alignment	not modelled	14.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase component c; **PDBTitle:** fad and nadh binding domain of methane monooxygenase2 reductase from methylococcus capsulatus (bath)
26	d2do3a1	Alignment	not modelled	14.2	25	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
27	c1qfjD_	Alignment	not modelled	13.8	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein (flavin reductase); **PDBTitle:** crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli
28	c1a3qA_	Alignment	not modelled	13.6	21	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (nuclear factor kappa-b p52); **PDBTitle:** human nf-kappa-b p52 bound to dna

29	d1vlra2	Alignment	not modelled	11.6	19	**Fold:**mRNA decapping enzyme DcpS N-terminal domain **Superfamily:**mRNA decapping enzyme DcpS N-terminal domain **Family:**mRNA decapping enzyme DcpS N-terminal domain
30	c2bgjB_	Alignment	not modelled	11.1	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp(h) reductase; **PDBTitle:** x-ray structure of the ferredoxin-nadp(h) reductase from2 rhodobacter capsulatus at 2.1 angstroms
31	d1ep3b1	Alignment	not modelled	10.9	13	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
32	c1s1iQ_	Alignment	not modelled	10.8	22	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l21-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
33	c2hdeA_	Alignment	not modelled	10.8	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone deacetylase complex subunit sap18; **PDBTitle:** solution structure of human sap18
34	d1uwfa1	Alignment	not modelled	10.2	18	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
35	c1khiA_	Alignment	not modelled	9.8	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hex1; **PDBTitle:** crystal structure of hex1
36	c3izcU_	Alignment	not modelled	9.5	22	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein rpl21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
37	c1le5E_	Alignment	not modelled	9.5	30	**PDB header:**transcription/dna **Chain:** E: **PDB Molecule:**nuclear factor nf-kappa-b p65 subunit; **PDBTitle:** crystal structure of a nf-kb heterodimer bound to an ifnb-kb
38	d2i6va1	Alignment	not modelled	9.4	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
39	d2zjrr1	Alignment	not modelled	9.4	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
40	d1vqot1	Alignment	not modelled	9.4	25	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
41	c1vpzB_	Alignment	not modelled	9.4	36	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**carbon storage regulator homolog; **PDBTitle:** crystal structure of a putative carbon storage regulator protein2 (csra, pa0905) from pseudomonas aeruginosa at 2.05 a resolution
42	c1lq8H_	Alignment	not modelled	9.4	17	**PDB header:**blood clotting **Chain:** H: **PDB Molecule:**plasma serine protease inhibitor; **PDBTitle:** crystal structure of cleaved protein c inhibitor
43	c4a1aP_	Alignment	not modelled	9.2	22	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l21; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
44	c3iz5U_	Alignment	not modelled	8.9	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein l21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
45	c3iz5Y_	Alignment	not modelled	8.7	31	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**60s ribosomal protein l26 (l24p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
46	c4a1cS_	Alignment	not modelled	8.3	19	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rpl26; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
47	c1zeqX_	Alignment	not modelled	8.1	13	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
48	c1nfiC_	Alignment	not modelled	8.1	30	**PDB header:**complex (transcription reg/ank repeat) **Chain:** C: **PDB Molecule:**nf-kappa-b p65; **PDBTitle:** i-kappa-b-alpha/nf-kappa-b complex
49	c1zuyB_	Alignment	not modelled	8.0	6	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin-5 isoform; **PDBTitle:** high-resolution structure of yeast myo5 sh3 domain
50	c1qgyA_	Alignment	not modelled	7.7	0	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp+ reductase; **PDBTitle:** ferredoxin:nadp+ reductase mutant with lys 75 replaced by glu (k75e)
51	d1khia1	Alignment	not modelled	7.6	16	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
52	c2ok8D_	Alignment	not modelled	7.5	0	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp+ reductase from plasmodium falciparum
53	c2vl6C_	Alignment	not modelled	7.5	33	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** structural analysis of the sulfolobus solfataricus mcm2

						protein n-terminal domain
54	c2jppB_	Alignment	not modelled	7.4	29	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**translational repressor; **PDBTitle:** structural basis of rsma/csra rna recognition: structure of2 rsme bound to the shine-dalgarno sequence of hcna mrna
55	c3a98A_	Alignment	not modelled	7.3	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dedicator of cytokinesis protein 2; **PDBTitle:** crystal structure of the complex of the interacting regions of dock22 and elmo1
56	c1cqxB_	Alignment	not modelled	7.2	18	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**flavohemoprotein; **PDBTitle:** crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
57	d1ikna2	Alignment	not modelled	7.1	33	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**Rel/Dorsal transcription factors, DNA-binding domain
58	c3s88I_	Alignment	not modelled	7.1	63	**PDB header:**immune system/viral protein **Chain:** I: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** crystal structure of sudan ebolavirus glycoprotein (strain gulu) bound2 to 16f6
59	d1sm4a1	Alignment	not modelled	6.9	10	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
60	c3mxnB_	Alignment	not modelled	6.8	25	**PDB header:**replication **Chain:** B: **PDB Molecule:**recq-mediated genome instability protein 2; **PDBTitle:** crystal structure of the rmi core complex
61	c1gvhA_	Alignment	not modelled	6.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavohemoprotein; **PDBTitle:** the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unespected geometry of the3 distal heme pocket
62	c1ep3B_	Alignment	not modelled	6.7	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydroorotate dehydrogenase b (pyrk subunit); **PDBTitle:** crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions.
63	c3csyK_	Alignment	not modelled	6.5	63	**PDB header:**immune system/viral protein **Chain:** K: **PDB Molecule:**envelope glycoprotein gp1; **PDBTitle:** crystal structure of the trimeric prefusion ebola virus glycoprotein2 in complex with a neutralizing antibody from a human survivor
64	d1cqxa2	Alignment	not modelled	6.4	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
65	c2piaA_	Alignment	not modelled	6.4	20	**PDB header:**reductase **Chain:** A: **PDB Molecule:**phthalate dioxygenase reductase; **PDBTitle:** phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]
66	c1krhA_	Alignment	not modelled	6.2	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
67	d1nyka_	Alignment	not modelled	6.0	23	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
68	c1i4oC_	Alignment	not modelled	6.0	19	**PDB header:**apoptosis/hydrolase **Chain:** C: **PDB Molecule:**baculoviral iap repeat-containing protein 4; **PDBTitle:** crystal structure of the xiap/caspase-7 complex
69	d1yb2a1	Alignment	not modelled	6.0	6	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
70	c1yb2A_	Alignment	not modelled	6.0	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0852; **PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum.
71	d1uwva1	Alignment	not modelled	5.8	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
72	d1vpza_	Alignment	not modelled	5.8	36	**Fold:**CsrA-like **Superfamily:**CsrA-like **Family:**CsrA-like
73	d1fnda1	Alignment	not modelled	5.8	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
74	d2bmwa1	Alignment	not modelled	5.6	0	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
75	d1gvha2	Alignment	not modelled	5.6	10	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
76	d2cwza1	Alignment	not modelled	5.6	22	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**TTHA0967-like
77	d2e9xc2	Alignment	not modelled	5.5	28	**Fold:**GINS/PriA/YqbF domain **Superfamily:**PriA/YqbF domain **Family:**PSF3 N-terminal domain-like
78	c3cxjB_	Alignment	not modelled	5.5	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
79	d1lcka1	Alignment	not modelled	5.2	6	**Fold:**SH3-like barrel **Superfamily:**SH3-domain

						Family:SH3-domain
80	c1t3oA_	Alignment	not modelled	5.1	32	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**carbon storage regulator; **PDBTitle:** solution structure of csra, a bacterial carbon storage2 regulatory protein
81	d1kuta_	Alignment	not modelled	5.1	26	**Fold:**SAICAR synthase-like **Superfamily:**SAICAR synthase-like **Family:**SAICAR synthase
82	c2b5oA_	Alignment	not modelled	5.0	0	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp reductase
83	d1ra0a1	Alignment	not modelled	5.0	16	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Cytosine deaminase