Phyre^2

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Description	P0A7U3
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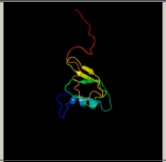
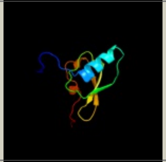
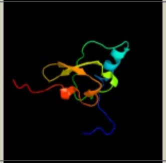
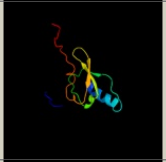
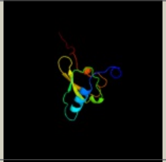
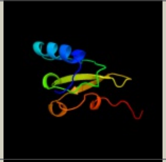
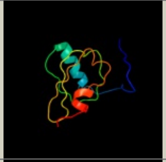
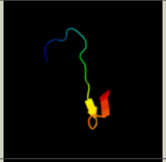
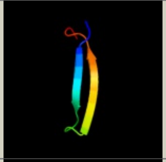
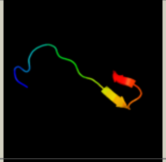
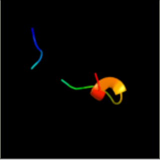
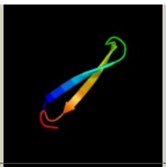
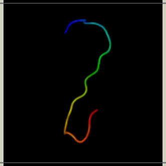
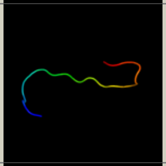
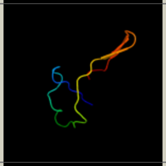
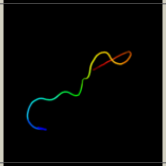
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bbnS_	Alignment		100.0	58	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**ribosomal protein s19; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
2	d2uubs1	Alignment		100.0	69	**Fold:**Ribosomal protein S19 **Superfamily:**Ribosomal protein S19 **Family:**Ribosomal protein S19
3	d2gy9s1	Alignment		100.0	100	**Fold:**Ribosomal protein S19 **Superfamily:**Ribosomal protein S19 **Family:**Ribosomal protein S19
4	c2zkqs_	Alignment		100.0	31	**PDB header:**ribosomal protein/rna **Chain:** S: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
5	c2xzmS_	Alignment		100.0	30	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rps15e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
6	c1s1hS_	Alignment		100.0	35	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**40s ribosomal protein s15; **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, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
7	c3izbR_	Alignment		100.0	32	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**40s ribosomal protein rps15 (s19p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
8	d1roca_	Alignment		18.4	30	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ASF1-like **Family:**ASF1-like
9	d1t3qa2	Alignment		14.8	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
10	c2idcA_	Alignment		12.5	30	**PDB header:**replication/chaperone **Chain:** A: **PDB Molecule:**anti-silencing protein 1 and histone h3 chimera; **PDBTitle:** structure of the histone h3-asf1 chaperone interaction
11	c3ezoA_	Alignment		11.9	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of acyl-carrier-protein s-2 malonyltransferase from burkholderia pseudomallei 1710b

12	d1vlba2	Alignment		11.2	43	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
13	d2i32a1	Alignment		10.5	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ASF1-like **Family:**ASF1-like
14	c2i32A_	Alignment		10.5	25	**PDB header:**replication chaperone **Chain:** A: **PDB Molecule:**anti-silencing factor 1 paralog a; **PDBTitle:** structure of a human asf1a-hira complex and insights into2 specificity of histone chaperone complex assembly
15	d1li1c1	Alignment		9.3	14	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Noncollagenous (NC1) domain of collagen IV
16	d1mlaa1	Alignment		7.9	60	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**FabD-like
17	d2cu9a1	Alignment		7.8	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ASF1-like **Family:**ASF1-like
18	c2cuyA_	Alignment		7.5	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-[acyl carrier protein] transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from thermus thermophilus hb8
19	d1quba5	Alignment		7.4	16	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
20	c3pntD_	Alignment		7.2	43	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**immunity factor for spn; **PDBTitle:** crystal structure of the streptococcus pyogenes nad+ glycohydrolase2 spn in complex with ifs, the immunity factor for spn
21	d1nm2a1	Alignment	not modelled	7.1	40	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**FabD-like
22	c3qatB_	Alignment	not modelled	7.1	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
23	d1c1za5	Alignment	not modelled	7.0	16	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
24	d2b5ea2	Alignment	not modelled	6.7	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
25	c1t60R_	Alignment	not modelled	6.6	15	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**type iv collagen; **PDBTitle:** crystal structure of type iv collagen nc1 domain from2 bovine lens capsule
26	c2jfkD_	Alignment	not modelled	6.6	70	**PDB header:**transferase **Chain:** D: **PDB Molecule:**fatty acid synthase; **PDBTitle:** structure of the mat domain of human fas with malonyl-coa
27	c3im8A_	Alignment	not modelled	6.4	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl acyl carrier protein transacylase; **PDBTitle:** crystal structure of mcat from streptococcus pneumoniae
28	d1t61a1	Alignment	not modelled	6.2	19	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Noncollagenous (NC1) domain of collagen IV

29	d1ex4a1	Alignment	not modelled	6.1	83	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase
30	d1x3ha2	Alignment	not modelled	5.9	14	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
31	c3im9A_	Alignment	not modelled	5.7	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of mcat from staphylococcus aureus
32	d1c6vx_	Alignment	not modelled	5.7	67	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase
33	c1c6vX_	Alignment	not modelled	5.7	67	**PDB header:**dna binding protein **Chain:** X: **PDB Molecule:**protein (siu89134); **PDBTitle:** siv integrase (catalytic domain + dna biding domain2 comprising residues 50-293) mutant with phe 185 replaced3 by his (f185h)
34	c2c2nA_	Alignment	not modelled	5.7	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** structure of human mitochondrial malonyltransferase
35	c3hhdC_	Alignment	not modelled	5.5	70	**PDB header:**transferase, hydrolase **Chain:** C: **PDB Molecule:**fatty acid synthase; **PDBTitle:** structure of the human fatty acid synthase ks-mat didomain2 as a framework for inhibitor design.
36	c1sqwA_	Alignment	not modelled	5.5	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**saccharomyces cerevisiae nip7p homolog; **PDBTitle:** crystal structure of kd93, a novel protein expressed in the2 human pro
37	c3g87A_	Alignment	not modelled	5.4	60	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from burkholderia pseudomallei using dried seaweed as nucleant or3 protease
38	c2cdh9_	Alignment	not modelled	5.4	40	**PDB header:**transferase **Chain:** 9: **PDB Molecule:**acetyl transferase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
39	d1d6za4	Alignment	not modelled	5.2	9	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Copper amine oxidase, domain N **Family:**Copper amine oxidase, domain N
40	c2qj3B_	Alignment	not modelled	5.2	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** mycobacterium tuberculosis fabd