Phyre^2

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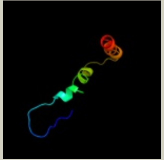
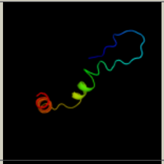
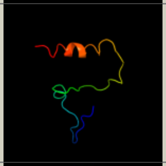
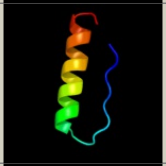
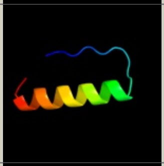
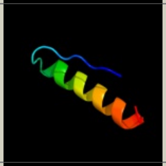
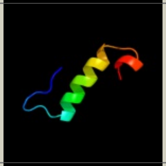
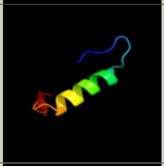
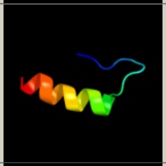
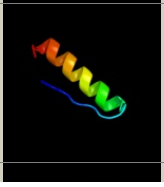
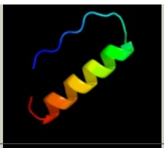
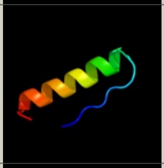
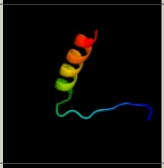
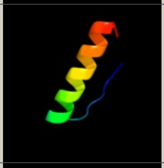
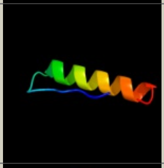
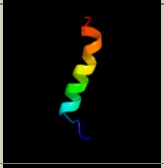
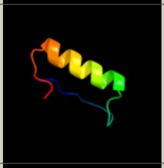
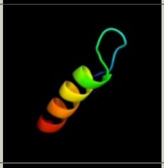
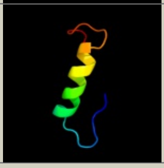
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z4mU_	Alignment		99.8	100	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein s21; **PDBTitle:** crystal structure of the bacterial ribosome from escherichia2 coli in complex with paromomycin and ribosome recycling3 factor (rrf). this file contains the 30s subunit of the4 second 70s ribosome, with paromomycin bound. the entire5 crystal structure contains two 70s ribosomes and is6 described in remark 400.
2	c3bbnU_	Alignment		99.8	40	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**ribosomal protein s21; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
3	c3fihU_	Alignment		99.8	100	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein s21; **PDBTitle:** ternary complex-bound e.coli 70s ribosome. this entry2 consists of the 30s subunit, trnas and the ternary complex.
4	d1edza2	Alignment		39.7	7	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
5	d1a4ia2	Alignment		33.8	11	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
6	d1b0aa2	Alignment		28.5	21	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
7	d1bvua2	Alignment		24.0	20	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
8	d2eiaa1	Alignment		23.1	19	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
9	d1eoqa_	Alignment		22.2	20	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
10	d1qrjb1	Alignment		18.0	18	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
11	c3nglA_	Alignment		15.6	25	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum

12	c1edzA_	Alignment		15.2	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate dehydrogenase; **PDBTitle:** structure of the nad-dependent 5,10-2 methylenetetrahydrofolate dehydrogenase from saccharomyces3 cerevisiae
13	c1b0aA_	Alignment		14.8	21	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
14	d1q9ua_	Alignment		13.9	19	**Fold:**TBP-like **Superfamily:**TT1751-like **Family:**TT1751-like
15	c1a4iB_	Alignment		13.8	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
16	c2c2xB_	Alignment		13.5	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
17	c3aogA_	Alignment		13.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
18	c3fiqA_	Alignment		13.1	6	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**odorant-binding protein 1f; **PDBTitle:** odorant binding protein obp1
19	d1d1da1	Alignment		13.1	20	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
20	c2k1cA_	Alignment		13.1	27	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**capsid protein p24; **PDBTitle:** nmr structure of the c-terminal domain of hiv-1 capsid in complex with2 peptide inhibitor
21	c1bajA_	Alignment	not modelled	12.7	27	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**gag polyprotein; **PDBTitle:** hiv-1 capsid protein c-terminal fragment plus gag p2 domain
22	c4a5oB_	Alignment	not modelled	12.2	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
23	d1e5pa_	Alignment	not modelled	11.9	10	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
24	c3p2oA_	Alignment	not modelled	11.4	25	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
25	d1p94a_	Alignment	not modelled	10.8	33	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
26	c3couA_	Alignment	not modelled	10.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 16; **PDBTitle:** crystal structure of human nudix motif 16 (nudt16)
27	d1gtma2	Alignment	not modelled	10.4	12	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
28	c3kvhA_	Alignment	not modelled	10.3	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein syndesmos; **PDBTitle:** crystal structure of human protein syndesmos (nudt16-like protein)
29	c3p2oB	Alignment	not modelled	9.7	25	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold;

29	[illegible]	Alignment	not modelled	[illegible]	[illegible]	**PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
30	c3l07B_	Alignment	not modelled	9.6	14	**PDB header:**oxidoreductase,hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
31	c2k87A_	Alignment	not modelled	9.6	14	**PDB header:**viral protein, rna binding protein **Chain:** A: **PDB Molecule:**non-structural protein 3 of replicase polyprotein 1a; **PDBTitle:** nmr structure of a putative rna binding protein (sars1) from sars2 coronavirus
32	c3gwyA_	Alignment	not modelled	9.4	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ctp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
33	c2jobA_	Alignment	not modelled	9.2	14	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
34	c4a26B_	Alignment	not modelled	8.7	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
35	d1a8oa_	Alignment	not modelled	8.5	27	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
36	d1dzka_	Alignment	not modelled	8.3	21	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
37	c2x8qA_	Alignment	not modelled	8.1	20	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein p27; **PDBTitle:** cryo-em 3d model of the icosahedral particle2 composed of rous sarcoma virus capsid protein pentamers
38	d1euza2	Alignment	not modelled	7.7	20	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
39	d1bj7a_	Alignment	not modelled	7.3	16	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
40	c1qrjB_	Alignment	not modelled	7.1	16	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**htlv-i capsid protein; **PDBTitle:** solution structure of htlv-i capsid protein
41	c2yfqA_	Alignment	not modelled	7.1	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
42	c3kwlA_	Alignment	not modelled	6.5	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from helicobacter pylori
43	c2r73C_	Alignment	not modelled	6.1	16	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**trichosurin; **PDBTitle:** crystal structure of the possum milk whey lipocalin2 trichosurin at ph 8.2
44	c1d1dA_	Alignment	not modelled	5.9	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (capsid protein); **PDBTitle:** nmr solution structure of the capsid protein from rous2 sarcoma virus
45	d1igna2	Alignment	not modelled	5.9	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**DNA-binding domain of rap1
46	c2fb1A_	Alignment	not modelled	5.9	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron
47	c3stgA_	Alignment	not modelled	5.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
48	c1bvuF_	Alignment	not modelled	5.2	19	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (glutamate dehydrogenase); **PDBTitle:** glutamate dehydrogenase from thermococcus litoralis