Phyre^2

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Description	Q9JMS7
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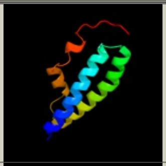
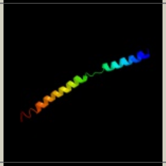
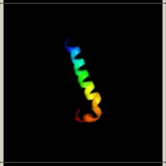
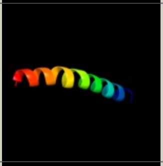
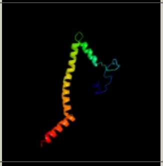
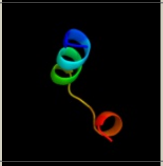
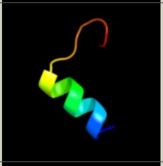
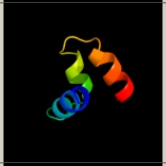
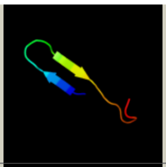
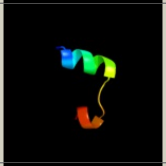
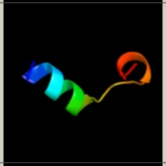
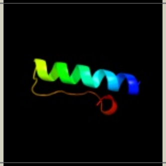
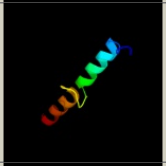
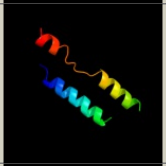
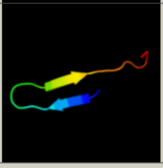
Unique Job ID	55c067a56976a548

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fseB_	Alignment		63.8	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**two-domain protein containing dj-1/thij/pfpi-like and **PDBTitle:** crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
2	c3ipdB_	Alignment		30.4	18	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
3	d2oc5a1	Alignment		25.6	10	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**PMT1231-like
4	c3lt7D_	Alignment		20.6	34	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**adhesin yada; **PDBTitle:** a transition from strong right-handed to canonical left-handed2 supercoiling in a conserved coiled coil segment of trimeric3 autotransporter adhesins - the m3 mutant structure
5	c2w8aC_	Alignment		19.7	14	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
6	d1v8ga1	Alignment		18.0	16	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
7	d1o17a1	Alignment		17.6	32	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
8	d1uoua1	Alignment		16.6	16	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
9	d1khda1	Alignment		14.1	17	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
10	c3izck_	Alignment		14.0	27	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein rpl16 (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
11	c2y0fD_	Alignment		13.9	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27

12	d2d0oa3	Alignment		13.0	35	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
13	d1brwa1	Alignment		12.8	16	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
14	d2tpta1	Alignment		11.8	16	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
15	d2qam31	Alignment		11.7	36	**Fold:**L35p-like **Superfamily:**L35p-like **Family:**Ribosomal protein L35p
16	d1muga_	Alignment		11.6	16	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Mug-like
17	d1rzsa_	Alignment		10.5	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
18	c2voyG_	Alignment		10.3	28	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
19	c2q9qF_	Alignment		10.1	17	**PDB header:**replication **Chain:** F: **PDB Molecule:**gins complex subunit 4; **PDBTitle:** the crystal structure of full length human gins complex
20	d1nbwa3	Alignment		9.8	37	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
21	c3kdpG_	Alignment	not modelled	9.3	33	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
22	c3kdpH_	Alignment	not modelled	9.3	33	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
23	c4a19Q_	Alignment	not modelled	8.4	13	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l36; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
24	c3mk7F_	Alignment	not modelled	8.4	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
25	d1nb9a_	Alignment	not modelled	8.3	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**ATP-dependent riboflavin kinase-like
26	c3iz5k_	Alignment	not modelled	7.7	22	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein l13a (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
27	d2elca1	Alignment	not modelled	7.5	17	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
28	d1t3ua_	Alignment	not modelled	7.5	15	**Fold:**Cell division protein ZapA-like **Superfamily:**Cell division protein ZapA-like

						Family: Cell division protein ZapA-like
29	c2f8sA_	Alignment	not modelled	7.3	15	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**argonaute protein; **PDBTitle:** crystal structure of aa-ago with externally-bound sirna
30	d2guka1	Alignment	not modelled	7.0	25	**Fold:**PG1857-like **Superfamily:**PG1857-like **Family:**PG1857-like
31	c2zdjA_	Alignment	not modelled	6.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttma177; **PDBTitle:** crystal structure of ttma177, a hypothetical protein from2 thermus thermophilus phage tma
32	c1nbwA_	Alignment	not modelled	6.6	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerol dehydratase reactivase alpha subunit; **PDBTitle:** glycerol dehydratase reactivase
33	c1khdD_	Alignment	not modelled	6.6	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.93 resolution (current name, pectobacterium carotovorum)
34	c3p45F_	Alignment	not modelled	6.5	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**caspase-6; **PDBTitle:** crystal structure of apo-caspase-6 at physiological ph
35	d1xmec1	Alignment	not modelled	6.3	24	**Fold:**Single transmembrane helix **Superfamily:**Bacterial ba3 type cytochrome c oxidase subunit IIa **Family:**Bacterial ba3 type cytochrome c oxidase subunit IIa
36	d1tzyc_	Alignment	not modelled	6.3	15	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
37	c3iuoA_	Alignment	not modelled	6.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase recq; **PDBTitle:** the crystal structure of the c-terminal domain of the atp-dependent2 dna helicase recq from porphyromonas gingivalis to 1.6a
38	c3mmyF_	Alignment	not modelled	6.2	31	**PDB header:**nuclear protein **Chain:** F: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1
39	d1f3va_	Alignment	not modelled	6.1	30	**Fold:**Ferredoxin-like **Superfamily:**TRADD, N-terminal domain **Family:**TRADD, N-terminal domain
40	c1unvA_	Alignment	not modelled	6.0	30	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
41	c1unvB_	Alignment	not modelled	5.9	29	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
42	c2ke4A_	Alignment	not modelled	5.7	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
43	c3p56B_	Alignment	not modelled	5.3	17	**PDB header:**hydrolase/replication **Chain:** B: **PDB Molecule:**ribonuclease h2 subunit b; **PDBTitle:** the human rnase h2 complex defines key interaction2 interfaces relevant to enzyme function and human disease
44	c1v8gB_	Alignment	not modelled	5.3	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
45	d2v7qi1	Alignment	not modelled	5.2	57	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Epsilon subunit of mitochondrial F1F0-ATP synthase **Family:**Epsilon subunit of mitochondrial F1F0-ATP synthase