Phyre²

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Description	P0ABC3
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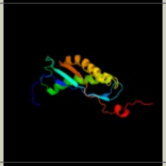
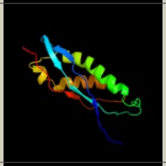
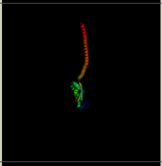
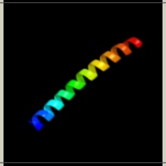
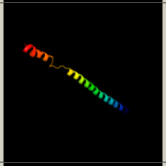
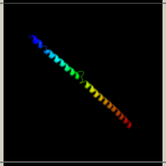
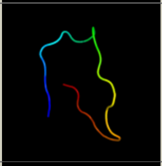
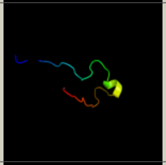
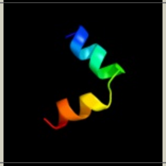
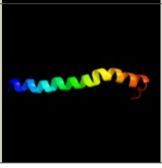
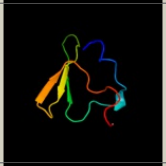
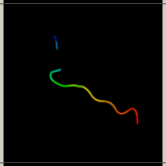
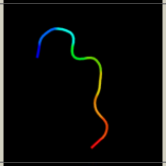
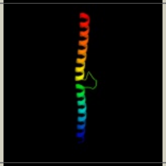
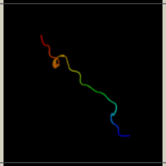
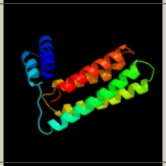
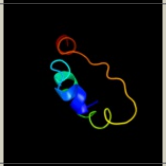
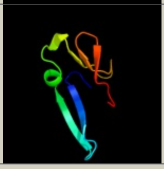
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bk6C_	Alignment		99.9	25	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ph stomatin; **PDBTitle:** crystal structure of a core domain of stomatin from2 pyrococcus horikoshii
2	d1wina_	Alignment		99.6	21	**Fold:**EF-Ts domain-like **Superfamily:**Band 7/SPFH domain **Family:**Band 7/SPFH domain
3	c2rpbA_	Alignment		99.5	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical membrane protein; **PDBTitle:** the solution structure of membrane protein
4	c2zv4O_	Alignment		98.8	15	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
5	c2kk7A_	Alignment		38.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**v-type atp synthase subunit e; **PDBTitle:** nmr solution structure of the n terminal domain of subunit e2 (e1-52) of a1ao atp synthase from methanocaldococcus3 jannaschii
6	c3k5bB_	Alignment		33.7	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**v-type atp synthase, subunit (vapc-therm); **PDBTitle:** crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
7	c3k5bE_	Alignment		16.7	13	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**v-type atp synthase subunit e; **PDBTitle:** crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
8	c3sbtB_	Alignment		16.3	42	**PDB header:**splicing **Chain:** B: **PDB Molecule:**a1 cistron-splicing factor aar2; **PDBTitle:** crystal structure of a aar2-prp8 complex
9	d1js8a2	Alignment		15.0	18	**Fold:**C-terminal domain of mollusc hemocyanin **Superfamily:**C-terminal domain of mollusc hemocyanin **Family:**C-terminal domain of mollusc hemocyanin
10	c2diiA_	Alignment		13.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex p62 **PDBTitle:** solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
11	c2ke4A_	Alignment		12.2	20	**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

12	d2diia1	Alignment		10.9	14	**Fold:**BSD domain-like **Superfamily:**BSD domain-like **Family:**BSD domain
13	c3l4hA_	Alignment		9.8	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hecw1; **PDBTitle:** helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
14	d1lnla2	Alignment		9.6	8	**Fold:**C-terminal domain of mollusc hemocyanin **Superfamily:**C-terminal domain of mollusc hemocyanin **Family:**C-terminal domain of mollusc hemocyanin
15	c1wd6B_	Alignment		9.4	44	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydhr; **PDBTitle:** crystal structure of jw1657 from escherichia coli
16	d1l2pa_	Alignment		8.8	20	**Fold:**Single transmembrane helix **Superfamily:**F1F0 ATP synthase subunit B, membrane domain **Family:**F1F0 ATP synthase subunit B, membrane domain
17	d1jeya1	Alignment		7.7	26	**Fold:**SPOC domain-like **Superfamily:**SPOC domain-like **Family:**Ku70 subunit middle domain
18	c1y4cA_	Alignment		7.2	11	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
19	d1nyoa_	Alignment		6.8	16	**Fold:**FAS1 domain **Superfamily:**FAS1 domain **Family:**FAS1 domain
20	d2ix0a3	Alignment		6.7	6	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
21	c1jeqA_	Alignment	not modelled	6.6	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ku70; **PDBTitle:** crystal structure of the ku heterodimer
22	c2l9uA_	Alignment	not modelled	6.6	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3; **PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain
23	d1o70a2	Alignment	not modelled	6.3	7	**Fold:**FAS1 domain **Superfamily:**FAS1 domain **Family:**FAS1 domain
24	d1if1a_	Alignment	not modelled	6.2	55	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Interferon regulatory factor
25	c2dllA_	Alignment	not modelled	6.2	55	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**interferon regulatory factor 4; **PDBTitle:** solution structure of the irf domain of human interferon2 regulator factors 4
26	c3lj5H_	Alignment	not modelled	6.0	12	**PDB header:**viral protein **Chain:** H: **PDB Molecule:**portal protein; **PDBTitle:** full length bacteriophage p22 portal protein
27	c2ko6A_	Alignment	not modelled	6.0	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yihd; **PDBTitle:** solution structure of protein sf3929 from shigella flexneri2 2a. northeast structural genomics consortium target3 sfr81/ontario center for structural proteomics target4 sf3929
28	d1p5dx4	Alignment	not modelled	5.9	15	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain

29	d2ix0a1	Alignment	not modelled	5.7	39	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
30	d2irfg_	Alignment	not modelled	5.7	55	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Interferon regulatory factor
31	c2k88A_	Alignment	not modelled	5.6	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vacuolar proton pump subunit g; **PDBTitle:** association of subunit d (vma6p) and e (vma4p) with g2 (vma10p) and the nmr solution structure of subunit g (g1-3 59) of the saccharomyces cerevisiae v1vo atpase
32	d1tf5a1	Alignment	not modelled	5.5	39	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
33	d2fhza1	Alignment	not modelled	5.5	30	**Fold:**ImmE5-like **Superfamily:**ImmE5-like **Family:**ImmE5-like
34	d1ueba3	Alignment	not modelled	5.5	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
35	d2f5tx2	Alignment	not modelled	5.4	18	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**TrmB middle domain-like
36	d1gvia1	Alignment	not modelled	5.4	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
37	d1tfra2	Alignment	not modelled	5.3	22	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
38	c3bmaC_	Alignment	not modelled	5.3	12	**PDB header:**ligase **Chain:** C: **PDB Molecule:**d-alanyl-lipoteichoic acid synthetase; **PDBTitle:** crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6
39	c2kseA_	Alignment	not modelled	5.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein qsec; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor qsec, center for structures of3 membrane proteins (csmp) target 4311c
40	c2iruA_	Alignment	not modelled	5.2	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative dna ligase-like protein rv0938/mt0965; **PDBTitle:** crystal structure of the polymerase domain from mycobacterium2 tuberculosis ligase d
41	d1h2ka_	Alignment	not modelled	5.1	23	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Hypoxia-inducible factor HIF ihhibitor (FIH1)
42	c1nohB_	Alignment	not modelled	5.1	16	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**head morphogenesis protein; **PDBTitle:** the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
43	d2o4ta1	Alignment	not modelled	5.1	12	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like