Phyre^2

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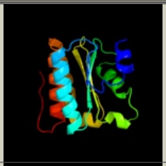
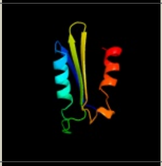
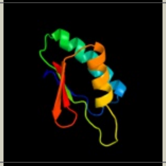
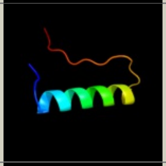
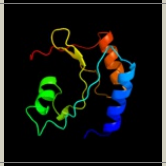
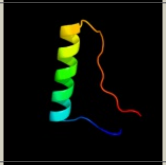
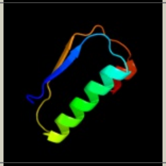
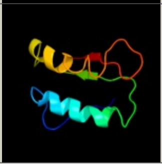
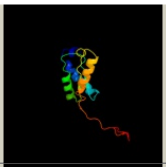
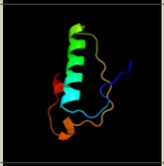
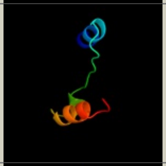
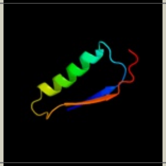
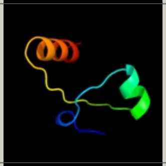
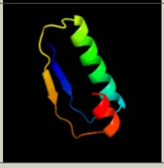
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ptjA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0603 protein at1g54780, chloroplastic; **PDBTitle:** structural and functional analysis of arabidopsis thaliana thylakoid2 lumen protein attlp18.3
2	c2kw7A_	Alignment		100.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** solution nmr structure of the n-terminal domain of protein pg_03612 from p.gingivalis, northeast structural genomics consortium target3 pgr37a
3	c2kptA_	Alignment		100.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative secreted protein; **PDBTitle:** solution nmr structure of the n-terminal domain of cg24962 protein from corynebacterium glutamicum. northeast3 structural genomics consortium target cgr26a
4	c3g98B_	Alignment		76.3	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of the c-ala domain from aquifex aeolicus2 alanyl-trna synthetase
5	d3b48a1	Alignment		42.3	14	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
6	c2vkcA_	Alignment		33.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nedd4-binding protein 2; **PDBTitle:** solution structure of the b3bp smr domain
7	d1j3wa_	Alignment		31.4	22	**Fold:**Profilin-like **Superfamily:**Roadblock/LC7 domain **Family:**Roadblock/LC7 domain
8	c3bj5A_	Alignment		30.8	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase; **PDBTitle:** alternative conformations of the x region of human protein disulphide-2 isomerase modulate exposure of the substrate binding b' domain
9	c1j3wB_	Alignment		25.7	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**giding protein-mglb; **PDBTitle:** structure of gliding protein-mglb from thermus thermophilus hb8
10	d1yg6a1	Alignment		25.2	8	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
11	c1qzwC_	Alignment		25.2	11	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication

12	c3pdiG_	Alignment		22.4	15	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
13	d2cbya1	Alignment		21.2	11	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
14	d1cvra2	Alignment		18.1	13	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Gingipain R (RgpB), N-terminal domain
15	d1y7oa1	Alignment		17.4	14	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
16	c2deoA_	Alignment		17.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**441aa long hypothetical nfed protein; **PDBTitle:** 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
17	c3ds8A_	Alignment		17.1	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2722 protein; **PDBTitle:** the crysatl structure of the gene lin2722 products from listeria2 innocua
18	d1y9ua_	Alignment		16.9	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
19	c2l8bA_	Alignment		16.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein trai; **PDBTitle:** trai (381-569)
20	c3kthD_	Alignment		15.5	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** structure of clpp from bacillus subtilis in orthorombic crystal form
21	d2d9ia1	Alignment	not modelled	15.4	19	**Fold:**IF3-like **Superfamily:**SMR domain-like **Family:**Smr domain
22	d1a1va1	Alignment	not modelled	15.2	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
23	c3iprC_	Alignment	not modelled	15.2	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
24	c1tg6G_	Alignment	not modelled	14.6	4	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**putative atp-dependent clp protease proteolytic subunit; **PDBTitle:** crystallography and mutagenesis point to an essential role for the n-2 terminus of human mitochondrial clpp
25	c2j37W_	Alignment	not modelled	14.4	13	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
26	c1cvrA_	Alignment	not modelled	14.2	13	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**gingipain r; **PDBTitle:** crystal structure of the arg specific cysteine proteinase gingipain r2 (rgpb)
27	c2zvfG_	Alignment	not modelled	13.9	16	**PDB header:**ligase **Chain:** G: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase c-terminal dimerization domain
28	c2cbyG_	Alignment	not modelled	13.6	12	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp-dependent clp protease proteolytic subunit 1; **PDBTitle:** crystal structure of the atp-dependent clp protease2

						proteolytic subunit 1 (clpp1) from mycobacterium3 tuberculosis
29	c1g6uB_	Alignment	not modelled	13.4	16	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**domain swapped dimer; **PDBTitle:** crystal structure of a domain swapped dimer
30	d1xvya_	Alignment	not modelled	13.2	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
31	d1omza_	Alignment	not modelled	13.1	7	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin
32	d1pdoa_	Alignment	not modelled	12.9	17	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
33	d1xc1a_	Alignment	not modelled	12.3	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
34	d1nnfa_	Alignment	not modelled	12.2	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
35	c2l69A_	Alignment	not modelled	12.1	24	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
36	c3lfjB_	Alignment	not modelled	11.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, mannose/fructose/n- **PDBTitle:** crystal structure of manxb from thermoanaerobacter tengcongensis
37	d1y4ta_	Alignment	not modelled	11.0	3	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
38	d1tg6a1	Alignment	not modelled	10.3	4	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
39	c3gdwA_	Alignment	not modelled	10.0	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
40	c2j289_	Alignment	not modelled	9.9	10	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
41	c3bqhA_	Alignment	not modelled	9.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb; **PDBTitle:** structure of the central domain (msra) of neisseria meningitidis pilb2 (oxidized form)
42	d1xvxa_	Alignment	not modelled	9.8	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
43	d3ct6a1	Alignment	not modelled	9.1	14	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
44	c2vqzB_	Alignment	not modelled	8.9	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**polymerase basic protein 2; **PDBTitle:** structure of the cap-binding domain of influenza virus2 polymerase subunit pb2 with bound m7gtp
45	d1u8sa1	Alignment	not modelled	8.7	4	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
46	c3p2lD_	Alignment	not modelled	8.7	6	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** crystal structure of atp-dependent clp protease subunit p from2 francisella tularensis
47	c2a02A_	Alignment	not modelled	8.6	7	**PDB header:**membrane protein, metal transport **Chain:** A: **PDB Molecule:**ferric-pseudobactin 358 receptor; **PDBTitle:** solution nmr structure of the periplasmic signaling domain2 of the outer membrane iron transporter pupa from3 pseudomonas putida.
48	d1ta8a_	Alignment	not modelled	8.5	19	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
49	c2ayaA_	Alignment	not modelled	8.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii subunit tau; **PDBTitle:** solution structure of the c-terminal 14 kda domain of the2 tau subunit from escherichia coli dna polymerase iii
50	c2iy3A_	Alignment	not modelled	8.2	13	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
51	d2vvpa1	Alignment	not modelled	8.1	13	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
52	c3pbjE_	Alignment	not modelled	8.1	21	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a designed2 metalloprotein
53	c3pbjC_	Alignment	not modelled	8.0	24	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a designed2 metalloprotein
						PDB header:de novo protein

54	c3pbjD_	Alignment	not modelled	8.0	24	**Chain:** D: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a designed2 metalloprotein
55	c3pbjA_	Alignment	not modelled	8.0	24	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a designed2 metalloprotein
56	c3pbjF_	Alignment	not modelled	8.0	24	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a designed2 metalloprotein
57	c3pbjB_	Alignment	not modelled	8.0	24	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l9l-pen l23h; **PDBTitle:** hydrolytic catalysis and structural stabilization in a designed2 metalloprotein
58	d2o8ia1	Alignment	not modelled	8.0	15	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
59	c3dm5A_	Alignment	not modelled	7.8	17	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
60	c3pilA_	Alignment	not modelled	7.5	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
61	c1ii8B_	Alignment	not modelled	7.4	9	**PDB header:**replication **Chain:** B: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
62	c2q37A_	Alignment	not modelled	7.3	10	**PDB header:**plant protein, lyase **Chain:** A: **PDB Molecule:**ohcu decarboxylase; **PDBTitle:** crystal structure of ohcu decarboxylase in the presence of2 (s)-allantoin
63	d2q37a1	Alignment	not modelled	7.3	10	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
64	c3pn1A_	Alignment	not modelled	7.3	19	**PDB header:**ligase/ligase inhibitor **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
65	c3gx1A_	Alignment	not modelled	7.1	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1832 protein; **PDBTitle:** crystal structure of a domain of lin1832 from listeria innocua
66	d1j3sa_	Alignment	not modelled	6.9	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
67	c2d3o1_	Alignment	not modelled	6.8	16	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**trigger factor; **PDBTitle:** structure of ribosome binding domain of the trigger factor2 on the 50s ribosomal subunit from d. radiodurans
68	c3c9hB_	Alignment	not modelled	6.7	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, substrate binding protein; **PDBTitle:** crystal structure of the substrate binding protein of the abc2 transporter from agrobacterium tumefaciens
69	d1ofda1	Alignment	not modelled	6.6	13	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Alpha subunit of glutamate synthase, C-terminal domain **Family:**Alpha subunit of glutamate synthase, C-terminal domain
70	d1nn4a_	Alignment	not modelled	6.4	19	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
71	d1xpja_	Alignment	not modelled	6.2	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
72	d1efpb_	Alignment	not modelled	6.1	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
73	d1sd4a_	Alignment	not modelled	6.1	37	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
74	c2z0sA_	Alignment	not modelled	5.9	5	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**probable exosome complex rna-binding protein 1; **PDBTitle:** crystal structure of putative exosome complex rna-binding2 protein
75	d1wejf_	Alignment	not modelled	5.8	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
76	c2h8lA_	Alignment	not modelled	5.6	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3; **PDBTitle:** crystal structure of the bb' fragment of erp57