Phyre2

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Description	P0A8E7
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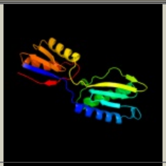
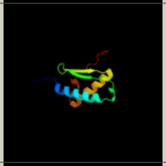
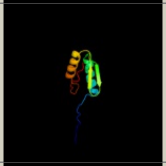
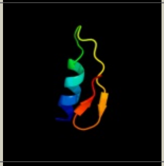
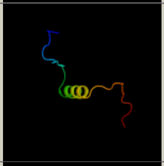
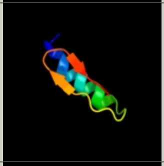
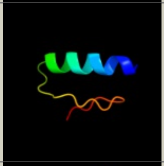
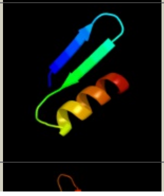
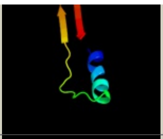
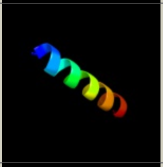
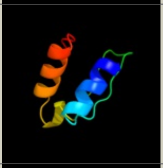
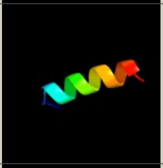
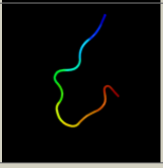
Unique Job ID	2d7fc682d2dc59c1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1in0B_	Alignment		100.0	62	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yajq protein; **PDBTitle:** yajq protein (hi1034)
2	d1in0a1	Alignment		100.0	58	**Fold:**Ferredoxin-like **Superfamily:**YajQ-like **Family:**YajQ-like
3	d1in0a2	Alignment		100.0	66	**Fold:**Ferredoxin-like **Superfamily:**YajQ-like **Family:**YajQ-like
4	d1wiha_	Alignment		75.1	18	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
5	d1eh1a_	Alignment		61.0	29	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
6	c2jpiA_	Alignment		60.9	9	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
7	d1ek8a_	Alignment		56.5	26	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
8	c3aqoD_	Alignment		54.2	21	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** structure and function of a membrane component secdf that enhances2 protein export
9	d1is1a_	Alignment		53.9	29	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
10	d1dd5a_	Alignment		46.6	26	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
11	d1vqoe2	Alignment		39.1	20	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6

12	d1pvga2	Alignment		34.5	32	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
13	d1ge9a_	Alignment		28.3	33	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
14	c3ci9B_	Alignment		25.7	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
15	d1jjcb4	Alignment		24.3	16	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
16	c2kyzA_	Alignment		22.5	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
17	d1j2jb_	Alignment		19.9	18	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
18	d1vpka2	Alignment		19.8	12	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase III, beta subunit
19	d1wxma1	Alignment		18.7	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
20	d1jz8a2	Alignment		18.0	42	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
21	d1wqga1	Alignment	not modelled	17.7	19	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
22	c1bo1A_	Alignment	not modelled	16.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (phosphatidylinositol phosphate kinase **PDBTitle:** phosphatidylinositol phosphate kinase type ii beta
23	d1bo1a_	Alignment	not modelled	16.6	17	**Fold:**SAICAR synthase-like **Superfamily:**SAICAR synthase-like **Family:**Phosphatidylinositol phosphate kinase IIbeta, PIPK IIbeta
24	d1yq2a1	Alignment	not modelled	16.5	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
25	d1e32a1	Alignment	not modelled	16.3	42	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
26	d1x7fa2	Alignment	not modelled	15.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Outer surface protein, N-terminal domain
27	c3ijmA_	Alignment	not modelled	14.3	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized restriction endonuclease-like fold **PDBTitle:** the structure of a restriction endonuclease-like fold superfamily2 protein from spirosoma linguale.
28	d1hywa_	Alignment	not modelled	14.3	24	**Fold:**gpW/XkdW-like **Superfamily:**Head-to-tail joining protein W, gpW **Family:**Head-to-tail joining protein W, gpW
29	d1qnaa1	Alignment	not modelled	14.1	13	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like

						Family:TATA-box binding protein (TBP), C-terminal domain
30	c2ftcF_	Alignment	not modelled	13.9	20	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**39s ribosomal protein l12, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
31	c3fblA_	Alignment	not modelled	13.8	38	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of orf132 of the archaeal virus acidianus2 filamentous virus 1 (afv1)
32	c2gk9D_	Alignment	not modelled	13.2	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**phosphatidylinositol-4-phosphate 5-kinase, type **PDBTitle:** human phosphatidylinositol-4-phosphate 5-kinase, type ii,2 gamma
33	d1ok7a2	Alignment	not modelled	11.8	4	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase III, beta subunit
34	c1x7fA_	Alignment	not modelled	11.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**outer surface protein; **PDBTitle:** crystal structure of an uncharacterized b. cereus protein
35	d1vjea_	Alignment	not modelled	11.0	30	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
36	d1nh2a1	Alignment	not modelled	10.9	13	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
37	c1qzrA_	Alignment	not modelled	9.8	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase ii; **PDBTitle:** crystal structure of the atpase region of saccharomyces cerevisiae2 topoisomerase ii bound to icrf-187 (dexrazoxane)
38	c1giyJ_	Alignment	not modelled	9.6	19	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** crystal structure of the ribosome at 5.5 a resolution. this2 file, 1giy, contains the 50s ribosome subunit. the 30s3 ribosome subunit, three trna, and mrna molecules are in the4 file 1gix
39	d1dd3a2	Alignment	not modelled	9.6	19	**Fold:**ClpS-like **Superfamily:**ClpS-like **Family:**Ribosomal protein L7/12, C-terminal domain
40	c2gya3_	Alignment	not modelled	9.4	20	**PDB header:**ribosome **Chain:** 3: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** structure of the 50s subunit of a pre-translocational e.2 coli ribosome obtained by fitting atomic models for rna and3 protein components into cryo-em map emd-1056
41	d1cdwa1	Alignment	not modelled	9.2	14	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
42	d1ctfa_	Alignment	not modelled	9.1	19	**Fold:**ClpS-like **Superfamily:**ClpS-like **Family:**Ribosomal protein L7/12, C-terminal domain
43	c2e70A_	Alignment	not modelled	8.6	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the fifth kow motif of human2 transcription elongation factor spt5
44	c1xyr6_	Alignment	not modelled	8.6	36	**PDB header:**virus **Chain:** 6: **PDB Molecule:**genome polyprotein, coat protein vp3; **PDB Fragment:**residues 620-630 **PDBTitle:** poliovirus 135s cell entry intermediate
45	c1vpkA_	Alignment	not modelled	8.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii, beta subunit; **PDBTitle:** crystal structure of dna polymerase iii, beta subunit (tm0262) from2 thermotoga maritima at 2.00 a resolution
46	d1vpra1	Alignment	not modelled	8.3	28	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Dinoflagellate luciferase repeat
47	c3k1tA_	Alignment	not modelled	8.1	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase gsha; **PDBTitle:** crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
48	c2h2mA_	Alignment	not modelled	7.8	31	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**comm domain-containing protein 1; **PDBTitle:** solution structure of the n-terminal domain of commd12 (murr1)
49	c1zxnB_	Alignment	not modelled	7.7	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme; **PDBTitle:** human dna topoisomerase iia atpase/adp
50	c3ke2A_	Alignment	not modelled	7.7	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_928783.1; **PDBTitle:** crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution
51	d1xmta_	Alignment	not modelled	7.6	8	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
52	c1mv4B_	Alignment	not modelled	7.5	67	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**tropomyosin 1 alpha chain; **PDBTitle:** tm9a251-284: a peptide model of the c-terminus of a rat2 striated alpha tropomyosin
53	c2zjq5_	Alignment	not modelled	7.3	20	**PDB header:**ribosome **Chain:** 5: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** interaction of l7 with l11 induced by micrococcin binding2 to the deinococcus radiodurans 50s subunit
						Fold: ClpS-like

54	d2zjq51	Alignment	not modelled	7.3	20	**Superfamily:**ClpS-like **Family:**Ribosomal protein L7/12, C-terminal domain
55	d1rfza_	Alignment	not modelled	7.3	29	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
56	c4a19Q_	Alignment	not modelled	7.2	14	**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.
57	c2egcA_	Alignment	not modelled	7.1	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 and px domain-containing protein 2a; **PDBTitle:** solution structure of the fifth sh3 domain from human2 kiaa0418 protein
58	c2joiA_	Alignment	not modelled	6.8	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0095; **PDBTitle:** nmr solution structure of hypothetical protein ta0095 from2 thermoplasma acidophilum
59	c3izck_	Alignment	not modelled	6.7	13	**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
60	d2a1jb1	Alignment	not modelled	6.6	18	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
61	c3okqA_	Alignment	not modelled	6.3	50	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bud site selection protein 6; **PDBTitle:** crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
62	d1cz5a1	Alignment	not modelled	6.2	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
63	d1c52a_	Alignment	not modelled	6.2	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
64	c3kowH_	Alignment	not modelled	5.8	36	**PDB header:**metal binding protein **Chain:** H: **PDB Molecule:**d-ornithine aminomutase s component; **PDBTitle:** crystal structure of ornithine 4,5 aminomutase backsoaked complex
65	d1cc8a_	Alignment	not modelled	5.7	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
66	c3fryB_	Alignment	not modelled	5.6	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable copper-exporting p-type atpase a; **PDBTitle:** crystal structure of the copa c-terminal metal binding domain
67	c3ossD_	Alignment	not modelled	5.5	13	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**type 2 secretion system, secretin gspd; **PDBTitle:** the crystal structure of enterotoxigenic escherichia coli gspc-gspd2 complex from the type ii secretion system
68	d1fyja_	Alignment	not modelled	5.5	27	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**a tRNA synthase domain
69	d1uaea_	Alignment	not modelled	5.4	28	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
70	c2d3o1_	Alignment	not modelled	5.3	15	**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
71	d2dlxa1	Alignment	not modelled	5.2	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**UAS domain