Phyre^2

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Description	P0A8B5
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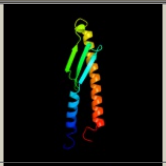
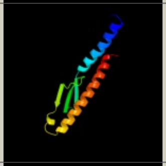
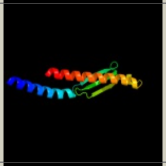
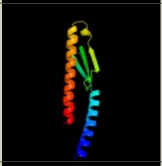
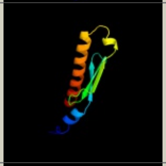
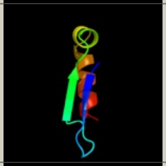
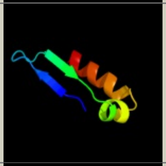
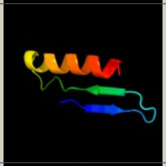
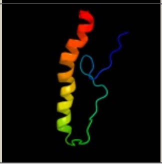
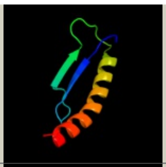
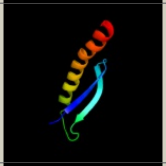
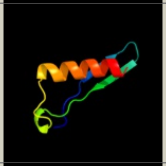
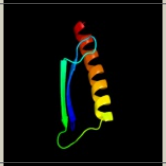
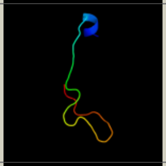
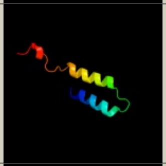
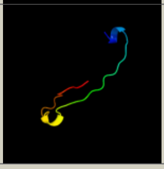
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1puga_	Alignment		99.9	100	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
2	d1j8ba_	Alignment		99.9	82	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
3	c1ybxA_	Alignment		99.9	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum
4	c3f42A_	Alignment		99.9	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hp0035; **PDBTitle:** crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
5	d1pugb_	Alignment		99.7	100	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
6	d1lr0a_	Alignment		78.2	11	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TolA
7	d2ba0g2	Alignment		74.0	18	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
8	c2x9aB_	Alignment		67.8	17	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**membrane spanning protein, required for outer membrane **PDBTitle:** crystal structure of g3p from phage if1 in complex with its2 coreceptor, the c-terminal domain of tola
9	d2nn6c2	Alignment		64.4	9	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
10	d1tola2	Alignment		61.1	17	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TolA
11	d2nn6e2	Alignment		51.2	7	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like

12	d2je6a2	Alignment		48.6	9	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
13	d2nn6a2	Alignment		46.4	15	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
14	c1xx3A_	Alignment		46.3	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tonb protein; **PDBTitle:** solution structure of escherichia coli tonb-ctd
15	c2v4uA_	Alignment		41.9	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthase 2; **PDBTitle:** human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
16	c3brcA_	Alignment		38.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein of unknown function; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
17	d1oysa2	Alignment		36.3	13	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
18	d2gskb1	Alignment		30.7	21	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
19	c3h7fB_	Alignment		30.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase 1; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
20	d1u07a_	Alignment		27.9	21	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
21	c2boiA_	Alignment	not modelled	26.8	24	**PDB header:**lectin **Chain:** A: **PDB Molecule:**cv-iil lectin; **PDBTitle:** 1.1a structure of chromobacterium violaceum lectin cv2l in2 complex with alpha-methyl-fucoside
22	d2chha1	Alignment	not modelled	26.4	16	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
23	c2vnvC_	Alignment	not modelled	26.4	21	**PDB header:**sugar-binding protein **Chain:** C: **PDB Molecule:**bcla; **PDBTitle:** crystal structure of bcla lectin from burkholderia2 cenocepacia in complex with alpha-methyl-mannoside at 1.73 angstrom resolution
24	d1uzva_	Alignment	not modelled	24.1	20	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
25	c2grxC_	Alignment	not modelled	23.8	21	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**protein tonb; **PDBTitle:** crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
26	d1ib8a2	Alignment	not modelled	23.7	8	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**YhbC-like, N-terminal domain **Family:**YhbC-like, N-terminal domain
27	c1udsA_	Alignment	not modelled	22.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of the trna processing enzyme rnase ph r126a mutant2 from aquifex aeolicus
28	c2xr4A_	Alignment	not modelled	22.1	24	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**lectin; **PDBTitle:** c-terminal domain of bc2l-c lectin from burkholderia cenocepacia

29	c2kzxA_	Alignment	not modelled	21.9	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a3dht5 from clostridium thermocellum,2 northeast structural genomics consortium target cmr116
30	c3nvaB_	Alignment	not modelled	21.6	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
31	c3b4tC_	Alignment	not modelled	21.5	6	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of mycobacterium tuberculosis rnase ph, the2 mycobacterium tuberculosis structural genomics consortium target3 rv1340
32	c3o6uB_	Alignment	not modelled	20.7	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein cpe2226; **PDBTitle:** crystal structure of cpe2226 protein from clostridium perfringens.2 northeast structural genomics consortium target cpr195
33	c2b1kA_	Alignment	not modelled	20.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of e. coli ccmg protein
34	c2npbA_	Alignment	not modelled	20.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**selenoprotein w; **PDBTitle:** nmr solution structure of mouse selw
35	c2k9kA_	Alignment	not modelled	20.3	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**tonb2; **PDBTitle:** molecular characterization of the tonb2 protein from vibrio2 anguillarum
36	c2owyB_	Alignment	not modelled	19.8	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**recombination-associated protein rdgc; **PDBTitle:** the recombination-associated protein rdgc adopts a novel toroidal2 architecture for dna binding
37	c1ib8A_	Alignment	not modelled	18.4	8	**PDB header:**nucleic acid binding protein **Chain:** A: **PDB Molecule:**conserved protein sp14.3; **PDBTitle:** solution structure and function of a conserved protein2 sp14.3 encoded by an essential streptococcus pneumoniae3 gene
38	c3eytA_	Alignment	not modelled	17.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
39	c3dd6A_	Alignment	not modelled	17.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of rph, an exoribonuclease from bacillus2 anthracis at 1.7 a resolution
40	d2fqla1	Alignment	not modelled	16.7	10	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
41	d1ihra_	Alignment	not modelled	16.3	24	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
42	d2ga5a1	Alignment	not modelled	16.0	10	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
43	c2pnzB_	Alignment	not modelled	15.9	18	**PDB header:**hydrolase/hydrolase **Chain:** B: **PDB Molecule:**probable exosome complex exonuclease 2; **PDBTitle:** crystal structure of the p. abyssi exosome rnase ph ring2 complexed with udp and gmp
44	c1r6mA_	Alignment	not modelled	15.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of the trna processing enzyme rnase ph from2 pseudomonas aeruginosa in complex with phosphate
45	d1e2ya_	Alignment	not modelled	15.2	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
46	c1x2gB_	Alignment	not modelled	14.3	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lipoate-protein ligase a; **PDBTitle:** crystal structure of lipate-protein ligase a from2 escherichia coli
47	c2nn6C_	Alignment	not modelled	14.1	11	**PDB header:**hydrolase/transferase **Chain:** C: **PDB Molecule:**exosome complex exonuclease rrp43; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
48	d1neia_	Alignment	not modelled	13.6	18	**Fold:**Hypothetical protein YoaG **Superfamily:**Hypothetical protein YoaG **Family:**Hypothetical protein YoaG
49	c2nn6E_	Alignment	not modelled	12.4	5	**PDB header:**hydrolase/transferase **Chain:** E: **PDB Molecule:**exosome complex exonuclease rrp42; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
50	c1vqzA_	Alignment	not modelled	12.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoate-protein ligase, putative; **PDBTitle:** crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
51	d1vqza1	Alignment	not modelled	12.0	18	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
52	c2z7eB_	Alignment	not modelled	11.1	8	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**nifu-like protein; **PDBTitle:** crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
53	c2qzbB_	Alignment	not modelled	10.8	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yfey; **PDBTitle:** crystal structure of the uncharacterized protein yfey from escherichia2 coli
						PDB header:hydrolase

54	c2wnrC_	Alignment	not modelled	9.8	9	**Chain:** C: **PDB Molecule:**probable exosome complex exonuclease 2; **PDBTitle:** the structure of methanothermobacter thermautotrophicus2 exosome core assembly
55	c2wp8A_	Alignment	not modelled	9.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exosome complex component rrp45; **PDBTitle:** yeast rrp44 nuclease
56	d1xvqa_	Alignment	not modelled	9.3	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
57	d1we0a1	Alignment	not modelled	9.2	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
58	c2vzkD_	Alignment	not modelled	8.7	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamate n-acetyltransferase 2 beta chain; **PDBTitle:** structure of the acyl-enzyme complex of an n-terminal2 nucleophile (ntn) hydrolase, oat2
59	c1vraB_	Alignment	not modelled	8.7	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arginine biosynthesis bifunctional protein argj; **PDBTitle:** crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
60	c2ad5B_	Alignment	not modelled	8.0	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
61	d1zofa1	Alignment	not modelled	8.0	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
62	c1zyeL_	Alignment	not modelled	7.8	15	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**thioredoxin-dependent peroxide reductase; **PDBTitle:** crystal strucutre analysis of bovine mitochondrial peroxiredoxin iii
63	d2cv4a1	Alignment	not modelled	7.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
64	c3fw2A_	Alignment	not modelled	7.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
65	c1jcgA_	Alignment	not modelled	7.5	8	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**rod shape-determining protein mreb; **PDBTitle:** mreb from thermotoga maritima, amppnp
66	c3uowB_	Alignment	not modelled	7.3	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
67	c1s94A_	Alignment	not modelled	7.3	11	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**s-syntaxin; **PDBTitle:** crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
68	d1s94a_	Alignment	not modelled	7.3	11	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
69	d1k28d2	Alignment	not modelled	7.1	38	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
70	c3h2dA_	Alignment	not modelled	7.1	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chec-like superfamily protein; **PDBTitle:** crystal structure of a chemotactic chec-like protein (so_3915) from2 shewanella oneidensis mr-1 at 1.86 a resolution
71	c2bmxB_	Alignment	not modelled	7.1	6	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxidase c; **PDBTitle:** mycobacterium tuberculosis ahpc
72	d1m98a2	Alignment	not modelled	7.1	29	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Orange carotenoid protein, C-terminal domain
73	c3lorB_	Alignment	not modelled	6.8	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**thiol-disulfide isomerase and thioredoxins; **PDBTitle:** the crystal structure of a thiol-disulfide isomerase from2 corynebacterium glutamicum to 2.2a
74	d2r7ka2	Alignment	not modelled	6.7	16	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
75	d1z5ye1	Alignment	not modelled	6.7	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
76	c1tolA_	Alignment	not modelled	6.7	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (fusion protein consisting of minor coat **PDBTitle:** fusion of n-terminal domain of the minor coat protein from2 gene iii in phage m13, and c-terminal domain of e. coli3 protein-tola
77	d1n8ja_	Alignment	not modelled	6.6	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
78	d3cdda1	Alignment	not modelled	6.6	7	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like

79	c3ghhA_	Alignment	not modelled	6.5	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ecto-nad+ glycohydrolase (cd38 molecule); **PDBTitle:** structural insights into the catalytic mechanism of cd38:2 evidence for a conformationally flexible covalent enzyme-3 substrate complex.
80	c3eukC_	Alignment	not modelled	6.4	13	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**chromosome partition protein mukb, linker; **PDBTitle:** crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, asymmetric dimer
81	c3kebB_	Alignment	not modelled	6.3	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** thiol peroxidase from chromobacterium violaceum
82	c2kxxA_	Alignment	not modelled	6.2	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small protein a; **PDBTitle:** nmr structure of escherichia coli bame, a lipoprotein component of the2 beta-barrel assembly machinery complex
83	d1x2ga1	Alignment	not modelled	6.2	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
84	d1knga_	Alignment	not modelled	5.9	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
85	c3mxnA_	Alignment	not modelled	5.9	20	**PDB header:**replication **Chain:** A: **PDB Molecule:**recq-mediated genome instability protein 1; **PDBTitle:** crystal structure of the rmi core complex
86	c2br2G_	Alignment	not modelled	5.8	9	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**exosome complex exonuclease 2; **PDBTitle:** rnase ph core of the archaeal exosome
87	d1yexa1	Alignment	not modelled	5.8	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
88	c3it4B_	Alignment	not modelled	5.7	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arginine biosynthesis bifunctional protein argj **PDBTitle:** the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
89	d1qmva_	Alignment	not modelled	5.7	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
90	d1l4sa_	Alignment	not modelled	5.7	7	**Fold:**Ribosome binding protein Y (YfiA homologue) **Superfamily:**Ribosome binding protein Y (YfiA homologue) **Family:**Ribosome binding protein Y (YfiA homologue)
91	c3fw6A_	Alignment	not modelled	5.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulase; **PDBTitle:** crystal structure of celm2, a bifunctional glucanase-2 xylanase protein from a metagenome library
92	d1yuwa1	Alignment	not modelled	5.2	20	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
93	d1kn0a_	Alignment	not modelled	5.1	23	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**The homologous-pairing domain of Rad52 recombinase