Phyre^{2}

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Description	P0A744
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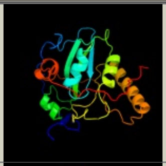
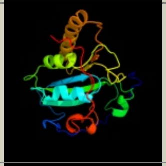
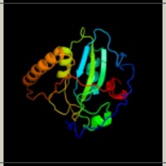
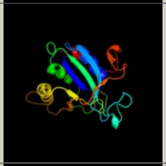
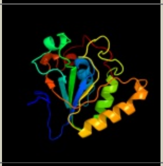
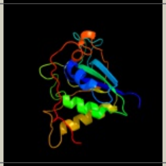
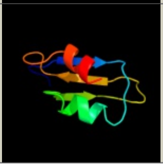
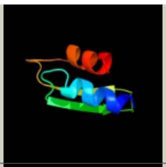
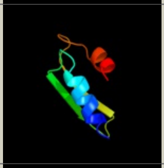
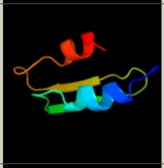
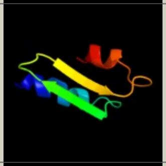
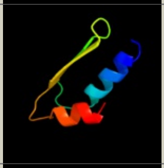
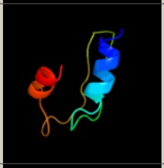
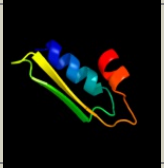
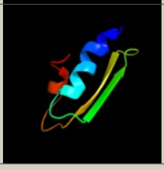
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ff3a_	Alignment		100.0	99	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
2	c1fvaA_	Alignment		100.0	62	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of bovine methionine sulfoxide reductase
3	d1fvga_	Alignment		100.0	60	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
4	d1ff3c_	Alignment		100.0	99	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
5	c2j89A_	Alignment		100.0	48	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine sulfoxide reductase a; **PDBTitle:** functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
6	c3bqhA_	Alignment		100.0	41	**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)
7	c3e0mB_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb **PDBTitle:** crystal structure of fusion protein of msra and msrb
8	c3pilA_	Alignment		100.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
9	c1nwaA_	Alignment		100.0	45	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msra; **PDBTitle:** structure of mycobacterium tuberculosis methionine2 sulfoxide reductase a in complex with protein-bound3 methionine
10	d1nwaa_	Alignment		100.0	45	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
11	d1kvja_	Alignment		96.1	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain

12	d1afia_	Alignment		95.1	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
13	d1cpza_	Alignment		95.0	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
14	d1q8la_	Alignment		94.7	26	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
15	c1yjrA_	Alignment		93.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
16	c2kkhA_	Alignment		93.9	23	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
17	d1p6ta2	Alignment		93.9	26	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
18	d1p6ta1	Alignment		93.9	24	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
19	d1s6ua_	Alignment		93.7	26	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
20	c2ldiA_	Alignment		93.6	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
21	d2qifa1	Alignment	not modelled	93.0	26	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
22	d1osda_	Alignment	not modelled	92.6	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
23	c2l3mA_	Alignment	not modelled	92.3	28	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
24	d2aw0a_	Alignment	not modelled	92.3	28	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
25	c2ga7A_	Alignment	not modelled	92.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
26	c2ropA_	Alignment	not modelled	92.1	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of domains 3 and 4 of human atp7b
27	c2ew9A_	Alignment	not modelled	92.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of apowln5-6
28	c2ofhX_	Alignment	not modelled	92.0	26	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
29	c2kt2A_	Alignment	not modelled	91.9	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase;

29	c2kt2A_	Alignment	not modelled	91.9	28	**PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
30	c3j09A_	Alignment	not modelled	91.9	27	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
31	c2rmlA_	Alignment	not modelled	91.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting p-type atpase copa; **PDBTitle:** solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
32	c3dxsX_	Alignment	not modelled	90.6	21	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
33	d2ggpb1	Alignment	not modelled	90.3	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
34	c1y3kA_	Alignment	not modelled	87.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
35	d1mwza_	Alignment	not modelled	86.6	24	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
36	c1yg0A_	Alignment	not modelled	84.8	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
37	c2aj1A_	Alignment	not modelled	80.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
38	c2gcfA_	Alignment	not modelled	79.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
39	c2k2pA_	Alignment	not modelled	68.8	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
40	d1vsra_	Alignment	not modelled	59.0	43	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
41	c2f40A_	Alignment	not modelled	58.5	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf1455; **PDBTitle:** structure of a novel protein from backbone-centered nmr data and nmr-2 assisted structure prediction
42	d2phcb2	Alignment	not modelled	57.5	32	**Fold:**DCoH-like **Superfamily:**PH0987 N-terminal domain-like **Family:**PH0987 N-terminal domain-like
43	c2phcB_	Alignment	not modelled	56.8	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
44	c2rogA_	Alignment	not modelled	43.4	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
45	d1qupa2	Alignment	not modelled	36.6	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
46	d1sb6a_	Alignment	not modelled	33.8	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
47	d1cw0a_	Alignment	not modelled	32.7	43	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
48	c2kwaA_	Alignment	not modelled	22.0	21	**PDB header:**transferase inhibitor **Chain:** A: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** 1h, 13c and 15n backbone and side chain resonance assignments of the2 n-terminal domain of the histidine kinase inhibitor kipi from3 bacillus subtilis
49	d2gz1a2	Alignment	not modelled	20.3	25	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
50	c3fryB_	Alignment	not modelled	19.5	12	**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
51	d1e3ha5	Alignment	not modelled	15.6	19	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
52	d1pugb_	Alignment	not modelled	14.6	25	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
53	c2kyzA_	Alignment	not modelled	14.6	15	**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
54	d1sl8a_	Alignment	not modelled	12.7	25	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
						PDB header:hydrolase

55	c3mmlD_	Alignment	not modelled	12.3	11	**Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
56	d1t4ba2	Alignment	not modelled	11.6	17	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
57	d1pqua2	Alignment	not modelled	10.7	17	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
58	c2crlA_	Alignment	not modelled	10.7	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** the apo form of hma domain of copper chaperone for2 superoxide dismutase
59	d1leha2	Alignment	not modelled	10.2	19	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
60	d1qv0a_	Alignment	not modelled	9.7	24	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
61	d1cc8a_	Alignment	not modelled	9.6	22	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
62	d1vqoa2	Alignment	not modelled	9.4	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
63	d2zjra2	Alignment	not modelled	9.4	45	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
64	c3dwqD_	Alignment	not modelled	9.2	33	**PDB header:**toxin **Chain:** D: **PDB Molecule:**subtilase cytotoxin, subunit b; **PDBTitle:** crystal structure of the a-subunit of the ab5 toxin from e.2 coli with neu5gc-2,3gal-1,3glcnac
65	d2b0ja2	Alignment	not modelled	9.2	55	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
66	c2kd1A_	Alignment	not modelled	9.1	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dna integration/recombination/invertion protein; **PDBTitle:** solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f
67	d2cqpa1	Alignment	not modelled	8.8	12	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
68	d1mb4a2	Alignment	not modelled	8.7	17	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
69	d1r6la2	Alignment	not modelled	8.2	18	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
70	c1qupA_	Alignment	not modelled	8.1	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase
71	d1rl2a2	Alignment	not modelled	8.1	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
72	c3oepA_	Alignment	not modelled	7.8	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0988; **PDBTitle:** crystal structure of ttha0988 in space group p43212
73	c3md1B_	Alignment	not modelled	7.7	10	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**nuclear and cytoplasmic polyadenylated rna-binding protein **PDBTitle:** crystal structure of the second rrm domain of yeast poly(u)-binding2 protein (pub1)
74	d2je6b2	Alignment	not modelled	7.7	25	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
75	c1jk9D_	Alignment	not modelled	7.4	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** heterodimer between h48f-ysod1 and yccs
76	d2nn6b2	Alignment	not modelled	6.7	23	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
77	d1uala_	Alignment	not modelled	6.6	25	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
78	c2dkhA_	Alignment	not modelled	6.5	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxybenzoate hydroxylase; **PDBTitle:** crystal structure of 3-hydroxybenzoate hydroxylase from comamonas2 testosteroni, in complex with the substrate
79	d2qdyb1	Alignment	not modelled	6.4	19	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
						PDB header:dna binding protein **Chain:** A: **PDB Molecule:**phage integrase;

80	c2kkpA_	Alignment	not modelled	6.1	33	**PDBTitle:** solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171).
81	d1fe0a_	Alignment	not modelled	6.1	27	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
82	d2p02a3	Alignment	not modelled	6.0	27	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
83	d1rlfa_	Alignment	not modelled	5.8	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
84	d1epwa2	Alignment	not modelled	5.8	50	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Clostridium neurotoxins, C-terminal domain
85	d2fura1	Alignment	not modelled	5.8	19	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
86	c3f42A_	Alignment	not modelled	5.6	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hp0035; **PDBTitle:** crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
87	c2h8bA_	Alignment	not modelled	5.5	50	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**insulin-like 3; **PDBTitle:** solution structure of insl3
88	c2k6tA_	Alignment	not modelled	5.5	50	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin-like 3 a chain; **PDBTitle:** solution structure of the relaxin-like factor
89	c2k6uA_	Alignment	not modelled	5.4	50	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin-like 3 a chain; **PDBTitle:** the solution structure of a conformationally restricted2 fully active derivative of the human relaxin-like factor3 (rlf)
90	c2kptA_	Alignment	not modelled	5.3	18	**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
91	d2j01d2	Alignment	not modelled	5.3	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
92	d1udsa2	Alignment	not modelled	5.2	14	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
93	c3f46A_	Alignment	not modelled	5.2	55	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methenyltetrahydromethanopterin hydrogenase; **PDBTitle:** the crystal structure of c176a mutated [fe]-hydrogenase (hmd)2 holoenzyme from methanocaldococcus jannaschii
94	c2dj9A_	Alignment	not modelled	5.2	80	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**growth-blocking peptide; **PDBTitle:** solution structure of growth-blocking peptide of the2 cabbage armyworm, mamestra brassicae
95	d2qamc2	Alignment	not modelled	5.2	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
96	c3enkB_	Alignment	not modelled	5.1	30	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
97	d2c0sa1	Alignment	not modelled	5.1	23	**Fold:**ROP-like **Superfamily:**BAS1536-like **Family:**BAS1536-like