























Phyre2

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Description	P0AE56
Date	Thu Jan 5 11:22:33 GMT 2012
Unique Job ID	0a9bc6243a5ca589

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y56A_	 Alignment		98.8	19	PDB header: oxidoreductase Chain: A; PDB Molecule: hypothetical protein ph1363; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
2	c1x31A_	 Alignment		98.5	18	PDB header: oxidoreductase Chain: A; PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
3	c2rghA_	 Alignment		97.6	6	PDB header: oxidoreductase Chain: A; PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
4	c2hu9B_	 Alignment		97.5	24	PDB header: metal transport Chain: B; PDB Molecule: mercuric transport protein periplasmic component; PDBTitle: x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
5	c3da1A_	 Alignment		97.0	10	PDB header: oxidoreductase Chain: A; PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
6	c2rgoA_	 Alignment		96.9	7	PDB header: oxidoreductase Chain: A; PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
7	c2r4iA_	 Alignment		94.4	11	PDB header: oxidoreductase Chain: A; PDB Molecule: aerobic glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap
8	d1fe0a_	 Alignment		43.5	30	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
9	d1l1ga1	 Alignment		38.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
10	c2kt2A_	 Alignment		37.5	29	PDB header: oxidoreductase Chain: A; PDB Molecule: mercuric reductase; PDBTitle: structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
11	c3fryB_	 Alignment		37.0	29	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

12	d1cpza_	Alignment		32.1	29	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
13	c2k2pA_	Alignment		31.7	24	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
14	c2kkaA_	Alignment		29.4	18	PDB header: metal transport Chain: A; PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
15	c1yg0A_	Alignment		28.6	18	PDB header: metal transport Chain: A; PDB Molecule: cop associated protein; PDBTitle: solution structure of apo-copp from helicobacter pylori
16	d1mwza_	Alignment		28.4	24	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
17	c2rogA_	Alignment		28.3	29	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
18	d1sb6a_	Alignment		27.6	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
19	d1s6ua_	Alignment		27.2	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
20	c1y3ka_	Alignment		26.8	24	PDB header: hydrolase Chain: A; PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the fifth domain of 2 menkes protein
21	c2kyzA_	Alignment	not modelled	26.6	18	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
22	d2cfxa1	Alignment	not modelled	26.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
23	d1afia_	Alignment	not modelled	24.7	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
24	c2ga7A_	Alignment	not modelled	24.2	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)
25	d1osda_	Alignment	not modelled	24.0	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
26	d2aw0a_	Alignment	not modelled	23.7	29	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
27	c3dxxX_	Alignment	not modelled	23.6	18	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
28	c1yjrA_	Alignment	not modelled	23.3	24	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
						Fold: DNA/RNA-binding 3-helical bundle

29	d2cyya1	Alignment	not modelled	23.2	19	Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
30	c2aj1A	Alignment	not modelled	23.0	19	PDB header: hydrolase Chain: A; PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada
31	c2gcfA	Alignment	not modelled	22.9	18	PDB header: hydrolase Chain: A; PDB Molecule: cation-transporting atpase pacs; PDBTitle: solution structure of the n-terminal domain of the copper(i) atpase2 pacs in its apo form
32	d1q8la	Alignment	not modelled	22.4	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
33	d1qupa2	Alignment	not modelled	21.3	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
34	d1p6ta2	Alignment	not modelled	21.0	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
35	d2ggpb1	Alignment	not modelled	20.9	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
36	d2cg4a1	Alignment	not modelled	20.7	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
37	c2ofhX	Alignment	not modelled	20.5	24	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
38	d1szpb1	Alignment	not modelled	20.0	19	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
39	c2ew9A	Alignment	not modelled	19.5	24	PDB header: hydrolase Chain: A; PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowln5-6
40	d1nera	Alignment	not modelled	19.2	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
41	d1p6ta1	Alignment	not modelled	18.1	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
42	d1t3qa1	Alignment	not modelled	17.7	25	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
43	d1szpa1	Alignment	not modelled	17.6	15	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
44	d1kvja	Alignment	not modelled	17.5	24	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
45	d1ffva1	Alignment	not modelled	17.4	29	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
46	d1zxia1	Alignment	not modelled	17.1	29	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
47	c1wygA	Alignment	not modelled	16.9	56	PDB header: oxidoreductase Chain: A; PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
48	d1n62a1	Alignment	not modelled	16.6	29	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
49	d1dgia1	Alignment	not modelled	16.5	21	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
50	d1v97a1	Alignment	not modelled	15.8	38	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
51	d1cc8a	Alignment	not modelled	15.7	26	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
52	d2qifa1	Alignment	not modelled	15.7	29	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
53	d1jroa1	Alignment	not modelled	15.1	25	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
54	c2ropA	Alignment	not modelled	15.0	31	PDB header: hydrolase Chain: A; PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b
55	c2ldiA	Alignment	not modelled	14.9	24	PDB header: hydrolase Chain: A; PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaa sub mutant
56	c2l3mA	Alignment	not modelled	14.2	35	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

57	c1ffuA	Alignment	not modelled	14.1	29	PDB header: hydrolase Chain: A: PDB Molecule: cuts, iron-sulfur protein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
58	c1ep3B	Alignment	not modelled	13.7	33	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase b (pyrk subunit); PDBTitle: crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions.
59	c2l4aA	Alignment	not modelled	13.5	19	PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
60	c2rmlA	Alignment	not modelled	13.1	20	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
61	d1s05a	Alignment	not modelled	13.0	22	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
62	d1xn7a	Alignment	not modelled	12.6	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein YhgG
63	c1rm6F	Alignment	not modelled	12.5	33	PDB header: oxidoreductase Chain: F: PDB Molecule: 4-hydroxybenzoyl-coa reductase gamma subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
64	c3eubl	Alignment	not modelled	12.2	38	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of desulfo-xanthine oxidase with xanthine
65	d1jmsa3	Alignment	not modelled	12.1	12	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
66	c3b9jl	Alignment	not modelled	11.9	38	PDB header: oxidoreductase Chain: I: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
67	d1gaqb	Alignment	not modelled	11.9	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
68	c1t3qD	Alignment	not modelled	11.8	25	PDB header: oxidoreductase Chain: D: PDB Molecule: quinoline 2-oxidoreductase small subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
69	c1vlbA	Alignment	not modelled	11.7	56	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
70	c3c6fD	Alignment	not modelled	11.7	26	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: yetf protein; PDBTitle: crystal structure of protein bsu07140 from bacillus subtilis
71	d1fxia	Alignment	not modelled	11.6	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
72	d1vlba1	Alignment	not modelled	11.6	25	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
73	d2vana1	Alignment	not modelled	11.5	24	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
74	d1awda	Alignment	not modelled	11.4	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
75	c2ldfA	Alignment	not modelled	11.4	60	PDB header: toxin Chain: A: PDB Molecule: sarafotoxin-m; PDBTitle: solution structure of the long sarafotoxin srTx-m
76	d1a70a	Alignment	not modelled	11.2	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
77	c1dgiA	Alignment	not modelled	11.1	44	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
78	d1ep3b2	Alignment	not modelled	10.7	30	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Dihydroorotate dehydrogenase B, PyrK subunit
79	c3hrdH	Alignment	not modelled	10.4	25	PDB header: oxidoreductase Chain: H: PDB Molecule: nicotinate dehydrogenase small fes subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
80	c1n60D	Alignment	not modelled	10.1	29	PDB header: oxidoreductase Chain: D: PDB Molecule: carbon monoxide dehydrogenase small chain; PDBTitle: crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
81	d2g7ga1	Alignment	not modelled	10.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain PDB header: structural genomics, unknown function

82	c2l02B_	Alignment	not modelled	10.0	19	Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
83	d1jroa2	Alignment	not modelled	9.7	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
84	d1iuea_	Alignment	not modelled	9.5	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
85	d1ffva2	Alignment	not modelled	9.1	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
86	c2ds8A_	Alignment	not modelled	9.1	25	PDB header: metal binding protein, protein binding Chain: A: PDB Molecule: atp-dependent clp protease atp-binding subunit PDBTitle: structure of the zbd-xb complex
87	d1czpa_	Alignment	not modelled	8.8	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
88	d2bs2b2	Alignment	not modelled	8.7	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
89	d1aipc1	Alignment	not modelled	8.4	14	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
90	d1n62a2	Alignment	not modelled	8.4	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
91	d1offa_	Alignment	not modelled	8.3	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
92	d1frda_	Alignment	not modelled	8.2	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
93	c2piaA_	Alignment	not modelled	8.2	33	PDB header: reductase Chain: A: PDB Molecule: phthalate dioxygenase reductase; PDBTitle: phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2Fe-2s]
94	d1vlba2	Alignment	not modelled	8.0	44	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
95	d1lloa_	Alignment	not modelled	7.8	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
96	d1lvaa4	Alignment	not modelled	7.8	4	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
97	d2fmpa2	Alignment	not modelled	7.5	24	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
98	d1t3qa2	Alignment	not modelled	7.5	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
99	d1efub3	Alignment	not modelled	7.5	21	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain