

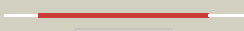





















Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	POA084
Date	Tue Jul 17 17:05:04 BST 2012
Unique Job ID	ff03cc090e036f4b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bqhA_	 Alignment		100.0	36	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)
2	c1fvaA_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: A; PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: crystal structure of bovine methionine sulfoxide reductase
3	d1fvga_	 Alignment		100.0	34	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
4	c3e0mB_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: B; PDB Molecule: peptide methionine sulfoxide reductase msra/msrb PDBTitle: crystal structure of fusion protein of msra and msrb
5	c3pi1A_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A; PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
6	c2j89A_	 Alignment		100.0	36	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
7	c1nwaA_	 Alignment		100.0	36	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
8	d1nwaa_	 Alignment		100.0	36	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
9	d1ff3a_	 Alignment		100.0	37	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
10	d1ff3c_	 Alignment		100.0	37	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
11	d1kvja_	 Alignment		96.3	22	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain

12	d1cpza_	Alignment		95.7	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
13	d1q8la_	Alignment		95.6	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
14	d1afia_	Alignment		95.4	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
15	d1p6ta1	Alignment		95.1	26	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
16	c2kkaA_	Alignment		95.0	15	PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
17	c1vjra_	Alignment		95.0	17	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
18	d1s6ua_	Alignment		94.8	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
19	c2ofhX_	Alignment		94.8	13	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
20	d1p6ta2	Alignment		94.7	23	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
21	c2ldiA_	Alignment	not modelled	94.4	17	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaa sub mutant
22	d2qifa1	Alignment	not modelled	94.3	22	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
23	c2ropA_	Alignment	not modelled	94.1	15	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b
24	d2aw0a_	Alignment	not modelled	93.9	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
25	c2ga7A_	Alignment	not modelled	93.8	11	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	c2l3ma_	Alignment	not modelled	93.6	26	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
27	c2ew9A_	Alignment	not modelled	93.5	15	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowln5-6
28	c2kt2A_	Alignment	not modelled	93.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
						Fold: Ferredoxin-like

29	d1osda_	Alignment	not modelled	93.4	22	Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
30	c2rmlA_	Alignment	not modelled	93.0	26	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
31	c3dxxX_	Alignment	not modelled	93.0	15	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
32	c3j09A_	Alignment	not modelled	93.0	17	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
33	d2ggpb1	Alignment	not modelled	92.8	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
34	c1y3kA_	Alignment	not modelled	91.9	17	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	c1yg0A_	Alignment	not modelled	88.8	18	PDB header: metal transport Chain: A: PDB Molecule: cop associated protein; PDBTitle: solution structure of apo-copp from helicobacter pylori
36	d1mwza_	Alignment	not modelled	88.8	11	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
37	c2gcfA_	Alignment	not modelled	86.6	16	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
38	d2phcb2	Alignment	not modelled	86.0	21	Fold: DCoH-like Superfamily: PH0987 N-terminal domain-like Family: PH0987 N-terminal domain-like
39	c2aj1A_	Alignment	not modelled	85.8	9	PDB header: hydrolase Chain: A: PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada
40	c2k2pA_	Alignment	not modelled	72.4	11	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
41	c2rogA_	Alignment	not modelled	71.4	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
42	c2phcB_	Alignment	not modelled	68.0	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein ph0987; PDBTitle: crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
43	c2kwaA_	Alignment	not modelled	61.9	17	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
44	d1vsra_	Alignment	not modelled	58.9	42	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
45	c2f40A_	Alignment	not modelled	56.0	16	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
46	c3oepA_	Alignment	not modelled	50.2	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha0988; PDBTitle: crystal structure of ttha0988 in space group p43212
47	d1qupa2	Alignment	not modelled	43.3	11	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
48	d1sb6a_	Alignment	not modelled	39.1	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
49	c2kyzA_	Alignment	not modelled	35.4	17	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
50	d1cw0a_	Alignment	not modelled	32.7	42	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
51	c1jk9D_	Alignment	not modelled	29.2	12	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-yosd1 and yccs
52	d2gz1a2	Alignment	not modelled	27.6	17	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
53	d1e3ha5	Alignment	not modelled	25.9	24	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
54	c3mmlD_	Alignment	not modelled	24.6	15	PDB header: hydrolase Chain: D: PDB Molecule: allophanate hydrolase subunit 1; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436 PDB header: rna binding protein

55	c3md1B_	Alignment	not modelled	22.5	7	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)
56	c3fryB_	Alignment	not modelled	22.1	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
57	d2cqpa1	Alignment	not modelled	19.2	11	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
58	d1fxla1	Alignment	not modelled	19.0	17	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
59	d1h2vz_	Alignment	not modelled	17.2	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
60	d1t4ba2	Alignment	not modelled	17.0	17	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
61	d2b0ja2	Alignment	not modelled	17.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
62	c3pgwS_	Alignment	not modelled	16.7	7	PDB header: splicing/dna/rna Chain: S: PDB Molecule: u1-70k; PDBTitle: crystal structure of human u1 snrnp
63	d1pugb_	Alignment	not modelled	16.4	18	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
64	d1pqua2	Alignment	not modelled	15.1	9	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
65	d1cc8a_	Alignment	not modelled	15.0	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
66	d1r6la2	Alignment	not modelled	14.8	22	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
67	d1tzfa_	Alignment	not modelled	14.5	36	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
68	d1udsa2	Alignment	not modelled	13.4	20	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
69	c1qupA_	Alignment	not modelled	13.2	11	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide2 dismutase
70	c3f46A_	Alignment	not modelled	12.1	27	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
71	d1fe0a_	Alignment	not modelled	11.4	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
72	c2crlA_	Alignment	not modelled	11.3	13	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
73	d1leha2	Alignment	not modelled	10.9	17	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
74	d1mb4a2	Alignment	not modelled	10.7	13	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
75	c2wqfA_	Alignment	not modelled	10.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: copper induced nitroreductase d; PDBTitle: crystal structure of the nitroreductase cind from2 lactococcus lactis in complex with fmn
76	d2je6b2	Alignment	not modelled	10.4	19	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
77	d1vqoa2	Alignment	not modelled	10.4	36	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
78	c2divA_	Alignment	not modelled	10.3	12	PDB header: rna binding protein Chain: A: PDB Molecule: trna selenocysteine associated protein; PDBTitle: solution structure of the rrm domain of trna selenocysteine2 associated protein
79	c2dnmA_	Alignment	not modelled	10.0	9	PDB header: rna binding protein Chain: A: PDB Molecule: srp46 splicing factor; PDBTitle: solution structure of rna binding domain in srp46 splicing2 factor
80	c2wzvB_	Alignment	not modelled	9.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nfnb protein; PDBTitle: crystal structure of the fmn-dependent nitroreductase

						nfnb2 from mycobacterium smegmatis
81	d1uala_	Alignment	not modelled	9.6	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
82	d1sl8a_	Alignment	not modelled	9.3	14	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
83	d1vjea_	Alignment	not modelled	9.2	21	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
84	d2cq3a1	Alignment	not modelled	8.9	20	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
85	c2e5hA_	Alignment	not modelled	8.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: zinc finger cchc-type and rna-binding motif- PDBTitle: solution structure of rna binding domain in zinc finger2 cchc-type and rna binding motif 1
86	c3va7A_	Alignment	not modelled	8.6	11	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
87	d2br2b2	Alignment	not modelled	8.4	20	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
88	d1whwa_	Alignment	not modelled	8.4	12	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
89	d2zjra2	Alignment	not modelled	8.2	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
90	d1rl2a2	Alignment	not modelled	8.1	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
91	d1ywqa1	Alignment	not modelled	8.1	10	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
92	d1bcoa1	Alignment	not modelled	7.6	20	Fold: mu transposase, C-terminal domain Superfamily: mu transposase, C-terminal domain Family: mu transposase, C-terminal domain
93	c2d9pA_	Alignment	not modelled	7.5	10	PDB header: rna binding protein Chain: A: PDB Molecule: polyadenylate-binding protein 3; PDBTitle: solution structure of rna binding domain 4 in2 polyadenylation binding protein 3
94	d2fura1	Alignment	not modelled	7.5	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
95	d1x5ta1	Alignment	not modelled	7.4	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
96	c3eo8A_	Alignment	not modelled	7.3	13	PDB header: flavoprotein Chain: A: PDB Molecule: blub-like flavoprotein; PDBTitle: crystal structure of blub-like flavoprotein (yp_001089088.1) from2 clostridium difficile 630 at 1.74 a resolution
97	c2b7lD_	Alignment	not modelled	7.2	10	PDB header: transferase Chain: D: PDB Molecule: glycerol-3-phosphate cytidyltransferase; PDBTitle: crystal structure of ctp:glycerol-3-phosphate2 cytidyltransferase from staphylococcus aureus
98	d2ghpa3	Alignment	not modelled	7.1	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
99	d1hl6a_	Alignment	not modelled	7.1	10	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD