

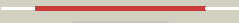





















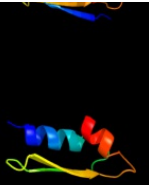
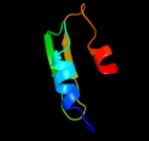

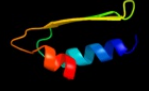






Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A086
Date	Tue Jul 17 17:05:04 BST 2012
Unique Job ID	f9ccc26106a810f1

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	c2j89A_	 Alignment		100.0	34	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
4	c1nwaA_	 Alignment		100.0	39	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
5	d1nwaA_	 Alignment		100.0	39	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
6	d1fvga_	 Alignment		100.0	35	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
7	c3e0mB_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: B; PDB Molecule: peptide methionine sulfoxide reductase msra/msrb PDBTitle: crystal structure of fusion protein of msra and msrb
8	d1ff3a_	 Alignment		100.0	35	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
9	c3pi1A_	 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
10	d1ff3c_	 Alignment		100.0	36	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
11	c1yjrA_	 Alignment		96.2	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
12	d1kvja_	 Alignment		95.9	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain

									Family: HMA, heavy metal-associated domain
13	d1cpza_	Alignment		95.8	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain			
14	d1q8la_	Alignment		95.7	17	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain			
15	d1afia_	Alignment		95.5	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain			
16	c2kkhA_	Alignment		95.2	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	d1p6ta1	Alignment		95.2	24	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain			
18	c2ew9A_	Alignment		95.1	22	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowIn5-6			
19	d1s6ua_	Alignment		94.9	17	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain			
20	c2ldiA_	Alignment		94.9	18	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaa sub mutant			
21	d2qifa1	Alignment	not modelled	94.7	24	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain			
22	d1p6ta2	Alignment	not modelled	94.6	17	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain			
23	c2ofhX_	Alignment	not modelled	94.5	16	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			
24	c2ropA_	Alignment	not modelled	94.2	15	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b			
25	d2aw0a_	Alignment	not modelled	94.1	22	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain			
26	c2ga7A_	Alignment	not modelled	94.1	9	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)			
27	c2l3mA_	Alignment	not modelled	94.0	24	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			
28	d1osda_	Alignment	not modelled	93.6	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain			
29	c2kt2A_	Alignment	not modelled	93.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmerA, the n-terminal hma domain of tn501 mercuric2 reductase			
30	c3dyeX_	Alignment	not modelled	93.4	20	PDB header: hydrolase Chain: X: PDB Molecule: copper-transporting atpase ran1;			

30	c0uxsA	Alignment	not modelled	93.4	20	PDBTitle: crystal structure of a copper binding domain from hma7, a p-2 type atpase PDB header: hydrolase
31	c2rmlA	Alignment	not modelled	93.2	17	Chain: A: PDB Molecule: copper-transporting p-type atpase copa; PDBTitle: solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
32	d2ggpb1	Alignment	not modelled	93.0	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
33	c3j09A	Alignment	not modelled	92.8	26	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
34	c1y3kA	Alignment	not modelled	91.7	15	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	89.2	16	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	88.7	14	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
37	c2gcfA	Alignment	not modelled	86.9	20	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	c2aj1A	Alignment	not modelled	85.4	7	PDB header: hydrolase Chain: A: PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada
39	d2phcb2	Alignment	not modelled	83.7	24	Fold: DCoH-like Superfamily: PH0987 N-terminal domain-like Family: PH0987 N-terminal domain-like
40	c2k2pA	Alignment	not modelled	73.1	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	70.6	16	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	68.1	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
43	d1vsra	Alignment	not modelled	66.1	33	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
44	c2f40A	Alignment	not modelled	62.5	8	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
45	c2kwaA	Alignment	not modelled	55.3	15	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
46	c3oepA	Alignment	not modelled	47.4	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	41.2	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
48	d1cw0a	Alignment	not modelled	40.3	33	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
49	c2hgnA	Alignment	not modelled	39.9	15	PDB header: rna binding protein Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein f; PDBTitle: nmr structure of the third qrrm domain of human hnrfp f
50	d1h2vz	Alignment	not modelled	39.1	14	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
51	d1sb6a	Alignment	not modelled	36.3	11	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
52	d1fxla1	Alignment	not modelled	35.1	14	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
53	c2kyzA	Alignment	not modelled	35.0	20	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	c3md1B	Alignment	not modelled	33.1	12	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)
55	d2gz1a2	Alignment	not modelled	30.8	30	Fold: FwdE/GAPDH domain-like Superfamily: Glycerol dehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like

56	d2cqpa1	Alignment	not modelled	28.4	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
57	c3pgw5_	Alignment	not modelled	28.1	5	PDB header: splicing/dna/rna Chain: S: PDB Molecule: u1-70k; PDBTitle: crystal structure of human u1 snrnp
58	d1e3ha5	Alignment	not modelled	27.8	25	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
59	c3mmlD_	Alignment	not modelled	26.2	14	PDB header: hydrolase Chain: D: PDB Molecule: allophanate hydrolase subunit 1; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
60	d2cq3a1	Alignment	not modelled	22.6	11	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
61	c3fryB_	Alignment	not modelled	20.2	15	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
62	c3f3mA_	Alignment	not modelled	18.5	33	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: six crystal structures of two phosphopantetheine adenylyltransferases2 reveal an alternative ligand binding mode and an associated3 structural change
63	c2d9pA_	Alignment	not modelled	18.2	9	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
64	d1t4ba2	Alignment	not modelled	17.8	17	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
65	c2divA_	Alignment	not modelled	17.8	7	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
66	d1pugb_	Alignment	not modelled	17.2	24	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
67	c2dnmA_	Alignment	not modelled	17.1	9	PDB header: rna binding protein Chain: A: PDB Molecule: srp46 splicing factor; PDBTitle: solution structure of rna binding domain in srp46 splicing2 factor
68	c3va7A_	Alignment	not modelled	17.1	11	PDB header: ligase Chain: A: PDB Molecule: kllA0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
69	d1pqua2	Alignment	not modelled	16.8	22	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
70	c1jk9D_	Alignment	not modelled	16.6	19	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-ysoD1 and yccs
71	d1x5ta1	Alignment	not modelled	16.5	9	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
72	d1hl6a_	Alignment	not modelled	16.4	16	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
73	d1fnxh1	Alignment	not modelled	16.3	10	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
74	d1udsA2	Alignment	not modelled	15.8	14	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
75	d2up1a2	Alignment	not modelled	15.7	12	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
76	d1whwa_	Alignment	not modelled	15.4	11	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
77	d1leha2	Alignment	not modelled	14.7	17	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
78	d1kgsa1	Alignment	not modelled	14.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
79	d1uala_	Alignment	not modelled	14.6	25	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
80	d1r6la2	Alignment	not modelled	14.4	16	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
81	c2crlA_	Alignment	not modelled	14.3	16	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

82	d1x4aa1	Alignment	not modelled	14.1	14	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
83	c2e5hA	Alignment	not modelled	13.9	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
84	d1cc8a	Alignment	not modelled	13.7	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
85	d1u7ka	Alignment	not modelled	12.8	26	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
86	d2erra1	Alignment	not modelled	12.8	12	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
87	d1mb4a2	Alignment	not modelled	12.7	17	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
88	c2dgaA	Alignment	not modelled	12.6	12	PDB header: rna binding protein Chain: A: PDB Molecule: probable rna-binding protein 19; PDBTitle: solution structure of the second rna recognition motif in2 rna-binding protein 19
89	c2wzvB	Alignment	not modelled	12.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nfnb protein; PDBTitle: crystal structure of the fnm-dependent nitroreductase nfnb2 from mycobacterium smegmatis
90	d2je6b2	Alignment	not modelled	12.5	16	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
91	c1m6vE	Alignment	not modelled	12.4	21	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
92	c2f3jA	Alignment	not modelled	12.2	12	PDB header: transport protein Chain: A: PDB Molecule: rna and export factor binding protein 2; PDBTitle: the solution structure of the ref2-i mrna export factor2 (residues 1-155).
93	d1a9xa4	Alignment	not modelled	12.0	22	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
94	d1sl8a	Alignment	not modelled	11.9	15	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
95	c1qapA	Alignment	not modelled	11.6	19	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide2 dismutase
96	c3cw18	Alignment	not modelled	10.8	7	PDB header: splicing Chain: 8: PDB Molecule: u1 small nuclear ribonucleoprotein 70 kda; PDB Fragment: nucleotides 57-82 absent, replaced with kissing loop; PDBTitle: crystal structure of human spliceosomal u1 snrnp
97	c2x1aA	Alignment	not modelled	10.7	14	PDB header: transcription/rna Chain: A: PDB Molecule: mrna 3'-end-processing protein rna15; PDBTitle: structure of rna15 rrm with rna bound (g)
98	d1rk8a	Alignment	not modelled	10.1	16	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
99	d2cqca1	Alignment	not modelled	10.1	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD