

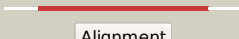

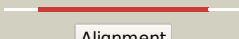



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0137c_msrA_164710_165258
Date	Tue Jul 23 14:50:18 BST 2019
Unique Job ID	80bcbbdb1eae7785

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nwaA_	 Alignment		100.0	100	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
2	d1nwaa_	 Alignment		100.0	100	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
3	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
4	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)
5	c2j89A_	 Alignment		100.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine sulfoxide reductase a; PDBTitle: functional and structural aspects of poplar cytosolic and2 plastidal type a methionine sulfoxide reductases
6	c1fvaA_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: crystal structure of bovine methionine sulfoxide reductase
7	c4d71B_	 Alignment		100.0	41	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: methionine sulfoxide reductase a of corynebacterium diphtheriae
8	c3pilA_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
9	d1fvga_	 Alignment		100.0	39	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
10	d1ff3a_	 Alignment		100.0	43	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
11	c5fa9B_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola

12	d1ff3c_	Alignment		100.0	43	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
13	c4lwIA_	Alignment		100.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: crystal structure of methionine sulfoxide reductase u16c/e55a from2 clostridium oremlandii
14	d1p6ta1	Alignment		96.8	23	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
15	d1kvja_	Alignment		96.4	24	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
16	c2ofgX_	Alignment		96.4	22	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
17	d1cpza_	Alignment		96.2	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
18	d1q8la_	Alignment		96.2	22	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
19	d1afia_	Alignment		96.0	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
20	c2lqbA_	Alignment		95.8	22	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: metal binding repeat 2 of the wilson disease protein (atp7b)
21	c1yjrA_	Alignment	not modelled	95.8	20	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
22	c2n7yA_	Alignment	not modelled	95.8	20	PDB header: metal binding protein Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: nmr structure of metal-binding domain 1 of atp7b
23	c2kkaA_	Alignment	not modelled	95.8	13	PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
24	c6ff2A_	Alignment	not modelled	95.8	26	PDB header: chaperone Chain: A: PDB Molecule: copper chaperone copz; PDBTitle: copz metallochaperone
25	d1p6ta2	Alignment	not modelled	95.7	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
26	d1s6ua_	Alignment	not modelled	95.6	22	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
27	c2ldiA_	Alignment	not modelled	95.5	21	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaan sub mutant
28	d2aw0a_	Alignment	not modelled	95.5	32	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
29	c1u9rA_	Alignment	not modelled	95.3	18	PDB header: hydrolase Chain: A: PDB Molecule: czcp cation efflux p1-atpase;

29	c4u91A	Alignment	not modelled	93.3	18	PDBTitle: structure of the n-terminal extension from cupriavidus metallidurans2 czcp
30	c2ofhX	Alignment	not modelled	95.3	19	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
31	d2qifa1	Alignment	not modelled	95.2	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
32	c2rmlA	Alignment	not modelled	95.2	22	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
33	c2ga7A	Alignment	not modelled	95.1	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)
34	c2ropA	Alignment	not modelled	95.1	17	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b
35	c2l3mA	Alignment	not modelled	94.9	22	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
36	c2ew9A	Alignment	not modelled	94.8	20	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowln5-6
37	c2kt2A	Alignment	not modelled	94.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
38	d1osda	Alignment	not modelled	94.7	24	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
39	d2ggpb1	Alignment	not modelled	94.4	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
40	c3j09A	Alignment	not modelled	94.4	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
41	c3dxxX	Alignment	not modelled	94.2	20	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
42	c1y3kA	Alignment	not modelled	94.0	24	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
43	d1mwza	Alignment	not modelled	91.7	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
44	c1yg0A	Alignment	not modelled	91.6	18	PDB header: metal transport Chain: A: PDB Molecule: cop associated protein; PDBTitle: solution structure of apo-copp from helicobacter pylori
45	c2aj1A	Alignment	not modelled	90.7	15	PDB header: hydrolase Chain: A: PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada
46	c2gcfA	Alignment	not modelled	90.5	23	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
47	d2phcb2	Alignment	not modelled	90.2	21	Fold: DCoH-like Superfamily: PH0987 N-terminal domain-like Family: PH0987 N-terminal domain-like
48	c4y2iA	Alignment	not modelled	82.6	19	PDB header: metal transport Chain: A: PDB Molecule: putative metal-binding transport protein; PDBTitle: gold ion bound to golb
49	c5i8iD	Alignment	not modelled	81.7	21	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
50	c2rogA	Alignment	not modelled	78.4	13	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
51	c2k2pA	Alignment	not modelled	78.2	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
52	c2phcB	Alignment	not modelled	77.4	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
53	c2kwaA	Alignment	not modelled	75.4	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
54	d1qupa2	Alignment	not modelled	67.7	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
						PDB header: structural genomics, unknown function

55	c3oepA_	Alignment	not modelled	67.3	30	Chain: A: PDB Molecule: putative uncharacterized protein ttha0988; PDBTitle: crystal structure of ttha0988 in space group p43212
56	c5dudB_	Alignment	not modelled	63.0	28	PDB header: unknown function Chain: B: PDB Molecule: ybgj; PDBTitle: crystal structure of e. coli ybgjk
57	d1vsra_	Alignment	not modelled	61.5	31	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
58	c2f40A_	Alignment	not modelled	57.8	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
59	d1sb6a_	Alignment	not modelled	50.8	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
60	c2kyzA_	Alignment	not modelled	49.6	14	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
61	c1jk9D_	Alignment	not modelled	40.3	14	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-ysoD1 and yccs
62	c3mmlD_	Alignment	not modelled	39.4	15	PDB header: hydrolase Chain: D: PDB Molecule: allophanate hydrolase subunit 1; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
63	c1ansA_	Alignment	not modelled	38.4	83	PDB header: toxin Chain: A: PDB Molecule: neurotoxin iii; PDBTitle: three-dimensional structure in solution of neurotoxin iii from the sea2 anemone anemonia sulcata
64	c3va7A_	Alignment	not modelled	37.7	11	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
65	c6nmiC_	Alignment	not modelled	36.3	17	PDB header: transcription Chain: C: PDB Molecule: general transcription factor iih subunit 1, p62; PDBTitle: cryo-em structure of the human tfiih core complex
66	c1qapA_	Alignment	not modelled	32.8	15	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide dismutase
67	d1cw0a_	Alignment	not modelled	30.9	42	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
68	c6o9l1_	Alignment	not modelled	29.1	18	PDB header: transcription/dna Chain: 1: PDB Molecule: general transcription factor iih subunit 1; PDBTitle: human holo-pic in the closed state
69	d2nn6b2	Alignment	not modelled	25.6	11	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
70	d2gz1a2	Alignment	not modelled	23.8	22	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
71	c2crlA_	Alignment	not modelled	23.8	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
72	d2je6b2	Alignment	not modelled	23.0	17	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
73	c3fryB_	Alignment	not modelled	22.9	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
74	c6fp6X_	Alignment	not modelled	22.3	10	PDB header: metal binding protein Chain: X: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: complex of human cu,zn sod1 with the human copper chaperone for sod12 in a compact conformation
75	d1cc8a_	Alignment	not modelled	20.9	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
76	c3md1B_	Alignment	not modelled	20.2	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)
77	d2br2b2	Alignment	not modelled	19.9	17	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
78	c4cwcC_	Alignment	not modelled	18.1	21	PDB header: isomerase Chain: C: PDB Molecule: replication initiation protein, replication initiation PDBTitle: structure of rolling circle replication initiator protein (2 repde) from staphylococcus aureus
79	d1leha2	Alignment	not modelled	16.1	20	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
						Fold: Ferredoxin-like

80	d1fxla1	Alignment	not modelled	16.0	12	Superfamily: RNA-binding domain, RBD Family: Canonical RBD
81	d1uala	Alignment	not modelled	15.7	25	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
82	c5gmk5	Alignment	not modelled	15.4	30	PDB header: rna binding protein/rna Chain: S; PDB Molecule: pre-mrna-splicing factor cwc15; PDBTitle: cryo-em structure of the catalytic step i spliceosome (c complex) at2 3.4 angstrom resolution
83	c4k6lG	Alignment	not modelled	15.3	12	PDB header: toxin Chain: G; PDB Molecule: putative pertussis-like toxin subunit; PDBTitle: structure of typhoid toxin
84	c6gg9A	Alignment	not modelled	15.2	33	PDB header: allergen Chain: A; PDB Molecule: major allergen cor a 1.0401; PDBTitle: solution structure of the hazel allergen cor a 1.0401
85	c5ensA	Alignment	not modelled	14.7	24	PDB header: transport protein Chain: A; PDB Molecule: multidrug efflux pump subunit acrb,multidrug efflux pump PDBTitle: rhodamine bound structure of bacterial efflux pump.
86	c4z9cA	Alignment	not modelled	14.4	16	PDB header: transferase Chain: A; PDB Molecule: pertussis toxin-like subunit arta; PDBTitle: ecpltab oxidized
87	d2cq3a1	Alignment	not modelled	13.9	14	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
88	d2nn6f2	Alignment	not modelled	13.1	17	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
89	d2cqpa1	Alignment	not modelled	12.6	11	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
90	d1u7ka	Alignment	not modelled	12.5	37	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
91	d1t4ba2	Alignment	not modelled	12.4	22	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
92	d1e3ha5	Alignment	not modelled	12.4	19	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
93	d1fe0a	Alignment	not modelled	12.3	33	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
94	d1sl8a	Alignment	not modelled	12.3	19	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
95	d1pqua2	Alignment	not modelled	11.6	9	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
96	c4f26A	Alignment	not modelled	11.1	14	PDB header: translation Chain: A; PDB Molecule: polyadenylate-binding protein 1; PDBTitle: crystal structure of the second rrm domain of human pabpc1 a ph 9.0
97	c2d9pA	Alignment	not modelled	10.9	8	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
98	c6hwwA	Alignment	not modelled	10.7	37	PDB header: viral protein Chain: A; PDB Molecule: putative gag polyprotein; PDBTitle: immature mlv capsid hexamer structure in intact virus particles
99	c2k2bA	Alignment	not modelled	10.6	26	PDB header: transport protein Chain: A; PDB Molecule: degenerin mec-4; PDBTitle: sparse-constraint solution nmr structure of micelle-2 solublized cytosolic amino terminal domain of c. elegans3 mechanosensory ion channel subunit mec-4. new york4 consortium on membrane protein structure (nycomps) (casp5 target)