



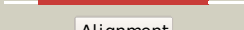


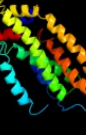

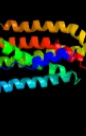

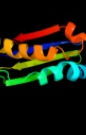




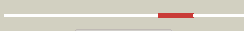


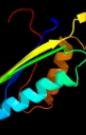











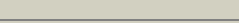

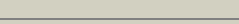
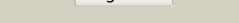
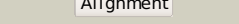
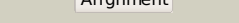
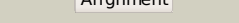
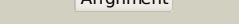
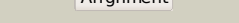
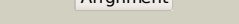
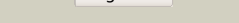
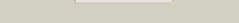
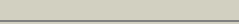
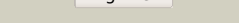
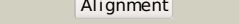
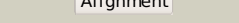
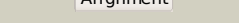
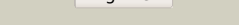
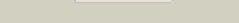
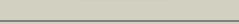

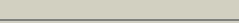



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">cloy8A_</a>	 Alignment		100.0	72	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein b; <b>PDBTitle:</b> structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
2	<a href="#">c3k07A_</a>	 Alignment		100.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cation efflux system protein cusa; <b>PDBTitle:</b> crystal structure of cusa
3	<a href="#">c3aqpB_</a>	 Alignment		100.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable secdf protein-export membrane protein; <b>PDBTitle:</b> crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
4	<a href="#">dliwga8</a>	 Alignment		100.0	72	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
5	<a href="#">dliwga7</a>	 Alignment		100.0	73	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
6	<a href="#">dliwga1</a>	 Alignment		99.9	76	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
7	<a href="#">dliwga2</a>	 Alignment		99.7	39	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
8	<a href="#">dliwga5</a>	 Alignment		99.6	68	<b>Fold:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Superfamily:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Family:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
9	<a href="#">dliwga6</a>	 Alignment		99.2	56	<b>Fold:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Superfamily:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Family:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
10	<a href="#">dliwga3</a>	 Alignment		98.8	65	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
11	<a href="#">dliwga4</a>	 Alignment		98.2	75	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains

12	<a href="#">c2ew9A_</a>	Alignment		96.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 2; <b>PDBTitle:</b> solution structure of apowln5-6
13	<a href="#">c2ropA_</a>	Alignment		95.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 2; <b>PDBTitle:</b> solution structure of domains 3 and 4 of human atp7b
14	<a href="#">c2rmlA_</a>	Alignment		94.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting p-type atpase copa; <b>PDBTitle:</b> solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
15	<a href="#">d1s6ua_</a>	Alignment		91.8	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
16	<a href="#">d2aw0a_</a>	Alignment		91.6	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
17	<a href="#">d1cpza_</a>	Alignment		91.2	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
18	<a href="#">d2qifa1</a>	Alignment		91.1	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
19	<a href="#">d1q8la_</a>	Alignment		91.0	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
20	<a href="#">c3dxsX_</a>	Alignment		90.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> copper-transporting atpase ran1; <b>PDBTitle:</b> crystal structure of a copper binding domain from hma7, a p-2 type atpase
21	<a href="#">c2l3mA_</a>	Alignment	not modelled	90.5	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> copper-ion-binding protein; <b>PDBTitle:</b> solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
22	<a href="#">d1p6ta1</a>	Alignment	not modelled	90.1	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
23	<a href="#">d1p6ta2</a>	Alignment	not modelled	90.0	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
24	<a href="#">d1kvja_</a>	Alignment	not modelled	89.8	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
25	<a href="#">c1yjrA_</a>	Alignment	not modelled	89.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
26	<a href="#">c2kkaA_</a>	Alignment	not modelled	89.3	13	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative heavy metal transporter; <b>PDBTitle:</b> structure of the zinc binding domain of the atpase hma4
27	<a href="#">c2ga7A_</a>	Alignment	not modelled	89.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
28	<a href="#">c1yg0A_</a>	Alignment	not modelled	89.2	9	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> cop associated protein; <b>PDBTitle:</b> solution structure of apo-copp from helicobacter pylori
						<b>PDB header:</b> hydrolase

29	<a href="#">c2ldiA_</a>	Alignment	not modelled	88.6	22	<b>Chain:</b> A: <b>PDB Molecule:</b> zinc-transporting atpase; <b>PDBTitle:</b> nmr solution structure of ziaa sub mutant
30	<a href="#">d1osda_</a>	Alignment	not modelled	88.5	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
31	<a href="#">c2ofhX_</a>	Alignment	not modelled	88.0	17	<b>PDB header:</b> hydrolase, membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> zinc-transporting atpase; <b>PDBTitle:</b> solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
32	<a href="#">c2kt2A_</a>	Alignment	not modelled	87.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
33	<a href="#">d1afia_</a>	Alignment	not modelled	87.0	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
34	<a href="#">c1y3kA_</a>	Alignment	not modelled	84.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the apo form of the fifth domain of2 menkes protein
35	<a href="#">d1qupa2_</a>	Alignment	not modelled	83.1	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
36	<a href="#">c1jk9D_</a>	Alignment	not modelled	81.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> copper chaperone for superoxide dismutase; <b>PDBTitle:</b> heterodimer between h48f-yso1 and yccs
37	<a href="#">c2k2pA_</a>	Alignment	not modelled	81.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1203; <b>PDBTitle:</b> solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
38	<a href="#">d2ggpb1_</a>	Alignment	not modelled	79.8	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
39	<a href="#">d1mwza_</a>	Alignment	not modelled	79.6	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
40	<a href="#">c2gcfA_</a>	Alignment	not modelled	78.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cation-transporting atpase pacs; <b>PDBTitle:</b> solution structure of the n-terminal domain of the copper(i) atpase2 pacs in its apo form
41	<a href="#">d1sb6a_</a>	Alignment	not modelled	77.4	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
42	<a href="#">c3j09A_</a>	Alignment	not modelled	77.2	20	<b>PDB header:</b> hydrolase, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper-exporting p-type atpase a; <b>PDBTitle:</b> high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
43	<a href="#">c2rogA_</a>	Alignment	not modelled	75.6	12	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heavy metal binding protein; <b>PDBTitle:</b> solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
44	<a href="#">c1qupA_</a>	Alignment	not modelled	75.2	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase 1 copper chaperone; <b>PDBTitle:</b> crystal structure of the copper chaperone for superoxide2 dismutase
45	<a href="#">c2crlA_</a>	Alignment	not modelled	74.7	16	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> copper chaperone for superoxide dismutase; <b>PDBTitle:</b> the apo form of hma domain of copper chaperone for2 superoxide dismutase
46	<a href="#">c2yvxD_</a>	Alignment	not modelled	67.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> mg2+ transporter mgte; <b>PDBTitle:</b> crystal structure of magnesium transporter mgte
47	<a href="#">d1cc8a_</a>	Alignment	not modelled	66.7	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
48	<a href="#">c2aj1A_</a>	Alignment	not modelled	66.5	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable cadmium-transporting atpase; <b>PDBTitle:</b> solution structure of apocada
49	<a href="#">c1yj7A_</a>	Alignment	not modelled	62.1	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> escj; <b>PDBTitle:</b> crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
50	<a href="#">c2kyzA_</a>	Alignment	not modelled	51.7	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heavy metal binding protein; <b>PDBTitle:</b> nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
51	<a href="#">c1ciiA_</a>	Alignment	not modelled	40.3	17	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
52	<a href="#">d2vv5a2_</a>	Alignment	not modelled	37.9	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain <b>Family:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain
53	<a href="#">d2cu6a1_</a>	Alignment	not modelled	37.8	20	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
54	<a href="#">d1uwda_</a>	Alignment	not modelled	36.6	13	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like

55	<a href="#">c3c6fD_</a>	 Alignment	not modelled	29.1	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> yefF protein; <b>PDBTitle:</b> crystal structure of protein bsu07140 from bacillus subtilis
56	<a href="#">c3gdzA_</a>	 Alignment	not modelled	28.1	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of arginyl-trna synthetase from klebsiella2 pneumoniae subsp. pneumoniae
57	<a href="#">c3fryB_</a>	 Alignment	not modelled	25.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable copper-exporting p-type atpase a; <b>PDBTitle:</b> crystal structure of the copa c-terminal metal binding domain
58	<a href="#">d1jb0i_</a>	 Alignment	not modelled	24.6	19	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit VIII of photosystem I reaction centre, Psal <b>Family:</b> Subunit VIII of photosystem I reaction centre, Psal
59	<a href="#">c3lnoA_</a>	 Alignment	not modelled	24.2	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of domain of unknown function duf59 from2 bacillus anthracis
60	<a href="#">d1f7ua3</a>	 Alignment	not modelled	21.2	13	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain <b>Family:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
61	<a href="#">d1fe0a_</a>	 Alignment	not modelled	20.6	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
62	<a href="#">c2bbjB_</a>	 Alignment	not modelled	19.6	9	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein; <b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
63	<a href="#">c2yy3B_</a>	 Alignment	not modelled	17.9	9	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 1-beta; <b>PDBTitle:</b> crystal structure of translation elongation factor ef-1 beta from2 pyrococcus horikoshii
64	<a href="#">d1ek8a_</a>	 Alignment	not modelled	16.5	27	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Ribosome recycling factor, RRF <b>Family:</b> Ribosome recycling factor, RRF
65	<a href="#">c3iplB_</a>	 Alignment	not modelled	16.1	12	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase; <b>PDBTitle:</b> crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
66	<a href="#">d1wqga1</a>	 Alignment	not modelled	15.8	19	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Ribosome recycling factor, RRF <b>Family:</b> Ribosome recycling factor, RRF
67	<a href="#">d1a87a_</a>	 Alignment	not modelled	15.7	15	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
68	<a href="#">c1a87A_</a>	 Alignment	not modelled	15.7	15	<b>PDB header:</b> bacteriocin <b>Chain:</b> A: <b>PDB Molecule:</b> colicin n; <b>PDBTitle:</b> colicin n
69	<a href="#">d1ydx2</a>	 Alignment	not modelled	14.6	19	<b>Fold:</b> DNA methylase specificity domain <b>Superfamily:</b> DNA methylase specificity domain <b>Family:</b> Type I restriction modification DNA specificity domain
70	<a href="#">c3g7sA_</a>	 Alignment	not modelled	13.8	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> long-chain-fatty-acid--coa ligase (fadd-1); <b>PDBTitle:</b> crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
71	<a href="#">d1dd5a_</a>	 Alignment	not modelled	13.6	15	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Ribosome recycling factor, RRF <b>Family:</b> Ribosome recycling factor, RRF
72	<a href="#">d1eh1a_</a>	 Alignment	not modelled	13.5	23	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Ribosome recycling factor, RRF <b>Family:</b> Ribosome recycling factor, RRF
73	<a href="#">d2phcb2</a>	 Alignment	not modelled	13.5	16	<b>Fold:</b> DCoH-like <b>Superfamily:</b> PH0987 N-terminal domain-like <b>Family:</b> PH0987 N-terminal domain-like
74	<a href="#">c2ki0A_</a>	 Alignment	not modelled	13.2	13	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> ds119; <b>PDBTitle:</b> nmr structure of a de novo designed beta alpha beta
75	<a href="#">d1is1a_</a>	 Alignment	not modelled	13.2	27	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Ribosome recycling factor, RRF <b>Family:</b> Ribosome recycling factor, RRF
76	<a href="#">d2nwwa1</a>	 Alignment	not modelled	13.0	10	<b>Fold:</b> Proton glutamate symport protein <b>Superfamily:</b> Proton glutamate symport protein <b>Family:</b> Proton glutamate symport protein
77	<a href="#">d2ffma1</a>	 Alignment	not modelled	12.9	9	<b>Fold:</b> Hypothetical protein SAV1430 <b>Superfamily:</b> Hypothetical protein SAV1430 <b>Family:</b> Hypothetical protein SAV1430
78	<a href="#">c1f7uA_</a>	 Alignment	not modelled	12.6	13	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg
79	<a href="#">d1kfta_</a>	 Alignment	not modelled	12.4	18	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Excinuclease UvrC C-terminal domain
80	<a href="#">c1kftA_</a>	 Alignment	not modelled	12.4	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc subunit c; <b>PDBTitle:</b> solution structure of the c-terminal domain of uvrC from e-2 coli

81	<a href="#">d2b3ya2</a>	Alignment	not modelled	12.2	43	<b>Fold:</b> Aconitase iron-sulfur domain <b>Superfamily:</b> Aconitase iron-sulfur domain <b>Family:</b> Aconitase iron-sulfur domain
82	<a href="#">c3g74B_</a>	Alignment	not modelled	12.1	42	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein of unknown function; <b>PDBTitle:</b> crystal structure of a functionally unknown protein from eubacterium2 ventriosum atcc 27560
83	<a href="#">d1x2ia1</a>	Alignment	not modelled	11.7	15	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
84	<a href="#">c2y9it</a>	Alignment	not modelled	11.6	14	<b>PDB header:</b> protein transport <b>Chain:</b> T: <b>PDB Molecule:</b> protein prgh; <b>PDBTitle:</b> three-dimensional model of salmonella's needle complex at2 subnanometer resolution
85	<a href="#">c2k1hA</a>	Alignment	not modelled	11.5	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ser13; <b>PDBTitle:</b> solution nmr structure of ser13 from staphylococcus epidermidis.2 northeast structural genomics consortium target ser13
86	<a href="#">c2vxaL_</a>	Alignment	not modelled	11.3	21	<b>PDB header:</b> flavoprotein <b>Chain:</b> L: <b>PDB Molecule:</b> dodecin; <b>PDBTitle:</b> h.halophila dodecin in complex with riboflavin
87	<a href="#">d1nwaa_</a>	Alignment	not modelled	11.2	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Peptide methionine sulfoxide reductase <b>Family:</b> Peptide methionine sulfoxide reductase
88	<a href="#">c1nwaA_</a>	Alignment	not modelled	11.2	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase msra; <b>PDBTitle:</b> structure of mycobacterium tuberculosis methionine2 sulfoxide reductase a in complex with protein-bound3 methionine
89	<a href="#">d2cfxa2</a>	Alignment	not modelled	11.2	7	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
90	<a href="#">c2hdiA_</a>	Alignment	not modelled	11.1	32	<b>PDB header:</b> protein transport,antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin i receptor; <b>PDBTitle:</b> crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
91	<a href="#">d1ge9a_</a>	Alignment	not modelled	10.9	15	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Ribosome recycling factor, RRF <b>Family:</b> Ribosome recycling factor, RRF
92	<a href="#">d1yvwa1</a>	Alignment	not modelled	10.9	27	<b>Fold:</b> all-alpha NTP pyrophosphatases <b>Superfamily:</b> all-alpha NTP pyrophosphatases <b>Family:</b> HisE-like (PRA-PH)
93	<a href="#">c1yvwD_</a>	Alignment	not modelled	10.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosyl-atp pyrophosphatase; <b>PDBTitle:</b> crystal structure of phosphoribosyl-atp2 pyrophosphohydrolase from bacillus cereus. nesgc target3 bcr13.
94	<a href="#">d2ux9a1</a>	Alignment	not modelled	10.8	14	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> Dodecin-like <b>Family:</b> Dodecin-like
95	<a href="#">d2cyya2</a>	Alignment	not modelled	10.7	4	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
96	<a href="#">c3oqtP_</a>	Alignment	not modelled	10.7	10	<b>PDB header:</b> flavoprotein <b>Chain:</b> P: <b>PDB Molecule:</b> rv1498a protein; <b>PDBTitle:</b> crystal structure of rv1498a protein from mycobacterium tuberculosis
97	<a href="#">d2cg4a2</a>	Alignment	not modelled	10.3	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
98	<a href="#">c2k9pA_</a>	Alignment	not modelled	10.3	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> pheromone alpha factor receptor; <b>PDBTitle:</b> structure of tm1_tm2 in lppg micelles
99	<a href="#">d2axti1</a>	Alignment	not modelled	10.3	12	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein I, Psbl <b>Family:</b> Psbl-like