Phyre^2

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Description	P76398
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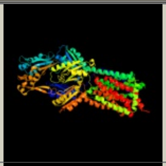
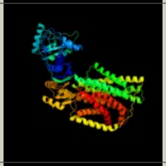
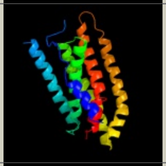
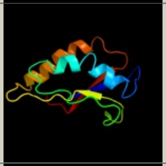
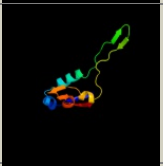
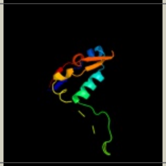
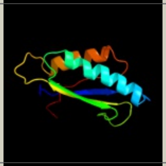
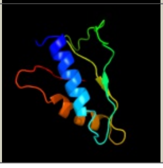
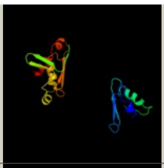
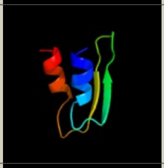
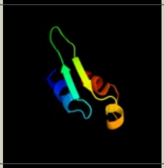
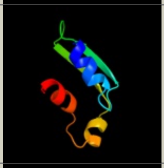
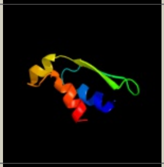
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k07A_	 Alignment		100.0	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
2	c1oy8A_	 Alignment		100.0	29	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
3	c3aqpB_	 Alignment		100.0	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
4	d1iwga8	 Alignment		100.0	30	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
5	d1iwga7	 Alignment		100.0	39	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
6	d1iwga1	 Alignment		99.9	30	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
7	d1iwga2	 Alignment		99.7	25	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
8	d1iwga5	 Alignment		99.5	32	**Fold:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Superfamily:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Family:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
9	d1iwga6	 Alignment		99.3	11	**Fold:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Superfamily:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Family:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
10	d1iwga3	 Alignment		98.9	16	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
11	d1iwga4	 Alignment		97.4	20	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains

12	c2ropA_	Alignment		95.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of domains 3 and 4 of human atp7b
13	c2ew9A_	Alignment		95.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of apowln5-6
14	c2rmlA_	Alignment		94.6	14	**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
15	d1q8la_	Alignment		89.5	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
16	c2kkhA_	Alignment		88.9	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
17	d1s6ua_	Alignment		88.4	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
18	d2aw0a_	Alignment		88.4	26	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
19	d2qifa1	Alignment		88.3	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
20	c2l3mA_	Alignment		88.0	15	**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
21	d1cpza_	Alignment	not modelled	87.3	22	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
22	d1osda_	Alignment	not modelled	87.3	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
23	d1afia_	Alignment	not modelled	86.4	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
24	c1yjrA_	Alignment	not modelled	86.3	9	**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
25	d1p6ta2	Alignment	not modelled	86.2	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
26	c2ofhX_	Alignment	not modelled	86.2	11	**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
27	d1p6ta1	Alignment	not modelled	86.1	13	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
28	c2ga7A_	Alignment	not modelled	85.8	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)
29	c3dxsX_	Alignment	not modelled	85.2	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1;

29	c3dxsX_	Alignment	not modelled	85.2	15	**PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
30	d1kvja_	Alignment	not modelled	85.2	22	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
31	c2ldiA_	Alignment	not modelled	84.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
32	c1y3kA_	Alignment	not modelled	83.7	7	**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
33	c2yvxD_	Alignment	not modelled	82.0	12	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
34	c2kt2A_	Alignment	not modelled	76.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
35	c1yg0A_	Alignment	not modelled	68.1	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
36	c2aj1A_	Alignment	not modelled	67.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
37	d1uwda_	Alignment	not modelled	66.6	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
38	d2cu6a1	Alignment	not modelled	65.6	23	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
39	c2gcfA_	Alignment	not modelled	60.2	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
40	d1mwza_	Alignment	not modelled	56.3	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
41	c1jk9D_	Alignment	not modelled	55.9	7	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** heterodimer between h48f-ysod1 and yccs
42	d1qupa2	Alignment	not modelled	54.9	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
43	d2ggpb1	Alignment	not modelled	53.9	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
44	c3j09A_	Alignment	not modelled	53.4	13	**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
45	c2zztA_	Alignment	not modelled	53.0	0	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
46	c1yj7A_	Alignment	not modelled	51.6	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**escj; **PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
47	c1ciiA_	Alignment	not modelled	49.5	12	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
48	c2k2pA_	Alignment	not modelled	45.9	5	**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
49	c2rogA_	Alignment	not modelled	42.7	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
50	c1qupA_	Alignment	not modelled	42.0	7	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase
51	c3lnoA_	Alignment	not modelled	40.8	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of domain of unknown function duf59 from2 bacillus anthracis
52	c2crlA_	Alignment	not modelled	40.1	23	**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
53	d2nwwa1	Alignment	not modelled	39.4	9	**Fold:**Proton glutamate symport protein **Superfamily:**Proton glutamate symport protein **Family:**Proton glutamate symport protein
54	d2cfxa2	Alignment	not modelled	37.2	0	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
						PDB header:oxidoreductase

55	c1nwaA_	Alignment	not modelled	35.0	21	**Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msra; **PDBTitle:** structure of mycobacterium tuberculosis methionine2 sulfoxide reductase a in complex with protein-bound3 methionine
56	d1nwaa_	Alignment	not modelled	35.0	21	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
57	d1sb6a_	Alignment	not modelled	33.4	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
58	c2bbjB_	Alignment	not modelled	32.5	15	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
59	d2cyya2	Alignment	not modelled	30.9	4	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
60	d2vv5a2	Alignment	not modelled	29.9	14	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain **Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain
61	c2yy3B_	Alignment	not modelled	29.3	4	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 1-beta; **PDBTitle:** crystal structure of translation elongation factor ef-1 beta from2 pyrococcus horikoshii
62	d1cc8a_	Alignment	not modelled	29.3	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
63	d2cg4a2	Alignment	not modelled	26.3	5	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
64	c2kncA_	Alignment	not modelled	25.9	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
65	d2phcb2	Alignment	not modelled	23.9	16	**Fold:**DCoH-like **Superfamily:**PH0987 N-terminal domain-like **Family:**PH0987 N-terminal domain-like
66	c3g7sA_	Alignment	not modelled	23.7	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1); **PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
67	c2zbcH_	Alignment	not modelled	21.3	7	**PDB header:**transcription **Chain:** H: **PDB Molecule:**83aa long hypothetical transcriptional regulator asnc; **PDBTitle:** crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
68	c3bqhA_	Alignment	not modelled	21.0	19	**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)
69	c2e1cA_	Alignment	not modelled	20.2	4	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
70	c2kyzA_	Alignment	not modelled	20.0	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
71	c2jnvA_	Alignment	not modelled	18.8	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 1, chloroplast; **PDBTitle:** solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
72	d1i1ga2	Alignment	not modelled	17.6	7	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
73	c3iplB_	Alignment	not modelled	16.7	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**2-succinylbenzoate--coa ligase; **PDBTitle:** crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
74	c2e1aD_	Alignment	not modelled	16.6	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
75	c2djwF_	Alignment	not modelled	15.9	13	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
76	c3e0mB_	Alignment	not modelled	15.6	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb **PDBTitle:** crystal structure of fusion protein of msra and msrb
77	c3aqoD_	Alignment	not modelled	14.6	18	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** structure and function of a membrane component secdf that enhances2 protein export
78	c2hdiA_	Alignment	not modelled	14.6	12	**PDB header:**protein transport,antimicrobial protein **Chain:** A: **PDB Molecule:**colicin i receptor; **PDBTitle:** crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
						PDB header:oxidoreductase

79	c2j89A_	Alignment	not modelled	14.4	16	**Chain:** A: **PDB Molecule:**methionine sulfoxide reductase a; **PDBTitle:** functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
80	d1oeya_	Alignment	not modelled	12.2	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
81	c3s6eB_	Alignment	not modelled	12.0	4	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**rna-binding protein 39; **PDBTitle:** crystal structure of a rna binding motif protein 39 (rbm39) from mus2 musculus at 0.95 a resolution
82	d1jb0i_	Alignment	not modelled	11.9	19	**Fold:**Single transmembrane helix **Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI **Family:**Subunit VIII of photosystem I reaction centre, PsaI
83	d2gufa1	Alignment	not modelled	11.8	17	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
84	c2vbzA_	Alignment	not modelled	11.8	9	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
85	d1xhja_	Alignment	not modelled	11.3	14	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
86	d1a87a_	Alignment	not modelled	10.6	13	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
87	c1a87A_	Alignment	not modelled	10.6	13	**PDB header:**bacteriocin **Chain:** A: **PDB Molecule:**colicin n; **PDBTitle:** colicin n
88	c3fryB_	Alignment	not modelled	10.4	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
89	c3pilA_	Alignment	not modelled	10.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
90	c2ki0A_	Alignment	not modelled	10.1	29	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**ds119; **PDBTitle:** nmr structure of a de novo designed beta alpha beta
91	d1th5a1	Alignment	not modelled	9.6	22	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
92	c1vbkA_	Alignment	not modelled	9.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
93	d1ff3a_	Alignment	not modelled	9.5	25	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
94	d1vbka2	Alignment	not modelled	9.5	18	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
95	c2vv5D_	Alignment	not modelled	9.3	14	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
96	d1j27a_	Alignment	not modelled	9.1	12	**Fold:**Ferredoxin-like **Superfamily:**Hypothetical protein TT1725 **Family:**Hypothetical protein TT1725
97	c3eynB_	Alignment	not modelled	9.0	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acyl-coenzyme a synthetase acsm2a; **PDBTitle:** crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa
98	d1dt9a3	Alignment	not modelled	8.9	18	**Fold:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 **Superfamily:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 **Family:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1
99	c2i88A_	Alignment	not modelled	8.9	6	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**colicin-e1; **PDBTitle:** crystal structure of the channel-forming domain of colicin2 e1