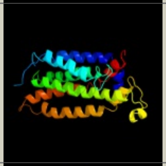
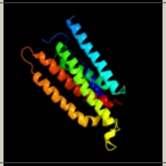
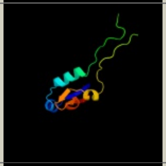
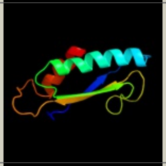
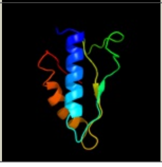
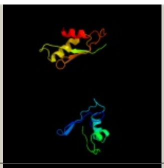
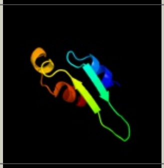
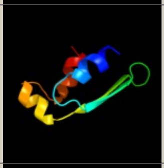
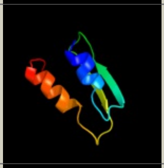
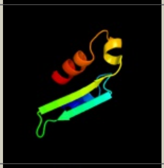
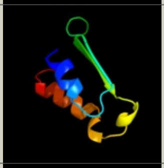
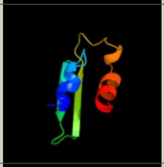
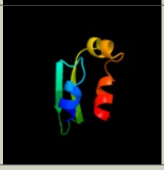
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P38054
Date	Thu Jan 5 11:57:54 GMT 2012
Unique Job ID	7903655c87458e30

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k07A_	Alignment		100.0	100	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
2	c1oy8A_	Alignment		100.0	20	**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	14	**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	19	**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	23	**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	24	**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	27	**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		99.6	26	**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	16	**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		98.1	14	**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		96.6	28	**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		94.6	15	**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		93.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of apowln5-6
14	d1s6ua_	Alignment		89.1	22	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
15	d2aw0a_	Alignment		88.4	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
16	d1q8la_	Alignment		87.9	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
17	c1yg0A_	Alignment		87.3	20	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
18	c1yjrA_	Alignment		87.0	10	**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
19	c2kkhA_	Alignment		86.5	27	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
20	d1cpza_	Alignment		86.4	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
21	d1kvja_	Alignment	not modelled	86.2	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
22	d2qifa1	Alignment	not modelled	86.2	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
23	d1p6ta2	Alignment	not modelled	85.3	22	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
24	c2rmlA_	Alignment	not modelled	84.9	21	**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
25	d1osda_	Alignment	not modelled	84.4	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
26	c2ldiA_	Alignment	not modelled	84.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
27	d1p6ta1	Alignment	not modelled	83.9	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
28	c2ofhX_	Alignment	not modelled	83.8	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
29	c2ga7A	Alignment	not modelled	83.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1;

		Alignment				**PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
30	c2kt2A_	Alignment	not modelled	83.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
31	c2l3mA_	Alignment	not modelled	82.4	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
32	c3dxsX_	Alignment	not modelled	81.4	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
33	c1y3kA_	Alignment	not modelled	79.2	8	**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
34	d2ggpb1	Alignment	not modelled	77.7	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
35	d1afia_	Alignment	not modelled	75.2	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
36	c2gcfA_	Alignment	not modelled	68.5	8	**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
37	d1mwza_	Alignment	not modelled	65.0	23	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
38	d1qupa2	Alignment	not modelled	64.4	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
39	c2k2pA_	Alignment	not modelled	62.8	14	**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
40	d1sb6a_	Alignment	not modelled	61.7	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
41	c1jk9D_	Alignment	not modelled	60.4	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** heterodimer between h48f-ysod1 and yccs
42	c1yj7A_	Alignment	not modelled	56.0	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**escj; **PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
43	c2yvxD_	Alignment	not modelled	53.8	12	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
44	c2aj1A_	Alignment	not modelled	52.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
45	c3j09A_	Alignment	not modelled	48.9	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
46	c2crlA_	Alignment	not modelled	48.7	15	**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
47	c2zztA_	Alignment	not modelled	45.0	6	**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
48	c2rogA_	Alignment	not modelled	44.6	17	**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
49	c1qupA_	Alignment	not modelled	42.9	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase
50	d1cc8a_	Alignment	not modelled	37.5	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
51	d1pw4a_	Alignment	not modelled	31.7	10	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
52	c1nwaA_	Alignment	not modelled	30.4	18	**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
53	d1nwaa_	Alignment	not modelled	30.4	18	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
54	d2cu6a1	Alignment	not modelled	30.1	17	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like

55	c2fyfB_	Alignment	not modelled	29.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
56	d2vv5a2	Alignment	not modelled	28.0	9	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain **Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain
57	c2kyzA_	Alignment	not modelled	24.5	16	**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
58	d1f7ua3	Alignment	not modelled	19.0	21	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain **Family:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
59	c3bqhA_	Alignment	not modelled	18.6	26	**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)
60	c2z51A_	Alignment	not modelled	17.6	11	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 2, chloroplast; **PDBTitle:** crystal structure of arabidopsis cnfu involved in iron-2 sulfur cluster biosynthesis
61	c2yy3B_	Alignment	not modelled	17.6	16	**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	c3g7sA_	Alignment	not modelled	16.5	16	**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
63	c2vxaL_	Alignment	not modelled	15.9	14	**PDB header:**flavoprotein **Chain:** L: **PDB Molecule:**dodecin; **PDBTitle:** h.halophila dodecin in complex with riboflavin
64	c3oqtP_	Alignment	not modelled	15.6	17	**PDB header:**flavoprotein **Chain:** P: **PDB Molecule:**rv1498a protein; **PDBTitle:** crystal structure of rv1498a protein from mycobacterium tuberculosis
65	c3fh6F_	Alignment	not modelled	15.5	12	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** crystal structure of the resting state maltose transporter from e.2 coli
66	c2y9jt_	Alignment	not modelled	15.0	15	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**protein prgh; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
67	d2ux9a1	Alignment	not modelled	14.8	11	**Fold:**Dodecin subunit-like **Superfamily:**Dodecin-like **Family:**Dodecin-like
68	c1u5tA_	Alignment	not modelled	13.9	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
69	c2j89A_	Alignment	not modelled	13.5	20	**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
70	c3e0mB_	Alignment	not modelled	13.4	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb **PDBTitle:** crystal structure of fusion protein of msra and msrb
71	c2yg8B_	Alignment	not modelled	13.4	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna-3-methyladenine glycosidase ii, putative; **PDBTitle:** structure of an unusual 3-methyladenine dna glycosylase ii (2 alka) from deinococcus radiodurans
72	d2cfxa2	Alignment	not modelled	13.2	5	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
73	c3c6fD_	Alignment	not modelled	13.2	12	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**yetf protein; **PDBTitle:** crystal structure of protein bsu07140 from bacillus subtilis
74	d1uwda_	Alignment	not modelled	13.2	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
75	c1vs3B_	Alignment	not modelled	12.7	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trna pseudouridine synthase a; **PDBTitle:** crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
76	c3fryB_	Alignment	not modelled	12.5	9	**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
77	c2jnvA_	Alignment	not modelled	12.4	22	**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
78	c3p14C_	Alignment	not modelled	12.1	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-rhamnose isomerase; **PDBTitle:** crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans
						PDB header:metal binding protein

79	c3onrl_	Alignment	not modelled	12.0	19	**Chain:** I: **PDB Molecule:**protein transport protein sece2; **PDBTitle:** crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
80	c2kssA_	Alignment	not modelled	12.0	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**carotenogenesis protein cars; **PDBTitle:** nmr structure of myxococcus xanthus antirepressor cars1
81	d1vkoa1	Alignment	not modelled	11.4	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
82	d1nh8a2	Alignment	not modelled	11.0	21	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
83	c3f10A_	Alignment	not modelled	10.8	32	**PDB header:**hydrolase, lyase **Chain:** A: **PDB Molecule:**8-oxoguanine-dna-glycosylase; **PDBTitle:** crystal structure of clostridium acetobutylicum 8-2 oxoguanine dna glycosylase in complex with 8-oxoguanosine
84	c2wzoA_	Alignment	not modelled	10.8	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**transforming growth factor beta regulator 1; **PDBTitle:** the structure of the fyr domain
85	c2hdiA_	Alignment	not modelled	10.7	27	**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.
86	d2cyya2	Alignment	not modelled	10.6	9	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
87	d2phcb2	Alignment	not modelled	10.5	15	**Fold:**DCoH-like **Superfamily:**PH0987 N-terminal domain-like **Family:**PH0987 N-terminal domain-like
88	d1nvmb2	Alignment	not modelled	10.4	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
89	c3iplB_	Alignment	not modelled	10.2	18	**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
90	d2cg4a2	Alignment	not modelled	10.0	5	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
91	d1xhja_	Alignment	not modelled	10.0	13	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
92	c3g74B_	Alignment	not modelled	9.9	50	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein of unknown function; **PDBTitle:** crystal structure of a functionally unknown protein from eubacterium2 ventriosum atcc 27560
93	d1s7ba_	Alignment	not modelled	9.9	13	**Fold:**Multidrug resistance efflux transporter EmrE **Superfamily:**Multidrug resistance efflux transporter EmrE **Family:**Multidrug resistance efflux transporter EmrE
94	d1wqga1	Alignment	not modelled	9.9	15	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
95	d1ib8a2	Alignment	not modelled	9.8	12	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**YhbC-like, N-terminal domain **Family:**YhbC-like, N-terminal domain
96	d2b3ya2	Alignment	not modelled	9.7	33	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
97	d1ciia1	Alignment	not modelled	9.7	21	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
98	d1ek8a_	Alignment	not modelled	9.5	31	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
99	c3p02A_	Alignment	not modelled	9.5	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein of unknown function (bacova_00267) from2 bacteroides ovatus at 1.55 a resolution