Email	l.a.kelley@imperial.ac.uk
Description	Q46798
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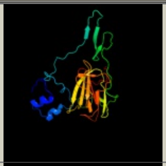
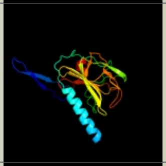
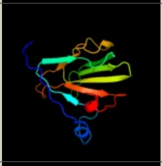
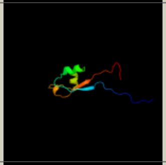
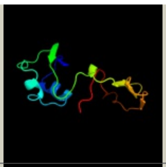
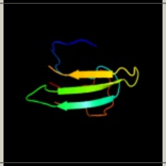
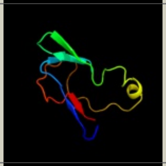
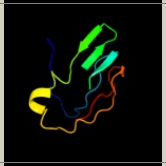
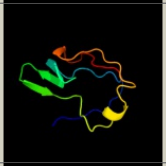
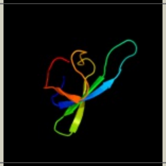
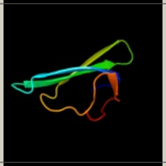
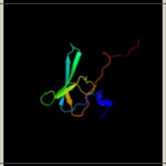
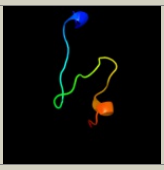
Unique Job ID	268d03a92a44ead4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gu1A_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
2	c2hsiB_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative peptidase m23; **PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
3	d1qwya_	Alignment		100.0	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Peptidoglycan hydrolase LytM
4	c3nyyA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycyl-glycine endopeptidase lytm; **PDBTitle:** crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
5	c2b44A_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm; **PDBTitle:** truncated s. aureus lytm, p 32 2 1 crystal form
6	c3it5B_	Alignment		99.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protease lasa; **PDBTitle:** crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
7	c3csqC_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
8	c2l9yA_	Alignment		98.8	23	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cvnh-lysm lectin; **PDBTitle:** solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)
9	c2djpA_	Alignment		98.6	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sb145; **PDBTitle:** the solution structure of the lysm domain of human2 hypothetical protein sb145
10	d1e0ga_	Alignment		98.3	29	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
11	d1y7ma2	Alignment		98.2	31	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain

12	c1y7mB_	Alignment		97.4	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14040; **PDBTitle:** crystal structure of the b. subtilis ykud protein at 2 a2 resolution
13	d2f3ga_	Alignment		96.2	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
14	d1glaf_	Alignment		95.9	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
15	d1gpra_	Alignment		95.7	29	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
16	d2gpra_	Alignment		95.7	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
17	d1e2wa2	Alignment		95.6	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
18	d1ci3m2	Alignment		95.1	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
19	c2aukA_	Alignment		94.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
20	c1e2vB_	Alignment		93.8	25	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
21	c1ctmA_	Alignment	not modelled	93.4	19	**PDB header:**electron transport(cytochrome) **Chain:** A: **PDB Molecule:**cytochrome f; **PDBTitle:** crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
22	c1q90A_	Alignment	not modelled	93.3	25	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**apocytochrome f; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
23	d1dcza_	Alignment	not modelled	92.7	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
24	c2ejgD_	Alignment	not modelled	91.8	31	**PDB header:**ligase **Chain:** D: **PDB Molecule:**149aa long hypothetical methylmalonyl-coa decarboxylase **PDBTitle:** crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
25	d1bdoa_	Alignment	not modelled	91.3	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
26	c2kccA_	Alignment	not modelled	90.6	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
27	c3n6rK_	Alignment	not modelled	90.4	28	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
28	c2b8gA_	Alignment	not modelled	90.4	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**biotin/lipoyl attachment protein;

28	c2b8gA_	Alignment	not modelled	90.4	18	**PDBTitle:** solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
29	d1hcza2	Alignment	not modelled	90.3	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
30	c1t5eB_	Alignment	not modelled	90.1	30	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
31	c2jxmB_	Alignment	not modelled	89.9	23	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
32	d1o78a_	Alignment	not modelled	89.7	35	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
33	c3lnnB_	Alignment	not modelled	89.7	26	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**membrane fusion protein (mfp) heavy metal cation efflux **PDBTitle:** crystal structure of zneb from cupriavidus metallidurans
34	c2aujD_	Alignment	not modelled	89.4	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
35	c2f1mA_	Alignment	not modelled	89.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
36	c1tu2B_	Alignment	not modelled	88.8	26	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**apocytochrome f; **PDBTitle:** the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
37	c2k33A_	Alignment	not modelled	88.7	26	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**acra; **PDBTitle:** solution structure of an n-glycosylated protein using in2 vitro glycosylation
38	c3fppB_	Alignment	not modelled	88.0	26	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**macrolide-specific efflux protein maca; **PDBTitle:** crystal structure of e.coli maca
39	d1vf7a_	Alignment	not modelled	87.9	30	**Fold:**HlyD-like secretion proteins **Superfamily:**HlyD-like secretion proteins **Family:**HlyD-like secretion proteins
40	c2ejmA_	Alignment	not modelled	87.5	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methylcrotonoyl-coa carboxylase subunit alpha; **PDBTitle:** solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
41	c2dn8A_	Alignment	not modelled	87.3	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
42	d1brwa3	Alignment	not modelled	87.0	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
43	d1laba_	Alignment	not modelled	86.9	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
44	d1tu2b2	Alignment	not modelled	85.9	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
45	c2q8iB_	Alignment	not modelled	85.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
46	c2l5tA_	Alignment	not modelled	84.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
47	d1y8ob1	Alignment	not modelled	84.3	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
48	d1qjoa_	Alignment	not modelled	83.7	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
49	d2pnrc1	Alignment	not modelled	82.1	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
50	c2dncA_	Alignment	not modelled	81.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component; **PDBTitle:** solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
51	d1ghja_	Alignment	not modelled	80.8	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
52	c2dneA_	Alignment	not modelled	80.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
53	c3h9iB_	Alignment	not modelled	78.2	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cation efflux system protein cusb; **PDBTitle:** crystal structure of the membrane fusion protein cusb

						from escherichia2 coli
54	c2j0fC_	Alignment	not modelled	77.9	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
55	c1otpA_	Alignment	not modelled	77.7	24	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
56	d1uoua3	Alignment	not modelled	77.2	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
57	d1k8ma_	Alignment	not modelled	76.7	9	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
58	c2dsjA_	Alignment	not modelled	76.6	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
59	c2jkuA_	Alignment	not modelled	76.1	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**propionyl-coa carboxylase alpha chain, **PDBTitle:** crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase
60	c3fmcC_	Alignment	not modelled	75.7	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative succinylglutamate desuccinylase / aspartoacylase; **PDBTitle:** crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
61	c2e75C_	Alignment	not modelled	75.6	21	**PDB header:**photosynthesis **Chain:** C: **PDB Molecule:**apocytochrome f; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
62	c2qj8B_	Alignment	not modelled	72.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
63	c2qf7A_	Alignment	not modelled	71.9	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
64	d1pmra_	Alignment	not modelled	71.3	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
65	c3cdxB_	Alignment	not modelled	70.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
66	d1gjxa_	Alignment	not modelled	70.7	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
67	c3na6A_	Alignment	not modelled	70.1	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinylglutamate desuccinylase/aspartoacylase; **PDBTitle:** crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
68	d2tpta3	Alignment	not modelled	70.1	21	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
69	d1mzya2	Alignment	not modelled	65.8	11	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
70	d1iyua_	Alignment	not modelled	65.8	14	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
71	c3ozxA_	Alignment	not modelled	65.4	14	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
72	c2xhaB_	Alignment	not modelled	62.1	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)
73	c2dafA_	Alignment		54.6	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flj35834 protein; **PDBTitle:** solution structure of the novel identified ubiquitin-like2 domain in the human hypothetical protein flj35834
74	c3h5qA_	Alignment	not modelled	54.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
75	c1brwB_	Alignment	not modelled	53.7	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
						Fold:alpha/beta-Hammerhead

76	d1o4ua2	Alignment	not modelled	49.5	16	**Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
77	d1qapa2	Alignment	not modelled	45.4	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
78	d1k8ga2	Alignment	not modelled	41.4	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
79	d1qpoa2	Alignment	not modelled	39.5	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
80	d1jb7a2	Alignment	not modelled	39.3	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
81	c2xhcA_	Alignment	not modelled	38.7	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
82	c3camB_	Alignment	not modelled	36.3	26	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**cold-shock domain family protein; **PDBTitle:** crystal structure of the cold shock domain protein from neisseria2 meningitidis
83	c3a5dB_	Alignment	not modelled	34.5	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**v-type atp synthase alpha chain; **PDBTitle:** inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
84	d1ndsa2	Alignment	not modelled	33.0	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
85	d2ns0a1	Alignment	not modelled	29.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
86	d2zjrt1	Alignment	not modelled	28.3	28	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**Ribosomal L27 protein
87	d1v8qa_	Alignment	not modelled	28.1	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**Ribosomal L27 protein
88	c3fin0_	Alignment	not modelled	25.6	20	**PDB header:**ribosome **Chain:** 0: **PDB Molecule:**50s ribosomal protein l27; **PDBTitle:** t. thermophilus 70s ribosome in complex with mrna, trnas2 and ef-tu.gdp.kirromycin ternary complex, fitted to a 6.43 a cryo-em map. this file contains the 50s subunit.
89	c2boyC_	Alignment	not modelled	25.3	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-chlorocatechol 1,2-dioxygenase; **PDBTitle:** crystal structure of 3-chlorocatechol 1,2-dioxygenase from2 rhodococcus opacus 1cp
90	d1vf5c2	Alignment	not modelled	24.3	44	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
91	d1snra2	Alignment	not modelled	24.2	16	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
92	c2elmA_	Alignment	not modelled	24.0	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 10th c2h2 zinc finger of human2 zinc finger protein 406
93	d3pcca_	Alignment	not modelled	23.5	9	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
94	c2kw8A_	Alignment	not modelled	23.5	3	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**lpxtg-site transpeptidase family protein; **PDBTitle:** solution structure of bacillus anthracis sortase a (srta)2 transpeptidase
95	d2awna2	Alignment	not modelled	23.1	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
96	d2bura1	Alignment	not modelled	22.7	18	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
97	d2es2a1	Alignment	not modelled	22.5	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
98	c2yz2B_	Alignment	not modelled	22.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative abc transporter atp-binding protein tm_0222; **PDBTitle:** crystal structure of the abc transporter in the cobalt transport2 system
99	d2burb1	Alignment	not modelled	21.6	18	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase