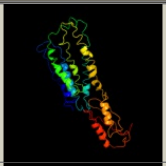
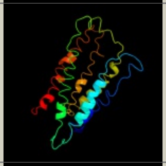
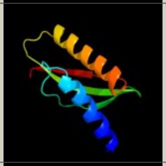
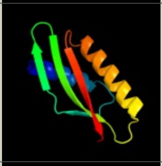
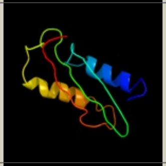
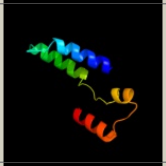
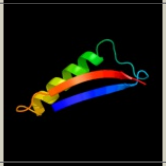
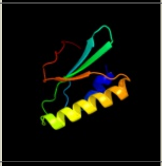
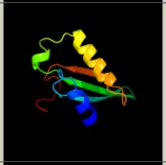
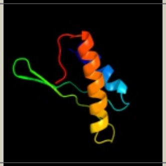
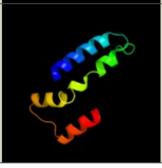
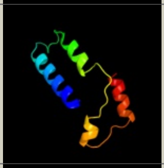
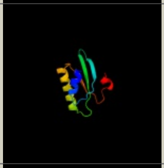
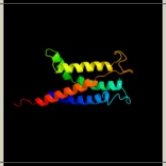
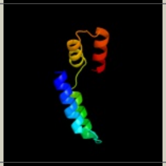
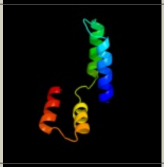
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P69380
Date	Thu Jan 5 12:11:26 GMT 2012
Unique Job ID	5ea24a0ec4e6877c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qfiB_	Alignment		100.0	100	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**ferrous-iron efflux pump fief; **PDBTitle:** structure of the zinc transporter yiip
2	d2qfia2	Alignment		100.0	100	**Fold:**Cation efflux protein transmembrane domain-like **Superfamily:**Cation efflux protein transmembrane domain-like **Family:**Cation efflux protein transmembrane domain-like
3	c2zztA_	Alignment		99.6	25	**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
4	d3bypa1	Alignment		99.6	34	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
5	d2qfia1	Alignment		99.5	100	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
6	d1dlca3	Alignment		58.5	18	**Fold:**Toxins' membrane translocation domains **Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain
7	d1ghha_	Alignment		57.6	15	**Fold:**DNA damage-inducible protein DinI **Superfamily:**DNA damage-inducible protein DinI **Family:**DNA damage-inducible protein DinI
8	c3qovD_	Alignment		56.2	9	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
9	c2y4oA_	Alignment		53.7	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak2 in complex with phenylacetyl adenylate
10	c3cd0B_	Alignment		53.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxy-3-methylglutaryl-coenzyme a reductase; **PDBTitle:** thermodynamic and structure guided design of statin hmg-coa2 reductase inhibitors
11	d1ji6a3	Alignment		45.8	15	**Fold:**Toxins' membrane translocation domains **Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain

12	c1hwjB_	Alignment		45.5	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**hmg-coa reductase; **PDBTitle:** complex of the catalytic portion of human hmg-coa reductase2 with cerivastatin
13	c1ji6A_	Alignment		42.2	16	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidial crystal protein cry3bb; **PDBTitle:** crystal structure of the insecticidal bacterial del2 endotoxin cry3bb1 bacillus thuringiensis
14	c2y27B_	Alignment		41.8	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
15	c3rfuC_	Alignment		39.6	11	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
16	d1f06a2	Alignment		35.8	19	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
17	d1dqaa1	Alignment		35.5	14	**Fold:**Ferredoxin-like **Superfamily:**NAD-binding domain of HMG-CoA reductase **Family:**NAD-binding domain of HMG-CoA reductase
18	c3eb7B_	Alignment		32.0	15	**PDB header:**toxin **Chain:** B: **PDB Molecule:**insecticidal delta-endotoxin cry8ea1; **PDBTitle:** crystal structure of insecticidal delta-endotoxin cry8ea1 from2 bacillus thuringiensis at 2.2 angstroms resolution
19	c1dlcA_	Alignment		31.5	18	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-endotoxin cryiiia; **PDBTitle:** crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution
20	d1wh9a_	Alignment		31.3	12	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
21	d1ib8a2	Alignment	not modelled	29.7	8	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**YhbC-like, N-terminal domain **Family:**YhbC-like, N-terminal domain
22	d1u8sa1	Alignment	not modelled	29.1	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
23	c2jo1A_	Alignment	not modelled	27.0	9	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
24	c3b64A_	Alignment	not modelled	24.4	13	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
25	c1u8sB_	Alignment	not modelled	21.7	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
26	d1uwda_	Alignment	not modelled	19.3	17	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
27	c2jp3A_	Alignment	not modelled	18.7	0	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
28	c3abfB_	Alignment	not modelled	17.4	9	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase

						homologue2 (tthb242)
29	d1fftb2	Alignment	not modelled	16.8	15	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
30	d1zpva1	Alignment	not modelled	16.7	6	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
31	c3laxA_	Alignment	not modelled	16.3	6	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
32	c3eynB_	Alignment	not modelled	16.1	8	**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
33	d1u8sa2	Alignment	not modelled	15.5	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
34	c3etcB_	Alignment	not modelled	14.8	7	**PDB header:**ligase **Chain:** B: **PDB Molecule:**amp-binding protein; **PDBTitle:** 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
35	c2zxeG_	Alignment	not modelled	12.8	6	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
36	d1x38a2	Alignment	not modelled	11.7	25	**Fold:**Flavodoxin-like **Superfamily:**Beta-D-glucan exohydrolase, C-terminal domain **Family:**Beta-D-glucan exohydrolase, C-terminal domain
37	c2ns6A_	Alignment	not modelled	11.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mobilization protein a; **PDBTitle:** crystal structure of the minimal relaxase domain of moba2 from plasmid r1162
38	c3kxwA_	Alignment	not modelled	11.6	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**saframycin mx1 synthetase b; **PDBTitle:** the crystal structure of fatty acid amp ligase from legionella2 pneumophila
39	c3hvwA_	Alignment	not modelled	11.1	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diguanylate-cyclase (dgc); **PDBTitle:** crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
40	c2iqcA_	Alignment	not modelled	9.8	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fanconi anemia group f protein; **PDBTitle:** crystal structure of human fancf protein that functions in2 the assembly of a dna damage signaling complex
41	d1q8ba_	Alignment	not modelled	9.8	10	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Hypothetical protein YjcS
42	c3gacD_	Alignment	not modelled	9.7	23	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** structure of mif with hpp
43	d2cu6a1	Alignment	not modelled	9.5	16	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
44	d1rq2a2	Alignment	not modelled	9.4	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
45	d1mlia_	Alignment	not modelled	9.4	5	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Muconalactone isomerase, MLI
46	d2aala1	Alignment	not modelled	9.2	13	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MSAD-like
47	c2x4kB_	Alignment	not modelled	8.9	7	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
48	d1wzua1	Alignment	not modelled	8.8	19	**Fold:**NadA-like **Superfamily:**NadA-like **Family:**NadA-like
49	c3mb2G_	Alignment	not modelled	8.3	16	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - alpha subunit; **PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
50	c1ex1A_	Alignment	not modelled	7.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (beta-d-glucan exohydrolase isoenzyme exo1); **PDBTitle:** beta-d-glucan exohydrolase from barley
51	d1lcia_	Alignment	not modelled	7.7	11	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
52	d1rwua_	Alignment	not modelled	7.7	8	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**YbeD-like
53	c1rwuA_	Alignment	not modelled	7.7	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0250 protein ybed;

						PDBTitle: solution structure of conserved protein ybed from e. coli
54	c3e7wA_	Alignment	not modelled	7.4	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** crystal structure of dlta: implications for the reaction2 mechanism of non-ribosomal peptide synthetase (nrps)3 adenylation domains
55	c1v55B_	Alignment	not modelled	7.3	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** bovine heart cytochrome c oxidase at the fully reduced state
56	c3mlcC_	Alignment	not modelled	7.2	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**fg41 malonate semialdehyde decarboxylase; **PDBTitle:** crystal structure of fg41msad inactivated by 3-chloropropiolate
57	c3m20A_	Alignment	not modelled	7.0	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative; **PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
58	d1uf0a_	Alignment	not modelled	6.8	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
59	d1xhja_	Alignment	not modelled	6.8	11	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
60	c2qs0A_	Alignment	not modelled	6.7	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**quinolinate synthetase a; **PDBTitle:** quinolinate synthase from pyrococcus furiosus
61	c3ry0A_	Alignment	not modelled	6.6	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
62	c2zkqc_	Alignment	not modelled	6.5	13	**PDB header:**ribosomal protein/rna **Chain:** C: **PDB Molecule:**rna expansion segment es4; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
63	c3dptB_	Alignment	not modelled	6.4	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**rab family protein; **PDBTitle:** cor domain of rab family protein (roco)
64	c1r7iB_	Alignment	not modelled	6.4	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxy-3-methylglutaryl-coenzyme a reductase; **PDBTitle:** hmg-coa reductase from p. mevalonii, native structure at 2.2 angstroms2 resolution.
65	c2kz0A_	Alignment	not modelled	6.4	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bola family protein; **PDBTitle:** solution structure of a bola protein (ech_0303) from ehrlichia2 chaffeensis. seattle structural genomics center for infectious3 disease target ehcha.10365.a
66	c3ibwA_	Alignment	not modelled	6.3	3	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
67	c2zw2B_	Alignment	not modelled	6.3	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
68	c3nyrA_	Alignment	not modelled	6.3	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**malonyl-coa ligase; **PDBTitle:** malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
69	c2dbbA_	Alignment	not modelled	6.2	11	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
70	d1uxya2	Alignment	not modelled	6.1	20	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
71	d2cfxa2	Alignment	not modelled	6.1	3	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
72	c2qieA_	Alignment	not modelled	6.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**molybdopterin-converting factor subunit 2; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
73	d1iwga3	Alignment	not modelled	6.0	8	**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
74	c3lnoA_	Alignment	not modelled	6.0	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of domain of unknown function duf59 from2 bacillus anthracis
75	d1gyxa_	Alignment	not modelled	6.0	18	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
76	c3ac0B_	Alignment	not modelled	6.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose

77	d2vapa2	Alignment	not modelled	5.9	28	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
78	d2ia7a1	Alignment	not modelled	5.8	7	**Fold:**gpW/gp25-like **Superfamily:**gpW/gp25-like **Family:**gpW/gp25-like
79	c2op8A_	Alignment	not modelled	5.8	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
80	d1ofua2	Alignment	not modelled	5.7	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
81	d2b3ja1	Alignment	not modelled	5.7	12	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
82	c2xq2A_	Alignment	not modelled	5.7	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
83	d2i1sa1	Alignment	not modelled	5.6	15	**Fold:**MM3350-like **Superfamily:**MM3350-like **Family:**MM3350-like
84	c2x41A_	Alignment	not modelled	5.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
85	c3brtC_	Alignment	not modelled	5.5	29	**PDB header:**transferase/transcription **Chain:** C: **PDB Molecule:**inhibitor of nuclear factor kappa-b kinase **PDBTitle:** nemo/ikk association domain structure
86	c2e1cA_	Alignment	not modelled	5.4	10	**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
87	d1otfa_	Alignment	not modelled	5.4	18	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
88	d1hp3a_	Alignment	not modelled	5.4	31	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
89	c3dhvA_	Alignment	not modelled	5.4	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase; **PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate
90	c3gdzA_	Alignment	not modelled	5.3	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of arginyl-trna synthetase from klebsiella2 pneumoniae subsp. pneumoniae
91	c1s1hC_	Alignment	not modelled	5.3	13	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**40s ribosomal protein s3; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
92	c1ypxA_	Alignment	not modelled	5.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative vitamin-b12 independent methionine synthase family **PDBTitle:** crystal structure of the putative vitamin-b12 independent methionine2 synthase from listeria monocytogenes, northeast structural genomics3 target lmr13
93	c2vv5D_	Alignment	not modelled	5.3	14	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
94	d2atza1	Alignment	not modelled	5.3	10	**Fold:**Prim-pol domain **Superfamily:**Prim-pol domain **Family:**HP0184-like
95	c1ib8A_	Alignment	not modelled	5.3	12	**PDB header:**nucleic acid binding protein **Chain:** A: **PDB Molecule:**conserved protein sp14.3; **PDBTitle:** solution structure and function of a conserved protein2 sp14.3 encoded by an essential streptococcus pneumoniae3 gene
96	c2khuA_	Alignment	not modelled	5.2	7	**PDB header:**transferase/protein binding **Chain:** A: **PDB Molecule:**immunoglobulin g-binding protein g, dna **PDBTitle:** solution structure of the ubiquitin-binding motif of human2 polymerase iota
97	c3fwtA_	Alignment	not modelled	5.0	10	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
98	c3lk6A_	Alignment	not modelled	5.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis
99	d1g9pa_	Alignment	not modelled	5.0	31	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins