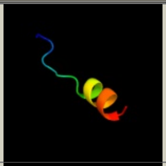
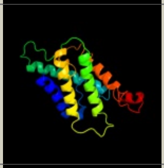
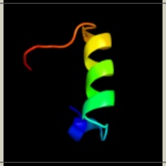
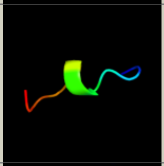
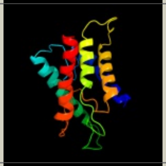
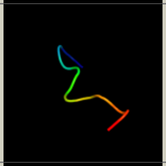
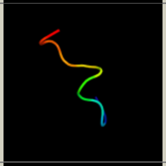
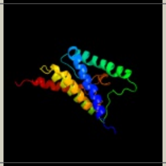
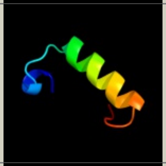
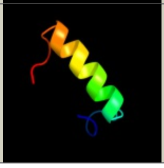
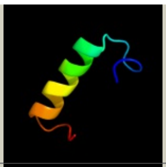
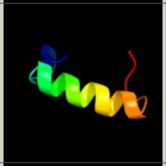
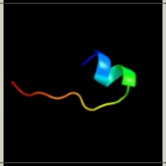
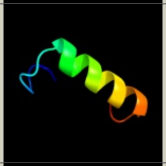
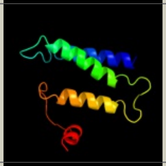
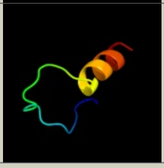
Email	l.a.kelley@imperial.ac.uk
Description	P43676
Date	Thu Jan 5 12:02:30 GMT 2012
Unique Job ID	fd5d3ed7605aeb3c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kncA_	Alignment		30.9	24	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
2	d1j4na_	Alignment		29.9	13	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
3	c2ia2D_	Alignment		28.8	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
4	c2bruC_	Alignment		26.3	42	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p) transhydrogenase subunit beta; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
5	d1h6ia_	Alignment		24.7	12	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
6	d1d4oa_	Alignment		24.3	42	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
7	c1pt9B_	Alignment		24.1	42	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
8	d1pnoa_	Alignment		23.9	33	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
9	c2w2eA_	Alignment		23.9	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin; **PDBTitle:** 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
10	c2g7uB_	Alignment		23.2	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
11	c3r4kD_	Alignment		20.4	22	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**transcriptional regulator, iclr family; **PDBTitle:** crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution

12	c1mkmA_	Alignment		17.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
13	c2xroE_	Alignment		16.8	26	**PDB header:**dna-binding protein/dna **Chain:** E: **PDB Molecule:**hth-type transcriptional regulator ttgv; **PDBTitle:** crystal structure of ttgv in complex with its dna operator
14	c2k1aA_	Alignment		15.2	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
15	d1vlpa2	Alignment		14.3	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase C-terminal domain
16	d1ybea1	Alignment		14.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase C-terminal domain
17	c2o0yB_	Alignment		13.9	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
18	d1mkma1	Alignment		13.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
19	d1s7ba_	Alignment		12.3	11	**Fold:**Multidrug resistance efflux transporter EmrE **Superfamily:**Multidrug resistance efflux transporter EmrE **Family:**Multidrug resistance efflux transporter EmrE
20	d2eiaa2	Alignment		11.9	11	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
21	d1yira1	Alignment	not modelled	11.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase C-terminal domain
22	c1vlpA_	Alignment	not modelled	11.5	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of a putative nicotinate phosphoribosyltransferase2 (yor209c, npt1) from saccharomyces cerevisiae at 1.75 a resolution
23	d1bw6a_	Alignment	not modelled	11.3	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
24	d2axtj1	Alignment	not modelled	10.3	23	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein J, PsbJ **Family:**PsbJ-like
25	d1vqo21	Alignment	not modelled	9.3	17	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Ribosomal protein L39e **Family:**Ribosomal protein L39e
26	c1l6nA_	Alignment	not modelled	9.2	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**gag polyprotein; **PDBTitle:** structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein
27	c2qksA_	Alignment	not modelled	9.2	14	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**kir3.1-prokaryotic kir channel chimera; **PDBTitle:** crystal structure of a kir3.1-prokaryotic kir channel chimera
28	d1oeya_	Alignment	not modelled	8.9	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain

29	d1wh7a_	Alignment	not modelled	8.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
30	c2wlvA_	Alignment	not modelled	8.5	26	**PDB header:**virus protein **Chain:** A: **PDB Molecule:**gag polyprotein; **PDBTitle:** structure of the n-terminal capsid domain of hiv-2
31	d1m9fd_	Alignment	not modelled	8.4	22	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
32	d2vv5a3	Alignment	not modelled	8.4	20	**Fold:**Mechanosensitive channel protein MscS (YggB), transmembrane region **Superfamily:**Mechanosensitive channel protein MscS (YggB), transmembrane region **Family:**Mechanosensitive channel protein MscS (YggB), transmembrane region
33	d1ymga1	Alignment	not modelled	8.4	13	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
34	c1ymgA_	Alignment	not modelled	8.4	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein; **PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution
35	c2kdpA_	Alignment	not modelled	8.2	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone deacetylase complex subunit sap30; **PDBTitle:** solution structure of the sap30 zinc finger motif
36	c2b2hA_	Alignment	not modelled	7.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
37	d2pxrc1	Alignment	not modelled	7.7	22	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
38	d1jb0i_	Alignment	not modelled	7.7	27	**Fold:**Single transmembrane helix **Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI **Family:**Subunit VIII of photosystem I reaction centre, PsaI
39	c2im5C_	Alignment	not modelled	7.6	47	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of nicotinate phosphoribosyltransferase2 from porphyromonas gingivalis
40	d2fhfa4	Alignment	not modelled	7.5	67	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
41	d2coba1	Alignment	not modelled	7.5	45	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
42	c2d57A_	Alignment	not modelled	7.3	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** double layered 2d crystal structure of aquaporin-4 (aqp4m23) at 3.2 a2 resolution by electron crystallography
43	d1uc8a1	Alignment	not modelled	7.0	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Lysine biosynthesis enzyme LysX, N-terminal domain
44	c1ifpA_	Alignment	not modelled	6.8	14	**PDB header:**virus **Chain:** A: **PDB Molecule:**major coat protein assembly; **PDBTitle:** inovirus (filamentous bacteriophage) strain pf3 major coat2 protein assembly
45	d1de4c3	Alignment	not modelled	6.8	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FolH catalytic domain-like
46	c2ajmA_	Alignment	not modelled	6.7	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**nonstructural protein 5a; **PDBTitle:** nmr structure of the in-plane membrane anchor domain [1-28]2 of the monotopic nonstructural protein 5a (ns5a) from the3 bovine viral diarrhea virus (bvdv)
47	d2ae9a1	Alignment	not modelled	6.6	30	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
48	c1ybeA_	Alignment	not modelled	6.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate phosphoribosyltransferase
49	c3a0bx_	Alignment	not modelled	6.6	9	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
50	c3a0hX_	Alignment	not modelled	6.6	9	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
51	c3a0hx_	Alignment	not modelled	6.6	9	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
52	c3a0bX_	Alignment	not modelled	6.6	9	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
53	c1z6fA_	Alignment	not modelled	6.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**penicillin-binding protein 5; **PDBTitle:** crystal structure of penicillin-binding protein 5 from e. coli in2 complex with a boronic acid inhibitor
54	c3d9sB_	Alignment	not modelled	6.5	18	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin-5; **PDBTitle:** human aquaporin 5 (aqp5) - high resolution x-ray structure
						PDB header:hydrolase

55	c2ootA_	Alignment	not modelled	6.5	20	**Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii
56	d1hlva1	Alignment	not modelled	6.4	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
57	d1sknp_	Alignment	not modelled	6.4	28	**Fold:**A DNA-binding domain in eukaryotic transcription factors **Superfamily:**A DNA-binding domain in eukaryotic transcription factors **Family:**A DNA-binding domain in eukaryotic transcription factors
58	d1j8yf2	Alignment	not modelled	6.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
59	d2idob1	Alignment	not modelled	6.4	25	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
60	c2xgyA_	Alignment	not modelled	6.3	15	**PDB header:**viral protein/isomerase **Chain:** A: **PDB Molecule:**relik capsid n-terminal domain; **PDBTitle:** complex of rabbit endogenous lentivirus (relik)capsid with2 cyclophilin a
61	d1m9dc_	Alignment	not modelled	6.3	26	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
62	d1fuia1	Alignment	not modelled	6.2	44	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**FucI/AraA C-terminal domain-like **Family:**L-fucose isomerase, C-terminal domain
63	c1q90R_	Alignment	not modelled	6.1	28	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
64	d1q90r_	Alignment	not modelled	6.1	28	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
65	c1s5lx_	Alignment	not modelled	6.1	9	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem ii psbx protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
66	d1c8za_	Alignment	not modelled	6.0	14	**Fold:**Tubby C-terminal domain-like **Superfamily:**Tubby C-terminal domain-like **Family:**Transcriptional factor tubby, C-terminal domain
67	d1fi4a1	Alignment	not modelled	6.0	24	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
68	c2rq5A_	Alignment	not modelled	5.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein jumonji; **PDBTitle:** solution structure of the at-rich interaction domain (arid)2 of jumonji/jarid2
69	c3b9yA_	Alignment	not modelled	5.9	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
70	d1se7a_	Alignment	not modelled	5.8	25	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
71	d2f7fa1	Alignment	not modelled	5.8	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
72	c1y32A_	Alignment	not modelled	5.8	35	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**humanin; **PDBTitle:** nmr structure of humanin in 30% tfe solution
73	d1obfo2	Alignment	not modelled	5.8	67	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
74	c2f7fA_	Alignment	not modelled	5.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase, putative; **PDBTitle:** crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
75	d2afwa1	Alignment	not modelled	5.7	33	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Glutaminyl-peptide cyclotransferase-like
76	d1wpga4	Alignment	not modelled	5.7	20	**Fold:**Calcium ATPase, transmembrane domain M **Superfamily:**Calcium ATPase, transmembrane domain M **Family:**Calcium ATPase, transmembrane domain M
77	c3mfdB_	Alignment	not modelled	5.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**d-alanyl-d-alanine carboxypeptidase dacb; **PDBTitle:** the structure of the beta-lactamase superfamily domain of d-alanyl-d-2 alanine carboxypeptidase from bacillus subtilis
78	c3os4A_	Alignment	not modelled	5.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** the crystal structure of nicotinate phosphoribosyltransferase from2 yersinia pestis
79	d1qd1a1	Alignment	not modelled	5.6	30	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. **Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.
80	d1ag7a_	Alignment	not modelled	5.6	50	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like

						Family: Conotoxin
81	c3gd8A_	Alignment	not modelled	5.6	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** crystal structure of human aquaporin 4 at 1.8 and its mechanism of2 conductance
82	d1iyxa2	Alignment	not modelled	5.6	15	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
83	c2h3oA_	Alignment	not modelled	5.5	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** structure of merft, a membrane protein with two trans-2 membrane helices
84	c2dvyA_	Alignment	not modelled	5.5	56	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease pabi; **PDBTitle:** crystal structure of restriction endonucleases pabi
85	d1bg6a1	Alignment	not modelled	5.5	4	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**N-(1-D-carboxylethyl)-L-norvaline dehydrogenase
86	d2h5na1	Alignment	not modelled	5.5	25	**Fold:**TerB-like **Superfamily:**TerB-like **Family:**PG1108-like
87	c1xooA_	Alignment	not modelled	5.5	56	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** nmr structure of g1s mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
88	c2kvlA_	Alignment	not modelled	5.4	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major outer capsid protein vp7; **PDBTitle:** nmr structure of the c-terminal domain of vp7
89	c1cx8F_	Alignment	not modelled	5.4	13	**PDB header:**metal transport **Chain:** F: **PDB Molecule:**transferrin receptor protein; **PDBTitle:** crytal structure of the ectodomain of human transferrin receptor
90	c2bsjB_	Alignment	not modelled	5.4	15	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein syct; **PDBTitle:** native crystal structure of the type iii secretion2 chaperone syct from yersinia enterocolitica
91	d1pvda1	Alignment	not modelled	5.4	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
92	c1fi4A_	Alignment	not modelled	5.3	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mevalonate 5-diphosphate decarboxylase; **PDBTitle:** the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
93	c1wazA_	Alignment	not modelled	5.3	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
94	d1c4ka1	Alignment	not modelled	5.3	50	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Ornithine decarboxylase N-terminal "wing" domain
95	c3ipdB_	Alignment	not modelled	5.3	5	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
96	d2ptza2	Alignment	not modelled	5.3	14	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
97	c3b8eB_	Alignment	not modelled	5.3	5	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
98	d1kjqa3	Alignment	not modelled	5.3	23	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
99	c1ot0A_	Alignment	not modelled	5.2	13	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**50s ribosomal protein l1; **PDBTitle:** structure of antimicrobial peptide, hp (2-20) and its2 analogues derived from helicobacter pylori, as determined3 by 1h nmr spectroscopy