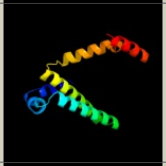
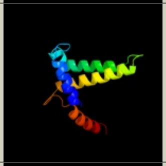
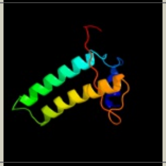
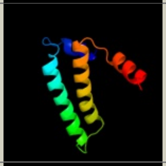
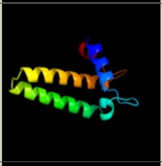
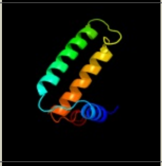
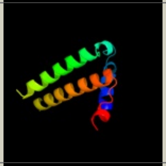
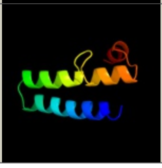
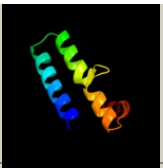
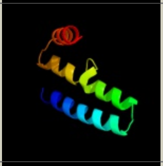
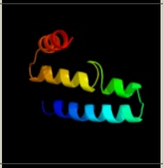
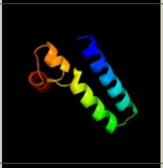
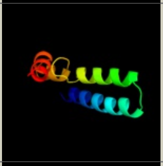
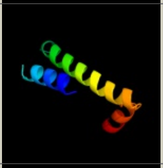
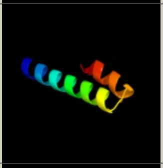
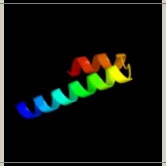
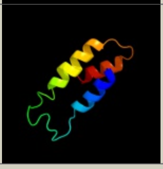
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AEY3
Date	Thu Jan 5 11:24:37 GMT 2012
Unique Job ID	8247e900352b15a5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3crcB_	 Alignment		100.0	94	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein mazg; **PDBTitle:** crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response
2	c2yxhB_	 Alignment		100.0	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mazg-related protein; **PDBTitle:** crystal structure of mazg-related protein from thermotoga maritima
3	d2a3qa1	 Alignment		99.6	17	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
4	c3obcB_	 Alignment		99.6	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pyrophosphatase; **PDBTitle:** crystal structure of a pyrophosphatase (af1178) from archaeoglobus2 fulgidus at 1.80 a resolution
5	c2q4pA_	 Alignment		99.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein rs21-c6; **PDBTitle:** ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
6	d2gtad1	 Alignment		99.3	25	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
7	d2gtaa1	 Alignment		99.1	27	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
8	d1vmga_	 Alignment		99.0	20	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
9	c2q9lA_	 Alignment		98.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
10	d2oiea1	 Alignment		98.3	17	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
11	d1yxba1	 Alignment		97.5	25	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)

12	d1y6xa1	Alignment		97.4	25	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
13	c1yvwD_	Alignment		97.0	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**phosphoribosyl-atp pyrophosphatase; **PDBTitle:** crystal structure of phosphoribosyl-atp2 pyrophosphohydrolase from bacillus cereus. nesgc target3 bcr13.
14	d1yvwa1	Alignment		97.0	18	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
15	c2a7wF_	Alignment		96.9	24	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**phosphoribosyl-atp pyrophosphatase; **PDBTitle:** crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7
16	d2a7wa1	Alignment		96.9	24	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
17	c2yf3F_	Alignment		93.9	32	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**mazg-like nucleoside triphosphate pyrophosphohydrolase; **PDBTitle:** crystal structure of dr2231, the mazg-like protein from2 deinococcus radiodurans, complex with manganese
18	c2p06A_	Alignment		92.5	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af_0060; **PDBTitle:** crystal structure of a predicted coding region af_0060 from2 archaeoglobus fulgidus dsm 4304
19	d2p06a1	Alignment		92.5	31	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**AF0060-like
20	c3nqwB_	Alignment		68.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cg11900; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
21	d2f02a1	Alignment	not modelled	56.5	22	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
22	d1zyma1	Alignment	not modelled	53.1	11	**Fold:**SAM domain-like **Superfamily:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain **Family:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain
23	c2hroA_	Alignment	not modelled	47.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
24	c3in1A_	Alignment	not modelled	38.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized sugar kinase ydjh; **PDBTitle:** crystal structure of a putative ribokinase in complex with2 adp from e.coli
25	c2lfcA_	Alignment	not modelled	35.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase, flavoprotein subunit; **PDBTitle:** solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
26	c3bf5A_	Alignment	not modelled	35.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribokinase related protein; **PDBTitle:** crystal structure of putative ribokinase (10640157) from thermoplasma2 acidophilum at 1.91 a resolution
27	d2dcna1	Alignment	not modelled	34.0	22	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase;

28	c2rfpA_	Alignment	not modelled	31.0	9	**PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
29	c3ah5E_	Alignment	not modelled	25.7	23	**PDB header:**transferase **Chain:** E: **PDB Molecule:**thymidylate synthase thyx; **PDBTitle:** crystal structure of flavin dependent thymidylate synthase thyx from2 helicobacter pylori complexed with fad and dump
30	d2j4ba1	Alignment	not modelled	24.1	19	**Fold:**Taf5 N-terminal domain-like **Superfamily:**Taf5 N-terminal domain-like **Family:**Taf5 N-terminal domain-like
31	c2jz8A_	Alignment	not modelled	23.3	80	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bh09830; **PDBTitle:** solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
32	c2varB_	Alignment	not modelled	22.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of sulfolobus solfataricus 2-keto-3-2 deoxygluconate kinase complexed with 2-keto-3-3 deoxygluconate
33	d1bpoa1	Alignment	not modelled	21.5	60	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Clathrin heavy-chain linker domain
34	d1qo8a3	Alignment	not modelled	19.7	24	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
35	d2afba1	Alignment	not modelled	19.0	15	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
36	d1y0pa3	Alignment	not modelled	18.8	20	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
37	c3muxB_	Alignment	not modelled	18.4	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative 4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
38	c2jg5B_	Alignment	not modelled	18.4	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructose 1-phosphate kinase; **PDBTitle:** crystal structure of a putative phosphofructokinase from2 staphylococcus aureus
39	d1vi9a_	Alignment	not modelled	18.1	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**PfkB-like kinase
40	c2nwhA_	Alignment	not modelled	18.1	17	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** carbohydrate kinase from agrobacterium tumefaciens
41	d2fv7a1	Alignment	not modelled	18.0	30	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
42	c3m6yA_	Alignment	not modelled	17.9	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
43	c3gbuD_	Alignment	not modelled	17.8	30	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uncharacterized sugar kinase ph1459; **PDBTitle:** crystal structure of an uncharacterized sugar kinase ph1459 from2 pyrococcus horikoshii in complex with atp
44	c2jg1C_	Alignment	not modelled	17.7	30	**PDB header:**transferase **Chain:** C: **PDB Molecule:**tagatose-6-phosphate kinase; **PDBTitle:** structure of staphylococcus aureus d-tagatose-6-phosphate2 kinase with cofactor and substrate
45	c3nybA_	Alignment	not modelled	17.6	14	**PDB header:**transferase/rna binding protein **Chain:** A: **PDB Molecule:**poly(a) rna polymerase protein 2; **PDBTitle:** structure and function of the polymerase core of tramp, a rna2 surveillance complex
46	d2fzpa1	Alignment	not modelled	17.4	42	**Fold:**NRDP1 C-terminal domain-like **Superfamily:**NRDP1 C-terminal domain-like **Family:**USP8 interacting domain
47	d1d4ca3	Alignment	not modelled	17.4	20	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
48	d1omha_	Alignment	not modelled	17.1	29	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Relaxase domain
49	c2i5bC_	Alignment	not modelled	16.9	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphomethylpyrimidine kinase; **PDBTitle:** the crystal structure of an adp complex of bacillus2 subtilis pyridoxal kinase provides evidence for the3 parralel emergence of enzyme activity during evolution
50	d3bvua1	Alignment	not modelled	16.7	12	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Families 57/38 glycoside transferase middle domain **Family:**alpha-mannosidase, domain 2
51	d1ogla_	Alignment	not modelled	16.6	25	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**Type II deoxyuridine triphosphatase
						PDB header:transferase

52	c3fnnA_	Alignment	not modelled	15.8	26	**Chain:** A: **PDB Molecule:**thymidylate synthase thyx; **PDBTitle:** biochemical and structural analysis of an atypical thyx:2 corynebacterium glutamicum nchu 87078 depends on thya for3 thymidine biosynthesis
53	d2f2aa1	Alignment	not modelled	15.6	19	**Fold:**Amidase signature (AS) enzymes **Superfamily:**Amidase signature (AS) enzymes **Family:**Amidase signature (AS) enzymes
54	c1iclA_	Alignment	not modelled	15.4	83	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**th1ox; **PDBTitle:** solution structure of designed beta-sheet mini-protein th1ox
55	c3hj6B_	Alignment	not modelled	15.4	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructokinase; **PDBTitle:** structure of halothermothrix orenii fructokinase (frk)
56	c2af6G_	Alignment	not modelled	15.3	29	**PDB header:**transferase **Chain:** G: **PDB Molecule:**thymidylate synthase thyx; **PDBTitle:** crystal structure of mycobacterium tuberculosis flavin dependent2 thymidylate synthase (mtb thyx) in the presence of co-factor fad and3 substrate analog 5-bromo-2'-deoxyuridine-5'-monophosphate (brdump)
57	d1vm7a_	Alignment	not modelled	15.2	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
58	d2ibge1	Alignment	not modelled	15.0	33	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**Hedgehog (development protein), N-terminal signaling domain
59	d1yvia1	Alignment	not modelled	14.7	2	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein-like
60	d2abqa1	Alignment	not modelled	14.5	30	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
61	c2rbcA_	Alignment	not modelled	14.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sugar kinase; **PDBTitle:** crystal structure of a putative ribokinase from agrobacterium2 tumefaciens
62	c2ddmA_	Alignment	not modelled	14.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxine kinase; **PDBTitle:** crystal structure of pyridoxal kinase from the escherichia2 coli pdxk gene at 2.1 a resolution
63	c2ld7B_	Alignment	not modelled	14.1	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**paired amphipathic helix protein sin3a; **PDBTitle:** solution structure of the msin3a pah3-sap30 sid complex
64	c2z36A_	Alignment	not modelled	13.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome p450 type compactin 3'',4''- **PDBTitle:** crystal structure of cytochrome p450 moxa from nonomuraea2 recticatena (cyp105)
65	c3cqdB_	Alignment	not modelled	13.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase isozyme 2; **PDBTitle:** structure of the tetrameric inhibited form of2 phosphofructokinase-2 from escherichia coli
66	c3egrB_	Alignment	not modelled	13.9	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phenylacetate-coa oxygenase subunit paab; **PDBTitle:** crystal structure of a phenylacetate-coa oxygenase subunit paab2 (reut_a2307) from ralstonia eutropha jmp134 at 2.65 a resolution
67	c1bpoA_	Alignment	not modelled	13.8	60	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein (clathrin); **PDBTitle:** clathrin heavy-chain terminal domain and linker
68	c3pl2D_	Alignment	not modelled	13.6	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sugar kinase, ribokinase family; **PDBTitle:** crystal structure of a 5-keto-2-deoxygluconokinase (ncgl0155, cgl0158)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.89 a3 resolution
69	d3d1ma1	Alignment	not modelled	13.6	33	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**Hedgehog (development protein), N-terminal signaling domain
70	d1wn0a1	Alignment	not modelled	13.6	5	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein-like
71	c3nnqA_	Alignment	not modelled	13.2	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**n-terminal domain of moloney murine leukemia virus **PDBTitle:** crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3
72	c2c49A_	Alignment	not modelled	13.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sugar kinase mj0406; **PDBTitle:** crystal structure of methanocaldococcus jannaschii2 nucleoside kinase - an archaeal member of the ribokinase3 family
73	d1ffgb_	Alignment	not modelled	12.9	38	**Fold:**Ferredoxin-like **Superfamily:**CheY-binding domain of CheA **Family:**CheY-binding domain of CheA
74	c2pmzL_	Alignment	not modelled	12.7	18	**PDB header:**translation, transferase **Chain:** L: **PDB Molecule:**dna-directed rna polymerase subunit l; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
75	c3skqA_	Alignment	not modelled	12.7	6	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**mitochondrial distribution and morphology protein 38; **PDBTitle:** mdm38 is a 14-3-3-like receptor and associates with the protein2 synthesis machinery at the inner mitochondrial membrane
						PDB header:protein transport

76	c1w7pD_	Alignment	not modelled	12.6	32	**Chain:** D: **PDB Molecule:**vps36p, ylr417w; **PDBTitle:** the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
77	c1a0oH_	Alignment	not modelled	12.5	38	**PDB header:**chemotaxis **Chain:** H: **PDB Molecule:**chea; **PDBTitle:** chey-binding domain of chea in complex with chey
78	c3lh5A_	Alignment	not modelled	12.5	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of the sh3-guanylate kinase core domain of zo-1
79	d2ix0a4	Alignment	not modelled	12.4	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RNB domain-like
80	c3ebnD_	Alignment	not modelled	12.3	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** a special dimerization of sars-cov main protease c-terminal2 domain due to domain-swapping
81	c3m1nB_	Alignment	not modelled	12.1	33	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**sonic hedgehog protein; **PDBTitle:** crystal structure of human sonic hedgehog n-terminal domain
82	c3e3vA_	Alignment	not modelled	11.9	11	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx from lactobacillus salivarius
83	d1rkda_	Alignment	not modelled	11.9	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
84	c3qk9B_	Alignment	not modelled	11.9	20	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**mitochondrial import inner membrane translocase subunit **PDBTitle:** yeast tim44 c-terminal domain complexed with cymal-3
85	c3kxaD_	Alignment	not modelled	11.4	31	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
86	c3ibqA_	Alignment	not modelled	11.2	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
87	c3fymA_	Alignment	not modelled	11.2	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus
88	d2absa1	Alignment	not modelled	11.1	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
89	c2absA_	Alignment	not modelled	11.1	19	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of t. gondii adenosine kinase complexed2 with amp-pcp
90	c3kzhA_	Alignment	not modelled	11.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable sugar kinase; **PDBTitle:** crystal structure of a putative sugar kinase from2 clostridium perfringens
91	c3l9qB_	Alignment	not modelled	10.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna primase large subunit; **PDBTitle:** crystal structure of human polymerase alpha-primase p58 iron-sulfur2 cluster domain
92	d1v19a_	Alignment	not modelled	10.8	30	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
93	c3lhxA_	Alignment	not modelled	10.8	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ketodeoxygluconokinase; **PDBTitle:** crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri
94	d1in0a1	Alignment	not modelled	10.8	15	**Fold:**Ferredoxin-like **Superfamily:**YajQ-like **Family:**YajQ-like
95	c2dydA_	Alignment	not modelled	10.8	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**poly(a)-binding protein; **PDBTitle:** solution structure of the pabc domain from triticum2 aevestium poly(a)-binding protein
96	d1bxya_	Alignment	not modelled	10.8	24	**Fold:**Ribosomal protein L30p/L7e **Superfamily:**Ribosomal protein L30p/L7e **Family:**Ribosomal protein L30p/L7e
97	d1sr2a_	Alignment	not modelled	10.5	5	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Sensor-like histidine kinase YojN, C-terminal domain
98	d1e85a_	Alignment	not modelled	10.5	23	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
99	c2pkkA_	Alignment	not modelled	10.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluro adenosine