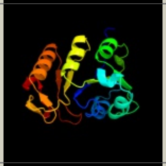
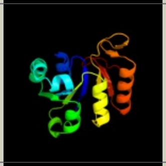
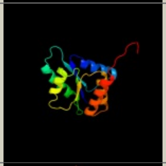
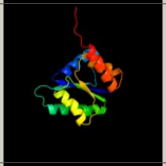
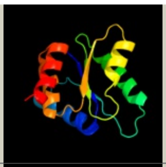
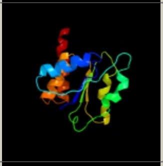
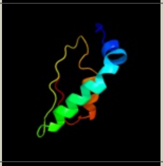
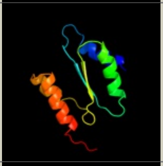
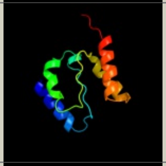
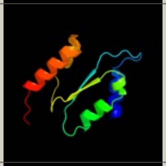
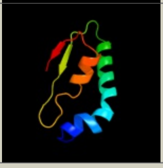
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P69797
Date	Thu Jan 5 12:12:00 GMT 2012
Unique Job ID	97a462c9829cb71f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vsqC_	Alignment		100.0	100	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannose-specific phosphotransferase enzyme iib **PDBTitle:** solution nmr structure of the productive complex between2 iiamannose and iibmannose of the mannose transporter of3 the e. coli phosphotransferase system
2	d1nrza_	Alignment		100.0	51	**Fold:**PTS IIb component **Superfamily:**PTS IIb component **Family:**PTS IIb component
3	d1blea_	Alignment		100.0	48	**Fold:**PTS IIb component **Superfamily:**PTS IIb component **Family:**PTS IIb component
4	c3lfjB_	Alignment		100.0	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, mannose/fructose/n- **PDBTitle:** crystal structure of manxb from thermoanaerobacter tengcongensis
5	c3p3vB_	Alignment		100.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts system, n-acetylgalactosamine-specific iib component; **PDBTitle:** crystal structure of a pts dependent n-acetyl-galactosamine-iib2 component (agav, spy_0631) from streptococcus pyogenes at 1.65 a3 resolution
6	c3eyeA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system n-acetylgalactosamine-specific iib **PDBTitle:** crystal structure of pts system n-acetylgalactosamine-2 specific iib component 1 from escherichia coli
7	d1pdoa_	Alignment		100.0	100	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
8	c3iprC_	Alignment		100.0	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
9	c3lfhF_	Alignment		100.0	34	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphotransferase system, mannose/fructose-specific **PDBTitle:** crystal structure of manxa from thermoanaerobacter tengcongensis
10	d3beda1	Alignment		100.0	23	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
11	c3mtqA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphoenolpyruvate-dependent sugar **PDBTitle:** crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution

12	c3gx1A_	Alignment		99.9	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1832 protein; **PDBTitle:** crystal structure of a domain of lin1832 from listeria innocua
13	d3b48a1	Alignment		99.8	11	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
14	c3gdwA_	Alignment		99.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
15	d3ct6a1	Alignment		99.1	15	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
16	c3edlA_	Alignment		87.9	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**alpha-tubulin; **PDBTitle:** kinesin13-microtubule ring complex
17	c2dt8A_	Alignment		86.2	15	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** fatty acid binding of a degv family protein from thermus thermophilus
18	c3lupA_	Alignment		82.2	12	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
19	c2g7zB_	Alignment		82.0	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein spy1493; **PDBTitle:** conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
20	c2btqB_	Alignment		80.8	17	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**tubulin btubb; **PDBTitle:** structure of btubab heterodimer from prosthecobacter2 dejongeii
21	c3lcmB_	Alignment	not modelled	74.2	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
22	c2btoA_	Alignment	not modelled	71.9	14	**PDB header:**cytoskeletal protein **Chain:** A: **PDB Molecule:**tubulin btuba; **PDBTitle:** structure of btuba from prosthecobacter dejongeii
23	c2p4nB_	Alignment	not modelled	71.8	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tubulin beta chain; **PDBTitle:** human monomeric kinesin (1bg2) and bovine tubulin (1jff)2 docked into the 9-angstrom cryo-em map of nucleotide-free3 kinesin complexed to the microtubule
24	c3nyiA_	Alignment	not modelled	70.4	15	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**fat acid-binding protein; **PDBTitle:** the crystal structure of a fat acid (stearic acid)-binding protein2 from eubacterium ventriosum atcc 27560.
25	d2czca2	Alignment	not modelled	70.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
26	c2qvcC_	Alignment	not modelled	69.6	9	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**sugar abc transporter, periplasmic sugar-binding **PDBTitle:** crystal structure of a periplasmic sugar abc transporter2 from thermotoga maritima
27	d2btoa1	Alignment	not modelled	68.3	14	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
28	c1mgpA_	Alignment	not modelled	66.3	17	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**hypothetical protein tm841; **PDBTitle:** hypothetical protein tm841 from thermotoga maritima

						reveals2 fatty acid binding function
29	d1mgpa_	Alignment	not modelled	66.3	17	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
30	d1pzxa_	Alignment	not modelled	66.3	12	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
31	d1tuba1	Alignment	not modelled	64.9	13	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
32	c3rfaA_	Alignment	not modelled	61.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase n; **PDBTitle:** x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
33	d1tubb1	Alignment	not modelled	60.8	8	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
34	c1z5wA_	Alignment	not modelled	57.7	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**tubulin gamma-1 chain; **PDBTitle:** crystal structure of gamma-tubulin bound to gtp
35	d1xm7a_	Alignment	not modelled	54.3	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Hypothetical protein aq 1666
36	c3ilhA_	Alignment	not modelled	51.4	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii
37	d1t0ia_	Alignment	not modelled	48.7	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
38	c2is8A_	Alignment	not modelled	48.6	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
39	c3l0gD_	Alignment	not modelled	48.3	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
40	c1qapA_	Alignment	not modelled	45.2	16	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
41	c3gl9B_	Alignment	not modelled	44.1	9	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
42	c4a26B_	Alignment	not modelled	43.8	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
43	d1rtta_	Alignment	not modelled	42.9	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
44	c3khtA_	Alignment	not modelled	41.5	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
45	c3p2oA_	Alignment	not modelled	40.8	11	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
46	c3p2oB_	Alignment	not modelled	40.6	11	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
47	c3q41B_	Alignment	not modelled	40.2	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate [nmda] receptor subunit zeta-1; **PDBTitle:** crystal structure of the glun1 n-terminal domain (ntd)
48	c3fysA_	Alignment	not modelled	39.9	13	**PDB header:**fatty acid-binding protein **Chain:** A: **PDB Molecule:**protein degv; **PDBTitle:** crystal structure of degv, a fatty acid binding protein2 from bacillus subtilis
49	c3eqzB_	Alignment	not modelled	39.3	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from colwellia2 psychrerythraea
50	d1tjna_	Alignment	not modelled	37.2	18	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**CbiX-like
51	c1tjnA_	Alignment	not modelled	37.2	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**sirohydrochlorin cobaltochelatase; **PDBTitle:** crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
52	d2obba1	Alignment	not modelled	36.8	10	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
53	d1r8ja2	Alignment	not modelled	36.0	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**N-terminal domain of the circadian clock protein KaiA

54	d1t0kb_	Alignment	not modelled	35.8	8	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
55	d2qwxa1	Alignment	not modelled	35.5	23	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
56	c3l07B_	Alignment	not modelled	35.1	10	**PDB header:**oxidoreductase,hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
57	c4a5oB_	Alignment	not modelled	34.7	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
58	c3n53B_	Alignment	not modelled	34.5	7	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase; **PDBTitle:** crystal structure of a response regulator receiver modulated2 diguanylate cyclase from pelobacter carbinolicus
59	c3eywA_	Alignment	not modelled	34.1	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
60	c3cz5B_	Alignment	not modelled	33.3	21	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**two-component response regulator, luxr family; **PDBTitle:** crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
61	c2qv0A_	Alignment	not modelled	33.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
62	c2p10D_	Alignment	not modelled	32.2	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
63	c2pjkA_	Alignment	not modelled	31.2	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
64	d1k66a_	Alignment	not modelled	30.9	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
65	c3h6hB_	Alignment	not modelled	30.1	9	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glutamate receptor, ionotropic kainate 2; **PDBTitle:** crystal structure of the glur6 amino terminal domain dimer assembly2 mpd form
66	c3sajB_	Alignment	not modelled	29.7	9	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate receptor 1; **PDBTitle:** crystal structure of glutamate receptor glua1 amino terminal domain
67	c2rjoA_	Alignment	not modelled	29.5	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
68	c1zfjA_	Alignment	not modelled	28.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
69	c3lftA_	Alignment	not modelled	28.2	8	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the abc domain in complex with l-trp from2 streptococcus pneumonia to 1.35a
70	d1a04a2	Alignment	not modelled	28.1	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
71	c1b0aA_	Alignment	not modelled	27.6	14	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
72	d1qrda_	Alignment	not modelled	27.5	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
73	c3cnbC_	Alignment	not modelled	26.9	11	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna-binding response regulator, merr family; **PDBTitle:** crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h
74	c3lyhB_	Alignment	not modelled	26.9	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cobalamin (vitamin b12) biosynthesis cbix protein; **PDBTitle:** crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution
75	c3pm7A_	Alignment	not modelled	26.7	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of ef_3132 protein from enterococcus faecalis at the2 resolution 2a, northeast structural genomics consortium target efr184
76	d2jfga2	Alignment	not modelled	26.5	15	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain

77	c2k1oA_	Alignment	not modelled	26.2	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative; **PDBTitle:** nmr structure of helicobacter pylori jhp0511 (hp0564).
78	d1w41a1	Alignment	not modelled	26.0	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
79	c2qsjB_	Alignment	not modelled	25.0	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-binding response regulator, luxr family; **PDBTitle:** crystal structure of a luxr family dna-binding response2 regulator from silicibacter pomeroyi
80	c3iefA_	Alignment	not modelled	24.8	19	**PDB header:**transferase, rna binding protein **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna guanine-n1-methyltransferase from2 bartonella henselae using mpcs.
81	c1mgtA_	Alignment	not modelled	24.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (o6-methylguanine-dna methyltransferase); **PDBTitle:** crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1
82	d2p10a1	Alignment	not modelled	23.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
83	c2hqbA_	Alignment	not modelled	23.4	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional activator of comk gene; **PDBTitle:** crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans
84	c3cg0A_	Alignment	not modelled	22.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase **PDBTitle:** crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
85	d1mb3a_	Alignment	not modelled	22.7	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
86	c3hebB_	Alignment	not modelled	22.6	8	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator receiver domain protein (chey); **PDBTitle:** crystal structure of response regulator receiver domain from2 rhodospirillum rubrum
87	c2qvgA_	Alignment	not modelled	22.0	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila
88	c3ho6B_	Alignment	not modelled	21.6	11	**PDB header:**toxin **Chain:** B: **PDB Molecule:**toxin a; **PDBTitle:** structure-function analysis of inositol hexakisphosphate-2 induced autoprocessing in clostridium difficile toxin a
89	c2qxyB_	Alignment	not modelled	21.4	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
90	c3eglC_	Alignment	not modelled	21.3	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of degv family protein cg2579 from corynebacterium2 glutamicum
91	c2p1zA_	Alignment	not modelled	21.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase; **PDBTitle:** crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
92	c1dd9A_	Alignment	not modelled	21.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** structure of the dnag catalytic core
93	d1dd9a_	Alignment	not modelled	21.0	18	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**DNA primase DnaG catalytic core
94	c1pd7B_	Alignment	not modelled	20.9	45	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mad1; **PDBTitle:** extended sid of mad1 bound to the pah2 domain of msin3b
95	c2c2xB_	Alignment	not modelled	20.9	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
96	d2i7pa1	Alignment	not modelled	20.7	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
97	c3kg2A_	Alignment	not modelled	20.6	11	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**glutamate receptor 2; **PDBTitle:** ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775
98	c3om1A_	Alignment	not modelled	20.6	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate receptor gluk5 (ka2); **PDBTitle:** crystal structure of the gluk5 (ka2) atd dimer at 1.7 angstrom2 resolution
99	c2kbfA_	Alignment	not modelled	20.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dbp5; **PDBTitle:** solution structure of carboxyl-terminal domain of dbp5p
100	d1qpoa1	Alignment	not modelled	20.4	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like