Email	l.a.kelley@imperial.ac.uk
Description	P64631
Date	Thu Jan 5 12:10:02 GMT 2012
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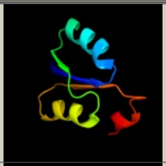
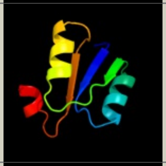
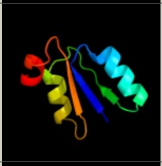
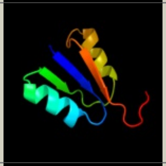
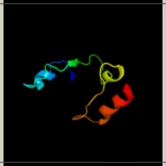
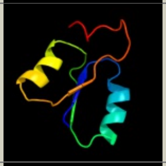
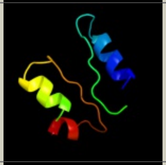
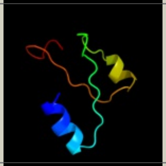
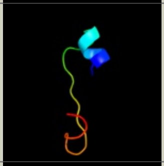
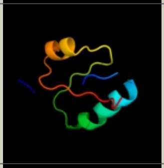
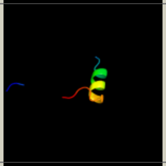
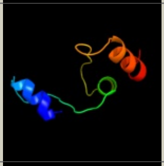
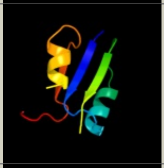
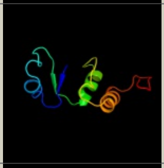
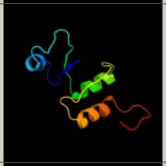
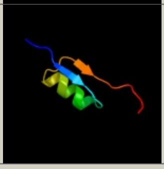
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3s5pA_	Alignment		90.4	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
2	d1nn4a_	Alignment		89.2	25	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
3	c3he8A_	Alignment		87.6	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
4	d2vvpa1	Alignment		83.9	15	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
5	d1o1xa_	Alignment		82.2	22	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
6	d2af4c1	Alignment		80.9	25	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
7	c3qd5B_	Alignment		78.1	25	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
8	c3m1pA_	Alignment		77.3	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
9	c3k7pA_	Alignment		76.4	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
10	c2ppwA_	Alignment		68.9	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
11	c3c5yD_	Alignment		67.5	24	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution

12	d1u5wa1	Alignment		64.8	14	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
13	c3onoA_	Alignment		58.6	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
14	c3s81A_	Alignment		58.5	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium
15	d2j85a1	Alignment		57.1	30	**Fold:**STIV B116-like **Superfamily:**STIV B116-like **Family:**STIV B116-like
16	d1r5ja_	Alignment		53.4	25	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
17	c1ycoA_	Alignment		49.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**branched-chain phosphotransacylase; **PDBTitle:** crystal structure of a branched-chain phosphotransacylase from2 enterococcus faecalis v583
18	c1vmiA_	Alignment		48.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphate acetyltransferase; **PDBTitle:** crystal structure of putative phosphate acetyltransferase2 (np_416953.1) from escherichia coli k12 at 2.32 a resolution
19	d1vmia_	Alignment		48.3	21	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
20	d1nsja_	Alignment		46.5	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
21	c3l6gA_	Alignment	not modelled	44.6	16	**PDB header:**glycine betaine-binding protein **Chain:** A: **PDB Molecule:**betaine abc transporter permease and substrate binding **PDBTitle:** crystal structure of lactococcal opuac in its open conformation
22	d1zbsa2	Alignment	not modelled	39.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
23	d1ni9a_	Alignment	not modelled	38.4	11	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**GlpX-like bacterial fructose-1,6-bisphosphatase
24	d1vi1a_	Alignment	not modelled	34.4	28	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
25	d1xcoa_	Alignment	not modelled	33.8	25	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
26	d2ch5a2	Alignment	not modelled	31.8	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
27	c3o66A_	Alignment	not modelled	30.3	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline abc transporter; **PDBTitle:** crystal structure of glycine betaine/carnitine/choline abc transporter
28	c2dx7B_	Alignment	not modelled	30.1	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**aspartate racemase; **PDBTitle:** crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid

29	c2kzhA_	Alignment	not modelled	28.3	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tryptophan biosynthesis protein trpcf; **PDBTitle:** three-dimensional structure of a truncated phosphoribosylanthranilate2 isomerase (residues 255-384) from escherichia coli
30	c3tngA_	Alignment	not modelled	27.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lmo1369 protein; **PDBTitle:** the crystal structure of a possible phosphate acetyl/butaryl2 transferase from listeria monocytogenes egd-e.
31	d2hrca1	Alignment	not modelled	27.9	21	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
32	d1zxoa1	Alignment	not modelled	27.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
33	d2cpwa1	Alignment	not modelled	27.2	13	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
34	c2rejA_	Alignment	not modelled	26.4	16	**PDB header:**choline-binding protein **Chain:** A: **PDB Molecule:**putative glycine betaine abc transporter protein; **PDBTitle:** abc-transporter choline binding protein in unliganded semi-2 closed conformation
35	c2x4iA_	Alignment	not modelled	25.1	39	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein 114; **PDBTitle:** orf 114a from sulfolobus islandicus rudivirus 1
36	d2gkea2	Alignment	not modelled	24.6	34	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Diaminopimelate epimerase
37	c3tmgA_	Alignment	not modelled	24.3	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine, l-proline abc transporter, **PDBTitle:** crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
38	d1vg5a_	Alignment	not modelled	21.0	37	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
39	d1p9qc2	Alignment	not modelled	18.2	25	**Fold:**FYSH domain **Superfamily:**FYSH domain **Family:**Hypothetical protein AF0491, N-terminal domain
40	c3uatA_	Alignment	not modelled	17.8	20	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**disks large homolog 1; **PDBTitle:** guanylate kinase domains of the maguk family scaffold proteins as2 specific phospho-protein binding modules
41	d1u7na_	Alignment	not modelled	17.3	44	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
42	c2jrlA_	Alignment	not modelled	16.9	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
43	c3fveA_	Alignment	not modelled	16.7	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**diaminopimelate epimerase; **PDBTitle:** crystal structure of diaminopimelate epimerase mycobacterium2 tuberculosis dapf
44	c3b2nA_	Alignment	not modelled	16.1	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
45	c2dakA_	Alignment	not modelled	16.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
46	d1zwya1	Alignment	not modelled	15.3	30	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
47	c3un6A_	Alignment	not modelled	14.6	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein saouhsc_00137; **PDBTitle:** 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
48	d1vmea1	Alignment	not modelled	13.8	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
49	d1o4ua1	Alignment	not modelled	13.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
50	d1rypd_	Alignment	not modelled	13.5	26	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
51	c2v25B_	Alignment	not modelled	13.3	6	**PDB header:**receptor **Chain:** B: **PDB Molecule:**major cell-binding factor; **PDBTitle:** structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate
52	d1rypg_	Alignment	not modelled	12.8	25	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
53	c3bdmF_	Alignment	not modelled	12.8	25	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome component c1; **PDBTitle:** yeast 20s proteasome:glidobactin a-complex
						Fold: Ntn hydrolase-like

54	d1j2pa_	Alignment	not modelled	12.7	24	**Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
55	c2crnA_	Alignment	not modelled	12.6	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**ubash3a protein; **PDBTitle:** solution structure of the uba domain of human ubash3a2 protein
56	c2cpwA_	Alignment	not modelled	12.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cbl-interacting protein sts-1 variant; **PDBTitle:** solution structure of rsgi ruh-031, a uba domain from human2 cdna
57	c1b74A_	Alignment	not modelled	12.1	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
58	c3kzgB_	Alignment	not modelled	12.1	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**arginine 3rd transport system periplasmic binding **PDBTitle:** crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
59	c3chgB_	Alignment	not modelled	11.7	16	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**glycine betaine-binding protein; **PDBTitle:** the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
60	c3c3wB_	Alignment	not modelled	11.5	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
61	c2cokA_	Alignment	not modelled	11.3	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase-1; **PDBTitle:** solution structure of brct domain of poly(adp-ribose)2 polymerase-1
62	c3czcA_	Alignment	not modelled	10.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
63	c3kn3C_	Alignment	not modelled	10.7	5	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative periplasmic protein; **PDBTitle:** crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinella succinogenes
64	d1dz3a_	Alignment	not modelled	10.6	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
65	d1irug_	Alignment	not modelled	10.6	25	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
66	d1o5ha_	Alignment	not modelled	10.4	15	**Fold:**Methenyltetrahydrofolate cyclohydrolase-like **Superfamily:**Methenyltetrahydrofolate cyclohydrolase-like **Family:**Methenyltetrahydrofolate cyclohydrolase-like
67	c3a16C_	Alignment	not modelled	10.2	35	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldoxime dehydratase; **PDBTitle:** crystal structure of aldoxime dehydratase (oxdre) in complex2 with propionaldoxime
68	d1lbqa_	Alignment	not modelled	9.3	19	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
69	c3lr1A_	Alignment	not modelled	9.2	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tungstate abc transporter, periplasmic tungstate- **PDBTitle:** the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
70	d1vega_	Alignment	not modelled	8.9	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
71	d2d9ra1	Alignment	not modelled	8.7	18	**Fold:**Double-split beta-barrel **Superfamily:**AF2212/PG0164-like **Family:**PG0164-like
72	c3dzmB_	Alignment	not modelled	8.7	60	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
73	c3s9xA_	Alignment	not modelled	8.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**asch domain; **PDBTitle:** high resolution crystal structure of asch domain from lactobacillus2 crispatus jv v101
74	d1u14a_	Alignment	not modelled	8.2	20	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
75	d1irue_	Alignment	not modelled	8.0	23	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
76	c3pamB_	Alignment	not modelled	8.0	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transmembrane protein; **PDBTitle:** crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
77	d1djqa1	Alignment	not modelled	7.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
78	c3b50A_	Alignment	not modelled	7.7	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sialic acid-binding periplasmic protein siap; **PDBTitle:** structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
						Fold:PRTase-like

79	d1hgxa_	Alignment	not modelled	7.7	22	**Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
80	c3ir1F_	Alignment	not modelled	7.6	22	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
81	c3t8yA_	Alignment	not modelled	7.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
82	d1nvta1	Alignment	not modelled	7.1	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
83	d1t62a_	Alignment	not modelled	7.0	26	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical protein EF3133
84	c2fmoA_	Alignment	not modelled	6.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate reductase; **PDBTitle:** ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
85	c3iwpK_	Alignment	not modelled	6.6	15	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
86	c1pzmB_	Alignment	not modelled	6.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
87	c3pppA_	Alignment	not modelled	6.6	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline-binding protein; **PDBTitle:** structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
88	c3bboV_	Alignment	not modelled	6.6	11	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**ribosomal protein l23; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
89	d1zc6a1	Alignment	not modelled	6.6	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
90	d1hw6a_	Alignment	not modelled	6.5	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
91	c3k4uA_	Alignment	not modelled	6.3	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**binding component of abc transporter; **PDBTitle:** crystal structure of putative binding component of abc transporter2 from wolinella succinogenes dsm 1740 complexed with lysine
92	d1a4pa_	Alignment	not modelled	6.3	25	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
93	c3qfnA_	Alignment	not modelled	6.2	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
94	d2hiya1	Alignment	not modelled	6.1	14	**Fold:**SP0830-like **Superfamily:**SP0830-like **Family:**SP0830-like
95	d1zpsa1	Alignment	not modelled	6.0	83	**Fold:**HisI-like **Superfamily:**HisI-like **Family:**HisI-like
96	d1irua_	Alignment	not modelled	6.0	25	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
97	c1su1A_	Alignment	not modelled	6.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yfce; **PDBTitle:** structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
98	d1su1a_	Alignment	not modelled	6.0	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
99	d1v5xa_	Alignment	not modelled	6.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes