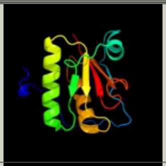
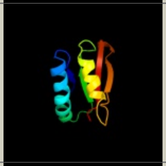
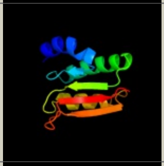
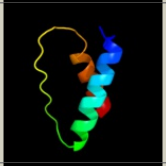
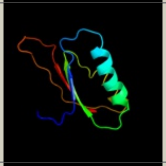
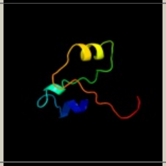
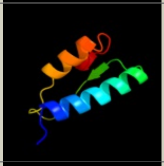
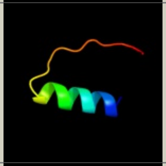
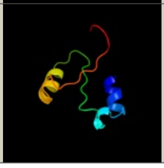
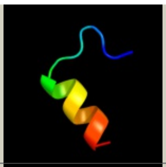
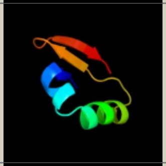
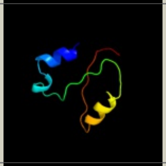
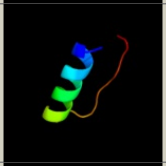
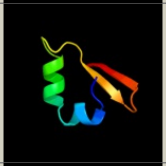
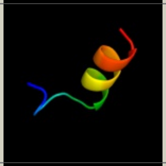
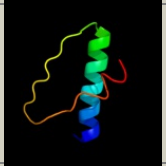
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8B2
Date	Thu Jan 5 11:07:22 GMT 2012
Unique Job ID	6b6254e2faed7843

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qd7X_	 Alignment		100.0	21	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
2	c2zqeA_	 Alignment		99.9	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
3	d2d9ia1	 Alignment		99.6	25	**Fold:**IF3-like **Superfamily:**SMR domain-like **Family:**Smr domain
4	c2vkcA_	 Alignment		99.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nedd4-binding protein 2; **PDBTitle:** solution structure of the b3bp smr domain
5	c3no4A_	 Alignment		52.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**creatinine amidohydrolase; **PDBTitle:** crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
6	d1jdqa_	 Alignment		46.9	14	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
7	c2q2eA_	 Alignment		44.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type ii dna topoisomerase vi subunit a; **PDBTitle:** crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
8	c3lubE_	 Alignment		43.9	11	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**putative creatinine amidohydrolase; **PDBTitle:** crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
9	d1dcja_	 Alignment		41.8	15	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
10	c2fmoA_	 Alignment		39.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate reductase; **PDBTitle:** ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
11	d1d3ya_	 Alignment		37.9	14	**Fold:**DNA topoisomerase IV, alpha subunit **Superfamily:**DNA topoisomerase IV, alpha subunit **Family:**DNA topoisomerase IV, alpha subunit

12	d1pyya2	Alignment		34.1	25	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
13	d2odka1	Alignment		32.5	18	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
14	c2zbkA_	Alignment		32.5	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type ii dna topoisomerase vi subunit a; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
15	d1b5ta_	Alignment		30.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
16	c2odkD_	Alignment		29.7	19	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
17	d1k25a2	Alignment		28.9	19	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
18	c3ouvA_	Alignment		28.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine protein kinase; **PDBTitle:** semet derivative of l512m mutant of pasta domain 3 of mycobacterium2 tuberculosis pknb
19	d1v7za_	Alignment		26.6	16	**Fold:**Creatininase **Superfamily:**Creatininase **Family:**Creatininase
20	c3k5wA_	Alignment		25.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori
21	c3eozB_	Alignment	not modelled	25.1	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
22	d2c2la2	Alignment	not modelled	23.0	11	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
23	d1rp5a2	Alignment	not modelled	22.5	29	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
24	c3cgxA_	Alignment	not modelled	21.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotide-diphospho-sugar transferase; **PDBTitle:** crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
25	c2q0xA_	Alignment	not modelled	20.6	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** alpha/beta hydrolase fold protein of unknown function
26	d2a6qb1	Alignment	not modelled	18.7	17	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
27	c3d3kD_	Alignment	not modelled	18.5	11	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
28	c3e0jF_	Alignment	not modelled	18.0	26	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna polymerase subunit delta-3; **PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta

29	c1x0lB_	Alignment	not modelled	16.9	6	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoisocitrate dehydrogenase; **PDBTitle:** crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
30	d1v93a_	Alignment	not modelled	16.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
31	c3g5oA_	Alignment	not modelled	14.9	17	**PDB header:**toxin/antitoxin **Chain:** A: **PDB Molecule:**uncharacterized protein rv2865; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
32	d1g8fa3	Alignment	not modelled	14.8	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
33	c1tyoA_	Alignment	not modelled	14.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** isocitrate dehydrogenase from the hyperthermophile aeropyrum pernix in2 complex with etheno-nadp
34	c3hryA_	Alignment	not modelled	13.9	9	**PDB header:**antitoxin **Chain:** A: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd in a trigonal space group and partially2 disordered
35	c3pzqA_	Alignment	not modelled	13.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mannan endo-1,4-beta-mannosidase. glycosyl hydrolase family **PDBTitle:** structure of the hyperthermostable endo-1,4-beta-d-mannanase from2 thermotoga petrophila rku-1 with maltose and glycerol
36	d1pava_	Alignment	not modelled	13.6	12	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
37	c2zc3F_	Alignment	not modelled	12.6	13	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**penicillin-binding protein 2x; **PDBTitle:** penicillin-binding protein 2x (pbp 2x) acyl-enzyme complex2 (biapenem) from streptococcus pneumoniae
38	c2g7zB_	Alignment	not modelled	12.5	11	**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
39	c2kueA_	Alignment	not modelled	11.9	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase pknb; **PDBTitle:** nmr structure of the pasta domain 2 and 3 of mycobacterium2 tuberculosis of pknb
40	d2c0ha1	Alignment	not modelled	11.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
41	c3odmE_	Alignment	not modelled	11.6	12	**PDB header:**lyase **Chain:** E: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** archaeal-type phosphoenolpyruvate carboxylase
42	c2ns6A_	Alignment	not modelled	11.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mobilization protein a; **PDBTitle:** crystal structure of the minimal relaxase domain of moba2 from plasmid r1162
43	c2kudA_	Alignment	not modelled	11.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase pknb; **PDBTitle:** nmr structure of the pasta domain 1 and 2 of mycobacterium2 tuberculosis of pknb
44	d2obba1	Alignment	not modelled	11.2	8	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
45	c3icgD_	Alignment	not modelled	11.2	6	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endoglucanase d; **PDBTitle:** crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
46	d3pgma_	Alignment	not modelled	11.1	11	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
47	d2i5ea1	Alignment	not modelled	11.0	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MM2497-like
48	c3fcyB_	Alignment	not modelled	10.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xylan esterase 1; **PDBTitle:** crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
49	c3u7vA_	Alignment	not modelled	10.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
50	c3lmaC_	Alignment	not modelled	10.4	12	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**stage v sporulation protein ad (spovad); **PDBTitle:** crystal structure of the stage v sporulation protein ad2 (spovad) from bacillus licheniformis. northeast structural3 genomics consortium target bir6.
51	c2f42A_	Alignment	not modelled	10.4	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stip1 homology and u-box containing protein 1; **PDBTitle:** dimerization and u-box domains of zebrafish c-terminal of hsp702 interacting protein
52	d2vo9a1	Alignment	not modelled	10.0	19	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**VanY-like
53	c3hs2H_	Alignment	not modelled	9.9	9	**PDB header:**antitoxin **Chain:** H: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd truncated to residue 57 in an

						orthorhombic2 space group
54	c3ir3B_	Alignment	not modelled	9.6	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-thioester dehydratase 2; **PDBTitle:** crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
55	c3l80A_	Alignment	not modelled	9.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
56	d1ceoa_	Alignment	not modelled	9.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
57	c3ndyA_	Alignment	not modelled	9.3	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase d; **PDBTitle:** the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
58	d1u7pa_	Alignment	not modelled	9.3	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Magnesium-dependent phosphatase-1, Mdp1
59	c2qniA_	Alignment	not modelled	9.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu0299; **PDBTitle:** crystal structure of uncharacterized protein atu0299
60	d1qhfa_	Alignment	not modelled	9.1	14	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
61	d1vjza_	Alignment	not modelled	9.1	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
62	c1cirA_	Alignment	not modelled	9.0	29	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**chymotrypsin inhibitor 2; **PDBTitle:** complex of two fragments of ci2 [(1-40)(dot)(41-64)]
63	d1gs5a_	Alignment	not modelled	8.9	24	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
64	d1riia_	Alignment	not modelled	8.9	14	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
65	c2y9xG_	Alignment	not modelled	8.7	19	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**lectin-like fold protein; **PDBTitle:** crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone
66	c3fpvC_	Alignment	not modelled	8.6	17	**PDB header:**heme binding protein **Chain:** C: **PDB Molecule:**extracellular haem-binding protein; **PDBTitle:** crystal structure of hbps
67	d1yh5a1	Alignment	not modelled	8.6	19	**Fold:**YggU-like **Superfamily:**YggU-like **Family:**YggU-like
68	c2xt0A_	Alignment	not modelled	8.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** dehalogenase dppa from plesiocystis pacifica sir-i
69	c3hz7A_	Alignment	not modelled	8.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the sira-like protein (dsy4693) from2 desulfitobacterium hafniense, northeast structural genomics3 consortium target dhr2a
70	d1hkha_	Alignment	not modelled	8.4	28	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
71	d2csba1	Alignment	not modelled	8.3	28	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
72	d2iw0a1	Alignment	not modelled	8.3	13	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
73	c2c2lD_	Alignment	not modelled	8.1	11	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**carboxy terminus of hsp70-interacting protein; **PDBTitle:** crystal structure of the chip u-box e3 ubiquitin ligase
74	d1uf3a_	Alignment	not modelled	8.0	11	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
75	c3ll4B_	Alignment	not modelled	7.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein ykr043c; **PDBTitle:** structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate
76	d2g5gx1	Alignment	not modelled	7.7	19	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**ChaN-like
77	d2a2la1	Alignment	not modelled	7.7	17	**Fold:**Profilin-like **Superfamily:**GlcG-like **Family:**GlcG-like
78	d1xpja_	Alignment	not modelled	7.6	10	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
79	c3i31A_	Alignment	not modelled	7.6	10	**PDB header:**rna binding protein,hydrolase **Chain:** A: **PDB Molecule:**heat resistant rna dependent atpase; **PDBTitle:** hera helicase rna binding domain is an rrm fold
						PDB header:isomerase

80	c2vx2D_	Alignment	not modelled	7.6	10	**Chain:** D: **PDB Molecule:**enoyl-coa hydratase domain-containing protein 3; **PDBTitle:** crystal structure of human enoyl coenzyme a hydratase2 domain-containing protein 3 (echdc3)
81	c3fdjA_	Alignment	not modelled	7.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** the structure of a degv family protein from eubacterium eligens.
82	c1yjxD_	Alignment	not modelled	7.5	12	**PDB header:**isomerase, hydrolase **Chain:** D: **PDB Molecule:**phosphoglycerate mutase 1; **PDBTitle:** crystal structure of human b type phosphoglycerate mutase
83	c3lupA_	Alignment	not modelled	7.5	15	**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
84	d2bi0a1	Alignment	not modelled	7.4	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
85	c3mmwB_	Alignment	not modelled	7.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase cel5a from the hyperthermophilic2 thermotoga maritima
86	c3d40A_	Alignment	not modelled	7.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**foma protein; **PDBTitle:** crystal structure of fosfomycin resistance kinase foma from2 streptomyces wedmorensis complexed with diphosphate
87	d2pb1a1	Alignment	not modelled	7.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
88	d2ax3a2	Alignment	not modelled	7.1	13	**Fold:**YjeF N-terminal domain-like **Superfamily:**YjeF N-terminal domain-like **Family:**YjeF N-terminal domain-like
89	d1r57a_	Alignment	not modelled	7.1	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
90	c3czcA_	Alignment	not modelled	7.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
91	c3l6wB_	Alignment	not modelled	7.0	26	**PDB header:**oxygen binding **Chain:** B: **PDB Molecule:**hemocyanin 1; **PDBTitle:** structure of the collar functional unit (klh1-h) of keyhole2 limpet hemocyanin
92	d1uuqa_	Alignment	not modelled	6.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
93	c1uz4A_	Alignment	not modelled	6.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**man5a; **PDBTitle:** common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 intineraries for glucoside and mannoside hydrolysis
94	d1e58a_	Alignment	not modelled	6.8	10	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
95	c1vkrA_	Alignment	not modelled	6.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components; **PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii
96	d1vkra_	Alignment	not modelled	6.6	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
97	d1wz8a1	Alignment	not modelled	6.5	13	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
98	c3t1iC_	Alignment	not modelled	6.5	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a; **PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations
99	d2a6qa1	Alignment	not modelled	6.4	17	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like