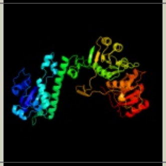
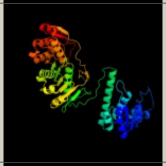
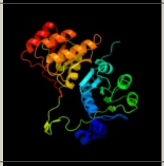
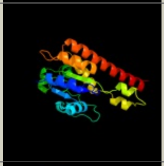
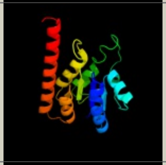
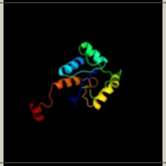
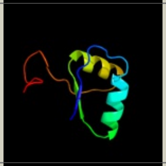
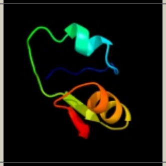
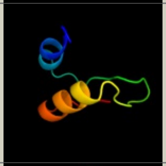
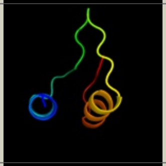
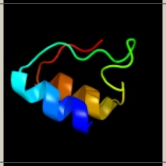
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P15639
Date	Thu Jan 5 11:34:47 GMT 2012
Unique Job ID	418385fa75a065e3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4a1oB_	Alignment		100.0	46	**PDB header:**transferase-hydrolase **Chain:** B: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
2	c1thzA_	Alignment		100.0	42	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
3	c1zczA_	Alignment		100.0	40	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
4	d1g8ma2	Alignment		100.0	37	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
5	d1pkxa2	Alignment		100.0	42	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
6	d1zcza2	Alignment		100.0	42	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
7	d1pkxa1	Alignment		100.0	51	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
8	d1g8ma1	Alignment		100.0	48	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
9	d1zcza1	Alignment		100.0	39	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
10	d1a9xa2	Alignment		99.4	25	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
11	c2yvqA_	Alignment		99.3	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens

12	d1wo8a1	Alignment		98.3	23	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
13	c1m6vE_	Alignment		98.0	44	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
14	d1vmda_	Alignment		96.9	26	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
15	c2pjuD_	Alignment		89.7	12	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
16	c3ff4A_	Alignment		89.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
17	d1iuka_	Alignment		88.0	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
18	d2d59a1	Alignment		85.4	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
19	d2pjua1	Alignment		85.1	11	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
20	c2q5cA_	Alignment		82.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
21	d2isba1	Alignment	not modelled	82.5	22	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
22	d2ioja1	Alignment	not modelled	81.8	24	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**DRTGG domain
23	d1wbha1	Alignment	not modelled	79.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
24	d2vzsa5	Alignment	not modelled	77.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
25	c2duwA_	Alignment	not modelled	76.1	18	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
26	d1y81a1	Alignment	not modelled	75.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
27	d1b93a_	Alignment	not modelled	75.0	21	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
28	d1ko7a1	Alignment	not modelled	71.4	15	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
						PDB header:lyase **Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-

29	c2yw3E_	Alignment	not modelled	70.3	34	deydro-3- **PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
30	c2hvwC_	Alignment	not modelled	69.6	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidylate deaminase; **PDBTitle:** crystal structure of dcmp deaminase from streptococcus2 mutans
31	d1mxsa_	Alignment	not modelled	68.4	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
32	c2o7pA_	Alignment	not modelled	64.6	28	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**riboflavin biosynthesis protein ribd; **PDBTitle:** the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
33	d1mkza_	Alignment	not modelled	63.8	22	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
34	d1vhca_	Alignment	not modelled	63.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
35	d1qt1a_	Alignment	not modelled	62.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
36	c2e3zB_	Alignment	not modelled	61.7	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of intracellular family 1 beta-2 glucosidase bgl1a from the basidiomycete phanerochaete3 chrysosporium in substrate-free form
37	c1ko7B_	Alignment	not modelled	60.7	15	**PDB header:**transferase,hydrolase **Chain:** B: **PDB Molecule:**hpr kinase/phosphatase; **PDBTitle:** x-ray structure of the hpr kinase/phosphatase from2 staphylococcus xylosus at 1.95 a resolution
38	d2obba1	Alignment	not modelled	60.1	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
39	d1ytla1	Alignment	not modelled	59.5	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**ACDE2-like
40	c3ia7A_	Alignment	not modelled	58.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
41	d2csua1	Alignment	not modelled	57.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
42	d1ujpa_	Alignment	not modelled	55.7	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
43	d1f75a_	Alignment	not modelled	55.5	14	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
44	d1f0ka_	Alignment	not modelled	55.0	26	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
45	c3u7jA_	Alignment	not modelled	54.7	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
46	c3dmyA_	Alignment	not modelled	52.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein fdra; **PDBTitle:** crystal structure of a predicated acyl-coa synthetase from e.coli
47	d1sjpa2	Alignment	not modelled	52.3	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
48	c3e2vA_	Alignment	not modelled	51.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3'-5'-exonuclease; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
49	d1cbga_	Alignment	not modelled	51.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
50	d1y5ea1	Alignment	not modelled	51.0	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
51	d2b3za2	Alignment	not modelled	50.2	19	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
52	d1ueha_	Alignment	not modelled	49.8	28	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
53	d1we3a2	Alignment	not modelled	46.8	22	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
54	c3p9zA_	Alignment	not modelled	44.5	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**uroporphyrinogen iii cosynthase (hemd); **PDBTitle:** crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
						PDB header:isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase;

55	c1xtzA_	Alignment	not modelled	44.2	25	**PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
56	d1pn3a_	Alignment	not modelled	43.3	19	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
57	c3orgB_	Alignment	not modelled	42.8	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cmclc; **PDBTitle:** crystal structure of a eukaryotic clc transporter
58	c3ahxC_	Alignment	not modelled	42.7	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-glucosidase a; **PDBTitle:** crystal structure of beta-glucosidase a from bacterium clostridium2 cellulovorans
59	d1rd5a_	Alignment	not modelled	42.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
60	c2v82A_	Alignment	not modelled	42.0	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
61	c3labA_	Alignment	not modelled	41.9	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate) **PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
62	d1tz9a_	Alignment	not modelled	41.4	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
63	c1nh7A_	Alignment	not modelled	40.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
64	c3sajB_	Alignment	not modelled	40.7	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate receptor 1; **PDBTitle:** crystal structure of glutamate receptor glua1 amino terminal domain
65	d2pq6a1	Alignment	not modelled	40.4	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
66	d1zpva1	Alignment	not modelled	40.2	27	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
67	c2z1sA_	Alignment	not modelled	40.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase b; **PDBTitle:** beta-glucosidase b from paenibacillus polymyxa complexed2 with cellotetraose
68	d1bqca_	Alignment	not modelled	39.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
69	d1rrva_	Alignment	not modelled	39.4	23	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
70	d1kida_	Alignment	not modelled	39.3	24	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
71	c3ktcB_	Alignment	not modelled	39.3	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
72	c3fuyC_	Alignment	not modelled	39.2	35	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative integron gene cassette protein; **PDBTitle:** structure from the mobile metagenome of cole harbour salt2 marsh: integron cassette protein hfx_cass1
73	d1k77a_	Alignment	not modelled	38.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Hypothetical protein YgbM (EC1530)
74	c3ahyD_	Alignment	not modelled	38.1	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of beta-glucosidase 2 from fungus trichoderma reesei2 in complex with tris
75	c2f00A_	Alignment	not modelled	37.3	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate--l-alanine ligase; **PDBTitle:** escherichia coli murc
76	d1vffa1	Alignment	not modelled	37.2	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
77	c2hxvA_	Alignment	not modelled	36.5	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5- **PDBTitle:** crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution
78	c2csuB_	Alignment	not modelled	35.6	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
79	c2vldA_	Alignment	not modelled	35.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0286 protein pyrab01260; **PDBTitle:** crystal structure of a repair endonuclease from pyrococcus2 abyssi
						Fold:TIM beta/alpha-barrel

80	d1xima_	Alignment	not modelled	34.8	24	**Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
81	d1wcga1	Alignment	not modelled	34.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
82	d1xsza2	Alignment	not modelled	33.2	39	**Fold:**TBP-like **Superfamily:**RalF, C-terminal domain **Family:**RalF, C-terminal domain
83	c2b8eB_	Alignment	not modelled	32.6	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**cation-transporting atpase; **PDBTitle:** copa atp binding domain
84	d1ht6a2	Alignment	not modelled	32.4	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
85	d1euca1	Alignment	not modelled	32.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
86	c2pjmA_	Alignment	not modelled	32.0	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
87	d1yrra2	Alignment	not modelled	31.7	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
88	d1uuqa_	Alignment	not modelled	31.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
89	c1uz4A_	Alignment	not modelled	31.3	18	**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
90	c3ptkB_	Alignment	not modelled	31.1	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase os4bglu12; **PDBTitle:** the crystal structure of rice (oryza sativa l.) os4bglu12
91	c3kg2A_	Alignment	not modelled	31.0	4	**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
92	d2nu7a1	Alignment	not modelled	30.7	34	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
93	c2wjxA_	Alignment	not modelled	30.2	4	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glutamate receptor 2; **PDBTitle:** crystal structure of the human ionotropic glutamate2 receptor glur2 atd region at 4.1 a resolution
94	c2vzvB_	Alignment	not modelled	30.2	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
95	d1snna_	Alignment	not modelled	30.1	22	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
96	c3iv4A_	Alignment	not modelled	29.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** a putative oxidoreductase with a thioredoxin fold
97	d1yx1a1	Alignment	not modelled	29.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
98	d1g57a_	Alignment	not modelled	29.3	32	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
99	c2f8mB_	Alignment	not modelled	29.1	31	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** ribose 5-phosphate isomerase from plasmodium falciparum
100	d1un7a2	Alignment	not modelled	29.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
101	c1i8tB_	Alignment	not modelled	29.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** strcuture of udp-galactopyranose mutase from e.coli
102	c1gqqA_	Alignment	not modelled	28.9	21	**PDB header:**cell wall biosynthesis **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** murc - crystal structure of the apo-enzyme from haemophilus2 influenzae
103	c3u57A_	Alignment	not modelled	28.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**raucaffricine-o-beta-d-glucosidase; **PDBTitle:** structures of alkaloid biosynthetic glucosidases decode substrate2 specificity
104	c2rbgB_	Alignment	not modelled	28.8	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein st0493; **PDBTitle:** crystal structure of hypothetical protein(st0493) from2 sulfolobus tokodaii
105	d1tg7a5	Alignment	not modelled	28.6	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Glycosyl hydrolases family 35 catalytic domain
106	c3qomA	Alignment	not modelled	28.1	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phospho-beta-glucosidase;

106	[illegible]	Alignment	not modelled	28.1	29	**PDBTitle:** crystal structure of 6-phospho-beta-glucosidase from lactobacillus2 plantarum
107	d1oela2	Alignment	not modelled	27.5	24	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
108	c2je8B_	Alignment	not modelled	27.2	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
109	d1srva_	Alignment	not modelled	27.0	24	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
110	c2d2rA_	Alignment	not modelled	26.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
111	c3c2qA_	Alignment	not modelled	26.8	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of conserved putative lor/sdh protein2 from methanococcus maripaludis s2
112	c2qyxB_	Alignment	not modelled	26.4	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein mj0159; **PDBTitle:** crystal structure of uncharacterized protein mj0159 from2 methanocaldococcus jannaschii
113	d2hxva2	Alignment	not modelled	26.1	22	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
114	c3mioA_	Alignment	not modelled	25.6	41	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3,4-dihydroxy-2-butanone 4-phosphate synthase; **PDBTitle:** crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
115	c3kwmC_	Alignment	not modelled	25.4	31	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
116	d1dk7a_	Alignment	not modelled	25.2	28	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
117	d1g2qa_	Alignment	not modelled	25.2	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
118	d1y5ha3	Alignment	not modelled	24.9	12	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
119	d2ooda2	Alignment	not modelled	24.8	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
120	d1ceoa_	Alignment	not modelled	24.4	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases