Phyre2

Email	l.a.kelley@imperial.ac.uk
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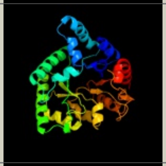
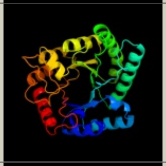
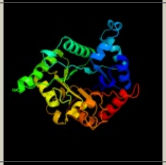
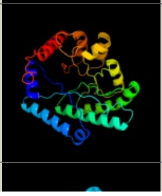
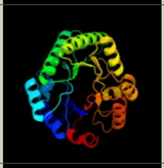
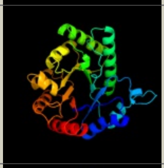
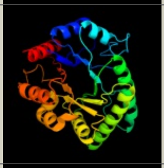
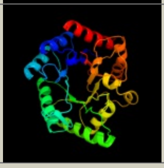
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cqkB_	Alignment		100.0	60	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-ribulose-5-phosphate 3-epimerase ulae; **PDBTitle:** crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
2	d1i60a_	Alignment		100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
3	c2zdsB_	Alignment		100.0	21	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
4	c3kwsB_	Alignment		100.0	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
5	c3dx5A_	Alignment		100.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
6	c3cnyA_	Alignment		100.0	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**inositol catabolism protein iole; **PDBTitle:** crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution
7	c2hk1D_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**d-psicose 3-epimerase; **PDBTitle:** crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
8	c2ou4C_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
9	d2g0wa1	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
10	c3ju2A_	Alignment		100.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
11	c2qw5B_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution

12	c3obeB_	Alignment		100.0	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
13	d1k77a_	Alignment		100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Hypothetical protein YgbM (EC1530)
14	c3qxbB_	Alignment		100.0	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative xylose isomerase; **PDBTitle:** crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
15	c3ktcB_	Alignment		100.0	16	**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
16	c2zvrA_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**uncharacterized protein tm_0416; **PDBTitle:** crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima
17	c3l23A_	Alignment		100.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
18	c3lmzA_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
19	c3p6lA_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
20	d2q02a1	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
21	c3ngfA_	Alignment	not modelled	100.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ap endonuclease, family 2; **PDBTitle:** crystal structure of ap endonuclease, family 2 from brucella2 melitensis
22	d1xp3a1	Alignment	not modelled	100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
23	d1qtwa_	Alignment	not modelled	100.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
24	c2x7vA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable endonuclease 4; **PDBTitle:** crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
25	d1yx1a1	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
26	d1muwa_	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
27	d1bxba_	Alignment	not modelled	100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
28	d1qt1a_	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
29	d1tz9a_	Alignment	not modelled	100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like

30	d2glka1	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
31	d1bxca_	Alignment	not modelled	100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
32	c3aamA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease iv; **PDBTitle:** crystal structure of endonuclease iv from thermus thermophilus hb8
33	d1xima_	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
34	c3bdkB_	Alignment	not modelled	100.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
35	d1xlma_	Alignment	not modelled	99.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
36	c2i56A_	Alignment	not modelled	99.8	17	**PDB header:**isomerase, metal-binding protein **Chain:** A: **PDB Molecule:**l-rhamnose isomerase; **PDBTitle:** crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose
37	d1a0ea_	Alignment	not modelled	99.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
38	d1a0ca_	Alignment	not modelled	99.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
39	d1a0da_	Alignment	not modelled	99.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
40	c3bzjA_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uv endonuclease; **PDBTitle:** uvde k229l
41	c3bwwA_	Alignment	not modelled	99.1	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein of unknown function duf692/cog3220; **PDBTitle:** crystal structure of a duf692 family protein (hs_1138) from2 haemophilus somnus 129pt at 2.20 a resolution
42	d1d8wa_	Alignment	not modelled	98.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**L-rhamnose isomerase
43	c3p14C_	Alignment	not modelled	98.2	11	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-rhamnose isomerase; **PDBTitle:** crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans
44	d1qwga_	Alignment	not modelled	96.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
45	c3a24A_	Alignment	not modelled	96.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of bt1871 retaining glycosidase
46	d1m5wa_	Alignment	not modelled	96.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
47	c2bdqA_	Alignment	not modelled	96.3	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
48	c2nx9B_	Alignment	not modelled	96.2	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxaloacetate decarboxylase 2, subunit alpha; **PDBTitle:** crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
49	d1h1ya_	Alignment	not modelled	96.2	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
50	c3gk0H_	Alignment	not modelled	96.1	21	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
51	d2fiqa1	Alignment	not modelled	96.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
52	c3ivuB_	Alignment	not modelled	96.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
53	c3qc3B_	Alignment	not modelled	95.7	9	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-ribulose-5-phosphate-3-epimerase; **PDBTitle:** crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
54	d1tqja_	Alignment	not modelled	95.4	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
55	d1d7ka2	Alignment	not modelled	95.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
						PDB header:transferase

56	c2vg2C_	Alignment	not modelled	95.1	8	**Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
57	c3o6cA_	Alignment	not modelled	95.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
58	d1f3ta2	Alignment	not modelled	94.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
59	c3bg3B_	Alignment	not modelled	94.4	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase, mitochondrial; **PDBTitle:** crystal structure of human pyruvate carboxylase (missing2 the biotin carboxylase domain at the n-terminus)
60	d1u83a_	Alignment	not modelled	94.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
61	c1u83A_	Alignment	not modelled	94.4	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
62	c2zq0B_	Alignment	not modelled	94.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase (alpha-glucosidase susb); **PDBTitle:** crystal structure of susb complexed with acarbose
63	c3b0vD_	Alignment	not modelled	94.3	9	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
64	c2h90A_	Alignment	not modelled	94.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
65	c1sr9A_	Alignment	not modelled	94.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of leua from mycobacterium tuberculosis
66	c3hf3A_	Alignment	not modelled	94.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
67	c2on3A_	Alignment	not modelled	93.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminooxy-3 1-aminopropane
68	d1ps9a1	Alignment	not modelled	93.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
69	c3bleA_	Alignment	not modelled	93.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
70	c1ydoC_	Alignment	not modelled	93.6	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
71	c1d7kB_	Alignment	not modelled	93.3	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**human ornithine decarboxylase; **PDBTitle:** crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
72	c3inpA_	Alignment	not modelled	92.8	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
73	c3aysA_	Alignment	not modelled	92.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** gh5 endoglucanase from a ruminal fungus in complex with cellotriose
74	d1vyra_	Alignment	not modelled	92.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
75	d1vlia2	Alignment	not modelled	92.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
76	c2xioA_	Alignment	not modelled	92.2	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn1; **PDBTitle:** structure of putative deoxyribonuclease tatdn1 isoform a
77	c1xc6A_	Alignment	not modelled	92.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
78	c3btnA_	Alignment	not modelled	92.2	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**antizyme inhibitor 1; **PDBTitle:** crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
79	d1gcya2	Alignment	not modelled	92.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
80	d1uuqa_	Alignment	not modelled	91.9	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
81	c1uz4A_	Alignment	not modelled	91.9	8	**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

82	d7odca2	Alignment	not modelled	91.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
83	c2ftpA_	Alignment	not modelled	91.7	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
84	d1f75a_	Alignment	not modelled	91.3	12	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
85	c3tr9A_	Alignment	not modelled	91.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
86	c2y5sA_	Alignment	not modelled	90.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
87	c2ekgB_	Alignment	not modelled	90.5	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**proline dehydrogenase/delta-1-pyrroline-5-carboxylate **PDBTitle:** structure of thermus thermophilus proline dehydrogenase inactivated by2 n-propargylglycine
88	d2zdra2	Alignment	not modelled	90.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
89	d1nvma2	Alignment	not modelled	90.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
90	c3ugsB_	Alignment	not modelled	89.9	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
91	c2p3eA_	Alignment	not modelled	89.8	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of aq1208 from aquifex aeolicus
92	c2d2rA_	Alignment	not modelled	89.5	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
93	d1olta_	Alignment	not modelled	89.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
94	d1tg7a5	Alignment	not modelled	89.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Glycosyl hydrolases family 35 catalytic domain
95	c2yswB_	Alignment	not modelled	88.6	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of the 3-dehydroquinate dehydratase from aquifex2 aeolicus vf5
96	c2qghA_	Alignment	not modelled	88.6	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
97	c1jp3A_	Alignment	not modelled	88.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** structure of e.coli undecaprenyl pyrophosphate synthase
98	d1g94a2	Alignment	not modelled	88.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
99	d1tqxa_	Alignment	not modelled	88.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
100	d2c0ha1	Alignment	not modelled	88.3	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
101	c1ydnA_	Alignment	not modelled	88.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
102	d1vema2	Alignment	not modelled	88.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
103	d1ji1a3	Alignment	not modelled	88.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
104	c3blpX_	Alignment	not modelled	88.1	20	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1; **PDBTitle:** role of aromatic residues in human salivary alpha-amylase
105	c1jdaA_	Alignment	not modelled	88.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase; **PDBTitle:** maltotetraose-forming exo-amylase
106	d1z41a1	Alignment	not modelled	88.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
107	c1j0yD_	Alignment	not modelled	88.0	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-amylase; **PDBTitle:** beta-amylase from bacillus cereus var. mycoides in complex2 with glucose
108	c2yfnA_	Alignment	not modelled	87.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask;

						PDBTitle: galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
109	d1e43a2	Alignment	not modelled	87.7	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
110	c2p10D_	Alignment	not modelled	87.6	12	**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
111	d1rh9a1	Alignment	not modelled	87.4	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
112	c2aaaA_	Alignment	not modelled	87.3	21	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** calcium binding in alpha-amylases: an x-ray diffraction2 study at 2.1 angstroms resolution of two enzymes from3 aspergillus
113	c3cu2A_	Alignment	not modelled	87.3	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribulose-5-phosphate 3-epimerase; **PDBTitle:** crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
114	c1ps9A_	Alignment	not modelled	87.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
115	d1rpxa_	Alignment	not modelled	87.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
116	d1e0ta2	Alignment	not modelled	87.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
117	c3pzqA_	Alignment	not modelled	87.0	20	**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
118	d1ea9c3	Alignment	not modelled	86.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
119	c1gcyA_	Alignment	not modelled	86.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
120	c3l55B_	Alignment	not modelled	86.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**b-1,4-endoglucanase/cellulase; **PDBTitle:** crystal structure of a putative beta-1,4-endoglucanase /2 cellulase from prevotella bryantii