
































# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P30136
Date	Thu Jan 5 11:45:53 GMT 2012
Unique Job ID	a986ba561ccc1d3a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3epmB_</a>	 Alignment		100.0	67	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> thiamine biosynthesis protein thic; <b>PDBTitle:</b> crystal structure of caulobacter crescentus thic
2	<a href="#">c3pnzD_</a>	 Alignment		95.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphotriesterase family protein; <b>PDBTitle:</b> crystal structure of the lactonase Imo2620 from listeria monocytogenes
3	<a href="#">dlad1a_</a>	 Alignment		93.9	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
4	<a href="#">dlub3a_</a>	 Alignment		91.1	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
5	<a href="#">c2hjpA_</a>	 Alignment		90.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonopyruvate hydrolase; <b>PDBTitle:</b> crystal structure of phosphonopyruvate hydrolase complex with 2 phosphonopyruvate and mg++
6	<a href="#">dlhl1a_</a>	 Alignment		90.3	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
7	<a href="#">c3qc3B_</a>	 Alignment		90.3	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-ribulose-5-phosphate-3-epimerase; <b>PDBTitle:</b> crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
8	<a href="#">dlmzha_</a>	 Alignment		90.1	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
9	<a href="#">c1bx2A_</a>	 Alignment		89.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dhps, dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
10	<a href="#">dlbx2a_</a>	 Alignment		89.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
11	<a href="#">c2zvra_</a>	 Alignment		89.5	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein tm_0416; <b>PDBTitle:</b> crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima

12	<a href="#">d3bofa1</a>	Alignment		89.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
13	<a href="#">c3db2C_</a>	Alignment		87.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative nadph-dependent oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
14	<a href="#">c2vefB_</a>	Alignment		87.2	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthase from streptococcus pneumoniae
15	<a href="#">d1ajza_</a>	Alignment		86.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
16	<a href="#">d2flia1</a>	Alignment		85.5	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
17	<a href="#">c3bolB_</a>	Alignment		85.2	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-methyltetrahydrofolate s-homocysteine <b>PDBTitle:</b> cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
18	<a href="#">c2o7qA_</a>	Alignment		84.4	24	<b>PDB header:</b> oxidoreductase,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional 3-dehydroquinate dehydratase/shikimate <b>PDBTitle:</b> crystal structure of the a. thaliana dhq-dehydroshikimate-sdh-2 shikimate-nadp(h)
19	<a href="#">d2zdra2</a>	Alignment		83.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
20	<a href="#">d2q02a1</a>	Alignment		83.6	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loli-like
21	<a href="#">d1sfla_</a>	Alignment	not modelled	83.4	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
22	<a href="#">d1i60a_</a>	Alignment	not modelled	83.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loli-like
23	<a href="#">c3k13A_</a>	Alignment	not modelled	82.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydrofolate-homocysteine methyltransferase; <b>PDBTitle:</b> structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
24	<a href="#">c2bdqA_</a>	Alignment	not modelled	81.1	14	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper homeostasis protein cutc; <b>PDBTitle:</b> crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
25	<a href="#">d1o0ya_</a>	Alignment	not modelled	80.3	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
26	<a href="#">c3ih1A_</a>	Alignment	not modelled	80.2	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
27	<a href="#">d1a3xa2</a>	Alignment	not modelled	80.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
28	<a href="#">c3d0cB_</a>	Alignment	not modelled	80.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2

					oceanobacillus iheyensis at 1.9 a resolution
29	<a href="#">c2y0fD_</a>	Alignment	not modelled	79.8	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl di phosphate synthase; <b>PDBTitle:</b> structure of gcpe (ispg) from thermus thermophilus hb27
30	<a href="#">c3eooL_</a>	Alignment	not modelled	79.8	15 <b>PDB header:</b> lyase <b>Chain:</b> L: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
31	<a href="#">c3q2kB_</a>	Alignment	not modelled	79.8	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of the wlbA dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaC
32	<a href="#">c1zlpA_</a>	Alignment	not modelled	79.3	15 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> petal death protein; <b>PDBTitle:</b> petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
33	<a href="#">c2c46B_</a>	Alignment	not modelled	79.2	15 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mrna capping enzyme; <b>PDBTitle:</b> crystal structure of the human rna guanylyltransferase and2 5'-phosphatase
34	<a href="#">c3k2gA_</a>	Alignment	not modelled	79.2	16 <b>PDB header:</b> resiniferatoxin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> resiniferatoxin-binding, phosphotriesterase- <b>PDBTitle:</b> crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
35	<a href="#">c3ngjC_</a>	Alignment	not modelled	78.5	17 <b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
36	<a href="#">c3rbvA_</a>	Alignment	not modelled	77.5	17 <b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar 3-ketoreductase; <b>PDBTitle:</b> crystal structure of kjd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
37	<a href="#">c2qlxD_</a>	Alignment	not modelled	77.3	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 1,5-anhydro-d-fructose reductase; <b>PDBTitle:</b> crystal structure analysis of bacterial 1,5-af reductase
38	<a href="#">c2vc7A_</a>	Alignment	not modelled	76.6	10 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aryldialkylphosphatase; <b>PDBTitle:</b> structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
39	<a href="#">d1rxda_</a>	Alignment	not modelled	76.6	10 <b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
40	<a href="#">c2hg4A_</a>	Alignment	not modelled	76.3	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-deoxyerythronolide b synthase; <b>PDBTitle:</b> structure of the ketosynthase-acyltransferase didomain of module 52 from debS.
41	<a href="#">c1vliA_</a>	Alignment	not modelled	75.7	17 <b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> spore coat polysaccharide biosynthesis protein spse; <b>PDBTitle:</b> crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
42	<a href="#">c2yciX_</a>	Alignment	not modelled	75.7	16 <b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 5-methyltetrahydrofolate corrinoid/iron sulfur protein <b>PDBTitle:</b> methyltransferase native
43	<a href="#">d1tqja_</a>	Alignment	not modelled	75.2	27 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
44	<a href="#">d1ccwb_</a>	Alignment	not modelled	74.6	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> Glutamate mutase, large subunit
45	<a href="#">c3oa3A_</a>	Alignment	not modelled	74.0	23 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aldolase; <b>PDBTitle:</b> crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
46	<a href="#">d2qtva4</a>	Alignment	not modelled	72.6	23 <b>Fold:</b> Gelsolin-like <b>Superfamily:</b> C-terminal, gelsolin-like domain of Sec23/24 <b>Family:</b> C-terminal, gelsolin-like domain of Sec23/24
47	<a href="#">c3l9cA_</a>	Alignment	not modelled	71.6	16 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> the crystal structure of smu.777 from streptococcus mutans ua159
48	<a href="#">c3ngfA_</a>	Alignment	not modelled	71.2	10 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ap endonuclease, family 2; <b>PDBTitle:</b> crystal structure of ap endonuclease, family 2 from brucella2 melitensis
49	<a href="#">c3ng3A_</a>	Alignment	not modelled	71.0	23 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
50	<a href="#">d1f6ya_</a>	Alignment	not modelled	71.0	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
51	<a href="#">c3cqkB_</a>	Alignment	not modelled	70.6	12 <b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ribulose-5-phosphate 3-epimerase ulae; <b>PDBTitle:</b> crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
52	<a href="#">d1qt1a_</a>	Alignment	not modelled	70.3	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
53	<a href="#">c3b0vD_</a>	Alignment	not modelled	70.1	26 <b>PDB header:</b> oxidoreductase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> trna-dihydrouridine synthase; <b>PDBTitle:</b> trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna

54	<a href="#">c3noeA</a>	Alignment	not modelled	70.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
55	<a href="#">d1ryda1</a>	Alignment	not modelled	70.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
56	<a href="#">c3hf3A</a>	Alignment	not modelled	69.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chromate reductase; <b>PDBTitle:</b> old yellow enzyme from thermus scotoductus sa-01
57	<a href="#">c3euwB</a>	Alignment	not modelled	69.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> myo-inositol dehydrogenase; <b>PDBTitle:</b> crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
58	<a href="#">d1vbga1</a>	Alignment	not modelled	69.3	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate phosphate dikinase, C-terminal domain
59	<a href="#">c3gr7A</a>	Alignment	not modelled	69.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph dehydrogenase; <b>PDBTitle:</b> structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
60	<a href="#">c3khdC</a>	Alignment	not modelled	68.2	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of pff1300w.
61	<a href="#">c2dzaA</a>	Alignment	not modelled	67.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
62	<a href="#">c3nt5B</a>	Alignment	not modelled	67.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
63	<a href="#">c3tr9A</a>	Alignment	not modelled	67.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> structure of a dihydropteroate synthase (folp) in complex with pteroi2 acid from coxiella burnetii
64	<a href="#">c3fokH</a>	Alignment	not modelled	67.4	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> uncharacterized protein cgl0159; <b>PDBTitle:</b> crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
65	<a href="#">d1vhna</a>	Alignment	not modelled	67.2	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
66	<a href="#">c3daqB</a>	Alignment	not modelled	67.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
67	<a href="#">c3e96B</a>	Alignment	not modelled	67.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
68	<a href="#">c3noyA</a>	Alignment	not modelled	65.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> crystal structure of ispg (gcpe)
69	<a href="#">d1h6za1</a>	Alignment	not modelled	65.9	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate phosphate dikinase, C-terminal domain
70	<a href="#">d1ojxa</a>	Alignment	not modelled	65.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
71	<a href="#">c3e18A</a>	Alignment	not modelled	65.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of nad-binding protein from listeria innocua
72	<a href="#">c1ps9A</a>	Alignment	not modelled	65.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
73	<a href="#">d1rpxa</a>	Alignment	not modelled	64.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
74	<a href="#">c3rggA</a>	Alignment	not modelled	64.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-tyrosine phosphatase mitochondrial 1; <b>PDBTitle:</b> crystal structure of ptpmt1 in complex with pi(5)p
75	<a href="#">c3fd8A</a>	Alignment	not modelled	63.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
76	<a href="#">c3kruC</a>	Alignment	not modelled	63.4	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
77	<a href="#">d1gkra2</a>	Alignment	not modelled	62.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
78	<a href="#">c3fluD</a>	Alignment	not modelled	62.5	14	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
79	<a href="#">c1ofgF</a>	Alignment	not modelled	62.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-fructose oxidoreductase;

					<b>PDBTitle:</b> glucose-fructose oxidoreductase
80	<a href="#">c1h6dL</a>	Alignment	not modelled	62.4	18 <b>PDB header:</b> protein translocation <b>Chain:</b> L: <b>PDB Molecule:</b> precursor form of glucose-fructose <b>PDBTitle:</b> oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
81	<a href="#">d1pkla2</a>	Alignment	not modelled	62.1	24 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
82	<a href="#">c2q4eB</a>	Alignment	not modelled	61.6	10 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable oxidoreductase at4g09670; <b>PDBTitle:</b> ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
83	<a href="#">d1xbta1</a>	Alignment	not modelled	61.5	19 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Type II thymidine kinase
84	<a href="#">c3nsnA</a>	Alignment	not modelled	60.6	30 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosaminidase; <b>PDBTitle:</b> crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
85	<a href="#">c3l5aA</a>	Alignment	not modelled	58.9	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh/flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
86	<a href="#">c3ceaA</a>	Alignment	not modelled	58.7	12 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> myo-inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
87	<a href="#">d1vjia</a>	Alignment	not modelled	58.4	24 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
88	<a href="#">c3p6lA</a>	Alignment	not modelled	58.4	12 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
89	<a href="#">c2yxgD</a>	Alignment	not modelled	57.9	18 <b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase (dapa)
90	<a href="#">d2glka1</a>	Alignment	not modelled	57.9	11 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
91	<a href="#">d1n7ka</a>	Alignment	not modelled	57.8	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
92	<a href="#">d2icsa2</a>	Alignment	not modelled	57.6	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-o-dependent hydrolases <b>Family:</b> Adenine deaminase-like
93	<a href="#">d1kbla1</a>	Alignment	not modelled	57.6	12 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate phosphate dikinase, C-terminal domain
94	<a href="#">d1vcva1</a>	Alignment	not modelled	57.1	20 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
95	<a href="#">d1eyea</a>	Alignment	not modelled	56.6	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
96	<a href="#">c1vrda</a>	Alignment	not modelled	56.6	27 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution
97	<a href="#">c3obkH</a>	Alignment	not modelled	56.1	20 <b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> delta-aminolevulinic acid dehydratase; <b>PDBTitle:</b> crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
98	<a href="#">c1zfja</a>	Alignment	not modelled	55.2	25 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
99	<a href="#">c3qyqC</a>	Alignment	not modelled	55.1	15 <b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase, putative; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of a putative deoxyribose-2 phosphate aldolase from toxoplasma gondii me49
100	<a href="#">c3js3C</a>	Alignment	not modelled	54.9	15 <b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
101	<a href="#">c3moiA</a>	Alignment	not modelled	54.7	10 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
102	<a href="#">c3gkaB</a>	Alignment	not modelled	54.5	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
103	<a href="#">d1xkya1</a>	Alignment	not modelled	54.5	12 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
					<b>Fold:</b> TIM beta/alpha-barrel

104	<a href="#">d1muwa_</a>	Alignment	not modelled	54.2	13	<b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
105	<a href="#">c3s4oB_</a>	Alignment	not modelled	54.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein tyrosine phosphatase-like protein; <b>PDBTitle:</b> protein tyrosine phosphatase (putative) from Leishmania major
106	<a href="#">c2imgA_</a>	Alignment	not modelled	53.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 23; <b>PDBTitle:</b> crystal structure of dual specificity protein phosphatase 23 from homo sapiens in complex with ligand malate ion
107	<a href="#">d1a53a_</a>	Alignment	not modelled	53.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
108	<a href="#">c2x5eA_</a>	Alignment	not modelled	52.5	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0271 protein pa4511; <b>PDBTitle:</b> crystal structure of the hypothetical protein pa4511 from <i>Pseudomonas aeruginosa</i>
109	<a href="#">c2qjhH_</a>	Alignment	not modelled	52.4	22	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> putative aldolase mj0400; <b>PDBTitle:</b> m. jannaschii adh synthase covalently bound to 2 dihydroxyacetone phosphate
110	<a href="#">c3eb2A_</a>	Alignment	not modelled	52.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from <i>Pseudomonas putida</i> at 2.0 Å resolution
111	<a href="#">d1fpza_</a>	Alignment	not modelled	51.2	17	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
112	<a href="#">c3dxeB_</a>	Alignment	not modelled	51.2	20	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> amyloid beta a4 protein; <b>PDBTitle:</b> crystal structure of the intracellular domain of human app2 (t668a mutant) in complex with fe65-ptb2
113	<a href="#">c1xuzA_</a>	Alignment	not modelled	50.2	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> polysialic acid capsule biosynthesis protein siaC; <b>PDBTitle:</b> crystal structure analysis of sialic acid synthase (neub) from <i>Neisseria meningitidis</i> , bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
114	<a href="#">c2ocza_</a>	Alignment	not modelled	49.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> the structure of a putative 3-dehydroquinate dehydratase from <i>Streptococcus pyogenes</i> .
115	<a href="#">c2o48X_</a>	Alignment	not modelled	49.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> dimeric dihydrodiol dehydrogenase; <b>PDBTitle:</b> crystal structure of mammalian dimeric dihydrodiol dehydrogenase
116	<a href="#">d1k77a_</a>	Alignment	not modelled	48.9	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Hypothetical protein YgbM (EC1530)
117	<a href="#">c2elrA_</a>	Alignment	not modelled	48.9	58	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 406; <b>PDBTitle:</b> solution structure of the 15th c2h2 zinc finger of human 2 zinc finger protein 406
118	<a href="#">d1vc4a_</a>	Alignment	not modelled	48.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
119	<a href="#">d1d3ga_</a>	Alignment	not modelled	48.1	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
120	<a href="#">c3dx5A_</a>	Alignment	not modelled	47.2	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein asbf; <b>PDBTitle:</b> crystal structure of the probable 3-dhs dehydratase asbf involved in the petrobactin synthesis from <i>Bacillus anthracis</i>