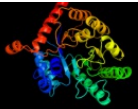










Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P00944
Date	Thu Jan 5 10:57:16 GMT 2012
Unique Job ID	136c47ff635c6295

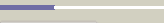

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1a0ca_	 Alignment		100.0	50	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
2	d1a0ea_	 Alignment		100.0	51	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
3	d1a0da_	 Alignment		100.0	53	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
4	d1x1ma_	 Alignment		100.0	26	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
5	d2glka1	 Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
6	d1x1ma_	 Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
7	d1muwa_	 Alignment		100.0	26	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
8	d1qt1a_	 Alignment		100.0	26	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
9	d1bxca_	 Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
10	d1bxba_	 Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
11	c2i56A_	 Alignment		100.0	18	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

12	c3ktcB_	Alignment		100.0	19	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
13	c2qw5B_	Alignment		99.9	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
14	c3qxbB_	Alignment		99.9	13	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	d1k77a_	Alignment		99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Hypothetical protein YgbM (EC1530)
16	d1d8wa_	Alignment		99.8	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: L-rhamnose isomerase
17	c2hk1D_	Alignment		99.8	16	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
18	c2zdsB_	Alignment		99.8	15	PDB header: dna binding protein Chain: B: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
19	c3kwsB_	Alignment		99.8	13	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
20	c3p14C_	Alignment		99.8	16	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
21	d1i60a_	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
22	d1xp3a1	Alignment	not modelled	99.7	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
23	c3ju2A_	Alignment	not modelled	99.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein smc04130; PDBTitle: crystal structure of protein smc04130 from sinorhizobium meliloti 1021
24	c2x7vA_	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
25	c3cqkB_	Alignment	not modelled	99.7	14	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
26	c2ou4C_	Alignment	not modelled	99.7	13	PDB header: isomerase Chain: C: PDB Molecule: d-tagatose 3-epimerase; PDBTitle: crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
27	c3ngfA_	Alignment	not modelled	99.7	15	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family 2; PDBTitle: crystal structure of ap endonuclease, family 2 from brucella2 melitensis
28	d1qtwa_	Alignment	not modelled	99.6	10	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
29	c3dx5A_	Alignment	not modelled	99.6	10	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
30	c2zvrA_	Alignment	not modelled	99.6	12	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
31	d2g0wa1	Alignment	not modelled	99.6	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lolI-like
32	c3obeB_	Alignment	not modelled	99.5	11	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
33	c3l23A_	Alignment	not modelled	99.5	9	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
34	c3aamA_	Alignment	not modelled	99.5	19	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease iv; PDBTitle: crystal structure of endonuclease iv from thermus thermophilus hb8
35	c3cnyA_	Alignment	not modelled	99.5	7	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 wcf51 at 1.85 a3 resolution
36	d2q02a1	Alignment	not modelled	99.4	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lolI-like
37	c3lmzA_	Alignment	not modelled	99.4	11	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
38	c3p6lA_	Alignment	not modelled	99.3	10	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
39	d1tz9a_	Alignment	not modelled	99.3	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like
40	d1yx1a1	Alignment	not modelled	99.2	9	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
41	c3bdkB_	Alignment	not modelled	99.0	16	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
42	c3bzjA_	Alignment	not modelled	98.1	16	PDB header: hydrolase Chain: A: PDB Molecule: uv endonuclease; PDBTitle: uvde k229l
43	c2xn1B_	Alignment	not modelled	90.7	25	PDB header: hydrolase Chain: B: PDB Molecule: alpha-galactosidase; PDBTitle: structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
44	c2yfnA_	Alignment	not modelled	87.6	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase-sucrose kinase agask; PDBTitle: galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
45	c3lw6A_	Alignment	not modelled	78.2	30	PDB header: transferase Chain: A: PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4-galactosyltransferase-7
46	d1pzta_	Alignment	not modelled	76.9	29	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
47	d1pbga_	Alignment	not modelled	68.6	14	Fold: TIM beta/(alpha)-barrel Superfamily: (Trans)glycosidases Family: Family 1 of glycosyl hydrolase
48	c2z1sA_	Alignment	not modelled	67.7	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase b; PDBTitle: beta-glucosidase b from paenibacillus polymyxa complexed2 with cellotetraose
49	c3mi6A_	Alignment	not modelled	65.7	23	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11.
50	c3ahxC_	Alignment	not modelled	61.1	16	PDB header: hydrolase Chain: C: PDB Molecule: beta-glucosidase a; PDBTitle: crystal structure of beta-glucosidase a from bacterium clostridium2 cellulovorans
51	c3n2oA_	Alignment	not modelled	52.2	20	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
52	c1jvnB_	Alignment	not modelled	52.0	24	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
53	d1cf3a2	Alignment	not modelled	46.0	18	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GMC oxidoreductases

54	d1ajza_	Alignment	not modelled	45.1	15	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
55	c3icgD_	Alignment	not modelled	44.3	13	PDB header: hydrolase Chain: D: PDB Molecule: endoglucanase d; PDBTitle: crystal structure of the catalytic and carbohydrate binding domain of 2 endoglucanase d from clostridium cellulovorans
56	d1qoxa_	Alignment	not modelled	43.6	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Family 1 of glycosyl hydrolase
57	d1gpea2	Alignment	not modelled	41.3	21	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GMC oxidoreductases
58	d1f3ta2	Alignment	not modelled	40.7	15	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
59	c1fcuA_	Alignment	not modelled	39.6	20	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: crystal structure (trigonal) of bee venom hyaluronidase
60	d1fcqa_	Alignment	not modelled	39.1	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Bee venom hyaluronidase
61	c2j75A_	Alignment	not modelled	38.8	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase a; PDBTitle: beta-glucosidase from thermotoga maritima in complex with 2 neuromycin
62	c3tdmD_	Alignment	not modelled	36.4	10	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, half flr
63	c2zoxA_	Alignment	not modelled	35.9	21	PDB header: hydrolase Chain: A: PDB Molecule: cytosolic beta-glucosidase; PDBTitle: crystal structure of the covalent intermediate of human cytosolic 2 beta-glucosidase
64	c1tvIA_	Alignment	not modelled	35.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
65	d1tvla_	Alignment	not modelled	35.7	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
66	c2atmA_	Alignment	not modelled	31.6	25	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: crystal structure of the recombinant allergen ves v 2
67	c2zunB_	Alignment	not modelled	30.4	11	PDB header: hydrolase Chain: B: PDB Molecule: 458aa long hypothetical endo-1,4-beta-glucanase; PDBTitle: functional analysis of hyperthermophilic endocellulase from 2 the archaeon pyrococcus horikoshii
68	c2pe4A_	Alignment	not modelled	30.2	20	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase-1; PDBTitle: structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme 2 involved in tumor growth and angiogenesis
69	d7odca2	Alignment	not modelled	29.2	13	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
70	c3aysA_	Alignment	not modelled	27.8	14	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: gh5 endoglucanase from a ruminal fungus in complex with cellotriose
71	d1b74a1	Alignment	not modelled	27.1	19	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
72	c3ianA_	Alignment	not modelled	26.9	17	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of a chitinase from lactococcus lactis 2 subsp. lactis
73	c2x1lC_	Alignment	not modelled	26.1	19	PDB header: ligase Chain: C: PDB Molecule: methionyl-trna synthetase; PDBTitle: crystal structure of mycobacterium smegmatis methionyl-trna 2 synthetase in complex with methionine and adenosine
74	c2yztA_	Alignment	not modelled	25.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha1756; PDBTitle: crystal structure of uncharacterized conserved protein from thermus 2 thermophilus hb8
75	c3raoB_	Alignment	not modelled	25.1	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus 2 cereus atcc 10987.
76	c2dgaA_	Alignment	not modelled	22.2	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of hexameric beta-glucosidase in wheat
77	d1eoka_	Alignment	not modelled	21.4	9	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
78	c3qomA_	Alignment	not modelled	20.9	16	PDB header: hydrolase Chain: A: PDB Molecule: 6-phospho-beta-glucosidase; PDBTitle: crystal structure of 6-phospho-beta-glucosidase from lactobacillus 2 plantarum
79	c3tqoA_	Alignment	not modelled	19.3	14	PDB header: ligase Chain: A: PDB Molecule: cysteinyI-trna synthetase; PDBTitle: structure of the cysteinyI-trna synthetase (cyss) from coxiella 2 burnetii.

80	c1j0yD_	 Alignment	not modelled	19.0	24	PDB header: hydrolase Chain: D: PDB Molecule: beta-amylase; PDBTitle: beta-amylase from bacillus cereus var. mycoides in complex2 with glucose
81	c1d7kB_	 Alignment	not modelled	19.0	12	PDB header: lyase Chain: B: PDB Molecule: human ornithine decarboxylase; PDBTitle: crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
82	c1uz4A_	 Alignment	not modelled	18.7	7	PDB header: hydrolase Chain: A: PDB Molecule: man5a; PDBTitle: common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 itineraries for glucoside and mannoside hydrolysis
83	d1uuqa_	 Alignment	not modelled	18.7	7	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
84	d1jvna1	 Alignment	not modelled	18.7	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
85	d1qo2a_	 Alignment	not modelled	18.1	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
86	c2w91A_	 Alignment	not modelled	17.8	19	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-n-acetylglucosaminidase d; PDBTitle: structure of a streptococcus pneumoniae family 85 glycoside2 hydrolase, endo-d.
87	c1zorB_	 Alignment	not modelled	16.3	22	PDB header: oxidoreductase Chain: B: PDB Molecule: isocitrate dehydrogenase; PDBTitle: isocitrate dehydrogenase from the hyperthermophile thermotoga maritima
88	c3pt5A_	 Alignment	not modelled	16.0	11	PDB header: hydrolase Chain: A: PDB Molecule: nans (yjhs), a 9-o-acetyl n-acetylneuraminic acid esterase; PDBTitle: crystal structure of nans
89	c2dwuA_	 Alignment	not modelled	15.0	17	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
90	d1kpga_	 Alignment	not modelled	14.4	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
91	c3gndC_	 Alignment	not modelled	12.9	16	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
92	d1d9ea_	 Alignment	not modelled	12.6	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
93	c3bwwA_	 Alignment	not modelled	12.1	7	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
94	d2j78a1	 Alignment	not modelled	12.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Family 1 of glycosyl hydrolase
95	d1d7ka2	 Alignment	not modelled	12.0	13	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
96	c1uasA_	 Alignment	not modelled	11.9	12	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of rice alpha-galactosidase
97	c3gnoA_	 Alignment	not modelled	11.9	14	PDB header: hydrolase Chain: A: PDB Molecule: os03g0212800 protein; PDBTitle: crystal structure of a rice os3bglu6 beta-glucosidase
98	c2yguA_	 Alignment	not modelled	11.8	24	PDB header: allergen Chain: A: PDB Molecule: venom allergen 2; PDBTitle: crystal structure of fire ant venom allergen, sol i 2
99	c3u57A_	 Alignment	not modelled	11.2	20	PDB header: hydrolase Chain: A: PDB Molecule: raucaffricine-o-beta-d-glucosidase; PDBTitle: structures of alkaloid biosynthetic glucosidases decode substrate2 specificity