Phyre^2

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Description	P0A9C3
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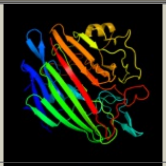
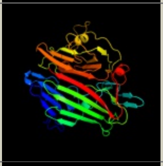
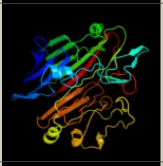
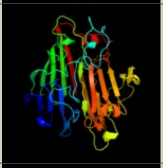
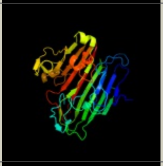
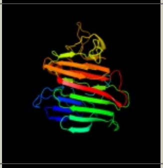
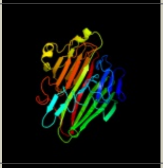
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1so0a_	Alignment		100.0	37	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
2	c1z45A_	Alignment		100.0	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**gal10 bifunctional protein; **PDBTitle:** crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces3 cerevisiae complexed with nad, udp-glucose, and galactose
3	d1lura_	Alignment		100.0	33	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
4	d1nsza_	Alignment		100.0	31	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
5	c3imhB_	Alignment		100.0	34	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**galactose-1-epimerase; **PDBTitle:** crystal structure of galactose 1-epimerase from lactobacillus2 acidophilus ncfm
6	d1z45a1	Alignment		100.0	25	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
7	c1ygaA_	Alignment		100.0	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**hypothetical 37.9 kda protein in bio3-hxt17 **PDBTitle:** crystal structure of saccharomyces cerevisiae yn9a protein,2 new york structural genomics consortium
8	c3os7D_	Alignment		100.0	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**galactose mutarotase-like protein; **PDBTitle:** crystal structure of a galactose mutarotase-like protein (ca_c0697)2 from clostridium acetobutylicum at 1.80 a resolution
9	c3os7B_	Alignment		100.0	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**galactose mutarotase-like protein; **PDBTitle:** crystal structure of a galactose mutarotase-like protein (ca_c0697)2 from clostridium acetobutylicum at 1.80 a resolution
10	c3nreB_	Alignment		100.0	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**aldose 1-epimerase; **PDBTitle:** crystal structure of a putative aldose 1-epimerase (b2544) from2 escherichia coli k12 at 1.59 a resolution
11	c3dcdA_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**galactose mutarotase related enzyme; **PDBTitle:** x-ray structure of the galactose mutarotase related enzyme q5fkd7 from2 lactobacillus acidophilus at the resolution 1.9a. northeast3 structural genomics consortium target lar33.

12	c3q1nA_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**galactose mutarotase related enzyme; **PDBTitle:** crystal structure of a galactose mutarotase-like protein (lsei_2598)2 from lactobacillus casei atcc 334 at 1.61 a resolution
13	c3mwxA_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**aldose 1-epimerase; **PDBTitle:** crystal structure of a putative galactose mutarotase (bsu18360) from2 bacillus subtilis at 1.45 a resolution
14	c3k25B_	Alignment		100.0	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**slr1438 protein; **PDBTitle:** crystal structure of slr1438 protein from synechocystis sp. pcc 6803,2 northeast structural genomics consortium target sgr112
15	c2cisA_	Alignment		100.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**hexose-6-phosphate mutarotase; **PDBTitle:** structure-based functional annotation: yeast ymr099c codes2 for a d-hexose-6-phosphate mutarotase. complex with3 tagatose-6-phosphate
16	c2htbB_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative enzyme related to aldose 1-epimerase; **PDBTitle:** crystal structure of a putative mutarotase (yead) from2 salmonella typhimurium in monoclinic form
17	d1jova_	Alignment		100.0	18	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Hypothetical protein HI1317
18	c3ty1B_	Alignment		99.9	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**hypothetical aldose 1-epimerase; **PDBTitle:** crystal structure of a hypothetical aldose 1-epimerase (kpn_04629)2 from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.90 a3 resolution
19	c3bs6B_	Alignment		97.3	17	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**inner membrane protein oxaa; **PDBTitle:** 1.8 angstrom crystal structure of the periplasmic domain of2 the membrane insertase yidc
20	c3blcB_	Alignment		96.2	17	**PDB header:**chaperone,protein transport **Chain:** B: **PDB Molecule:**inner membrane protein oxaa; **PDBTitle:** crystal structure of the periplasmic domain of the escherichia coli2 yidc
21	c1so9A_	Alignment	not modelled	59.9	24	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cytochrome c oxidase assembly protein ctag; **PDBTitle:** solution structure of apocox11, 30 structures
22	d1so9a_	Alignment	not modelled	59.9	24	**Fold:**Ctag/Cox11 **Superfamily:**Ctag/Cox11 **Family:**Ctag/Cox11
23	d1k1xa2	Alignment	not modelled	45.1	13	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**4-alpha-glucanotransferase, C-terminal domain
24	d1jz8a4	Alignment	not modelled	19.0	20	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**beta-Galactosidase, domain 5
25	c2xn1B_	Alignment	not modelled	18.6	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
26	d2hkja2	Alignment	not modelled	14.6	45	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
27	c2zooA_	Alignment	not modelled	14.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
28	d1f2ri_	Alignment	not modelled	13.9	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
						Fold:beta-clip

29	d4ubpb_	Alignment	not modelled	12.8	18	**Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
30	d1oe1a1	Alignment	not modelled	12.8	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
31	d1e9ya1	Alignment	not modelled	12.2	18	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
32	d1ibxb_	Alignment	not modelled	10.0	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
33	c1ibxB_	Alignment	not modelled	10.0	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**chimera of igg binding protein g and dna **PDBTitle:** nmr structure of dff40 and dff45 n-terminal domain complex
34	d1c9fa_	Alignment	not modelled	9.9	32	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
35	d1q2la4	Alignment	not modelled	9.9	29	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
36	d1ejxb_	Alignment	not modelled	9.5	17	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
37	d1ibxa_	Alignment	not modelled	9.3	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
38	c2zf9D_	Alignment	not modelled	8.9	6	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**scae cell-surface anchored scaffoldin protein; **PDBTitle:** crystal structure of a type iii cohesin module from the cellulosomal2 scae cell-surface anchoring scaffoldin of ruminococcus flavefaciens
39	d1ndsa1	Alignment	not modelled	8.1	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
40	c3cw3A_	Alignment	not modelled	8.0	16	**PDB header:**oncoprotein **Chain:** A: **PDB Molecule:**absent in melanoma 1 protein; **PDBTitle:** crystal structure of aim1g1
41	c2g8gA_	Alignment	not modelled	7.2	40	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid; **PDBTitle:** structurally mapping the diverse phenotype of adeno-2 associated virus serotype 4
42	d1m53a1	Alignment	not modelled	7.0	9	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
43	c3mi6A_	Alignment	not modelled	6.5	13	**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.
44	c3kieF_	Alignment	not modelled	6.4	33	**PDB header:**virus **Chain:** F: **PDB Molecule:**capsid protein vp1; **PDBTitle:** crystal structure of adeno-associated virus serotype 3b
45	c1v06A_	Alignment	not modelled	6.3	33	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**hmg box-containing protein 1; **PDBTitle:** axh domain of the transcription factor hbp1 from m.musculus
46	d1yq2a5	Alignment	not modelled	6.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
47	c2x3bB_	Alignment	not modelled	6.2	34	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**toxic extracellular endopeptidase; **PDBTitle:** asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
48	c2kl8A_	Alignment	not modelled	6.1	44	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
49	c1wa1X_	Alignment	not modelled	6.0	14	**PDB header:**reductase **Chain:** X: **PDB Molecule:**dissimilatory copper-containing nitrite **PDBTitle:** crystal structure of h313q mutant of alcaligenes2 xylosoxidans nitrite reductase
50	c3nttA_	Alignment	not modelled	5.9	39	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** structural insights of adeno-associated virus 5. a gene therapy vector2 for cystic fibrosis
51	c3dqgC_	Alignment	not modelled	5.9	11	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock 70 kda protein f; **PDBTitle:** peptide-binding domain of heat shock 70 kda protein f, mitochondrial2 precursor, from caenorhabditis elegans.
52	d1s58a_	Alignment	not modelled	5.5	29	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Parvoviridae-like VP
53	c2eelA_	Alignment	not modelled	5.4	22	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**cell death activator cide-a; **PDBTitle:** solution structure of the cide-n domain of human cell death2 activator cide-a
54	c3qgaD_	Alignment	not modelled	5.4	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**fusion of urease beta and gamma subunits; **PDBTitle:** 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae

55	d1mzya1	Alignment	not modelled	5.3	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
56	d1vlba2	Alignment	not modelled	5.3	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins