Phyre^2

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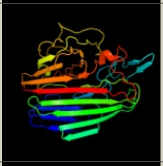
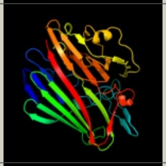
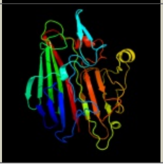
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nreB_	Alignment		100.0	20	**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
2	d1z45a1	Alignment		100.0	23	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
3	d1so0a_	Alignment		100.0	23	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
4	c3imhB_	Alignment		100.0	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**galactose-1-epimerase; **PDBTitle:** crystal structure of galactose 1-epimerase from lactobacillus2 acidophilus ncfm
5	c1ygaA_	Alignment		100.0	22	**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
6	c1z45A_	Alignment		100.0	22	**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
7	d1lura_	Alignment		100.0	22	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
8	d1nsza_	Alignment		100.0	20	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
9	c3os7B_	Alignment		100.0	19	**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	c3os7D_	Alignment		100.0	19	**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
11	c3dcdA_	Alignment		100.0	16	**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	20	**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	22	**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	13	**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	15	**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		100.0	11	**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	c3blcB_	Alignment		98.1	12	**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
20	c3bs6B_	Alignment		98.1	10	**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
21	d1jz8a4	Alignment	not modelled	93.2	12	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**beta-Galactosidase, domain 5
22	c2yfnA_	Alignment	not modelled	89.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
23	c2xn1B_	Alignment	not modelled	89.0	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
24	c3rgbA_	Alignment	not modelled	86.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
25	c1yewI_	Alignment	not modelled	86.3	14	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
26	c3mi6A_	Alignment	not modelled	83.2	11	**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.
27	c3rfrI_	Alignment	not modelled	82.2	17	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
28	c3bgaB_	Alignment	not modelled	75.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of beta-galactosidase from

						bacteroides2 thetaiotaomicron vpi-5482
29	c1jz6C_	Alignment	not modelled	74.5	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole
30	c3mv14_	Alignment	not modelled	71.1	14	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e.coli (lacz) beta-galactosidase (r599a) in complex with guanidinium
31	c1so9A_	Alignment	not modelled	65.5	10	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cytochrome c oxidase assembly protein ctag; **PDBTitle:** solution structure of apocox11, 30 structures
32	d1so9a_	Alignment	not modelled	65.5	10	**Fold:**Ctag/Cox11 **Superfamily:**Ctag/Cox11 **Family:**Ctag/Cox11
33	d1ejxb_	Alignment	not modelled	63.0	17	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
34	d4ubpb_	Alignment	not modelled	62.3	26	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
35	d1e9ya1	Alignment	not modelled	52.4	22	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
36	c3qgaD_	Alignment	not modelled	50.7	22	**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
37	d1ji1a2	Alignment	not modelled	49.2	8	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
38	c3qbtH_	Alignment	not modelled	47.2	26	**PDB header:**protein transport/hydrolase **Chain:** H: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** crystal structure of ocrl1 540-678 in complex with rab8a:gppnhp
39	c1e9zA_	Alignment	not modelled	44.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
40	c3obaA_	Alignment	not modelled	39.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** structure of the beta-galactosidase from kluyveromyces lactis
41	d1nkga3	Alignment	not modelled	38.0	11	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Rhamnogalacturonase B, RhgB, N-terminal domain
42	c1nkgA_	Alignment	not modelled	32.3	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**rhamnogalacturonase b; **PDBTitle:** rhamnogalacturonan lyase from aspergillus aculeatus
43	d1wzla2	Alignment	not modelled	25.0	17	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
44	c3isyA_	Alignment	not modelled	24.4	6	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor; **PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
45	c2r39A_	Alignment	not modelled	19.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fixg-related protein; **PDBTitle:** crystal structure of fixg-related protein from vibrio parahaemolyticus
46	c2x3bB_	Alignment	not modelled	19.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**toxic extracellular endopeptidase; **PDBTitle:** asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
47	c3ac0B_	Alignment	not modelled	16.7	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
48	c2cqtA_	Alignment	not modelled	16.2	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cellobiose phosphorylase; **PDBTitle:** crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
49	d2je8a2	Alignment	not modelled	15.1	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
50	c2zf9D_	Alignment	not modelled	12.6	15	**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
51	c2kl8A_	Alignment	not modelled	11.5	31	**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
52	d1cc3a_	Alignment	not modelled	10.7	20	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
53	d1g94a1	Alignment	not modelled	10.4	21	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain

54	d1cx1a_	Alignment	not modelled	9.8	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**CBM4/9
55	d1nbca_	Alignment	not modelled	9.0	15	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
56	c3cfuA_	Alignment	not modelled	8.7	33	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yjha; **PDBTitle:** crystal structure of the yjha protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr562
57	c1v7wA_	Alignment	not modelled	8.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
58	d1gu3a_	Alignment	not modelled	8.1	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**CBM4/9
59	d1v7wa2	Alignment	not modelled	8.1	12	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain
60	d1ktba1	Alignment	not modelled	8.0	14	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
61	d1g43a_	Alignment	not modelled	7.9	5	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
62	c3zqwA_	Alignment	not modelled	7.7	15	**PDB header:**carbohydrate-binding protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin; **PDBTitle:** structure of cbm3b of major scaffoldin subunit scaa from2 acetivibrio cellulolyticus
63	c2l8aA_	Alignment	not modelled	7.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** structure of a novel cbm3 lacking the calcium-binding site
64	d1dkza2	Alignment	not modelled	7.4	23	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
65	d2ccwa1	Alignment	not modelled	7.3	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
66	c3dqgC_	Alignment	not modelled	7.0	13	**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.
67	d1u00a2	Alignment	not modelled	6.7	20	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
68	c3qfgA_	Alignment	not modelled	6.6	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of a putative lipoprotein from staphylococcus aureus subsp.2 aureus nctc 8325
69	d1cuoa_	Alignment	not modelled	6.4	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
70	d3dhpa1	Alignment	not modelled	6.4	19	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
71	d1mspa_	Alignment	not modelled	6.4	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
72	c2wo4A_	Alignment	not modelled	6.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase, family 9; **PDBTitle:** 3b' carbohydrate-binding module from the cel9v glycoside2 hydrolase from clostridium thermocellum, in-house data
73	d2vzsa2	Alignment	not modelled	6.2	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
74	d3es6b1	Alignment	not modelled	6.0	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SVA-like
75	d2j5wa3	Alignment	not modelled	5.9	0	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
76	d1hfua2	Alignment	not modelled	5.8	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
77	d2f2ha2	Alignment	not modelled	5.8	8	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**YicI N-terminal domain-like
78	d1azca_	Alignment	not modelled	5.6	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
79	c3tdqB_	Alignment	not modelled	5.6	19	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**pily2 protein; **PDBTitle:** crystal structure of a fimbrial biogenesis protein pily22 (pily2_pa4555) from pseudomonas aeruginosa pao1 at 2.10 a resolution
80	d1jaea1	Alignment	not modelled	5.2	16	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain

						Family:alpha-Amylases, C-terminal beta-sheet domain
81	c2aenH_	Alignment	not modelled	5.2	12	**PDB header:**viral protein **Chain:** H: **PDB Molecule:**outer capsid protein vp4, vp8* core; **PDBTitle:** crystal structure of the rotavirus strain ds-1 vp8* core