Phyre^2

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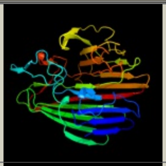
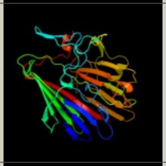
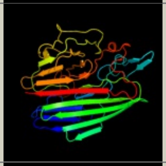
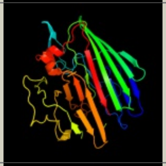
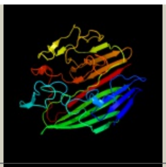
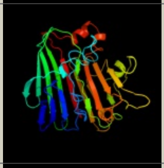
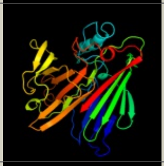
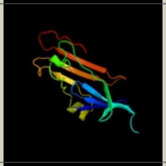
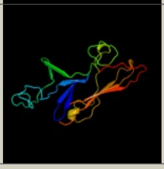
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nreB_	Alignment		100.0	99	**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	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
3	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
4	c1ygaA_	Alignment		100.0	15	**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
5	d1z45a1	Alignment		100.0	17	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
6	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
7	c3imhB_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**galactose-1-epimerase; **PDBTitle:** crystal structure of galactose 1-epimerase from lactobacillus2 acidophilus ncfm
8	c3dcdA_	Alignment		100.0	17	**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.
9	c3q1nA_	Alignment		100.0	17	**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
10	d1so0a_	Alignment		100.0	20	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
11	d1lura_	Alignment		100.0	15	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)

12	d1nsza_	Alignment		100.0	16	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
13	c3k25B_	Alignment		100.0	19	**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
14	c1z45A_	Alignment		100.0	17	**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
15	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
16	c2cisA_	Alignment		100.0	16	**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
17	d1jova_	Alignment		100.0	20	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Hypothetical protein HI1317
18	c3ty1B_	Alignment		100.0	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		97.1	16	**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		96.4	16	**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	d1k1xa2	Alignment	not modelled	89.8	12	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**4-alpha-glucanotransferase, C-terminal domain
22	c2xn1B_	Alignment	not modelled	85.6	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
23	c2cqtA_	Alignment	not modelled	80.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cellobiose phosphorylase; **PDBTitle:** crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
24	c3rgbA_	Alignment	not modelled	74.6	17	**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	74.6	17	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
26	c2yfnA_	Alignment	not modelled	72.9	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
27	d1ejxb_	Alignment	not modelled	72.8	23	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
28	d4ubpb_	Alignment	not modelled	68.5	23	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit

29	c3mi6A_	Alignment	not modelled	66.9	15	**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.
30	c3rfrI_	Alignment	not modelled	65.4	17	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
31	d1jz8a4	Alignment	not modelled	61.3	13	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**beta-Galactosidase, domain 5
32	d1e9ya1	Alignment	not modelled	60.0	19	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
33	c3qgaD_	Alignment	not modelled	57.7	32	**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
34	c1v7wA_	Alignment	not modelled	56.9	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
35	d1v7wa2	Alignment	not modelled	54.8	8	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain
36	c1e9zA_	Alignment	not modelled	50.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
37	c3isyA_	Alignment	not modelled	45.5	15	**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
38	c2kl8A_	Alignment	not modelled	40.2	13	**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
39	c3ndyG_	Alignment	not modelled	40.1	19	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**endoglucanase d; **PDBTitle:** the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
40	c1k1yA_	Alignment	not modelled	36.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
41	c3qbtH_	Alignment	not modelled	33.4	22	**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
42	c3bgaB_	Alignment	not modelled	21.6	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of beta-galactosidase from bacteroides2 thetaiotaomicron vpi-5482
43	d2vzsa2	Alignment	not modelled	20.9	37	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
44	c3obaA_	Alignment	not modelled	18.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** structure of the beta-galactosidase from kluyveromyces lactis
45	d1w8oa1	Alignment	not modelled	18.0	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
46	c2x3bB_	Alignment	not modelled	12.2	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**toxic extracellular endopeptidase; **PDBTitle:** asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
47	d1f2ri_	Alignment	not modelled	12.2	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
48	d2exna1	Alignment	not modelled	10.8	12	**Fold:**MOSC N-terminal domain-like **Superfamily:**MOSC N-terminal domain-like **Family:**MOSC N-terminal domain-like
49	d1c9fa_	Alignment	not modelled	10.7	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
50	c2zf9D_	Alignment	not modelled	10.4	31	**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	c2p28A_	Alignment	not modelled	9.9	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of the phe2 and phe3 fragments of the integrin beta2 subunit
52	c2x41A_	Alignment	not modelled	9.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
53	c2kutA_	Alignment	not modelled	8.4	37	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target

						gmr58a
54	d1ibxa_	Alignment	not modelled	8.3	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
55	d1wn7a1	Alignment	not modelled	8.2	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
56	c3qfgA_	Alignment	not modelled	8.2	15	**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
57	d1nkga3	Alignment	not modelled	7.9	24	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Rhamnogalacturonase B, RhgB, N-terminal domain
58	d1s58a_	Alignment	not modelled	7.8	20	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Parvoviridae-like VP
59	c3nttA_	Alignment	not modelled	7.6	28	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** structural insights of adeno-associated virus 5. a gene therapy vector2 for cystic fibrosis
60	c3cfuA_	Alignment	not modelled	7.6	17	**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
61	d2je8a2	Alignment	not modelled	7.4	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
62	d1mspa_	Alignment	not modelled	7.3	30	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
63	d1ny721	Alignment	not modelled	7.2	9	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
64	d1jv2a2	Alignment	not modelled	7.1	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Integrin domains **Family:**Integrin domains
65	c3ac0B_	Alignment	not modelled	7.1	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
66	d1oe1a1	Alignment	not modelled	6.9	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
67	c1ibxB_	Alignment	not modelled	6.6	29	**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
68	d1ibxb_	Alignment	not modelled	6.6	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
69	d1pgl21	Alignment	not modelled	6.3	15	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
70	c3cdzA_	Alignment	not modelled	6.1	31	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor viii heavy chain; **PDBTitle:** crystal structure of human factor viii
71	d1exha_	Alignment	not modelled	6.1	15	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family II
72	d1pgw21	Alignment	not modelled	6.1	15	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
73	c2r5kE_	Alignment	not modelled	6.0	11	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**major capsid protein l1; **PDBTitle:** pentamer structure of major capsid protein l1 of human2 papilloma virus type 11
74	c2zooA_	Alignment	not modelled	5.9	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
75	c2l8aA_	Alignment	not modelled	5.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** structure of a novel cbm3 lacking the calcium-binding site
76	c3qisA_	Alignment	not modelled	5.4	25	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** recognition of the f&h motif by the lowe syndrome protein ocrl
77	c3mpbA_	Alignment	not modelled	5.2	43	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
78	c2eelA_	Alignment	not modelled	5.1	12	**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
79	c2aenH_	Alignment	not modelled	5.1	11	**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
						PDB header:hydrolase

80	c1lf6A_	Alignment	not modelled	5.0	10	**Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** crystal structure of bacterial glucoamylase