Phyre^2

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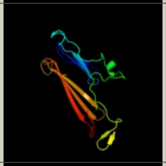
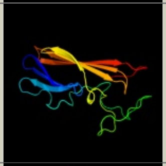
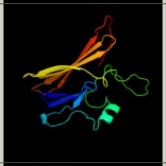
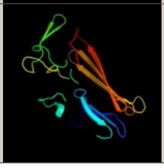
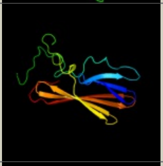
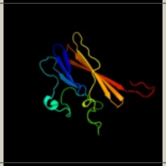
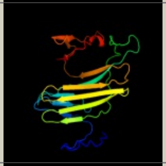
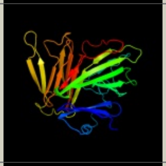
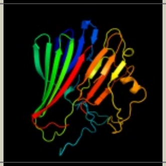
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3blcB_	Alignment		100.0	94	**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
2	c3bs6B_	Alignment		100.0	98	**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
3	d1z45a1	Alignment		97.7	9	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
4	c1ygaA_	Alignment		97.4	12	**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	c2htbB_	Alignment		97.3	8	**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
6	d1lura_	Alignment		97.3	13	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
7	c3dcdA_	Alignment		97.0	9	**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.
8	c3nreB_	Alignment		97.0	13	**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
9	c3q1nA_	Alignment		97.0	21	**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	c3mwxA_	Alignment		96.9	13	**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
11	c1z45A_	Alignment		96.6	10	**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

12	c3imhB_	Alignment		96.5	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**galactose-1-epimerase; **PDBTitle:** crystal structure of galactose 1-epimerase from lactobacillus2 acidophilus ncfm
13	d1nsza_	Alignment		96.4	13	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
14	d1so0a_	Alignment		96.4	13	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
15	c2cisA_	Alignment		95.7	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
16	c3k25B_	Alignment		94.1	10	**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
17	d3bvua2	Alignment		72.7	10	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**alpha-mannosidase, C-terminal domain
18	c2yfnA_	Alignment		70.9	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
19	c3os7D_	Alignment		69.6	13	**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
20	c3os7B_	Alignment		69.6	13	**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
21	d1jova_	Alignment	not modelled	66.3	7	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Hypothetical protein HI1317
22	c1o7dD_	Alignment	not modelled	53.8	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
23	d1jz8a4	Alignment	not modelled	52.5	8	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**beta-Galactosidase, domain 5
24	d1x9la_	Alignment	not modelled	51.7	16	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**DR1885-like metal-binding protein **Family:**DR1885-like metal-binding protein
25	c3ty1B_	Alignment	not modelled	50.1	10	**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
26	c3mi6A_	Alignment	not modelled	46.0	10	**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	c2xn1B_	Alignment	not modelled	42.6	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
28	c3mv14_	Alignment	not modelled	38.2	6	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e.coli (lacz) beta-galactosidase (r599a) in complex with

						guanidinium
29	c1jz6C_	Alignment	not modelled	31.9	6	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole
30	d1k1xa2	Alignment	not modelled	26.0	13	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**4-alpha-glucanotransferase, C-terminal domain
31	d1e42a1	Alignment	not modelled	24.6	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like
32	c1z65A_	Alignment	not modelled	24.1	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**prion-like protein doppel; **PDBTitle:** mouse doppel 1-30 peptide
33	c2rmrA_	Alignment	not modelled	20.3	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**paired amphipathic helix protein sin3a; **PDBTitle:** solution structure of msin3a pah1 domain
34	c2ow7A_	Alignment	not modelled	18.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase 2; **PDBTitle:** golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thioniabicyclo[4.3.0]nonan-7,8-diol chloride
35	c4a1qB_	Alignment	not modelled	18.4	36	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**orf e73; **PDBTitle:** solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
36	d1lvaa3	Alignment	not modelled	15.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
37	c3rgbA_	Alignment	not modelled	13.7	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
38	c1e42A_	Alignment	not modelled	13.6	17	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**ap-2 complex subunit beta; **PDBTitle:** beta2-adaptin appendage domain, from clathrin adaptor ap2
39	c2kmuA_	Alignment	not modelled	13.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase q4; **PDBTitle:** recql4 amino-terminal domain
40	c3r45C_	Alignment	not modelled	12.5	17	**PDB header:**nuclear protein **Chain:** C: **PDB Molecule:**holliday junction recognition protein; **PDBTitle:** structure of a cenp-a-histone h4 heterodimer in complex with chaperone2 hjurp
41	c1v7wA_	Alignment	not modelled	12.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
42	c1w8xP_	Alignment	not modelled	11.3	22	**PDB header:**virus **Chain:** P: **PDB Molecule:**protein p16; **PDBTitle:** structural analysis of prd1
43	c2y69Q_	Alignment	not modelled	11.1	18	**PDB header:**electron transport **Chain:** Q: **PDB Molecule:**cytochrome c oxidase subunit 4 isoform 1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
44	c2f1eA_	Alignment	not modelled	10.9	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein apag; **PDBTitle:** solution structure of apag protein
45	d1qbaa2	Alignment	not modelled	10.3	13	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Bacterial chitobiase, n-terminal domain
46	d1xvsa_	Alignment	not modelled	10.0	4	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ApaG-like **Family:**ApaG-like
47	d1xq4a_	Alignment	not modelled	9.9	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ApaG-like **Family:**ApaG-like
48	d1v54d_	Alignment	not modelled	9.2	18	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit IV **Family:**Mitochondrial cytochrome c oxidase subunit IV
49	c1k1yA_	Alignment	not modelled	9.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
50	c2jo8B_	Alignment	not modelled	9.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase 4; **PDBTitle:** solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
51	d1v7wa2	Alignment	not modelled	8.9	17	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain
52	c2avuF_	Alignment	not modelled	8.7	21	**PDB header:**transcription activator **Chain:** F: **PDB Molecule:**flagellar transcriptional activator flhc; **PDBTitle:** structure of the escherichia coli flhdc complex, a2 prokaryotic heteromeric regulator of transcription
53	d2avue1	Alignment	not modelled	8.7	21	**Fold:**FlhC-like **Superfamily:**FlhC-like **Family:**FlhC-like
54	c3oq9C_	Alignment	not modelled	8.6	13	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6; **PDBTitle:** structure of the fas/fadd death domain assembly

55	c3hfdA_	Alignment	not modelled	8.6	19	**PDB header:**chaperone, protein transport **Chain:** A: **PDB Molecule:**nucleosome assembly protein 1; **PDBTitle:** nucleosome assembly protein 1 from plasmodium knowlesi
56	d2e50a1	Alignment	not modelled	8.5	16	**Fold:**NAP-like **Superfamily:**NAP-like **Family:**NAP-like
57	d1tzaa_	Alignment	not modelled	8.3	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ApaG-like **Family:**ApaG-like
58	d1s5qb_	Alignment	not modelled	8.2	15	**Fold:**PAH2 domain **Superfamily:**PAH2 domain **Family:**PAH2 domain
59	d2f05a1	Alignment	not modelled	7.5	18	**Fold:**PAH2 domain **Superfamily:**PAH2 domain **Family:**PAH2 domain
60	d1hn0a3	Alignment	not modelled	7.4	17	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
61	d1g43a_	Alignment	not modelled	7.2	13	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
62	c2ayuA_	Alignment	not modelled	6.9	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**nucleosome assembly protein; **PDBTitle:** the structure of nucleosome assembly protein suggests a mechanism for2 histone binding and shuttling
63	d2ayua1	Alignment	not modelled	6.9	13	**Fold:**NAP-like **Superfamily:**NAP-like **Family:**NAP-like
64	c2rddB_	Alignment	not modelled	6.9	23	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
65	d1cwva4	Alignment	not modelled	6.7	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
66	c2kfeA_	Alignment	not modelled	6.5	22	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**meucin-24; **PDBTitle:** solution structure of meucin-24
67	c2do5A_	Alignment	not modelled	6.4	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**splicing factor 3b subunit 2; **PDBTitle:** solution structure of the sap domain of human splicing2 factor 3b subunit 2
68	c3fs3A_	Alignment	not modelled	6.4	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**nucleosome assembly protein 1, putative; **PDBTitle:** crystal structure of malaria parasite nucleosome assembly protein2 (nap)
69	c2jtvA_	Alignment	not modelled	6.3	50	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**protein of unknown function; **PDBTitle:** solution structure of protein rpa3401, northeast structural genomics2 consortium target rpt7, ontario center for structural proteomics3 target rp3384
70	c2of5A_	Alignment	not modelled	6.2	14	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain-containing protein cradd; **PDBTitle:** oligomeric death domain complex
71	d1w1wa_	Alignment	not modelled	5.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
72	c1wsuA_	Alignment	not modelled	5.7	10	**PDB header:**translation/rna **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** c-terminal domain of elongation factor selb complexed with2 secis rna
73	d1ojra_	Alignment	not modelled	5.7	35	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
74	c1htyA_	Alignment	not modelled	5.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase ii; **PDBTitle:** golgi alpha-mannosidase ii
75	d1flca2	Alignment	not modelled	5.6	21	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Esterase domain of haemagglutinin-esterase-fusion glycoprotein HEF1
76	c3oobaA_	Alignment	not modelled	5.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** structure of the beta-galactosidase from kluyveromyces lactis
77	c3h9pB_	Alignment	not modelled	5.5	33	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative triphosphoribosyl-dephospho-coa synthase; **PDBTitle:** crystal structure of putative triphosphoribosyl-dephospho-coa synthase2 from archaeoglobus fulgidus
78	d1fada_	Alignment	not modelled	5.5	12	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
79	c3cazA_	Alignment	not modelled	5.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**bar protein; **PDBTitle:** crystal structure of a bar protein from galdieria sulphuraria
80	d1ryka_	Alignment	not modelled	5.1	19	**Fold:**SAM domain-like **Superfamily:**Hypothetical protein YjbJ

Family: Hypothetical protein YjbJ