Phyre2

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Description	P39173
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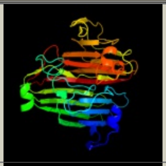
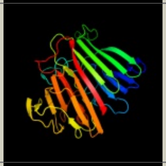
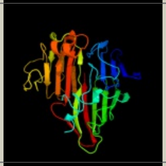
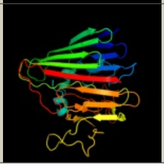
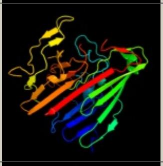
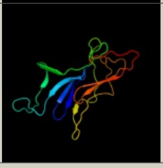
Unique Job ID	d92deb62fefb6fcb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2htbB_	Alignment		100.0	83	**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
2	d1jova_	Alignment		100.0	35	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Hypothetical protein HI1317
3	c2cisA_	Alignment		100.0	28	**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
4	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
5	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.
6	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
7	c3q1nA_	Alignment		100.0	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
8	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
9	c3nreB_	Alignment		100.0	17	**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
10	c3mwxA_	Alignment		100.0	15	**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	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

12	d1nsza_	Alignment		100.0	17	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
13	d1lura_	Alignment		100.0	15	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
14	c1ygaA_	Alignment		100.0	13	**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
15	d1so0a_	Alignment		100.0	13	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
16	d1z45a1	Alignment		100.0	14	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
17	c1z45A_	Alignment		100.0	15	**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
18	c3ty1B_	Alignment		99.9	14	**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		96.6	11	**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	10	**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	d1ejxb_	Alignment	not modelled	37.9	10	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
22	d4ubpb_	Alignment	not modelled	36.4	14	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
23	c2yfnA_	Alignment	not modelled	35.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
24	d1e9ya1	Alignment	not modelled	35.3	10	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
25	d1jz8a4	Alignment	not modelled	32.7	15	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**beta-Galactosidase, domain 5
26	c2js4A_	Alignment	not modelled	31.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein bb2007; **PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
27	c3qgaD_	Alignment	not modelled	29.4	10	**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
28	c1e9zA_	Alignment	not modelled	26.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha;

						PDBTitle: crystal structure of helicobacter pylori urease
29	d1fcqa_	Alignment	not modelled	21.2	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Bee venom hyaluronidase
30	c2jr6A_	Alignment	not modelled	18.6	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein nma0874; **PDBTitle:** solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
31	d2pk7a1	Alignment	not modelled	17.7	45	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
32	d2jnya1	Alignment	not modelled	16.8	36	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
33	d2hf1a1	Alignment	not modelled	16.6	27	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
34	c2k5rA_	Alignment	not modelled	14.6	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein xf2673; **PDBTitle:** solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
35	c2kpiA_	Alignment	not modelled	14.3	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco3027; **PDBTitle:** solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
36	d1pxva_	Alignment	not modelled	11.4	29	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
37	c1y4hA_	Alignment	not modelled	9.8	29	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**cysteine protease; **PDBTitle:** wild type staphopain-staphostatin complex
38	c1h4tD_	Alignment	not modelled	9.0	16	**PDB header:**aminoacyl-trna synthetase **Chain:** D: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline
39	c1qf6A_	Alignment	not modelled	8.9	25	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
40	c2qeaB_	Alignment	not modelled	8.4	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative general stress protein 26; **PDBTitle:** crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution
41	c1nj8C_	Alignment	not modelled	8.3	8	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from2 methanocaldococcus janaschii
42	d1pgw21	Alignment	not modelled	7.8	21	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
43	d1ny721	Alignment	not modelled	7.4	26	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
44	d1pgl21	Alignment	not modelled	7.3	21	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
45	c3qbtH_	Alignment	not modelled	7.2	7	**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
46	c3dmbA_	Alignment	not modelled	7.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative general stress protein 26 with a pnp-oxidase like **PDBTitle:** crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
47	c1yewI_	Alignment	not modelled	6.6	5	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
48	c3rgbA_	Alignment	not modelled	6.6	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
49	d1k1xa2	Alignment	not modelled	6.6	15	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**4-alpha-glucanotransferase, C-terminal domain
50	c3ialB_	Alignment	not modelled	6.6	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** giardia lamblia prolyl-trna synthetase in complex with prolyl-2 adenylate
51	d1th5a1	Alignment	not modelled	6.4	21	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
52	c3bmzA_	Alignment	not modelled	5.1	22	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** violacein biosynthetic enzyme vioe
53	c2r5iL_	Alignment	not modelled	5.1	26	**PDB header:**viral protein **Chain:** L: **PDB Molecule:**l1 protein; **PDBTitle:** pentamer structure of major capsid protein l1 of human2 papilloma virus type 18