Phyre2

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Description	P37680
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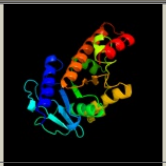
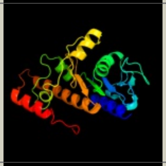
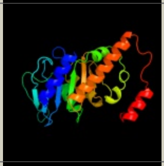
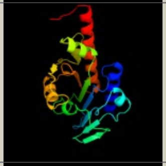
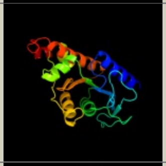
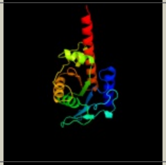
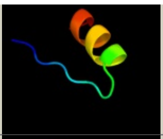
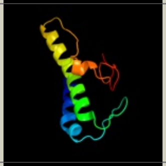
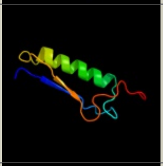
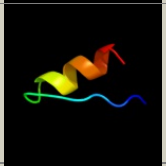
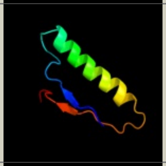
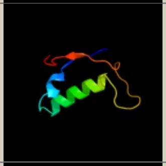
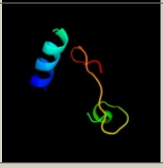
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k0wa_	Alignment		100.0	74	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
2	c3ocrA_	Alignment		100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**class ii aldolase/adducin domain protein; **PDBTitle:** crystal structure of aldolase ii superfamily protein from pseudomonas2 syringae
3	d1e4cp_	Alignment		100.0	27	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
4	d1ojra_	Alignment		100.0	15	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
5	c2z7bA_	Alignment		100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mlr6791 protein; **PDBTitle:** crystal structure of mesorhizobium loti 3-hydroxy-2-methylpyridine-4,2 5-dicarboxylate decarboxylase
6	d1pvta_	Alignment		100.0	22	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
7	c2opiB_	Alignment		100.0	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
8	c2irpA_	Alignment		100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative aldolase class 2 protein aq_1979; **PDBTitle:** crystal structure of the l-fuculose-1-phosphate aldolase (aq_1979)2 from aquifex aeolicus vf5
9	c2fk5B_	Alignment		100.0	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from thermus2 thermophilus hb8
10	c3m4rA_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of the n-terminal class ii aldolase domain of a conserved2 protein from thermoplasma acidophilum
11	c2cfuA_	Alignment		34.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.

12	c2yztA_	Alignment		34.1	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1756; **PDBTitle:** crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
13	d2cfua2	Alignment		27.0	11	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
14	c3kvaA_	Alignment		19.2	20	**PDB header:**h3k4me3 binding protein, transferase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 1d; **PDBTitle:** structure of kiaa1718 jumonji domain in complex with alpha-2 ketoglutarate
15	d1j5ua_	Alignment		16.4	11	**Fold:**MTH1598-like **Superfamily:**MTH1598-like **Family:**MTH1598-like
16	c2w3pB_	Alignment		15.7	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**benzoyl-coa-dihydrodiol lyase; **PDBTitle:** boxc crystal structure
17	d1jw3a_	Alignment		14.2	26	**Fold:**MTH1598-like **Superfamily:**MTH1598-like **Family:**MTH1598-like
18	d1gp6a_	Alignment		12.9	12	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
19	d1odma_	Alignment		12.4	14	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
20	c2btwA_	Alignment		12.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alr0975 protein; **PDBTitle:** crystal structure of alr0975
21	c2ra9A_	Alignment	not modelled	9.1	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf1285; **PDBTitle:** crystal structure of a duf1285 family protein (sbal_2486) from2 shewanella baltica os155 at 1.40 a resolution
22	d2bu3a1	Alignment	not modelled	8.4	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Phytochelatin synthase
23	c2kouA_	Alignment	not modelled	7.8	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dicer-like protein 4; **PDBTitle:** dicer like protein
24	c1gn4B_	Alignment	not modelled	7.5	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**superoxide dismutase; **PDBTitle:** h145e mutant of mycobacterium tuberculosis iron-superoxide2 dismutase.
25	c1fcuA_	Alignment	not modelled	7.4	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure (trigonal) of bee venom hyaluronidase
26	c3kv4A_	Alignment	not modelled	7.1	20	**PDB header:**h3k4me3 binding protein, transferase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** structure of phf8 in complex with histone h3
27	c2i0tB_	Alignment	not modelled	7.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aromatic amine dehydrogenase; **PDBTitle:** crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
28	c2yz3B_	Alignment	not modelled	7.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystallographic investigation of inhibition mode of the2 vim-2 metallo-beta-lactamase from pseudomonas aeruginosa3 with mercaptocarboxylate inhibitor
						PDB header:cell cycle

29	c3euhF_	Alignment	not modelled	7.0	23	**Chain:** F: **PDB Molecule:**muke; **PDBTitle:** crystal structure of the muke-mukf complex
30	c2oqkA_	Alignment	not modelled	6.8	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
31	d1y67a2	Alignment	not modelled	6.7	10	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
32	d1fcqa_	Alignment	not modelled	6.4	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Bee venom hyaluronidase
33	d1wi9a_	Alignment	not modelled	6.3	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
34	d1f28a_	Alignment	not modelled	5.9	11	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
35	d1a9xa5	Alignment	not modelled	5.9	19	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
36	c2e1nA_	Alignment	not modelled	5.6	14	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**pex; **PDBTitle:** crystal structure of the cyanobacterium circadian clock modifier pex
37	d1kzyc2	Alignment	not modelled	5.6	14	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**53BP1
38	c1ibtC_	Alignment	not modelled	5.6	50	**PDB header:**lyase **Chain:** C: **PDB Molecule:**histidine decarboxylase beta chain; **PDBTitle:** structure of the d53,54n mutant of histidine decarboxylase at-170 c
39	d1uerc2	Alignment	not modelled	5.6	24	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
40	d1b06a2	Alignment	not modelled	5.5	19	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
41	c1kkcB_	Alignment	not modelled	5.3	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**manganese superoxide dismutase; **PDBTitle:** crystal structure of aspergillus fumigatus mnsod
42	c3pu3A_	Alignment	not modelled	5.2	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 2; **PDBTitle:** phf2 jumonji domain-nog complex
43	c3da4B_	Alignment	not modelled	5.1	20	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m; **PDBTitle:** crystal structure of colicin m, a novel phosphatase2 specifically imported by escherichia coli
44	d1gv3a2	Alignment	not modelled	5.1	19	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain