Phyre2

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Description	Q46890
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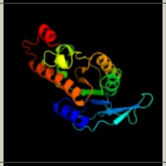
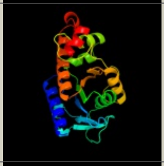
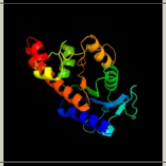
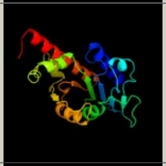
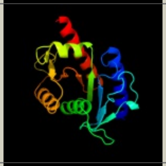
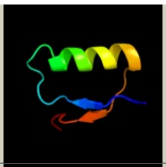
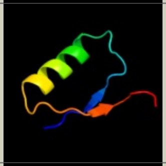
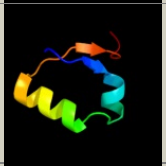
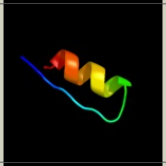
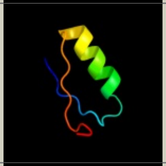
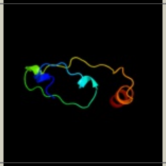
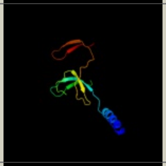
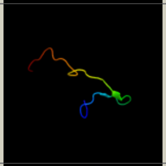
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1e4cp_	Alignment		100.0	28	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
2	d1ojra_	Alignment		100.0	25	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
3	c3ocrA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**class ii aldolase/adducin domain protein; **PDBTitle:** crystal structure of aldolase ii superfamily protein from pseudomonas2 syringae
4	c2z7bA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mlr6791 protein; **PDBTitle:** crystal structure of mesorhizobium loti 3-hydroxy-2-methylpyridine-4,2 5-dicarboxylate decarboxylase
5	c2opiB_	Alignment		100.0	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
6	c2fk5B_	Alignment		100.0	29	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from thermus2 thermophilus hb8
7	d1k0wa_	Alignment		100.0	23	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
8	d1pvta_	Alignment		100.0	26	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
9	c2irpA_	Alignment		100.0	25	**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
10	c3m4rA_	Alignment		100.0	23	**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	d1w9ya1	Alignment		48.7	19	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like

12	d1gp6a_	Alignment		40.5	25	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
13	d1odma_	Alignment		38.2	36	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
14	d1dcsa_	Alignment		32.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
15	c2yztA_	Alignment		31.5	16	**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
16	c3on7C_	Alignment		25.2	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, iron/ascorbate family; **PDBTitle:** crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution
17	c3kv4A_	Alignment		15.0	26	**PDB header:**h3k4me3 binding protein, transferase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** structure of phf8 in complex with histone h3
18	c3m9bK_	Alignment		14.9	13	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
19	c2ra9A_	Alignment		13.2	19	**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
20	d1chda_	Alignment		12.5	18	**Fold:**Methylesterase CheB, C-terminal domain **Superfamily:**Methylesterase CheB, C-terminal domain **Family:**Methylesterase CheB, C-terminal domain
21	d1jw3a_	Alignment	not modelled	10.6	28	**Fold:**MTH1598-like **Superfamily:**MTH1598-like **Family:**MTH1598-like
22	c3pvjB_	Alignment	not modelled	10.2	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440
23	d1j5ua_	Alignment	not modelled	10.2	16	**Fold:**MTH1598-like **Superfamily:**MTH1598-like **Family:**MTH1598-like
24	c3ooxA_	Alignment	not modelled	9.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 2og-fe(ii) oxygenase family protein; **PDBTitle:** crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution
25	c1a2oB_	Alignment	not modelled	8.8	18	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
26	d1hj3a1	Alignment	not modelled	7.9	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
27	d1w96c1	Alignment	not modelled	7.4	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
28	d2dsya1	Alignment	not modelled	7.0	25	**Fold:**TTHA1013/TTHA0281-like **Superfamily:**TTHA1013/TTHA0281-like

						Family:TTHA0281-like
29	c3sftA_	Alignment	not modelled	6.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
30	c2ri0B_	Alignment	not modelled	6.5	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans
31	c2re3A_	Alignment	not modelled	6.2	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
32	c3dclC_	Alignment	not modelled	6.2	27	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**tm1086; **PDBTitle:** crystal structure of tm1086
33	d2c9wa2	Alignment	not modelled	6.1	19	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
34	c1w7vD_	Alignment	not modelled	6.0	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** znmg substituted aminopeptidase p from e. coli
35	d1ulza1	Alignment	not modelled	5.9	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
36	d1w96a1	Alignment	not modelled	5.8	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
37	d1otja_	Alignment	not modelled	5.5	13	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like