Phyre2

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Description	P39306
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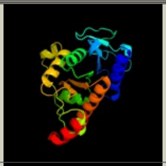
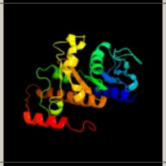
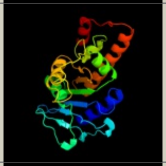
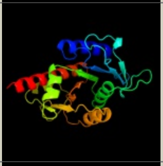
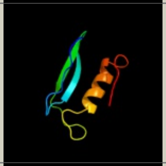
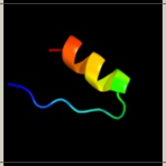
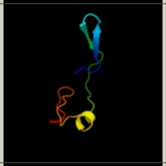
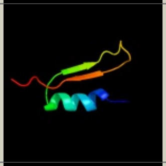
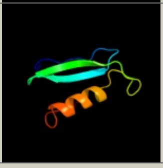
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k0wa_	Alignment		100.0	61	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
2	c3ocrA_	Alignment		100.0	15	**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	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
5	d1ojra_	Alignment		100.0	18	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
6	d1pvta_	Alignment		100.0	23	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
7	c2opiB_	Alignment		100.0	18	**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	c2fk5B_	Alignment		100.0	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from thermus2 thermophilus hb8
9	c2irpA_	Alignment		100.0	20	**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	20	**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	c2yztA_	Alignment		43.3	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

12	c1gph1_	Alignment		22.4	7	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
13	d1jw3a_	Alignment		22.4	38	**Fold:**MTH1598-like **Superfamily:**MTH1598-like **Family:**MTH1598-like
14	d1chda_	Alignment		20.1	17	**Fold:**Methylesterase CheB, C-terminal domain **Superfamily:**Methylesterase CheB, C-terminal domain **Family:**Methylesterase CheB, C-terminal domain
15	d1j5ua_	Alignment		19.3	11	**Fold:**MTH1598-like **Superfamily:**MTH1598-like **Family:**MTH1598-like
16	d1mqoa_	Alignment		16.7	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
17	c1ecjB_	Alignment		16.0	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
18	c3p04A_	Alignment		15.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
19	c3p04B_	Alignment		13.4	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
20	c3sftA_	Alignment		13.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
21	d1eexg_	Alignment	not modelled	12.4	14	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Diol dehydratase, gamma subunit **Family:**Diol dehydratase, gamma subunit
22	c1uc5M_	Alignment	not modelled	12.4	14	**PDB header:**lyase **Chain:** M: **PDB Molecule:**diol dehydrase gamma subunit; **PDBTitle:** structure of diol dehydratase complexed with (r)-1,2-2 propanediol
23	c7mdhA_	Alignment	not modelled	11.1	9	**PDB header:**chloroplastic malate dehydrogenase **Chain:** A: **PDB Molecule:**protein (malate dehydrogenase); **PDBTitle:** structural basis for light acitvation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
24	d1iwpg_	Alignment	not modelled	10.7	22	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Diol dehydratase, gamma subunit **Family:**Diol dehydratase, gamma subunit
25	c3da4B_	Alignment	not modelled	10.1	22	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m; **PDBTitle:** crystal structure of colicin m, a novel phosphatase2 specifically imported by escherichia coli
26	c1zq1B_	Alignment	not modelled	9.9	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
27	c1a2oB_	Alignment	not modelled	9.9	17	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
28	c2vf7B_	Alignment	not modelled	9.2	25	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
						PDB header:structural genomics, unknown function

29	c3ikbB_	Alignment	not modelled	7.2	3	**Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the structure of a conserved protein from streptococcus2 mutans ua159.
30	d2czra1	Alignment	not modelled	6.8	11	**Fold:**Restriction endonuclease-like **Superfamily:**TBP-interacting protein-like **Family:**TBP-interacting protein-like
31	c3q2oB_	Alignment	not modelled	6.5	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
32	d1a9xa5	Alignment	not modelled	6.4	19	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
33	c2ra9A_	Alignment	not modelled	6.3	15	**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
34	c2p09A_	Alignment	not modelled	5.7	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**a non-biological atp binding protein with two mutations **PDBTitle:** structural insights into the evolution of a non-biological protein
35	c2kouA_	Alignment	not modelled	5.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dicer-like protein 4; **PDBTitle:** dicer like protein
36	d3e9va1	Alignment	not modelled	5.3	27	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
37	d1iuqa_	Alignment	not modelled	5.1	4	**Fold:**Glycerol-3-phosphate (1)-acyltransferase **Superfamily:**Glycerol-3-phosphate (1)-acyltransferase **Family:**Glycerol-3-phosphate (1)-acyltransferase