Phyre^2

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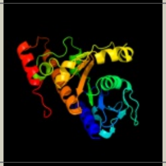
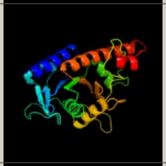
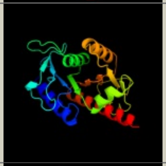
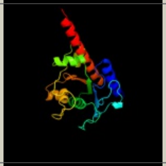
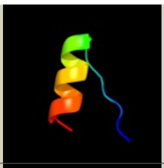
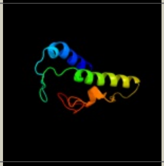
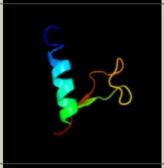
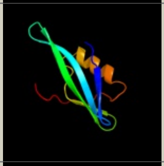
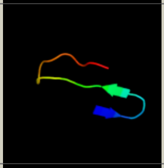
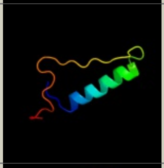
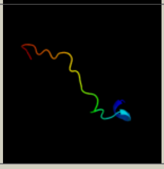
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k0wa_	Alignment		100.0	98	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
2	c3ocrA_	Alignment		100.0	16	**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	26	**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	18	**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	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
7	d1pvta_	Alignment		100.0	25	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
8	c2irpA_	Alignment		100.0	23	**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	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
10	c3m4rA_	Alignment		100.0	21	**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		35.6	8	**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	d1j5ua_	Alignment		23.2	16	**Fold:**MTH1598-like **Superfamily:**MTH1598-like **Family:**MTH1598-like
13	c2cfuA_	Alignment		20.2	14	**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.
14	c3euhF_	Alignment		18.1	20	**PDB header:**cell cycle **Chain:** F: **PDB Molecule:**muke; **PDBTitle:** crystal structure of the muke-mukf complex
15	d1jw3a_	Alignment		16.9	32	**Fold:**MTH1598-like **Superfamily:**MTH1598-like **Family:**MTH1598-like
16	c2yz3B_	Alignment		10.0	14	**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
17	d3e9va1	Alignment		9.6	26	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
18	c2w3pB_	Alignment		8.5	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**benzoyl-coa-dihydrodiol lyase; **PDBTitle:** boxc crystal structure
19	c7mdhA_	Alignment		8.0	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
20	c3da4B_	Alignment		7.7	22	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m; **PDBTitle:** crystal structure of colicin m, a novel phosphatase2 specifically imported by escherichia coli
21	c1b8vA_	Alignment	not modelled	7.7	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (malate dehydrogenase); **PDBTitle:** malate dehydrogenase from aquaspirillum arcticum
22	d1w96c1	Alignment	not modelled	7.1	28	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
23	c3ikbB_	Alignment	not modelled	6.7	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the structure of a conserved protein from streptococcus2 mutans ua159.
24	d1q0qa3	Alignment	not modelled	6.7	16	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
25	d1r0ka3	Alignment	not modelled	6.6	21	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
26	d1a9xa5	Alignment	not modelled	6.5	17	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
27	d1ulza1	Alignment	not modelled	5.9	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
28	c2atmA_	Alignment	not modelled	5.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure of the recombinant allergen ves v 2
						Fold:BTG domain-like

29	d2z15a1	Alignment	not modelled	5.8	17	**Superfamily:**BTG domain-like **Family:**BTG domain-like
30	d2j9ga1	Alignment	not modelled	5.6	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
31	c1gph1_	Alignment	not modelled	5.6	10	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
32	c3q2oB_	Alignment	not modelled	5.4	30	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
33	d2cfua2	Alignment	not modelled	5.4	8	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
34	c1fcuA_	Alignment	not modelled	5.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure (trigonal) of bee venom hyaluronidase
35	d1k75a_	Alignment	not modelled	5.4	10	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
36	c1k5hB_	Alignment	not modelled	5.3	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose-5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose-5-phosphate reductoisomerase
37	c3pqeD_	Alignment	not modelled	5.3	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
38	d1y67a2	Alignment	not modelled	5.2	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
39	c1gn4B_	Alignment	not modelled	5.2	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**superoxide dismutase; **PDBTitle:** h145e mutant of mycobacterium tuberculosis iron-superoxide2 dismutase.