



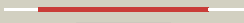
















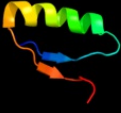
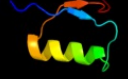
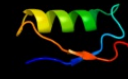
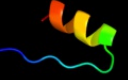
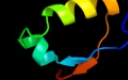

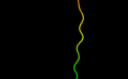
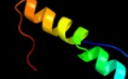




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dle4cp_	 Alignment		100.0	100	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
2	dl0jra_	 Alignment		100.0	19	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
3	c3ocrA_	 Alignment		100.0	21	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	19	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	24	PDB header: lyase Chain: B: PDB Molecule: l-fucose-1-phosphate aldolase; PDBTitle: crystal structure of l-fucose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
6	dlk0wa_	 Alignment		100.0	27	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
7	c2fk5B_	 Alignment		100.0	30	PDB header: lyase Chain: B: PDB Molecule: fucose-1-phosphate aldolase; PDBTitle: crystal structure of l-fucose-1-phosphate aldolase from thermus2 thermophilus hb8
8	dlpvta_	 Alignment		100.0	24	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
9	c2irpA_	 Alignment		100.0	26	PDB header: lyase Chain: A: PDB Molecule: putative aldolase class 2 protein aq_1979; PDBTitle: crystal structure of the l-fucose-1-phosphate aldolase (aq_1979)2 from aquifex aeolicus vf5
10	c3m4rA_	 Alignment		100.0	19	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	dlw9ya1	 Alignment		57.5	19	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: Penicillin synthase-like

12	d1gp6a_	Alignment		56.4	21	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
13	d1odma_	Alignment		52.2	11	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
14	c2yztA_	Alignment		50.3	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
15	d1dcsa_	Alignment		45.9	15	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
16	c3on7C_	Alignment		37.5	12	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	c1w7vD_	Alignment		28.9	25	PDB header: hydrolase Chain: D: PDB Molecule: xaa-pro aminopeptidase; PDBTitle: znmg substituted aminopeptidase p from e. coli
18	d2dsya1	Alignment		25.3	22	Fold: TTHA1013/TTHA0281-like Superfamily: TTHA1013/TTHA0281-like Family: TTHA0281-like
19	d1b6aa2	Alignment		20.1	13	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
20	c3kv4A_	Alignment		19.4	28	PDB header: h3k4me3 binding protein, transferase Chain: A: PDB Molecule: phd finger protein 8; PDBTitle: structure of phf8 in complex with histone h3
21	d1u5tb1	Alignment	not modelled	18.5	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
22	c7mdhA_	Alignment	not modelled	17.8	15	PDB header: chloroplastic malate dehydrogenase Chain: A: PDB Molecule: protein (malate dehydrogenase); PDBTitle: structural basis for light activation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
23	c3pviB_	Alignment	not modelled	17.6	15	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
24	d1chda_	Alignment	not modelled	17.2	19	Fold: Methylesterase CheB, C-terminal domain Superfamily: Methylesterase CheB, C-terminal domain Family: Methylesterase CheB, C-terminal domain
25	d1j5ua_	Alignment	not modelled	17.1	16	Fold: MTH1598-like Superfamily: MTH1598-like Family: MTH1598-like
26	d1jw3a_	Alignment	not modelled	16.7	26	Fold: MTH1598-like Superfamily: MTH1598-like Family: MTH1598-like
27	c3cb5A_	Alignment	not modelled	15.0	16	PDB header: transcription Chain: A: PDB Molecule: fact complex subunit spt16; PDBTitle: crystal structure of the s. pombe peptidase homology domain of fact2 complex subunit spt16 (form a)
28	d2v3za2	Alignment	not modelled	14.5	25	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase

29	c3ooxA	Alignment	not modelled	12.9	9	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
30	c3euhF	Alignment	not modelled	12.2	23	PDB header: cell cycle Chain: F: PDB Molecule: muke; PDBTitle: crystal structure of the muke-mukf complex
31	c3kv5D	Alignment	not modelled	11.2	20	PDB header: h3k4me3 binding protein, transferase Chain: D: PDB Molecule: jmjc domain-containing histone demethylation PDBTitle: structure of kiaa1718, human jumonji demethylase, in complex2 with n-oxalylglycine
32	c3mx6A	Alignment	not modelled	11.1	14	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
33	c3da4B	Alignment	not modelled	10.7	17	PDB header: antibiotic Chain: B: PDB Molecule: colicin-m; PDBTitle: crystal structure of colicin m, a novel phosphatase2 specifically imported by escherichia coli
34	d1jq5a	Alignment	not modelled	10.6	7	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
35	c1a2oB	Alignment	not modelled	10.4	21	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
36	c3pu3A	Alignment	not modelled	10.1	26	PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 2; PDBTitle: phf2 jumonji domain-nog complex
37	d2gg2a1	Alignment	not modelled	9.8	15	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
38	c2v6cA	Alignment	not modelled	9.4	22	PDB header: transcription regulator Chain: A: PDB Molecule: proliferation-associated protein 2g4; PDBTitle: crystal structure of erbb3 binding protein 1 (ebp1)
39	c3sftA	Alignment	not modelled	9.4	16	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of thermotoga maritima cheb methyltransferase catalytic2 domain
40	d1otja	Alignment	not modelled	9.0	15	Fold: Double-stranded beta-helix Superfamily: Clavaminase synthase-like Family: TauD/TfdA-like
41	d1xxaa	Alignment	not modelled	8.9	19	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
42	d1xgsa2	Alignment	not modelled	8.2	20	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
43	c3n9mC	Alignment	not modelled	7.9	26	PDB header: oxidoreductase Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: cekdm7a from c.elegans, alone
44	c1v8gB	Alignment	not modelled	7.8	12	PDB header: transferase Chain: B: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
45	c3jywX	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l35; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
46	c3k2zA	Alignment	not modelled	7.7	18	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
47	c1s1iX	Alignment	not modelled	7.5	19	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l35; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
48	d1w96c1	Alignment	not modelled	7.4	11	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
49	c3kvaA	Alignment	not modelled	7.4	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
50	c3p42D	Alignment	not modelled	7.2	12	PDB header: unknown function Chain: D: PDB Molecule: predicted protein; PDBTitle: structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
51	c3uhjE	Alignment	not modelled	7.2	5	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
52	c2yu1A	Alignment	not modelled	7.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: jmjc domain-containing histone demethylation protein 1a; PDBTitle: crystal structure of hjhdm1a complexed with a-ketoglutarate
						PDB header: chaperone

53	c3m9bK_	Alignment	not modelled	6.8	21	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
54	d1luaa2	Alignment	not modelled	6.8	9	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
55	d1ulza1	Alignment	not modelled	6.8	17	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
56	d1eucb2	Alignment	not modelled	6.7	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Succinyl-CoA synthetase, beta-chain, N-terminal domain
57	c3s6bA_	Alignment	not modelled	6.6	25	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150
58	c3ig4E_	Alignment	not modelled	6.3	28	PDB header: hydrolase Chain: E: PDB Molecule: xaa-pro aminopeptidase; PDBTitle: structure of a putative aminopeptidase p from bacillus anthracis
59	d1ov9a_	Alignment	not modelled	6.3	20	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
60	c2vg2C_	Alignment	not modelled	6.1	17	PDB header: transferase Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp
61	d2j9ga1	Alignment	not modelled	6.1	22	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
62	d2okga1	Alignment	not modelled	6.1	4	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
63	c1b8vA_	Alignment	not modelled	5.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (malate dehydrogenase); PDBTitle: malate dehydrogenase from aquaspirillum arcticum
64	c3q2oB_	Alignment	not modelled	5.6	30	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
65	c2ftpA_	Alignment	not modelled	5.6	7	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
66	c2wl8D_	Alignment	not modelled	5.4	16	PDB header: protein transport Chain: D: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: x-ray crystal structure of pex19p
67	d1w96a1	Alignment	not modelled	5.4	11	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
68	c2g6pA_	Alignment	not modelled	5.3	35	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 1; PDBTitle: crystal structure of truncated (delta 1-89) human methionine2 aminopeptidase type 1 in complex with pyridyl pyrimidine derivative
69	c2gz5A_	Alignment	not modelled	5.3	35	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 1; PDBTitle: human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang
70	d1chma2	Alignment	not modelled	5.3	24	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
71	c1ta9A_	Alignment	not modelled	5.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
72	c3cagF_	Alignment	not modelled	5.0	9	PDB header: dna binding protein Chain: F: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
73	d1a9xa5	Alignment	not modelled	5.0	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like