Phyre^2

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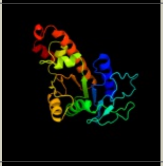
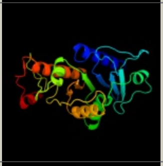
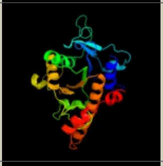
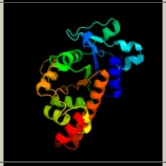
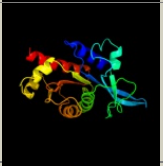
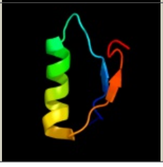
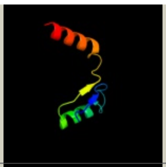
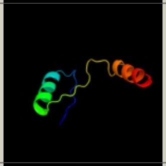
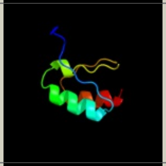
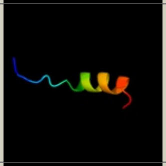
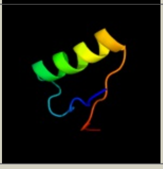
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ojra_	Alignment		100.0	100	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
2	d1pvta_	Alignment		100.0	24	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
3	d1e4cp_	Alignment		100.0	19	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
4	c3ocrA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**class ii aldolase/adducin domain protein; **PDBTitle:** crystal structure of aldolase ii superfamily protein from pseudomonas2 syringae
5	c2opiB_	Alignment		100.0	20	**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	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
7	d1k0wa_	Alignment		100.0	16	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
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	17	**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	17	**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		61.5	8	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like

12	d1gp6a_	Alignment		59.9	10	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
13	c3on7C_	Alignment		49.8	2	**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
14	d1dcsa_	Alignment		48.0	10	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
15	d1odma_	Alignment		46.5	11	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
16	d1eucb2	Alignment		39.1	13	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
17	c2yztA_	Alignment		32.5	11	**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
18	d1nz8a_	Alignment		29.6	19	**Fold:**Ferredoxin-like **Superfamily:**N-utilization substance G protein NusG, N-terminal domain **Family:**N-utilization substance G protein NusG, N-terminal domain
19	d1gjja2	Alignment		28.0	24	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
20	c3ooxA_	Alignment		25.8	3	**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
21	c3p45F_	Alignment	not modelled	20.1	23	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**caspase-6; **PDBTitle:** crystal structure of apo-caspase-6 at physiological ph
22	d2odgc1	Alignment	not modelled	19.1	31	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
23	d1jeia_	Alignment	not modelled	18.7	24	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
24	d1luaa2	Alignment	not modelled	17.8	11	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Methylene-tetrahydromethanopterin dehydrogenase
25	c2h51B_	Alignment	not modelled	17.6	23	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**caspase-1; **PDBTitle:** crystal structure of human caspase-1 (glu390->asp and arg286->lys) in2 complex with 3-[2-(2-benzyloxycarbonylamino-3-methyl-butyrylamino)-3 propionylamino]-4-oxo-pentanoic acid (z-vad-fmk)
26	d2pw6a1	Alignment	not modelled	17.2	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
27	c2pmzV_	Alignment	not modelled	16.8	20	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
28	d1dzfa2	Alignment	not modelled	16.5	28	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5

29	d1wi9a_	Alignment	not modelled	16.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
30	c2c1eB_	Alignment	not modelled	15.8	31	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**caspase-3 subunit p12; **PDBTitle:** crystal structures of caspase-3 in complex with aza-peptide michael2 acceptor inhibitors.
31	c2ra9A_	Alignment	not modelled	15.4	23	**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
32	c2p2cD_	Alignment	not modelled	15.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase-2; **PDBTitle:** inhibition of caspase-2 by a designed ankyrin repeat2 protein (darpin)
33	c2qs0A_	Alignment	not modelled	14.1	5	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**quinolinate synthetase a; **PDBTitle:** quinolinate synthase from pyrococcus furiosus
34	d1hmja_	Alignment	not modelled	14.0	22	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
35	c3sipB_	Alignment	not modelled	14.0	31	**PDB header:**hydrolase/ligase/hydrolase **Chain:** B: **PDB Molecule:**caspase; **PDBTitle:** crystal structure of drice and diap1-bir1 complex
36	d1eika_	Alignment	not modelled	13.7	17	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
37	c2c2zB_	Alignment	not modelled	13.6	17	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**caspase-8 p10 subunit; **PDBTitle:** crystal structure of caspase-8 in complex with aza-peptide michael2 acceptor inhibitor
38	d1j5ua_	Alignment	not modelled	13.4	25	**Fold:**MTH1598-like **Superfamily:**MTH1598-like **Family:**MTH1598-like
39	d2bfdb2	Alignment	not modelled	13.4	10	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
40	d1h9fa_	Alignment	not modelled	12.9	24	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
41	d2d6fa1	Alignment	not modelled	12.7	8	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
42	c3fmyA_	Alignment	not modelled	12.6	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
43	c2qljB_	Alignment	not modelled	12.4	38	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**caspase-7; **PDBTitle:** crystal structure of caspase-7 with inhibitor ac-wehd-cho
44	d1e0fi_	Alignment	not modelled	11.3	30	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
45	c1e0fI_	Alignment	not modelled	11.3	30	**PDB header:**coagulation/crystal structure/heparin-b **Chain:** I: **PDB Molecule:**haemadin; **PDBTitle:** crystal structure of the human alpha-thrombin-haemadin2 complex: an exosite ii-binding inhibitor
46	c3b1qD_	Alignment	not modelled	11.3	26	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribokinase, putative; **PDBTitle:** structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
47	d1ikpa2	Alignment	not modelled	11.1	27	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
48	c1eucB_	Alignment	not modelled	11.1	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**succinyl-coa synthetase, beta chain; **PDBTitle:** crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
49	d1jw3a_	Alignment	not modelled	10.8	31	**Fold:**MTH1598-like **Superfamily:**MTH1598-like **Family:**MTH1598-like
50	d1wzua1	Alignment	not modelled	10.7	0	**Fold:**NadA-like **Superfamily:**NadA-like **Family:**NadA-like
51	c1e0fJ_	Alignment	not modelled	10.7	30	**PDB header:**coagulation/crystal structure/heparin-b **Chain:** J: **PDB Molecule:**haemadin; **PDBTitle:** crystal structure of the human alpha-thrombin-haemadin2 complex: an exosite ii-binding inhibitor
52	d1m1ha2	Alignment	not modelled	10.7	22	**Fold:**Ferredoxin-like **Superfamily:**N-utilization substance G protein NusG, N-terminal domain **Family:**N-utilization substance G protein NusG, N-terminal domain
53	c3r1fO_	Alignment	not modelled	10.7	16	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
54	c3kv4A_	Alignment	not modelled	10.5	4	**PDB header:**h3k4me3 binding protein, transferase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** structure of phf8 in complex with histone h3
55	c3s6bA_	Alignment	not modelled	10.4	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase 1b from

						plasmodium2 falciparum, pf10_0150
56	d1dwka1	Alignment	not modelled	10.4	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
57	d2nu7b2	Alignment	not modelled	10.2	9	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
58	d1ig4a_	Alignment	not modelled	10.2	9	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
59	d1kx5b_	Alignment	not modelled	10.0	18	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
60	d1gvfa_	Alignment	not modelled	9.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
61	d1alna1	Alignment	not modelled	9.6	29	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
62	d1qk9a_	Alignment	not modelled	9.5	13	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
63	c2nu9E_	Alignment	not modelled	9.4	11	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
64	d1w85b2	Alignment	not modelled	9.3	18	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
65	c1e0fK_	Alignment	not modelled	9.1	30	**PDB header:**coagulation/crystal structure/heparin-b **Chain:** K: **PDB Molecule:**haemadin; **PDBTitle:** crystal structure of the human alpha-thrombin-haemadin2 complex: an exosite ii-binding inhibitor
66	d1u5tb1	Alignment	not modelled	8.9	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
67	c3pvjB_	Alignment	not modelled	8.6	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
68	c2ky8A_	Alignment	not modelled	8.6	23	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**methyl-cpg-binding domain protein 2; **PDBTitle:** solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
69	c2z5wA_	Alignment	not modelled	8.5	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**bcla protein; **PDBTitle:** tbcla, a recombinant spore surface protein from bacillus anthracis
70	c3h02F_	Alignment	not modelled	8.5	12	**PDB header:**lyase **Chain:** F: **PDB Molecule:**naphthoate synthase; **PDBTitle:** 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.
71	d1zq1c2	Alignment	not modelled	8.2	22	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
72	c3ju3A_	Alignment	not modelled	8.2	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; **PDBTitle:** crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
73	c3ox4D_	Alignment	not modelled	8.0	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
74	d2a6aa2	Alignment	not modelled	7.9	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
75	d1ub1a_	Alignment	not modelled	7.9	22	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
76	d1rrma_	Alignment	not modelled	7.8	18	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
77	d1uasa1	Alignment	not modelled	7.8	19	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
78	d1o2da_	Alignment	not modelled	7.5	12	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
79	d1a9xa5	Alignment	not modelled	7.3	25	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
80	d2huec1	Alignment	not modelled	7.3	19	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
81	c3q94B_	Alignment	not modelled	7.2	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'

82	d1rvga_	Alignment	not modelled	7.0	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
83	d2d6fc2	Alignment	not modelled	6.9	22	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
84	c1v8gB_	Alignment	not modelled	6.6	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
85	c1wckA_	Alignment	not modelled	6.6	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**bcla protein; **PDBTitle:** crystal structure of the c-terminal domain of bcla, the2 major antigen of the exosporium of the bacillus anthracis3 spore.
86	c3p04A_	Alignment	not modelled	6.6	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
87	c1w7vD_	Alignment	not modelled	6.5	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** znmg substituted aminopeptidase p from e. coli
88	c3a1yF_	Alignment	not modelled	6.5	20	**PDB header:**ribosomal protein **Chain:** F: **PDB Molecule:**50s ribosomal protein p1 (l12p); **PDBTitle:** the structure of protein complex
89	c1olsB_	Alignment	not modelled	6.4	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxoisovalerate dehydrogenase beta subunit; **PDBTitle:** roles of his291-alpha and his146-beta' in the reductive2 acylation reaction catalyzed by human branched-chain3 alpha-ketoacid dehydrogenase
90	c3p04B_	Alignment	not modelled	6.3	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
91	d1hzda_	Alignment	not modelled	6.2	20	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
92	c3h0gE_	Alignment	not modelled	6.1	20	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
93	c3q2oB_	Alignment	not modelled	6.0	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
94	d1hj3a1	Alignment	not modelled	5.8	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
95	d1b4ub_	Alignment	not modelled	5.8	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
96	c2qlcC_	Alignment	not modelled	5.7	10	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein radc homolog; **PDBTitle:** the crystal structure of dna repair protein radc from chlorobium2 tepidum tls
97	d2d69a1	Alignment	not modelled	5.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
98	c3bfjK_	Alignment	not modelled	5.5	12	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
99	c2k06A_	Alignment	not modelled	5.4	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of the aminoterminal domain of e. coli2 nusg