Phyre^{2}

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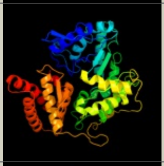
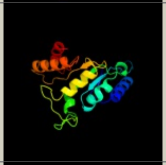
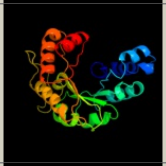
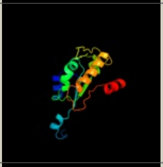
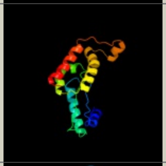
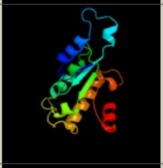
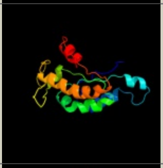
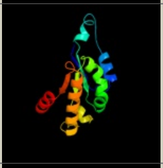
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1d8ca_	Alignment		100.0	97	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
2	d1n8ia_	Alignment		100.0	60	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
3	c3cuzA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase a; **PDBTitle:** atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
4	c3cuxA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
5	c3pugA_	Alignment		99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** haloferax volcanii malate synthase native at 3mm glyoxylate
6	c3r4iB_	Alignment		99.7	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase; **PDBTitle:** crystal structure of a citrate lyase (bxe_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution
7	c1sgjB_	Alignment		99.6	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase, beta subunit; **PDBTitle:** crystal structure of citrate lyase beta subunit
8	c3qqwC_	Alignment		99.6	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**putative citrate lyase; **PDBTitle:** crystal structure of a hypothetical lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution
9	d1sgja_	Alignment		99.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
10	c1u5vA_	Alignment		99.6	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cite; **PDBTitle:** structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis
11	d1u5ha_	Alignment		99.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase

12	c2hroA_	Alignment		97.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
13	c2bg5C_	Alignment		96.8	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphoenolpyruvate-protein kinase; **PDBTitle:** crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts)
14	d1dxea_	Alignment		96.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
15	c2hwgA_	Alignment		96.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
16	c2v5jB_	Alignment		96.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
17	c3qz6A_	Alignment		96.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
18	c2vwtA_	Alignment		95.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yfau, 2-keto-3-deoxy sugar aldolase; **PDBTitle:** crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
19	c2olsA_	Alignment		93.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate synthase; **PDBTitle:** the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
20	c1izcA_	Alignment		93.1	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular diels-alderase; **PDBTitle:** crystal structure analysis of macrophomate synthase
21	d1izca_	Alignment	not modelled	93.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
22	d1e0ta2	Alignment	not modelled	93.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
23	d1vbga1	Alignment	not modelled	92.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
24	c1h6zA_	Alignment	not modelled	88.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei
25	d1kbla1	Alignment	not modelled	88.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
26	d1pkla2	Alignment	not modelled	88.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
27	d1h6za1	Alignment	not modelled	86.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
28	c1vbhA_	Alignment	not modelled	85.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate,orthophosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase with bound mg-pep from maize
29	d1a3xa2	Alignment	not modelled	81.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase

30	c1kblA_	Alignment	not modelled	74.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase
31	d1liua2	Alignment	not modelled	62.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
32	d2g50a2	Alignment	not modelled	59.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
33	c2kz6A_	Alignment	not modelled	59.1	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein cv0426 from chromobacterium violaceum,2 northeast structural genomics consortium (nesg) target cvt2
34	d1njra_	Alignment	not modelled	48.1	17	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
35	c2zzxD_	Alignment	not modelled	45.9	12	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**abc transporter, solute-binding protein; **PDBTitle:** crystal structure of a periplasmic substrate binding protein in2 complex with lactate
36	d1zela1	Alignment	not modelled	43.8	32	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rv2827c N-terminal domain-like
37	c2q4oA_	Alignment	not modelled	39.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein at2g37210/t2n18.3; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
38	d2q4oa1	Alignment	not modelled	39.1	17	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
39	d1rg6a_	Alignment	not modelled	37.5	30	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
40	c1zelA_	Alignment	not modelled	36.7	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv2827c; **PDBTitle:** crystal structure of rv2827c protein from mycobacterium tuberculosis
41	d1ic8a2	Alignment	not modelled	35.1	27	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
42	c2gbbA_	Alignment	not modelled	31.2	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative chorismate mutase; **PDBTitle:** crystal structure of secreted chorismate mutase from2 yersinia pestis
43	c1zr5B_	Alignment	not modelled	29.7	24	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**h2afy protein; **PDBTitle:** crystal structure of the macro-domain of human core histone variant2 macroh2a1.2
44	c3q3jA_	Alignment	not modelled	28.2	23	**PDB header:**membrane protein/protein binding **Chain:** A: **PDB Molecule:**plexin-a2; **PDBTitle:** crystal structure of plexin a2 rbd in complex with rnd1
45	d1s9va2	Alignment	not modelled	26.4	22	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
46	d1t35a_	Alignment	not modelled	25.1	10	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
47	c3q71A_	Alignment	not modelled	23.6	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8) - macro domain 2 in complex with adenosine-5-2 diphosphoribose
48	d1ydha_	Alignment	not modelled	23.5	12	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
49	d1rh6a_	Alignment	not modelled	23.3	21	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
50	d1w0ba_	Alignment	not modelled	21.7	21	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
51	d1muja2	Alignment	not modelled	21.7	34	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
52	c3rmrA_	Alignment	not modelled	19.9	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**avirulence protein; **PDBTitle:** crystal structure of hyaloperonospora arabidopsidis atr1 effector2 domain
53	d1jk8a2	Alignment	not modelled	19.9	24	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
54	d1vj7a2	Alignment	not modelled	18.9	26	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**RelA/SpoT domain
55	c2q4dB_	Alignment	not modelled	18.7	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene

						at5g11950
56	c2zc2A_	Alignment	not modelled	18.3	12	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnad-like replication protein; **PDBTitle:** crystal structure of dnad-like replication protein from2 streptococcus mutans ua159, gi 24377835, residues 127-199
57	d1es0a2	Alignment	not modelled	17.9	26	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
58	d2jn4a1	Alignment	not modelled	17.8	23	**Fold:**NifT/FixU barrel-like **Superfamily:**NifT/FixU-like **Family:**NifT/FixU
59	c2jn4A_	Alignment	not modelled	17.8	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein fixu, nift; **PDBTitle:** solution nmr structure of protein rp4601 from2 rhodopseudomonas palustris. northeast structural genomics3 consortium target rpt2; ontario center for structural4 proteomics target rp4601.
60	c2pxgA_	Alignment	not modelled	17.3	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein; **PDBTitle:** nmr solution structure of omla
61	d1dxsa_	Alignment	not modelled	17.1	32	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
62	d3bzra1	Alignment	not modelled	16.6	25	**Fold:**EscU C-terminal domain-like **Superfamily:**EscU C-terminal domain-like **Family:**EscU C-terminal domain-like
63	c3bzrA_	Alignment	not modelled	16.6	25	**PDB header:**membrane protein, protein transport **Chain:** A: **PDB Molecule:**escu; **PDBTitle:** crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
64	c3bd1B_	Alignment	not modelled	16.3	28	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cro protein; **PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
65	c3hlzA_	Alignment	not modelled	16.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bt_1490; **PDBTitle:** crystal structure of bt_1490 (np_810393.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.50 a resolution
66	d1mvla_	Alignment	not modelled	15.9	26	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
67	c1mvlA_	Alignment	not modelled	15.9	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ppc decarboxylase athal3a; **PDBTitle:** ppc decarboxylase mutant c175s
68	c3g80B_	Alignment	not modelled	15.7	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**protein b2; **PDBTitle:** nodamura virus protein b2, rna-binding domain
69	c2vy2A_	Alignment	not modelled	15.7	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein leafy; **PDBTitle:** structure of leafy transcription factor from arabidopsis2 thaliana in complex with dna from ag-i promoter
70	c2dnrA_	Alignment	not modelled	15.5	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**synaptojanin-1; **PDBTitle:** solution structure of rna binding domain in synaptojanin 1
71	c3odmE_	Alignment	not modelled	15.0	17	**PDB header:**lyase **Chain:** E: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** archaeal-type phosphoenolpyruvate carboxylase
72	c3ogfA_	Alignment	not modelled	14.7	14	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed dimeric trefoil-fold sub-domain which **PDBTitle:** crystal structure of difoil-4p homo-trimer: de novo designed dimeric2 trefoil-fold sub-domain which forms homo-trimer assembly
73	d2ipqx1	Alignment	not modelled	14.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**STY4665 C-terminal domain-like
74	d2ffca1	Alignment	not modelled	14.1	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
75	d1gsma1	Alignment	not modelled	13.7	34	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
76	d1ev7a_	Alignment	not modelled	13.1	29	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease NaeI
77	d1wuua1	Alignment	not modelled	13.0	18	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
78	d1zbsa1	Alignment	not modelled	12.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
79	d1u04a1	Alignment	not modelled	12.6	80	**Fold:**SH3-like barrel **Superfamily:**PAZ domain **Family:**PAZ domain
80	d1k82a1	Alignment	not modelled	12.2	10	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
						Fold:DNA/RNA-binding 3-helical bundle

81	d2v9va2	Alignment	not modelled	11.9	33	**Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
82	d1ei7a_	Alignment	not modelled	11.8	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**TMV-like viral coat proteins **Family:**TMV-like viral coat proteins
83	c3da5A_	Alignment	not modelled	11.1	67	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**argonaute; **PDBTitle:** crystal structure of piwi/argonaute/zwille(paz) domain from2 thermococcus thioreducens
84	c1pprO_	Alignment	not modelled	10.9	23	**PDB header:**light-harvesting protein **Chain:** O: **PDB Molecule:**peridinin-chlorophyll protein; **PDBTitle:** peridinin-chlorophyll-protein of amphidinium carterae
85	c3ofgA_	Alignment	not modelled	10.8	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**boca/mesd chaperone for ywtd beta-propeller-egf protein 1; **PDBTitle:** structured domain of caenorhabditis elegans bmy-1
86	d1qasa3	Alignment	not modelled	10.7	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Mammalian PLC
87	c2vx6A_	Alignment	not modelled	10.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellvibrio japonicus mannanase cjman26c; **PDBTitle:** cellvibrio japonicus mannanase cjman26c gal1man4-bound form
88	d1sv0c_	Alignment	not modelled	10.0	18	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
89	d1umya_	Alignment	not modelled	10.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
90	d1ykhb1	Alignment	not modelled	9.7	19	**Fold:**Mediator hinge subcomplex-like **Superfamily:**Mediator hinge subcomplex-like **Family:**CSE2-like
91	d1pava_	Alignment	not modelled	9.7	16	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
92	d1xzpa3	Alignment	not modelled	9.7	35	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**TrmE formyl-THF-binding domain
93	c1xzqB_	Alignment	not modelled	9.7	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable trna modification gtpase trme; **PDBTitle:** structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
94	c3k6qB_	Alignment	not modelled	9.6	27	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative ligand binding protein; **PDBTitle:** crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
95	c3cwyA_	Alignment	not modelled	9.5	38	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein cagd; **PDBTitle:** structure of cagd from h. pylori pathogenicity island2 crystallized in the presence of cu(ii) ions
96	d1alna1	Alignment	not modelled	9.5	16	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
97	c3c01H_	Alignment	not modelled	9.4	10	**PDB header:**membrane protein, protein transport **Chain:** H: **PDB Molecule:**surface presentation of antigens protein spas; **PDBTitle:** crystal structural of native spas c-terminal domain
98	d1ug3a1	Alignment	not modelled	9.4	15	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
99	c3czoD_	Alignment	not modelled	9.3	17	**PDB header:**lyase **Chain:** D: **PDB Molecule:**histidine ammonia-lyase; **PDBTitle:** crystal structure of double mutant phenylalanine ammonia-2 lyase from anabaena variabilis