Phyre^{2}

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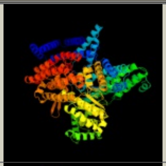
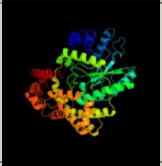
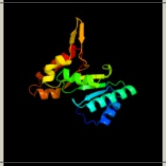
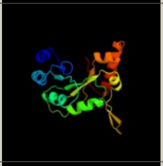
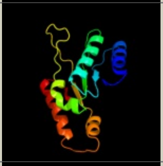
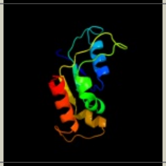
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jqna_	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
2	c1jqoA_	Alignment		100.0	42	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
3	d1jqoa_	Alignment		100.0	42	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
4	c3odmE_	Alignment		100.0	17	**PDB header:**lyase **Chain:** E: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** archaeal-type phosphoenolpyruvate carboxylase
5	d1e0ta2	Alignment		97.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
6	d1pkla2	Alignment		97.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
7	d1a3xa2	Alignment		97.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
8	d2g50a2	Alignment		96.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
9	c2vwtA_	Alignment		96.5	21	**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
10	d1dxea_	Alignment		95.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
11	d1liua2	Alignment		95.3	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase

12	c2v5jB_	Alignment		95.3	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
13	c3qqwC_	Alignment		95.1	16	**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
14	d1izca_	Alignment		94.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
15	c1izcA_	Alignment		94.7	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular diels-alderase; **PDBTitle:** crystal structure analysis of macrophomate synthase
16	c3qz6A_	Alignment		94.2	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
17	c3r4iB_	Alignment		93.8	18	**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
18	c1sgjB_	Alignment		92.3	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase, beta subunit; **PDBTitle:** crystal structure of citrate lyase beta subunit
19	d1sgja_	Alignment		92.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
20	d1u5ha_	Alignment		91.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
21	c1u5vA_	Alignment	not modelled	90.5	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cite; **PDBTitle:** structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis
22	c1a3wB_	Alignment	not modelled	88.9	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
23	c1pklB_	Alignment	not modelled	88.6	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
24	c3pugA_	Alignment	not modelled	88.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** haloferax volcanii malate synthase native at 3mm glyoxylate
25	c3qllB_	Alignment	not modelled	87.5	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase; **PDBTitle:** crystal structure of ripc from yersinia pestis
26	c1e0tD_	Alignment	not modelled	87.2	30	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
27	c3eoeC_	Alignment	not modelled	86.3	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
28	c2vgbB_	Alignment	not modelled	83.9	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l; **PDBTitle:** human erythrocyte pyruvate kinase
						PDB header:transferase/transferase inhibitor

29	c3t07D_	Alignment	not modelled	83.8	29	**Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
30	c1aqfB_	Alignment	not modelled	83.8	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
31	c3e0vB_	Alignment	not modelled	81.6	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
32	c3cuzA_	Alignment	not modelled	78.1	18	**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
33	c1t5aB_	Alignment	not modelled	77.5	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
34	c3khdC_	Alignment	not modelled	76.9	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
35	c3ma8A_	Alignment	not modelled	75.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
36	c2e28A_	Alignment	not modelled	74.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
37	d1wdpa1	Alignment	not modelled	62.5	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
38	c1j0yD_	Alignment	not modelled	61.7	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-amylase; **PDBTitle:** beta-amylase from bacillus cereus var. mycoides in complex2 with glucose
39	c2xfyA_	Alignment	not modelled	61.5	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-amylase; **PDBTitle:** crystal structure of barley beta-amylase complexed with2 alpha-cyclodextrin
40	c1q7tA_	Alignment	not modelled	59.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein rv1170; **PDBTitle:** rv1170 (mshb) from mycobacterium tuberculosis
41	d1q74a_	Alignment	not modelled	59.4	19	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
42	c2yxgD_	Alignment	not modelled	58.0	9	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
43	c3godA_	Alignment	not modelled	52.9	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cas1; **PDBTitle:** structural basis for dnase activity of a conserved protein2 implicated in crispr-mediated antiviral defense
44	c1ahuB_	Alignment	not modelled	52.6	25	**PDB header:**flavoenzyme **Chain:** B: **PDB Molecule:**vanillyl-alcohol oxidase; **PDBTitle:** structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
45	c3tekA_	Alignment	not modelled	52.2	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**thermodbp-single stranded dna binding protein; **PDBTitle:** thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
46	c3fluD_	Alignment	not modelled	50.3	12	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
47	c3nkdB_	Alignment	not modelled	50.1	23	**PDB header:**immune system **Chain:** B: **PDB Molecule:**crispr-associated protein cas1; **PDBTitle:** structure of crisp-associated protein cas1 from escherichia coli str.2 k-12
48	d1vema2	Alignment	not modelled	48.9	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
49	d2hf5a1	Alignment	not modelled	47.2	47	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
50	c3io3A_	Alignment	not modelled	46.8	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**deha2d07832p; **PDBTitle:** get3 with adp from d. hansenii in closed form
51	c2yr1B_	Alignment	not modelled	44.5	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
52	d1wota_	Alignment	not modelled	44.1	28	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
53	c2k7rA_	Alignment	not modelled	43.3	11	**PDB header:**replication **Chain:** A: **PDB Molecule:**primosomal protein dnai; **PDBTitle:** n-terminal domain of the bacillus subtilis helicase-loading2 protein dnai
54	d2csua1	Alignment	not modelled	42.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
						PDB header:transferase

55	c3cuxA_	Alignment	not modelled	42.0	16	**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
56	c3noeA_	Alignment	not modelled	39.8	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
57	d1b1ya_	Alignment	not modelled	39.4	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
58	c3d0cB_	Alignment	not modelled	38.8	4	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
59	d1fa2a_	Alignment	not modelled	36.1	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
60	c3cyqM_	Alignment	not modelled	33.3	12	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** the crystal structure of the complex of the c-terminal domain of2 helicobacter pylori motb (residues 125-256) with n-acetylmuramic acid
61	c3e96B_	Alignment	not modelled	33.3	7	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
62	d1fp3a_	Alignment	not modelled	32.5	12	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
63	d1bg5a1	Alignment	not modelled	32.2	14	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
64	d1scta_	Alignment	not modelled	31.1	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
65	d1rd5a_	Alignment	not modelled	28.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
66	c2o98P_	Alignment	not modelled	27.6	29	**PDB header:**protein binding **Chain:** P: **PDB Molecule:**plasma membrane h+ atpase; **PDBTitle:** structure of the 14-3-3 / h+-atpase plant complex
67	c3h8hA_	Alignment	not modelled	27.6	43	**PDB header:**transcription **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase ring2; **PDBTitle:** structure of the c-terminal domain of human rnf2/ring1b;
68	c3lfxE_	Alignment	not modelled	27.3	16	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of tm1797, a cas1 protein from thermotoga maritima
69	d1a9xa1	Alignment	not modelled	27.1	19	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
70	d1z7aa1	Alignment	not modelled	26.9	13	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**PA1517-like
71	c2gljR_	Alignment	not modelled	26.8	21	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:** **PDBTitle:** crystal structure of aminopeptidase i from clostridium2 acetobutylicum
72	c3si9B_	Alignment	not modelled	25.2	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
73	c3ibgF_	Alignment	not modelled	24.9	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**atpase, subunit of the get complex; **PDBTitle:** crystal structure of aspergillus fumigatus get3 with bound2 adp
74	c2ehbD_	Alignment	not modelled	24.8	19	**PDB header:**signalling protein/transferase **Chain:** D: **PDB Molecule:**cbl-interacting serine/threonine-protein kinase 24; **PDBTitle:** the structure of the c-terminal domain of the protein kinase atsos22 bound to the calcium sensor atsos3
75	d2r8ba1	Alignment	not modelled	24.4	50	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
76	c3u0vA_	Alignment	not modelled	24.4	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysophospholipase-like protein 1; **PDBTitle:** crystal structure analysis of human lyplal1
77	d1p4ca_	Alignment	not modelled	24.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
78	c2hmcA_	Alignment	not modelled	24.1	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
79	d2vl8a1	Alignment	not modelled	23.7	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycosylating toxin catalytic domain-like
80	d1hzfa_	Alignment	not modelled	23.5	26	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Complement components

81	c1hzfA_	Alignment	not modelled	23.5	26	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement factor c4a; **PDBTitle:** c4adg fragment of human complement factor c4a
82	c3og9A_	Alignment	not modelled	23.4	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein yahd a copper inducible hydrolase; **PDBTitle:** structure of yahd with malic acid
83	d1gtma1	Alignment	not modelled	23.4	41	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
84	d1xnya1	Alignment	not modelled	22.7	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
85	c2gedB_	Alignment	not modelled	22.6	30	**PDB header:**protein transport, signaling protein **Chain:** B: **PDB Molecule:**signal recognition particle receptor beta **PDBTitle:** signal recognition particle receptor beta-subunit in2 nucleotide-free dimerized form
86	c3epmB_	Alignment	not modelled	22.4	21	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiamine biosynthesis protein thic; **PDBTitle:** crystal structure of caulobacter crescentus thic
87	c2cdh1_	Alignment	not modelled	22.4	11	**PDB header:**transferase **Chain:** 1: **PDB Molecule:**enoyl reductase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
88	d1k0ma1	Alignment	not modelled	21.9	11	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
89	d1vrga1	Alignment	not modelled	21.7	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
90	d1z1za1	Alignment	not modelled	21.6	30	**Fold:**Phage tail protein-like **Superfamily:**Phage tail protein-like **Family:**Lambda phage gpU-like
91	d1gzda_	Alignment	not modelled	21.3	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
92	d1fj2a_	Alignment	not modelled	21.1	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
93	d1jmsa3	Alignment	not modelled	21.1	18	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
94	c3pv9D_	Alignment	not modelled	20.9	20	**PDB header:**immune system **Chain:** D: **PDB Molecule:**putative uncharacterized protein ph1245; **PDBTitle:** structure of ph1245, a cas1 from pyrococcus horikoshii
95	d1zl0a2	Alignment	not modelled	20.3	36	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
96	c3dz1A_	Alignment	not modelled	20.1	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
97	d1auoa_	Alignment	not modelled	19.9	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
98	d1xhoa_	Alignment	not modelled	19.7	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
99	c1xhoB_	Alignment	not modelled	19.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**chorismate mutase; **PDBTitle:** chorismate mutase from clostridium thermocellum cth-682