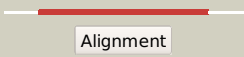
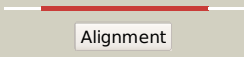
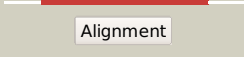
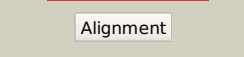
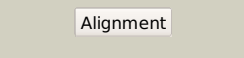
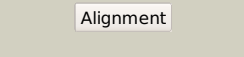
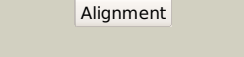
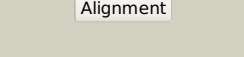
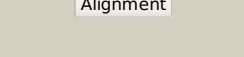
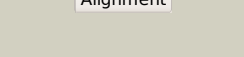
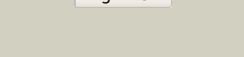
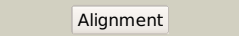
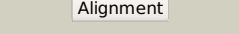
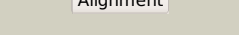
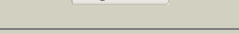
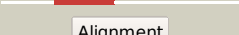
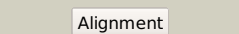
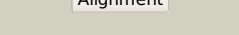
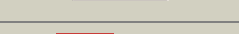
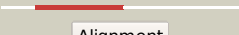
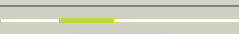
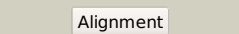
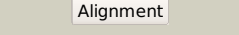


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3odmE_	 Alignment		100.0	29	PDB header: lyase Chain: E: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: archaeal-type phosphoenolpyruvate carboxylase
2	c1jqoA_	 Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
3	d1jqoa_	 Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
4	d1jqna_	 Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
5	d1e0ta2	 Alignment		98.7	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
6	d1dxea_	 Alignment		98.0	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpal aldolase
7	d1pkla2	 Alignment		97.9	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
8	c4mf4F_	 Alignment		97.9	19	PDB header: lyase Chain: F: PDB Molecule: hpch/hpai aldolase/citrate lyase family protein; PDBTitle: crystal structure of a hpch/hpal aldolase/citrate lyase family protein2 from burkholderia cenocepacia j2315
9	d2g50a2	 Alignment		97.9	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
10	d1a3xa2	 Alignment		97.8	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
11	d1liua2	 Alignment		97.8	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase

12	c2vwtA_	Alignment		97.8	15	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
13	c3qqwC_	Alignment		97.8	18	PDB header: lyase Chain: C: PDB Molecule: putative citrate lyase; PDBTitle: crystal structure of a putative lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution
14	c4b5sB_	Alignment		97.7	14	PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-2-oxo-heptane-1,7-dioate aldolase; PDBTitle: crystal structures of divalent metal dependent pyruvate aldolase,2 hpai, in complex with pyruvate
15	c4l9zA_	Alignment		97.7	17	PDB header: lyase Chain: A: PDB Molecule: malyl-coa lyase; PDBTitle: crystal structure of rhodobacter sphaeroides malyl-coa lyase in2 complex with magnesium, oxalate, and coa
16	c4tv6A_	Alignment		97.7	20	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxyglucarate aldolase; PDBTitle: crystal structure of citrate synthase variant sbng e151q
17	d1izca_	Alignment		97.6	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpai aldolase
18	c1izcA_	Alignment		97.6	19	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
19	c3cuzA_	Alignment		97.6	17	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
20	c2v5jB_	Alignment		97.5	13	PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
21	c3qz6A_	Alignment	not modelled	97.4	18	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
22	c1sgjB_	Alignment	not modelled	97.4	20	PDB header: lyase Chain: B: PDB Molecule: citrate lyase, beta subunit; PDBTitle: crystal structure of citrate lyase beta subunit
23	d1sgja_	Alignment	not modelled	97.4	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpai aldolase
24	c1u5vA_	Alignment	not modelled	97.4	23	PDB header: lyase Chain: A: PDB Molecule: cite; PDBTitle: structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis
25	c4roqA_	Alignment	not modelled	97.4	15	PDB header: lyase Chain: A: PDB Molecule: malyl-coa lyase/beta-methylmalyl-coa lyase; PDBTitle: crystal structure of malyl-coa lyase from methylobacterium extorquens
26	d1u5ha_	Alignment	not modelled	97.2	22	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpai aldolase
27	c3qlIB_	Alignment	not modelled	97.2	19	PDB header: lyase Chain: B: PDB Molecule: citrate lyase; PDBTitle: crystal structure of ripc from yersinia pestis
28	c3r4iB_	Alignment	not modelled	97.0	16	PDB header: lyase Chain: B: PDB Molecule: citrate lyase; PDBTitle: crystal structure of a citrate lyase (bx_e_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution

29	c3cuxA	 Alignment	not modelled	97.0	20	PDB header: transferase Chain: A: PDB Molecule: malate synthase; PDBTitle: atomic resolution structures of escherichia coli and2 bacillus anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
30	c4l7zC	 Alignment	not modelled	96.9	16	PDB header: lyase Chain: C: PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of chloroflexus aurantiacus malyi-coa lyase
31	c3pugA	 Alignment	not modelled	96.4	11	PDB header: transferase Chain: A: PDB Molecule: malate synthase; PDBTitle: haloferax volcanii malate synthase native at 3mm glyoxylate
32	c1e0tD	 Alignment	not modelled	95.8	20	PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase
33	c3e0vB	 Alignment	not modelled	95.7	21	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
34	c3ma8A	 Alignment	not modelled	95.7	16	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
35	c4imaD	 Alignment	not modelled	95.4	23	PDB header: transferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: the structure of c436m-hlpyk in complex with citrate/mn/atp/fru-1,6-bp
36	c3qtgA	 Alignment	not modelled	95.4	13	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from pyrobaculum aerophilum
37	c1a3wB	 Alignment	not modelled	95.0	17	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
38	c4fxjB	 Alignment	not modelled	94.8	24	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes m1/m2; PDBTitle: structure of m2 pyruvate kinase in complex with phenylalanine
39	c3khdA	 Alignment	not modelled	94.6	20	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
40	c3eoeC	 Alignment	not modelled	94.4	19	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
41	c3t07D	 Alignment	not modelled	94.3	18	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
42	c1pkIB	 Alignment	not modelled	94.3	21	PDB header: transferase Chain: B: PDB Molecule: protein (pyruvate kinase); PDBTitle: the structure of leishmania pyruvate kinase
43	c1aqfB	 Alignment	not modelled	94.1	21	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
44	c1t5aB	 Alignment	not modelled	94.1	22	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase, m2 isozyme; PDBTitle: human pyruvate kinase m2
45	c2e28A	 Alignment	not modelled	93.8	18	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
46	c3khdC	 Alignment	not modelled	93.6	20	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
47	c2vgbB	 Alignment	not modelled	93.6	22	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes r/l; PDBTitle: human erythrocyte pyruvate kinase
48	c2bg5C	 Alignment	not modelled	90.0	13	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)
49	c3gycB	 Alignment	not modelled	66.0	22	PDB header: hydrolase Chain: B: PDB Molecule: putative glycoside hydrolase; PDBTitle: crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
50	c2olsA	 Alignment	not modelled	62.8	16	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
51	c1kblA	 Alignment	not modelled	56.1	17	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
52	d1kbla1	 Alignment	not modelled	51.2	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
53	c1ahuB	 Alignment	not modelled	43.7	22	PDB header: flavoenzyme Chain: B: PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
54	c2vngA	Alignment	not modelled	37.7	44	PDB header: dna-binding protein Chain: A: PDB Molecule: hypothetical 13.2 kda protein;

54	c2vqA_	Alignment	not modelled	37.7	44	PDBTitle: structure of a dna binding winged-helix protein, f-112,2 from sulfobolus spindle-shaped virus 1.
55	d2vqca1	Alignment	not modelled	37.7	44	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: F112-like
56	c2hroA_	Alignment	not modelled	35.3	11	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
57	c2hwgA_	Alignment	not modelled	35.0	9	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
58	d1xnya1	Alignment	not modelled	35.0	19	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
59	d1vrqa1	Alignment	not modelled	33.8	19	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
60	c2f9iD_	Alignment	not modelled	30.7	16	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl PDBTitle: crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
61	d1h6za1	Alignment	not modelled	29.6	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
62	d1rd5a_	Alignment	not modelled	29.0	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
63	c4n7qA_	Alignment	not modelled	28.0	6	PDB header: lyase Chain: A: PDB Molecule: phosphomethylpyrimidine synthase, chloroplastic; PDBTitle: crystal structure of eukaryotic thic from a. thaliana
64	c3epmB_	Alignment	not modelled	27.3	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiamine biosynthesis protein thic; PDBTitle: crystal structure of caulobacter crescentus thic
65	c4clqB_	Alignment	not modelled	27.2	21	PDB header: translation Chain: B: PDB Molecule: ribosome biogenesis protein bms1; PDBTitle: structure of rcl1p - bms1p complex
66	c4a1sE_	Alignment	not modelled	26.2	63	PDB header: cell cycle Chain: E: PDB Molecule: re60102p; PDBTitle: crystallographic structure of the pins:insc complex
67	c1vbaA_	Alignment	not modelled	24.7	20	PDB header: transferase Chain: A: PDB Molecule: pyruvate,orthophosphate dikinase; PDBTitle: pyruvate phosphate dikinase with bound mg-pep from maize
68	c2ghjD_	Alignment	not modelled	24.3	26	PDB header: structural protein Chain: D: PDB Molecule: 50s ribosomal protein l20; PDBTitle: crystal structure of folded and partially unfolded forms of2 aquifex aeolicus ribosomal protein l20
69	c3vkbA_	Alignment	not modelled	23.8	19	PDB header: transferase Chain: A: PDB Molecule: moeo5; PDBTitle: crystal structure of moeo5 soaked with fspp overnight
70	d1pixa2	Alignment	not modelled	22.1	15	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
71	c2xfyA_	Alignment	not modelled	21.8	4	PDB header: hydrolase Chain: A: PDB Molecule: beta-amylase; PDBTitle: crystal structure of barley beta-amylase complexed with2 alpha-cyclodextrin
72	c2guzD_	Alignment	not modelled	21.0	18	PDB header: chaperone, protein transport Chain: D: PDB Molecule: mitochondrial import inner membrane translocase PDBTitle: structure of the tim14-tim16 complex of the mitochondrial2 protein import motor
73	c4e5sC_	Alignment	not modelled	20.1	44	PDB header: hydrolase Chain: C: PDB Molecule: mccflike protein (ba_5613); PDBTitle: crystal structure of mccflike protein (ba_5613) from bacillus2 anthracis str. ames
74	c1o0wB_	Alignment	not modelled	19.9	11	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease iii; PDBTitle: crystal structure of ribonuclease iii (tm1102) from2 thermotoga maritima at 2.0 a resolution
75	d2j5wa4	Alignment	not modelled	19.9	25	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
76	d2j5wa1	Alignment	not modelled	19.8	33	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
77	c4v19U_	Alignment	not modelled	19.8	21	PDB header: ribosome Chain: U: PDB Molecule: mitoribosomal protein bl20m, mrpl20; PDBTitle: structure of the large subunit of the mammalian2 mitochondrial ribosome, part 1 of 2
78	d1on3a1	Alignment	not modelled	19.7	10	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
79	c3tlgB_	Alignment	not modelled	19.6	44	PDB header: hydrolase Chain: B: PDB Molecule: mccf; PDBTitle: microcin c7 self immunity protein mccf in the inactive mutant apo2 state
						Fold: TIM beta/alpha-barrel

80	d1fa2a_	Alignment	not modelled	19.4	4	Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
81	d1n8ia_	Alignment	not modelled	19.3	14	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
82	c4mjsQ_	Alignment	not modelled	18.6	26	PDB header: transferase/protein binding Chain: Q: PDB Molecule: protein kinase c zeta type; PDBTitle: crystal structure of a pb1 complex
83	d2j5wa3	Alignment	not modelled	18.6	17	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
84	c2jmka_	Alignment	not modelled	18.5	24	PDB header: protein binding Chain: A: PDB Molecule: hypothetical protein ta0956; PDBTitle: solution structure of ta0956
85	c3g23A_	Alignment	not modelled	18.5	43	PDB header: hydrolase Chain: A: PDB Molecule: ld-carboxypeptidase a; PDBTitle: crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution
86	d1mxaa2	Alignment	not modelled	18.2	37	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
87	c3gjzB_	Alignment	not modelled	17.8	44	PDB header: immune system Chain: B: PDB Molecule: microcin immunity protein mccf; PDBTitle: crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
88	d1gyza_	Alignment	not modelled	17.7	26	Fold: PABP domain-like Superfamily: Ribosomal protein L20 Family: Ribosomal protein L20
89	d1ccwb_	Alignment	not modelled	17.5	16	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Glutamate mutase, large subunit
90	d1wdpa1	Alignment	not modelled	17.4	4	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
91	d1zl0a2	Alignment	not modelled	17.2	43	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
92	c2qazC_	Alignment	not modelled	17.1	15	PDB header: hydrolase activator Chain: C: PDB Molecule: sspb protein; PDBTitle: structure of c. crescentus sspb ortholog
93	d1sqra_	Alignment	not modelled	17.1	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Ribosomal protein L35ae
94	d1b1ya_	Alignment	not modelled	16.7	4	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
95	c4h1hB_	Alignment	not modelled	16.6	57	PDB header: hydrolase Chain: B: PDB Molecule: lmo1638 protein; PDBTitle: crystal structure of mccf homolog from listeria monocytogenes egd-e
96	c4l6wB_	Alignment	not modelled	16.5	10	PDB header: ligase Chain: B: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (acc6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
97	c2qasA_	Alignment	not modelled	16.4	14	PDB header: hydrolase activator Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of caulobacter crescentus sspb ortholog
98	c2uuvC_	Alignment	not modelled	16.3	10	PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase; PDBTitle: alkyldihydroxyacetonephosphate synthase in p1
99	d1h4pa_	Alignment	not modelled	16.3	8	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases