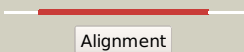
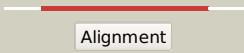
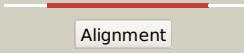
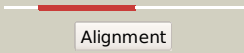
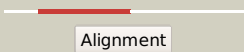
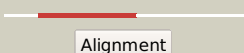
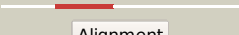
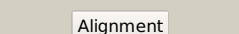
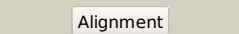
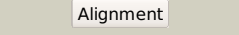
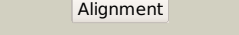
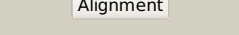
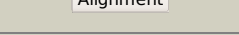
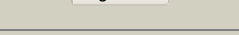
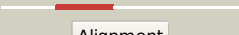
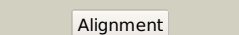
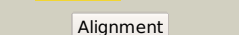
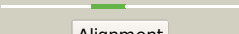
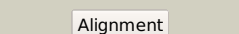
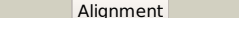


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3odmE_	 Alignment		100.0	30	PDB header: lyase Chain: E; PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: archaeal-type phosphoenolpyruvate carboxylase
2	c1jqoA_	 Alignment		100.0	16	PDB header: lyase Chain: A; PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
3	d1jqoa_	 Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
4	d1jqna_	 Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
5	d1e0ta2	 Alignment		98.7	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
6	d1pkla2	 Alignment		98.1	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
7	d1dxea_	 Alignment		98.0	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpal aldolase
8	d1liua2	 Alignment		97.9	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
9	d1a3xa2	 Alignment		97.9	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
10	d2g50a2	 Alignment		97.9	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
11	c4mf4F_	 Alignment		97.8	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

12	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
13	c3cuza_	Alignment		97.8	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
14	c2vwtA_	Alignment		97.7	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
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	c2v5jB_	Alignment		97.6	18	PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
17	c1sgjB_	Alignment		97.6	18	PDB header: lyase Chain: B: PDB Molecule: citrate lyase, beta subunit; PDBTitle: crystal structure of citrate lyase beta subunit
18	c3qllB_	Alignment		97.6	16	PDB header: lyase Chain: B: PDB Molecule: citrate lyase; PDBTitle: crystal structure of ripc from yersinia pestis
19	c4roqA_	Alignment		97.6	12	PDB header: lyase Chain: A: PDB Molecule: malyl-coa lyase/beta-methylmalyl-coa lyase; PDBTitle: crystal structure of malyl-coa lyase from methylobacterium extorquens
20	d1sgja_	Alignment		97.6	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpai aldolase
21	c4b5sB_	Alignment	not modelled	97.6	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
22	c4tv6A_	Alignment	not modelled	97.5	19	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxyglucarate aldolase; PDBTitle: crystal structure of citrate synthase variant sbng e151q
23	c1izca_	Alignment	not modelled	97.5	17	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
24	d1izca_	Alignment	not modelled	97.5	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpai aldolase
25	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
26	c3qz6A_	Alignment	not modelled	97.3	20	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
27	d1u5ha_	Alignment	not modelled	97.3	23	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpai aldolase
28	c4l7zC_	Alignment	not modelled	97.0	20	PDB header: lyase Chain: C: PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of chloroflexus aurantiacus malyl-coa lyase

29	c3cuxA	 Alignment	not modelled	97.0	21	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	c1e0tD	 Alignment	not modelled	96.5	18	PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase
31	c3pugA	 Alignment	not modelled	96.1	11	PDB header: transferase Chain: A: PDB Molecule: malate synthase; PDBTitle: haloferax volcanii malate synthase native at 3mm glyoxylate
32	c3r4iB	 Alignment	not modelled	96.0	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
33	c3qtgA	 Alignment	not modelled	95.9	16	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from pyrobaculum aerophilum
34	c4imaD	 Alignment	not modelled	95.9	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
35	c3e0vB	 Alignment	not modelled	95.9	20	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
36	c3ma8A	 Alignment	not modelled	95.8	18	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
37	c1a3wB	 Alignment	not modelled	95.6	15	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
38	c2e28A	 Alignment	not modelled	95.2	19	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure analysis of pyruvate kinase from bacillus2 stearrowthermophilus
39	c3khdA	 Alignment	not modelled	95.2	22	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
40	c1aqfB	 Alignment	not modelled	95.2	20	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
41	c4fxjB	 Alignment	not modelled	95.1	20	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes m1/m2; PDBTitle: structure of m2 pyruvate kinase in complex with phenylalanine
42	c3eoeC	 Alignment	not modelled	95.1	21	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
43	c1t5aB	 Alignment	not modelled	95.0	20	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase, m2 isozyme; PDBTitle: human pyruvate kinase m2
44	c3t07D	 Alignment	not modelled	95.0	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
45	c1pkIB	 Alignment	not modelled	95.0	20	PDB header: transferase Chain: B: PDB Molecule: protein (pyruvate kinase); PDBTitle: the structure of leishmania pyruvate kinase
46	c2vgbB	 Alignment	not modelled	94.8	19	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes r/l; PDBTitle: human erythrocyte pyruvate kinase
47	c3khdC	 Alignment	not modelled	94.6	22	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
48	c2bg5C	 Alignment	not modelled	79.4	12	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	63.4	31	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	c1kblA	 Alignment	not modelled	56.7	20	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
51	d1xnya1	 Alignment	not modelled	50.0	17	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
52	d1vrqa1	 Alignment	not modelled	49.9	15	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
53	c2f9iD	 Alignment	not modelled	47.9	14	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl PDBTitle: crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
54	d1rd5a	 Alignment	not modelled	47.8	26	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel

						Family: Tryptophan biosynthesis enzymes
55	c4u0pB_	Alignment	not modelled	47.8	11	PDB header: transferase Chain: B: PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
56	c1ahuB_	Alignment	not modelled	45.0	24	PDB header: flavoenzyme Chain: B: PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
57	d1kbla1	Alignment	not modelled	41.8	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
58	c4n7qA_	Alignment	not modelled	41.4	6	PDB header: lyase Chain: A: PDB Molecule: phosphomethylpyrimidine synthase, chloroplastic; PDBTitle: crystal structure of eukaryotic thic from a. thaliana
59	c4mjsQ_	Alignment	not modelled	40.4	30	PDB header: transferase/protein binding Chain: Q: PDB Molecule: protein kinase c zeta type; PDBTitle: crystal structure of a pb1 complex
60	c3epmB_	Alignment	not modelled	40.4	10	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiamine biosynthesis protein thic; PDBTitle: crystal structure of caulobacter crescentus thic
61	d1h4pa_	Alignment	not modelled	39.9	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
62	c2vqcA_	Alignment	not modelled	37.9	44	PDB header: dna-binding protein Chain: A: PDB Molecule: hypothetical 13.2 kda protein; PDBTitle: structure of a dna binding winged-helix protein, f-112,2 from sulfolobus spindle-shaped virus 1.
63	d2vqca1	Alignment	not modelled	37.9	44	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: F112-like
64	c2hwgA_	Alignment	not modelled	35.0	12	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
65	d1pixa2	Alignment	not modelled	34.8	13	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
66	c4clqB_	Alignment	not modelled	34.6	29	PDB header: translation Chain: B: PDB Molecule: ribosome biogenesis protein bms1; PDBTitle: structure of rcl1p - bms1p complex
67	c2olsA_	Alignment	not modelled	34.0	13	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
68	c2hroA_	Alignment	not modelled	33.5	10	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
69	c3vkbA_	Alignment	not modelled	33.0	21	PDB header: transferase Chain: A: PDB Molecule: moeo5; PDBTitle: crystal structure of moeo5 soaked with fspp overnight
70	d1on3a1	Alignment	not modelled	32.9	8	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
71	c4l6wB_	Alignment	not modelled	28.5	10	PDB header: ligase Chain: B: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
72	d2a7sa1	Alignment	not modelled	26.4	12	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
73	d1kqpa_	Alignment	not modelled	26.1	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
74	d2e9xb1	Alignment	not modelled	25.7	16	Fold: GINs helical bundle-like Superfamily: GINs helical bundle-like Family: PSF2 C-terminal domain-like
75	c2f9yB_	Alignment	not modelled	25.4	10	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
76	d2f9yb1	Alignment	not modelled	25.4	10	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
77	c4a1sE_	Alignment	not modelled	24.5	63	PDB header: cell cycle Chain: E: PDB Molecule: re60102p; PDBTitle: crystallographic structure of the pins:insc complex
78	d2a5yb2	Alignment	not modelled	24.4	27	Fold: DEATH domain Superfamily: DEATH domain Family: Caspase recruitment domain, CARD
79	d2a7sa2	Alignment	not modelled	23.6	2	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
80	d1vbga1	Alignment	not modelled	23.5	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain

						Family: Pyruvate phosphate dikinase, C-terminal domain
81	c4l6wA_	Alignment	not modelled	23.4	10	PDB header: ligase Chain: A: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (acc6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
82	c2ghjD_	Alignment	not modelled	23.2	32	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
83	c1pixB_	Alignment	not modelled	22.2	15	PDB header: lyase Chain: B: PDB Molecule: glutaconyl-coa decarboxylase a subunit; PDBTitle: crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase
84	d1f0ja_	Alignment	not modelled	22.1	17	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
85	c4e5sC_	Alignment	not modelled	21.3	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
86	d2pb1a1	Alignment	not modelled	21.2	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
87	c2xfyA_	Alignment	not modelled	21.0	11	PDB header: hydrolase Chain: A: PDB Molecule: beta-amylase; PDBTitle: crystal structure of barley beta-amylase complexed with2 alpha-cyclodextrin
88	c3tlgB_	Alignment	not modelled	20.7	44	PDB header: hydrolase Chain: B: PDB Molecule: mccf; PDBTitle: microcin c7 self immunity protein mccf in the inactive mutant apo2 state
89	d3c7ba2	Alignment	not modelled	19.9	9	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
90	d1fa2a_	Alignment	not modelled	19.1	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
91	c4v19U_	Alignment	not modelled	18.9	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
92	c3g23A_	Alignment	not modelled	18.9	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
93	c3gjzB_	Alignment	not modelled	18.8	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
94	d1mxaa2	Alignment	not modelled	18.6	30	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
95	c2eeeA_	Alignment	not modelled	18.5	6	PDB header: gene regulation Chain: A: PDB Molecule: uncharacterized protein c6orf130; PDBTitle: solution structure of the a1pp domain from human protein2 c6orf130
96	d1sqra_	Alignment	not modelled	17.8	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Ribosomal protein L35ae
97	d1zl0a2	Alignment	not modelled	17.5	43	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
98	c3glmD_	Alignment	not modelled	17.3	10	PDB header: lyase Chain: D: PDB Molecule: glutaconyl-coa decarboxylase subunit a; PDBTitle: glutaconyl-coa decarboxylase a subunit from clostridium symbiosum co-2 crystallized with crotonyl-coa
99	c3ijeB_	Alignment	not modelled	17.3	16	PDB header: protein binding Chain: B: PDB Molecule: integrin beta-3; PDBTitle: crystal structure of the complete integrin alhavbeta3 ectodomain plus2 an alpha/beta transmembrane fragment