



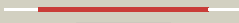


















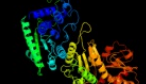
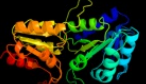






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2o1sC_</a>	 Alignment		100.0	98	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 1-deoxy-d-xylulose-5-phosphate synthase; <b>PDBTitle:</b> 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 escherichia coli
2	<a href="#">c2o1xA_</a>	 Alignment		100.0	48	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose-5-phosphate synthase; <b>PDBTitle:</b> 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 deinococcus radiodurans
3	<a href="#">c3mosA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> the structure of human transketolase
4	<a href="#">c2r8pA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase 1; <b>PDBTitle:</b> transketolase from e. coli in complex with substrate d-2 fructose-6-phosphate
5	<a href="#">c2g28A_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase e1 component; <b>PDBTitle:</b> e. coli pyruvate dehydrogenase h407a variant2 phosphonolactylthiamin diphosphate complex
6	<a href="#">c1r9jB_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> transketolase from leishmania mexicana
7	<a href="#">c3hylB_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase from bacillus anthracis
8	<a href="#">c3m7iA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase in complex with thiamine2 diphosphate, ribose-5-phosphate(pyranose form) and3 magnesium ion
9	<a href="#">c2e6kB_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> x-ray structure of thermus thermophilus hb8 tt0505
10	<a href="#">c3uk1A_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of a transketolase from burkholderia thailandensis2 with an oxidized cysteinesulfonic acid in the active site
11	<a href="#">c1tkcA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> specificity of coenzyme binding in thiamin diphosphate2 dependent enzymes: crystal structures of yeast3 transketolase in complex with analogs of thiamin4 diphosphate

12	<a href="#">c1itzC_</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> maize transketolase in complex with tpp
13	<a href="#">c3komB_</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of apo transketolase from francisella tularensis
14	<a href="#">c3ahhA_</a>	Alignment		100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose 5-phosphate/fructose 6-phosphate phosphoketolase; <b>PDBTitle:</b> h142a mutant of phosphoketolase from bifidobacterium breve complexed2 with acetyl thiamine diphosphate
15	<a href="#">c1ni4D_</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate dehydrogenase e1 component: beta <b>PDBTitle:</b> human pyruvate dehydrogenase
16	<a href="#">c1olsB_</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoisovalerate dehydrogenase beta subunit; <b>PDBTitle:</b> roles of his291-alpha and his146-beta' in the reductive2 acylation reaction catalyzed by human branched-chain3 alpha-ketoacid dehydrogenase
17	<a href="#">c1um9D_</a>	Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-oxo acid dehydrogenase beta subunit; <b>PDBTitle:</b> branched-chain 2-oxo acid dehydrogenase (e1) from thermus2 thermophilus hb8 in apo-form
18	<a href="#">c3dufD_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate dehydrogenase e1 component subunit beta; <b>PDBTitle:</b> snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
19	<a href="#">c2bp7F_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 2-oxoisovalerate dehydrogenase beta subunit; <b>PDBTitle:</b> new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
20	<a href="#">d2ieaa2</a>	Alignment		100.0	19	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like PP module
21	<a href="#">d1itza1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like PP module
22	<a href="#">d2r8oa2</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like PP module
23	<a href="#">d1r9ja2</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like PP module
24	<a href="#">d1gpua1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like PP module
25	<a href="#">c1ik6A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase; <b>PDBTitle:</b> 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum
26	<a href="#">d2r8oa1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
27	<a href="#">d1gpua2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
28	<a href="#">d1itza2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
29	<a href="#">d1r9ja1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding)

						<b>Family:</b> TK-like Pyr module
30	<a href="#">c2jgdA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e1 component; <b>PDBTitle:</b> e. coli 2-oxoglutarate dehydrogenase (e1o)
31	<a href="#">c2yicC</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-oxoglutarate decarboxylase; <b>PDBTitle:</b> crystal structure of the suca domain of mycobacterium smegmatis2 alpha-ketoglutarate decarboxylase (triclinic form)
32	<a href="#">d2ieaa1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
33	<a href="#">d1umdb1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
34	<a href="#">d1w85b1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
35	<a href="#">c2xt6B</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoglutarate decarboxylase; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
36	<a href="#">d2ozlb1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
37	<a href="#">d1qs0b1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
38	<a href="#">d2bfdb1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
39	<a href="#">d1w85a</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
40	<a href="#">d2ozla1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
41	<a href="#">dlik6a1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
42	<a href="#">d1umda</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
43	<a href="#">d2bfda1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
44	<a href="#">d1qs0a</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
45	<a href="#">d1qs0b2</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
46	<a href="#">d2ozlb2</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
47	<a href="#">d2bfdb2</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
48	<a href="#">d1umdb2</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
49	<a href="#">d1w85b2</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
50	<a href="#">dlik6a2</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
51	<a href="#">d1itza3</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
52	<a href="#">d1r9ja3</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
53	<a href="#">d2r8oa3</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
54	<a href="#">d1gpua3</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
55	<a href="#">d2ieaa3</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
56	<a href="#">d1t9ba3</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding)

					<b>Family:</b> Pyruvate oxidase and decarboxylase PP module
57	<a href="#">d1q6za3</a>	Alignment	not modelled	99.4	21 <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
58	<a href="#">d2ihta3</a>	Alignment	not modelled	99.3	16 <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
59	<a href="#">c2c3yA</a>	Alignment	not modelled	99.3	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase; <b>PDBTitle:</b> crystal structure of the radical form of 2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
60	<a href="#">d1jsca3</a>	Alignment	not modelled	99.3	23 <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
61	<a href="#">d2ji7a3</a>	Alignment	not modelled	99.3	10 <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
62	<a href="#">d2djia3</a>	Alignment	not modelled	99.2	16 <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
63	<a href="#">d1ozha3</a>	Alignment	not modelled	99.2	18 <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
64	<a href="#">c2pgnA</a>	Alignment	not modelled	99.2	17 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexane-1,2-dione hydrolase (cdh); <b>PDBTitle:</b> the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
65	<a href="#">d1ybha3</a>	Alignment	not modelled	99.2	17 <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
66	<a href="#">c2v3wC</a>	Alignment	not modelled	99.2	20 <b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> benzoylformate decarboxylase; <b>PDBTitle:</b> crystal structure of the benzoylformate decarboxylase2 variant I461a from pseudomonas putida
67	<a href="#">d1ovma3</a>	Alignment	not modelled	99.2	20 <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
68	<a href="#">d2ez9a3</a>	Alignment	not modelled	99.1	12 <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
69	<a href="#">c2djia</a>	Alignment	not modelled	99.1	12 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate oxidase; <b>PDBTitle:</b> crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
70	<a href="#">c3ju3A</a>	Alignment	not modelled	99.1	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; <b>PDBTitle:</b> crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
71	<a href="#">c1t9dB</a>	Alignment	not modelled	99.1	21 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetolactate synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of yeast acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, metsulfuron methyl
72	<a href="#">c2q27B</a>	Alignment	not modelled	99.0	15 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxalyl-coa decarboxylase; <b>PDBTitle:</b> crystal structure of oxalyl-coa decarboxylase from escherichia coli
73	<a href="#">c1powA</a>	Alignment	not modelled	99.0	9 <b>PDB header:</b> oxidoreductase(oxygen as acceptor) <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate oxidase; <b>PDBTitle:</b> the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
74	<a href="#">c1jscA</a>	Alignment	not modelled	99.0	22 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> acetohydroxy-acid synthase; <b>PDBTitle:</b> crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
75	<a href="#">d1pvda3</a>	Alignment	not modelled	99.0	21 <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
76	<a href="#">c1upaC</a>	Alignment	not modelled	99.0	16 <b>PDB header:</b> synthase <b>Chain:</b> C: <b>PDB Molecule:</b> carboxyethylarginine synthase; <b>PDBTitle:</b> carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
77	<a href="#">c1ovmC</a>	Alignment	not modelled	99.0	18 <b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> indole-3-pyruvate decarboxylase; <b>PDBTitle:</b> crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
78	<a href="#">c3eyaE</a>	Alignment	not modelled	98.9	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase [cytochrome]; <b>PDBTitle:</b> structural basis for membrane binding and catalytic2 activation of the peripheral membrane enzyme pyruvate3 oxidase from escherichia coli
79	<a href="#">c2ag1A</a>	Alignment	not modelled	98.9	16 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> benzaldehyde lyase; <b>PDBTitle:</b> crystal structure of benzaldehyde lyase (bal)- semet
80	<a href="#">c2panF</a>	Alignment	not modelled	98.9	15 <b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> glyoxylate carboligase; <b>PDBTitle:</b> crystal structure of e. coli glyoxylate carboligase
81	<a href="#">c1yi1A</a>	Alignment	not modelled	98.9	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
					<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding)

82	<a href="#">d1zpd3</a>	Alignment	not modelled	98.9	17	<b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
83	<a href="#">c1zpdA</a>	Alignment	not modelled	98.9	21	<b>PDB header:</b> alcohol fermentation <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> pyruvate decarboxylase from zymomonas mobilis
84	<a href="#">c2ji6B</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxalyl-coa decarboxylase; <b>PDBTitle:</b> x-ray structure of oxalyl-coa decarboxylase in complex with 2 3-deaza-thdp and oxalyl-coa
85	<a href="#">c1ozhD</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> acetolactate synthase, catabolic; <b>PDBTitle:</b> the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusual3 intermediate.
86	<a href="#">c2w93A</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate decarboxylase isozyme 1; <b>PDBTitle:</b> crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate3 pyruvamide
87	<a href="#">c3lq1A</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene- <b>PDBTitle:</b> crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene2 1-carboxylic acid synthase/2-oxoglutarate decarboxylase3 from listeria monocytogenes str. 4b f2365
88	<a href="#">c2vbiF</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> holostucture of pyruvate decarboxylase from acetobacter2 pasteurianus
89	<a href="#">c2x7jA</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene <b>PDBTitle:</b> structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
90	<a href="#">c2jlaD</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene <b>PDBTitle:</b> crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase - semet3 protein
91	<a href="#">c2vbgB</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> branched-chain alpha-ketoacid decarboxylase; <b>PDBTitle:</b> the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
92	<a href="#">c2nxwB</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phenyl-3-pyruvate decarboxylase; <b>PDBTitle:</b> crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
93	<a href="#">d2c42a3</a>	Alignment	not modelled	98.4	14	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
94	<a href="#">d2ez9a2</a>	Alignment	not modelled	98.0	15	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
95	<a href="#">d2djia2</a>	Alignment	not modelled	97.8	11	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
96	<a href="#">d2c42a1</a>	Alignment	not modelled	97.8	16	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> PFOR Pyr module
97	<a href="#">d1t9ba2</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
98	<a href="#">d1pvda2</a>	Alignment	not modelled	97.8	12	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
99	<a href="#">d1ybha2</a>	Alignment	not modelled	97.7	15	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
100	<a href="#">d2c42a2</a>	Alignment	not modelled	97.6	22	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> PFOR PP module
101	<a href="#">d1zpd2</a>	Alignment	not modelled	97.6	16	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
102	<a href="#">d1q6za2</a>	Alignment	not modelled	97.5	14	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
103	<a href="#">d1ovma2</a>	Alignment	not modelled	97.1	15	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
104	<a href="#">d1ozha2</a>	Alignment	not modelled	96.7	11	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
105	<a href="#">d2ihta2</a>	Alignment	not modelled	95.7	13	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
106	<a href="#">c1yd7A</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-keto acid:ferredoxin oxidoreductase subunit <b>PDBTitle:</b> conserved hypothetical protein pfu-1647980-001 from2



					pyrococcus furiosus
107	<a href="#">d2ji7a2</a>	Alignment	not modelled	95.6	12 <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
108	<a href="#">c3tovB</a>	Alignment	not modelled	65.8	12 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase family 9; <b>PDBTitle:</b> the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
109	<a href="#">d2glza1</a>	Alignment	not modelled	45.0	17 <b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> FwdE-like <b>Family:</b> FwdE-like
110	<a href="#">d2gvia1</a>	Alignment	not modelled	41.4	18 <b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> FwdE-like <b>Family:</b> FwdE-like
111	<a href="#">d1pswa</a>	Alignment	not modelled	37.7	14 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> ADP-heptose LPS heptosyltransferase II
112	<a href="#">d1wi9a</a>	Alignment	not modelled	34.8	22 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PCI domain (PINT motif)
113	<a href="#">d1z67a1</a>	Alignment	not modelled	31.5	18 <b>Fold:</b> YidB-like <b>Superfamily:</b> YidB-like <b>Family:</b> YidB-like
114	<a href="#">c2vxob</a>	Alignment	not modelled	30.1	11 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> human gmp synthetase in complex with xmp
115	<a href="#">d2zjrv1</a>	Alignment	not modelled	29.3	22 <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Ribosomal protein L29 (L29p) <b>Family:</b> Ribosomal protein L29 (L29p)
116	<a href="#">c3bboZ</a>	Alignment	not modelled	25.0	22 <b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> ribosomal protein l29; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
117	<a href="#">c2l6pA</a>	Alignment	not modelled	24.0	23 <b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phac1, phac2 and phad genes; <b>PDBTitle:</b> nmr solution structure of the protein np_253742.1
118	<a href="#">c2gviA</a>	Alignment	not modelled	23.9	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative formylmethanofuran dehydrogenase2 subunit e (ta1109) from thermoplasma acidophilum at 1.87 a resolution
119	<a href="#">d2aq0a1</a>	Alignment	not modelled	23.6	17 <b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
120	<a href="#">c2kvuA</a>	Alignment	not modelled	22.4	11 <b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> mkl/myocardin-like protein 1; <b>PDBTitle:</b> solution nmr structure of sap domain of mkl/myocardin-like2 protein 1 from h.sapiens, northeast structural genomics3 consortium target target hr4547e