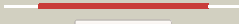



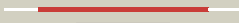


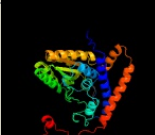













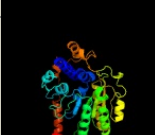











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0843 (-) _939391_940395
Date	Fri Jul 26 01:50:43 BST 2019
Unique Job ID	7e9c7bb375f429cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1qs0a_</a>	 Alignment		100.0	23	<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
2	<a href="#">d2ozla1</a>	 Alignment		100.0	24	<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
3	<a href="#">d1umda_</a>	 Alignment		100.0	27	<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
4	<a href="#">d2bfdal</a>	 Alignment		100.0	23	<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
5	<a href="#">d1w85a_</a>	 Alignment		100.0	28	<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
6	<a href="#">c2yicC</a>	 Alignment		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)
7	<a href="#">c2xt6B</a>	 Alignment		100.0	17	<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)
8	<a href="#">c2jgdA</a>	 Alignment		100.0	15	<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)
9	<a href="#">d1gpua1</a>	 Alignment		100.0	16	<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
10	<a href="#">d1r9ja2</a>	 Alignment		100.0	15	<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
11	<a href="#">d2r8oa2</a>	 Alignment		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 PP module

12	<a href="#">dlitza1</a>	Alignment		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 PP module
13	<a href="#">c4c7vA_</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> apo transketolase from lactobacillus salivarius at 2.2a resolution
14	<a href="#">c1tkcA_</a>	Alignment		100.0	16	<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
15	<a href="#">c5nd5A_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase from chlamydomonas reinhardtii in2 complex with tpp and mg2+
16	<a href="#">c5vrbB_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of a transketolase from neisseria gonorrhoeae
17	<a href="#">c3m7iA_</a>	Alignment		100.0	16	<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) and magnesium ion
18	<a href="#">c3rimA_</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis transketolase2 (rv1449c)
19	<a href="#">c3mosA_</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> the structure of human transketolase
20	<a href="#">c1itcC_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> maize transketolase in complex with tpp
21	<a href="#">c2o1xA_</a>	Alignment	not modelled	100.0	16	<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) from deinococcus2 radiodurans
22	<a href="#">c5hgxA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase mutant - h261f from pichia stipitis
23	<a href="#">c3hylB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase from bacillus anthracis
24	<a href="#">c2e6kB_</a>	Alignment	not modelled	100.0	21	<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
25	<a href="#">c2r8pA_</a>	Alignment	not modelled	100.0	19	<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-fructose-6-2 phosphate
26	<a href="#">c3uk1A_</a>	Alignment	not modelled	100.0	16	<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
27	<a href="#">c1r9jB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> transketolase from leishmania mexicana
28	<a href="#">c2o1sC_</a>	Alignment	not modelled	100.0	17	<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
						<b>PDB header:</b> transferase

29	<a href="#">c6ouwA_</a>	Alignment	not modelled	100.0	19	<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 (dxps) from deinococcus2 radiodurans with enamine intermediate bound
30	<a href="#">c3komB_</a>	Alignment	not modelled	100.0	16	<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
31	<a href="#">d2ieaa2</a>	Alignment	not modelled	100.0	15	<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
32	<a href="#">c2g28A_</a>	Alignment	not modelled	100.0	16	<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
33	<a href="#">c4qoyC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase e1 component; <b>PDBTitle:</b> novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydrolipoyl acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
34	<a href="#">c3ahhA_</a>	Alignment	not modelled	99.9	11	<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
35	<a href="#">d2dja3</a>	Alignment	not modelled	99.9	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
36	<a href="#">c2dja_</a>	Alignment	not modelled	99.9	14	<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
37	<a href="#">d2ez9a3</a>	Alignment	not modelled	99.7	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 PP module
38	<a href="#">d1t9ba3</a>	Alignment	not modelled	99.7	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
39	<a href="#">c1powA_</a>	Alignment	not modelled	99.7	17	<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
40	<a href="#">d1q6za3</a>	Alignment	not modelled	99.7	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
41	<a href="#">c4k9qB_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoylformate decarboxylase; <b>PDBTitle:</b> the crystal structure of benzoylformate decarboxylase from2 polynucleobacter necessarius
42	<a href="#">d1jsca3</a>	Alignment	not modelled	99.7	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
43	<a href="#">c4q9dA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> benzoylformate decarboxylase; <b>PDBTitle:</b> x-ray structure of a putative thiamin diphosphate-dependent enzyme2 isolated from mycobacterium smegmatis
44	<a href="#">d1ybha3</a>	Alignment	not modelled	99.7	19	<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
45	<a href="#">c2panF_</a>	Alignment	not modelled	99.6	17	<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
46	<a href="#">d2ihta3</a>	Alignment	not modelled	99.6	22	<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
47	<a href="#">d1ozha3</a>	Alignment	not modelled	99.6	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
48	<a href="#">c3eyaE_</a>	Alignment	not modelled	99.6	23	<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
49	<a href="#">c1t9dB_</a>	Alignment	not modelled	99.6	15	<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 in complex with a2 sulfonyleurea herbicide, metsulfuron methyl
50	<a href="#">c2ag1A_</a>	Alignment	not modelled	99.6	23	<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
51	<a href="#">c4rjB_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> acetolactate synthase; <b>PDBTitle:</b> acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii
52	<a href="#">c3ey9B_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate dehydrogenase [cytochrome]; <b>PDBTitle:</b> structural basis for membrane binding and catalytic activation of the2 peripheral membrane enzyme pyruvate oxidase from escherichia coli
53	<a href="#">d2ji7a3</a>	Alignment	not modelled	99.5	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
54	<a href="#">c2v3wC_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> benzoylformate decarboxylase; <b>PDBTitle:</b> crystal structure of the benzoylformate decarboxylase

						variant I461a2 from pseudomonas putida
55	<a href="#">c1jscA_</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> acetoxyhydroxy-acid synthase; <b>PDBTitle:</b> crystal structure of the catalytic subunit of yeast2 acetoxyhydroxyacid synthase: a target for herbicidal3 inhibitors
56	<a href="#">c6n2oB_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate ferredoxin/ferredoxin oxidoreductase, beta <b>PDBTitle:</b> 2-oxoglutarate:ferredoxin oxidoreductase from magnetococcus marinus2 with 2-oxoglutarate, coenzyme a and succinyl-coa bound
57	<a href="#">d1pvda3</a>	Alignment	not modelled	99.5	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
58	<a href="#">c5ahkB_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetolactate synthase ii, large subunit; <b>PDBTitle:</b> crystal structure of acetoxyhydroxy acid synthase pf5 from2 pseudomonas protegens
59	<a href="#">c2pgnA_</a>	Alignment	not modelled	99.5	21	<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
60	<a href="#">c1upaC_</a>	Alignment	not modelled	99.5	22	<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)
61	<a href="#">c1ozhD_</a>	Alignment	not modelled	99.5	17	<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.
62	<a href="#">c1yi1A_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana acetoxyhydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
63	<a href="#">c2ji6B_</a>	Alignment	not modelled	99.5	19	<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 3-deaza-2 thdp and oxalyl-coa
64	<a href="#">d1lovma3</a>	Alignment	not modelled	99.5	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 PP module
65	<a href="#">c2nxwB_</a>	Alignment	not modelled	99.5	16	<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
66	<a href="#">c2q27B_</a>	Alignment	not modelled	99.4	18	<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
67	<a href="#">c2jlaD_</a>	Alignment	not modelled	99.4	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
68	<a href="#">c2vbgB_</a>	Alignment	not modelled	99.4	11	<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
69	<a href="#">c2w93A_</a>	Alignment	not modelled	99.4	10	<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 surrogate pyruvamide
70	<a href="#">c3lq1A_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- <b>PDBTitle:</b> crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene 1-2 carboxylic acid synthase/2-oxoglutarate decarboxylase from listeria3 monocytogenes str. 4b f2365
71	<a href="#">c5essB_</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- <b>PDBTitle:</b> crystal structure of m. tuberculosis mend bound to mg2+ and covalent2 intermediate i (a thdp and decarboxylated 2-oxoglutarate adduct)
72	<a href="#">c1zpdA_</a>	Alignment	not modelled	99.4	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
73	<a href="#">c2x7jA_</a>	Alignment	not modelled	99.4	18	<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
74	<a href="#">d1zpdA3</a>	Alignment	not modelled	99.4	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
75	<a href="#">c2vbiF_</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> holostructure of pyruvate decarboxylase from acetobacter pasteurianus
76	<a href="#">c5b46B_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoacid--ferredoxin oxidoreductase beta subunit; <b>PDBTitle:</b> 2-oxoacid:ferredoxin oxidoreductase 2 from sulfolobus

						tokodai - ligand2 free form
77	<a href="#">c1ovmC</a>	Alignment	not modelled	99.3	13	<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="#">c5c4iC</a>	Alignment	not modelled	99.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxalate oxidoreductase subunit beta; <b>PDBTitle:</b> structure of an oxalate oxidoreductase
79	<a href="#">d2c42a2</a>	Alignment	not modelled	98.5	20	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> PFOR PP module
80	<a href="#">c6cipD</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase; <b>PDBTitle:</b> pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpp bound
81	<a href="#">c2c3yA</a>	Alignment	not modelled	97.7	18	<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 f2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
82	<a href="#">d1zpdA2</a>	Alignment	not modelled	97.5	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
83	<a href="#">d2dja2</a>	Alignment	not modelled	97.4	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
84	<a href="#">d1pvdA2</a>	Alignment	not modelled	97.2	7	<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
85	<a href="#">d2ji7a2</a>	Alignment	not modelled	97.2	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 Pyr module
86	<a href="#">d1ybha2</a>	Alignment	not modelled	96.9	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
87	<a href="#">d2ez9a2</a>	Alignment	not modelled	96.9	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
88	<a href="#">d1ozha2</a>	Alignment	not modelled	96.8	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 Pyr module
89	<a href="#">d1t9ba2</a>	Alignment	not modelled	96.7	19	<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
90	<a href="#">d2ihta2</a>	Alignment	not modelled	96.6	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
91	<a href="#">d1q6za2</a>	Alignment	not modelled	96.4	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 Pyr module
92	<a href="#">c4wbxC</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-keto acid:ferredoxin oxidoreductase subunit alpha; <b>PDBTitle:</b> conserved hypothetical protein pf1771 from pyrococcus furiosus solved2 by sulfur sad using swiss light source data
93	<a href="#">c5b47A</a>	Alignment	not modelled	95.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-oxoacid--ferredoxin oxidoreductase alpha subunit; <b>PDBTitle:</b> 2-oxoacid:ferredoxin oxidoreductase 2 from sulfolobus tokodai -2 pyruvate complex
94	<a href="#">c5b48A</a>	Alignment	not modelled	95.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-oxoacid--ferredoxin oxidoreductase alpha subunit; <b>PDBTitle:</b> 2-oxoacid:ferredoxin oxidoreductase 1 from sulfolobus tokodai
95	<a href="#">d1ovma2</a>	Alignment	not modelled	95.6	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 Pyr module
96	<a href="#">c6n2nA</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate flavodoxin/ferredoxin oxidoreductase domain <b>PDBTitle:</b> crystal structure of 2-oxoglutarate:ferredoxin oxidoreductase from2 magnetococcus marinus
97	<a href="#">d2c42a1</a>	Alignment	not modelled	94.2	18	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> PFOR Pyr module
98	<a href="#">d2r8oa1</a>	Alignment	not modelled	94.2	15	<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
99	<a href="#">d1itza2</a>	Alignment	not modelled	93.7	14	<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
100	<a href="#">d1r9ja1</a>	Alignment	not modelled	93.0	12	<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
101	<a href="#">d1gpua2</a>	Alignment	not modelled	92.7	8	<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
102	<a href="#">c5c4iA</a>	Alignment	not modelled	88.5	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxalate oxidoreductase subunit alpha; <b>PDBTitle:</b> structure of an oxalate oxidoreductase



103	<a href="#">c4hhuA</a>	Alignment	not modelled	87.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> or280; <b>PDBTitle:</b> crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
104	<a href="#">d2ozlb1</a>	Alignment	not modelled	74.9	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 Pyr module
105	<a href="#">d1qs0b1</a>	Alignment	not modelled	72.9	13	<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
106	<a href="#">d2bfdb1</a>	Alignment	not modelled	68.6	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
107	<a href="#">c5cw9A</a>	Alignment	not modelled	57.6	26	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed ferredoxin-ferredoxin domain insertion <b>PDBTitle:</b> crystal structure of de novo designed ferredoxin-ferredoxin domain2 insertion protein
108	<a href="#">d1w85b1</a>	Alignment	not modelled	56.2	15	<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
109	<a href="#">c1jqkE</a>	Alignment	not modelled	49.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> carbon monoxide dehydrogenase; <b>PDBTitle:</b> crystal structure of carbon monoxide dehydrogenase from2 rhodospirillum rubrum
110	<a href="#">d1jqka</a>	Alignment	not modelled	49.9	19	<b>Fold:</b> Prismane protein-like <b>Superfamily:</b> Prismane protein-like <b>Family:</b> Carbon monoxide dehydrogenase
111	<a href="#">d1on3a2</a>	Alignment	not modelled	48.4	21	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
112	<a href="#">d1su7a</a>	Alignment	not modelled	46.2	20	<b>Fold:</b> Prismane protein-like <b>Superfamily:</b> Prismane protein-like <b>Family:</b> Carbon monoxide dehydrogenase
113	<a href="#">d1fvpa</a>	Alignment	not modelled	46.1	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (LuxF, FP390)
114	<a href="#">d1vrqa2</a>	Alignment	not modelled	45.9	18	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
115	<a href="#">c1lw7A</a>	Alignment	not modelled	41.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator nadr; <b>PDBTitle:</b> nadr protein from haemophilus influenzae
116	<a href="#">d2pjua1</a>	Alignment	not modelled	41.0	14	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> PrpR receptor domain-like <b>Family:</b> PrpR receptor domain-like
117	<a href="#">c1pixB</a>	Alignment	not modelled	39.9	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaconyl-coa decarboxylase a subunit; <b>PDBTitle:</b> crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase
118	<a href="#">d2a7sa2</a>	Alignment	not modelled	38.5	23	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
119	<a href="#">d2a7sa1</a>	Alignment	not modelled	38.3	17	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
120	<a href="#">c4l6wB</a>	Alignment	not modelled	37.9	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> probable propionyl-coa carboxylase beta chain 6; <b>PDBTitle:</b> carboxyltransferase subunit (acc6) of mycobacterium tuberculosis2 acetyl-coa carboxylase