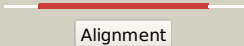

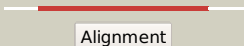

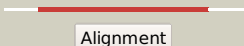







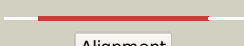














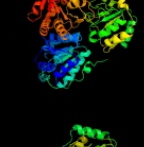


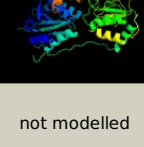


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3509c_(ilvX)_3937056_3938603
Date	Fri Aug 9 18:20:18 BST 2019
Unique Job ID	150bb5f7901b7411

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ey9B_</a>	 Alignment		100.0	20	<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
2	<a href="#">c1powA_</a>	 Alignment		100.0	22	<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
3	<a href="#">c1yi1A_</a>	 Alignment		100.0	22	<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 sulfonyleurea herbicide, tribenuron methyl
4	<a href="#">c4rj1B_</a>	 Alignment		100.0	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
5	<a href="#">c2djiA_</a>	 Alignment		100.0	19	<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
6	<a href="#">c2panF_</a>	 Alignment		100.0	20	<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
7	<a href="#">c2v3wC_</a>	 Alignment		100.0	25	<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 l461a2 from pseudomonas putida
8	<a href="#">c1ozhD_</a>	 Alignment		100.0	21	<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.
9	<a href="#">c2pgnA_</a>	 Alignment		100.0	18	<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
10	<a href="#">c1t9dB_</a>	 Alignment		100.0	22	<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
11	<a href="#">c4k9qB_</a>	 Alignment		100.0	20	<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

12	<a href="#">c1jscA_</a>	Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> acetoxy-acid synthase; <b>PDBTitle:</b> crystal structure of the catalytic subunit of yeast2 acetoxy-acid synthase: a target for herbicidal3 inhibitors
13	<a href="#">c3eyaE_</a>	Alignment		100.0	21	<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
14	<a href="#">c4q9dA_</a>	Alignment		100.0	24	<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
15	<a href="#">c2vbiF_</a>	Alignment		100.0	18	<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
16	<a href="#">c5ahkB_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> acetolactate synthase ii, large subunit; <b>PDBTitle:</b> crystal structure of acetoxy acid synthase pf5 from2 pseudomonas protegens
17	<a href="#">c1zpdA_</a>	Alignment		100.0	19	<b>PDB header:</b> alcohol fermentation <b>Chain:</b> A; <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> pyruvate decarboxylase from zymomonas mobilis
18	<a href="#">c2ag1A_</a>	Alignment		100.0	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
19	<a href="#">c2vbgB_</a>	Alignment		100.0	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
20	<a href="#">c2x7jA_</a>	Alignment		100.0	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
21	<a href="#">c2q27B_</a>	Alignment	not modelled	100.0	20	<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
22	<a href="#">c2w93A_</a>	Alignment	not modelled	100.0	17	<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
23	<a href="#">c1upaC_</a>	Alignment	not modelled	100.0	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)
24	<a href="#">c2ji6B_</a>	Alignment	not modelled	100.0	22	<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
25	<a href="#">c1ovmC_</a>	Alignment	not modelled	100.0	20	<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
26	<a href="#">c2nxwB_</a>	Alignment	not modelled	100.0	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 brasiliense
27	<a href="#">c2jlaD_</a>	Alignment	not modelled	100.0	14	<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
						<b>PDB header:</b> transferase

28	<a href="#">c3lq1A</a>	Alignment	not modelled	100.0	16	<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
29	<a href="#">c5essB</a>	Alignment	not modelled	100.0	19	<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)
30	<a href="#">d2djia2</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> Pyruvate oxidase and decarboxylase Pyr module
31	<a href="#">d1ybha2</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> Pyruvate oxidase and decarboxylase Pyr module
32	<a href="#">d1ozha2</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> Pyruvate oxidase and decarboxylase Pyr module
33	<a href="#">d1t9ba2</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> Pyruvate oxidase and decarboxylase Pyr module
34	<a href="#">d1q6za2</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> Pyruvate oxidase and decarboxylase Pyr module
35	<a href="#">d1zpa2</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> Pyruvate oxidase and decarboxylase Pyr module
36	<a href="#">d1pvda2</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> Pyruvate oxidase and decarboxylase Pyr module
37	<a href="#">d2ji7a2</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> Pyruvate oxidase and decarboxylase Pyr module
38	<a href="#">d1ybha3</a>	Alignment	not modelled	100.0	27	<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="#">d2ihta2</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> Pyruvate oxidase and decarboxylase Pyr module
40	<a href="#">d2ez9a2</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> Pyruvate oxidase and decarboxylase Pyr module
41	<a href="#">d2ez9a3</a>	Alignment	not modelled	100.0	28	<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
42	<a href="#">d2djia3</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> Pyruvate oxidase and decarboxylase PP module
43	<a href="#">d1t9ba3</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> Pyruvate oxidase and decarboxylase PP module
44	<a href="#">d1lovma2</a>	Alignment	not modelled	100.0	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 Pyr module
45	<a href="#">d1ozha3</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> Pyruvate oxidase and decarboxylase PP module
46	<a href="#">d1lovma3</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> Pyruvate oxidase and decarboxylase PP module
47	<a href="#">d2ihta3</a>	Alignment	not modelled	100.0	29	<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="#">d1q6za3</a>	Alignment	not modelled	100.0	32	<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
49	<a href="#">d1zpa3</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> Pyruvate oxidase and decarboxylase PP module
50	<a href="#">d2ji7a3</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> Pyruvate oxidase and decarboxylase PP module
51	<a href="#">d1pvda3</a>	Alignment	not modelled	100.0	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
52	<a href="#">d1jsca3</a>	Alignment	not modelled	100.0	28	<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
53	<a href="#">c6n2oB</a>	Alignment	not modelled	100.0	15	<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 <b>PDB header:</b> oxidoreductase

54	<a href="#">c5b46B</a>	Alignment	not modelled	100.0	15	<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
55	<a href="#">c2c3yA</a>	Alignment	not modelled	99.9	19	<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
56	<a href="#">c4wbxC</a>	Alignment	not modelled	99.9	17	<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
57	<a href="#">c5c4iC</a>	Alignment	not modelled	99.9	16	<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
58	<a href="#">d2c42a1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> PFOR Pyr module
59	<a href="#">c6cipD</a>	Alignment	not modelled	99.8	13	<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-tpg bound
60	<a href="#">c6n2nA</a>	Alignment	not modelled	99.8	17	<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
61	<a href="#">d2ez9a1</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
62	<a href="#">c5b47A</a>	Alignment	not modelled	99.8	16	<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
63	<a href="#">d2djia1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
64	<a href="#">c5c4iA</a>	Alignment	not modelled	99.8	12	<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
65	<a href="#">c5b48A</a>	Alignment	not modelled	99.8	19	<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
66	<a href="#">d1ozha1</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
67	<a href="#">d1t9ba1</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
68	<a href="#">d1pvda1</a>	Alignment	not modelled	99.7	8	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
69	<a href="#">d2ji7a1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
70	<a href="#">d1ybha1</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
71	<a href="#">d1zpdA1</a>	Alignment	not modelled	99.7	10	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
72	<a href="#">d2ihta1</a>	Alignment	not modelled	99.7	6	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
73	<a href="#">d1q6za1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
74	<a href="#">d1lovma1</a>	Alignment	not modelled	99.6	9	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
75	<a href="#">d2r8oa2</a>	Alignment	not modelled	99.6	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
76	<a href="#">d2c42a2</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> PFOR PP module
77	<a href="#">d2bfda1</a>	Alignment	not modelled	99.6	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
78	<a href="#">d1w85a</a>	Alignment	not modelled	99.6	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
79	<a href="#">c1yd7A</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-keto acid:ferredoxin oxidoreductase subunit alpha; <b>PDBTitle:</b> conserved hypothetical protein pfu-1647980-001 from pyrococcus2 furiosus

80	<a href="#">d1gpua1</a>	Alignment	not modelled	99.6	27	<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
81	<a href="#">d1r9ja2</a>	Alignment	not modelled	99.6	31	<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
82	<a href="#">d1itza1</a>	Alignment	not modelled	99.5	29	<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
83	<a href="#">d2ozla1</a>	Alignment	not modelled	99.5	25	<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
84	<a href="#">d1umda_</a>	Alignment	not modelled	99.5	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 PP module
85	<a href="#">c3m7iA_</a>	Alignment	not modelled	99.4	26	<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
86	<a href="#">c3cf4G_</a>	Alignment	not modelled	99.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase epsilon subunit; <b>PDBTitle:</b> structure of the codh component of the m. barkeri acids complex
87	<a href="#">c5nd5A_</a>	Alignment	not modelled	99.4	32	<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+
88	<a href="#">c2o1xA_</a>	Alignment	not modelled	99.3	22	<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
89	<a href="#">c2o1sC_</a>	Alignment	not modelled	99.3	24	<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
90	<a href="#">c3rimA_</a>	Alignment	not modelled	99.3	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis transketolase2 (rv1449c)
91	<a href="#">c5hgxA_</a>	Alignment	not modelled	99.3	26	<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
92	<a href="#">c2e6kB_</a>	Alignment	not modelled	99.3	30	<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
93	<a href="#">c3hylB_</a>	Alignment	not modelled	99.3	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase from bacillus anthracis
94	<a href="#">c1itzC_</a>	Alignment	not modelled	99.3	28	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> maize transketolase in complex with tpp
95	<a href="#">c3uk1A_</a>	Alignment	not modelled	99.3	23	<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
96	<a href="#">c4c7vA_</a>	Alignment	not modelled	99.3	29	<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
97	<a href="#">c1tkcA_</a>	Alignment	not modelled	99.3	27	<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
98	<a href="#">c1r9jB_</a>	Alignment	not modelled	99.3	31	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> transketolase from leishmania mexicana
99	<a href="#">c3mosA_</a>	Alignment	not modelled	99.3	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> the structure of human transketolase
100	<a href="#">c2r8pA_</a>	Alignment	not modelled	99.2	26	<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
101	<a href="#">c5vrbB_</a>	Alignment	not modelled	99.2	26	<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
102	<a href="#">c6ouwA_</a>	Alignment	not modelled	99.2	27	<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 (dxps) from deinococcus2 radiodurans with enamine intermediate bound
103	<a href="#">c3komB_</a>	Alignment	not modelled	99.1	19	<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
104	<a href="#">c2g28A_</a>	Alignment	not modelled	99.1	24	<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
105	<a href="#">d2ieaa2</a>	Alignment	not modelled	99.1	23	<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

106	<a href="#">d1qs0a_</a>	Alignment	not modelled	99.1	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
107	<a href="#">c5ol2D_</a>	Alignment	not modelled	99.0	10	<b>PDB header:</b> flavoprotein <b>Chain:</b> D: <b>PDB Molecule:</b> electron transfer flavoprotein large subunit; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
108	<a href="#">c4qoyC_</a>	Alignment	not modelled	98.9	24	<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
109	<a href="#">c3ahhA_</a>	Alignment	not modelled	98.8	22	<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
110	<a href="#">c2jgdA_</a>	Alignment	not modelled	98.1	22	<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)
111	<a href="#">c1olsB_</a>	Alignment	not modelled	97.8	12	<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 reductive acylation2 reaction catalyzed by human branched-chain alpha-ketoacid3 dehydrogenase
112	<a href="#">c4l2iA_</a>	Alignment	not modelled	97.7	8	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein alpha subunit; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
113	<a href="#">d1gpua2</a>	Alignment	not modelled	97.7	9	<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
114	<a href="#">c2yicC_</a>	Alignment	not modelled	97.6	24	<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)
115	<a href="#">d2r8oa1</a>	Alignment	not modelled	97.5	11	<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
116	<a href="#">d1r9ja1</a>	Alignment	not modelled	97.5	13	<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
117	<a href="#">d1itza2</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> TK-like Pyr module
118	<a href="#">d1ytia1</a>	Alignment	not modelled	97.0	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> ACDE2-like
119	<a href="#">c1ni4D_</a>	Alignment	not modelled	96.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate dehydrogenase e1 component: beta <b>PDBTitle:</b> human pyruvate dehydrogenase
120	<a href="#">c3dufD_</a>	Alignment	not modelled	96.2	14	<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