







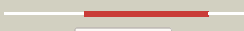















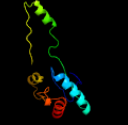








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2455c (- )_2754753_2756714
Date	Wed Aug 7 12:50:08 BST 2019
Unique Job ID	2b6332c2bff0be4f

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6n2nA_</a>	 Alignment		100.0	32	<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
2	<a href="#">c5b47A_</a>	 Alignment		100.0	27	<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
3	<a href="#">c5b48A_</a>	 Alignment		100.0	29	<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
4	<a href="#">c5c4iA_</a>	 Alignment		100.0	24	<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
5	<a href="#">c6cipD_</a>	 Alignment		100.0	19	<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
6	<a href="#">c2c3yA_</a>	 Alignment		100.0	20	<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 of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
7	<a href="#">c4wbxC_</a>	 Alignment		100.0	34	<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
8	<a href="#">d2c42a1</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> PFOR Pyr module
9	<a href="#">c1yd7A_</a>	 Alignment		100.0	39	<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
10	<a href="#">c3g2eA_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oorc subunit of 2-oxoglutarate:acceptor oxidoreductase; <b>PDBTitle:</b> structure of putative oorc subunit of 2-oxoglutarate:acceptor2 oxidoreductase from campylobacter jejuni
11	<a href="#">d2c42a4</a>	 Alignment		100.0	15	<b>Fold:</b> Pyruvate-ferredoxin oxidoreductase, PFOR, domain III <b>Superfamily:</b> Pyruvate-ferredoxin oxidoreductase, PFOR, domain III <b>Family:</b> Pyruvate-ferredoxin oxidoreductase, PFOR, domain III

12	<a href="#">c3on3B_</a>	Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> keto/oxoacid ferredoxin oxidoreductase, gamma subunit; <b>PDBTitle:</b> the crystal structure of keto/oxoacid ferredoxin oxidoreductase, gamma2 subunit from geobacter sulfurreducens pca
13	<a href="#">c2raaA_</a>	Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate synthase subunit porc; <b>PDBTitle:</b> crystal structure of pyruvate oxidoreductase subunit porc (ec 1.2.7.1)2 (tm0015) from thermotoga maritima at 2.12 a resolution
14	<a href="#">c3ju3A_</a>	Alignment		99.9	25	<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
15	<a href="#">c5c4iB_</a>	Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxalate oxidoreductase subunit delta; <b>PDBTitle:</b> structure of an oxalate oxidoreductase
16	<a href="#">d2c42a3</a>	Alignment		99.8	16	<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
17	<a href="#">d1t9ba2</a>	Alignment		99.8	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
18	<a href="#">d2ez9a2</a>	Alignment		99.8	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
19	<a href="#">d2ji7a2</a>	Alignment		99.7	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
20	<a href="#">c2bp7F_</a>	Alignment		99.7	17	<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)
21	<a href="#">c1ni4D_</a>	Alignment	not modelled	99.7	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
22	<a href="#">c1jscA_</a>	Alignment	not modelled	99.7	18	<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
23	<a href="#">c2ji6B_</a>	Alignment	not modelled	99.7	17	<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
24	<a href="#">c2ag1A_</a>	Alignment	not modelled	99.7	20	<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
25	<a href="#">c1t9dB_</a>	Alignment	not modelled	99.7	18	<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 sulfonylurea herbicide, metsulfuron methyl
26	<a href="#">d1ybha2</a>	Alignment	not modelled	99.7	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
27	<a href="#">c5ahkB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetolactate synthase ii, large subunit; <b>PDBTitle:</b> crystal structure of acetohydroxy acid synthase pf5 from2 pseudomonas protegens
28	<a href="#">c3mosA_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> the structure of human transketolase
						<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding)

29	<a href="#">d1pvda2</a>	Alignment	not modelled	99.7	12	<b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
30	<a href="#">d2dja2</a>	Alignment	not modelled	99.6	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
31	<a href="#">c1ozhD_</a>	Alignment	not modelled	99.6	13	<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.
32	<a href="#">c1um9D_</a>	Alignment	not modelled	99.6	22	<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
33	<a href="#">c1olsB_</a>	Alignment	not modelled	99.6	16	<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
34	<a href="#">c2w93A_</a>	Alignment	not modelled	99.6	12	<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
35	<a href="#">c3dufD_</a>	Alignment	not modelled	99.6	16	<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
36	<a href="#">c3eyaE_</a>	Alignment	not modelled	99.6	17	<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
37	<a href="#">c1zpdA_</a>	Alignment	not modelled	99.6	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
38	<a href="#">c2pgnA_</a>	Alignment	not modelled	99.6	16	<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
39	<a href="#">c2nxwB_</a>	Alignment	not modelled	99.6	21	<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 braslense
40	<a href="#">c1yi1A_</a>	Alignment	not modelled	99.6	23	<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
41	<a href="#">c1powA_</a>	Alignment	not modelled	99.6	18	<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
42	<a href="#">c4rjB_</a>	Alignment	not modelled	99.6	16	<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
43	<a href="#">c1tkcA_</a>	Alignment	not modelled	99.5	18	<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
44	<a href="#">c2panF_</a>	Alignment	not modelled	99.5	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
45	<a href="#">c2o1sC_</a>	Alignment	not modelled	99.5	19	<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
46	<a href="#">c2djiA_</a>	Alignment	not modelled	99.5	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
47	<a href="#">c2q27B_</a>	Alignment	not modelled	99.5	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
48	<a href="#">c2vbiF_</a>	Alignment	not modelled	99.5	19	<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
49	<a href="#">c5hgxA_</a>	Alignment	not modelled	99.5	20	<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
50	<a href="#">c1upaC_</a>	Alignment	not modelled	99.5	17	<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)
51	<a href="#">c2r8pA_</a>	Alignment	not modelled	99.5	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
52	<a href="#">c5vrB_</a>	Alignment	not modelled	99.5	20	<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

53	<a href="#">c2o1xA</a>	Alignment	not modelled	99.5	17	<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
54	<a href="#">c1ik6A</a>	Alignment	not modelled	99.4	20	<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
55	<a href="#">c6ouwA</a>	Alignment	not modelled	99.4	19	<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
56	<a href="#">c2x7jA</a>	Alignment	not modelled	99.4	17	<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
57	<a href="#">c3ey9B</a>	Alignment	not modelled	99.4	19	<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
58	<a href="#">c1ovmC</a>	Alignment	not modelled	99.4	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
59	<a href="#">c3m7iA</a>	Alignment	not modelled	99.4	13	<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
60	<a href="#">c1r9jB</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> transketolase from leishmania mexicana
61	<a href="#">c4q9dA</a>	Alignment	not modelled	99.4	13	<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
62	<a href="#">c3uk1A</a>	Alignment	not modelled	99.4	18	<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
63	<a href="#">c4c7vA</a>	Alignment	not modelled	99.4	22	<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
64	<a href="#">c1itzC</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> maize transketolase in complex with tpp
65	<a href="#">c3komB</a>	Alignment	not modelled	99.4	15	<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
66	<a href="#">c5nd5A</a>	Alignment	not modelled	99.3	17	<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+
67	<a href="#">c3hylB</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase from bacillus anthracis
68	<a href="#">c3rimA</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis transketolase2 (rv1449c)
69	<a href="#">c2vbgB</a>	Alignment	not modelled	99.3	14	<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
70	<a href="#">c3lq1A</a>	Alignment	not modelled	99.3	19	<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="#">c2e6kB</a>	Alignment	not modelled	99.3	23	<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
72	<a href="#">c4k9gB</a>	Alignment	not modelled	99.3	17	<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
73	<a href="#">d1zpdA2</a>	Alignment	not modelled	99.3	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
74	<a href="#">d2ozlb2</a>	Alignment	not modelled	99.2	13	<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
75	<a href="#">d1ozha2</a>	Alignment	not modelled	99.2	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
76	<a href="#">c5essB</a>	Alignment	not modelled	99.2	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)

77	<a href="#">c2v3wC</a>	Alignment	not modelled	99.2	17	<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
78	<a href="#">d1q6za2</a>	Alignment	not modelled	99.2	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
79	<a href="#">c2jlaD</a>	Alignment	not modelled	99.1	16	<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
80	<a href="#">d1umdb2</a>	Alignment	not modelled	99.1	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
81	<a href="#">d2ihta2</a>	Alignment	not modelled	99.0	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
82	<a href="#">d1w85b2</a>	Alignment	not modelled	99.0	12	<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
83	<a href="#">d1ovma2</a>	Alignment	not modelled	99.0	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="#">c2xt6B</a>	Alignment	not modelled	98.8	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)
85	<a href="#">d2bfdb2</a>	Alignment	not modelled	98.8	15	<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
86	<a href="#">d1ik6a2</a>	Alignment	not modelled	98.8	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
87	<a href="#">c2jgdA</a>	Alignment	not modelled	98.8	18	<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)
88	<a href="#">c2yicC</a>	Alignment	not modelled	98.7	19	<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)
89	<a href="#">c2g28A</a>	Alignment	not modelled	98.7	15	<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
90	<a href="#">d1qs0b2</a>	Alignment	not modelled	98.5	12	<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
91	<a href="#">c3ahhA</a>	Alignment	not modelled	98.1	13	<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
92	<a href="#">d2r8oa3</a>	Alignment	not modelled	98.1	18	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
93	<a href="#">d2r8oa1</a>	Alignment	not modelled	98.1	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
94	<a href="#">d2ozlb1</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> Branched-chain alpha-keto acid dehydrogenase Pyr module
95	<a href="#">d1gpua3</a>	Alignment	not modelled	98.0	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
96	<a href="#">d1r9ja3</a>	Alignment	not modelled	98.0	18	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
97	<a href="#">d1itza3</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
98	<a href="#">d1w85b1</a>	Alignment	not modelled	97.8	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
99	<a href="#">d1r9ja1</a>	Alignment	not modelled	97.8	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
100	<a href="#">d1umdb1</a>	Alignment	not modelled	97.8	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 Pyr module
101	<a href="#">d1gpua2</a>	Alignment	not modelled	97.7	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
102	<a href="#">d1itza2</a>	Alignment	not modelled	97.6	18	<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



103	<a href="#">d1qs0a_</a>	Alignment	not modelled	97.6	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 PP module
104	<a href="#">d2bfdb1</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> Branched-chain alpha-keto acid dehydrogenase Pyr module
105	<a href="#">d1qs0b1</a>	Alignment	not modelled	97.4	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
106	<a href="#">c4qoyC_</a>	Alignment	not modelled	97.4	13	<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
107	<a href="#">d2bfdal</a>	Alignment	not modelled	96.8	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
108	<a href="#">d2ozla1</a>	Alignment	not modelled	96.6	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
109	<a href="#">d1umda_</a>	Alignment	not modelled	96.4	12	<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
110	<a href="#">d1w85a_</a>	Alignment	not modelled	96.3	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 PP module
111	<a href="#">d2ieaa3</a>	Alignment	not modelled	96.0	18	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
112	<a href="#">d2r8oa2</a>	Alignment	not modelled	95.8	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
113	<a href="#">d1r9ja2</a>	Alignment	not modelled	95.5	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
114	<a href="#">d1itza1</a>	Alignment	not modelled	95.1	12	<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
115	<a href="#">d1ik6a1</a>	Alignment	not modelled	94.0	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
116	<a href="#">d1gpua1</a>	Alignment	not modelled	93.0	14	<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
117	<a href="#">d2djia3</a>	Alignment	not modelled	91.5	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 PP module
118	<a href="#">c1gg4A_</a>	Alignment	not modelled	82.5	20	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramoylalanyl-d-glutamyl-2,6-diaminopimelate- <b>PDBTitle:</b> crystal structure of escherichia coli udpmurnac-tripeptide d-alanyl-d-2 alanine-adding enzyme (murf) at 2.3 angstrom resolution
119	<a href="#">c1gqqA_</a>	Alignment	not modelled	81.7	19	<b>PDB header:</b> cell wall biosynthesis <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramate-l-alanine ligase; <b>PDBTitle:</b> murc - crystal structure of the apo-enzyme from haemophilus influenzae
120	<a href="#">c5u4uA_</a>	Alignment	not modelled	81.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> mgc81300 protein; <b>PDBTitle:</b> pseudogtpase domain (pg1) of p190rhogap-a