

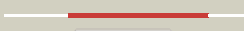


















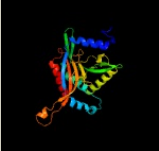











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1248c_(kgd)_1389363_1393058
Date	Wed Jul 31 22:05:34 BST 2019
Unique Job ID	9a0127a4185fcb99

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2xt6B_</a>	 Alignment		100.0	88	<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)
2	<a href="#">c2yicC_</a>	 Alignment		100.0	88	<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)
3	<a href="#">c2jgdA_</a>	 Alignment		100.0	44	<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)
4	<a href="#">c4n72B_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> pyruvate dehydrogenase (dihydrolipoiltransacetylase) <b>PDBTitle:</b> catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
5	<a href="#">d1b5sa_</a>	 Alignment		100.0	25	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
6	<a href="#">d1dpba_</a>	 Alignment		100.0	21	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
7	<a href="#">c2ii4C_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> lipoamide acyltransferase component of branched-chain <b>PDBTitle:</b> crystal structure of a cubic core of the dihydrolipoamide2 acyltransferase (e2b) component in the branched-chain alpha-ketoacid3 dehydrogenase complex (bckdc), coenzyme a-bound form
8	<a href="#">c3i60A_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> branched-chain alpha-keto acid dehydrogenase; <b>PDBTitle:</b> crystal structure of branched-chain alpha-keto acid dehydrogenase2 subunit e2 from mycobacterium tuberculosis
9	<a href="#">c3b8kA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydrolipoillysine-residue acetyltransferase; <b>PDBTitle:</b> structure of the truncated human dihydrolipoil acetyltransferase (e2)
10	<a href="#">d1scza_</a>	 Alignment		100.0	27	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
11	<a href="#">c6h60A_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component, mitochondrial; <b>PDBTitle:</b> pseudo-atomic structural model of the e3bp component of the human2 pyruvate dehydrogenase multienzyme complex

12	<a href="#">c3maeA_</a>	Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-oxoisovalerate dehydrogenase e2 component, <b>PDBTitle:</b> crystal structure of probable dihydrolipoamide acetyltransferase from <i>listeria monocytogenes</i> 4b f2365
13	<a href="#">c3rqcB_</a>	Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable lipoamide acyltransferase; <b>PDBTitle:</b> crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from <i>thermoplasma acidophilum</i>
14	<a href="#">d1umda_</a>	Alignment		100.0	19	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
15	<a href="#">c1olsB_</a>	Alignment		100.0	20	<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
16	<a href="#">d2ozla1</a>	Alignment		100.0	19	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
17	<a href="#">d1q23a_</a>	Alignment		100.0	12	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
18	<a href="#">c3mosA_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> the structure of human transketolase
19	<a href="#">d3claa_</a>	Alignment		100.0	12	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
20	<a href="#">c2bp7F_</a>	Alignment		100.0	21	<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 <i>pseudomonas putida</i> branched-chain2 dehydrogenase (e1)
21	<a href="#">c1ni4D_</a>	Alignment	not modelled	100.0	11	<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="#">c3dufD_</a>	Alignment	not modelled	100.0	19	<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
23	<a href="#">c1um9D_</a>	Alignment	not modelled	100.0	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 <i>thermus2 thermophilus</i> hb8 in apo-form
24	<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 <i>deinococcus2 radiodurans</i>
25	<a href="#">c4c7vA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> apo transketolase from <i>lactobacillus salivarius</i> at 2.2a resolution
26	<a href="#">c6ouwA_</a>	Alignment	not modelled	100.0	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 (dxps) from <i>deinococcus2 radiodurans</i> with enamine intermediate bound
27	<a href="#">d1w85a_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
28	<a href="#">c1itzC_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> maize transketolase in complex with tpp
						<b>PDB header:</b> transferase

29	<a href="#">c2o1sC_</a>	Alignment	not modelled	100.0	20	<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) from <i>Escherichia coli</i>
30	<a href="#">c1ik6A_</a>	Alignment	not modelled	100.0	21	<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 <i>Pyrobaculum aerophilum</i>
31	<a href="#">d1qs0b1</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> Branched-chain alpha-keto acid dehydrogenase Pyr module
32	<a href="#">c5vrB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of a transketolase from <i>Neisseria gonorrhoeae</i>
33	<a href="#">c1tkcA_</a>	Alignment	not modelled	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
34	<a href="#">d1qs0a_</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> Branched-chain alpha-keto acid dehydrogenase PP module
35	<a href="#">d2bfdA1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
36	<a href="#">c2i9dC_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> chloramphenicol acetyltransferase
37	<a href="#">c2r8pA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase 1; <b>PDBTitle:</b> transketolase from <i>E. coli</i> in complex with substrate d-fructose-6-2 phosphate
38	<a href="#">c3hylB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase from <i>Bacillus anthracis</i>
39	<a href="#">c2e6kB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> x-ray structure of <i>Thermus thermophilus</i> hb8 tt0505
40	<a href="#">c5nd5A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase from <i>Chlamydomonas reinhardtii</i> in2 complex with tpp and mg2+
41	<a href="#">c3m7iA_</a>	Alignment	not modelled	100.0	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
42	<a href="#">c3rimA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of <i>Mycobacterium tuberculosis</i> transketolase2 (rv1449c)
43	<a href="#">c5hgxA_</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 transketolase mutant - h261f from <i>Pichia stipitis</i>
44	<a href="#">d2bfdb1</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> Branched-chain alpha-keto acid dehydrogenase Pyr module
45	<a href="#">c3uk1A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of a transketolase from <i>Burkholderia thailandensis</i> 2 with an oxidized cysteinesulfonic acid in the active site
46	<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 <i>Leishmania mexicana</i>
47	<a href="#">d2ozlb1</a>	Alignment	not modelled	100.0	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
48	<a href="#">d1w85b1</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> Branched-chain alpha-keto acid dehydrogenase Pyr module
49	<a href="#">c3komB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of apo transketolase from <i>Francisella tularensis</i>
50	<a href="#">d1umdb1</a>	Alignment	not modelled	99.9	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
51	<a href="#">d1ik6a1</a>	Alignment	not modelled	99.9	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 Pyr module
52	<a href="#">c2g28A_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase e1 component; <b>PDBTitle:</b> <i>E. coli</i> pyruvate dehydrogenase h407a variant2 phosphonolactylthiamin diphosphate complex
53	<a href="#">d2r8oa2</a>	Alignment	not modelled	99.5	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
54	<a href="#">d1gpua1</a>	Alignment	not modelled	99.5	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
						<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose 5-phosphate/fructose 6-

55	<a href="#">c3ahhA</a>	Alignment	not modelled	99.4	14	phosphate phosphoketolase; <b>PDBTitle:</b> h142a mutant of phosphoketolase from bifidobacterium breve complexed2 with acetyl thiamine diphosphate
56	<a href="#">d1r9ja2</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like PP module
57	<a href="#">d1itza1</a>	Alignment	not modelled	99.4	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
58	<a href="#">d2r8oa1</a>	Alignment	not modelled	99.3	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
59	<a href="#">d1qs0b2</a>	Alignment	not modelled	99.3	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
60	<a href="#">d2bfdb2</a>	Alignment	not modelled	99.3	10	<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
61	<a href="#">d1r9ja1</a>	Alignment	not modelled	99.2	16	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
62	<a href="#">d1umdb2</a>	Alignment	not modelled	99.2	16	<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
63	<a href="#">d1ik6a2</a>	Alignment	not modelled	99.2	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
64	<a href="#">d2ozlb2</a>	Alignment	not modelled	99.1	8	<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
65	<a href="#">d1itza2</a>	Alignment	not modelled	99.1	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
66	<a href="#">c5c4iA</a>	Alignment	not modelled	99.1	18	<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
67	<a href="#">d1w85b2</a>	Alignment	not modelled	99.1	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
68	<a href="#">d1gpua2</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> TK-like Pyr module
69	<a href="#">c5b48A</a>	Alignment	not modelled	98.9	14	<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
70	<a href="#">c4qoyC</a>	Alignment	not modelled	98.9	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
71	<a href="#">c5b47A</a>	Alignment	not modelled	98.8	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
72	<a href="#">c4wbxC</a>	Alignment	not modelled	98.8	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
73	<a href="#">c2c3yA</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase; <b>PDBTitle:</b> crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
74	<a href="#">c6n2nA</a>	Alignment	not modelled	98.8	12	<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
75	<a href="#">c6cipD</a>	Alignment	not modelled	98.8	15	<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
76	<a href="#">d2djia3</a>	Alignment	not modelled	98.7	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
77	<a href="#">c2djiA</a>	Alignment	not modelled	98.6	22	<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
78	<a href="#">c3ju3A</a>	Alignment	not modelled	98.0	13	<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
79	<a href="#">d1t9ba3</a>	Alignment	not modelled	97.7	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

80	<a href="#">d1jsca3</a>	Alignment	not modelled	97.6	22	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
81	<a href="#">d2c42a3</a>	Alignment	not modelled	97.6	11	<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
82	<a href="#">c2panF_</a>	Alignment	not modelled	97.4	25	<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
83	<a href="#">d1ybha3</a>	Alignment	not modelled	97.2	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
84	<a href="#">d2ieaa2</a>	Alignment	not modelled	97.1	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
85	<a href="#">d1q6za3</a>	Alignment	not modelled	96.9	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
86	<a href="#">c6n2oB_</a>	Alignment	not modelled	96.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate ferredoxin/ flavodoxin oxidoreductase, beta <b>PDBTitle:</b> 2-oxoglutarate:ferredoxin oxidoreductase from magnetococcus marinus2 with 2-oxoglutarate, coenzyme a and succinyl-coa bound
87	<a href="#">d2ez9a3</a>	Alignment	not modelled	96.9	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
88	<a href="#">d2ihta3</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> Pyruvate oxidase and decarboxylase PP module
89	<a href="#">d1ozha3</a>	Alignment	not modelled	96.4	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
90	<a href="#">d2ji7a3</a>	Alignment	not modelled	96.4	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
91	<a href="#">c3eyaE_</a>	Alignment	not modelled	96.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase [cytochrome]; <b>PDBTitle:</b> structural basis for membrane binding and catalytic2 activation of the peripheral membrane enzyme pyruvate3 oxidase from escherichia coli
92	<a href="#">c1powA_</a>	Alignment	not modelled	96.3	20	<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
93	<a href="#">c1jscA_</a>	Alignment	not modelled	96.2	21	<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
94	<a href="#">c1t9dB_</a>	Alignment	not modelled	96.1	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetolactate synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of yeast acetoxyhydroxyacid synthase in complex with a2 sulfonylurea herbicide, metsulfuron methyl
95	<a href="#">c5ahkB_</a>	Alignment	not modelled	96.1	12	<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
96	<a href="#">d1r9ja3</a>	Alignment	not modelled	96.1	11	<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="#">c4q9dA_</a>	Alignment	not modelled	96.0	15	<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
98	<a href="#">c5essB_</a>	Alignment	not modelled	96.0	17	<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)
99	<a href="#">c3ey9B_</a>	Alignment	not modelled	96.0	18	<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
100	<a href="#">d1itza3</a>	Alignment	not modelled	95.8	11	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
101	<a href="#">d1gpua3</a>	Alignment	not modelled	95.7	15	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
102	<a href="#">d1pvda3</a>	Alignment	not modelled	95.6	12	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
103	<a href="#">c5b46B_</a>	Alignment	not modelled	95.2	19	<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
104	<a href="#">c2nxwB_</a>	Alignment	not modelled	95.1	17	<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



105	<a href="#">c2v3wC</a>	Alignment	not modelled	95.0	20	<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
106	<a href="#">c4rjIB</a>	Alignment	not modelled	95.0	19	<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
107	<a href="#">c2pgnA</a>	Alignment	not modelled	94.9	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
108	<a href="#">c1upaC</a>	Alignment	not modelled	94.7	13	<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)
109	<a href="#">c2jlaD</a>	Alignment	not modelled	94.5	15	<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
110	<a href="#">d1ovma3</a>	Alignment	not modelled	94.4	16	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
111	<a href="#">c2q27B</a>	Alignment	not modelled	94.1	22	<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
112	<a href="#">c4k9qB</a>	Alignment	not modelled	94.1	18	<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
113	<a href="#">c2ag1A</a>	Alignment	not modelled	93.9	25	<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
114	<a href="#">d2r8oa3</a>	Alignment	not modelled	93.7	8	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
115	<a href="#">c2ji6B</a>	Alignment	not modelled	93.7	23	<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
116	<a href="#">c1yi1A</a>	Alignment	not modelled	93.4	21	<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
117	<a href="#">c1yd7A</a>	Alignment	not modelled	92.3	24	<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
118	<a href="#">c3lq1A</a>	Alignment	not modelled	90.5	21	<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
119	<a href="#">c1ovmC</a>	Alignment	not modelled	89.6	19	<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
120	<a href="#">d2c42a1</a>	Alignment	not modelled	89.2	12	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> PFOR Pyr module