

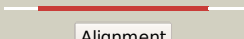

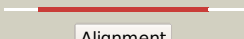



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2496c_(pdhB)_2809946_2810992
Date	Wed Aug 7 12:50:12 BST 2019
Unique Job ID	da5ad71a0d4b507e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1olsB_	 Alignment		100.0	38	PDB header: oxidoreductase Chain: B; PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: roles of his291-alpha and his146-beta' in the reductive acylation2 reaction catalyzed by human branched-chain alpha-ketoacid3 dehydrogenase
2	c1ni4D_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: D; PDB Molecule: pyruvate dehydrogenase e1 component: beta PDBTitle: human pyruvate dehydrogenase
3	c2bp7F_	 Alignment		100.0	46	PDB header: oxidoreductase Chain: F; PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
4	c3dufD_	 Alignment		100.0	48	PDB header: oxidoreductase/transferase Chain: D; PDB Molecule: pyruvate dehydrogenase e1 component subunit beta; PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
5	c1um9D_	 Alignment		100.0	48	PDB header: oxidoreductase Chain: D; PDB Molecule: 2-oxo acid dehydrogenase beta subunit; PDBTitle: branched-chain 2-oxo acid dehydrogenase (e1) from thermus2 thermophilus hb8 in apo-form
6	c1ik6A_	 Alignment		100.0	48	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate dehydrogenase; PDBTitle: 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum
7	c6ouwA_	 Alignment		100.0	19	PDB header: transferase Chain: A; PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxps) from deinococcus2 radiodurans with enamine intermediate bound
8	c2o1xA_	 Alignment		100.0	19	PDB header: transferase Chain: A; PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from deinococcus2 radiodurans
9	c2o1sC_	 Alignment		100.0	22	PDB header: transferase Chain: C; PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 escherichia coli
10	c3mosA_	 Alignment		100.0	18	PDB header: transferase Chain: A; PDB Molecule: transketolase; PDBTitle: the structure of human transketolase
11	c2r8pA_	 Alignment		100.0	13	PDB header: transferase Chain: A; PDB Molecule: transketolase 1; PDBTitle: transketolase from e. coli in complex with substrate d-fructose-6-2 phosphate

12	c1tkcA_	Alignment		100.0	14	PDB header: transferase Chain: A; PDB Molecule: transketolase; PDBTitle: specificity of coenzyme binding in thiamin diphosphate2 dependent enzymes: crystal structures of yeast3 transketolase in complex with analogs of thiamin4 diphosphate
13	c5nd5A_	Alignment		100.0	15	PDB header: transferase Chain: A; PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from chlamydomonas reinhardtii in2 complex with tpp and mg2+
14	c4c7vA_	Alignment		100.0	11	PDB header: transferase Chain: A; PDB Molecule: transketolase; PDBTitle: apo transketolase from lactobacillus salivarius at 2.2a resolution
15	c3rimA_	Alignment		100.0	14	PDB header: transferase Chain: A; PDB Molecule: transketolase; PDBTitle: crystal structure of mycobacterium tuberculosis transketolase2 (rv1449c)
16	c3hylB_	Alignment		100.0	14	PDB header: transferase Chain: B; PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from bacillus anthracis
17	c5hgxA_	Alignment		100.0	14	PDB header: transferase Chain: A; PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase mutant - h261f from pichia stipitis
18	c1r9jB_	Alignment		100.0	15	PDB header: transferase Chain: B; PDB Molecule: transketolase; PDBTitle: transketolase from leishmania mexicana
19	c3komB_	Alignment		100.0	15	PDB header: transferase Chain: B; PDB Molecule: transketolase; PDBTitle: crystal structure of apo transketolase from francisella tularensis
20	c3uk1A_	Alignment		100.0	14	PDB header: transferase Chain: A; PDB Molecule: transketolase; PDBTitle: crystal structure of a transketolase from burkholderia thailandensis2 with an oxidized cysteinesulfonic acid in the active site
21	c2e6kB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B; PDB Molecule: transketolase; PDBTitle: x-ray structure of thermus thermophilus hb8 tt0505
22	c1itzC_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: C; PDB Molecule: transketolase; PDBTitle: maize transketolase in complex with tpp
23	c5vrB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B; PDB Molecule: transketolase; PDBTitle: crystal structure of a transketolase from neisseria gonorrhoeae
24	c3m7iA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A; PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase in complex with thiamine2 diphosphate, ribose-5-phosphate(pyranose form) and magnesium ion
25	d1qs0b1	Alignment	not modelled	100.0	45	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
26	d2ozl1	Alignment	not modelled	100.0	33	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
27	d1w85b1	Alignment	not modelled	100.0	53	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
28	d1umdb1	Alignment	not modelled	100.0	55	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
29	c2g28A_	Alignment	not modelled	100.0	10	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate dehydrogenase e1 component; PDBTitle: e. coli pyruvate dehydrogenase h407a variant2

						phosphonolactylthiamin diphosphate complex
30	d2bfdb1	Alignment	not modelled	100.0	40	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
31	c2xt6B	Alignment	not modelled	100.0	18	PDB header: lyase Chain: B: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
32	c2yicC	Alignment	not modelled	100.0	18	PDB header: lyase Chain: C: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of the suca domain of mycobacterium smegmatis2 alpha-ketoglutarate decarboxylase (triclinic form)
33	c2jgdA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoglutarate dehydrogenase e1 component; PDBTitle: e. coli 2-oxoglutarate dehydrogenase (e1o)
34	c4qoyC	Alignment	not modelled	100.0	10	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase e1 component; PDBTitle: 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
35	d2r8oa1	Alignment	not modelled	100.0	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
36	d1ik6a1	Alignment	not modelled	100.0	52	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
37	d1r9ja1	Alignment	not modelled	100.0	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
38	d1itza2	Alignment	not modelled	100.0	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
39	d1gpua2	Alignment	not modelled	100.0	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
40	c3ahhA	Alignment	not modelled	100.0	11	PDB header: lyase Chain: A: PDB Molecule: xylulose 5-phosphate/fructose 6-phosphate phosphoketolase; PDBTitle: h142a mutant of phosphoketolase from bifidobacterium breve complexed2 with acetyl thiamine diphosphate
41	d2bfdb2	Alignment	not modelled	100.0	36	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
42	d1lumdb2	Alignment	not modelled	100.0	39	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
43	d1qs0b2	Alignment	not modelled	100.0	47	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
44	d2ozlb2	Alignment	not modelled	100.0	35	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
45	d1w85b2	Alignment	not modelled	100.0	40	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
46	d2ieaa1	Alignment	not modelled	100.0	10	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
47	d1ik6a2	Alignment	not modelled	100.0	45	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
48	c4wbxC	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-keto acid:ferredoxin oxidoreductase subunit alpha; PDBTitle: conserved hypothetical protein pf1771 from pyrococcus furiosus solved2 by sulfur sad using swiss light source data
49	c5c4iA	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxalate oxidoreductase subunit alpha; PDBTitle: structure of an oxalate oxidoreductase
50	c5b47A	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase alpha subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 2 from sulfolobus tokodai-2 pyruvate complex
51	d2r8oa3	Alignment	not modelled	99.8	13	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
52	d1itza3	Alignment	not modelled	99.8	12	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
53	d1r9ja3	Alignment	not modelled	99.8	15	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
54	c6n2nA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate flavodoxin/ferredoxin oxidoreductase domain PDBTitle: crystal structure of 2-oxoglutarate:ferredoxin

						oxidoreductase from2 magnetococcus marinus
55	d1gpua3	Alignment	not modelled	99.7	12	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
56	c2c3yA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
57	c5b48A	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase alpha subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 1 from sulfolobus tokodai
58	c6cipD	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpp bound
59	c3ju3A	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; PDBTitle: crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
60	d2ieaa3	Alignment	not modelled	99.6	11	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
61	d2c42a3	Alignment	not modelled	99.2	13	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
62	c1powA	Alignment	not modelled	98.1	13	PDB header: oxidoreductase(oxygen as acceptor) Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
63	c3ey9B	Alignment	not modelled	98.1	15	PDB header: oxidoreductase Chain: B: PDB Molecule: pyruvate dehydrogenase [cytochrome]; PDBTitle: structural basis for membrane binding and catalytic activation of the2 peripheral membrane enzyme pyruvate oxidase from escherichia coli
64	c1t9dB	Alignment	not modelled	98.0	16	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase, mitochondrial; PDBTitle: crystal structure of yeast acetohydroxyacid synthase in complex with a2 sulfonyleurea herbicide, metsulfuron methyl
65	c3eyaE	Alignment	not modelled	98.0	13	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase [cytochrome]; PDBTitle: structural basis for membrane binding and catalytic2 activation of the peripheral membrane enzyme pyruvate3 oxidase from escherichia coli
66	c1yi1A	Alignment	not modelled	98.0	14	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonyleurea herbicide, tribenuron methyl
67	d2c42a1	Alignment	not modelled	97.9	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR Pyr module
68	d1pvda2	Alignment	not modelled	97.9	10	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
69	c2x7jA	Alignment	not modelled	97.8	13	PDB header: transferase Chain: A: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
70	c2djiA	Alignment	not modelled	97.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
71	c2q27B	Alignment	not modelled	97.8	11	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from escherichia coli
72	c5ahkB	Alignment	not modelled	97.8	11	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase ii, large subunit; PDBTitle: crystal structure of acetohydroxy acid synthase pf5 from2 pseudomonas protegens
73	c2nxwB	Alignment	not modelled	97.8	16	PDB header: lyase Chain: B: PDB Molecule: phenyl-3-pyruvate decarboxylase; PDBTitle: crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
74	c2ji6B	Alignment	not modelled	97.8	13	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: x-ray structure of oxalyl-coa decarboxylase in complex with 3-deaza-2 thdp and oxalyl-coa
75	c2ag1A	Alignment	not modelled	97.8	16	PDB header: lyase Chain: A: PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
76	c2vbgB	Alignment	not modelled	97.7	12	PDB header: lyase Chain: B: PDB Molecule: branched-chain alpha-ketoacid decarboxylase; PDBTitle: the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
77	c1upaC	Alignment	not modelled	97.7	15	PDB header: synthase Chain: C: PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
78	d1zpa2	Alignment	not modelled	97.7	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module

79	c2vbiF_	Alignment	not modelled	97.7	13	PDB header: lyase Chain: F; PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter pasteurianus
80	c2v3wC_	Alignment	not modelled	97.7	13	PDB header: lyase Chain: C; PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase variant l461a2 from pseudomonas putida
81	c2pgnA_	Alignment	not modelled	97.6	12	PDB header: hydrolase Chain: A; PDB Molecule: cyclohexane-1,2-dione hydrolase (cdh); PDBTitle: the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
82	d2djia2	Alignment	not modelled	97.6	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
83	d2ez9a2	Alignment	not modelled	97.6	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
84	c2panF_	Alignment	not modelled	97.6	13	PDB header: lyase Chain: F; PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
85	c1jscA_	Alignment	not modelled	97.5	13	PDB header: lyase Chain: A; PDB Molecule: acetoxyacid synthase; PDBTitle: crystal structure of the catalytic subunit of yeast2 acetoxyacid synthase: a target for herbicidal3 inhibitors
86	d1q6za2	Alignment	not modelled	97.4	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
87	d1t9ba2	Alignment	not modelled	97.4	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
88	c4k9qB_	Alignment	not modelled	97.4	14	PDB header: lyase Chain: B; PDB Molecule: benzoylformate decarboxylase; PDBTitle: the crystal structure of benzoylformate decarboxylase from2 polynucleobacter necessarius
89	c4rjB_	Alignment	not modelled	97.3	14	PDB header: lyase Chain: B; PDB Molecule: acetolactate synthase; PDBTitle: acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii
90	d2ji7a3	Alignment	not modelled	97.3	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
91	d1ybha2	Alignment	not modelled	97.3	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
92	c2w93A_	Alignment	not modelled	97.3	9	PDB header: lyase Chain: A; PDB Molecule: pyruvate decarboxylase isozyme 1; PDBTitle: crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate pyruvamide
93	d1jsca3	Alignment	not modelled	97.2	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
94	d1ovma2	Alignment	not modelled	97.2	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
95	c3lq1A_	Alignment	not modelled	96.9	11	PDB header: transferase Chain: A; PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- PDBTitle: crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene 1-2 carboxylic acid synthase/2-oxoglutarate decarboxylase from listeria3 monocytogenes str. 4b f2365
96	d1t9ba3	Alignment	not modelled	96.9	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
97	c1ozhD_	Alignment	not modelled	96.7	12	PDB header: lyase Chain: D; PDB Molecule: acetolactate synthase, catabolic; PDBTitle: the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusual3 intermediate.
98	c1yd7A_	Alignment	not modelled	96.5	19	PDB header: oxidoreductase Chain: A; PDB Molecule: 2-keto acid:ferredoxin oxidoreductase subunit alpha; PDBTitle: conserved hypothetical protein pfu-1647980-001 from pyrococcus2 furiosus
99	c2jlaD_	Alignment	not modelled	96.5	11	PDB header: transferase Chain: D; PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase - semet3 protein
100	c4q9dA_	Alignment	not modelled	96.5	15	PDB header: lyase Chain: A; PDB Molecule: benzoylformate decarboxylase; PDBTitle: x-ray structure of a putative thiamin diphosphate-dependent enzyme2 isolated from mycobacterium smegmatis
101	c1zpdA_	Alignment	not modelled	96.4	14	PDB header: alcohol fermentation Chain: A; PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from zymomonas mobilis
102	d1ozha3	Alignment	not modelled	96.2	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
103	d2ji7a2	Alignment	not modelled	96.1	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding)

						Family: Pyruvate oxidase and decarboxylase Pyr module
104	d1ozha2	Alignment	not modelled	96.1	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
105	d2ihia2	Alignment	not modelled	95.9	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
106	c5b46B	Alignment	not modelled	95.4	18	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase beta subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 2 from sulfolobus tokodai - ligand2 free form
107	d1ybha3	Alignment	not modelled	95.0	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
108	c5essB	Alignment	not modelled	94.6	19	PDB header: transferase Chain: B: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- PDBTitle: crystal structure of m. tuberculosis mend bound to mg2+ and covalent2 intermediate i (a thdp and decarboxylated 2-oxoglutarate adduct)
109	c1ovmC	Alignment	not modelled	93.8	14	PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
110	d1q6za3	Alignment	not modelled	92.7	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
111	d2ez9a3	Alignment	not modelled	85.0	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
112	d2djia3	Alignment	not modelled	83.8	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
113	c6n2oB	Alignment	not modelled	82.4	11	PDB header: oxidoreductase Chain: B: PDB Molecule: pyruvate ferredoxin/flavodoxin oxidoreductase, beta PDBTitle: 2-oxoglutarate:ferredoxin oxidoreductase from magnetococcus marinus2 with 2-oxoglutarate, coenzyme a and succinyl-coa bound
114	d1uxya1	Alignment	not modelled	81.9	12	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
115	d2ozla1	Alignment	not modelled	75.5	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
116	d1vmea1	Alignment	not modelled	75.2	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
117	d1zpa3	Alignment	not modelled	73.6	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
118	d2ihia3	Alignment	not modelled	73.4	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
119	d1ovma3	Alignment	not modelled	71.7	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
120	c2eguA	Alignment	not modelled	69.8	15	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of o-acetylserine sulphydrase from geobacillus2 kaustophilus hta426