


















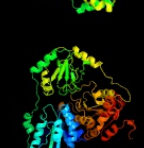

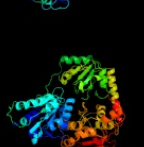











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0555_(menD)_646301_647965
Date	Fri Jul 26 01:50:10 BST 2019
Unique Job ID	c9fda3024501ccb4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5essB_	 Alignment		100.0	100	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)
2	c2x7jA_	 Alignment		100.0	32	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
3	c1powA_	 Alignment		100.0	15	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
4	c3ey9B_	 Alignment		100.0	17	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
5	c2djiA_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
6	c4rjB_	 Alignment		100.0	19	PDB header: lyase Chain: B: PDB Molecule: acetolactate synthase; PDBTitle: acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii
7	c2jlaD_	 Alignment		100.0	28	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
8	c2pgnA_	 Alignment		100.0	16	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
9	c1yi1A_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
10	c2panF_	 Alignment		100.0	17	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
11	c1ozhD_	 Alignment		100.0	19	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.

12	c4k9qB_	Alignment		100.0	20	PDB header: lyase Chain: B: PDB Molecule: benzoylformate decarboxylase; PDBTitle: the crystal structure of benzoylformate decarboxylase from <i>Pseudomonas putida</i>
13	c1t9dB_	Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase, mitochondrial; PDBTitle: crystal structure of yeast acetohydroxyacid synthase in complex with α 2 sulfonyleurea herbicide, metsulfuron methyl
14	c2v3wC_	Alignment		100.0	16	PDB header: lyase Chain: C: PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase variant I461A2 from <i>Pseudomonas putida</i>
15	c2ag1A_	Alignment		100.0	16	PDB header: lyase Chain: A: PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
16	c5ahkB_	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase ii, large subunit; PDBTitle: crystal structure of acetohydroxy acid synthase pf5 from <i>Pseudomonas protegens</i>
17	c1zpdA_	Alignment		100.0	18	PDB header: alcohol fermentation Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from <i>Zymomonas mobilis</i>
18	c3lq1A_	Alignment		100.0	31	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 <i>Listeria monocytogenes</i> str. 4b f2365
19	c3eyaE_	Alignment		100.0	18	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 <i>Escherichia coli</i>
20	c2ji6B_	Alignment		100.0	16	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
21	c1jscA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: acetohydroxy-acid synthase; PDBTitle: crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
22	c2vbiF_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from <i>Acetobacter pasteurianus</i>
23	c4q9dA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: benzoylformate decarboxylase; PDBTitle: x-ray structure of a putative thiamin diphosphate-dependent enzyme2 isolated from <i>Mycobacterium smegmatis</i>
24	c2q27B_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from <i>Escherichia coli</i>
25	c2vbgB_	Alignment	not modelled	100.0	15	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 <i>Lactococcus lactis</i> with 2r-1-3 hydroxyethyl-deazathdp
26	c1upaC_	Alignment	not modelled	100.0	20	PDB header: synthase Chain: C: PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from <i>Streptomyces clavuligerus</i> (semet structure)
27	c1ovmC_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from <i>Enterobacter cloacae</i>
						PDB header: lyase Chain: A: PDB Molecule: pyruvate decarboxylase isozyme 1;

28	c2w93A_	Alignment	not modelled	100.0	14	PDBTitle: crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate pyruvamide
29	c2nxwB_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: phenyl-3-pyruvate decarboxylase; PDBTitle: crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasileense
30	d1q6za2	Alignment	not modelled	100.0	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
31	d2djia2	Alignment	not modelled	100.0	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
32	d1ozha2	Alignment	not modelled	100.0	24	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
33	d1ybha2	Alignment	not modelled	100.0	25	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
34	d1zpa2	Alignment	not modelled	100.0	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
35	d2ji7a2	Alignment	not modelled	100.0	24	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
36	d2ihta2	Alignment	not modelled	100.0	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
37	d1t9ba2	Alignment	not modelled	100.0	25	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
38	d1pvda2	Alignment	not modelled	100.0	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
39	d2ez9a2	Alignment	not modelled	100.0	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
40	d1lovma2	Alignment	not modelled	100.0	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
41	d2ez9a3	Alignment	not modelled	100.0	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
42	d1ybha3	Alignment	not modelled	100.0	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
43	d1ozha3	Alignment	not modelled	100.0	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
44	d2djia3	Alignment	not modelled	100.0	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
45	d1t9ba3	Alignment	not modelled	100.0	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
46	d1pvda3	Alignment	not modelled	100.0	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
47	d1lovma3	Alignment	not modelled	100.0	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
48	d1zpa3	Alignment	not modelled	100.0	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
49	d2ihta3	Alignment	not modelled	100.0	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
50	d1q6za3	Alignment	not modelled	100.0	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
51	d2ji7a3	Alignment	not modelled	100.0	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
52	d1jsca3	Alignment	not modelled	100.0	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
53	c5b46B_	Alignment	not modelled	99.8	14	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
54	c6n2oB_	Alignment	not modelled	99.8	13	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

55	c4wbxC	Alignment	not modelled	99.7	14	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
56	d2c42a1	Alignment	not modelled	99.6	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR Pyr module
57	c5c4iC	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: C: PDB Molecule: oxalate oxidoreductase subunit beta; PDBTitle: structure of an oxalate oxidoreductase
58	c6n2nA	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate flavodoxin/ferredoxin oxidoreductase domain PDBTitle: crystal structure of 2-oxoglutarate:ferredoxin oxidoreductase from2 magnetococcus marinus
59	c5c4iA	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: oxalate oxidoreductase subunit alpha; PDBTitle: structure of an oxalate oxidoreductase
60	d2ez9a1	Alignment	not modelled	99.4	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
61	d2ji7a1	Alignment	not modelled	99.4	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
62	d2dja1	Alignment	not modelled	99.4	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
63	c5b47A	Alignment	not modelled	99.4	18	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
64	d2bfdal	Alignment	not modelled	99.4	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
65	c5b48A	Alignment	not modelled	99.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase alpha subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 1 from sulfolobus tokodai
66	d1w85a	Alignment	not modelled	99.4	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
67	d2r8oa2	Alignment	not modelled	99.4	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
68	d1umda	Alignment	not modelled	99.3	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
69	d1ybha1	Alignment	not modelled	99.3	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
70	d2ozla1	Alignment	not modelled	99.3	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
71	d1gpua1	Alignment	not modelled	99.2	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
72	d1r9ja2	Alignment	not modelled	99.2	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
73	d1t9ba1	Alignment	not modelled	99.2	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
74	c6cipD	Alignment	not modelled	99.2	12	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpp bound
75	d1ozha1	Alignment	not modelled	99.2	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
76	d1itza1	Alignment	not modelled	99.2	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
77	c2c3yA	Alignment	not modelled	99.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
78	c1yd7A	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-keto acid:ferredoxin oxidoreductase subunit alpha; PDBTitle: conserved hypothetical protein pfu-1647980-001 from pyrococcus2 furiosus
79	d2ihta1	Alignment	not modelled	99.2	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
80	c3mosA	Alignment	not modelled	99.1	18	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: the structure of human transketolase

81	d1q6za1	Alignment	not modelled	99.1	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
82	c3m7iA	Alignment	not modelled	99.1	19	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
83	d1zpdA1	Alignment	not modelled	99.1	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
84	c5nd5A	Alignment	not modelled	99.1	18	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from chlamydomonas reinhardtii in2 complex with tpp and mg2+
85	c2o1xA	Alignment	not modelled	99.0	21	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
86	c3rimA	Alignment	not modelled	99.0	13	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of mycobacterium tuberculosis transketolase2 (rv1449c)
87	c2r8pA	Alignment	not modelled	99.0	17	PDB header: transferase Chain: A: PDB Molecule: transketolase 1; PDBTitle: transketolase from e. coli in complex with substrate d-fructose-6-2 phosphate
88	c4c7vA	Alignment	not modelled	99.0	21	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: apo transketolase from lactobacillus salivarius at 2.2a resolution
89	c3uk1A	Alignment	not modelled	99.0	16	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
90	d1qs0a	Alignment	not modelled	99.0	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
91	c5hqxA	Alignment	not modelled	99.0	16	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase mutant - h261f from pichia stipitis
92	c3hylB	Alignment	not modelled	99.0	15	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from bacillus anthracis
93	c1itzC	Alignment	not modelled	99.0	15	PDB header: transferase Chain: C: PDB Molecule: transketolase; PDBTitle: maize transketolase in complex with tpp
94	c2o1sC	Alignment	not modelled	99.0	25	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
95	d1ovma1	Alignment	not modelled	99.0	5	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
96	c2e6kB	Alignment	not modelled	98.9	22	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: x-ray structure of thermus thermophilus hb8 tt0505
97	c1tkcA	Alignment	not modelled	98.9	18	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
98	c5vrB	Alignment	not modelled	98.9	14	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of a transketolase from neisseria gonorrhoeae
99	c1r9jB	Alignment	not modelled	98.8	13	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: transketolase from leishmania mexicana
100	d2c42a2	Alignment	not modelled	98.8	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module
101	c2g28A	Alignment	not modelled	98.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase e1 component; PDBTitle: e. coli pyruvate dehydrogenase h407a variant2 phosphonolactylthiamin diphosphate complex
102	c6ouwA	Alignment	not modelled	98.8	24	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
103	d1pvdA1	Alignment	not modelled	98.7	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
104	d2ieaa2	Alignment	not modelled	98.7	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
105	c3komB	Alignment	not modelled	98.7	14	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of apo transketolase from francisella tularensis
106	c4qoyC	Alignment	not modelled	98.6	15	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
107	c3ahhA_	Alignment	not modelled	98.4	12	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
108	c5ol2D_	Alignment	not modelled	98.3	17	PDB header: flavoprotein Chain: D: PDB Molecule: electron transfer flavoprotein large subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
109	c3cf4G_	Alignment	not modelled	98.1	16	PDB header: oxidoreductase Chain: G: PDB Molecule: acetyl-coa decarboxylase/synthase epsilon subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex
110	d1gpua2	Alignment	not modelled	97.5	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
111	c2yicC_	Alignment	not modelled	97.5	12	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)
112	d2r8oa1	Alignment	not modelled	97.4	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
113	c2jgdA_	Alignment	not modelled	97.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoglutarate dehydrogenase e1 component; PDBTitle: e. coli 2-oxoglutarate dehydrogenase (e1o)
114	d1r9ja1	Alignment	not modelled	97.1	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
115	d1itza2	Alignment	not modelled	97.0	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
116	c4l2iA_	Alignment	not modelled	96.7	11	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
117	c2xt6B_	Alignment	not modelled	95.4	13	PDB header: lyase Chain: B: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
118	c2bp7F_	Alignment	not modelled	92.1	15	PDB header: oxidoreductase Chain: F: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
119	c1olsB_	Alignment	not modelled	91.9	11	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
120	d1w85b1	Alignment	not modelled	85.9	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module