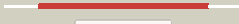



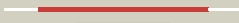





















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2497c_(pdhA)_2811003_2812106
Date	Wed Aug 7 12:50:12 BST 2019
Unique Job ID	58f97dcdcf8fa4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qs0a_	 Alignment		100.0	32	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
2	d1umda_	 Alignment		100.0	40	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
3	d1w85a_	 Alignment		100.0	36	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
4	d2bfdal	 Alignment		100.0	35	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
5	d2ozla1	 Alignment		100.0	26	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
6	c2yicC	 Alignment		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)
7	c2xt6B	 Alignment		100.0	17	PDB header: lyase Chain: B: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
8	c2jgdA	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoglutarate dehydrogenase e1 component; PDBTitle: e. coli 2-oxoglutarate dehydrogenase (e1o)
9	d1gpua1	 Alignment		100.0	21	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
10	d2r8oa2	 Alignment		100.0	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
11	d1r9ja2	 Alignment		100.0	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module

12	d1itza1	Alignment		100.0	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
13	c4c7vA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: apo transketolase from lactobacillus salivarius at 2.2a resolution
14	c5nd5A_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from chlamydomonas reinhardtii in2 complex with tpp and mg2+
15	c5vrbB_	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of a transketolase from neisseria gonorrhoeae
16	c3mosA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: the structure of human transketolase
17	c1itzC_	Alignment		100.0	18	PDB header: transferase Chain: C: PDB Molecule: transketolase; PDBTitle: maize transketolase in complex with tpp
18	c3rimA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of mycobacterium tuberculosis transketolase2 (rv1449c)
19	c1tkcA_	Alignment		100.0	20	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
20	c5hgxA_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase mutant - h261f from pichia stipitis
21	c3m7iA_	Alignment	not modelled	100.0	17	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
22	c2r8pA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: transketolase 1; PDBTitle: transketolase from e. coli in complex with substrate d-fructose-6-2 phosphate
23	c1r9jB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: transketolase from leishmania mexicana
24	c3uk1A_	Alignment	not modelled	100.0	24	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
25	c2e6kB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: x-ray structure of thermus thermophilus hb8 tt0505
26	c3hylB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from bacillus anthracis
27	c2o1xA_	Alignment	not modelled	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
28	c3komB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of apo transketolase from francisella tularensis

29	c2o1sC	Alignment	not modelled	100.0	18	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
30	c6ouwA	Alignment	not modelled	100.0	18	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
31	c2g28A	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase e1 component; PDBTitle: e. coli pyruvate dehydrogenase h407a variant2 phosphonolactylthiamin diphosphate complex
32	d2ieaa2	Alignment	not modelled	99.9	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
33	c4qoyC	Alignment	not modelled	99.9	18	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
34	d2djia3	Alignment	not modelled	99.9	21	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
35	c2djiA	Alignment	not modelled	99.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
36	c3ahhA	Alignment	not modelled	99.9	15	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
37	c1powA	Alignment	not modelled	99.8	23	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
38	d1t9ba3	Alignment	not modelled	99.8	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
39	d1jsca3	Alignment	not modelled	99.7	21	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
40	c4k9qB	Alignment	not modelled	99.7	20	PDB header: lyase Chain: B: PDB Molecule: benzoylformate decarboxylase; PDBTitle: the crystal structure of benzoylformate decarboxylase from2 polynucleobacter necessarius
41	c4q9dA	Alignment	not modelled	99.7	28	PDB header: lyase Chain: A: PDB Molecule: benzoylformate decarboxylase; PDBTitle: x-ray structure of a putative thiamin diphosphate- dependent enzyme2 isolated from mycobacterium smegmatis
42	d2ez9a3	Alignment	not modelled	99.7	24	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
43	d1ybha3	Alignment	not modelled	99.7	28	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
44	d1q6za3	Alignment	not modelled	99.7	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
45	c2panF	Alignment	not modelled	99.6	23	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
46	d1ozha3	Alignment	not modelled	99.6	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
47	c6n2oB	Alignment	not modelled	99.6	18	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
48	d2ihta3	Alignment	not modelled	99.6	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
49	c3eyaE	Alignment	not modelled	99.6	26	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
50	c4rjJB	Alignment	not modelled	99.6	22	PDB header: lyase Chain: B: PDB Molecule: acetolactate synthase; PDBTitle: acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii
51	c1t9dB	Alignment	not modelled	99.6	19	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
52	c1yi1A	Alignment	not modelled	99.6	26	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
53	c3ey9B	Alignment	not modelled	99.6	25	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
54	c5ahkB_	Alignment	not modelled	99.6	18	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase ii, large subunit; PDBTitle: crystal structure of acetohydroxy acid synthase pf5 from2 pseudomonas protegens
55	c1upaC_	Alignment	not modelled	99.5	24	PDB header: synthase Chain: C: PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
56	c1jscA_	Alignment	not modelled	99.5	21	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
57	c2ag1A_	Alignment	not modelled	99.5	22	PDB header: lyase Chain: A: PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
58	d2ji7a3	Alignment	not modelled	99.5	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
59	d1pvda3	Alignment	not modelled	99.5	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
60	c2v3wC_	Alignment	not modelled	99.5	23	PDB header: lyase Chain: C: PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase variant l461a2 from pseudomonas putida
61	d1ovma3	Alignment	not modelled	99.5	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
62	c2vbgB_	Alignment	not modelled	99.5	23	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
63	c2w93A_	Alignment	not modelled	99.5	19	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
64	c2nxwB_	Alignment	not modelled	99.5	23	PDB header: lyase Chain: B: PDB Molecule: phenyl-3-pyruvate decarboxylase; PDBTitle: crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
65	c1ozhD_	Alignment	not modelled	99.5	16	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.
66	c2pgnA_	Alignment	not modelled	99.5	24	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
67	c2ji6B_	Alignment	not modelled	99.5	19	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
68	c2q27B_	Alignment	not modelled	99.5	16	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from escherichia coli
69	c2x7jA_	Alignment	not modelled	99.4	21	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	c2jlaD_	Alignment	not modelled	99.4	22	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
71	c1zpdA_	Alignment	not modelled	99.4	25	PDB header: alcohol fermentation Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from zymomonas mobilis
72	c3lq1A_	Alignment	not modelled	99.4	18	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
73	d1zpdA3	Alignment	not modelled	99.4	23	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
74	c1ovmC_	Alignment	not modelled	99.4	21	PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
75	c5essB_	Alignment	not modelled	99.4	17	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)
76	c5b46B_	Alignment	not modelled	99.4	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
77	c2vbiF_	Alignment	not modelled	99.4	24	PDB header: lyase Chain: F; PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter pasteurianus
78	c5c4iC_	Alignment	not modelled	99.0	14	PDB header: oxidoreductase Chain: C; PDB Molecule: oxalate oxidoreductase subunit beta; PDBTitle: structure of an oxalate oxidoreductase
79	d2c42a2	Alignment	not modelled	98.3	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module
80	c6cipD_	Alignment	not modelled	97.8	21	PDB header: oxidoreductase Chain: D; PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpp bound
81	d1zpa2	Alignment	not modelled	97.5	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
82	d1pvda2	Alignment	not modelled	97.3	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
83	d2djia2	Alignment	not modelled	97.3	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
84	c5b47A_	Alignment	not modelled	97.2	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
85	c5b48A_	Alignment	not modelled	97.2	17	PDB header: oxidoreductase Chain: A; PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase alpha subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 1 from sulfolobus tokodai
86	c6n2nA_	Alignment	not modelled	97.0	14	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate flavodoxin/ferredoxin oxidoreductase domain PDBTitle: crystal structure of 2-oxoglutarate:ferredoxin oxidoreductase from2 magnetococcus marinus
87	d2ez9a2	Alignment	not modelled	97.0	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
88	d2ji7a2	Alignment	not modelled	96.9	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
89	d1t9ba2	Alignment	not modelled	96.8	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
90	d2c42a1	Alignment	not modelled	96.8	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR Pyr module
91	d2r8oa1	Alignment	not modelled	96.6	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
92	d1ozha2	Alignment	not modelled	96.4	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
93	d1ybha2	Alignment	not modelled	96.3	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
94	d2ihta2	Alignment	not modelled	96.3	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
95	d1itza2	Alignment	not modelled	96.3	9	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
96	d1r9ja1	Alignment	not modelled	96.2	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
97	c4wbxC_	Alignment	not modelled	96.2	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
98	c2c3yA_	Alignment	not modelled	96.0	13	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
99	d1q6za2	Alignment	not modelled	95.9	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
100	d1gpua2	Alignment	not modelled	95.7	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
101	d1ovma2	Alignment	not modelled	95.1	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
102	c5c4iA_	Alignment	not modelled	94.7	5	PDB header: oxidoreductase Chain: A; PDB Molecule: oxalate oxidoreductase subunit alpha;

						PDBTitle: structure of an oxalate oxidoreductase
103	c1yd7A	Alignment	not modelled	67.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-keto acid:ferredoxin oxidoreductase subunit alpha; PDBTitle: conserved hypothetical protein pfu-1647980-001 from pyrococcus2 furiosus
104	d1on3a2	Alignment	not modelled	55.7	20	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
105	c1ik6A	Alignment	not modelled	52.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase; PDBTitle: 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum
106	d1ugpa	Alignment	not modelled	48.8	10	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
107	d1e5xa	Alignment	not modelled	48.7	18	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
108	c5cw9A	Alignment	not modelled	47.5	28	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed ferredoxin-ferredoxin domain insertion PDBTitle: crystal structure of de novo designed ferredoxin-ferredoxin domain2 insertion protein
109	c1olsB	Alignment	not modelled	47.5	14	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
110	d1umdb1	Alignment	not modelled	46.6	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
111	d1ik6a1	Alignment	not modelled	44.0	21	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
112	c1vrgE	Alignment	not modelled	43.8	18	PDB header: ligase Chain: E: PDB Molecule: propionyl-coa carboxylase, beta subunit; PDBTitle: crystal structure of propionyl-coa carboxylase, beta subunit (tm0716)2 from thermotoga maritima at 2.30 a resolution
113	d2a7sa2	Alignment	not modelled	43.3	18	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
114	d2a7sa1	Alignment	not modelled	40.7	17	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
115	d1w85b1	Alignment	not modelled	40.3	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
116	d1vrga2	Alignment	not modelled	40.3	19	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
117	c6e28D	Alignment	not modelled	40.3	16	PDB header: signaling protein Chain: D: PDB Molecule: caspase recruitment domain-containing protein 9; PDBTitle: the card9 card domain-swapped dimer
118	d2pja1	Alignment	not modelled	39.8	14	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
119	d1xnya2	Alignment	not modelled	39.1	14	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
120	c4l6wB	Alignment	not modelled	38.9	11	PDB header: ligase Chain: B: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase