


















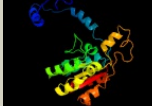




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2454c (-)_2753635_2754756
Date	Wed Aug 7 12:50:08 BST 2019
Unique Job ID	59e7af153048332e

Detailed template
information

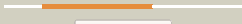



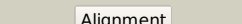

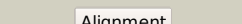
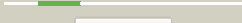
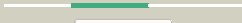
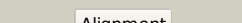
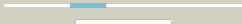

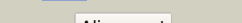
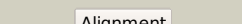
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5b46B_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase beta subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 2 from sulfolobus tokodai - ligand2 free form
2	c6n2oB_	 Alignment		100.0	40	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
3	c5c4iC_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: oxalate oxidoreductase subunit beta; PDBTitle: structure of an oxalate oxidoreductase
4	d2c42a2	 Alignment		100.0	21	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module
5	c6cipD_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpp bound
6	c2c3yA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
7	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
8	c2djiA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
9	c1yi1A_	 Alignment		100.0	16	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	c1t9dB_	 Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase, mitochondrial; PDBTitle: crystal structure of yeast acetohydroxyacid synthase in complex with a2 sulfonylurea herbicide, metsulfuron methyl
11	c4rjB_	 Alignment		100.0	18	PDB header: lyase Chain: B: PDB Molecule: acetolactate synthase; PDBTitle: acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii

12	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 escherichia coli
13	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.
14	c2pgnA_	Alignment		100.0	20	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
15	c1powA_	Alignment		100.0	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
16	c1jscA_	Alignment		100.0	19	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
17	d2ihta3	Alignment		100.0	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
18	c5ahkB_	Alignment		100.0	13	PDB header: transferase Chain: B; PDB Molecule: acetolactate synthase ii, large subunit; PDBTitle: crystal structure of acetoxy acid synthase pf5 from2 pseudomonas protegens
19	c2v3wC_	Alignment		100.0	19	PDB header: lyase Chain: C; PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase variant l461a2 from pseudomonas putida
20	c2panF_	Alignment		100.0	15	PDB header: lyase Chain: F; PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
21	c2x7jA_	Alignment	not modelled	100.0	15	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
22	c1upaC_	Alignment	not modelled	100.0	18	PDB header: synthase Chain: C; PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
23	c4q9dA_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A; PDB Molecule: benzoylformate decarboxylase; PDBTitle: x-ray structure of a putative thiamin diphosphate-dependent enzyme2 isolated from mycobacterium smegmatis
24	d1ybha3	Alignment	not modelled	100.0	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
25	c2ag1A_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A; PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
26	d2djia3	Alignment	not modelled	100.0	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
27	c1ovmC_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: C; PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
28	c2q27B_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B; PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from escherichia coli
						PDB header: lyase Chain: B; PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from escherichia coli

29	c4k9qB_	Alignment	not modelled	100.0	15	Chain: B; PDB Molecule: benzoylformate decarboxylase; PDBTitle: the crystal structure of benzoylformate decarboxylase from <i>2 polynucleobacter necessarius</i>
30	c2ji6B_	Alignment	not modelled	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
31	d1t9ba3	Alignment	not modelled	100.0	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
32	d2ez9a3	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 PP module
33	c2nxwB_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B; PDB Molecule: phenyl-3-pyruvate decarboxylase; PDBTitle: crystal structure of phenylpyruvate decarboxylase of <i>azospirillum2 brasiliense</i>
34	d1ozha3	Alignment	not modelled	100.0	21	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
35	c1zpdA_	Alignment	not modelled	100.0	16	PDB header: alcohol fermentation Chain: A; PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from <i>zymomonas mobilis</i>
36	d1jsca3	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
37	d1ovma3	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
38	c2vbgB_	Alignment	not modelled	99.9	18	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
39	c2jlaD_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: D; PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: crystal structure of <i>e.coli mend</i> , 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase - semet3 protein
40	c3lq1A_	Alignment	not modelled	99.9	17	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>listeria3 monocytogenes str. 4b f2365</i>
41	d2ji7a3	Alignment	not modelled	99.9	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
42	d1pvda3	Alignment	not modelled	99.9	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
43	d1zpdA3	Alignment	not modelled	99.9	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
44	c2w93A_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: A; PDB Molecule: pyruvate decarboxylase isozyme 1; PDBTitle: crystal structure of the <i>saccharomyces cerevisiae</i> pyruvate2 decarboxylase variant e477q in complex with the surrogate pyruvamide
45	c2vbiF_	Alignment	not modelled	99.9	21	PDB header: lyase Chain: F; PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from <i>acetobacter pasteurianus</i>
46	d1q6za3	Alignment	not modelled	99.9	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
47	c5essB_	Alignment	not modelled	99.7	14	PDB header: transferase Chain: B; PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- PDBTitle: crystal structure of <i>m. tuberculosis mend</i> bound to mg2+ and covalent2 intermediate i (a thdp and decarboxylated 2-oxoglutarate adduct)
48	d2bfda1	Alignment	not modelled	99.3	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
49	d1w85a_	Alignment	not modelled	99.3	23	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
50	d2r8oa2	Alignment	not modelled	99.3	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
51	d2ozla1	Alignment	not modelled	99.2	26	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
52	d1umda_	Alignment	not modelled	99.2	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
53	c2o1xA_	Alignment	not modelled	99.2	26	PDB header: transferase Chain: A; PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from <i>deinococcus2 radiodurans</i>

54	d1r9ja2	Alignment	not modelled	99.1	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
55	d1itza1	Alignment	not modelled	99.0	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
56	c2o1sC	Alignment	not modelled	99.0	24	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
57	d1gpua1	Alignment	not modelled	99.0	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
58	c5vrB	Alignment	not modelled	98.9	20	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of a transketolase from neisseria gonorrhoeae
59	c5nd5A	Alignment	not modelled	98.9	18	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from chlamydomonas reinhardtii in2 complex with tpp and mg2+
60	c3uk1A	Alignment	not modelled	98.9	20	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
61	c6ouwA	Alignment	not modelled	98.8	27	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
62	c4c7vA	Alignment	not modelled	98.8	16	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: apo transketolase from lactobacillus salivarius at 2.2a resolution
63	c2r8pA	Alignment	not modelled	98.8	18	PDB header: transferase Chain: A: PDB Molecule: transketolase 1; PDBTitle: transketolase from e. coli in complex with substrate d-fructose-6-2 phosphate
64	c3m7iA	Alignment	not modelled	98.8	21	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
65	c3komB	Alignment	not modelled	98.8	19	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of apo transketolase from francisella tularensis
66	c2e6kB	Alignment	not modelled	98.7	21	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: x-ray structure of thermus thermophilus hb8 tt0505
67	c3mosA	Alignment	not modelled	98.7	19	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: the structure of human transketolase
68	c3rimA	Alignment	not modelled	98.7	16	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of mycobacterium tuberculosis transketolase2 (rv1449c)
69	c3hylB	Alignment	not modelled	98.7	15	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from bacillus anthracis
70	d1qs0a	Alignment	not modelled	98.6	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
71	c1itzC	Alignment	not modelled	98.6	18	PDB header: transferase Chain: C: PDB Molecule: transketolase; PDBTitle: maize transketolase in complex with tpp
72	c5hgxA	Alignment	not modelled	98.6	18	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase mutant - h261f from pichia stipitis
73	c1r9jB	Alignment	not modelled	98.5	21	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: transketolase from leishmania mexicana
74	c1tkcA	Alignment	not modelled	98.5	16	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
75	d2ieaa2	Alignment	not modelled	98.5	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
76	c4qoyC	Alignment	not modelled	98.3	21	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
77	c3ahhA	Alignment	not modelled	98.3	22	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
78	c2g28A	Alignment	not modelled	98.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase e1 component; PDBTitle: e. coli pyruvate dehydrogenase h407a variant2 phosphonolactylthiamin diphosphate complex
						Fold: Thiamin diphosphate-binding fold (THDP-binding)

79	d1itza2	Alignment	not modelled	97.2	14	Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
80	c2jgdA	Alignment	not modelled	96.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoglutarate dehydrogenase e1 component; PDBTitle: e. coli 2-oxoglutarate dehydrogenase (e1o)
81	d1zpdA2	Alignment	not modelled	96.4	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
82	d1gpua2	Alignment	not modelled	96.0	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
83	d1w85b1	Alignment	not modelled	95.4	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
84	d1ybha1	Alignment	not modelled	95.4	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
85	c2vicC	Alignment	not modelled	95.4	24	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)
86	d2ez9a2	Alignment	not modelled	95.4	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
87	d2r8oa1	Alignment	not modelled	95.2	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
88	d2ji7a2	Alignment	not modelled	94.7	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
89	d1r9ja1	Alignment	not modelled	94.5	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
90	d1q6za2	Alignment	not modelled	94.4	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
91	d2djia2	Alignment	not modelled	94.3	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
92	d2djia1	Alignment	not modelled	93.9	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
93	d2ozb1	Alignment	not modelled	93.1	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
94	d1ovma2	Alignment	not modelled	92.8	10	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
95	d2ji7a1	Alignment	not modelled	92.6	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
96	d2ihta2	Alignment	not modelled	90.7	10	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
97	d1ozha2	Alignment	not modelled	89.8	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
98	d1pvda2	Alignment	not modelled	89.2	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
99	d1t9ba2	Alignment	not modelled	88.6	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
100	d1qs0b1	Alignment	not modelled	88.4	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
101	c1ni4D	Alignment	not modelled	87.0	12	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate dehydrogenase e1 component: beta PDBTitle: human pyruvate dehydrogenase
102	d1ybha2	Alignment	not modelled	86.7	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
103	c1um9D	Alignment	not modelled	86.2	18	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
104	c1ik6A	Alignment	not modelled	85.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase; PDBTitle: 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum
105	d1umdb1	Alignment	not modelled	84.8	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
106	d1ik6a1	Alignment	not modelled	81.7	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module

107	c3dufD	 Alignment	not modelled	80.6	17	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
108	c1olsB	 Alignment	not modelled	80.1	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
109	d2bfdb1	 Alignment	not modelled	79.9	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
110	c5ftwA	 Alignment	not modelled	76.8	15	PDB header: transferase Chain: A: PDB Molecule: chemotaxis protein methyltransferase; PDBTitle: crystal structure of glutamate o-methyltransferase in2 complex with s- adenosyl-l-homocysteine (sah) from3 bacillus subtilis
111	c2bp7F	 Alignment	not modelled	71.7	10	PDB header: oxidoreductase Chain: F: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
112	c2xt6B	 Alignment	not modelled	63.9	28	PDB header: lyase Chain: B: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
113	c3vs9F	 Alignment	not modelled	56.7	12	PDB header: transferase Chain: F: PDB Molecule: type iii polyketide synthase; PDBTitle: crystal structure of type iii pks arsc mutant
114	c5xlyA	 Alignment	not modelled	52.9	13	PDB header: transferase Chain: A: PDB Molecule: chemotaxis protein methyltransferase 1; PDBTitle: crystal structure of cher1 in complex with c-di-gmp-bound mapz
115	c3ibsA	 Alignment	not modelled	45.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein batb; PDBTitle: crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron
116	c4wbcC	 Alignment	not modelled	39.9	13	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
117	d2okfa1	 Alignment	not modelled	36.0	12	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: XisH-like
118	d2inba1	 Alignment	not modelled	35.1	10	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: XisH-like
119	d1bi5a1	 Alignment	not modelled	28.2	20	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
120	c2x98A	 Alignment	not modelled	27.5	22	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase