Phyre^2

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Description	P0AFG8
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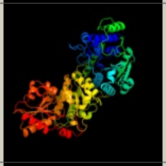
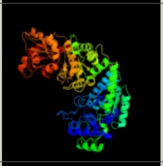
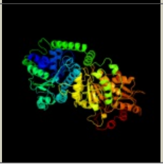
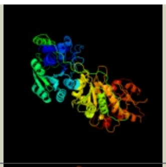
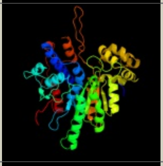
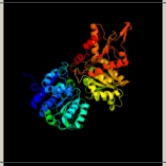
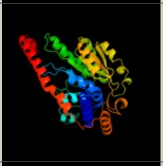
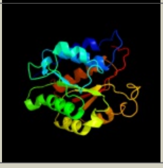
Detailed template information

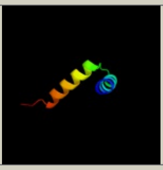
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g28A_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase e1 component; **PDBTitle:** e. coli pyruvate dehydrogenase h407a variant2 phosphonolactylthiamin diphosphate complex
2	c3ahhA_	Alignment		100.0	16	**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
3	c1r9jB_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** transketolase from leishmania mexicana
4	c2r8pA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transketolase 1; **PDBTitle:** transketolase from e. coli in complex with substrate d-2 fructose-6-phosphate
5	c3hylB_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** crystal structure of transketolase from bacillus anthracis
6	c3komB_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** crystal structure of apo transketolase from francisella tularensis
7	c3m7iA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transketolase; **PDBTitle:** crystal structure of transketolase in complex with thiamine2 diphosphate, ribose-5-phosphate(pyranose form) and3 magnesium ion
8	c1tkcA_	Alignment		100.0	22	**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
9	c1itzC_	Alignment		100.0	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**transketolase; **PDBTitle:** maize transketolase in complex with tpp
10	c2e6kB_	Alignment		100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** x-ray structure of thermus thermopilus hb8 tt0505
11	c3uk1A_	Alignment		100.0	25	**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

12	c3mosA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transketolase; **PDBTitle:** the structure of human transketolase
13	d2ieaa2	Alignment		100.0	100	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
14	c2o1sC_	Alignment		100.0	19	**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
15	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) from2 deinococcus radiodurans
16	d1itza1	Alignment		100.0	25	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
17	d1r9ja2	Alignment		100.0	23	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
18	d1gpua1	Alignment		100.0	26	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
19	d2r8oa2	Alignment		100.0	26	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
20	d2ieaa1	Alignment		100.0	100	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
21	d2ieaa3	Alignment	not modelled	100.0	100	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
22	c1um9D_	Alignment	not modelled	100.0	13	**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
23	d1gpua2	Alignment	not modelled	100.0	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
24	c3dufD_	Alignment	not modelled	100.0	12	**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
25	d1r9ja1	Alignment	not modelled	100.0	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
26	d1itza2	Alignment	not modelled	100.0	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
27	c1olsB_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxoisovalerate dehydrogenase beta subunit; **PDBTitle:** roles of his291-alpha and his146-beta' in the reductive2 acylation reaction catalyzed by human branched-chain3 alpha-ketoacid dehydrogenase
28	d2r8oa1	Alignment	not modelled	100.0	19	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding)

						Family:TK-like Pyr module
29	c1ni4D_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**pyruvate dehydrogenase e1 component: beta **PDBTitle:** human pyruvate dehydrogenase
30	c2bp7F_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**2-oxoisovalerate dehydrogenase beta subunit; **PDBTitle:** new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
31	c1ik6A_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase; **PDBTitle:** 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum
32	d2bfda1	Alignment	not modelled	99.9	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
33	d1w85a_	Alignment	not modelled	99.9	20	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
34	d1itza3	Alignment	not modelled	99.9	24	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
35	d1r9ja3	Alignment	not modelled	99.9	18	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
36	d2ozla1	Alignment	not modelled	99.9	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
37	d1umda_	Alignment	not modelled	99.9	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
38	d1umdb1	Alignment	not modelled	99.9	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
39	d2r8oa3	Alignment	not modelled	99.9	24	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
40	d1gpua3	Alignment	not modelled	99.9	21	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
41	d1w85b1	Alignment	not modelled	99.9	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
42	d2ozlb1	Alignment	not modelled	99.8	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
43	d1qs0a_	Alignment	not modelled	99.8	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
44	d2bfdb1	Alignment	not modelled	99.8	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
45	d1qs0b1	Alignment	not modelled	99.7	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
46	c2yicC_	Alignment	not modelled	99.7	15	**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)
47	d1ik6a1	Alignment	not modelled	99.7	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
48	d1w85b2	Alignment	not modelled	99.5	10	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
49	d1q6za3	Alignment	not modelled	99.4	25	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
50	d1umdb2	Alignment	not modelled	99.3	18	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
51	d1t9ba3	Alignment	not modelled	99.3	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
52	d2ozlb2	Alignment	not modelled	99.3	13	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
53	c2jgdA_	Alignment	not modelled	99.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-oxoglutarate dehydrogenase e1 component; **PDBTitle:** e. coli 2-oxoglutarate dehydrogenase (e1o)
54	d2djia3	Alignment	not modelled	99.3	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
55	d2bfdb2	Alignment	not modelled	99.3	11	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like

		Alignment	not modelled			**Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
56	d2ez9a3	Alignment	not modelled	99.3	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
57	d1jsca3	Alignment	not modelled	99.2	22	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
58	c1powA_	Alignment	not modelled	99.2	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
59	d2ihta3	Alignment	not modelled	99.2	23	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
60	c2djiA_	Alignment	not modelled	99.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate oxidase; **PDBTitle:** crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
61	c2xt6B_	Alignment	not modelled	99.2	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
62	d1ozha3	Alignment	not modelled	99.2	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
63	d1ybha3	Alignment	not modelled	99.2	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
64	d2ji7a3	Alignment	not modelled	99.1	24	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
65	c2nxwB_	Alignment	not modelled	99.0	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phenyl-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
66	d1pvda3	Alignment	not modelled	99.0	22	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
67	c1jscA_	Alignment	not modelled	99.0	19	**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
68	c1t9dB_	Alignment	not modelled	99.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetolactate synthase, mitochondrial; **PDBTitle:** crystal structure of yeast acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, metsulfuron methyl
69	c1upaC_	Alignment	not modelled	99.0	24	**PDB header:**synthase **Chain:** C: **PDB Molecule:**carboxyethylarginine synthase; **PDBTitle:** carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
70	c2ag1A_	Alignment	not modelled	99.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**benzaldehyde lyase; **PDBTitle:** crystal structure of benzaldehyde lyase (bal)- semet
71	c2v3wC_	Alignment	not modelled	99.0	23	**PDB header:**lyase **Chain:** C: **PDB Molecule:**benzoylformate decarboxylase; **PDBTitle:** crystal structure of the benzoylformate decarboxylase2 variant l461a from pseudomonas putida
72	d1ovma3	Alignment	not modelled	98.9	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
73	c3eyaE_	Alignment	not modelled	98.9	23	**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
74	c2pgnA_	Alignment	not modelled	98.9	22	**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
75	d1qs0b2	Alignment	not modelled	98.9	16	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
76	c1yi1A_	Alignment	not modelled	98.9	21	**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
77	c2q27B_	Alignment	not modelled	98.9	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxalyl-coa decarboxylase; **PDBTitle:** crystal structure of oxalyl-coa decarboxylase from escherichia coli
78	c2vbiF_	Alignment	not modelled	98.9	24	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
79	c2panF_	Alignment	not modelled	98.8	21	**PDB header:**lyase **Chain:** F: **PDB Molecule:**glyoxylate carboligase; **PDBTitle:** crystal structure of e. coli glyoxylate carboligase
80	c1ozhD_	Alignment	not modelled	98.8	21	**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.

81	c1zpdA_	Alignment	not modelled	98.8	21	**PDB header:**alcohol fermentation **Chain:** A: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** pyruvate decarboxylase from zymomonas mobilis
82	c2w93A_	Alignment	not modelled	98.8	24	**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 surrogate3 pyruvamide
83	c3lq1A_	Alignment	not modelled	98.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene- **PDBTitle:** crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene2 1-carboxylic acid synthase/2-oxoglutarate decarboxylase3 from listeria monocytogenes str. 4b f2365
84	c1ovmC_	Alignment	not modelled	98.7	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**indole-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
85	c2vbgB_	Alignment	not modelled	98.7	28	**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
86	d1zpda3	Alignment	not modelled	98.7	23	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
87	c2ji6B_	Alignment	not modelled	98.7	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxalyl-coa decarboxylase; **PDBTitle:** x-ray structure of oxalyl-coa decarboxylase in complex with2 3-deaza-thdp and oxalyl-coa
88	c2jlaD_	Alignment	not modelled	98.7	18	**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
89	c2x7jA_	Alignment	not modelled	98.5	16	**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
90	d1ik6a2	Alignment	not modelled	98.5	13	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
91	c3ju3A_	Alignment	not modelled	98.1	11	**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
92	c2c3yA_	Alignment	not modelled	97.8	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
93	d2c42a2	Alignment	not modelled	97.7	23	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR PP module
94	d2c42a3	Alignment	not modelled	97.3	13	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
95	d1q6za2	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 Pyr module
96	c3a9rA_	Alignment	not modelled	94.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-arabinose isomerase; **PDBTitle:** x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
97	d1ybha2	Alignment	not modelled	92.1	12	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
98	d2ihta2	Alignment	not modelled	90.2	7	**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	87.0	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
100	c1fuiB_	Alignment	not modelled	83.7	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
101	d2ez9a2	Alignment	not modelled	79.2	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
102	d2c42a1	Alignment	not modelled	79.2	9	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR Pyr module
103	d1vm0a_	Alignment	not modelled	77.5	28	**Fold:**IF3-like **Superfamily:**AlbA-like **Family:**Hypothetical protein At2g34160
104	d1ozha2	Alignment	not modelled	75.9	7	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
105	c2g3vB	Ali	not modelled	75.6	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein at2g34160;

105	c2q3vB_	Alignment	not modelled	75.6	24	**PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g34160
106	c2k2eA_	Alignment	not modelled	74.1	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bp2786; **PDBTitle:** solution nmr structure of bordetella pertussis protein2 bp2786, a mth938-like domain. northeast structural3 genomics consortium target ber31
107	c2gm2A_	Alignment	not modelled	73.3	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
108	c3o8nA_	Alignment	not modelled	72.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase, muscle type; **PDBTitle:** structure of phosphofructokinase from rabbit skeletal muscle
109	c2h9uA_	Alignment	not modelled	72.8	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna/rna-binding protein alba 2; **PDBTitle:** crystal structure of the archaea specific dna binding protein
110	d2q4qa1	Alignment	not modelled	69.6	26	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
111	c3h87D_	Alignment		69.1	25	**PDB header:**toxin/antitoxin **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
112	d2fi9a1	Alignment	not modelled	69.0	28	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
113	c2oaq1_	Alignment	not modelled	68.5	19	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**type ii secretion system protein; **PDBTitle:** crystal structure of the archaeal secretion atpase gspe in complex2 with phosphate
114	d1fuia2	Alignment	not modelled	63.3	16	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**L-fucose isomerase, N-terminal and second domains
115	c3l3bA_	Alignment	not modelled	62.1	25	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**es1 family protein; **PDBTitle:** crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
116	c3lp6D_	Alignment	not modelled	60.5	29	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
117	c3opyG_	Alignment	not modelled	57.0	12	**PDB header:**transferase **Chain:** G: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
118	c3o8oC_	Alignment	not modelled	56.7	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**6-phosphofructokinase subunit alpha; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
119	c3c3jA_	Alignment	not modelled	54.3	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
120	d1pfka_	Alignment	not modelled	53.4	19	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase