Phyre2

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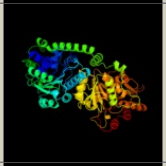
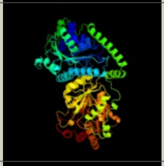
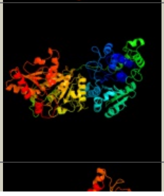
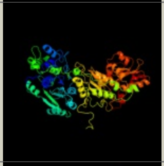
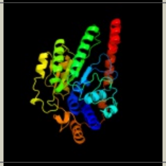
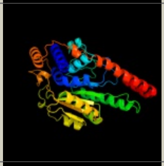
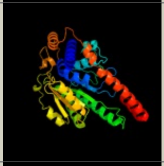
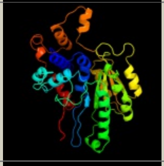
Description	P33570
Date	Thu Jan 5 11:52:13 GMT 2012
Unique Job ID	f5591e449b54229e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r8pA_	Alignment		100.0	75	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transketolase 1; **PDBTitle:** transketolase from e. coli in complex with substrate d-2 fructose-6-phosphate
2	c3hylB_	Alignment		100.0	49	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** crystal structure of transketolase from bacillus anthracis
3	c1itzC_	Alignment		100.0	50	**PDB header:**transferase **Chain:** C: **PDB Molecule:**transketolase; **PDBTitle:** maize transketolase in complex with tpp
4	c3uk1A_	Alignment		100.0	60	**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
5	c3komB_	Alignment		100.0	52	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** crystal structure of apo transketolase from francisella tularensis
6	c1r9jB_	Alignment		100.0	47	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** transketolase from leishmania mexicana
7	c2e6kB_	Alignment		100.0	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** x-ray structure of thermus thermopilus hb8 tt0505
8	c1tkcA_	Alignment		100.0	48	**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	c3m7iA_	Alignment		100.0	43	**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
10	c3mosA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transketolase; **PDBTitle:** the structure of human transketolase
11	c2g28A_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase e1 component; **PDBTitle:** e. coli pyruvate dehydrogenase h407a variant2 phosphonolactylthiamin diphosphate complex

12	c2o1xA_	Alignment		100.0	23	**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
13	c2o1sC_	Alignment		100.0	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1-deoxy-d-xylulose-5-phosphate synthase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 escherichia coli
14	c3ahhA_	Alignment		100.0	17	**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
15	d2r8oa2	Alignment		100.0	77	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
16	d1itza1	Alignment		100.0	54	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
17	d1r9ja2	Alignment		100.0	50	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
18	d1gpua1	Alignment		100.0	53	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
19	d2ieaa2	Alignment		100.0	27	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
20	c1ni4D_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**pyruvate dehydrogenase e1 component: beta **PDBTitle:** human pyruvate dehydrogenase
21	c1olsB_	Alignment	not modelled	100.0	15	**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
22	c1um9D_	Alignment	not modelled	100.0	19	**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	c3dufD_	Alignment	not modelled	100.0	21	**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
24	c2bp7F_	Alignment	not modelled	100.0	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)
25	c1ik6A_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase; **PDBTitle:** 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum
26	d2r8oa1	Alignment	not modelled	100.0	77	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
27	d1gpua2	Alignment	not modelled	100.0	49	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
28	d1itza2	Alignment	not modelled	100.0	48	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding)

						Family:TK-like Pyr module
29	d1r9ja1	Alignment	not modelled	100.0	48	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
30	c2yicC_	Alignment	not modelled	100.0	14	**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)
31	c2xt6B_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
32	c2jgdA_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-oxoglutarate dehydrogenase e1 component; **PDBTitle:** e. coli 2-oxoglutarate dehydrogenase (e1o)
33	d1w85b1	Alignment	not modelled	100.0	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
34	d1umdb1	Alignment	not modelled	100.0	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
35	d2ieaa1	Alignment	not modelled	100.0	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
36	d2ozlb1	Alignment	not modelled	100.0	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
37	d1qs0b1	Alignment	not modelled	100.0	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
38	d2bfdb1	Alignment	not modelled	100.0	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
39	d1w85a_	Alignment	not modelled	100.0	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
40	d1umda_	Alignment	not modelled	100.0	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
41	d2ozla1	Alignment	not modelled	100.0	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
42	d1qs0a_	Alignment	not modelled	100.0	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
43	d2bfda1	Alignment	not modelled	100.0	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
44	d1ik6a1	Alignment	not modelled	100.0	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
45	d2r8oa3	Alignment	not modelled	100.0	68	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
46	d1itza3	Alignment	not modelled	99.9	43	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
47	d1r9ja3	Alignment	not modelled	99.9	38	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
48	d1gpua3	Alignment	not modelled	99.9	41	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
49	d2ieaa3	Alignment	not modelled	99.9	25	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
50	d1w85b2	Alignment	not modelled	99.9	27	**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	d2ozlb2	Alignment	not modelled	99.8	17	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
52	d1umdb2	Alignment	not modelled	99.8	22	**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	d2bfdb2	Alignment	not modelled	99.8	14	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
54	d1qs0b2	Alignment	not modelled	99.8	19	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
55	d1ik6a2	Alignment	not modelled	99.7	22	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-

						subunit, C-terminal-domain
56	d2djia3	Alignment	not modelled	99.6	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
57	d1t9ba3	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
58	c2djiA_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate oxidase; **PDBTitle:** crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
59	d1q6za3	Alignment	not modelled	99.5	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
60	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
61	d1jsca3	Alignment	not modelled	99.4	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
62	d1ybha3	Alignment	not modelled	99.4	20	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
63	d2ez9a3	Alignment	not modelled	99.4	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
64	d1ozha3	Alignment	not modelled	99.4	19	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
65	d2ihta3	Alignment	not modelled	99.4	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
66	c1powA_	Alignment	not modelled	99.4	14	**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
67	c3ju3A_	Alignment	not modelled	99.3	20	**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
68	c2c3yA_	Alignment	not modelled	99.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
69	c1t9dB_	Alignment	not modelled	99.3	18	**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
70	c2pgnA_	Alignment	not modelled	99.3	21	**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
71	d1pvda3	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
72	c2v3wC_	Alignment	not modelled	99.3	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**benzoylformate decarboxylase; **PDBTitle:** crystal structure of the benzoylformate decarboxylase2 variant l461a from pseudomonas putida
73	c2nxwB_	Alignment	not modelled	99.3	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phenyl-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
74	c1jscA_	Alignment	not modelled	99.3	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
75	c3eyaE_	Alignment	not modelled	99.3	21	**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
76	c2panF_	Alignment	not modelled	99.2	18	**PDB header:**lyase **Chain:** F: **PDB Molecule:**glyoxylate carboligase; **PDBTitle:** crystal structure of e. coli glyoxylate carboligase
77	c2vbiF_	Alignment	not modelled	99.2	28	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
78	c2vbgB_	Alignment	not modelled	99.2	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 lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
79	c2ag1A_	Alignment	not modelled	99.2	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**benzaldehyde lyase; **PDBTitle:** crystal structure of benzaldehyde lyase (bal)- semet
80	c1zpdA_	Alignment	not modelled	99.2	25	**PDB header:**alcohol fermentation **Chain:** A: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** pyruvate decarboxylase from zymomonas mobilis
						PDB header:transferase

81	c1yi1A_	Alignment	not modelled	99.2	18	**Chain:** A: **PDB Molecule:**acetolactate synthase; **PDBTitle:** crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
82	d1ovma3	Alignment	not modelled	99.2	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
83	d1zpda3	Alignment	not modelled	99.2	25	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
84	c1upaC_	Alignment	not modelled	99.2	19	**PDB header:**synthase **Chain:** C: **PDB Molecule:**carboxyethylarginine synthase; **PDBTitle:** carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
85	c2q27B_	Alignment	not modelled	99.2	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxalyl-coa decarboxylase; **PDBTitle:** crystal structure of oxalyl-coa decarboxylase from escherichia coli
86	c2w93A_	Alignment	not modelled	99.2	16	**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
87	c1ozhD_	Alignment	not modelled	99.2	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.
88	c2ji6B_	Alignment	not modelled	99.2	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxalyl-coa decarboxylase; **PDBTitle:** crystal structure of oxalyl-coa decarboxylase in complex with2 3-deaza-thdp and oxalyl-coa
89	c1ovmC_	Alignment	not modelled	99.1	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**indole-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
90	c3lq1A_	Alignment	not modelled	99.1	15	**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
91	c2jlaD_	Alignment	not modelled	99.1	13	**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
92	c2x7jA_	Alignment	not modelled	99.1	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
93	d2c42a3	Alignment	not modelled	98.5	16	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
94	d2c42a1	Alignment	not modelled	98.1	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR Pyr module
95	d2c42a2	Alignment	not modelled	97.7	25	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR PP module
96	d2djia2	Alignment	not modelled	97.5	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
97	d1q6za2	Alignment	not modelled	97.5	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
98	d2ez9a2	Alignment	not modelled	97.5	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
99	d1zpda2	Alignment	not modelled	97.2	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
100	d1ovma2	Alignment	not modelled	97.1	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
101	d1ybha2	Alignment	not modelled	97.0	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
102	d1pvda2	Alignment	not modelled	97.0	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
103	d1t9ba2	Alignment	not modelled	96.9	10	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
104	d2ihta2	Alignment	not modelled	96.6	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
105	d1ozha2	Alignment	not modelled	96.5	8	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module

106	d2ji7a2	Alignment	not modelled	96.2	12	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
107	c1yd7A_	Alignment	not modelled	95.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-keto acid:ferredoxin oxidoreductase subunit **PDBTitle:** conserved hypothetical protein pfu-1647980-001 from2 pyrococcus furiosus
108	c3f8rD_	Alignment	not modelled	79.9	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**thioredoxin reductase (trxb-3); **PDBTitle:** crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
109	c2zkiH_	Alignment	not modelled	79.9	23	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
110	d1wu7a1	Alignment	not modelled	77.6	21	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
111	c2zbwA_	Alignment	not modelled	76.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
112	d1djqa3	Alignment	not modelled	76.5	19	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
113	d2a5la1	Alignment	not modelled	76.0	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
114	d1dxla1	Alignment	not modelled	75.9	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
115	d1trba1	Alignment	not modelled	75.0	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
116	c3ipzA_	Alignment	not modelled	74.8	5	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic; **PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
117	d1jnra2	Alignment	not modelled	74.0	27	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
118	d1d5ta1	Alignment	not modelled	73.9	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
119	d1gesa1	Alignment	not modelled	73.7	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
120	c3ctyA_	Alignment	not modelled	72.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of t. acidophilum thioredoxin reductase