Phyre2

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Description	P00893
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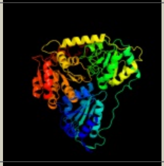
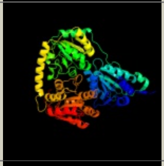
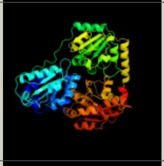
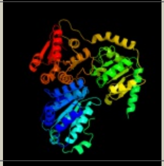
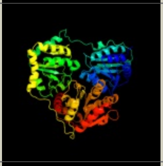
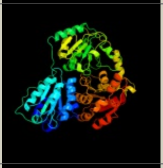
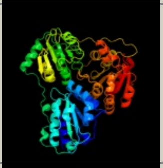
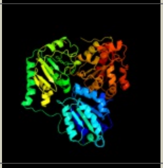
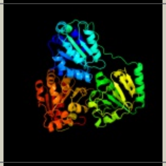
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yi1A_	Alignment		100.0	40	**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
2	c1powA_	Alignment		100.0	26	**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
3	c2djiA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate oxidase; **PDBTitle:** crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
4	c2panF_	Alignment		100.0	32	**PDB header:**lyase **Chain:** F: **PDB Molecule:**glyoxylate carboligase; **PDBTitle:** crystal structure of e. coli glyoxylate carboligase
5	c2pgnA_	Alignment		100.0	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
6	c1t9dB_	Alignment		100.0	44	**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
7	c3eyaE_	Alignment		100.0	29	**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
8	c2q27B_	Alignment		100.0	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxalyl-coa decarboxylase; **PDBTitle:** crystal structure of oxalyl-coa decarboxylase from escherichia coli
9	c1ozhD_	Alignment		100.0	28	**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.
10	c1jscA_	Alignment		100.0	43	**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
11	c2ag1A_	Alignment		100.0	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**benzaldehyde lyase; **PDBTitle:** crystal structure of benzaldehyde lyase (bal)- semet

12	c2ji6B_	Alignment		100.0	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
13	c1zpdA_	Alignment		100.0	19	**PDB header:**alcohol fermentation **Chain:** A: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** pyruvate decarboxylase from zymomonas mobilis
14	c1upaC_	Alignment		100.0	26	**PDB header:**synthase **Chain:** C: **PDB Molecule:**carboxyethylarginine synthase; **PDBTitle:** carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
15	c2v3wC_	Alignment		100.0	24	**PDB header:**lyase **Chain:** C: **PDB Molecule:**benzoylformate decarboxylase; **PDBTitle:** crystal structure of the benzoylformate decarboxylase2 variant l461a from pseudomonas putida
16	c2x7jA_	Alignment		100.0	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
17	c2vbiF_	Alignment		100.0	19	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
18	c2vbgB_	Alignment		100.0	24	**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
19	c1ovmC_	Alignment		100.0	22	**PDB header:**lyase **Chain:** C: **PDB Molecule:**indole-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
20	c2w93A_	Alignment		100.0	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 surrogate3 pyruvamide
21	c2nxwB_	Alignment	not modelled	100.0	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phenyl-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
22	c3lq1A_	Alignment	not modelled	100.0	20	**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
23	c2jlaD_	Alignment	not modelled	100.0	15	**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
24	d1ybha2	Alignment	not modelled	100.0	46	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
25	d1ybha3	Alignment	not modelled	100.0	41	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
26	d2djia2	Alignment	not modelled	100.0	25	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
27	d1t9ba3	Alignment	not modelled	100.0	44	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
						Fold: Thiamin diphosphate-binding fold (THDP-binding)

28	d2ji7a2	Alignment	not modelled	100.0	27	**Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
29	d1ozha2	Alignment	not modelled	100.0	39	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
30	d1t9ba2	Alignment	not modelled	100.0	53	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
31	d1q6za2	Alignment	not modelled	100.0	26	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
32	d2djia3	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
33	d2ez9a3	Alignment	not modelled	100.0	24	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
34	d2ihta2	Alignment	not modelled	100.0	34	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
35	d1zpda2	Alignment	not modelled	100.0	20	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
36	d1pvda2	Alignment	not modelled	100.0	20	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
37	d2ez9a2	Alignment	not modelled	100.0	29	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
38	d1ozha3	Alignment	not modelled	100.0	24	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
39	d2ihta3	Alignment	not modelled	100.0	26	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
40	d1ovma2	Alignment	not modelled	100.0	25	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
41	d1zpda3	Alignment	not modelled	100.0	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
42	d1ovma3	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
43	d1q6za3	Alignment	not modelled	100.0	27	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
44	d2ji7a3	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
45	d1pvda3	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
46	d1jsca3	Alignment	not modelled	100.0	45	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
47	d2ez9a1	Alignment	not modelled	100.0	24	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
48	d2djia1	Alignment	not modelled	100.0	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
49	d1ybha1	Alignment	not modelled	100.0	34	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
50	d2ihta1	Alignment	not modelled	100.0	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
51	d1t9ba1	Alignment	not modelled	100.0	39	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
52	d2ji7a1	Alignment	not modelled	100.0	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
53	d1ozha1	Alignment	not modelled	100.0	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
54	d1q6za1	Alignment	not modelled	99.9	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
55	d1zpda1	Alignment	not modelled	99.9	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
						Fold:DHS-like NAD/FAD-binding domain

56	d1ovma1	Alignment	not modelled	99.9	20	**Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
57	d1pvda1	Alignment	not modelled	99.9	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
58	c2c3yA_	Alignment	not modelled	99.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
59	d2c42a1	Alignment	not modelled	99.8	12	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR Pyr module
60	c3cf4G_	Alignment	not modelled	99.7	15	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**acetyl-coa decarboxylase/synthase epsilon subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
61	d2r8oa2	Alignment	not modelled	99.6	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
62	d2bfda1	Alignment	not modelled	99.6	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
63	d2ozla1	Alignment	not modelled	99.6	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
64	d1umda_	Alignment	not modelled	99.6	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
65	d1gpua1	Alignment	not modelled	99.6	20	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
66	d1r9ja2	Alignment	not modelled	99.6	23	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
67	c1yd7A_	Alignment	not modelled	99.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-keto acid:ferredoxin oxidoreductase subunit **PDBTitle:** conserved hypothetical protein pfu-1647980-001 from2 pyrococcus furiosus
68	d1itza1	Alignment	not modelled	99.6	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
69	d1w85a_	Alignment	not modelled	99.6	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
70	d2c42a2	Alignment	not modelled	99.5	21	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR PP module
71	c3hylB_	Alignment	not modelled	99.4	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** crystal structure of transketolase from bacillus anthracis
72	c1itzC_	Alignment	not modelled	99.4	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**transketolase; **PDBTitle:** maize transketolase in complex with tpp
73	c2o1sC_	Alignment	not modelled	99.3	23	**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
74	c1tkcA_	Alignment	not modelled	99.3	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
75	c1r9jB_	Alignment	not modelled	99.3	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** transketolase from leishmania mexicana
76	c2r8pA_	Alignment	not modelled	99.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transketolase 1; **PDBTitle:** transketolase from e. coli in complex with substrate d-2 fructose-6-phosphate
77	c3m7iA_	Alignment	not modelled	99.3	19	**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
78	c3uk1A_	Alignment	not modelled	99.3	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
79	c2o1xA_	Alignment	not modelled	99.3	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
80	d1qs0a_	Alignment	not modelled	99.3	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
81	c3mosA_	Alignment	not modelled	99.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transketolase;

						PDBTitle: the structure of human transketolase
82	c2e6kB_	Alignment	not modelled	99.3	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** x-ray structure of thermus thermopilus hb8 tt0505
83	c3komB_	Alignment	not modelled	99.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** crystal structure of apo transketolase from francisella tularensis
84	c2g28A_	Alignment	not modelled	99.2	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase e1 component; **PDBTitle:** e. coli pyruvate dehydrogenase h407a variant2 phosphonolactylthiamin diphosphate complex
85	d2ieaa2	Alignment	not modelled	99.2	24	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
86	c3ahhA_	Alignment	not modelled	99.0	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
87	c2jgdA_	Alignment	not modelled	98.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-oxoglutarate dehydrogenase e1 component; **PDBTitle:** e. coli 2-oxoglutarate dehydrogenase (e1o)
88	c1olsB_	Alignment	not modelled	98.1	11	**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
89	c1efpC_	Alignment	not modelled	98.1	21	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**protein (electron transfer flavoprotein); **PDBTitle:** electron transfer flavoprotein (etf) from paracoccus2 denitrificans
90	c2yicC_	Alignment	not modelled	98.0	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)
91	d1gpua2	Alignment	not modelled	98.0	10	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
92	d2r8oa1	Alignment	not modelled	97.9	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
93	c2bp7F_	Alignment	not modelled	97.8	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**2-oxoisovalerate dehydrogenase beta subunit; **PDBTitle:** new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
94	d1r9ja1	Alignment	not modelled	97.8	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
95	d1efva2	Alignment	not modelled	97.8	28	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
96	d1ytla1	Alignment	not modelled	97.7	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**ACDE2-like
97	d1itza2	Alignment	not modelled	97.7	12	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
98	d3clsd2	Alignment	not modelled	97.6	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
99	d1efpa2	Alignment	not modelled	97.6	24	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
100	c1ni4D_	Alignment	not modelled	97.6	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**pyruvate dehydrogenase e1 component: beta **PDBTitle:** human pyruvate dehydrogenase
101	d1w85b1	Alignment	not modelled	97.0	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
102	c1um9D_	Alignment	not modelled	96.9	14	**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
103	c2xt6B_	Alignment	not modelled	96.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
104	d2ozlb1	Alignment	not modelled	96.9	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
105	d1umdb1	Alignment	not modelled	96.6	19	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
106	c3pkiF_	Alignment	not modelled	96.6	24	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
						PDB header:hydrolase

107	c3k35D_	Alignment	not modelled	96.5	23	**Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
108	c3glsC_	Alignment	not modelled	96.4	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
109	d1qs0b1	Alignment	not modelled	96.4	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
110	d1j8fa_	Alignment	not modelled	96.4	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
111	d1m2ka_	Alignment	not modelled	96.3	22	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
112	d1yc5a1	Alignment	not modelled	96.2	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
113	c1q14A_	Alignment	not modelled	96.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
114	c2hjhB_	Alignment	not modelled	96.1	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2; **PDBTitle:** crystal structure of the sir2 deacetylase
115	d1q1aa_	Alignment	not modelled	96.0	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
116	d2b4ya1	Alignment	not modelled	96.0	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
117	c2iv2X_	Alignment	not modelled	95.9	8	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**formate dehydrogenase h; **PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
118	d1s5pa_	Alignment	not modelled	95.9	24	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
119	d1ma3a_	Alignment	not modelled	95.6	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
120	c3dufD_	Alignment	not modelled	95.6	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