







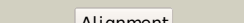

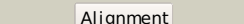

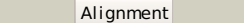

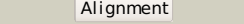

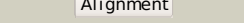

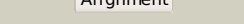
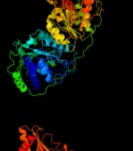
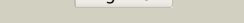
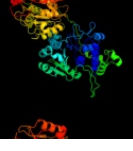



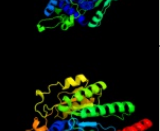




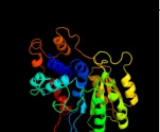


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r8pA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: transketolase 1; PDBTitle: transketolase from e. coli in complex with substrate d-2 fructose-6-phosphate
2	c3hylB_	 Alignment		100.0	50	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from bacillus anthracis
3	c1itzC_	 Alignment		100.0	49	PDB header: transferase Chain: C: PDB Molecule: transketolase; PDBTitle: maize transketolase in complex with tpp
4	c3uk1A_	 Alignment		100.0	63	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	c1r9jB_	 Alignment		100.0	48	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: transketolase from leishmania mexicana
6	c3komB_	 Alignment		100.0	53	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of apo transketolase from francisella tularensis
7	c2e6kB_	 Alignment		100.0	48	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: x-ray structure of thermus thermophilus hb8 tt0505
8	c1tkcA_	 Alignment		100.0	47	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	45	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	27	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	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
14	c3ahhA	Alignment		100.0	18	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	100	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
16	d1r9ja2	Alignment		100.0	52	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
17	d1lta1	Alignment		100.0	56	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
18	d1gpua1	Alignment		100.0	52	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
19	d2ieaa2	Alignment		100.0	28	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
20	c1olsB	Alignment		100.0	12	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
21	c1ni4D	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate dehydrogenase e1 component: beta PDBTitle: human pyruvate dehydrogenase
22	c1um9D	Alignment	not modelled	100.0	15	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	16	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	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)
25	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
26	d2r8oa1	Alignment	not modelled	100.0	100	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
27	d1lta2	Alignment	not modelled	100.0	43	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
28	d1gpua2	Alignment	not modelled	100.0	46	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	50	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	13	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	12	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	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoglutarate dehydrogenase e1 component; PDBTitle: e. coli 2-oxoglutarate dehydrogenase (e1o)
33	d1umdb1	Alignment	not modelled	100.0	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
34	d2ieaa1	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
35	d1w85b1	Alignment	not modelled	100.0	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
36	d2ozlb1	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
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	12	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	16	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	16	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	18	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	19	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	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
44	dlik6a1	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
45	d2r8oa3	Alignment	not modelled	100.0	100	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	38	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	36	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	38	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
49	d1w85b2	Alignment	not modelled	99.9	20	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
50	d2ozlb2	Alignment	not modelled	99.9	15	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	d1umdb2	Alignment	not modelled	99.9	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	d2bfdb2	Alignment	not modelled	99.8	11	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	d2ieaa3	Alignment	not modelled	99.8	22	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
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	dlik6a2	Alignment	not modelled	99.7	12	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	d1t9ba3	Alignment	not modelled	99.5	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
57	d2dja3	Alignment	not modelled	99.5	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
58	c3ju3A	Alignment	not modelled	99.5	14	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
59	d1q6za3	Alignment	not modelled	99.5	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
60	c2djiA	Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
61	d1jsca3	Alignment	not modelled	99.4	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
62	d2ihta3	Alignment	not modelled	99.4	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
63	d2ji7a3	Alignment	not modelled	99.4	23	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
64	c2c3yA	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
65	d1ybha3	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
66	d2ez9a3	Alignment	not modelled	99.3	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
67	d1ozha3	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
68	c1powA	Alignment	not modelled	99.3	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
69	c1t9dB	Alignment	not modelled	99.3	17	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	d1pvda3	Alignment	not modelled	99.3	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
71	c2pgnA	Alignment	not modelled	99.3	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
72	c2v3wC	Alignment	not modelled	99.2	18	PDB header: lyase Chain: C: PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase2 variant I461a from pseudomonas putida
73	c2q27B	Alignment	not modelled	99.2	15	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from escherichia coli
74	c2nxwB	Alignment	not modelled	99.2	15	PDB header: lyase Chain: B: PDB Molecule: phenyl-3-pyruvate decarboxylase; PDBTitle: crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasiliense
75	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
76	c1jscA	Alignment	not modelled	99.2	20	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
77	c2panF	Alignment	not modelled	99.2	20	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
78	c2vbiF	Alignment	not modelled	99.2	25	PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
79	c3eyaE	Alignment	not modelled	99.2	22	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
80	c2ag1A	Alignment	not modelled	99.2	19	PDB header: lyase Chain: A: PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
81	c1un3C	Alignment	not modelled	99.2	22	PDB header: synthase Chain: C: PDB Molecule: carboxyethylarginine synthase;

81	c1updc	Alignment	not modelled	99.2	42	PDBTitle: carboxyethylarginine synthase from streptomyces2 clavigerous (semet structure) PDB header: lyase
82	c2w93A	Alignment	not modelled	99.2	15	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	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
84	c1yi1A	Alignment	not modelled	99.2	20	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
85	c1zpdA	Alignment	not modelled	99.1	28	PDB header: alcohol fermentation Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from zymomonas mobilis
86	d1zpdA3	Alignment	not modelled	99.1	25	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	99.1	19	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	c1ozhD	Alignment	not modelled	99.1	20	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.
89	c3lq1A	Alignment	not modelled	99.0	13	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
90	c1ovmC	Alignment	not modelled	99.0	16	PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
91	c2x7jA	Alignment	not modelled	99.0	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
92	c2jlaD	Alignment	not modelled	99.0	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
93	d2c42a3	Alignment	not modelled	98.8	17	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
94	d2c42a1	Alignment	not modelled	97.9	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR Pyr module
95	d2c42a2	Alignment	not modelled	97.8	25	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module
96	d1q6za2	Alignment	not modelled	97.4	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
97	d2djia2	Alignment	not modelled	97.3	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	97.2	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
99	d1pvda2	Alignment	not modelled	97.1	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
100	d2ihta2	Alignment	not modelled	96.7	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
101	d1t9ba2	Alignment	not modelled	96.6	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
102	d1ozha2	Alignment	not modelled	96.5	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
103	d1zpdA2	Alignment	not modelled	96.4	10	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
104	d1yba2	Alignment	not modelled	96.1	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
105	d2ji7a2	Alignment	not modelled	96.1	10	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
						Fold: Thiamin diphosphate-binding fold (THDP-binding)

106	d1ovma2	Alignment	not modelled	95.4	10	Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
107	c1yd7A	Alignment	not modelled	95.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-keto acid:ferredoxin oxidoreductase subunit PDBTitle: conserved hypothetical protein pfu-1647980-001 from2 pyrococcus furiosus
108	d1wu7a1	Alignment	not modelled	82.8	14	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
109	c2zkiH	Alignment	not modelled	76.4	16	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	d2a5la1	Alignment	not modelled	75.1	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
111	d1fx0a3	Alignment	not modelled	72.7	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
112	c2zbwA	Alignment	not modelled	68.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
113	d1djq3	Alignment	not modelled	68.1	11	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: N-terminal domain of adrenodoxin reductase-like
114	d1vmea1	Alignment	not modelled	66.8	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
115	d1trba1	Alignment	not modelled	66.1	9	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
116	c2qe7C	Alignment	not modelled	65.5	14	PDB header: hydrolase Chain: C: PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
117	d1dsla1	Alignment	not modelled	65.0	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
118	d1skyb3	Alignment	not modelled	64.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
119	d1jnra2	Alignment	not modelled	62.0	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
120	c2q7vA	Alignment	not modelled	61.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin2 reductase