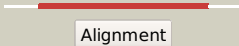



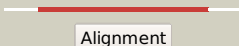

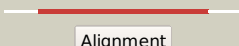

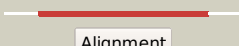

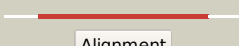

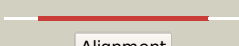











Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1449c_(tkk)_1628103_1630205
 Date Fri Aug 2 13:30:02 BST 2019
 Unique Job ID c01fa5a57f7caf43

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rimA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of mycobacterium tuberculosis transketolase2 (rv1449c)
2	c5nd5A_	 Alignment		100.0	46	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from chlamydomonas reinhardtii in2 complex with tpp and mg2+
3	c3hylB_	 Alignment		100.0	46	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from bacillus anthracis
4	c1itzC_	 Alignment		100.0	45	PDB header: transferase Chain: C: PDB Molecule: transketolase; PDBTitle: maize transketolase in complex with tpp
5	c4c7vA_	 Alignment		100.0	42	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: apo transketolase from lactobacillus salivarius at 2.2a resolution
6	c1r9jB_	 Alignment		100.0	42	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: transketolase from leishmania mexicana
7	c5hqxA_	 Alignment		100.0	44	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase mutant - h261f from pichia stipitis
8	c2r8pA_	 Alignment		100.0	44	PDB header: transferase Chain: A: PDB Molecule: transketolase 1; PDBTitle: transketolase from e. coli in complex with substrate d-fructose-6-2 phosphate
9	c5vrbB_	 Alignment		100.0	43	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of a transketolase from neisseria gonorrhoeae
10	c1tkcA_	 Alignment		100.0	45	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
11	c3uk1A_	 Alignment		100.0	43	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	c2e6kB	Alignment		100.0	51	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: x-ray structure of thermus thermophilus hb8 tt0505
13	c3komB	Alignment		100.0	38	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of apo transketolase from francisella tularensis
14	c3m7iA	Alignment		100.0	38	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase in complex with thiamine2 diphosphate, ribose-5-phosphate(pyranose form) and magnesium ion
15	c3mosA	Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: the structure of human transketolase
16	c4qoyC	Alignment		100.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase e1 component; PDBTitle: novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydrolipoyl acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
17	c2g28A	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase e1 component; PDBTitle: e. coli pyruvate dehydrogenase h407a variant2 phosphonolactylthiamin diphosphate complex
18	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) from deinococcus2 radiodurans
19	c2o1sC	Alignment		100.0	18	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
20	c6ouwA	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxps) from deinococcus2 radiodurans with enamine intermediate bound
21	c3ahhA	Alignment	not modelled	100.0	20	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
22	d1itza1	Alignment	not modelled	100.0	44	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
23	d1r9ja2	Alignment	not modelled	100.0	40	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
24	d1gpua1	Alignment	not modelled	100.0	46	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
25	d2r8oa2	Alignment	not modelled	100.0	40	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
26	d2ieaa2	Alignment	not modelled	100.0	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
27	c1ni4D	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate dehydrogenase e1 component: beta PDBTitle: human pyruvate dehydrogenase
28	c1olsB	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: roles of his291-alpha and his146-beta' in the reductive acylation2 reaction catalyzed by human branched-chain alpha-

						ketoacid3 dehydrogenase 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
29	c1um9D_	Alignment	not modelled	100.0	18	
30	c3dufD_	Alignment	not modelled	100.0	15	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
31	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)
32	d1gpua2	Alignment	not modelled	100.0	47	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
33	d1itza2	Alignment	not modelled	100.0	52	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
34	c1ik6A_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase; PDBTitle: 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum
35	d2r8oa1	Alignment	not modelled	100.0	45	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
36	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
37	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)
38	d2ieaa1	Alignment	not modelled	100.0	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
39	c2jgdA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoglutarate dehydrogenase e1 component; PDBTitle: e. coli 2-oxoglutarate dehydrogenase (e1o)
40	c2xt6B_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: B: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
41	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
42	d1umdb1	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
43	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
44	d2bfdb1	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
45	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
46	d1w85a_	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 PP module
47	d2ozla1	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 PP module
48	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
49	d1qs0a_	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
50	d2bfda1	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
51	d1ik6a1	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
52	d2r8oa3	Alignment	not modelled	99.9	50	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
53	d1itza3	Alignment	not modelled	99.9	41	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
54	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
						Fold: TK C-terminal domain-like

55	d1gpua3	Alignment	not modelled	99.9	41	Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
56	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
57	d1w85b2	Alignment	not modelled	99.8	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
58	d1umdb2	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
59	d2ozlb2	Alignment	not modelled	99.8	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
60	d2bfdb2	Alignment	not modelled	99.8	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
61	d1qs0b2	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
62	d1ik6a2	Alignment	not modelled	99.7	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
63	c5b47A_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A; PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase alpha subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 2 from sulfolobus tokodai -2 pyruvate complex
64	d2djia3	Alignment	not modelled	99.6	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
65	c4wbxC_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: C; PDB Molecule: 2-keto acid:ferredoxin oxidoreductase subunit alpha; PDBTitle: conserved hypothetical protein pf1771 from pyrococcus furiosus solved2 by sulfur sad using swiss light source data
66	c6n2nA_	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate flavodoxin/ferredoxin oxidoreductase domain PDBTitle: crystal structure of 2-oxoglutarate:ferredoxin oxidoreductase from2 magnetococcus marinus
67	d1t9ba3	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
68	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
69	c2djiA_	Alignment	not modelled	99.5	20	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
70	c5c4iA_	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: A; PDB Molecule: oxalate oxidoreductase subunit alpha; PDBTitle: structure of an oxalate oxidoreductase
71	c4q9dA_	Alignment	not modelled	99.5	21	PDB header: lyase Chain: A; PDB Molecule: benzoylformate decarboxylase; PDBTitle: x-ray structure of a putative thiamin diphosphate-dependent enzyme2 isolated from mycobacterium smegmatis
72	d2ez9a3	Alignment	not modelled	99.5	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
73	d2ji7a3	Alignment	not modelled	99.5	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
74	c1powA_	Alignment	not modelled	99.5	16	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
75	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
76	d1ozha3	Alignment	not modelled	99.4	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
77	d1ybha3	Alignment	not modelled	99.4	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
78	d2ihta3	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
79	c2pgnA_	Alignment	not modelled	99.4	16	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
80	c4rjB_	Alignment	not modelled	99.4	12	PDB header: lyase Chain: B; PDB Molecule: acetolactate synthase; PDBTitle: acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii

81	c2q27B_	Alignment	not modelled	99.4	13	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from escherichia coli
82	c4k9qB_	Alignment	not modelled	99.3	21	PDB header: lyase Chain: B: PDB Molecule: benzoylformate decarboxylase; PDBTitle: the crystal structure of benzoylformate decarboxylase from2 polynucleobacter necessarius
83	c2v3wC_	Alignment	not modelled	99.3	20	PDB header: lyase Chain: C: PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase variant l461a2 from pseudomonas putida
84	c5ahkB_	Alignment	not modelled	99.3	18	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase ii, large subunit; PDBTitle: crystal structure of acetohydroxy acid synthase pf5 from2 pseudomonas protegens
85	c1t9dB_	Alignment	not modelled	99.3	18	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase, mitochondrial; PDBTitle: crystal structure of yeast acetohydroxyacid synthase in complex with a2 sulfonyleurea herbicide, metsulfuron methyl
86	d1ovma3	Alignment	not modelled	99.3	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
87	c2nxwB_	Alignment	not modelled	99.3	16	PDB header: lyase Chain: B: PDB Molecule: phenyl-3-pyruvate decarboxylase; PDBTitle: crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
88	c3ey9B_	Alignment	not modelled	99.3	20	PDB header: oxidoreductase Chain: B: PDB Molecule: pyruvate dehydrogenase [cytochrome]; PDBTitle: structural basis for membrane binding and catalytic activation of the2 peripheral membrane enzyme pyruvate oxidase from escherichia coli
89	c2ji6B_	Alignment	not modelled	99.3	13	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: x-ray structure of oxalyl-coa decarboxylase in complex with 3-deaza-2 thdp and oxalyl-coa
90	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
91	c2vbiF_	Alignment	not modelled	99.3	26	PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter pasteurianus
92	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
93	c3eyaE_	Alignment	not modelled	99.3	20	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
94	c3ju3A_	Alignment	not modelled	99.3	16	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
95	c2panF_	Alignment	not modelled	99.3	21	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
96	d1zpdA3	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
97	c1yi1A_	Alignment	not modelled	99.2	22	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonyleurea herbicide, tribenuron methyl
98	c2vbgB_	Alignment	not modelled	99.2	16	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
99	c1zpdA_	Alignment	not modelled	99.2	26	PDB header: alcohol fermentation Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from zymomonas mobilis
100	c1upaC_	Alignment	not modelled	99.2	24	PDB header: synthase Chain: C: PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
101	c2ag1A_	Alignment	not modelled	99.2	19	PDB header: lyase Chain: A: PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
102	c5b48A_	Alignment	not modelled	99.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase alpha subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 1 from sulfolobus tokodai
103	c1ozhD_	Alignment	not modelled	99.2	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.
104	c6cipD_	Alignment	not modelled	99.2	17	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpp bound PDB header: lyase

105	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 surrogate pyruvamide
106	c3lq1A	Alignment	not modelled	99.1	18	PDB header: transferase Chain: A; PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- PDBTitle: crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene 1-2 carboxylic acid synthase/2-oxoglutarate decarboxylase from listeria3 monocytogenes str. 4b f2365
107	c1ovmC	Alignment	not modelled	99.1	20	PDB header: lyase Chain: C; PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
108	c2x7jA	Alignment	not modelled	99.1	13	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
109	c2jlaD	Alignment	not modelled	99.1	19	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
110	c2c3yA	Alignment	not modelled	99.0	15	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
111	c6n2oB	Alignment	not modelled	99.0	22	PDB header: oxidoreductase Chain: B; PDB Molecule: pyruvate ferredoxin/ferredoxin oxidoreductase, beta PDBTitle: 2-oxoglutarate:ferredoxin oxidoreductase from magnetococcus marinus2 with 2-oxoglutarate, coenzyme a and succinyl-coa bound
112	c5b46B	Alignment	not modelled	98.9	19	PDB header: oxidoreductase Chain: B; PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase beta subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 2 from sulfobolus tokodai - ligand2 free form
113	c5essB	Alignment	not modelled	98.7	12	PDB header: transferase Chain: B; PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- PDBTitle: crystal structure of m. tuberculosis mend bound to mg2+ and covalent2 intermediate i (a thdp and decarboxylated 2-oxoglutarate adduct)
114	c5c4iC	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: C; PDB Molecule: oxalate oxidoreductase subunit beta; PDBTitle: structure of an oxalate oxidoreductase
115	d2c42a3	Alignment	not modelled	98.2	13	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
116	d2c42a1	Alignment	not modelled	97.7	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR Pyr module
117	d2djia2	Alignment	not modelled	97.6	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
118	d1q6za2	Alignment	not modelled	97.6	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
119	d1zpd2	Alignment	not modelled	97.5	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
120	d2c42a2	Alignment	not modelled	97.5	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module