





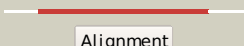

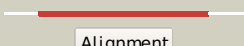
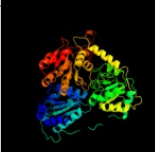
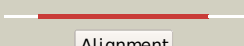

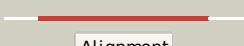
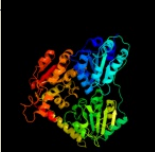

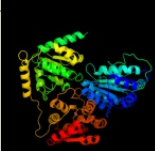








# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0AEP7
Date	Thu Jan 5 11:23:52 GMT 2012
Unique Job ID	383a2279049ab466

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2panF_</a>	 Alignment		100.0	96	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> glyoxylate carboligase; <b>PDBTitle:</b> crystal structure of e. coli glyoxylate carboligase
2	<a href="#">c2djiA_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate oxidase; <b>PDBTitle:</b> crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
3	<a href="#">c1powA_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase(oxygen as acceptor) <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate oxidase; <b>PDBTitle:</b> the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
4	<a href="#">c1yi1A_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana acetoxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
5	<a href="#">c2pgnA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexane-1,2-dione hydrolase (cdh); <b>PDBTitle:</b> the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
6	<a href="#">c1t9dB_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetolactate synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of yeast acetoxyacid synthase in2 complex with a sulfonylurea herbicide, metsulfuron methyl
7	<a href="#">c1ozhD_</a>	 Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> acetolactate synthase, catabolic; <b>PDBTitle:</b> the crystal structure of klebsiella pneumoniae acetoxyacid synthase with enzyme-bound cofactor and with an unusual3 intermediate.
8	<a href="#">c1jscA_</a>	 Alignment		100.0	32	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> acetoxyacid synthase; <b>PDBTitle:</b> crystal structure of the catalytic subunit of yeast2 acetoxyacid synthase: a target for herbicidal3 inhibitors
9	<a href="#">c3eyaE_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase [cytochrome]; <b>PDBTitle:</b> structural basis for membrane binding and catalytic2 activation of the peripheral membrane enzyme pyruvate3 oxidase from escherichia coli
10	<a href="#">c2q27B_</a>	 Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxalyl-coa decarboxylase; <b>PDBTitle:</b> crystal structure of oxalyl-coa decarboxylase from escherichia coli
11	<a href="#">c2ag1A_</a>	 Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> benzaldehyde lyase; <b>PDBTitle:</b> crystal structure of benzaldehyde lyase (bal)- semet

12	<a href="#">c2x7jA_</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene <b>PDBTitle:</b> structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
13	<a href="#">c1zpdA_</a>	Alignment		100.0	17	<b>PDB header:</b> alcohol fermentation <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> pyruvate decarboxylase from zymomonas mobilis
14	<a href="#">c2ji6B_</a>	Alignment		100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxalyl-coa decarboxylase; <b>PDBTitle:</b> x-ray structure of oxalyl-coa decarboxylase in complex with2 3-deaza-thdp and oxalyl-coa
15	<a href="#">c2vbiF_</a>	Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
16	<a href="#">c2v3wC_</a>	Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> benzoylformate decarboxylase; <b>PDBTitle:</b> crystal structure of the benzoylformate decarboxylase2 variant l461a from pseudomonas putida
17	<a href="#">c1upaC_</a>	Alignment		100.0	24	<b>PDB header:</b> synthase <b>Chain:</b> C: <b>PDB Molecule:</b> carboxyethyl arginine synthase; <b>PDBTitle:</b> carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
18	<a href="#">c2vbgB_</a>	Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> branched-chain alpha-ketoacid decarboxylase; <b>PDBTitle:</b> the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
19	<a href="#">c1ovmC_</a>	Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> indole-3-pyruvate decarboxylase; <b>PDBTitle:</b> crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
20	<a href="#">c2w93A_</a>	Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate decarboxylase isozyme 1; <b>PDBTitle:</b> crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate3 pyruvamide
21	<a href="#">c2nxwB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phenyl-3-pyruvate decarboxylase; <b>PDBTitle:</b> crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
22	<a href="#">c2jlaD_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene <b>PDBTitle:</b> crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase - semet3 protein
23	<a href="#">c3lq1A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene- <b>PDBTitle:</b> crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene2 1-carboxylic acid synthase/2-oxoglutarate decarboxylase3 from listeria monocytogenes str. 4b f2365
24	<a href="#">d2djia3</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
25	<a href="#">d1yba2</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
26	<a href="#">d1ozha2</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
27	<a href="#">d2djia2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
28	<a href="#">d2ez9a3</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module



57	<a href="#">d1pvdA1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
58	<a href="#">c2c3yA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase; <b>PDBTitle:</b> crystal structure of the radical form of 2 pyruvate:ferredoxin oxidoreductase from <i>Desulfovibrio3 africanus</i>
59	<a href="#">d2c42a1</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> PFOR Pyr module
60	<a href="#">c3cf4G</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase epsilon subunit; <b>PDBTitle:</b> structure of the codh component of the <i>m. barkeri</i> acds complex
61	<a href="#">d2oz1a1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
62	<a href="#">d1w85a</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
63	<a href="#">d2bfdA1</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
64	<a href="#">d1umda</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
65	<a href="#">d2r8oa2</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like PP module
66	<a href="#">d1gpua1</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like PP module
67	<a href="#">c1yd7A</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-keto acid:ferredoxin oxidoreductase subunit <b>PDBTitle:</b> conserved hypothetical protein pfu-1647980-001 from 2 <i>pyrococcus furiosus</i>
68	<a href="#">d1r9ja2</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like PP module
69	<a href="#">d1itza1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like PP module
70	<a href="#">d1qs0a</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase PP module
71	<a href="#">d2c42a2</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> PFOR PP module
72	<a href="#">c3hylB</a>	Alignment	not modelled	99.3	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase from <i>Bacillus anthracis</i>
73	<a href="#">c1tkcA</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> specificity of coenzyme binding in thiamin diphosphate2 dependent enzymes: crystal structures of yeast3 transketolase in complex with analogs of thiamin4 diphosphate
74	<a href="#">c3m7iA</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of transketolase in complex with thiamine2 diphosphate, ribose-5-phosphate(pyranose form) and3 magnesium ion
75	<a href="#">c2o1xA</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose-5-phosphate synthase; <b>PDBTitle:</b> 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from 2 <i>deinococcus radiodurans</i>
76	<a href="#">c1itzC</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> maize transketolase in complex with tpp
77	<a href="#">c3uk1A</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of a transketolase from <i>Burkholderia thailandensis</i> 2 with an oxidized cysteinesulfonic acid in the active site
78	<a href="#">c3mosA</a>	Alignment	not modelled	99.3	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> the structure of human transketolase
79	<a href="#">c2e6kB</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> x-ray structure of <i>Thermus thermophilus</i> hb8 tt0505
80	<a href="#">c1r9jB</a>	Alignment	not modelled	99.3	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> transketolase from <i>Leishmania mexicana</i>
81	<a href="#">c2r8pA</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase 1; <b>PDBTitle:</b> transketolase from <i>E. coli</i> in complex with substrate d-2 fructose-6-phosphate <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 1-deoxy-d-xylulose-5-phosphate

82	<a href="#">c2o1sC</a>	Alignment	not modelled	99.3	19	synthase; <b>PDBTitle:</b> 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 escherichia coli
83	<a href="#">c3komB</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> crystal structure of apo transketolase from francisella tularensis
84	<a href="#">c2g28A</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase e1 component; <b>PDBTitle:</b> e. coli pyruvate dehydrogenase h407a variant2 phosphonolactylthiamin diphosphate complex
85	<a href="#">d2ieaa2</a>	Alignment	not modelled	99.0	20	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like PP module
86	<a href="#">c3ahhA</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose 5-phosphate/fructose 6- phosphate phosphoketolase; <b>PDBTitle:</b> h142a mutant of phosphoketolase from bifidobacterium breve complexed2 with acetyl thiamine diphosphate
87	<a href="#">c2jgdA</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e1 component; <b>PDBTitle:</b> e. coli 2-oxoglutarate dehydrogenase (e1o)
88	<a href="#">c2yicC</a>	Alignment	not modelled	98.3	26	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-oxoglutarate decarboxylase; <b>PDBTitle:</b> crystal structure of the suca domain of mycobacterium smegmatis2 alpha-ketoglutarate decarboxylase (tri clinic form)
89	<a href="#">c1efpC</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> protein (electron transfer flavoprotein); <b>PDBTitle:</b> electron transfer flavoprotein (etf) from paracoccus2 denitrificans
90	<a href="#">d1ytlA1</a>	Alignment	not modelled	97.9	17	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> ACDE2-like
91	<a href="#">c1olsB</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoisovalerate dehydrogenase beta subunit; <b>PDBTitle:</b> roles of his291-alpha and his146-beta' in the reductive2 acylation reaction catalyzed by human branched-chain3 alpha- ketoacid dehydrogenase
92	<a href="#">d1efva2</a>	Alignment	not modelled	97.8	22	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> C-terminal domain of the electron transfer flavoprotein alpha subunit
93	<a href="#">d3clsd2</a>	Alignment	not modelled	97.7	15	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> C-terminal domain of the electron transfer flavoprotein alpha subunit
94	<a href="#">d1efpa2</a>	Alignment	not modelled	97.6	21	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> C-terminal domain of the electron transfer flavoprotein alpha subunit
95	<a href="#">d2r8oa1</a>	Alignment	not modelled	97.6	11	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
96	<a href="#">c2xt6B</a>	Alignment	not modelled	97.6	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoglutarate decarboxylase; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis alpha- ketoglutarate2 decarboxylase homodimer (orthorhombic form)
97	<a href="#">d1gpua2</a>	Alignment	not modelled	97.5	10	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
98	<a href="#">c1ni4D</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate dehydrogenase e1 component: beta <b>PDBTitle:</b> human pyruvate dehydrogenase
99	<a href="#">d1w85b1</a>	Alignment	not modelled	97.3	15	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
100	<a href="#">c3dufD</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate dehydrogenase e1 component subunit beta; <b>PDBTitle:</b> snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
101	<a href="#">d1r9ja1</a>	Alignment	not modelled	97.2	14	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
102	<a href="#">d2ozlb1</a>	Alignment	not modelled	97.1	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
103	<a href="#">d1itza2</a>	Alignment	not modelled	96.8	10	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
104	<a href="#">c1um9D</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-oxo acid dehydrogenase beta subunit; <b>PDBTitle:</b> branched-chain 2-oxo acid dehydrogenase (e1) from thermus2 thermophilus hb8 in apo-form
105	<a href="#">d1umdb1</a>	Alignment	not modelled	96.5	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module
106	<a href="#">c3glsC</a>	Alignment	not modelled	96.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-3, <b>PDBTitle:</b> crystal structure of human sirt3
107	<a href="#">d2bfdb1</a>	Alignment	not modelled	96.4	15	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase Pyr module

108	<a href="#">c3pkiF_</a>	Alignment	not modelled	96.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> human sirt6 crystal structure in complex with adp ribose
109	<a href="#">c2hjhB_</a>	Alignment	not modelled	96.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent histone deacetylase sir2; <b>PDBTitle:</b> crystal structure of the sir2 deacetylase
110	<a href="#">c1pt9B_</a>	Alignment	not modelled	96.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase, mitochondrial; <b>PDBTitle:</b> crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
111	<a href="#">d1ma3a_</a>	Alignment	not modelled	95.8	12	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
112	<a href="#">c2bruC_</a>	Alignment	not modelled	95.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit beta; <b>PDBTitle:</b> complex of the domain i and domain iii of escherichia coli2 transhydrogenase
113	<a href="#">c3k35D_</a>	Alignment	not modelled	95.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> crystal structure of human sirt6
114	<a href="#">c1q14A_</a>	Alignment	not modelled	95.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hst2 protein; <b>PDBTitle:</b> structure and autoregulation of the yeast hst2 homolog of sir2
115	<a href="#">d1m2ka_</a>	Alignment	not modelled	95.8	15	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
116	<a href="#">d1d4oa_</a>	Alignment	not modelled	95.7	19	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Transhydrogenase domain III (dIII)
117	<a href="#">d1s5pa_</a>	Alignment	not modelled	95.7	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
118	<a href="#">d1yc5a1</a>	Alignment	not modelled	95.6	8	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
119	<a href="#">d1q1aa_</a>	Alignment	not modelled	95.6	18	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
120	<a href="#">c3c2qA_</a>	Alignment	not modelled	95.5	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> crystal structure of conserved putative lor/sdh protein2 from methanococcus maripaludis s2