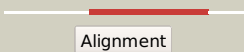

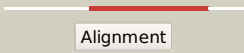



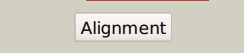



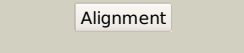

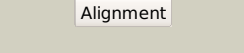



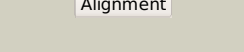

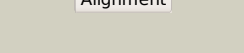

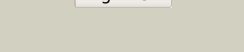




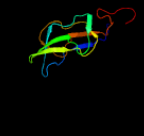


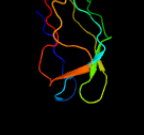
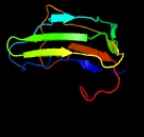
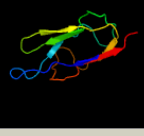


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2495c_(pdhC)_2808768_2809949
Date	Wed Aug 7 12:50:12 BST 2019
Unique Job ID	14e2a315c818ebe7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3l60A_</a>	 Alignment		100.0	100	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> branched-chain alpha-keto acid dehydrogenase; <b>PDBTitle:</b> crystal structure of branched-chain alpha-keto acid dehydrogenase2 subunit e2 from mycobacterium tuberculosis
2	<a href="#">c2ii4C_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> lipoamide acyltransferase component of branched-chain <b>PDBTitle:</b> crystal structure of a cubic core of the dihydrolipoamide2 acyltransferase (e2b) component in the branched-chain alpha-ketoacid3 dehydrogenase complex (bckdc), coenzyme a-bound form
3	<a href="#">d1b5sa_</a>	 Alignment		100.0	33	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
4	<a href="#">d1dpba_</a>	 Alignment		100.0	29	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
5	<a href="#">c4n72B_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate dehydrogenase (dihydrolipoyl)transacetylase <b>PDBTitle:</b> catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
6	<a href="#">c3b8kA_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase; <b>PDBTitle:</b> structure of the truncated human dihydrolipoyl acetyltransferase (e2)
7	<a href="#">d1scza_</a>	 Alignment		100.0	29	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
8	<a href="#">c6h60A_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component, mitochondrial; <b>PDBTitle:</b> pseudo-atomic structural model of the e3bp component of the human2 pyruvate dehydrogenase multienzyme complex
9	<a href="#">c3maeA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-oxoisovalerate dehydrogenase e2 component, <b>PDBTitle:</b> crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
10	<a href="#">c3rqcB_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable lipoamide acyltransferase; <b>PDBTitle:</b> crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum
11	<a href="#">d1q23a_</a>	 Alignment		100.0	15	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like

12	<a href="#">d3claa_</a>	Alignment		100.0	14	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
13	<a href="#">c2i9dC_</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> chloramphenicol acetyltransferase
14	<a href="#">c2dneA_</a>	Alignment		99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
15	<a href="#">c2dncA_</a>	Alignment		99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component; <b>PDBTitle:</b> solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
16	<a href="#">d1y8ob1</a>	Alignment		99.9	20	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
17	<a href="#">c2q8iB_</a>	Alignment		99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase component of <b>PDBTitle:</b> pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
18	<a href="#">c2i5tA_</a>	Alignment		99.9	45	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipoamide acyltransferase; <b>PDBTitle:</b> solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
19	<a href="#">d1k8ma_</a>	Alignment		99.9	37	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
20	<a href="#">d1ghja_</a>	Alignment		99.9	26	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
21	<a href="#">d1gjxa_</a>	Alignment	not modelled	99.8	32	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
22	<a href="#">d1qjoa_</a>	Alignment	not modelled	99.8	39	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
23	<a href="#">d1laba_</a>	Alignment	not modelled	99.8	41	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
24	<a href="#">d1iyua_</a>	Alignment	not modelled	99.8	36	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
25	<a href="#">d1pmra_</a>	Alignment	not modelled	99.8	30	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
26	<a href="#">d2pnrc1</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
27	<a href="#">c2ejmA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methylcrotonoyl-coa carboxylase subunit alpha; <b>PDBTitle:</b> solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
28	<a href="#">c2xt6B_</a>	Alignment	not modelled	99.7	20	<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) <b>PDB header:</b> ligase

29	<a href="#">c2dn8A</a>	Alignment	not modelled	99.7	20	<b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
30	<a href="#">c2kccA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
31	<a href="#">c2b8gA</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> biotin/lipoyl attachment protein; <b>PDBTitle:</b> solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
32	<a href="#">c2ejgD</a>	Alignment	not modelled	99.6	35	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> 149aa long hypothetical methylmalonyl-coa decarboxylase <b>PDBTitle:</b> crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
33	<a href="#">d1dcza</a>	Alignment	not modelled	99.6	34	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
34	<a href="#">d1o78a</a>	Alignment	not modelled	99.5	33	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
35	<a href="#">c3n6rK</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> ligase <b>Chain:</b> K: <b>PDB Molecule:</b> propionyl-coa carboxylase, alpha subunit; <b>PDBTitle:</b> crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
36	<a href="#">d1bdoa</a>	Alignment	not modelled	99.5	26	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
37	<a href="#">c5ks8D</a>	Alignment	not modelled	99.5	27	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
38	<a href="#">c3bg5B</a>	Alignment	not modelled	99.4	34	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus pyruvate carboxylase
39	<a href="#">c3hblA</a>	Alignment	not modelled	99.4	34	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of s. aureus pyruvate carboxylase t908a mutant
40	<a href="#">c4hnbB</a>	Alignment	not modelled	99.4	34	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of r54e mutant of s. aureus pyruvate carboxylase
41	<a href="#">c5vz0D</a>	Alignment	not modelled	99.4	31	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
42	<a href="#">c5ks8F</a>	Alignment	not modelled	99.4	27	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
43	<a href="#">c4qskB</a>	Alignment	not modelled	99.4	26	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
44	<a href="#">c3u9sA</a>	Alignment	not modelled	99.4	33	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
45	<a href="#">c5cslA</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
46	<a href="#">c6g2dC</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa carboxylase 1; <b>PDBTitle:</b> citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
47	<a href="#">c4rcnA</a>	Alignment	not modelled	99.3	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> long-chain acyl-coa carboxylase; <b>PDBTitle:</b> structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase
48	<a href="#">c3bg3A</a>	Alignment	not modelled	99.3	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase, mitochondrial; <b>PDBTitle:</b> crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
49	<a href="#">c5csaA</a>	Alignment	not modelled	99.3	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of domains bt-bccp-ac1-ac5 of yeast acetyl-coa2 carboxylase
50	<a href="#">c3va7A</a>	Alignment	not modelled	99.2	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> klla0e08119p; <b>PDBTitle:</b> crystal structure of the kluyveromyces lactis urea carboxylase
51	<a href="#">c2cooA</a>	Alignment	not modelled	99.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipoamide acyltransferase component of branched- <b>PDBTitle:</b> solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
52	<a href="#">c1w3dA</a>	Alignment	not modelled	99.0	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase component of <b>PDBTitle:</b> nmr structure of the peripheral-subunit binding domain of bacillus2 stearothermophilus e2p
53	<a href="#">c2eq9C</a>	Alignment	not modelled	98.9	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from

						thermus thermophilus2 hb8 with psbdb
54	<a href="#">c1zwvA</a>	Alignment	not modelled	98.9	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipamide acyltransferase component of branched- <b>PDBTitle:</b> solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
55	<a href="#">c4qoyE</a>	Alignment	not modelled	98.9	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase (dihydrolipoyltransacetylase) <b>PDBTitle:</b> 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
56	<a href="#">d1bala</a>	Alignment	not modelled	98.9	28	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
57	<a href="#">d1w85i</a>	Alignment	not modelled	98.9	40	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
58	<a href="#">c1w4kA</a>	Alignment	not modelled	98.9	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase e2; <b>PDBTitle:</b> peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
59	<a href="#">c3dv0l</a>	Alignment	not modelled	98.9	40	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> I: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
60	<a href="#">c2eq8C</a>	Alignment	not modelled	98.8	59	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
61	<a href="#">d1w4ha1</a>	Alignment	not modelled	98.8	32	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
62	<a href="#">c2eq7C</a>	Alignment	not modelled	98.8	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e2 component; <b>PDBTitle:</b> crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
63	<a href="#">d2cyua1</a>	Alignment	not modelled	98.8	37	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
64	<a href="#">c2qf7A</a>	Alignment	not modelled	98.7	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase protein; <b>PDBTitle:</b> crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
65	<a href="#">c2k33A</a>	Alignment	not modelled	98.4	33	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> acra; <b>PDBTitle:</b> solution structure of an n-glycosylated protein using in2 vitro glycosylation
66	<a href="#">c3tw6B</a>	Alignment	not modelled	98.3	24	<b>PDB header:</b> ligase/activator <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase protein; <b>PDBTitle:</b> structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a
67	<a href="#">c5a35A</a>	Alignment	not modelled	98.2	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> crystal structure of glycine cleavage protein h-like (gcvh-1)2 from streptococcus pyogenes
68	<a href="#">c4kkuD</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> membrane fusion protein; <b>PDBTitle:</b> structure of besa (selenomethionone derivative - p212121)
69	<a href="#">c3t51C</a>	Alignment	not modelled	97.6	23	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> cation efflux system protein cusb; <b>PDBTitle:</b> crystal structures of the pre-extrusion and extrusion states of the2 cusba adaptor-transporter complex
70	<a href="#">c3h9iB</a>	Alignment	not modelled	97.6	25	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> cation efflux system protein cusb; <b>PDBTitle:</b> crystal structure of the membrane fusion protein cusb from escherichia2 coli
71	<a href="#">d1hpca</a>	Alignment	not modelled	97.5	26	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
72	<a href="#">d1onla</a>	Alignment	not modelled	97.5	38	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
73	<a href="#">c3iftA</a>	Alignment	not modelled	97.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
74	<a href="#">c3mxuA</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> crystal structure of glycine cleavage system protein h from bartonella2 henselae <b>PDB header:</b> biosynthetic protein

75	<a href="#">c2edgA</a>	Alignment	not modelled	97.4	27	<b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> solution structure of the gcv_h domain from mouse glycine
76	<a href="#">c2qj8B</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mlr6093 protein; <b>PDBTitle:</b> crystal structure of an aspartoacylase family protein (mlr6093) from <i>Mesorhizobium loti</i> maff303099 at 2.00 Å resolution
77	<a href="#">c2ka7A</a>	Alignment	not modelled	97.0	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> nmr solution structure of tm0212 at 40 °C
78	<a href="#">c3a8jF</a>	Alignment	not modelled	97.0	24	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> crystal structure of et-ehred complex
79	<a href="#">c5c22A</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chromosomal hemolysin d; <b>PDBTitle:</b> crystal structure of zn-bound hlyd from <i>E. coli</i>
80	<a href="#">c2aukA</a>	Alignment	not modelled	96.5	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain; <b>PDBTitle:</b> structure of <i>E. coli</i> rna polymerase beta' g/g' insert
81	<a href="#">c5xu0B</a>	Alignment	not modelled	96.5	21	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> membrane-fusion protein; <b>PDBTitle:</b> structure of the membrane fusion protein spr0693 from <i>Streptococcus pneumoniae</i> r6
82	<a href="#">c4tkoB</a>	Alignment	not modelled	96.4	22	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> emra; <b>PDBTitle:</b> structure of the periplasmic adaptor protein emra
83	<a href="#">c3fmcC</a>	Alignment	not modelled	96.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> putative succinylglutamate desuccinylase / aspartoacylase; <b>PDBTitle:</b> crystal structure of a putative succinylglutamate desuccinylase / aspartoacylase family protein (sama_0604) from <i>Shewanella amazonensis</i> sb2b at 1.80 Å resolution
84	<a href="#">c3na6A</a>	Alignment	not modelled	96.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> succinylglutamate desuccinylase/aspartoacylase; <b>PDBTitle:</b> crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from <i>Silicibacter</i> sp. tm1040 at 2.00 Å resolution
85	<a href="#">c3fppB</a>	Alignment	not modelled	96.3	23	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> macrolide-specific efflux protein maca; <b>PDBTitle:</b> crystal structure of <i>E. coli</i> maca
86	<a href="#">c5nilG</a>	Alignment	not modelled	96.1	24	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> macrolide export protein maca; <b>PDBTitle:</b> structure of the macab-tolc abc-type tripartite multidrug efflux pump-2 macb section
87	<a href="#">c1t5eB</a>	Alignment	not modelled	96.0	29	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> multidrug resistance protein mexa; <b>PDBTitle:</b> the structure of mexa
88	<a href="#">c5v5sH</a>	Alignment	not modelled	96.0	18	<b>PDB header:</b> membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> multidrug efflux pump subunit acra; <b>PDBTitle:</b> multi-drug efflux; membrane transport; rnd superfamily; drug2 resistance
89	<a href="#">c2f5zK</a>	Alignment	not modelled	95.9	22	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> K: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component; <b>PDBTitle:</b> crystal structure of human dihydrolipoamide dehydrogenase2 (e3) complexed to the e3-binding domain of human e3-3 binding protein
90	<a href="#">c1zy8M</a>	Alignment	not modelled	95.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component, <b>PDBTitle:</b> the crystal structure of dihydrolipoamide dehydrogenase and2 dihydrolipoamide dehydrogenase-binding protein (didomain)3 subcomplex of human pyruvate dehydrogenase complex.
91	<a href="#">c4p6vA</a>	Alignment	not modelled	95.9	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> na(+)-translocating nadh-quinone reductase subunit a; <b>PDBTitle:</b> crystal structure of the na <sup>+</sup> -translocating nadh: ubiquinone2 oxidoreductase from <i>Vibrio cholerae</i>
92	<a href="#">d1vf7a</a>	Alignment	not modelled	95.9	29	<b>Fold:</b> HlyD-like secretion proteins <b>Superfamily:</b> HlyD-like secretion proteins <b>Family:</b> HlyD-like secretion proteins
93	<a href="#">c4dk1B</a>	Alignment	not modelled	95.8	26	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative maca, multidrug resistance protein mexa; <b>PDBTitle:</b> crystal structure of maca-mexa chimeric protein, containing the2 pseudomonas aeruginosa mexa alpha-hairpin domain.
94	<a href="#">c2f60K</a>	Alignment	not modelled	95.8	22	<b>PDB header:</b> protein binding <b>Chain:</b> K: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component; <b>PDBTitle:</b> crystal structure of the dihydrolipoamide dehydrogenase (e3)-binding2 domain of human e3-binding protein
95	<a href="#">c2v4dM</a>	Alignment	not modelled	95.7	18	<b>PDB header:</b> membrane protein <b>Chain:</b> M: <b>PDB Molecule:</b> multidrug resistance protein mexa; <b>PDBTitle:</b> re-refinement of mexa adaptor protein
96	<a href="#">c2f1mA</a>	Alignment	not modelled	95.6	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein a; <b>PDBTitle:</b> conformational flexibility in the multidrug efflux system protein acra
97	<a href="#">c3lnnB</a>	Alignment	not modelled	95.6	44	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> membrane fusion protein (mfp) heavy metal cation efflux <b>PDBTitle:</b> crystal structure of zneb from <i>Cupriavidus metallidurans</i>
98	<a href="#">c3lnnA</a>	Alignment	not modelled	95.6	28	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> membrane fusion protein (mfp) heavy metal cation efflux <b>PDBTitle:</b> crystal structure of zneb from <i>Cupriavidus metallidurans</i>

99	<a href="#">c3cdxB</a>	Alignment	not modelled	95.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> succinylglutamatedesuccinylase/aspartoacylase; <b>PDBTitle:</b> crystal structure of succinylglutamatedesuccinylase/aspartoacylase2 from rhodobacter sphaeroides
100	<a href="#">c4l8jA</a>	Alignment	not modelled	95.2	29	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative efflux transporter; <b>PDBTitle:</b> crystal structure of a putative efflux transporter (bacegg_01895) from bacteroides eggerthii dsm 20697 at 2.06 a resolution
101	<a href="#">c2jkuA</a>	Alignment	not modelled	95.0	38	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> propionyl-coa carboxylase alpha chain, mitochondrial; <b>PDBTitle:</b> crystal structure of the n-terminal region of the biotin acceptor2 domain of human propionyl-coa carboxylase
102	<a href="#">c4dk0A</a>	Alignment	not modelled	94.8	26	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative maca; <b>PDBTitle:</b> crystal structure of maca from actinobacillus actinomycetemcomitans
103	<a href="#">c5nenA</a>	Alignment	not modelled	94.7	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase c; <b>PDBTitle:</b> crystal structure of the soluble domain of lipc, a membrane fusion2 protein of a type i secretion system
104	<a href="#">d2gpra</a>	Alignment	not modelled	94.7	21	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
105	<a href="#">c2aujD</a>	Alignment	not modelled	94.2	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain; <b>PDBTitle:</b> structure of thermus aquaticus rna polymerase beta'-subunit2 insert
106	<a href="#">d1brwa3</a>	Alignment	not modelled	93.9	17	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
107	<a href="#">c3d4rE</a>	Alignment	not modelled	93.7	24	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> domain of unknown function from the pfam-b_34464 family; <b>PDBTitle:</b> crystal structure of a duf2118 family protein (mmp0046) from methanococcus maripaludis at 2.20 a resolution
108	<a href="#">c3h5qA</a>	Alignment	not modelled	91.6	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine-nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
109	<a href="#">d1uoua3</a>	Alignment	not modelled	91.3	17	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
110	<a href="#">c2dsjA</a>	Alignment	not modelled	91.2	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine-nucleoside (thymidine) phosphorylase; <b>PDBTitle:</b> crystal structure of project id tt0128 from thermus thermophilus hb8
111	<a href="#">d2tpta3</a>	Alignment	not modelled	91.2	17	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
112	<a href="#">c1brwB</a>	Alignment	not modelled	91.1	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (pyrimidine nucleoside phosphorylase); <b>PDBTitle:</b> the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
113	<a href="#">d2f3ga</a>	Alignment	not modelled	91.0	19	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
114	<a href="#">d1o4ua2</a>	Alignment	not modelled	90.9	19	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like
115	<a href="#">d1glaf</a>	Alignment	not modelled	90.8	19	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
116	<a href="#">c2j0fC</a>	Alignment	not modelled	90.7	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> thymidine phosphorylase; <b>PDBTitle:</b> structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
117	<a href="#">c4ga5H</a>	Alignment	not modelled	90.4	21	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> putative thymidine phosphorylase; <b>PDBTitle:</b> crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
118	<a href="#">c4g0bA</a>	Alignment	not modelled	90.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxycinnamoyl-coa shikimate/quinatate <b>PDBTitle:</b> structure of native hct from coffea canephora
119	<a href="#">c1otpA</a>	Alignment	not modelled	89.1	17	<b>PDB header:</b> phosphorylase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine phosphorylase; <b>PDBTitle:</b> structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
120	<a href="#">d1qapa2</a>	Alignment	not modelled	88.8	33	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like