

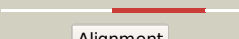





















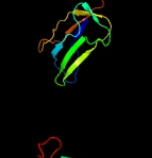

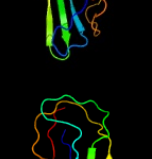

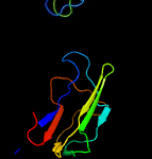
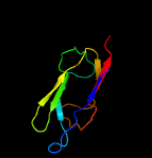
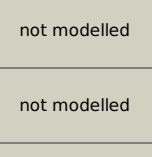


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2215_(dlaT)_2481973_2483634
Date	Mon Aug 5 13:25:34 BST 2019
Unique Job ID	b68c52988ec56580

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4n72B_	 Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase (dihydrolipoiltransacetylase PDBTitle: catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
2	d1b5sa_	 Alignment		100.0	39	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
3	c2ii4C_	 Alignment		100.0	32	PDB header: transferase Chain: C: PDB Molecule: lipoamide acyltransferase component of branched-chain PDBTitle: 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
4	d1dpba_	 Alignment		100.0	34	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
5	c3i60A_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: branched-chain alpha-keto acid dehydrogenase; PDBTitle: crystal structure of branched-chain alpha-keto acid dehydrogenase2 subunit e2 from mycobacterium tuberculosis
6	c3b8kA_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoilysine-residue acetyltransferase; PDBTitle: structure of the truncated human dihydrolipoil acetyltransferase (e2)
7	c6h60A_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component, mitochondrial; PDBTitle: pseudo-atomic structural model of the e3bp component of the human2 pyruvate dehydrogenase multienzyme complex
8	d1scza_	 Alignment		100.0	40	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
9	c3maeA_	 Alignment		100.0	35	PDB header: transferase Chain: A: PDB Molecule: 2-oxoisovalerate dehydrogenase e2 component, PDBTitle: crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
10	c3rqcB_	 Alignment		100.0	39	PDB header: transferase Chain: B: PDB Molecule: probable lipoamide acyltransferase; PDBTitle: crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum
11	d1q23a_	 Alignment		100.0	16	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like

12	d3claa_	Alignment		100.0	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
13	c2i9dC_	Alignment		100.0	18	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
14	c2dneA_	Alignment		99.9	28	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
15	c2dncA_	Alignment		99.9	27	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
16	d1y8ob1	Alignment		99.8	33	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
17	c2l5tA_	Alignment		99.8	47	PDB header: transferase Chain: A: PDB Molecule: lipoamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
18	c2q8iB_	Alignment		99.8	33	PDB header: transferase Chain: B: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
19	d1k8ma_	Alignment		99.8	33	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
20	d1ghja_	Alignment		99.8	37	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
21	d1qjoa_	Alignment	not modelled	99.8	30	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
22	d1laba_	Alignment	not modelled	99.8	35	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
23	d1gjxa_	Alignment	not modelled	99.8	24	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
24	c2xt6B_	Alignment	not modelled	99.7	26	PDB header: lyase Chain: B: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
25	d1pmra_	Alignment	not modelled	99.7	38	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
26	d1iyua_	Alignment	not modelled	99.7	28	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
27	d2pnrc1	Alignment	not modelled	99.7	36	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
28	c2ejmA_	Alignment	not modelled	99.6	18	PDB header: ligase Chain: A: PDB Molecule: methylcrotonoyl-coa carboxylase subunit alpha; PDBTitle: solution structure of ruh-072, an apo-biotinyl domain form2 human acetyl coenzyme a carboxylase PDB header: ligase

29	c2dn8A	Alignment	not modelled	99.6	19	Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of rsg1 ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
30	c2b8gA	Alignment	not modelled	99.5	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: biotin/lipoyl attachment protein; PDBTitle: solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
31	c2kccA	Alignment	not modelled	99.5	20	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
32	c2ejgD	Alignment	not modelled	99.5	36	PDB header: ligase Chain: D: PDB Molecule: 149aa long hypothetical methylmalonyl-coa decarboxylase PDBTitle: crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
33	d1dcza	Alignment	not modelled	99.5	37	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
34	d1o78a	Alignment	not modelled	99.4	37	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
35	c3n6rK	Alignment	not modelled	99.4	18	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
36	d1bdoa	Alignment	not modelled	99.4	25	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
37	c5ks8D	Alignment	not modelled	99.3	24	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
38	c3bg5B	Alignment	not modelled	99.3	31	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
39	c3hblA	Alignment	not modelled	99.3	31	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
40	c4hnbB	Alignment	not modelled	99.3	31	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
41	c5ks8F	Alignment	not modelled	99.3	24	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
42	c5vz0D	Alignment	not modelled	99.3	23	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
43	c4qskB	Alignment	not modelled	99.2	30	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
44	c3u9sA	Alignment	not modelled	99.2	33	PDB header: ligase Chain: A: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
45	c3bg3A	Alignment	not modelled	99.2	28	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
46	c4rcnA	Alignment	not modelled	99.2	21	PDB header: ligase Chain: A: PDB Molecule: long-chain acyl-coa carboxylase; PDBTitle: structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase
47	c5cslA	Alignment	not modelled	99.1	19	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
48	c3va7A	Alignment	not modelled	99.1	27	PDB header: ligase Chain: A: PDB Molecule: kla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
49	c5c22A	Alignment	not modelled	99.1	17	PDB header: protein transport Chain: A: PDB Molecule: chromosomal hemolysin d; PDBTitle: crystal structure of zn-bound hlyd from e. coli
50	c6g2dC	Alignment	not modelled	99.0	14	PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
51	c5csaA	Alignment	not modelled	99.0	19	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of domains bt-bccp-ac1-ac5 of yeast acetyl-coa2 carboxylase
52	c2cooA	Alignment	not modelled	98.9	34	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase component of branched- PDBTitle: solution structure of the e3 binding domain of2 dihydrolipoamide branched chaintransacylase
53	c2k33A	Alignment	not modelled	98.9	22	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: acrca; PDBTitle: solution structure of an n-glycosylated protein using in2 vitro glycosylation
						PDB header: hydrolase

54	c5nenA	Alignment	not modelled	98.8	21	Chain: A: PDB Molecule: lipase c; PDBTitle: crystal structure of the soluble domain of lipc, a membrane fusion2 protein of a type i secretion system
55	c3fppB	Alignment	not modelled	98.7	14	PDB header: membrane protein Chain: B: PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
56	c2f1mA	Alignment	not modelled	98.7	14	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
57	c4dk0A	Alignment	not modelled	98.7	14	PDB header: membrane protein Chain: A: PDB Molecule: putative maca; PDBTitle: crystal structure of maca from actinobacillus actinomycetemcomitans
58	c3h9iB	Alignment	not modelled	98.7	14	PDB header: transport protein Chain: B: PDB Molecule: cation efflux system protein cusb; PDBTitle: crystal structure of the membrane fusion protein cusb from escherichia2 coli
59	c4tkoB	Alignment	not modelled	98.7	20	PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
60	c1w4kA	Alignment	not modelled	98.7	40	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase e2; PDBTitle: peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
61	c1zwvA	Alignment	not modelled	98.6	41	PDB header: transferase Chain: A: PDB Molecule: lipoamide acyltransferase component of branched- PDBTitle: solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
62	c5v5sH	Alignment	not modelled	98.6	14	PDB header: membrane protein Chain: H: PDB Molecule: multidrug efflux pump subunit acra; PDBTitle: multi-drug efflux; membrane transport; rnd superfamily; drug2 resistance
63	c1w3dA	Alignment	not modelled	98.6	36	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoalysine-residue acetyltransferase component of PDBTitle: nmr structure of the peripheral-subunit binding domain of bacillus2 stearothermophilus e2p
64	c2eq9C	Alignment	not modelled	98.6	45	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
65	c4qoyE	Alignment	not modelled	98.6	41	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase (dihydrolipoalysine-residue) PDBTitle: novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydrolipoal acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
66	c5niIG	Alignment	not modelled	98.6	14	PDB header: transport protein Chain: G: PDB Molecule: macrolide export protein maca; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump-2 macb section
67	d1w85i	Alignment	not modelled	98.6	39	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
68	c4l8jA	Alignment	not modelled	98.6	15	PDB header: transport protein Chain: A: PDB Molecule: putative efflux transporter; PDBTitle: crystal structure of a putative efflux transporter (bacegg_01895) from2 bacteroides eggerthii dsm 20697 at 2.06 a resolution
69	c2v4dM	Alignment	not modelled	98.6	14	PDB header: membrane protein Chain: M: PDB Molecule: multidrug resistance protein mexa; PDBTitle: re-refinement of mexa adaptor protein
70	d1w4ha1	Alignment	not modelled	98.6	35	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
71	c2eq8C	Alignment	not modelled	98.6	44	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
72	d1bala	Alignment	not modelled	98.6	30	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
73	c3dv0L	Alignment	not modelled	98.6	39	PDB header: oxidoreductase/transferase Chain: I: PDB Molecule: dihydrolipoalysine-residue acetyltransferase PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
74	d2cyua1	Alignment	not modelled	98.5	38	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
75	c3lppA	Alignment	not modelled	98.5	13	PDB header: metal transport Chain: A: PDB Molecule: membrane fusion protein (mfp) heavy

75	c3lnnA	Alignment	not modelled	98.5	13	metal cation efflux PDB header: crystal structure of zneb from cupriavidus metallidurans PDB header: transport protein
76	c3t51C	Alignment	not modelled	98.5	14	Chain: C; PDB Molecule: cation efflux system protein cusb; PDBTitle: crystal structures of the pre-extrusion and extrusion states of the2 cusba adaptor-transporter complex
77	c5xu0B	Alignment	not modelled	98.5	10	PDB header: transport protein Chain: B; PDB Molecule: membrane-fusion protein; PDBTitle: structure of the membrane fusion protein spr0693 from streptococcus2 pneumoniae r6
78	c4dk1B	Alignment	not modelled	98.4	14	PDB header: membrane protein Chain: B; PDB Molecule: putative maca, multidrug resistance protein mexa; PDBTitle: crystal structure of maca-mexa chimeric protein, containing the2 pseudomonas aeruginosa mexa alpha-hairpin domain.
79	c2eq7C	Alignment	not modelled	98.4	41	PDB header: oxidoreductase Chain: C; PDB Molecule: 2-oxoglutarate dehydrogenase e2 component; PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
80	d1vf7a	Alignment	not modelled	98.4	15	Fold: HlyD-like secretion proteins Superfamily: HlyD-like secretion proteins Family: HlyD-like secretion proteins
81	c3lnnB	Alignment	not modelled	98.3	13	PDB header: metal transport Chain: B; PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
82	c2qf7A	Alignment	not modelled	98.3	20	PDB header: ligase Chain: A; PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
83	c1t5eB	Alignment	not modelled	98.3	17	PDB header: transport protein Chain: B; PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa
84	c5a35A	Alignment	not modelled	98.2	25	PDB header: transport protein Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage protein h-like (gcvh-1)2 from streptococcus pyogenes
85	c4kkuD	Alignment	not modelled	98.1	20	PDB header: membrane protein Chain: D; PDB Molecule: membrane fusion protein; PDBTitle: structure of besa (selenomethionone derivative - p212121)
86	c3tw6B	Alignment	not modelled	97.8	20	PDB header: ligase/activator Chain: B; PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a
87	d1onla	Alignment	not modelled	97.5	28	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
88	c2edgA	Alignment	not modelled	97.5	20	PDB header: biosynthetic protein Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: solution structure of the gcv_h domain from mouse glycine
89	d1hpca	Alignment	not modelled	97.5	21	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
90	c3iftA	Alignment	not modelled	97.4	23	PDB header: oxidoreductase Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
91	c3mxuA	Alignment	not modelled	97.4	20	PDB header: oxidoreductase Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from bartonella2 henselae
92	c2aukA	Alignment	not modelled	97.1	25	PDB header: transferase Chain: A; PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
93	c3a8jF	Alignment	not modelled	97.0	17	PDB header: transferase/transport protein Chain: F; PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of et-ehred complex
94	c2ka7A	Alignment	not modelled	96.8	18	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: nmr solution structure of tm0212 at 40 c
95	c2qj8B	Alignment	not modelled	96.7	14	PDB header: hydrolase Chain: B; PDB Molecule: mlr6093 protein; PDBTitle: crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
96	c4p6vA	Alignment	not modelled	96.6	19	PDB header: oxidoreductase Chain: A; PDB Molecule: na(+)-translocating nadh-quinone reductase subunit a; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
97	c3na6A	Alignment	not modelled	96.3	23	PDB header: hydrolase Chain: A; PDB Molecule: succinylglutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
98	c3fmcC	Alignment	not modelled	96.2	25	PDB header: hydrolase Chain: C; PDB Molecule: putative succinylglutamate desuccinylase / aspartoacylase; PDBTitle: crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
99	c2f5zK	Alignment	not modelled	95.4	26	PDB header: oxidoreductase/protein binding Chain: K; PDB Molecule: pyruvate dehydrogenase protein x component;

99	c2f2zK	Alignment	not modelled	95.4	20	PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 (e3) complexed to the e3-binding domain of human e3-3 binding protein
100	d2gpra	Alignment	not modelled	95.4	17	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
101	c1zy8M	Alignment	not modelled	95.3	26	PDB header: oxidoreductase Chain: M: PDB Molecule: pyruvate dehydrogenase protein x component, PDBTitle: the crystal structure of dihydrolipoamide dehydrogenase and2 dihydrolipoamide dehydrogenase-binding protein (didomain)3 subcomplex of human pyruvate dehydrogenase complex.
102	c2aujD	Alignment	not modelled	95.2	22	PDB header: transferase Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert
103	c2f60K	Alignment	not modelled	95.2	25	PDB header: protein binding Chain: K: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: crystal structure of the dihydrolipoamide dehydrogenase (e3)-binding2 domain of human e3-binding protein
104	c3cdxB	Alignment	not modelled	95.1	18	PDB header: hydrolase Chain: B: PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of succinylglutamatedesuccinylase/aspartoacylase2 from rhodobacter sphaeroides
105	c2jkuA	Alignment	not modelled	94.0	21	PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, mitochondrial; PDBTitle: crystal structure of the n-terminal region of the biotin acceptor2 domain of human propionyl-coa carboxylase
106	c3d4rE	Alignment	not modelled	93.9	26	PDB header: unknown function Chain: E: PDB Molecule: domain of unknown function from the pfam-b_34464 family; PDBTitle: crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
107	d1glaf	Alignment	not modelled	93.4	13	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
108	d2f3ga	Alignment	not modelled	93.3	13	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
109	d1brwa3	Alignment	not modelled	93.3	25	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
110	d1gpra	Alignment	not modelled	91.6	21	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
111	c5t3eA	Alignment	not modelled	91.4	15	PDB header: ligase Chain: A: PDB Molecule: bacillamide synthetase heterocyclization domain; PDBTitle: crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
112	d1uoua3	Alignment	not modelled	91.2	21	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
113	c3h5qA	Alignment	not modelled	90.6	29	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
114	d2tpa3	Alignment	not modelled	90.4	21	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
115	c2dsjA	Alignment	not modelled	90.3	38	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
116	c1brwB	Alignment	not modelled	90.2	25	PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
117	d1o4ua2	Alignment	not modelled	89.8	14	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
118	c2j0fC	Alignment	not modelled	89.6	21	PDB header: transferase Chain: C: PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
119	c4ga5H	Alignment	not modelled	89.5	17	PDB header: transferase Chain: H: PDB Molecule: putative thymidine phosphorylase; PDBTitle: crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
120	c1otpA	Alignment	not modelled	88.0	21	PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase