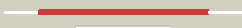








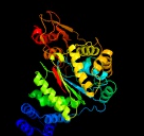























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3314c_(deoA)_3702355_3703638
Date	Thu Aug 8 16:20:52 BST 2019
Unique Job ID	1dba835e83e2d532

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2dsjA_</a>	 Alignment		100.0	44	<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
2	<a href="#">c1brwB_</a>	 Alignment		100.0	47	<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
3	<a href="#">c2j0fC_</a>	 Alignment		100.0	47	<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
4	<a href="#">c1otpA_</a>	 Alignment		100.0	42	<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
5	<a href="#">c3h5gA_</a>	 Alignment		100.0	40	<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
6	<a href="#">c4ga5H_</a>	 Alignment		100.0	34	<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
7	<a href="#">c1khdD_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.9 resolution3 (current name, pectobacterium carotovorum)
8	<a href="#">d1brwa2</a>	 Alignment		100.0	52	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
9	<a href="#">c1vquB_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase 2; <b>PDBTitle:</b> crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
10	<a href="#">d1uoua2</a>	 Alignment		100.0	52	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
11	<a href="#">c1v8gB_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8

12	<a href="#">d2tpa2</a>	Alignment		100.0	52	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
13	<a href="#">c1o17A</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyl-transferase (trpd)
14	<a href="#">c2bpgB</a>	Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
15	<a href="#">c5nofB</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyltransferase from thermococcus kodakaraensis
16	<a href="#">c4hkmA</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of an anthranilate phosphoribosyltransferase (target2 id nysgrc-016600) from xanthomonas campestris
17	<a href="#">c4gtnA</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> structure of anthranilate phosphoribosyl transferase from2 acinetobacter baylyi
18	<a href="#">c4muoB</a>	Alignment		100.0	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ybib; <b>PDBTitle:</b> the trpd2 enzyme from e.coli: ybib
19	<a href="#">d2elca2</a>	Alignment		100.0	24	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
20	<a href="#">d1o17a2</a>	Alignment		100.0	12	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
21	<a href="#">d1khda2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
22	<a href="#">d2tpa3</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
23	<a href="#">d1brwa3</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
24	<a href="#">d1uoua3</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
25	<a href="#">d2tpa1</a>	Alignment	not modelled	99.8	38	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
26	<a href="#">d1brwa1</a>	Alignment	not modelled	99.8	47	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
27	<a href="#">d1uoua1</a>	Alignment	not modelled	99.7	47	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-

						terminal domain
28	<a href="#">d1o17a1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
29	<a href="#">d1khdal</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
30	<a href="#">d1v8ga1</a>	Alignment	not modelled	99.6	25	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
31	<a href="#">d2elca1</a>	Alignment	not modelled	99.3	25	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
32	<a href="#">c4gjjC</a>	Alignment	not modelled	94.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> pseudouridine-5'-phosphate glycosidase; <b>PDBTitle:</b> crystal structure of pseudouridine monophosphate glycosidase complexed2 with sulfate
33	<a href="#">d1qpoa2</a>	Alignment	not modelled	93.3	21	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like
34	<a href="#">c4ex8A</a>	Alignment	not modelled	93.2	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alna; <b>PDBTitle:</b> crystal structure of the prealnumycin c-glycosynthase alna
35	<a href="#">d1vkma</a>	Alignment	not modelled	92.7	18	<b>Fold:</b> Indigoidine synthase A-like <b>Superfamily:</b> Indigoidine synthase A-like <b>Family:</b> Indigoidine synthase A-like
36	<a href="#">d1vf7a</a>	Alignment	not modelled	92.4	23	<b>Fold:</b> HlyD-like secretion proteins <b>Superfamily:</b> HlyD-like secretion proteins <b>Family:</b> HlyD-like secretion proteins
37	<a href="#">c3lnnB</a>	Alignment	not modelled	92.2	21	<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 cupriavidus metallidurans
38	<a href="#">c4l8jA</a>	Alignment	not modelled	90.9	15	<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) from2 bacteroides eggerthii dsm 20697 at 2.06 a resolution
39	<a href="#">c2v4dM</a>	Alignment	not modelled	90.5	20	<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
40	<a href="#">c2gu1A</a>	Alignment	not modelled	90.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc peptidase; <b>PDBTitle:</b> crystal structure of a zinc containing peptidase from2 vibrio cholerae
41	<a href="#">c2f1mA</a>	Alignment	not modelled	90.3	21	<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
42	<a href="#">d1o4ua2</a>	Alignment	not modelled	90.1	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
43	<a href="#">c5v5sH</a>	Alignment	not modelled	89.7	22	<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
44	<a href="#">c3h9iB</a>	Alignment	not modelled	88.9	19	<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
45	<a href="#">c1t5eB</a>	Alignment	not modelled	88.8	17	<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
46	<a href="#">d1dcza</a>	Alignment	not modelled	88.4	27	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
47	<a href="#">c5xu0B</a>	Alignment	not modelled	87.5	14	<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 streptococcus2 pneumoniae r6
48	<a href="#">d1qapa2</a>	Alignment	not modelled	87.3	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
49	<a href="#">c3lnnA</a>	Alignment	not modelled	86.8	18	<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 cupriavidus metallidurans
50	<a href="#">c4tkoB</a>	Alignment	not modelled	86.7	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
51	<a href="#">c5c22A</a>	Alignment	not modelled	86.3	24	<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 e. coli
52	<a href="#">d2pnrc1</a>	Alignment	not modelled	85.7	21	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains

53	<a href="#">c2hsiB_</a>	Alignment	not modelled	84.8	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative peptidase m23; <b>PDBTitle:</b> crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
54	<a href="#">c5niIG_</a>	Alignment	not modelled	84.5	14	<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
55	<a href="#">c2jbmA_</a>	Alignment	not modelled	84.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> qprtase structure from human
56	<a href="#">c2q8iB_</a>	Alignment	not modelled	84.0	25	<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
57	<a href="#">d1gjxa_</a>	Alignment	not modelled	83.6	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
58	<a href="#">d1o78a_</a>	Alignment	not modelled	83.4	31	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
59	<a href="#">c5ks8D_</a>	Alignment	not modelled	83.4	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
60	<a href="#">d2qpaa_</a>	Alignment	not modelled	83.3	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
61	<a href="#">c2dneA_</a>	Alignment	not modelled	83.0	17	<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
62	<a href="#">d1y8ob1</a>	Alignment	not modelled	82.8	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
63	<a href="#">c2dncA_</a>	Alignment	not modelled	82.8	29	<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
64	<a href="#">d1iyua_</a>	Alignment	not modelled	82.6	17	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
65	<a href="#">d1glaf_</a>	Alignment	not modelled	82.6	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
66	<a href="#">d1gpaa_</a>	Alignment	not modelled	82.4	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
67	<a href="#">c2ejmA_</a>	Alignment	not modelled	82.3	17	<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-biotinyl domain from2 human acetyl coenzyme a carboxylase
68	<a href="#">c2yvqA_</a>	Alignment	not modelled	81.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
69	<a href="#">c2ejgD_</a>	Alignment	not modelled	80.9	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
70	<a href="#">c2k33A_</a>	Alignment	not modelled	80.6	22	<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
71	<a href="#">d2f3ga_</a>	Alignment	not modelled	80.6	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
72	<a href="#">c3fppB_</a>	Alignment	not modelled	80.5	16	<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 e.coli maca
73	<a href="#">c3sluB_</a>	Alignment	not modelled	80.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> m23 peptidase domain protein; <b>PDBTitle:</b> crystal structure of nmb0315
74	<a href="#">c4dk0A_</a>	Alignment	not modelled	80.3	19	<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
75	<a href="#">c3uz0D_</a>	Alignment	not modelled	80.3	22	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> stage ii sporulation protein q; <b>PDBTitle:</b> crystal structure of spoiiah and spoiq complex
76	<a href="#">d1qjoa_</a>	Alignment	not modelled	80.0	17	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
77	<a href="#">d1k8ma_</a>	Alignment	not modelled	79.9	9	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains

78	<a href="#">c2b8gA</a>	Alignment	not modelled	79.9	17	<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)
79	<a href="#">c3n6rK</a>	Alignment	not modelled	79.6	28	<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)
80	<a href="#">c3l0gD</a>	Alignment	not modelled	78.6	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
81	<a href="#">d1laba</a>	Alignment	not modelled	78.5	21	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
82	<a href="#">c3c2vA</a>	Alignment	not modelled	78.2	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of the quinolinate phosphoribosyl transferase (bna6)2 from saccharomyces cerevisiae complexed with prpp and the inhibitor3 phthalate
83	<a href="#">d1ghja</a>	Alignment	not modelled	78.2	29	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
84	<a href="#">c3t51C</a>	Alignment	not modelled	77.9	18	<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
85	<a href="#">c2dn8A</a>	Alignment	not modelled	77.4	13	<b>PDB header:</b> ligase <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
86	<a href="#">c3tufB</a>	Alignment	not modelled	75.6	22	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> stage ii sporulation protein q; <b>PDBTitle:</b> structure of the spoiiq-spoiiiah pore forming complex.
87	<a href="#">c4bh5B</a>	Alignment	not modelled	74.9	32	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> murein hydrolase activator envc; <b>PDBTitle:</b> lytm domain of envc, an activator of cell wall amidases in2 escherichia coli
88	<a href="#">c2l5tA</a>	Alignment	not modelled	74.8	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipamide acyltransferase; <b>PDBTitle:</b> solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
89	<a href="#">c5b0hB</a>	Alignment	not modelled	74.7	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> leukocyte cell-derived chemotaxin-2; <b>PDBTitle:</b> crystal structure of human leukocyte cell-derived chemotaxin 2
90	<a href="#">c2m0nA</a>	Alignment	not modelled	74.6	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c, seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
91	<a href="#">d2pa2a1</a>	Alignment	not modelled	74.3	14	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Ribosomal protein L16p/L10e <b>Family:</b> Ribosomal protein L10e
92	<a href="#">c2kccA</a>	Alignment	not modelled	74.1	13	<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
93	<a href="#">c4dk1B</a>	Alignment	not modelled	73.8	14	<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="#">c1x1oC</a>	Alignment	not modelled	72.4	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of project id tt0268 from thermus thermophilus hb8
95	<a href="#">c2kvcA</a>	Alignment	not modelled	71.9	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of the mycobacterium tuberculosis protein rv0543c.2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
96	<a href="#">c3pajA</a>	Alignment	not modelled	70.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase, carboxylating; <b>PDBTitle:</b> 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
97	<a href="#">c5nenA</a>	Alignment	not modelled	68.8	29	<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
98	<a href="#">d1e2wa2</a>	Alignment	not modelled	68.5	32	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
99	<a href="#">d1bdoa</a>	Alignment	not modelled	67.9	18	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
100	<a href="#">c2qj8B</a>	Alignment	not modelled	67.9	14	<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) from2 mesorhizobium loti maff303099 at 2.00 a resolution
101	<a href="#">d1ci3m2</a>	Alignment	not modelled	67.6	37	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
						<b>PDB header:</b> transferase

102	<a href="#">c5bufA_</a>	Alignment	not modelled	67.6	11	<b>Chain:</b> A; <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase; <b>PDBTitle:</b> 2.37 angstrom structure of epsp synthase from acinetobacter baumannii
103	<a href="#">c2b7pA_</a>	Alignment	not modelled	67.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> probable nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori with phthalic acid
104	<a href="#">c4rnzA_</a>	Alignment	not modelled	66.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> conserved hypothetical secreted protein; <b>PDBTitle:</b> structure of helicobacter pylori csd3 from the hexagonal crystal
105	<a href="#">c2qguA_</a>	Alignment	not modelled	65.5	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> probable signal peptide protein; <b>PDBTitle:</b> three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
106	<a href="#">c3tqvA_</a>	Alignment	not modelled	65.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
107	<a href="#">c1qapA_</a>	Alignment	not modelled	64.5	20	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> A; <b>PDB Molecule:</b> quinolinic acid phosphoribosyltransferase; <b>PDBTitle:</b> quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
108	<a href="#">c3nyyA_</a>	Alignment	not modelled	64.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative glycyl-glycine endopeptidase lytm; <b>PDBTitle:</b> crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
109	<a href="#">c3gnnA_</a>	Alignment	not modelled	63.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of nicotinate-nucleotide pyrophosphorylase from2 burkholderi pseudomallei
110	<a href="#">d1pmra_</a>	Alignment	not modelled	63.1	27	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
111	<a href="#">c3fmcC_</a>	Alignment	not modelled	63.0	29	<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 /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
112	<a href="#">c2lkyA_</a>	Alignment	not modelled	62.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of msmeq_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target myma.17112.b
113	<a href="#">c3zf7K_</a>	Alignment	not modelled	62.2	21	<b>PDB header:</b> ribosome <b>Chain:</b> K; <b>PDB Molecule:</b> 60s ribosomal protein l10, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
114	<a href="#">c2jxmB_</a>	Alignment	not modelled	62.0	19	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> cytochrome f; <b>PDBTitle:</b> ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
115	<a href="#">c4hnbB_</a>	Alignment	not modelled	61.7	25	<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
116	<a href="#">c3bg5B_</a>	Alignment	not modelled	61.2	25	<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
117	<a href="#">c3hblA_</a>	Alignment	not modelled	59.9	25	<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
118	<a href="#">c3j39I_</a>	Alignment	not modelled	59.6	14	<b>PDB header:</b> ribosome <b>Chain:</b> l; <b>PDB Molecule:</b> 60s ribosomal protein l10; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
119	<a href="#">c5gt1A_</a>	Alignment	not modelled	59.6	18	<b>PDB header:</b> choline-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> choline binding protein a; <b>PDBTitle:</b> crystal structure of cbpa from l. salivarius ren
120	<a href="#">c5vz0D_</a>	Alignment	not modelled	59.3	25	<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