

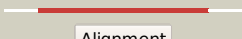













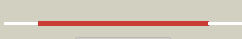







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1416_(ribH)_1591677_1592159
Date	Wed Jul 31 22:05:52 BST 2019
Unique Job ID	1c0ab7a1c29f8dd8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w19E_	 Alignment		100.0	100	PDB header: transferase Chain: E: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase; PDBTitle: lumazine synthase from mycobacterium tuberculosis bound to 3-(1,3,7-2 trihydro-9-d-ribityl-2,6,8-purinetrione-7-yl)propane 1-phosphate
2	d1c41a_	 Alignment		100.0	36	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
3	c4j07E_	 Alignment		100.0	81	PDB header: transferase Chain: E: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase; PDBTitle: crystal structure of a probable riboflavin synthase, beta chain ribh2 (6,7-dimethyl-8-ribityllumazine synthase, dmrl synthase, lumazine3 synthase) from mycobacterium leprae
4	d1ejba_	 Alignment		100.0	36	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
5	d1rvv1_	 Alignment		100.0	37	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
6	d1nqua_	 Alignment		100.0	47	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
7	c3mk3L_	 Alignment		100.0	46	PDB header: transferase Chain: L: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase; PDBTitle: crystal structure of lumazine synthase from salmonella typhimurium lt2
8	d1kz1a_	 Alignment		100.0	34	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
9	c2f59B_	 Alignment		100.0	40	PDB header: transferase Chain: B: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase 1; PDBTitle: lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
10	d1c2ya_	 Alignment		100.0	34	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
11	d1di0a_	 Alignment		100.0	28	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase

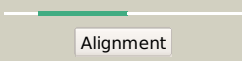
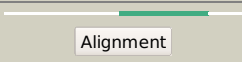
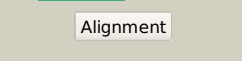
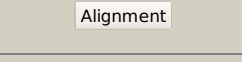
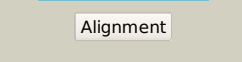
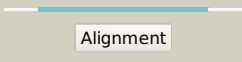
12	c2obxH_	Alignment		100.0	28	PDB header: transferase Chain: H: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase 1; PDBTitle: lumazine synthase ribh2 from mesorhizobium loti (gene ml7281, swiss-2 prot entry q986n2) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
13	c2b99A_	Alignment		97.6	17	PDB header: transferase Chain: A: PDB Molecule: riboflavin synthase; PDBTitle: crystal structure of an archaeal pentameric riboflavin2 synthase complex with a substrate analog inhibitor
14	c4y7jE_	Alignment		97.4	17	PDB header: membrane protein,transport protein Chain: E: PDB Molecule: large conductance mechanosensitive channel protein, PDBTitle: structure of an archaeal mechanosensitive channel in expanded state
15	c5ulbA_	Alignment		95.6	18	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter from yersinia2 enterocolitica subsp. enterocolitica 8081
16	c5z6vA_	Alignment		93.2	19	PDB header: protein transport Chain: A: PDB Molecule: abc-type uncharacterized transport system periplasmic PDBTitle: crystal structure of a substrate-binding protein from rhodothermus2 marinus
17	c3ma0A_	Alignment		92.6	16	PDB header: sugar binding protein Chain: A: PDB Molecule: d-xylose-binding periplasmic protein; PDBTitle: closed liganded crystal structure of xylose binding protein from2 escherichia coli
18	c4kzkA_	Alignment		92.2	11	PDB header: sugar binding protein Chain: A: PDB Molecule: l-arabinose abc transporter, periplasmic l-arabinose- PDBTitle: the structure of the periplasmic l-arabinose binding protein from2 burkholderia thailandensis
19	c3lftA_	Alignment		92.1	19	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the abc domain in complex with l-trp from2 streptococcus pneumonia to 1.35a
20	c4yhsA_	Alignment		91.5	17	PDB header: solute-binding protein Chain: A: PDB Molecule: monosaccharide abc transporter substrate-binding protein, PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from bradyrhizobium sp. btai1 (bbta_2440, target efi-3 511490) with bound bis-tris
21	c5dkvD_	Alignment	not modelled	90.4	20	PDB header: sugar binding protein Chain: D: PDB Molecule: abc transporter substrate binding protein (ribose); PDBTitle: crystal structure of an abc transporter solute binding protein from2 agrobacterium vitis(avis_5339, target efi-511225) bound with alpha-d-3 tagatopyranose
22	c3l6uA_	Alignment	not modelled	90.1	16	PDB header: transport protein Chain: A: PDB Molecule: abc-type sugar transport system periplasmic component; PDBTitle: crystal structure of abc-type sugar transport system, periplasmic2 component from exiguobacterium sibiricum
23	c5hsgA_	Alignment	not modelled	90.0	14	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter, nucleotide binding/atpase PDBTitle: crystal structure of an abc transporter solute binding protein from2 klebsiella pneumoniae (kpn_01730, target efi-511059), apo open3 structure
24	c5dteD_	Alignment	not modelled	89.2	19	PDB header: transport protein Chain: D: PDB Molecule: monosaccharide-transporting atpase; PDBTitle: crystal structure of an abc transporter periplasmic solute binding2 protein (ipr025997) from actinobacillus succinogenes 130z(asuc_0081,3 target efi-511065) with bound d-allose
25	d8abpa_	Alignment	not modelled	89.2	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
26	c4lrxA_	Alignment	not modelled	88.5	13	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, periplasmic sugar-binding protein; PDBTitle: crystal structure of caulobacter myo-inositol binding protein bound to2 myo-inositol
27	c3o1hB_	Alignment	not modelled	87.9	15	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic protein tort; PDBTitle: crystal structure of the tors sensor domain - tort complex

						in the2 presence of tmao
28	d1gcaa_	Alignment	not modelled	86.9	8	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
29	c4ry8D_	Alignment	not modelled	86.8	20	PDB header: transport protein Chain: D: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of 5-methylthioribose transporter solute binding2 protein tlet_1677 from thermotoga lettingae tmo target efi-511109 in3 complex with 5-methylthioribose
30	c4z0nA_	Alignment	not modelled	86.8	7	PDB header: transcription Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of a periplasmic solute binding protein (ipr025997)2 from streptobacillus moniliformis dsm-12112 (smon_0317, target efi-3 511281) with bound d-galactose
31	d1guda_	Alignment	not modelled	86.5	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
32	c2qh8A_	Alignment	not modelled	86.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved domain protein from vibrio2 cholerae o1 biovar eltor str. n16961
33	c4kqcA_	Alignment	not modelled	86.0	20	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: abc transporter, laci family transcriptional regulator from2 brachyspira murdochii
34	c6gq0A_	Alignment	not modelled	85.3	16	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar binding protein; PDBTitle: crystal structure of ganp, a glucose-galactose binding protein from2 geobacillus stearothermophilus
35	c6hyhA_	Alignment	not modelled	84.6	13	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of msmeg_1712 from mycobacterium smegmatis in2 complex with beta-d-fucofuranose
36	c4yleA_	Alignment	not modelled	84.5	21	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from burkholderia multivorans (bmul_1631, target efi-3 511115) with an unknown ligand modelled as alpha-d-erythrofuranose
37	c4yv7A_	Alignment	not modelled	84.5	16	PDB header: solute-binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from mycobacterium smegmatis (msmei_3018, target efi-3 511327) with bound glycerol
38	c3ksmA_	Alignment	not modelled	83.8	20	PDB header: transport protein Chain: A: PDB Molecule: abc-type sugar transport system, periplasmic component; PDBTitle: crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
39	c2vk2A_	Alignment	not modelled	83.3	15	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
40	c4kq9A_	Alignment	not modelled	82.2	17	PDB header: transport protein Chain: A: PDB Molecule: ribose abc transporter, substrate binding protein; PDBTitle: crystal structure of periplasmic ribose abc transporter from2 conexibacter woesei dsm 14684
41	c4rxtA_	Alignment	not modelled	81.8	18	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter; PDBTitle: crystal structure of carbohydrate transporter solute binding protein2 arad_9553 from agrobacterium radiobacter, target efi-511541, in3 complex with d-arabinose
42	c4rk1F_	Alignment	not modelled	81.8	11	PDB header: transcription regulator Chain: F: PDB Molecule: ribose transcriptional regulator; PDBTitle: crystal structure of laci family transcriptional regulator from2 enterococcus faecium, target efi-512930, with bound ribose
43	c4wt7B_	Alignment	not modelled	81.5	17	PDB header: transport protein Chain: B: PDB Molecule: abc transporter substrate binding protein (ribose); PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis (avi_5165, target efi-511223)3 with bound allitol
44	c4ry9A_	Alignment	not modelled	81.5	11	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of carbohydrate transporter solute binding protein2 veis_2079 from verminephrobacter eiseniae ef01-2, target efi-511009,3 a complex with d-talitol
45	c4kvfA_	Alignment	not modelled	80.2	11	PDB header: transport protein Chain: A: PDB Molecule: rhamnose abc transporter, periplasmic rhamnose-binding PDBTitle: the crystal structure of a rhamnose abc transporter, periplasmic2 rhamnose-binding protein from kribbella flavida dsm 17836
46	c5ix8A_	Alignment	not modelled	76.8	11	PDB header: transport protein Chain: A: PDB Molecule: putative sugar abc transport system, substrate-binding PDBTitle: crystal structure of sugar abc transport system, substrate-binding2 protein from bordetella parapertussis 12822
47	c3k9cA_	Alignment	not modelled	75.0	24	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family protein; PDBTitle: crystal structure of laci transcriptional regulator from rhodococcus2 species.
48	c2kkaA_	Alignment	not modelled	74.8	13	PDB header: transcription regulator Chain: A: PDB Molecule: laci family transcriptional regulator;

48	c3kkaA	Alignment	not modelled	74.8	13	PDBTitle: crystal structure of a lacI family transcriptional regulator from2 mycobacterium smegmatis
49	d2a5la1	Alignment	not modelled	74.8	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
50	c6ndiB	Alignment	not modelled	73.9	13	PDB header: sugar binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: 2.60 angstrom resolution crystal structure of periplasmic binding and2 sugar binding domain of lacI family protein from klebsiella3 pneumoniae.
51	c4rk6B	Alignment	not modelled	73.3	15	PDB header: transcription regulator Chain: B: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of lacI family transcriptional regulator ccpa from2 weissella paramesenteroides, target efi-512926, with bound glucose
52	c2fn9A	Alignment	not modelled	72.9	22	PDB header: sugar binding protein Chain: A: PDB Molecule: ribose abc transporter, periplasmic ribose-binding protein; PDBTitle: thermotoga maritima ribose binding protein unliganded form
53	c5hqjA	Alignment	not modelled	72.7	19	PDB header: solute-binding protein Chain: A: PDB Molecule: periplasmic binding protein/lacI transcriptional regulator; PDBTitle: crystal structure of abc transporter solute binding protein b1g1h72 from burkholderia graminis c4d1m, target efi-511179, in complex with3 d-arabinose
54	c3tb6B	Alignment	not modelled	72.3	12	PDB header: dna binding protein Chain: B: PDB Molecule: arabinose metabolism transcriptional repressor; PDBTitle: structure of the effector-binding domain of arabinose repressor arar2 from bacillus subtilis
55	c5bq3A	Alignment	not modelled	72.1	16	PDB header: transport protein Chain: A: PDB Molecule: rhamnose abc transporter, rhamnose-binding protein; PDBTitle: crystal structure of a sugar abc transporter (actodo_00688) from2 actinomyces odontolyticus atcc 17982 at 2.60 a resolution
56	d1u11a	Alignment	not modelled	71.1	17	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
57	c2fqxA	Alignment	not modelled	71.1	21	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
58	c2fw9A	Alignment	not modelled	70.8	17	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
59	c3rotA	Alignment	not modelled	70.3	18	PDB header: transport protein Chain: A: PDB Molecule: abc sugar transporter, periplasmic sugar binding protein; PDBTitle: crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
60	c3h5oB	Alignment	not modelled	70.2	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
61	c3qk7C	Alignment	not modelled	66.8	19	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
62	c4ry0A	Alignment	not modelled	66.1	17	PDB header: transport protein Chain: A: PDB Molecule: probable ribose abc transporter, substrate-binding protein; PDBTitle: crystal structure of ribose transporter solute binding protein2 rhe_pf00037 from rhizobium etil cfn 42, target efi-511357, in complex3 with d-ribose
63	c4rxuA	Alignment	not modelled	66.0	8	PDB header: transport protein Chain: A: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
64	d1y5ea1	Alignment	not modelled	65.5	20	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
65	c6dspB	Alignment	not modelled	65.4	13	PDB header: signaling protein Chain: B: PDB Molecule: autoinducer 2-binding protein lsrb; PDBTitle: lsrb from clostridium saccharobutylicum in complex with ai-2
66	c3orsD	Alignment	not modelled	64.6	15	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
67	d2fyva1	Alignment	not modelled	64.2	8	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
68	c3glwB	Alignment	not modelled	63.7	14	PDB header: transport protein Chain: B: PDB Molecule: sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans
69	c4rweA	Alignment	not modelled	63.7	13	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar-binding transport protein; PDBTitle: the crystal structure of a sugar-binding transport protein from2 yersinia pestis co92
						PDB header: transport protein Chain: A: PDB Molecule: abc transporter;

70	c4wwhA_	Alignment	not modelled	63.6	8	PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from mycobacterium smegmatis (msmeg_1704, target efi-3 510967) with bound d-galactose
71	c5xsdA_	Alignment	not modelled	63.6	13	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: xylii-lytsn complex mutant - d103a
72	c2rjoA_	Alignment	not modelled	61.9	19	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
73	c5braA_	Alignment	not modelled	61.5	17	PDB header: solute-binding protein Chain: A: PDB Molecule: putative periplasmic binding protein with substrate ribose; PDBTitle: crystal structure of a putative periplasmic solute binding protein2 (ipr025997) from ochrobactrum anthropi atcc49188 (oant_2843, target3 efi-511085)
74	d2nqra3	Alignment	not modelled	59.2	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
75	c4qccA_	Alignment	not modelled	58.1	14	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
76	c4o5aA_	Alignment	not modelled	57.4	14	PDB header: transcription regulator Chain: A: PDB Molecule: laci family transcription regulator; PDBTitle: the crystal structure of a laci family transcriptional regulator from2 bifidobacterium animalis subsp. lactis dsm 10140
77	c2h0aA_	Alignment	not modelled	56.8	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of probable transcription regulator from2 thermus thermophilus
78	c4ycsC_	Alignment	not modelled	56.6	14	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
79	c4wzzA_	Alignment	not modelled	56.4	14	PDB header: transport protein Chain: A: PDB Molecule: putative sugar abc transporter, substrate-binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentas (cphy_0583, target efi-3 511148) with bound l-rhamnose
80	c4joqA_	Alignment	not modelled	55.2	17	PDB header: transport protein Chain: A: PDB Molecule: abc ribose transporter, periplasmic solute-binding protein; PDBTitle: putative ribose abc transporter, periplasmic solute-binding protein2 from rhodobacter sphaeroides
81	c4pevB_	Alignment	not modelled	55.1	19	PDB header: solute-binding protein Chain: B: PDB Molecule: membrane lipoprotein family protein; PDBTitle: crystal structure of abc transporter system solute-binding proteins2 from aeropyrum pernix k1
82	c3lp6D_	Alignment	not modelled	54.9	23	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
83	c3cs3A_	Alignment	not modelled	54.6	8	PDB header: transcription regulator Chain: A: PDB Molecule: sugar-binding transcriptional regulator, laci family; PDBTitle: crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
84	c4yo7A_	Alignment	not modelled	54.4	12	PDB header: solute binding protein Chain: A: PDB Molecule: sugar abc transporter (sugar-binding protein); PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from bacillus halodurans c-125 (bh2323, target efi-3 511484) with bound myo-inositol
85	c5er3A_	Alignment	not modelled	53.2	22	PDB header: solute-binding protein Chain: A: PDB Molecule: sugar abc transporter, periplasmic sugar-binding protein; PDBTitle: crystal structure of abc transporter system solute-binding protein2 from rhodopirellula baltica sh 1
86	c3bilA_	Alignment	not modelled	53.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable laci-family transcriptional regulator; PDBTitle: crystal structure of a probable laci family transcriptional regulator2 from corynebacterium glutamicum
87	c4fr2A_	Alignment	not modelled	52.1	15	PDB header: oxidoreductase, metal binding protein Chain: A: PDB Molecule: 1,3-propanediol dehydrogenase; PDBTitle: alcohol dehydrogenase from oenococcus oeni
88	c5mp4C_	Alignment	not modelled	51.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: protoplast secreted protein 2; PDBTitle: the structure of pst2p from saccharomyces cerevisiae
89	c4pe6B_	Alignment	not modelled	50.9	18	PDB header: solute-binding protein Chain: B: PDB Molecule: putative abc transporter; PDBTitle: crystal structure of abc transporter solute binding protein from2 thermobispora bispora dsm 43833
90	d1o4va_	Alignment	not modelled	49.3	22	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
91	c3s40C_	Alignment	not modelled	48.8	19	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
92	c3h75A_	Alignment	not modelled	48.6	13	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic sugar-binding domain protein; PDBTitle: crystal structure of a periplasmic sugar-binding protein

						from the2 pseudomonas fluorescens
93	d1ydgA	Alignment	not modelled	48.2	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
94	c3l49D	Alignment	not modelled	48.0	11	PDB header: transport protein Chain: D: PDB Molecule: abc sugar (ribose) transporter, periplasmic substrate- PDBTitle: crystal structure of abc sugar transporter subunit from rhodobacter2 sphaeroides 2.4.1
95	c2zkiH	Alignment	not modelled	47.6	18	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
96	c4gudA	Alignment	not modelled	47.6	14	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
97	c3e3mA	Alignment	not modelled	46.7	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a lacI family transcriptional regulator from2 silicibacter pomeroyi
98	c2qvcC	Alignment	not modelled	46.1	8	PDB header: transport protein Chain: C: PDB Molecule: sugar abc transporter, periplasmic sugar-binding protein; PDBTitle: crystal structure of a periplasmic sugar abc transporter from2 thermotoga maritima
99	c2r94B	Alignment	not modelled	45.8	22	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
100	d2f7wa1	Alignment	not modelled	45.4	15	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
101	c5ocpA	Alignment	not modelled	45.2	16	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: the periplasmic binding protein component of the arabinose abc2 transporter from shewanella sp. ana-3 bound to alpha and beta-l-3 arabinofuranose
102	c4rk5A	Alignment	not modelled	44.9	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI family transcriptional regulator from2 lactobacillus casei, target efi-512911, with bound sucrose
103	c3clkB	Alignment	not modelled	44.5	12	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
104	c4rxmA	Alignment	not modelled	44.5	6	PDB header: transport protein Chain: A: PDB Molecule: possible sugar abc superfamily atp binding cassette PDBTitle: crystal structure of periplasmic abc transporter solute binding2 protein a7jw62 from mannheimia haemolytica phl213, target efi-511105,3 in complex with myo-inositol
105	c2hmcA	Alignment	not modelled	44.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
106	c3rggD	Alignment	not modelled	43.9	8	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
107	c3lq1A	Alignment	not modelled	43.7	15	PDB header: transferase Chain: A: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- PDBTitle: crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene 1-2 carboxylic acid synthase/2-oxoglutarate decarboxylase from listeria3 monocytogenes str. 4b f2365
108	c2nqqA	Alignment	not modelled	43.2	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
109	c2qu7B	Alignment	not modelled	42.8	10	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcription regulator from2 staphylococcus saprophyticus subsp. saprophyticus
110	c3d8uA	Alignment	not modelled	42.7	17	PDB header: transcription regulator Chain: A: PDB Molecule: purr transcriptional regulator; PDBTitle: the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
111	c3o74A	Alignment	not modelled	42.6	15	PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
112	c4ru1C	Alignment	not modelled	42.6	15	PDB header: transport protein Chain: C: PDB Molecule: monosaccharide abc transporter substrate-binding protein, PDBTitle: crystal structure of carbohydrate transporter acei_1806 from2 acidothermus cellulolyticus 11b, target efi-510965, in complex with3 myo-inositol
113	c6bsvB	Alignment	not modelled	42.3	16	PDB header: transferase Chain: B: PDB Molecule: xyloglucan 6-xylosyltransferase 1; PDBTitle: crystal structure of xyloglucan xylosyltransferase binary form
114	c3ctpB	Alignment	not modelled	42.0	7	PDB header: transcription regulator Chain: B: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of periplasmic binding protein/laci transcriptional2 regulator from alkaliphilus metalliredigens qymf complexed with d-3 xylulofuranose

115	c3mizB_	 Alignment	not modelled	41.0	15	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator protein, lacI PDBTitle: crystal structure of a putative transcriptional regulator2 protein, lacI family from rhizobium etli
116	d1w3ia_	 Alignment	not modelled	40.4	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
117	d1dbqa_	 Alignment	not modelled	40.3	8	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
118	c3c3kA_	 Alignment	not modelled	40.2	17	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
119	c4wutA_	 Alignment	not modelled	39.9	8	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate binding protein (ribose); PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis (avi_5133, target efi-511220)3 with bound d-fucose
120	c2ioyB_	 Alignment	not modelled	39.6	12	PDB header: sugar binding protein Chain: B: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of thermoanaerobacter tengcongensis ribose binding2 protein