







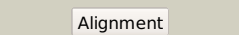

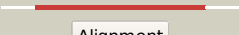









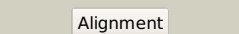



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3275c_purE_3658111_3658635
Date	Thu Aug 8 16:20:48 BST 2019
Unique Job ID	9c1a6340248504e9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lp6D_	 Alignment		100.0	99	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
2	d1o4va_	 Alignment		100.0	58	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
3	c3trhI_	 Alignment		100.0	41	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
4	c3orsD_	 Alignment		100.0	57	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
5	c4grdA_	 Alignment		100.0	57	PDB header: lyase,isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
6	c2fw9A_	 Alignment		100.0	57	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
7	d1u11a_	 Alignment		100.0	58	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
8	d1qcza_	 Alignment		100.0	49	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
9	c2ywxA_	 Alignment		100.0	44	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
10	c2h31A_	 Alignment		100.0	25	PDB header: ligase, lyase Chain: A: PDB Molecule: multifunctional protein ade2; PDBTitle: crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
11	c3rggD_	 Alignment		100.0	27	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air

12	c4b4kK_	Alignment		100.0	61	PDB header: isomerase Chain: K: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of bacillus anthracis pure
13	c6o55B_	Alignment		100.0	54	PDB header: isomerase Chain: B: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 (pure) from legionella pneumophila
14	d1xmpa_	Alignment		100.0	61	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
15	c4ja0A_	Alignment		100.0	26	PDB header: protein binding Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase; PDBTitle: crystal structure of the invertebrate bi-functional purine2 biosynthesis enzyme paics at 2.8 a resolution
16	c5zxlD_	Alignment		98.1	12	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of glda from e.coli
17	d1jq5a_	Alignment		98.0	19	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
18	c4mcaB_	Alignment		97.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from serratia to 1.9a
19	c5tprB_	Alignment		97.8	14	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: desmethyl-4-deoxygadusol synthase from anabaena variabilis (ava_3858)2 with nad+ and zn2+ bound
20	c6csjD_	Alignment		97.7	12	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of a bacillus coagulans polyol dehydrogenase double mutant2 with an acquired d-lactate dehydrogenase activity
21	c4p53A_	Alignment	not modelled	97.6	20	PDB header: lyase Chain: A: PDB Molecule: cyclase; PDBTitle: vala (2-epi-5-epi-valiolone synthase) from streptomyces hygrosopicus2 subsp. jinggangensis 5008 with nad+ and zn2+ bound
22	c3qbeA_	Alignment	not modelled	97.5	18	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of the 3-dehydroquinase synthase (arob) from2 mycobacterium tuberculosis
23	c1ta9A_	Alignment	not modelled	97.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
24	c3ce9A_	Alignment	not modelled	97.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
25	c3okfA_	Alignment	not modelled	97.3	21	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: 2.5 angstrom resolution crystal structure of 3-dehydroquinase synthase2 (arob) from vibrio cholerae
26	d1o2da_	Alignment	not modelled	97.3	20	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
27	c5eksB_	Alignment	not modelled	97.3	19	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: structure of 3-dehydroquinase synthase from acinetobacter baumannii in2 complex with nad
28	d1vlja_	Alignment	not modelled	97.2	19	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase

29	c3ox4D	Alignment	not modelled	97.2	18	PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
30	c3bfjK	Alignment	not modelled	97.2	14	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
31	c3zokB	Alignment	not modelled	97.1	20	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: structure of 3-dehydroquinase synthase from actinidia chinensis in2 complex with nad
32	c6c76A	Alignment	not modelled	97.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: structure of iron containing alcohol dehydrogenase from thermococcus2 thioreducens in an orthorhombic crystal form
33	c3jzdA	Alignment	not modelled	96.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of putative alcohol dehydrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
34	d1rrma	Alignment	not modelled	96.9	14	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
35	c3zdrA	Alignment	not modelled	96.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase domain of the bifunctional PDBTitle: structure of the alcohol dehydrogenase (adh) domain of a2 bifunctional adhe dehydrogenase from geobacillus3 thermoglucosidasius ncimb 11955
36	c3uhjE	Alignment	not modelled	96.9	15	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
37	c6c5cA	Alignment	not modelled	96.9	20	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of aro1p from candida albicans sc5314 in complex2 with nadh
38	c5yvmA	Alignment	not modelled	96.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq
39	c3iv7B	Alignment	not modelled	96.7	24	PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase iv; PDBTitle: crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution
40	c3hl0B	Alignment	not modelled	96.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
41	d1sg6a	Alignment	not modelled	96.6	19	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
42	c4fr2A	Alignment	not modelled	96.4	16	PDB header: oxidoreductase, metal binding protein Chain: A: PDB Molecule: 1,3-propanediol dehydrogenase; PDBTitle: alcohol dehydrogenase from oenococcus oeni
43	c5hvnA	Alignment	not modelled	96.4	20	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: 3.0 angstrom crystal structure of 3-dehydroquinase synthase (arob)2 from francisella tularensis in complex with nad.
44	c2gruB	Alignment	not modelled	96.4	19	PDB header: lyase Chain: B: PDB Molecule: 2-deoxy-scylo-inosose synthase; PDBTitle: crystal structure of 2-deoxy-scylo-inosose synthase2 complexed with carbaglucose-6-phosphate, nad+ and co2+
45	c3clhA	Alignment	not modelled	96.0	19	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of 3-dehydroquinase synthase (dhqs)from2 helicobacter pylori
46	d1oj7a	Alignment	not modelled	95.9	18	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
47	c2q5cA	Alignment	not modelled	95.6	12	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
48	d2pju1	Alignment	not modelled	95.5	17	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
49	d1kq3a	Alignment	not modelled	95.4	16	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
50	c2bonB	Alignment	not modelled	95.3	20	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
51	d2bon1	Alignment	not modelled	95.1	20	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
52	c3rf7A	Alignment	not modelled	95.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
53	d1ujna	Alignment	not modelled	94.6	21	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
54	c6ibnD	Alignment	not modelled	94.2	19	PDB header: oxidoreductase Chain: D: PDB Molecule: methanol dehydrogenase;

54	c0jxpd_	Alignment	not modelled	94.2	19	PDBTitle: crystal structure of sulfoacetaldehyde reductase from bifidobacterium2 kashiwanohense in complex with nad+ PDB header: transport protein
55	c4kqcA_	Alignment	not modelled	93.9	13	Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: abc transporter, laci family transcriptional regulator from2 brachyspira murdochii
56	d2jgra1	Alignment	not modelled	93.7	20	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
57	d2p1ra1	Alignment	not modelled	93.7	20	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
58	c4zhtB_	Alignment	not modelled	93.6	17	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcna2 2-epimerase
59	c2qq1A_	Alignment	not modelled	92.8	18	PDB header: structural protein Chain: A: PDB Molecule: molybdenum cofactor biosynthesis mog; PDBTitle: crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from aquifex aeolicus vf5
60	d1guda_	Alignment	not modelled	92.8	14	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
61	c4pe6B_	Alignment	not modelled	92.7	12	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
62	c1xahA_	Alignment	not modelled	92.7	24	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinate synthase; PDBTitle: crystal structure of staphylococcus aureus 3-dehydroquinate2 synthase (dhqs) in complex with zn2+ and nad+
63	c5fb3C_	Alignment	not modelled	92.7	16	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerophosphate dehydrogenase in complex with nadph
64	d2qv7a1	Alignment	not modelled	92.5	20	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
65	c3rotA_	Alignment	not modelled	92.0	12	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
66	c3s99A_	Alignment	not modelled	91.6	12	PDB header: lipid binding protein Chain: A: PDB Molecule: basic membrane lipoprotein; PDBTitle: crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
67	c2qv7A_	Alignment	not modelled	91.2	17	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
68	c4irxA_	Alignment	not modelled	90.8	20	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
69	c5z9aB_	Alignment	not modelled	90.8	24	PDB header: lyase Chain: B: PDB Molecule: chorismate synthase; PDBTitle: crystal structure of chorismate synthase from pseudomonas aeruginosa
70	c4z0nA_	Alignment	not modelled	90.8	15	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
71	c4werA_	Alignment	not modelled	90.7	19	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase catalytic domain protein; PDBTitle: crystal structure of diacylglycerol kinase catalytic domain protein2 from enterococcus faecalis v583
72	c5ulbA_	Alignment	not modelled	90.6	13	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
73	c2pjuD_	Alignment	not modelled	90.5	17	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon regulatory protein2 prpr
74	d1um0a_	Alignment	not modelled	90.2	23	Fold: Chorismate synthase, AroC Superfamily: Chorismate synthase, AroC Family: Chorismate synthase, AroC
75	c3lftA_	Alignment	not modelled	90.0	16	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
76	c5hsgA_	Alignment	not modelled	89.7	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
77	c2fn9A_	Alignment	not modelled	89.4	14	PDB header: sugar binding protein Chain: A: PDB Molecule: ribose abc transporter, periplasmic ribose-binding protein; PDBTitle: thermotoga maritima ribose binding protein unliganded form

78	c4rk5A_	Alignment	not modelled	89.4	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
79	c3u7rB_	Alignment	not modelled	89.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent frn reductase; PDBTitle: ferb - flavoenzyme nad(p)h:(acceptor) oxidoreductase (ferb) from2 paracoccus denitrificans
80	c5dkvD_	Alignment	not modelled	88.6	15	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
81	c4yleA_	Alignment	not modelled	88.5	14	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
82	c4ycsC_	Alignment	not modelled	88.5	15	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
83	c4kvfA_	Alignment	not modelled	88.5	14	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
84	c5tt0A_	Alignment	not modelled	88.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: crystal structure of an oxidoreductase (short chain2 dehydrogenase/reductase family) from burkholderia thailandensis
85	c4lj2A_	Alignment	not modelled	87.3	22	PDB header: lyase Chain: A: PDB Molecule: chorismate synthase; PDBTitle: crystal structure of chorismate synthase from acinetobacter baumannii2 at 3.15a resolution
86	c4rfiB_	Alignment	not modelled	86.6	15	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p)+]; PDBTitle: crystal structure of g1pdh with nadph from methanocaldococcus2 jannaschii
87	c5dteD_	Alignment	not modelled	86.5	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
88	c3hcbW_	Alignment	not modelled	86.2	8	PDB header: rna binding protein Chain: B: PDB Molecule: maltose operon transcriptional repressor; PDBTitle: crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus aureus
89	d1q1la_	Alignment	not modelled	85.8	24	Fold: Chorismate synthase, AroC Superfamily: Chorismate synthase, AroC Family: Chorismate synthase, AroC
90	c1zuwA_	Alignment	not modelled	85.7	23	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase 1; PDBTitle: crystal structure of b.subtilis glutamate racemase (race) with d-glu
91	d1sq1a_	Alignment	not modelled	85.5	31	Fold: Chorismate synthase, AroC Superfamily: Chorismate synthase, AroC Family: Chorismate synthase, AroC
92	c1ztbA_	Alignment	not modelled	85.3	26	PDB header: ligase Chain: A: PDB Molecule: chorismate synthase; PDBTitle: crystal structure of chorismate synthase from mycobacterium2 tuberculosis
93	d1qxoA_	Alignment	not modelled	84.7	30	Fold: Chorismate synthase, AroC Superfamily: Chorismate synthase, AroC Family: Chorismate synthase, AroC
94	c2fqxA_	Alignment	not modelled	84.5	15	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
95	c4rxuA_	Alignment	not modelled	84.5	15	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
96	c3h75A_	Alignment	not modelled	84.2	18	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
97	c3h8qB_	Alignment	not modelled	84.0	9	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 3; PDBTitle: crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
98	d1xi8a3	Alignment	not modelled	83.9	13	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
99	c4trrH_	Alignment	not modelled	83.6	20	PDB header: oxidoreductase Chain: H: PDB Molecule: putative d-beta-hydroxybutyrate dehydrogenase; PDBTitle: crystal structure of a putative putative d-beta-hydroxybutyrate2 dehydrogenase from burkholderia cenocepacia j2315
100	d2gm3a1	Alignment	not modelled	83.6	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like

101	c2jfoB_	Alignment	not modelled	83.4	25	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
102	c4y9tA_	Alignment	not modelled	83.1	18	PDB header: solute-binding protein Chain: A: PDB Molecule: abc transporter, solute binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis s4 (avi_5305, target efi-511224)3 with bound alpha-d-glucosamine
103	c5w16D_	Alignment	not modelled	82.9	18	PDB header: isomerase Chain: D: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from thermus thermophilus in2 complex with d-glutamate
104	c3opyH_	Alignment	not modelled	82.8	18	PDB header: transferase Chain: H: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
105	c3opyB_	Alignment	not modelled	82.8	18	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
106	c2iy3A_	Alignment	not modelled	82.8	20	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal regognition particle
107	c4rxmA_	Alignment	not modelled	82.5	14	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
108	c3ksmA_	Alignment	not modelled	82.4	17	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
109	c2f59B_	Alignment	not modelled	82.2	22	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
110	c4pevB_	Alignment	not modelled	81.3	14	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
111	c5zvB_	Alignment	not modelled	81.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: glutaredoxin; PDBTitle: crystal structure of wheat glutarredoxin
112	c3ak4C_	Alignment	not modelled	81.1	23	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
113	c1z0zC_	Alignment	not modelled	81.1	17	PDB header: transferase Chain: C: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
114	c4o5aA_	Alignment	not modelled	80.7	16	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
115	c3brsA_	Alignment	not modelled	80.7	15	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
116	c3s40C_	Alignment	not modelled	80.6	13	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
117	c3h7aC_	Alignment	not modelled	79.9	15	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of short-chain dehydrogenase from rhodospseudomonas2 palustris
118	d2f7wa1	Alignment	not modelled	79.7	13	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
119	d1z0sa1	Alignment	not modelled	79.5	16	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
120	c3l49D_	Alignment	not modelled	78.7	14	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