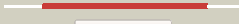



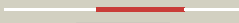



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0207c_(-)_247384_248112
Date	Tue Jul 23 14:50:26 BST 2019
Unique Job ID	d8c1ec196315dff8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qipA_	 Alignment		99.9	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: protein of unknown function vpa0982; PDBTitle: crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
2	c5yaaD_	 Alignment		99.6	17	PDB header: hydrolase Chain: D; PDB Molecule: meiosis regulator and mrna stability factor 1; PDBTitle: crystal structure of marf1 nyn domain from mus musculus
3	d2jgra1	 Alignment		96.6	17	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
4	c2bonB_	 Alignment		96.2	17	PDB header: transferase Chain: B; PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
5	d2bona1	 Alignment		96.0	17	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
6	d2p1ra1	 Alignment		95.9	17	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
7	d2qv7a1	 Alignment		95.7	18	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
8	c2qv7A_	 Alignment		94.7	13	PDB header: transferase Chain: A; PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
9	c3s40C_	 Alignment		93.5	8	PDB header: transferase Chain: C; PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
10	d1tfra2	 Alignment		93.4	26	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
11	c4rxuA_	 Alignment		92.8	18	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

12	c3uugB_	Alignment		92.7	23	PDB header: sugar binding protein Chain: B: PDB Molecule: multiple sugar-binding periplasmic receptor chve; PDBTitle: crystal structure of the periplasmic sugar binding protein chve
13	c5ocpA_	Alignment		91.8	11	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
14	c4kzkA_	Alignment		91.6	13	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
15	c4wwhA_	Alignment		91.2	21	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from mycobacterium smegmatis (msmeg_1704, target efi-3 510967) with bound d-galactose
16	c4werA_	Alignment		91.1	16	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
17	c4y9tA_	Alignment		90.7	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
18	c3vzdB_	Alignment		90.6	18	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
19	c3d8tB_	Alignment		90.1	18	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
20	c6dspB_	Alignment		89.6	18	PDB header: signaling protein Chain: B: PDB Molecule: autoinducer 2-binding protein lsrb; PDBTitle: lsrb from clostridium saccharobutylicum in complex with ai-2
21	c2dc1A_	Alignment	not modelled	89.1	23	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
22	c6hyhA_	Alignment	not modelled	88.8	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
23	c3brsA_	Alignment	not modelled	88.5	14	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
24	c4es6A_	Alignment	not modelled	87.9	12	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of hemd (pa5259) from pseudomonas aeruginosa (pao1)2 at 2.22 a resolution
25	c2ihnA_	Alignment	not modelled	87.4	27	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
26	c5ulbA_	Alignment	not modelled	86.8	11	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
27	c3mw8A_	Alignment	not modelled	86.8	11	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from2 shewanella amazonensis sb2b at 1.65 a resolution
28	d2d59a1	Alignment	not modelled	86.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

						Family: CoA-binding domain
29	d1cmwa2	Alignment	not modelled	86.1	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
30	d1jr2a_	Alignment	not modelled	84.8	13	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
31	c1jr2A_	Alignment	not modelled	84.8	13	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: structure of uroporphyrinogen iii synthase
32	c4n03A_	Alignment	not modelled	84.6	19	PDB header: transport protein Chain: A: PDB Molecule: abc-type branched-chain amino acid transport systems PDBTitle: fatty acid abc transporter substrate-binding protein from2 thermomonospora curvata
33	c3g1wB_	Alignment	not modelled	83.4	11	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
34	d1wd7a_	Alignment	not modelled	83.4	17	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
35	c4ry0A_	Alignment	not modelled	82.9	14	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 etli cfn 42, target efi-511357, in complex3 with d-ribose
36	c4irxA_	Alignment	not modelled	82.2	17	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
37	c2vk2A_	Alignment	not modelled	82.2	11	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
38	c5bq3A_	Alignment	not modelled	82.1	23	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
39	c3lopA_	Alignment	not modelled	82.0	13	PDB header: substrate binding protein Chain: A: PDB Molecule: substrate binding periplasmic protein; PDBTitle: crystal structure of substrate-binding periplasmic protein2 (pbp) from ralstonia solanacearum
40	c5hsgA_	Alignment	not modelled	81.9	17	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
41	c1cmwA_	Alignment	not modelled	81.7	19	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
42	d1guda_	Alignment	not modelled	81.0	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
43	c4m88A_	Alignment	not modelled	80.1	9	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: crystal structure of extracellular ligand-binding receptor from2 verminephrobacter eiseniae ef01-2
44	d3dhxa1	Alignment	not modelled	79.9	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: NIL domain-like
45	d2qrra1	Alignment	not modelled	79.7	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: NIL domain-like
46	d2liva_	Alignment	not modelled	79.2	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
47	c4yleA_	Alignment	not modelled	78.9	12	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-erythrofurranose
48	c4yhsA_	Alignment	not modelled	78.7	12	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
49	c5dkvD_	Alignment	not modelled	78.2	18	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
50	c3n0wA_	Alignment	not modelled	77.6	12	PDB header: transport protein Chain: A: PDB Molecule: abc branched chain amino acid family transporter, PDBTitle: crystal structure of a branched chain amino acid abc transporter2 periplasmic ligand-binding protein (bx_e_c0949) from

						burkholderia3 xenovorans lb400 at 1.88 a resolution
51	d1xo1a2	Alignment	not modelled	77.4	31	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
52	c3re1B	Alignment	not modelled	76.8	15	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthetase; PDBTitle: crystal structure of uroporphyrinogen iii synthase from pseudomonas2 syringae pv. tomato dc3000
53	c4ry8D	Alignment	not modelled	76.6	11	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
54	d2dria	Alignment	not modelled	76.0	14	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
55	c4z0nA	Alignment	not modelled	75.7	11	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
56	d8abpa	Alignment	not modelled	75.3	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
57	c6gq0A	Alignment	not modelled	74.1	11	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
58	c3ma0A	Alignment	not modelled	73.8	17	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
59	c2qbuA	Alignment	not modelled	73.1	9	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 methyltransferase; PDBTitle: crystal structure of methanothermobacter thermautotrophicus cbil
60	c4rs3A	Alignment	not modelled	72.9	11	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, carbohydrate uptake transporter-2 (cut2) PDBTitle: crystal structure of carbohydrate transporter a0qyb3 from2 mycobacterium smegmatis str. mc2 155, target efi-510969, in complex3 with xylitol
61	d1a9xb2	Alignment	not modelled	72.7	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
62	d1usga	Alignment	not modelled	72.4	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
63	c4jc0B	Alignment	not modelled	71.8	13	PDB header: transferase Chain: B: PDB Molecule: ribosomal protein s12 methylthiotransferase rimo; PDBTitle: crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77
64	c4ry9A	Alignment	not modelled	71.4	14	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
65	c3l6uA	Alignment	not modelled	71.1	11	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
66	c4xfkA	Alignment	not modelled	70.7	13	PDB header: transport protein Chain: A: PDB Molecule: putative branched chain amino acid abc transporter, PDBTitle: crystal structure of leucine-, isoleucine-, valine-, threonine-, and2 alanine-binding protein from brucella ovis
67	c3kwpA	Alignment	not modelled	70.5	14	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis
68	c4ggmX	Alignment	not modelled	70.2	19	PDB header: hydrolase Chain: X: PDB Molecule: udp-2,3-diacylglucosamine pyrophosphatase lpxi; PDBTitle: structure of lpxi
69	d1s4da	Alignment	not modelled	70.1	20	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
70	c4wzzA	Alignment	not modelled	70.0	17	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
71	c3brqA	Alignment	not modelled	69.2	10	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator ascg; PDBTitle: crystal structure of the escherichia coli transcriptional repressor2 ascg
72	d2qswa1	Alignment	not modelled	68.7	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: NIL domain-like
73	c2rjoA	Alignment	not modelled	67.8	17	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
74	c3bb1A	Alignment	not modelled	67.8	14	PDB header: regulatory protein Chain: A: PDB Molecule: regulatory protein of laci family; PDBTitle: crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
75	c3pfnB	Alignment	not modelled	67.5	14	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
76	c4wt7B	Alignment	not modelled	67.2	14	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
77	c5t6oA	Alignment	not modelled	67.0	22	PDB header: biosynthetic protein Chain: A: PDB Molecule: poly-beta-hydroxybuterate polymerase; PDBTitle: structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator
78	c3eafA	Alignment	not modelled	66.9	11	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
79	c2iksA	Alignment	not modelled	66.5	13	PDB header: transcription Chain: A: PDB Molecule: dna-binding transcriptional dual regulator; PDBTitle: crystal structure of n-terminal truncated dna-binding transcriptional2 dual regulator from escherichia coli k12
80	c4wutA	Alignment	not modelled	66.4	14	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
81	c3zddA	Alignment	not modelled	65.8	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
82	c6nmiE	Alignment	not modelled	65.8	8	PDB header: transcription Chain: E: PDB Molecule: general transcription factor iih subunit 2, p44; PDBTitle: cryo-em structure of the human tfiih core complex
83	c3dbiA	Alignment	not modelled	65.6	10	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 escherichia coli complexed with phosphate
84	c3o74A	Alignment	not modelled	65.4	17	PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
85	c4joqA	Alignment	not modelled	64.8	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
86	c4rxmA	Alignment	not modelled	64.8	10	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
87	c2x7xA	Alignment	not modelled	64.5	19	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component system2 bt1754
88	c4evrA	Alignment	not modelled	63.9	15	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter subunit, substrate-binding PDBTitle: crystal structure of abc transporter from r. palustris - solute2 binding protein (rpa0668) in complex with benzoate
89	c4ru0B	Alignment	not modelled	63.7	18	PDB header: transport protein Chain: B: PDB Molecule: putative branched-chain amino acid abc transporter, PDBTitle: the crystal structure of abc transporter permease from pseudomonas2 fluorescens group
90	c4yv7A	Alignment	not modelled	63.2	14	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
91	c4pe6B	Alignment	not modelled	62.9	19	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
92	c3rotA	Alignment	not modelled	62.5	11	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
93	c2duwA	Alignment	not modelled	62.3	13	PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae
94	c3ksmA	Alignment	not modelled	62.1	14	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
95	c4vc6A	Alignment	not modelled	61.8	18	PDB header: solute-binding protein Chain: A: PDB Molecule: putative solute-binding component of abc transporter;

95	c4ysvA	Alignment	not modelled	61.8	18	PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentans (cphy_1585, target efi-3 511156) with bound beta-d-glucose PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelataase for3 siroheme synthesis
96	c1pjtB	Alignment	not modelled	60.7	18	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
97	c4kq9A	Alignment	not modelled	60.2	15	PDB header: peptide binding protein Chain: D: PDB Molecule: protein memo1; PDBTitle: crystal structure of memo, form ii
98	c3bd0D	Alignment	not modelled	60.2	15	PDB header: peptide binding protein Chain: D: PDB Molecule: protein memo1; PDBTitle: crystal structure of memo, form ii
99	d1wyza1	Alignment	not modelled	59.8	19	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
100	c4yo7A	Alignment	not modelled	59.2	13	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
101	d1qo0a	Alignment	not modelled	59.2	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
102	d1u0ta	Alignment	not modelled	59.1	19	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
103	c2dwcB	Alignment	not modelled	58.6	17	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
104	c2l82A	Alignment	not modelled	58.5	25	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or32; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
105	d1iuka	Alignment	not modelled	57.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
106	c1d4cB	Alignment	not modelled	56.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the uncomplexed form of the flavocytochrome c2 fumarate reductase of shewanella putrefaciens strain mr-1
107	c3fxaA	Alignment	not modelled	56.4	15	PDB header: sugar binding protein Chain: A: PDB Molecule: sis domain protein; PDBTitle: crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
108	c4pz0A	Alignment	not modelled	55.9	15	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar abc transporter, sugar-binding protein; PDBTitle: the crystal structure of a solute binding protein from bacillus2 anthracis str. ames in complex with quorum-sensing signal3 autoinducer-2 (ai-2)
109	c3gv0A	Alignment	not modelled	55.8	7	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI family transcription regulator from2 agrobacterium tumefaciens
110	c3om1A	Alignment	not modelled	55.6	8	PDB header: membrane protein Chain: A: PDB Molecule: glutamate receptor gluk5 (ka2); PDBTitle: crystal structure of the gluk5 (ka2) atd dimer at 1.7 angstrom2 resolution
111	c5xavB	Alignment	not modelled	55.5	19	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
112	d1tifa	Alignment	not modelled	54.7	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
113	c4ribA	Alignment	not modelled	54.7	15	PDB header: hydrolase/dna Chain: A: PDB Molecule: fanconi-associated nuclease 1; PDBTitle: fan1 nuclease bound to 5' phosphorylated p(dt) single flap dna
114	c5h06C	Alignment	not modelled	54.1	12	PDB header: hydrolase Chain: C: PDB Molecule: amyp; PDBTitle: crystal structure of amyp in complex with maltose
115	c3o1hB	Alignment	not modelled	53.9	11	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
116	c4o5aA	Alignment	not modelled	53.1	12	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
117	c5braA	Alignment	not modelled	53.0	13	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)

118	c3g68A_	Alignment	not modelled	52.6	6	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
119	c2xecD_	Alignment	not modelled	52.5	16	PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to2 tris
120	c5oqj6_	Alignment	not modelled	52.1	10	PDB header: transcription Chain: 6: PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih