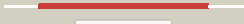



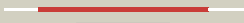



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1166_(lpqW)_1296157_1298064
Date	Wed Jul 31 22:05:25 BST 2019
Unique Job ID	92522c7ff3d72e4f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2grvC_	 Alignment		100.0	85	PDB header: biosynthetic protein Chain: C: PDB Molecule: lpqw; PDBTitle: crystal structure of lpqw
2	c4onyB_	 Alignment		100.0	17	PDB header: transport protein Chain: B: PDB Molecule: extracellular solute-binding protein family 5; PDBTitle: crystal structure of a abc transporter, periplasmic substrate-binding2 protein from brucella melitensis
3	c4oetA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: putative peptide abc-transport system periplasmic peptide- PDBTitle: crystal structure of nikz from campylobacter jejuni, unliganded form
4	c5icqA_	 Alignment		100.0	19	PDB header: periplasmic binding protein Chain: A: PDB Molecule: methylocystis parvus obbp mbne; PDBTitle: methanobactin periplasmic binding protein
5	c4oerA_	 Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: nika protein; PDBTitle: crystal structure of nika from brucella suis, unliganded form
6	d1xoca1	 Alignment		100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
7	c5isuA_	 Alignment		100.0	19	PDB header: transport protein Chain: A: PDB Molecule: lmo0135 protein; PDBTitle: 2.2 angstrom crystal structure of abc transporter substrate binding2 protein ctap (lmo0135) from listeria monocytogenes.
8	c3tpaA_	 Alignment		100.0	15	PDB header: heme binding protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: structure of hbpa2 from haemophilus parasuis
9	d1zlqa1	 Alignment		100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
10	c2wokA_	 Alignment		100.0	21	PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: clavulanic acid biosynthesis oligopeptide binding protein PDBTitle: clavulanic acid biosynthesis oligopeptide binding protein 2 complexed2 with bradykinin
11	d1dpea_	 Alignment		100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like

12	c2o7jA_	Alignment		100.0	15	PDB header: sugar binding protein Chain: A: PDB Molecule: oligopeptide abc transporter, periplasmic PDBTitle: the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
13	c1ztyA_	Alignment		100.0	16	PDB header: sugar binding protein, signaling protein Chain: A: PDB Molecule: chitin oligosaccharide binding protein; PDBTitle: crystal structure of the chitin oligosaccharide binding2 protein
14	c3t66A_	Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: nickel abc transporter (nickel-binding protein); PDBTitle: crystal structure of nickel abc transporter from bacillus halodurans
15	c3m8uA_	Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg)
16	c6hlxA_	Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: agaa; PDBTitle: structure of the pbp agaa in complex with agropinic acid from2 a.tumefacien r10
17	c3o9pA_	Alignment		100.0	18	PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: periplasmic murein peptide-binding protein; PDBTitle: the structure of the escherichia coli murein tripeptide binding2 protein mppa
18	c4qfkG_	Alignment		100.0	16	PDB header: peptide binding protein Chain: G: PDB Molecule: abc transporter periplasmic peptide-binding protein; PDBTitle: crystal structure of dipeptide binding protein from pseudoalteromonas2 sp. sm9913
19	c5yheA_	Alignment		100.0	15	PDB header: metal binding protein Chain: A: PDB Molecule: nickel abc transporter substrate-binding protein; PDBTitle: the crystal structure of staphylococcus aureus cnta in complex with2 staphylopine and cobalt
20	d1jeta_	Alignment		100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
21	c6dtfA_	Alignment	not modelled	100.0	16	PDB header: peptide binding protein Chain: A: PDB Molecule: periplasmic oligopeptide-binding protein; PDBTitle: crystal structure of haemophilus influenzae oppa complex with kkk
22	c4pfwA_	Alignment	not modelled	100.0	15	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: crystal structure of mannohexaose bound oligopeptide abc transporter,2 periplasmic oligopeptide-binding protein (tm1226) from thermotoga3 maritima at 2.2 a resolution
23	d1uqwa_	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
24	d1vr5a1	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
25	c3zs6A_	Alignment	not modelled	100.0	16	PDB header: peptide binding protein Chain: A: PDB Molecule: periplasmic oligopeptide-binding protein; PDBTitle: the structural characterization of burkholderia pseudomallei oppa.
26	c5u4oA_	Alignment	not modelled	100.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: a 2.05a x-ray structure of a bacterial extracellular solute-binding2 protein, family 5 for bacillus anthracis str. ames
27	c4wedA_	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, periplasmic solute-binding protein; PDBTitle: crystal structure of abc transporter substrate-binding protein from2 sinorhizobium meliloti
28	c3ry3B_	Alignment	not modelled	100.0	15	PDB header: transport protein Chain: B: PDB Molecule: putative solute-binding protein; PDBTitle: putative solute-binding protein from yersinia pestis.

29	c4zebA_		Alignment	not modelled	100.0	13	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein (agrociniopines a) PDBTitle: pbp acca from a. tumefaciens c58 in complex with agrociniopine a
30	c2d5wA_		Alignment	not modelled	100.0	14	PDB header: peptide binding protein Chain: A: PDB Molecule: peptide abc transporter, peptide-binding protein; PDBTitle: the crystal structure of oligopeptide binding protein from thermus2 thermophilus hb8 complexed with pentapeptide
31	c6epzA_		Alignment	not modelled	100.0	16	PDB header: transport protein Chain: A: PDB Molecule: periplasmic alpha-galactoside-binding protein; PDBTitle: structure of the periplasmic binding protein melb (atu4661) in complex2 with melibiose from agrobacterium fabrum c58
32	c3rqtA_		Alignment	not modelled	100.0	14	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of the complex of ligand binding2 component of abc-type import system from staphylococcus aureus with3 nickel and two histidines
33	c3ftoA_		Alignment	not modelled	100.0	19	PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide-binding protein oppa; PDBTitle: crystal structure of oppa in a open conformation
34	c6i3gA_		Alignment	not modelled	100.0	15	PDB header: peptide binding protein Chain: A: PDB Molecule: abc transporter, substrate-binding protein, family 5; PDBTitle: crystal structure of a putative peptide binding protein oppa from2 clostridium difficile
35	c4fajA_		Alignment	not modelled	100.0	18	PDB header: peptide binding protein Chain: A: PDB Molecule: prgz; PDBTitle: structure and mode of peptide binding of pheromone receptor prgz
36	c6npaA_		Alignment	not modelled	100.0	16	PDB header: transport protein Chain: A: PDB Molecule: oligopeptide abc transporter, oligopeptide-binding protein; PDBTitle: crystal structure of oligopeptide abc transporter from bacillus2 anthracis str. ames (substrate-binding domain)
37	c4gl8B_		Alignment	not modelled	100.0	15	PDB header: protein transport Chain: B: PDB Molecule: oligopeptide abc transporter oppaiv; PDBTitle: x-ray crystal structure of a periplasmic oligopeptide-binding2 protein/oligopeptide abc transporter(oppaiv) from borrelia3 burgdorferi
38	c5yybA_		Alignment	not modelled	100.0	16	PDB header: sugar binding protein Chain: A: PDB Molecule: putative abc transporter periplasmic binding protein; PDBTitle: crystal structure of sialic acid binding protein from haemophilus2 ducreyi with neu5gc
39	c5ipwA_		Alignment	not modelled	100.0	14	PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide abc transporter, periplasmic oligopeptide- PDBTitle: oligopeptide-binding protein oppa
40	c5kztB_		Alignment	not modelled	100.0	12	PDB header: peptide binding protein Chain: B: PDB Molecule: peptide/nickel transport system substrate-binding protein; PDBTitle: listeria monocytogenes oppa bound to peptide
41	c3lvuB_		Alignment	not modelled	100.0	21	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
42	c3pamB_		Alignment	not modelled	100.0	23	PDB header: transport protein Chain: B: PDB Molecule: transmembrane protein; PDBTitle: crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
43	c3o6pA_		Alignment	not modelled	100.0	17	PDB header: protein binding Chain: A: PDB Molecule: peptide abc transporter, peptide-binding protein; PDBTitle: crystal structure of peptide abc transporter, peptide-binding protein
44	c3chgB_		Alignment	not modelled	95.6	20	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
45	c3tmgA_		Alignment	not modelled	93.2	21	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine, l-proline abc transporter, 2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
46	c3l6gA_		Alignment	not modelled	92.9	16	PDB header: glycine betaine-binding protein Chain: A: PDB Molecule: betaine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcal opuac in its open conformation
47	c2rejA_		Alignment	not modelled	91.6	21	PDB header: choline-binding protein Chain: A: PDB Molecule: putative glycine betaine abc transporter protein; PDBTitle: abc-transporter choline binding protein in unliganded semi-2 closed conformation
48	d1r9la_		Alignment	not modelled	90.8	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
49	c6jf1A_		Alignment	not modelled	90.1	13	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of the substrate binding protein of a methionine2 transporter from streptococcus pneumoniae
50	c4q0cA_		Alignment	not modelled	90.0	16	PDB header: transferase Chain: A: PDB Molecule: virulence sensor protein bvgs; PDBTitle: 3.1 a resolution crystal structure of the b. pertussis bvgs2 periplasmic domain

51	c4xz6A	Alignment	not modelled	82.9	16	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/proline abc transporter, periplasmic PDBTitle: tmox in complex with tmao
52	d1sw5a	Alignment	not modelled	81.9	26	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
53	c4q5tA	Alignment	not modelled	80.9	15	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of an atmb (putative membrane lipoprotein) from2 streptococcus mutans ua159 at 1.91 a resolution
54	c3hlyA	Alignment	not modelled	79.2	14	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from synechococcus sp2 q5mzp6_synp6 protein. northeast structural genomics consortium target3 snr135d.
55	c3r6uA	Alignment	not modelled	77.9	18	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
56	c4oteA	Alignment	not modelled	76.6	20	PDB header: protein transport Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of a putative lipoprotein (cd630_1653) from2 clostridium difficile 630 at 2.20 a resolution
57	c3up9A	Alignment	not modelled	76.2	22	PDB header: methionine-binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative lipoprotein (actodo_00931) from2 actinomyces odontolyticus atcc 17982 at 2.35 a resolution
58	c3nohA	Alignment	not modelled	75.9	23	PDB header: peptide binding protein Chain: A: PDB Molecule: putative peptide binding protein; PDBTitle: crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
59	c6esvA	Alignment	not modelled	75.7	10	PDB header: signaling protein Chain: A: PDB Molecule: putative periplasmic phosphite-binding-like protein (pbl) PDBTitle: structure of the phosphate-bound form of aix from rhizobium sp. str.2 nt-26
60	d2p0la1	Alignment	not modelled	75.6	10	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
61	c3gxaA	Alignment	not modelled	74.2	16	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
62	d1e5da1	Alignment	not modelled	74.2	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
63	c4ntlA	Alignment	not modelled	72.6	17	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein, yaec family; PDBTitle: crystal structure of a lipoprotein, yaec family (ef3198) from2 enterococcus faecalis v583 at 1.80 a resolution
64	c5b3kA	Alignment	not modelled	72.6	17	PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from pseudomonas aeruginosa
65	d1ycga1	Alignment	not modelled	71.6	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
66	c3ir1F	Alignment	not modelled	68.6	16	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria meningitidis
67	c5o2kE	Alignment	not modelled	67.0	11	PDB header: transport protein Chain: E: PDB Molecule: probable phosphite transport system-binding protein ptxb; PDBTitle: native apo-structure of pseudomonas stutzeri ptxb to 2.1 a resolution
68	c3f6sl	Alignment	not modelled	66.2	10	PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin alternate2 conformers
69	c4ef2A	Alignment	not modelled	65.8	19	PDB header: methionine-binding protein Chain: A: PDB Molecule: pheromone cob1/lipoprotein, yaec family; PDBTitle: crystal structure of a pheromone cob1 precursor/lipoprotein, yaec2 family (ef2496) from enterococcus faecalis v583 at 2.10 a resolution
70	d1xs5a	Alignment	not modelled	64.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
71	c4gotA	Alignment	not modelled	61.8	26	PDB header: lipid binding protein Chain: A: PDB Molecule: methionine-binding lipoprotein metq; PDBTitle: crystal structure of a putative methionine-binding lipoprotein2 (bsu32730) from bacillus subtilis subsp. subtilis str. 168 at 1.95 a3 resolution
72	c4z7eB	Alignment	not modelled	61.4	11	PDB header: transport protein Chain: B: PDB Molecule: lmo1422 protein; PDBTitle: soluble binding domain of lmo1422 abc-transporter
73	c3woaA	Alignment	not modelled	61.2	7	PDB header: dna binding protein, sugar binding prote Chain: A: PDB Molecule: repressor protein ci, maltose-binding periplasmic protein; PDBTitle: crystal structure of lambda repressor (1-45) fused with maltose-2 binding protein
74	c4wepA	Alignment	not modelled	60.0	12	PDB header: transport protein Chain: A: PDB Molecule: putative osmoprotectant uptake system substrate-binding PDBTitle: apo_yehz from escherichia coli
75	c4h2dR	Alignment	not modelled	59.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent diflavin oxidoreductase

75	c41z6B_	Alignment	not modelled	55.4	17	PDB header: crystal structure of ndor1 PDB header: transport protein
76	c4k3fA_	Alignment	not modelled	59.0	13	Chain: A; PDB Molecule: probable tonb-dependent receptor; PDBTitle: crystal structure of a putative tonb-dependent receptor (pa5505) from <i>Pseudomonas aeruginosa</i> pao1 at 1.60 Å resolution
77	c5vegC_	Alignment	not modelled	57.0	17	PDB header: electron transport Chain: C; PDB Molecule: flavodoxin; PDBTitle: structure of a short-chain flavodoxin associated with a non-canonical <i>Pdu</i> bacterial microcompartment
78	c6onpA_	Alignment	not modelled	56.8	11	PDB header: unknown function Chain: A; PDB Molecule: periplasmic binding protein xoxj; PDBTitle: crystal structure of periplasmic binding protein xoxj from <i>Methylobacterium extorquens</i> am1
79	c3qslA_	Alignment	not modelled	56.3	10	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from <i>Bordetella bronchiseptica</i> rb50
80	c4ne4A_	Alignment	not modelled	56.0	13	PDB header: transport protein Chain: A; PDB Molecule: abc transporter, substrate binding protein PDBTitle: crystal structure of abc transporter substrate binding protein prox2 from <i>Agrobacterium tumefaciens</i> cocrystallized with btb
81	c2zykA_	Alignment	not modelled	53.3	16	PDB header: sugar binding protein Chain: A; PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
82	d1tlla2	Alignment	not modelled	52.1	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
83	d1v6ta_	Alignment	not modelled	50.7	24	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
84	c4ib2B_	Alignment	not modelled	48.5	19	PDB header: transport protein Chain: B; PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of a putative lipoprotein (rumgna_00858) from <i>Ruminococcus gnavus</i> atcc 29149 at 1.76 Å resolution
85	d1f4pa_	Alignment	not modelled	48.4	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
86	c3pppA_	Alignment	not modelled	48.0	25	PDB header: transport protein Chain: A; PDB Molecule: glycine betaine/carnitine/choline-binding protein; PDBTitle: structures of the substrate-binding protein provide insights into the multiple compatible solutes binding specificities of <i>Bacillus subtilis</i> abc transporter opuc
87	c4esxA_	Alignment	not modelled	45.4	10	PDB header: transferase Chain: A; PDB Molecule: pyrimidine biosynthesis enzyme thi13; PDBTitle: crystal structure of <i>C. albicans</i> thi5 complexed with plp
88	c4heqB_	Alignment	not modelled	45.4	22	PDB header: electron transport Chain: B; PDB Molecule: flavodoxin; PDBTitle: the crystal structure of flavodoxin from <i>Desulfovibrio gigas</i>
89	c2m6rA_	Alignment	not modelled	45.2	20	PDB header: electron transport Chain: A; PDB Molecule: flavodoxin; PDBTitle: apo_yqca
90	c4n82B_	Alignment	not modelled	44.5	15	PDB header: oxidoreductase Chain: B; PDB Molecule: ribonucleotide reductase; PDBTitle: x-ray crystal structure of <i>Streptococcus sanguinis</i> nrdox
91	c6h0cA_	Alignment	not modelled	44.4	11	PDB header: oxidoreductase Chain: A; PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: flv1 flavodiiron core from <i>Synechocystis</i> sp. pcc6803
92	c5hqjA_	Alignment	not modelled	44.1	13	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 <i>Burkholderia graminis</i> c4d1m, target efi-511179, in complex with 3 d-arabinose
93	c5me4A_	Alignment	not modelled	43.4	19	PDB header: transport protein Chain: A; PDB Molecule: probable phosphite transport system-binding protein htxb; PDBTitle: the structure of htxb from <i>Pseudomonas stutzeri</i> in complex with 2 hypophosphite to 1.52 Å resolution
94	c4r6kA_	Alignment	not modelled	42.7	10	PDB header: transport protein Chain: A; PDB Molecule: solute-binding protein; PDBTitle: crystal structure of abc transporter substrate-binding protein yeso2 from <i>Bacillus subtilis</i> , target efi-510761, an open conformation
95	d1p99a_	Alignment	not modelled	41.3	25	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
96	c1p99A_	Alignment	not modelled	41.3	25	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7 Å crystal structure of protein pg110 from <i>Staphylococcus aureus</i>
97	c3p7iA_	Alignment	not modelled	41.1	10	PDB header: transport protein Chain: A; PDB Molecule: phnd, subunit of alkylphosphonate abc transporter; PDBTitle: crystal structure of <i>Escherichia coli</i> phnd in complex with 2-2 aminoethyl phosphonate
98	c3k2dA_	Alignment	not modelled	40.3	12	PDB header: immune system Chain: A; PDB Molecule: abc-type metal ion transport system, periplasmic component; PDBTitle: crystal structure of immunogenic lipoprotein a from <i>Vibrio vulnificus</i>
99	c5widB_	Alignment	not modelled	40.3	13	PDB header: flavoprotein Chain: B; PDB Molecule: flavodoxin;

						PDBTitle: structure of a flavodoxin from the domain archaea
100	c3ombA_	Alignment	not modelled	40.2	13	PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein, family 1; PDBTitle: crystal structure of extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis
101	d2fz5a1	Alignment	not modelled	39.8	9	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
102	d1ykga1	Alignment	not modelled	39.4	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
103	c6detA_	Alignment	not modelled	39.1	11	PDB header: transport protein Chain: A: PDB Molecule: tv2483; PDBTitle: the crystal structure of tv2483 bound to l-arginine
104	c1x2gB_	Alignment	not modelled	38.1	9	PDB header: ligase Chain: B: PDB Molecule: lipoate-protein ligase a; PDBTitle: crystal structure of lipate-protein ligase a from2 escherichia coli
105	c4qhga_	Alignment	not modelled	37.8	9	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: the structure of a nutrient binding protein from burkholderia2 cenocepacia bound to methionine
106	c2x26A_	Alignment	not modelled	37.5	13	PDB header: transport protein Chain: A: PDB Molecule: periplasmic aliphatic sulphonates-binding protein; PDBTitle: crystal structure of the periplasmic aliphatic sulphonate binding2 protein ssua from escherichia coli
107	c5jvbB_	Alignment	not modelled	37.3	8	PDB header: transport protein Chain: B: PDB Molecule: phosphonate abc transporter, periplasmic phosphonate- PDBTitle: 1.95a resolution structure of ptxb from trichodesmium erythraeum2 ims101 in complex with phosphite
108	d1us5a_	Alignment	not modelled	37.2	21	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
109	c4eq9A_	Alignment	not modelled	36.4	7	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate-binding protein-amino acid PDBTitle: 1.4 angstrom crystal structure of abc transporter glutathione-binding2 protein gsht from streptococcus pneumoniae strain canada mdr_19a in3 complex with glutathione
110	c3fniA_	Alignment	not modelled	36.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
111	c3zkkA_	Alignment	not modelled	36.2	10	PDB header: transport protein Chain: A: PDB Molecule: xos binding protein; PDBTitle: structure of the xylo-oligosaccharide specific solute binding protein2 from bifidobacterium animalis subsp. lactis bl-04 in complex with3 xylotetraose
112	c2ek8A_	Alignment	not modelled	35.6	16	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: aminopeptidase from aneurinibacillus sp. strain am-1
113	d5nula_	Alignment	not modelled	35.4	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
114	c2z8fB_	Alignment	not modelled	35.1	13	PDB header: sugar binding protein Chain: B: PDB Molecule: galacto-n-biose/lacto-n-biose i transporter substrate- PDBTitle: the galacto-n-biose-/lacto-n-biose i-binding protein (gl-bp) of the2 abc transporter from bifidobacterium longum in complex with lacto-n-3 tetraose
115	c4yo3G_	Alignment	not modelled	33.7	24	PDB header: transport protein Chain: G: PDB Molecule: tssa; PDBTitle: enteroaggregative escherichia coli tssa n-terminal fragment
116	c3i6vA_	Alignment	not modelled	33.3	12	PDB header: transport protein Chain: A: PDB Molecule: periplasmic his/glu/gln/arg/opine family-binding protein; PDBTitle: crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine
117	c3ix1A_	Alignment	not modelled	32.8	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
118	c3ix1B_	Alignment	not modelled	32.8	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
119	c2hnbA_	Alignment	not modelled	32.4	16	PDB header: electron transport Chain: A: PDB Molecule: protein mioc; PDBTitle: solution structure of a bacterial holo-flavodoxin
120	c3kzgb_	Alignment	not modelled	32.0	20	PDB header: transport protein Chain: B: PDB Molecule: arginine 3rd transport system periplasmic binding PDBTitle: crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila