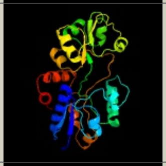
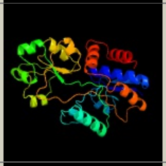
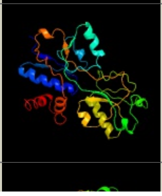
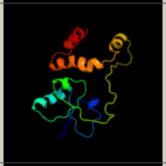
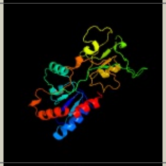
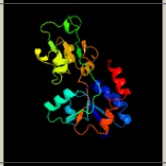
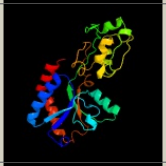
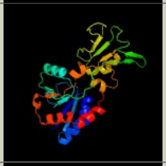
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1244_(lpqZ)_1386863_1387723
Date	Wed Jul 31 22:05:33 BST 2019
Unique Job ID	ee6f76f7295b71a9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ne4A_	Alignment		100.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein **PDBTitle:** crystal structure of abc transporter substrate binding protein prox2 from agrobacterium tumefaciens cocrystalized with btb
2	c4wepA_	Alignment		100.0	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative osmoprotectant uptake system substrate-binding **PDBTitle:** apo yehz from escerichia coli
3	c3o66A_	Alignment		100.0	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline abc transporter; **PDBTitle:** crystal structure of glycine betaine/carnitine/choline abc transporter
4	c4z7eB_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**lmo1422 protein; **PDBTitle:** soluble binding domain of lmo1422 abc-transporter
5	d1sw5a_	Alignment		100.0	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
6	c3r6uA_	Alignment		100.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**choline-binding protein; **PDBTitle:** crystal structure of choline binding protein opubc from bacillus2 subtilis
7	c3pppA_	Alignment		100.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline-binding protein; **PDBTitle:** structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
8	c4xz6A_	Alignment		100.0	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/proline abc transporter, periplasmic **PDBTitle:** tmox in complex with tmao
9	d1r9la_	Alignment		100.0	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
10	c6efrA_	Alignment		100.0	18	**PDB header:**choline-binding protein **Chain:** A: **PDB Molecule:**inicsnfr 1.0, a genetically encoded nicotine biosensor, **PDBTitle:** crystal structure of inicsnfr 1.0
11	c2rejA_	Alignment		100.0	15	**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

12	c3tmgA_	Alignment		100.0	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine, l-proline abc transporter, **PDBTitle:** crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
13	c3l6gA_	Alignment		100.0	10	**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
14	c3chgB_	Alignment		100.0	16	**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
15	c4ntlA_	Alignment		98.8	10	**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
16	c6jf1A_	Alignment		98.8	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure of the substrate binding protein of a methionine2 transporter from streptococcus pneumoniae
17	c4gotA_	Alignment		98.8	13	**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
18	c4q5tA_	Alignment		98.7	12	**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
19	c3gxaA_	Alignment		98.6	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
20	c3k2dA_	Alignment		98.5	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**abc-type metal ion transport system, periplasmic component; **PDBTitle:** crystal structure of immunogenic lipoprotein a from vibrio vulnificus
21	c3un6A_	Alignment	not modelled	98.5	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein saouhsc_00137; **PDBTitle:** 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
22	c3e4rA_	Alignment	not modelled	98.4	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein; **PDBTitle:** crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes
23	c4ib2B_	Alignment	not modelled	98.4	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of a putative lipoprotein (rumgna_00858) from2 ruminococcus gnavus atcc 29149 at 1.76 a resolution
24	c2x26A_	Alignment	not modelled	98.4	14	**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
25	c3ix1A_	Alignment	not modelled	98.3	11	**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
26	c3tqwA_	Alignment	not modelled	98.3	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**methionine-binding protein; **PDBTitle:** structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
27	c3ix1B_	Alignment	not modelled	98.3	11	**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
						PDB header:methionine-binding protein

28	c3up9A_	Alignment	not modelled	98.2	14	**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
29	c3ir1F_	Alignment	not modelled	98.2	13	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria meningitidis
30	c4ef2A_	Alignment	not modelled	98.2	13	**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
31	c4oteA_	Alignment	not modelled	98.1	14	**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
32	c3uifA_	Alignment	not modelled	98.1	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfonate abc transporter, periplasmic sulfonate-binding **PDBTitle:** crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
33	d1xs5a_	Alignment	not modelled	98.1	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
34	c4k3fA_	Alignment	not modelled	98.1	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable tonb-dependent receptor; **PDBTitle:** crystal structure of a putative tonb-dependent receptor (pa5505) from2 pseudomonas aeruginosa pao1 at 1.60 a resolution
35	c4qhqA_	Alignment	not modelled	98.1	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipoprotein; **PDBTitle:** the structure of a nutrient binding protein from burkholderia2 cenocepacia bound to methionine
36	c4h67D_	Alignment	not modelled	98.1	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**pyrimidine precursor biosynthesis enzyme thi5; **PDBTitle:** crystal structure of hmp synthase thi5 from s. cerevisiae
37	c3hn0A_	Alignment	not modelled	98.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein; **PDBTitle:** crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
38	c3p7iA_	Alignment	not modelled	97.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**phnd, subunit of alkylphosphonate abc transporter; **PDBTitle:** crystal structure of escherichia coli phnd in complex with 2-2 aminoethyl phosphonate
39	d1p99a_	Alignment	not modelled	97.9	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
40	c1p99A_	Alignment	not modelled	97.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg110; **PDBTitle:** 1.7a crystal structure of protein pg110 from staphylococcus aureus
41	c6esvA_	Alignment	not modelled	97.8	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative periplasmic phosphite-binding-like protein (pbl) **PDBTitle:** structure of the phosphate-bound form of aiox from rhizobium sp. str.2 nt-26
42	c3qslA_	Alignment	not modelled	97.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of cae31940 from bordetella bronchiseptica rb50
43	c2de4B_	Alignment	not modelled	97.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dibenzothiophene desulfurization enzyme b; **PDBTitle:** crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid
44	c5me4A_	Alignment	not modelled	97.7	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable phosphite transport system-binding protein htxb; **PDBTitle:** the structure of htxb from pseudomonas stutzeri in complex with2 hypophosphite to 1.52 a resolution
45	c2x7pA_	Alignment	not modelled	97.7	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**possible thiamine biosynthesis enzyme; **PDBTitle:** the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
46	c5lv1C_	Alignment	not modelled	97.5	12	**PDB header:**periplasmic binding protein **Chain:** C: **PDB Molecule:**ptxb; **PDBTitle:** 2.12 a resolution structure of ptxb from prochlorococcus marinus (mit2 9301) in complex with phosphite
47	c4esxA_	Alignment	not modelled	97.5	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine biosynthesis enzyme thi13; **PDBTitle:** crystal structure of c. albicans thi5 complexed with plp
48	c5lq8A_	Alignment	not modelled	97.2	10	**PDB header:**periplasmic binding protein **Chain:** A: **PDB Molecule:**putative phosphonate binding protein for abc transporter; **PDBTitle:** 1.52 a resolution structure of phnd1 from prochlorococcus marinus (mit2 9301) in complex with methylphosphonate
49	c2g29A_	Alignment	not modelled	97.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein nrta; **PDBTitle:** crystal structure of the periplasmic nitrate-binding2 protein nrta from synechocystis pcc 6803
50	c3n5lA_	Alignment	not modelled	97.1	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**binding protein component of abc phosphonate transporter; **PDBTitle:** crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
						Fold: Periplasmic binding protein-like II

51	d1us5a_	Alignment	not modelled	97.1	10	**Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
52	c4dddA_	Alignment	not modelled	96.9	5	**PDB header:**immune system **Chain:** A: **PDB Molecule:**immunogenic protein; **PDBTitle:** crystal structure of an immunogenic protein from ehrlichia chaffeensis
53	c5o2kE_	Alignment	not modelled	96.8	14	**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
54	c4nmyA_	Alignment	not modelled	96.7	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type transport system, extracellular solute-binding **PDBTitle:** crystal structure of the thiamin-bound form of substrate-binding2 protein of abc transporter from clostridium difficile
55	c4q0cA_	Alignment	not modelled	96.5	18	**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
56	c5jvbB_	Alignment	not modelled	96.1	10	**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
57	c4pshA_	Alignment	not modelled	95.5	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**abc-type transporter, periplasmic subunit family 3; **PDBTitle:** structure of holo argbp from t. maritima
58	d2fyia1	Alignment	not modelled	95.2	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
59	c5ub6B_	Alignment	not modelled	94.8	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**phosphate-binding protein; **PDBTitle:** xac2383 from xanthomonas citri bound to pyrophosphate
60	c5tpiA_	Alignment	not modelled	94.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative transcriptional regulator (lysr family); **PDBTitle:** 1.47 angstrom crystal structure of the c-terminal substrate binding2 domain of lysr family transcriptional regulator from klebsiella3 pneumoniae.
61	c5z50A_	Alignment	not modelled	94.0	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cys regulon transcriptional activator; **PDBTitle:** crystal structure of pacysb regulatory domain
62	c2i4cA_	Alignment	not modelled	94.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**bicarbonate transporter; **PDBTitle:** crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
63	c3fj7A_	Alignment	not modelled	93.5	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**major antigenic peptide peb3; **PDBTitle:** crystal structure of l-phospholactate bound peb3
64	c3woaA_	Alignment	not modelled	93.3	14	**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
65	c5gzsA_	Alignment	not modelled	93.2	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef family protein; **PDBTitle:** structure of vc protein
66	d1amfa_	Alignment	not modelled	93.1	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
67	c3lr1A_	Alignment	not modelled	92.5	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tungstate abc transporter, periplasmic tungstate- **PDBTitle:** the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
68	c2h5yC_	Alignment	not modelled	92.3	15	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**molybdate-binding periplasmic protein; **PDBTitle:** crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate
69	c4jb7A_	Alignment	not modelled	92.0	9	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**accessory colonization factor acfc; **PDBTitle:** 1.42 angstrom resolution crystal structure of accessory colonization2 factor acfc (acfc) in complex with d-aspartic acid
70	c1al3A_	Alignment	not modelled	90.0	13	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**cys regulon transcriptional activator cysb; **PDBTitle:** cofactor binding fragment of cysb from klebsiella aerogenes
71	d1al3a_	Alignment	not modelled	90.0	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
72	c3muqB_	Alignment	not modelled	89.7	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
73	d2esna2	Alignment	not modelled	89.5	21	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
74	c6onpA_	Alignment	not modelled	88.8	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**periplasmic binding protein xoxj; **PDBTitle:** crystal structure of periplasmic binding protein xoxj from2 methylobacterium extorquens am1
						PDB header:transport protein **Chain:** B: **PDB Molecule:**amino acid abc transporter, periplasmic

75	c4z9nB_	Alignment	not modelled	88.6	15	amino acid-binding **PDBTitle:** abc transporter / periplasmic binding protein from brucella ovis with2 glutathione bound
76	c4rnsA_	Alignment	not modelled	88.4	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**pcp degradation transcriptional activation protein; **PDBTitle:** pcpr inducer binding domain (apo-form)
77	c3mplA_	Alignment	not modelled	87.3	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**virulence sensor protein bvgs; **PDBTitle:** crystal structure of bordetella pertussis bvgs vft2 domain (double2 mutant f375e/q461e)
78	c5z72B_	Alignment	not modelled	87.2	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**ccpc; **PDBTitle:** crystal structure of ccpc regulatory domain in complex with citrate2 from bacillus amyloliquefaciens
79	c2q2aD_	Alignment	not modelled	87.1	16	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**artj; **PDBTitle:** crystal structures of the arginine-, lysine-, histidine-binding2 protein artj from the thermophilic bacterium geobacillus3 stearothermophilus
80	c2ypnA_	Alignment	not modelled	86.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hydroxymethylbilane synthase); **PDBTitle:** hydroxymethylbilane synthase
81	c5b70B_	Alignment	not modelled	85.6	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**lysr family transcriptional regulator; **PDBTitle:** oxyr2 e204g regulatory domain from vibrio vulnificus
82	c4eq9A_	Alignment	not modelled	85.1	11	**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
83	c4c0rB_	Alignment	not modelled	84.5	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative amino acid binding protein; **PDBTitle:** molecular and structural basis of glutathione import in2 gram-positive bacteria via gsht and the cystine abc3 importer tcybc of streptococcus mutans.
84	c5b3zB_	Alignment	not modelled	84.3	11	**PDB header:**isomerase,sugar binding protein **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase nima-interacting 1, **PDBTitle:** crystal structure of hpin1 ww domain (5-39) fused with maltose-binding2 protein
85	d1zbma1	Alignment	not modelled	83.9	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
86	c3c9hB_	Alignment	not modelled	83.4	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, substrate binding protein; **PDBTitle:** crystal structure of the substrate binding protein of the abc2 transporter from agrobacterium tumefaciens
87	c4ng7A_	Alignment	not modelled	83.3	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**trap periplasmic solute binding protein; **PDBTitle:** crystal structure of a trap periplasmic solute binding protein from2 citrobacter koseri (cko_04899), target efi-510094, apo, open3 structure
88	d1xvxa_	Alignment	not modelled	83.0	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
89	c3kzgB_	Alignment	not modelled	82.7	10	**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
90	c6ddnB_	Alignment	not modelled	82.7	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**probable sulfate-binding lipoprotein subi; **PDBTitle:** the sulfate-binding protein subi from mycobacterium tuberculosis h37rv
91	c2f7cA_	Alignment	not modelled	80.8	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** catm effector binding domain with its effector cis,cis-muconate
92	c2hxrA_	Alignment	not modelled	80.1	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator cynr; **PDBTitle:** structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
93	d1utha_	Alignment	not modelled	79.9	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
94	c4mlqA_	Alignment	not modelled	79.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**porphobilinogen deaminase; **PDBTitle:** crystal structure of bacillus megaterium porphobilinogen deaminase
95	c3vvfA_	Alignment	not modelled	78.0	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**amino acid abc transporter, binding protein; **PDBTitle:** crystal structure of ttc0807 complexed with arginine
96	c4ovtA_	Alignment	not modelled	77.8	12	**PDB header:**solute-binding protein **Chain:** A: **PDB Molecule:**trap dicarboxylate transporter, dctp subunit; **PDBTitle:** crystal structure of a trap periplasmic solute binding protein from2 ochrobacterium anthropi (oant_3902), target efi-510153, with bound l-3 fuconate
97	c2uyeA_	Alignment	not modelled	77.6	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein; **PDBTitle:** double mutant y110s,f111v dntr from burkholderia sp. strain2 dnt in complex with thiocyanate
98	c4i1dB_	Alignment	not modelled	77.3	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter substrate-binding protein; **PDBTitle:** the crystal structure of an abc transporter substrate-binding protein2 from bradyrhizobium japonicum usda 110

99	c3jv9B_	Alignment	not modelled	76.7	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** the structure of a reduced form of oxyr from n. meningitidis
100	d1i6aa_	Alignment	not modelled	76.7	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
101	c4oz9A_	Alignment	not modelled	76.2	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**membrane-bound lytic murein transglycosylase f; **PDBTitle:** crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine
102	c5uh0A_	Alignment	not modelled	75.7	10	**PDB header:**hydrolase,oxidoreductase **Chain:** A: **PDB Molecule:**membrane-bound lytic murein transglycosylase f; **PDBTitle:** 1.95 angstrom resolution crystal structure of fragment (35-274) of2 membrane-bound lytic murein transglycosylase f from yersinia pestis.
103	c3k4uA_	Alignment	not modelled	75.2	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**binding component of abc transporter; **PDBTitle:** crystal structure of putative binding component of abc transporter2 from wolinella succinogenes dsm 1740 complexed with lysine
104	d1pdaa1	Alignment	not modelled	74.9	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
105	c6detA_	Alignment	not modelled	74.7	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tv2483; **PDBTitle:** the crystal structure of tv2483 bound to l-arginine
106	c3oxnD_	Alignment	not modelled	74.4	5	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator, lysr family; **PDBTitle:** the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
107	c2ql3G_	Alignment	not modelled	74.3	15	**PDB header:**transcription **Chain:** G: **PDB Molecule:**probable transcriptional regulator, lysr family protein; **PDBTitle:** crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
108	c5vvhE_	Alignment	not modelled	74.2	11	**PDB header:**transcription **Chain:** E: **PDB Molecule:**octopine catabolism/uptake operon regulatory protein occr; **PDBTitle:** crystal structure of the effector binding domain of lysr-type2 transcriptional regulator, occr from agrobacterium tumefaciens
109	c4zdmA_	Alignment	not modelled	72.5	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate receptor kainate-like protein; **PDBTitle:** pleurobrachia bachei iglur3 lbd glycine complex
110	c2pt1A_	Alignment	not modelled	72.3	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron transport protein; **PDBTitle:** futa1 synechocystis pcc 6803
111	c4h5fB_	Alignment	not modelled	72.3	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**amino acid abc superfamily atp binding cassette **PDBTitle:** crystal structure of an amino acid abc transporter substrate-binding2 protein from streptococcus pneumoniae canada mdr_19a bound to l-3 arginine, form 1
112	c3eq1A_	Alignment	not modelled	72.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**porphobilinogen deaminase; **PDBTitle:** the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
113	c3n6uA_	Alignment	not modelled	71.9	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
114	c2qryD_	Alignment	not modelled	71.6	9	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**thiamine-binding periplasmic protein; **PDBTitle:** periplasmic thiamin binding protein
115	c6h2tA_	Alignment	not modelled	70.9	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable glutamine-binding lipoprotein glnh (glnbp); **PDBTitle:** glnh bound to glu, mycobacterium tuberculosis
116	c2h9bB_	Alignment	not modelled	69.7	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
117	c4fajA_	Alignment	not modelled	68.7	10	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**prgz; **PDBTitle:** structure and mode of peptide binding of pheromone receptor prgz
118	c4oenA_	Alignment	not modelled	67.7	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**second substrate binding domain of putative amino acid abc **PDBTitle:** crystal structure of the second substrate binding domain of a putative2 amino acid abc transporter from streptococcus pneumoniae canada3 mdr_19a
119	c4yicA_	Alignment	not modelled	67.3	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**trap transporter solute binding protein; **PDBTitle:** crystal structure of a trap transporter solute binding protein2 (ipr025997) from bordetella bronchiseptica rb50 (bb0280, target efi-3 500035) with bound picolinic acid
120	c2q89A_	Alignment	not modelled	67.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative abc transporter amino acid-binding protein; **PDBTitle:** crystal structure of ehub in complex with hydroxyectoine