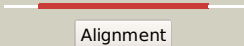

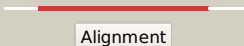

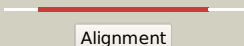







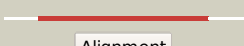




















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3759c_(proX)_4204604_4205551
Date	Fri Aug 9 18:20:46 BST 2019
Unique Job ID	a5a06263576dcbae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ne4A_</a>	 Alignment		100.0	28	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate binding protein <b>PDBTitle:</b> crystal structure of abc transporter substrate binding protein prox2 from agrobacterium tumefaciens cocrystalized with btb
2	<a href="#">c4wepA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative osmoprotectant uptake system substrate-binding <b>PDBTitle:</b> apo yehz from escherichia coli
3	<a href="#">d1sw5a_</a>	 Alignment		100.0	22	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
4	<a href="#">c4z7eB_</a>	 Alignment		100.0	25	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lmo1422 protein; <b>PDBTitle:</b> soluble binding domain of lmo1422 abc-transporter
5	<a href="#">c3r6uA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> choline-binding protein; <b>PDBTitle:</b> crystal structure of choline binding protein opubc from bacillus2 subtilis
6	<a href="#">c3o66A_</a>	 Alignment		100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/carnitine/choline abc transporter; <b>PDBTitle:</b> crystal structure of glycine betaine/carnitine/choline abc transporter
7	<a href="#">c3pppA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/carnitine/choline-binding protein; <b>PDBTitle:</b> structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
8	<a href="#">d1r9la_</a>	 Alignment		100.0	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
9	<a href="#">c4xz6A_</a>	 Alignment		100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/proline abc transporter, periplasmic <b>PDBTitle:</b> tmox in complex with tmao
10	<a href="#">c6efrA_</a>	 Alignment		100.0	33	<b>PDB header:</b> choline-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> inicsnfr 1.0, a genetically encoded nicotine biosensor, <b>PDBTitle:</b> crystal structure of inicsnfr 1.0
11	<a href="#">c2rejA_</a>	 Alignment		100.0	17	<b>PDB header:</b> choline-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycine betaine abc transporter protein; <b>PDBTitle:</b> abc-transporter choline binding protein in unliganded semi-2 closed conformation

12	<a href="#">c3tmgA</a>	Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine, l-proline abc transporter, <b>PDBTitle:</b> crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
13	<a href="#">c3l6gA</a>	Alignment		100.0	15	<b>PDB header:</b> glycine betaine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> betaine abc transporter permease and substrate binding <b>PDBTitle:</b> crystal structure of lactococcal opuac in its open conformation
14	<a href="#">c3chgB</a>	Alignment		100.0	13	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine-binding protein; <b>PDBTitle:</b> the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
15	<a href="#">c3un6A</a>	Alignment		99.6	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein saouhsc_00137; <b>PDBTitle:</b> 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
16	<a href="#">c3e4rA</a>	Alignment		99.6	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein; <b>PDBTitle:</b> crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes
17	<a href="#">c3uifA</a>	Alignment		99.6	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfonate abc transporter, periplasmic sulfonate-binding <b>PDBTitle:</b> crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
18	<a href="#">c2x26A</a>	Alignment		99.5	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic aliphatic sulphonates-binding protein; <b>PDBTitle:</b> crystal structure of the periplasmic aliphatic sulphonate binding2 protein ssua from escherichia coli
19	<a href="#">c6jf1A</a>	Alignment		99.5	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein; <b>PDBTitle:</b> crystal structure of the substrate binding protein of a methionine2 transporter from streptococcus pneumoniae
20	<a href="#">c4ntlA</a>	Alignment		99.5	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein, yaec family; <b>PDBTitle:</b> crystal structure of a lipoprotein, yaec family (ef3198) from2 enterococcus faecalis v583 at 1.80 a resolution
21	<a href="#">c4gotA</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-binding lipoprotein metq; <b>PDBTitle:</b> crystal structure of a putative methionine-binding lipoprotein2 (bsu32730) from bacillus subtilis subsp. subtilis str. 168 at 1.95 a3 resolution
22	<a href="#">c3gxaA</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946; <b>PDBTitle:</b> crystal structure of gna1946
23	<a href="#">c2de4B</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dibenzothiophene desulfurization enzyme b; <b>PDBTitle:</b> crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfenic acid
24	<a href="#">c3ix1A</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding <b>PDBTitle:</b> periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
25	<a href="#">c3ix1B</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding <b>PDBTitle:</b> periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
26	<a href="#">c2x7pA</a>	Alignment	not modelled	99.4	7	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> possible thiamine biosynthesis enzyme; <b>PDBTitle:</b> the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
27	<a href="#">c3k2dA</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type metal ion transport system, periplasmic component; <b>PDBTitle:</b> crystal structure of immunogenic lipoprotein a from vibrio vulnificus

28	<a href="#">c3qsIA_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> structure of cae31940 from bordetella bronchiseptica rb50
29	<a href="#">c4q5tA_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein; <b>PDBTitle:</b> crystal structure of an atmb (putative membrane lipoprotein) from2 streptococcus mutans ua159 at 1.91 a resolution
30	<a href="#">c3ir1F_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946; <b>PDBTitle:</b> crystal structure of lipoprotein gna1946 from neisseria meningitidis
31	<a href="#">c3hn0A_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein; <b>PDBTitle:</b> crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
32	<a href="#">c3tqwA_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-binding protein; <b>PDBTitle:</b> structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
33	<a href="#">c4k3fA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable tonb-dependent receptor; <b>PDBTitle:</b> crystal structure of a putative tonb-dependent receptor (pa5505) from2 pseudomonas aeruginosa pao1 at 1.60 a resolution
34	<a href="#">c2g29A_</a>	Alignment	not modelled	99.3	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein nrtA; <b>PDBTitle:</b> crystal structure of the periplasmic nitrate-binding2 protein nrtA from synechocystis pcc 6803
35	<a href="#">c4ef2A_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> methionine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pheromone cob1/lipoprotein, yaec family; <b>PDBTitle:</b> crystal structure of a pheromone cob1 precursor/lipoprotein, yaec2 family (ef2496) from enterococcus faecalis v583 at 2.10 a resolution
36	<a href="#">c2i4cA_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> bicarbonate transporter; <b>PDBTitle:</b> crystal structure of bicarbonate transport protein cmpA from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
37	<a href="#">c3up9A_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> methionine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative lipoprotein (actodo_00931) from2 actinomyces odontolyticus atcc 17982 at 2.35 a resolution
38	<a href="#">c4ib2B_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> crystal structure of a putative lipoprotein (rumgna_00858) from2 ruminococcus gnavus atcc 29149 at 1.76 a resolution
39	<a href="#">c4h67D_</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> pyrimidine precursor biosynthesis enzyme thi5; <b>PDBTitle:</b> crystal structure of hmp synthase thi5 from s. cerevisiae
40	<a href="#">c4oteA_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein; <b>PDBTitle:</b> crystal structure of a putative lipoprotein (cd630_1653) from2 clostridium difficile 630 at 2.20 a resolution
41	<a href="#">c6esvA_</a>	Alignment	not modelled	99.2	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative periplasmic phosphite-binding-like protein (pbl) <b>PDBTitle:</b> structure of the phosphate-bound form of aixo from rhizobium sp. str.2 nt-26
42	<a href="#">c4qhqA_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein; <b>PDBTitle:</b> the structure of a nutrient binding protein from burkholderia2 cenocepacia bound to methionine
43	<a href="#">c4esxA_</a>	Alignment	not modelled	99.2	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine biosynthesis enzyme thi13; <b>PDBTitle:</b> crystal structure of c. albicans thi5 complexed with plp
44	<a href="#">c4dddA_</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> immunogenic protein; <b>PDBTitle:</b> crystal structure of an immunogenic protein from ehrlichia chaffeensis
45	<a href="#">d1xs5a_</a>	Alignment	not modelled	99.1	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
46	<a href="#">c3p7iA_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phnd, subunit of alkylphosphonate abc transporter; <b>PDBTitle:</b> crystal structure of escherichia coli phnd in complex with 2-2 aminoethyl phosphonate
47	<a href="#">d1p99a_</a>	Alignment	not modelled	99.1	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
48	<a href="#">c1p99A_</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pg110; <b>PDBTitle:</b> 1.7a crystal structure of protein pg110 from staphylococcus aureus
49	<a href="#">c5me4A_</a>	Alignment	not modelled	99.0	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable phosphite transport system-binding protein htxb; <b>PDBTitle:</b> the structure of htxb from pseudomonas stutzeri in complex with2 hypophosphite to 1.52 a resolution
50	<a href="#">d1us5a_</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
51	<a href="#">c4nmyA_</a>	Alignment	not modelled	99.0	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type transport system, extracellular solute-binding <b>PDBTitle:</b> crystal structure of the thiamin-bound form of substrate-binding2 protein of abc transporter from clostridium difficile
52	<a href="#">c5lv1C_</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> periplasmic binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> ptxb;

52	<a href="#">c5v1C_</a>	Alignment	not modelled	98.9	11	<b>PDBTitle:</b> 2.12 a resolution structure of ptxb from prochlorococcus marinus (mit2 9301) in complex with phosphite <b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> probable phosphite transport system-binding protein ptxb;
53	<a href="#">c5o2kE_</a>	Alignment	not modelled	98.8	13	<b>PDBTitle:</b> native apo-structure of pseudomonas stutzeri ptxb to 2.1 a resolution <b>PDB header:</b> periplasmic binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphonate binding protein for abc transporter;
54	<a href="#">c5lq8A_</a>	Alignment	not modelled	98.7	13	<b>PDBTitle:</b> 1.52 a resolution structure of phnd1 from prochlorococcus marinus (mit2 9301) in complex with methylphosphonate <b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphonate abc transporter, periplasmic phosphonate-
55	<a href="#">c5jvbB_</a>	Alignment	not modelled	98.6	12	<b>PDBTitle:</b> 1.95a resolution structure of ptxb from trichodesmium erythraeum2 ims101 in complex with phosphite <b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphate-binding protein;
56	<a href="#">c5ub6B_</a>	Alignment	not modelled	98.6	12	<b>PDBTitle:</b> xac2383 from xanthomonas citri bound to pyrophosphate <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> binding protein component of abc phosphonate transporter;
57	<a href="#">c3n5lA_</a>	Alignment	not modelled	98.5	14	<b>PDBTitle:</b> crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution <b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
58	<a href="#">d2nxoa1</a>	Alignment	not modelled	98.5	13	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> molybdate-binding periplasmic protein;
59	<a href="#">c2h5yC_</a>	Alignment	not modelled	98.3	11	<b>PDBTitle:</b> crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate <b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable sulfate-binding lipoprotein subi;
60	<a href="#">c6ddnB_</a>	Alignment	not modelled	98.2	15	<b>PDBTitle:</b> the sulfate-binding protein subi from mycobacterium tuberculosis h37rv <b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
61	<a href="#">d1amfa_</a>	Alignment	not modelled	98.2	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate abc transporter, periplasmic phosphate-binding <b>PDBTitle:</b> crystal structure of psts (bb_0215) from borrelia burgdorferi
62	<a href="#">c4n13A_</a>	Alignment	not modelled	98.1	10	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
63	<a href="#">d1atga_</a>	Alignment	not modelled	98.1	9	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
64	<a href="#">d1zbma1</a>	Alignment	not modelled	98.1	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
65	<a href="#">c3muqB_</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein;
66	<a href="#">c4kd5A_</a>	Alignment	not modelled	97.8	9	<b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type transport system, molybdenum-specific <b>PDBTitle:</b> substrate binding domain of putative molybdenum abc transporter from2 clostridium difficile
67	<a href="#">c4nhbB_</a>	Alignment	not modelled	97.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter-dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio desulfuricans (ddes_1525), target efi-510107, with3 bound sn-glycerol-3-phosphate
68	<a href="#">c4q0cA_</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> virulence sensor protein bvgs; <b>PDBTitle:</b> 3.1 a resolution crystal structure of the b. pertussis bvgs2 periplasmic domain
69	<a href="#">c4pfbA_</a>	Alignment	not modelled	97.7	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c4-dicarboxylate-binding protein; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 fusobacterium nucleatum (fn1258, target efi-510120) with bound sn-3 glycerol-3-phosphate
70	<a href="#">c4jb7A_</a>	Alignment	not modelled	97.7	10	<b>PDB header:</b> cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> accessory colonization factor acfc; <b>PDBTitle:</b> 1.42 angstrom resolution crystal structure of accessory colonization2 factor acfc (acfc) in complex with d-aspartic acid
71	<a href="#">c3lr1A_</a>	Alignment	not modelled	97.7	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> tungstate abc transporter, periplasmic tungstate- <b>PDBTitle:</b> the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
72	<a href="#">c4o8mA_</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein2 actinobacillus succinogenes 130z, target efi-510004, with bound l-3 galactonate
73	<a href="#">c4nq8B_</a>	Alignment	not modelled	97.7	16	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> putative periplasmic substrate-binding transport protein; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 bordetella bronchiseptica (bb3421), target efi-510039, with density3 modeled as pantoate
						<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap periplasmic solute binding protein;

74	<a href="#">c4ng7A_</a>	Alignment	not modelled	97.6	11	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 citrobacter koseri (cko_04899), target efi-510094, apo, open3 structure
75	<a href="#">c3fj7A_</a>	Alignment	not modelled	97.6	8	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> major antigenic peptide peb3; <b>PDBTitle:</b> crystal structure of l-phospholactate bound peb3
76	<a href="#">c4p1eA_</a>	Alignment	not modelled	97.6	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 escherichia fergusonii (efer_1530), target efi-510119, apo open3 structure, phased with iodide
77	<a href="#">d2czla1</a>	Alignment	not modelled	97.5	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
78	<a href="#">c4ovsB_</a>	Alignment	not modelled	97.5	13	<b>PDB header:</b> solute-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 sulfurospirillum deleyianum dsm 6946 (sdel_0447), target efi-510309,3 with bound succinate
79	<a href="#">c3cvgD_</a>	Alignment	not modelled	97.5	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative metal binding protein; <b>PDBTitle:</b> crystal structure of a periplasmic putative metal binding protein
80	<a href="#">c3gyyC_</a>	Alignment	not modelled	97.5	9	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> periplasmic substrate binding protein; <b>PDBTitle:</b> the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
81	<a href="#">c4rxlA_</a>	Alignment	not modelled	97.5	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum abc transporter, periplasmic molybdenum-binding <b>PDBTitle:</b> crystal structure of molybdenum abc transporter solute binding protein2 vc_a0726 from vibrio cholerae, target efi-510913, in complex with3 tungstate
82	<a href="#">c4n8yA_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative trap-type c4-dicarboxylate transport system, <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 bradyrhizobium sp. btai1 b (bbta_0128), target efi-5100563 (bbta_0128), complex with alpha/beta-d-galacturonate
83	<a href="#">c4p47A_</a>	Alignment	not modelled	97.5	13	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 ochrobactrum anthropi (oant_4429), target efi-510151, c-terminus bound3 in ligand binding pocket
84	<a href="#">c4pddA_</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 polaromonas sp js666 (bpro_0088, target efi-510167) bound to d-3 erythronate
85	<a href="#">c2hpgB_</a>	Alignment	not modelled	97.5	11	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding <b>PDBTitle:</b> the crystal structure of a thermophilic trap periplasmic2 binding protein
86	<a href="#">c3woaA_</a>	Alignment	not modelled	97.5	9	<b>PDB header:</b> dna binding protein, sugar binding prote <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein ci, maltose-binding periplasmic protein; <b>PDBTitle:</b> crystal structure of lambda repressor (1-45) fused with maltose-2 binding protein
87	<a href="#">c4pakA_</a>	Alignment	not modelled	97.5	11	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 verminephrobacter eiseniae ef01-2 (veis_3954, target efi-510324) a3 nephridial symbiont of the earthworm eisenia foetida, bound to (r)-4 pantoic acid
88	<a href="#">c4ovtA_</a>	Alignment	not modelled	97.4	11	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 ochrobacterium anthropi (oant_3902), target efi-510153, with bound l-3 fuconate
89	<a href="#">c5my5A_</a>	Alignment	not modelled	97.4	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter periplasmic substrate-binding protein; <b>PDBTitle:</b> tungstate binding protein - tupa - from desulfovibrio alaskensis g20
90	<a href="#">d1xvxa_</a>	Alignment	not modelled	97.4	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
91	<a href="#">c4o94B_</a>	Alignment	not modelled	97.4	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 rhodopseudomonas palustris haa2 (rpb_3329), target efi-510223, with3 bound succinate
92	<a href="#">c4pfrA_</a>	Alignment	not modelled	97.3	12	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_3541, target efi-510203), apo open3 partially disordered
93	<a href="#">c4p56C_</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> solute-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative extracellular solute-binding protein; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 bordetella bronchiseptica, target efi-510038 (bb2442),



						with bound3 (r)-mandelate and (s)-mandelate
94	<a href="#">c4p1A_</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 chromohalobacter salexigens dsm 3043 (csal_2479), target efi-510085,3 with bound d-glucuronate, spg i213
95	<a href="#">c2f5xC_</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> bugd; <b>PDBTitle:</b> structure of periplasmic binding protein bugd
96	<a href="#">c4oz9A_</a>	Alignment	not modelled	97.3	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> membrane-bound lytic murein transglycosylase f; <b>PDBTitle:</b> crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine
97	<a href="#">c4nn3A_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio salexigens (desal_2161), target efi-510109, with bound3 orotic acid
98	<a href="#">c4n91A_</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 anaerococcus prevotii dsm 20548 (apre_1383), target efi-510023, with3 bound alpha/beta d-glucuronate
99	<a href="#">c4x8rB_</a>	Alignment	not modelled	97.2	10	<b>PDB header:</b> solute-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_2138, target efi-510205) with3 bound glucuronate
100	<a href="#">c4oanB_</a>	Alignment	not modelled	97.2	9	<b>PDB header:</b> membrane protein/protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 rhodospseudomonas palustris haa2 (rpb_2686), target efi-510221, with3 density modeled as (s)-2-hydroxy-2-methyl-3-oxobutanoate ((s)-2-4 acetolactate)
101	<a href="#">c6hkeB_</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> possible tctc subunit of the tripartite tricarboxylate <b>PDBTitle:</b> matc (rpa3494) from rhodospseudomonas palustris with bound malate
102	<a href="#">d1sbpa_</a>	Alignment	not modelled	97.2	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
103	<a href="#">c4nf0E_</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> probable c4-dicarboxylate-binding protein; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 pseudomonas aeruginosa pao1 (pa4616), target efi-510182, with bound3 l-malate
104	<a href="#">c4zdmA_</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate receptor kainate-like protein; <b>PDBTitle:</b> pleurobrachia bachei iglur3 lbd glycine complex
105	<a href="#">c4pbhA_</a>	Alignment	not modelled	97.1	15	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit, putative; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 ruegeria pomeroyi dss-3 (spo1773, target efi-510260) with bound3 benzoic acid
106	<a href="#">c2vpnB_</a>	Alignment	not modelled	97.0	11	<b>PDB header:</b> transport <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic substrate binding protein; <b>PDBTitle:</b> high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata
107	<a href="#">c4magA_</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sialic acid binding protein; <b>PDBTitle:</b> crystal structure of the periplasmic sialic acid binding protein from2 vibrio cholerae
108	<a href="#">c4ovqA_</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate abc transporter, substrate-binding <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 roseobacter denitrificans, target efi-510230, with bound beta-d-3 glucuronate
109	<a href="#">c4pe3A_</a>	Alignment	not modelled	96.9	14	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter-dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_3620, target efi-510199), apo open3 structure
110	<a href="#">d2fyia1</a>	Alignment	not modelled	96.9	10	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
111	<a href="#">c4ovpB_</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> solute-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> c4-dicarboxylate transport system substrate-binding <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 sulfitebacter sp. nas-14.1, target efi-510292, with bound alpha-d-3 manuronate
112	<a href="#">c6onpA_</a>	Alignment	not modelled	96.9	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein xoxj; <b>PDBTitle:</b> crystal structure of periplasmic binding protein xoxj from2 methylobacterium extorquens am1
113	<a href="#">c4mnpA_</a>	Alignment	not modelled	96.8	10	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminate-binding protein; <b>PDBTitle:</b> structure of the sialic acid binding protein from fusobacterium2 nucleatum subsp. nucleatum atcc 25586

114	<a href="#">c3fxbB_</a>	Alignment	not modelled	96.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of the ectoine-binding protein ueha
115	<a href="#">c4nguA_</a>	Alignment	not modelled	96.8	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio alaskensis g20 (dde_1548), target efi-510103, with3 bound d-ala-d-ala
116	<a href="#">c4x9tA_</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein upf0065; <b>PDBTitle:</b> crystal structure of a tctc solute binding protein from polaromonas2 (bpro_3516, target efi-510338), no ligand
117	<a href="#">c4n6kA_</a>	Alignment	not modelled	96.8	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter-dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio salexigens dsm2638, target efi-510113 (desal_0342),3 complex with diglycerolphosphate
118	<a href="#">c4xeqC_</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio vulgaris (deval_0042, target efi-510114) bound to3 copurified (r)-pantoic acid
119	<a href="#">c2pfyA_</a>	Alignment	not modelled	96.7	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
120	<a href="#">c4gd5B_</a>	Alignment	not modelled	96.6	9	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphate abc transporter, phosphate-binding protein; <b>PDBTitle:</b> x-ray crystal structure of a putative phosphate abc transporter2 substrate-binding protein with bound phosphate from clostridium3 perfringens