

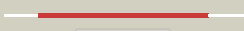






























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1680_(-)_1904436_1905260
Date	Fri Aug 2 13:30:27 BST 2019
Unique Job ID	1e5552b8b3c607a4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3n5lA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> binding protein component of abc phosphonate transporter; <b>PDBTitle:</b> crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
2	<a href="#">c5ub6B_</a>	 Alignment		100.0	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphate-binding protein; <b>PDBTitle:</b> xac2383 from xanthomonas citri bound to pyrophosphate
3	<a href="#">c3p7lA_</a>	 Alignment		100.0	16	<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
4	<a href="#">c5me4A_</a>	 Alignment		100.0	18	<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
5	<a href="#">c5lq8A_</a>	 Alignment		100.0	19	<b>PDB header:</b> periplasmic binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphonate binding protein for abc transporter; <b>PDBTitle:</b> 1.52 a resolution structure of phnd1 from prochlorococcus marinus (mit2 9301) in complex with methylphosphonate
6	<a href="#">c5o2kE_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> probable phosphite transport system-binding protein ptxb; <b>PDBTitle:</b> native apo-structure of pseudomonas stutzeri ptxb to 2.1 a resolution
7	<a href="#">c5lv1C_</a>	 Alignment		100.0	17	<b>PDB header:</b> periplasmic binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> ptxb; <b>PDBTitle:</b> 2.12 a resolution structure of ptxb from prochlorococcus marinus (mit2 9301) in complex with phosphite
8	<a href="#">c6esvA_</a>	 Alignment		100.0	15	<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 aix from rhizobium sp. str.2 nt-26
9	<a href="#">c5jvbB_</a>	 Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphonate abc transporter, periplasmic phosphonate- <b>PDBTitle:</b> 1.95a resolution structure of ptxb from trichodesmium erythraeum2 ims101 in complex with phosphite
10	<a href="#">c3e4rA_</a>	 Alignment		99.9	19	<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
11	<a href="#">c6jflA_</a>	 Alignment		99.9	11	<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

12	<a href="#">c2x26A</a>	Alignment		99.9	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
13	<a href="#">c3uifA</a>	Alignment		99.9	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
14	<a href="#">c3qslA</a>	Alignment		99.9	14	<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
15	<a href="#">c3un6A</a>	Alignment		99.9	12	<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="#">c3ix1B</a>	Alignment		99.9	13	<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
17	<a href="#">c3ix1A</a>	Alignment		99.9	13	<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
18	<a href="#">c4q5tA</a>	Alignment		99.9	15	<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
19	<a href="#">c2x7pA</a>	Alignment		99.9	11	<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
20	<a href="#">c4k3fA</a>	Alignment		99.9	15	<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
21	<a href="#">d1xs5a</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
22	<a href="#">c2de4B</a>	Alignment	not modelled	99.9	13	<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 sulfonic acid
23	<a href="#">c4gotA</a>	Alignment	not modelled	99.8	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
24	<a href="#">c4oteA</a>	Alignment	not modelled	99.8	14	<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
25	<a href="#">c3k2dA</a>	Alignment	not modelled	99.8	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
26	<a href="#">c4h67D</a>	Alignment	not modelled	99.8	15	<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
27	<a href="#">c4esxA</a>	Alignment	not modelled	99.8	16	<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
28	<a href="#">c3gxaA</a>	Alignment	not modelled	99.8	13	<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

29	<a href="#">c4qhgA</a>	Alignment	not modelled	99.8	13	<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
30	<a href="#">c4ef2A</a>	Alignment	not modelled	99.8	17	<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
31	<a href="#">c4nmyA</a>	Alignment	not modelled	99.8	13	<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
32	<a href="#">c4ib2B</a>	Alignment	not modelled	99.8	15	<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
33	<a href="#">d1eh3a</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
34	<a href="#">d1dtza1</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
35	<a href="#">c3up9A</a>	Alignment	not modelled	99.8	15	<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
36	<a href="#">d1b1xa1</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
37	<a href="#">c3tqwA</a>	Alignment	not modelled	99.8	15	<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
38	<a href="#">c3ir1F</a>	Alignment	not modelled	99.8	14	<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
39	<a href="#">d1p99a</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
40	<a href="#">c1p99A</a>	Alignment	not modelled	99.8	17	<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
41	<a href="#">c4ntIA</a>	Alignment	not modelled	99.8	11	<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
42	<a href="#">d1h76a1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
43	<a href="#">d1ryoa</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
44	<a href="#">d1ce2a1</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
45	<a href="#">c2g29A</a>	Alignment	not modelled	99.8	13	<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
46	<a href="#">d1us5a</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
47	<a href="#">c4dddA</a>	Alignment	not modelled	99.8	15	<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
48	<a href="#">c3hn0A</a>	Alignment	not modelled	99.7	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
49	<a href="#">d1ieja</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
50	<a href="#">d1jnfa1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
51	<a href="#">c5oeiA</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein family upf0065:tat pathway signal; <b>PDBTitle:</b> r. palustris rpa4515 with oxoadipate
52	<a href="#">c2i4cA</a>	Alignment	not modelled	99.7	11	<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
53	<a href="#">c3tmgA</a>	Alignment	not modelled	99.7	11	<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
54	<a href="#">d2hava1</a>	Alianment	not modelled	99.7	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II

						<b>Family:</b> Transferrin
55	<a href="#">c3l6gA</a>	Alignment	not modelled	99.6	11	<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
56	<a href="#">c2qpqC</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> protein bug27; <b>PDBTitle:</b> structure of bug27 from bordetella pertussis
57	<a href="#">c2f5xC</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> bugd; <b>PDBTitle:</b> structure of periplasmic binding protein bugd
58	<a href="#">d1tfda</a>	Alignment	not modelled	99.6	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
59	<a href="#">d2b6da1</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
60	<a href="#">d2nxoa1</a>	Alignment	not modelled	99.6	18	<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="#">c4x9tA</a>	Alignment	not modelled	99.6	9	<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
62	<a href="#">c2dvzA</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> structure of a periplasmic transporter
63	<a href="#">d2czla1</a>	Alignment	not modelled	99.5	17	<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="#">c6hkeB</a>	Alignment	not modelled	99.4	13	<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 rhodopseudomonas palustris with bound malate
65	<a href="#">d1cb6a2</a>	Alignment	not modelled	99.4	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
66	<a href="#">d1zbma1</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
67	<a href="#">d1jnfa2</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
68	<a href="#">d1dota1</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
69	<a href="#">d1jw1a1</a>	Alignment	not modelled	99.4	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
70	<a href="#">d1b1xa2</a>	Alignment	not modelled	99.3	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
71	<a href="#">c4z9nB</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> amino acid abc transporter, periplasmic amino acid-binding <b>PDBTitle:</b> abc transporter / periplasmic binding protein from brucella ovis with2 glutathione bound
72	<a href="#">d2d3ia2</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
73	<a href="#">c4q0cA</a>	Alignment	not modelled	99.3	21	<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
74	<a href="#">c1lfgA</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> transferrin <b>Chain:</b> A: <b>PDB Molecule:</b> lactoferrin; <b>PDBTitle:</b> structure of diferric human lactoferrin
75	<a href="#">c4oz9A</a>	Alignment	not modelled	99.2	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
76	<a href="#">c2hpgB</a>	Alignment	not modelled	99.1	15	<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
77	<a href="#">c2pfzA</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
78	<a href="#">c4p47A</a>	Alignment	not modelled	99.1	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 ochrobactrum anthropi (oant_4429), target efi-510151, c-terminus bound3 in ligand binding pocket
79	<a href="#">c6onpA</a>	Alignment	not modelled	99.1	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
80	<a href="#">c4p8bA_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap-type transporter, periplasmic component; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 ralstonia eutropha h16 (h16_a1328), target efi-510189, with bound3 (s)-2-hydroxy-2-methyl-3-oxobutanoate ((s)-2-acetolactate)
81	<a href="#">c4c0rB_</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative amino acid binding protein; <b>PDBTitle:</b> molecular and structural basis of glutathione import in2 gram-positive bacteria via gshst and the cystine abc3 importer tcybc of streptococcus mutans.
82	<a href="#">c1ce2A_</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein (lactoferrin); <b>PDBTitle:</b> structure of diferric buffalo lactoferrin at 2.5a resolution
83	<a href="#">c4pbhA_</a>	Alignment	not modelled	99.0	13	<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
84	<a href="#">d1h76a2</a>	Alignment	not modelled	99.0	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
85	<a href="#">c2pfyA_</a>	Alignment	not modelled	99.0	18	<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
86	<a href="#">d1dtza2</a>	Alignment	not modelled	99.0	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
87	<a href="#">c3kzgB_</a>	Alignment	not modelled	99.0	10	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> arginine 3rd transport system periplasmic binding <b>PDBTitle:</b> crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
88	<a href="#">c5orgA_</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> octopine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> octopine-binding periplasmic protein; <b>PDBTitle:</b> structure of the periplasmic binding protein (pbp) occj from a.2 tumefaciens b6 in complex with octopine.
89	<a href="#">c4de8A_</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cps2a; <b>PDBTitle:</b> lytr-cps2a-psr family protein with bound octaprenyl monophosphate2 lipid
90	<a href="#">c5sv6A_</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular solute-binding protein, family 3; <b>PDBTitle:</b> crystal structure of mxaj from methlophaga aminisulfidivorans mpt
91	<a href="#">c4nhbB_</a>	Alignment	not modelled	99.0	13	<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
92	<a href="#">c4pddA_</a>	Alignment	not modelled	99.0	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 polaromonas sp js666 (bpro_0088, target efi-510167) bound to d-3 erythronate
93	<a href="#">c3mplA_</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence sensor protein bvgs; <b>PDBTitle:</b> crystal structure of bordetella pertussis bvgs vft2 domain (double2 mutant f375e/q461e)
94	<a href="#">c4pfiA_</a>	Alignment	not modelled	99.0	16	<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 marinobacter aquaeolei vt8 (maqu_2829, target efi-510133), apo open3 structure
95	<a href="#">c4napD_</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> extracellular solute-binding protein, family 7; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio alaskensis g20 (dde_0634), target efi-510102, with3 bound d-tryptophan
96	<a href="#">c6h2tA_</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutamine-binding lipoprotein glnh (glnbp); <b>PDBTitle:</b> glnh bound to glu, mycobacterium tuberculosis
97	<a href="#">c5uh0A_</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> hydrolase,oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> membrane-bound lytic murein transglycosylase f; <b>PDBTitle:</b> 1.95 angstrom resolution crystal structure of fragment (35-274) of2 membrane-bound lytic murein transglycosylase f from yersinia pestis.
98	<a href="#">c4pp0B_</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nopaline-binding periplasmic protein; <b>PDBTitle:</b> structure of the pbp noct-m117n in complex with pyronopaline
99	<a href="#">c4o94B_</a>	Alignment	not modelled	99.0	13	<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
						<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter-dctp subunit;



100	<a href="#">c4n6dA</a>	Alignment	not modelled	99.0	12	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio salexigens dsm2638 (desal_3247), target efi-510112,3 phased with i3c, open complex, c-terminus of symmetry mate bound in4 ligand binding site <b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit;
101	<a href="#">c4ovtA</a>	Alignment	not modelled	99.0	11	<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 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter subunit dctp;
102	<a href="#">c4xfeA</a>	Alignment	not modelled	98.9	13	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 pseudomonas putida f1 (pput_1203), target efi-500184, with bound d-3 glucuronate <b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sialic acid binding protein;
103	<a href="#">c4magA</a>	Alignment	not modelled	98.9	16	<b>PDBTitle:</b> crystal structure of the periplasmic sialic acid binding protein from2 vibrio cholerae <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit;
104	<a href="#">c4nn3A</a>	Alignment	not modelled	98.9	11	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio salexigens (desal_2161), target efi-510109, with bound3 orotic acid <b>PDB header:</b> solute-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative extracellular solute-binding protein;
105	<a href="#">c4p56C</a>	Alignment	not modelled	98.9	12	<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 <b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminate-binding protein;
106	<a href="#">c4mnpA</a>	Alignment	not modelled	98.9	17	<b>PDBTitle:</b> structure of the sialic acid binding protein from fusobacterium2 nucleatum subsp. nucleatum atcc 25586 <b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> serotransferrin;
107	<a href="#">c2hauA</a>	Alignment	not modelled	98.9	13	<b>PDBTitle:</b> apo-human serum transferrin (non-glycosylated) <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter substrate-binding protein-amino acid
108	<a href="#">c4eq9A</a>	Alignment	not modelled	98.9	11	<b>PDBTitle:</b> 1.4 angstrom crystal structure of abc transporter glutathione-binding2 protein gsht from streptococcus pneumoniae strain canada mdr_19a in3 complex with glutathione <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit;
109	<a href="#">c4o8mA</a>	Alignment	not modelled	98.9	14	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein2 actinobacillus succinogenes 130z, target efi-510004, with bound l-3 galactonate <b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit;
110	<a href="#">c4pfrA</a>	Alignment	not modelled	98.9	12	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_3541, target efi-510203), apo open3 partially disordered <b>PDB header:</b> choline-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycine betaine abc transporter protein;
111	<a href="#">c2rejA</a>	Alignment	not modelled	98.9	14	<b>PDBTitle:</b> abc-transporter choline binding protein in unliganded semi-2 closed conformation <b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
112	<a href="#">d1dota2</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative trap-type c4-dicarboxylate transport system,
113	<a href="#">c4n8yA</a>	Alignment	not modelled	98.9	13	<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 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter periplasmic solute-binding
114	<a href="#">c4n4uA</a>	Alignment	not modelled	98.9	17	<b>PDBTitle:</b> crystal structure of abc transporter solute binding protein bb07192 from bordetella bronchiseptica rb50, target efi-510049 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c4-dicarboxylate-binding protein;
115	<a href="#">c4pf6A</a>	Alignment	not modelled	98.9	14	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 roseobacter denitrificans (rd1_0742, target efi-510239) with bound 3-3 deoxy-d-manno-oct-2-ulosonic acid (kdo) <b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> trap dicarboxylate transporter-dctp subunit;
116	<a href="#">c4mcoC</a>	Alignment	not modelled	98.9	17	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 rhodoferax ferrireducens (rfer_1840), target efi-510211, with bound3 malonate <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap-type c4-dicarboxylate:h+ symport system substrate-
117	<a href="#">c4mx6A</a>	Alignment	not modelled	98.9	12	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 shewanella oneidensis (so_3134), target efi-510275, with bound3 succinate <b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit;
118	<a href="#">c4pakA</a>	Alignment	not modelled	98.9	13	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 verminophrobacter eiseniae efi01-2 (veis_3954, target efi-510324) a3 nephridial symbiont of the earthworm eisenia foetida, bound to (r)-4 pantoic acid <b>PDB header:</b> solute-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative trap periplasmic solute binding

119	<a href="#">c4pbqC_</a>	Alignment	not modelled	98.9	13	protein; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 haemophilus influenzae rdaw (hicg_00826, target efi-510123) with3 bound l-gulonate
120	<a href="#">c4ng7A_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap periplasmic solute binding protein; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 citrobacter koseri (cko_04899), target efi-510094, apo, open3 structure