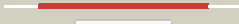



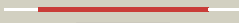



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2121c_(hisG)_2379814_2380668
Date	Mon Aug 5 13:25:24 BST 2019
Unique Job ID	b0a2cf660437b079

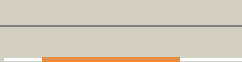
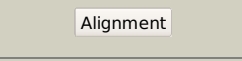
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1nh7A_</a>	 Alignment		100.0	99	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
2	<a href="#">c4yb5B_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> adenosine triphosphate phosphoribosyltransferase from campylobacter2 jejuni in complex with the allosteric inhibitor histidine
3	<a href="#">c2vd3B_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
4	<a href="#">c1q1kA_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
5	<a href="#">c6cz1A_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase catalytic subunit; <b>PDBTitle:</b> crystal structure of medicago truncatula atp-phosphoribosyltransferase2 in relaxed form
6	<a href="#">d1nh8a1</a>	 Alignment		100.0	100	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
7	<a href="#">d1h3da1</a>	 Alignment		100.0	32	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
8	<a href="#">c2vd2A_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> the crystal structure of hisg from b. subtilis
9	<a href="#">c5m8hH_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> atp phosphoribosyltransferase (hiszg atpprt) from psychrobacter2 arcticus
10	<a href="#">d1ve4a1</a>	 Alignment		100.0	30	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
11	<a href="#">d1z7me1</a>	 Alignment		100.0	25	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like

12	<a href="#">d1o63a_</a>	Alignment		100.0	25	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
13	<a href="#">d1nh8a2</a>	Alignment		100.0	100	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
14	<a href="#">d1h3da2</a>	Alignment		99.8	31	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
15	<a href="#">c3ix1A_</a>	Alignment		97.4	19	<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
16	<a href="#">c4h67D_</a>	Alignment		97.2	16	<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
17	<a href="#">c3ix1B_</a>	Alignment		97.1	19	<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
18	<a href="#">c4nmyA_</a>	Alignment		97.1	14	<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
19	<a href="#">c4esxA_</a>	Alignment		97.0	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 p1p
20	<a href="#">c3qslA_</a>	Alignment		97.0	15	<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
21	<a href="#">c3uifA_</a>	Alignment	not modelled	96.8	18	<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
22	<a href="#">c5ub6B_</a>	Alignment	not modelled	96.7	16	<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
23	<a href="#">c1p99A_</a>	Alignment	not modelled	96.5	13	<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
24	<a href="#">d1p99a_</a>	Alignment	not modelled	96.5	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
25	<a href="#">c3e4rA_</a>	Alignment	not modelled	96.2	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
26	<a href="#">c3un6A_</a>	Alignment	not modelled	96.1	11	<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
27	<a href="#">c6h2tA_</a>	Alignment	not modelled	96.1	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutamine-binding lipoprotein glnh (glbnp); <b>PDBTitle:</b> glnh bound to glu, mycobacterium tuberculosis
						<b>Fold:</b> Periplasmic binding protein-like II

28	<a href="#">d1zba1</a>	Alignment	not modelled	96.0	13	<b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
29	<a href="#">c3hn0A_</a>	Alignment	not modelled	95.7	14	<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
30	<a href="#">c6esvA_</a>	Alignment	not modelled	95.4	13	<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
31	<a href="#">c5me4A_</a>	Alignment	not modelled	95.2	13	<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
32	<a href="#">c4z9nB_</a>	Alignment	not modelled	95.1	17	<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
33	<a href="#">d2czla1</a>	Alignment	not modelled	94.6	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
34	<a href="#">c2de4B_</a>	Alignment	not modelled	93.7	18	<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
35	<a href="#">c2x26A_</a>	Alignment	not modelled	93.5	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
36	<a href="#">c5kuhB_</a>	Alignment	not modelled	93.3	9	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate receptor ionotropic, kainate 2; <b>PDBTitle:</b> gluk2em with ly466195
37	<a href="#">c3p7iA_</a>	Alignment	not modelled	93.1	12	<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
38	<a href="#">c2x7pA_</a>	Alignment	not modelled	92.8	14	<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
39	<a href="#">d2nxoa1</a>	Alignment	not modelled	91.9	14	<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="#">c5o2kE_</a>	Alignment	not modelled	91.5	16	<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
41	<a href="#">c4p56C_</a>	Alignment	not modelled	91.5	17	<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
42	<a href="#">c2rd5D_</a>	Alignment	not modelled	91.5	23	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> pii protein; <b>PDBTitle:</b> structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
43	<a href="#">c4pp0B_</a>	Alignment	not modelled	90.4	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
44	<a href="#">c5lv1C_</a>	Alignment	not modelled	89.8	13	<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
45	<a href="#">c4n6dA_</a>	Alignment	not modelled	89.7	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 desulfovibrio salexigens dsm2638 (desa_3247), target efi-510112,3 phased with i3c, open complex, c-terminus of symmetry mate bound in4 ligand binding site
46	<a href="#">c5jvbB_</a>	Alignment	not modelled	88.9	16	<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
47	<a href="#">c3n5IA_</a>	Alignment	not modelled	88.9	13	<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
48	<a href="#">c4ozIA_</a>	Alignment	not modelled	88.9	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii; <b>PDBTitle:</b> glnk2 from haloferax mediterranei complexed with amp
49	<a href="#">c4n8yA_</a>	Alignment	not modelled	88.8	17	<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. bta1 b (bbta_0128), target efi-5100563 (bbta_0128), complex with alpha/beta-d-galacturonate

50	<a href="#">c4q0cA</a>	Alignment	not modelled	88.6	17	<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
51	<a href="#">c3kzgB</a>	Alignment	not modelled	88.5	13	<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
52	<a href="#">c4mncA</a>	Alignment	not modelled	88.4	11	<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 polaromonas sp. js666 (bpro_4736), target efi-510156, with bound3 benzoyl formate, space group p21
53	<a href="#">c4p1eA</a>	Alignment	not modelled	87.9	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
54	<a href="#">c5lq8A</a>	Alignment	not modelled	87.9	13	<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
55	<a href="#">c4p1IA</a>	Alignment	not modelled	87.5	18	<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
56	<a href="#">c4napD</a>	Alignment	not modelled	87.1	17	<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
57	<a href="#">c4xeqC</a>	Alignment	not modelled	87.0	14	<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
58	<a href="#">c2pfzA</a>	Alignment	not modelled	86.9	15	<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
59	<a href="#">c4usiC</a>	Alignment	not modelled	86.8	13	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> nitrogen regulatory protein pii; <b>PDBTitle:</b> nitrogen regulatory protein pii from chlamydomonas2 reinhardtii in complex with mgatp and 2-oxoglutarate
60	<a href="#">c4de8A</a>	Alignment	not modelled	85.6	22	<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
61	<a href="#">c6jf1A</a>	Alignment	not modelled	85.6	15	<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
62	<a href="#">c4pakA</a>	Alignment	not modelled	84.9	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 verminephrobacter eiseniae ef01-2 (veis_3954, target efi-510324) a3 nephridial symbiont of the earthworm eisenia foetida, bound to (r)-4 pantoic acid
63	<a href="#">c3tmgA</a>	Alignment	not modelled	84.8	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
64	<a href="#">c3l7pA</a>	Alignment	not modelled	84.7	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative nitrogen regulatory protein pii; <b>PDBTitle:</b> crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
65	<a href="#">c4mx6A</a>	Alignment	not modelled	84.2	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap-type c4-dicarboxylate:h+ symport system substrate- <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 shewanella oneidensis (so_3134), target efi-510275, with bound3 succinate
66	<a href="#">c3fxbB</a>	Alignment	not modelled	83.7	12	<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
67	<a href="#">c4ovsB</a>	Alignment	not modelled	83.5	12	<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 deleyanum dsm 6946 (sdel_0447), target efi-510309,3 with bound succinate
68	<a href="#">c4pe3A</a>	Alignment	not modelled	83.2	20	<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
69	<a href="#">c4r25A</a>	Alignment	not modelled	82.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory pii-like protein; <b>PDBTitle:</b> structure of b. subtilis glnk

70	<a href="#">c4pfbA</a>		not modelled	82.8	16	<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 nucleatun (fn1258, target efi-510120) with bound sn-3 glycerol-3-phosphate
71	<a href="#">c3bzqA</a>		not modelled	82.3	19	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii; <b>PDBTitle:</b> high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
72	<a href="#">c4ln5A</a>		not modelled	81.7	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 burkholderia ambifaria (bamb_6123), target efi-510059, with bound3 glycerol and chloride ion
73	<a href="#">c4nn3A</a>		not modelled	80.5	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 desulfovibrio salexigens (desal_2161), target efi-510109, with bound3 orotic acid
74	<a href="#">c4mcoC</a>		not modelled	79.9	16	<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 rhodoferrax ferrireducens (rfer_1840), target efi-510211, with bound3 malonate
75	<a href="#">d1qy7a</a>		not modelled	79.9	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
76	<a href="#">c3mhyC</a>		not modelled	79.6	11	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> pii-like protein pz; <b>PDBTitle:</b> a new pii protein structure
77	<a href="#">c4xfeA</a>		not modelled	79.3	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter subunit dctp; <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
78	<a href="#">c4pddA</a>		not modelled	79.2	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
79	<a href="#">c2j9dG</a>		not modelled	79.1	11	<b>PDB header:</b> membrane transport <b>Chain:</b> G: <b>PDB Molecule:</b> hypothetical nitrogen regulatory pii-like <b>PDBTitle:</b> structure of glnk1 with bound effectors indicates2 regulatory mechanism for ammonia uptake
80	<a href="#">c2hzkB</a>		not modelled	78.8	20	<b>PDB header:</b> ligand binding, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap-t family sorbitol/mannitol transporter, periplasmic <b>PDBTitle:</b> crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
81	<a href="#">c3b50A</a>		not modelled	78.7	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sialic acid-binding periplasmic protein siap; <b>PDBTitle:</b> structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
82	<a href="#">d2ns1b1</a>		not modelled	78.5	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
83	<a href="#">c5l2eB</a>		not modelled	77.8	13	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate receptor ionotropic, delta-2, glutamate receptor <b>PDBTitle:</b> crystal structure of rat glutamate receptor delta-2 extracellular2 domain
84	<a href="#">c4n5wB</a>		not modelled	77.6	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> twin-arginine translocation pathway signal; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 chromohalobacter salexigens dsm 3043 (csal_0678), target efi-501078,3 with bound 1,2-ethanediol
85	<a href="#">c4pbqC</a>		not modelled	77.1	15	<b>PDB header:</b> solute-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative trap periplasmic solute binding 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
86	<a href="#">c2rc9A</a>		not modelled	76.6	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate [nmda] receptor subunit 3a; <b>PDBTitle:</b> crystal structure of the nr3a ligand binding core complex with acpc at2 1.96 angstrom resolution
87	<a href="#">c4pf6A</a>		not modelled	76.5	15	<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 roseobacter denitrificans (rd1_0742, target efi-510239) with bound 3-3 deoxy-d-manno-oct-2-ulosonic acid (kdo)
88	<a href="#">d2piia</a>		not modelled	76.4	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
89	<a href="#">c4pbhA</a>		not modelled	76.1	18	<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
90	<a href="#">c4f3pB</a>		not modelled	76.0	10	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> glutamine-binding periplasmic protein; <b>PDBTitle:</b> crystal structure of a glutamine-binding periplasmic protein from2 burkholderia pseudomallei in complex with glutamine <b>PDB header:</b> membrane protein/protein transport

91	<a href="#">c4oanB</a>		Alignment	not modelled	75.5	10	<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)
92	<a href="#">c3o8wA</a>		Alignment	not modelled	75.4	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii (glnb-1); <b>PDBTitle:</b> archaeoglobus fulgidus glnk1
93	<a href="#">c5t0wA</a>		Alignment	not modelled	74.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> anccdt-1; <b>PDBTitle:</b> crystal structure of the ancestral amino acid-binding protein anccdt-2 1, a precursor of cyclohexadienyl dehydratase
94	<a href="#">c4o8mA</a>		Alignment	not modelled	74.3	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 protein2 actinobacillus succinogenes 130z, target efi-510004, with bound l-3 galactonate
95	<a href="#">c5i7iB</a>		Alignment	not modelled	73.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap solute binding protein; <b>PDBTitle:</b> crystal structure of a marine metagenome trap solute binding protein2 specific for aromatic acid ligands (sorcerer ii global ocean sampling3 expedition, unidentified microbe, locus tag os_1523157) in complex4 with co-crystallized 3-hydroxybenzoate
96	<a href="#">c4o94B</a>		Alignment	not modelled	73.4	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 rhodospseudomonas palustris haa2 (rpb_3329), target efi-510223, with3 bound succinate
97	<a href="#">d1vm0a</a>		Alignment	not modelled	73.1	26	<b>Fold:</b> IF3-like <b>Superfamily:</b> AlbA-like <b>Family:</b> Hypothetical protein At2g34160
98	<a href="#">c2ylnA</a>		Alignment	not modelled	72.6	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter, periplasmic binding protein, <b>PDBTitle:</b> crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
99	<a href="#">d1hwua</a>		Alignment	not modelled	72.4	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
100	<a href="#">c4nq8B</a>		Alignment	not modelled	72.4	14	<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
101	<a href="#">c4n4uA</a>		Alignment	not modelled	71.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter periplasmic solute-binding <b>PDBTitle:</b> crystal structure of abc transporter solute binding protein bb07192 from bordetella bronchiseptica rb50, target efi-510049
102	<a href="#">c3ir1F</a>		Alignment	not modelled	71.4	13	<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
103	<a href="#">c4p8bA</a>		Alignment	not modelled	71.2	12	<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)
104	<a href="#">c4petA</a>		Alignment	not modelled	71.1	21	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular solute-binding protein, family 7; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 colwellia psychrerythraea (cps_0129, target efi-510097) with bound3 calcium and pyruvate
105	<a href="#">c3ncpD</a>		Alignment	not modelled	70.7	17	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii (glnb-2); <b>PDBTitle:</b> glnk2 from archaeoglobus fulgidus
106	<a href="#">c3gxA</a>		Alignment	not modelled	70.2	12	<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
107	<a href="#">d1ul3a</a>		Alignment	not modelled	70.0	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
108	<a href="#">c4dddA</a>		Alignment	not modelled	69.4	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
109	<a href="#">c3l6gA</a>		Alignment	not modelled	69.0	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
110	<a href="#">c4pfrA</a>		Alignment	not modelled	68.7	16	<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
111	<a href="#">c4ng7A</a>		Alignment	not modelled	67.8	18	<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

112	<a href="#">c2q3vB_</a>	Alignment	not modelled	67.5	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein at2g34160; <b>PDBTitle:</b> ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g34160
113	<a href="#">c3vvfA_</a>	Alignment	not modelled	66.1	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid abc transporter, binding protein; <b>PDBTitle:</b> crystal structure of ttc0807 complexed with arginine
114	<a href="#">c5tpiA_</a>	Alignment	not modelled	66.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator (lysr family); <b>PDBTitle:</b> 1.47 angstrom crystal structure of the c-terminal substrate binding2 domain of lysr family transcriptional regulator from klebsiella3 pneumoniae.
115	<a href="#">c6mmvC_</a>	Alignment	not modelled	65.7	11	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate receptor ionotropic, nmda 1; <b>PDBTitle:</b> triheteromeric nmda receptor glun1/glun2a/glun2a* extracellular domain2 in the '2-knuckle-asymmetric' conformation, in complex with glycine3 and glutamate, in the presence of 1 micromolar zinc chloride, and at4 ph 7.4
116	<a href="#">c3ce8A_</a>	Alignment	not modelled	65.6	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative pii-like nitrogen regulatory protein; <b>PDBTitle:</b> crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution
117	<a href="#">c4yicA_</a>	Alignment	not modelled	65.3	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap transporter solute binding protein; <b>PDBTitle:</b> crystal structure of a trap transporter solute binding protein2 (ipr025997) from bordetella bronchiseptica rb50 (bb0280, target efi-3 500035) with bound picolinic acid
118	<a href="#">c3gmgB_</a>	Alignment	not modelled	65.2	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein rv1825/mt1873; <b>PDBTitle:</b> crystal structure of an uncharacterized conserved protein from2 mycobacterium tuberculosis
119	<a href="#">c4pf8A_</a>	Alignment	not modelled	65.1	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap-t family transporter, dctp (periplasmic binding) <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 sulfitobacter sp. nas-14.1 (target efi-510299) with bound beta-d-3 galacturonate
120	<a href="#">d3c7bb2</a>	Alignment	not modelled	64.7	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like