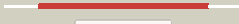



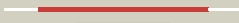



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3575c_(- )_4017268_4018347
Date	Fri Aug 9 18:20:25 BST 2019
Unique Job ID	63cc32356da7322e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3h5tA_</a>	 Alignment		100.0	42	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
2	<a href="#">c3kxD_</a>	 Alignment		100.0	25	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
3	<a href="#">c1zvvA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-resistance amylase regulator; <b>PDBTitle:</b> crystal structure of a ccpa-crh-dna complex
4	<a href="#">c5syszA_</a>	 Alignment		100.0	31	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> transcriptional regulator celr-cellobiose complex
5	<a href="#">c1efaA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> lac repressor; <b>PDBTitle:</b> crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf
6	<a href="#">c1lbgB_</a>	 Alignment		100.0	23	<b>PDB header:</b> <b>PDB COMPND:</b>
7	<a href="#">c1bdhA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (purine repressor); <b>PDBTitle:</b> purine repressor mutant-hypoxanthine-palindromic operator2 complex
8	<a href="#">c3qk7C_</a>	 Alignment		100.0	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulators; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
9	<a href="#">c3dbiA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of sugar-binding transcriptional regulator (lacI2 family) from escherichia coli complexed with phosphate
10	<a href="#">c4o5aA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lacI family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a lacI family transcriptional regulator from2 bifidobacterium animalis subsp. lactis dsm 10140
11	<a href="#">c3e3mA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a lacI family transcriptional regulator from2 silicibacter pomeroyi

12	<a href="#">c3k9cA_</a>	Alignment		100.0	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family protein; <b>PDBTitle:</b> crystal structure of lacI transcriptional regulator from rhodococcus2 species.
13	<a href="#">c3k4hA_</a>	Alignment		100.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator lacI from2 bacillus cereus subsp. cytotoxis nvh 391-98
14	<a href="#">c3hcwB_</a>	Alignment		100.0	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> maltose operon transcriptional repressor; <b>PDBTitle:</b> crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus aureus
15	<a href="#">d2nzug1</a>	Alignment		100.0	20	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
16	<a href="#">c3c3kA_</a>	Alignment		100.0	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
17	<a href="#">c3h5oB_</a>	Alignment		100.0	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator gntr; <b>PDBTitle:</b> the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
18	<a href="#">c3mizB_</a>	Alignment		100.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator protein, lacI <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator2 protein, lacI family from rhizobium etli
19	<a href="#">c2iksA_</a>	Alignment		100.0	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding transcriptional dual regulator; <b>PDBTitle:</b> crystal structure of n-terminal truncated dna-binding transcriptional2 dual regulator from escherichia coli k12
20	<a href="#">c3kkeA_</a>	Alignment		100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lacI family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a lacI family transcriptional regulator from2 mycobacterium smegmatis
21	<a href="#">c3cs3A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of sugar-binding transcriptional regulator (lacI2 family) from enterococcus faecalis
22	<a href="#">c5ufhA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lacI-type transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a lacI-type transcriptional regulator from2 bifidobacterium animalis subsp. lactis dsm 10140
23	<a href="#">c3d8uA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> purr transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
24	<a href="#">c3bbIA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> regulatory protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein of lacI family; <b>PDBTitle:</b> crystal structure of a regulatory protein of lacI family from2 chloroflexus aggregans
25	<a href="#">c4rk5A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of lacI family transcriptional regulator from2 lactobacillus casei, target efi-512911, with bound sucrose
26	<a href="#">c4rk6B_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-resistance amylase regulator; <b>PDBTitle:</b> crystal structure of lacI family transcriptional regulator ccpa from2 weissella paramesenteroides, target efi-512926, with bound glucose
27	<a href="#">c4kmrB_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> structure of a putative transcriptional regulator of lacI family from2 sanguibacter keddii dsm 10542.
28	<a href="#">c2o20H_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> catabolite control protein a; <b>PDBTitle:</b> crystal structure of transcription regulator ccpa of lactococcus2 lactis

29	<a href="#">d1tifa_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
30	<a href="#">c2rgyA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of transcriptional regulator of lacI family from2 burkholderia phymatum
31	<a href="#">c3egcF_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative ribose operon repressor; <b>PDBTitle:</b> crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis
32	<a href="#">c3brqA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator ascg; <b>PDBTitle:</b> crystal structure of the escherichia coli transcriptional repressor2 ascg
33	<a href="#">d1jyea_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
34	<a href="#">c1jyeA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lactose operon repressor; <b>PDBTitle:</b> structure of a dimeric lac repressor with c-terminal deletion and k84I2 substitution
35	<a href="#">c3huuC_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcription regulator like protein; <b>PDBTitle:</b> crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
36	<a href="#">c4rk1F_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> F: <b>PDB Molecule:</b> ribose transcriptional regulator; <b>PDBTitle:</b> crystal structure of lacI family transcriptional regulator from2 enterococcus faecium, target efi-512930, with bound ribose
37	<a href="#">c2qu7B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative transcription regulator from2 staphylococcus saprophyticus subsp. saprophyticus
38	<a href="#">c3gv0A_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of lacI family transcription regulator from2 agrobacterium tumefaciens
39	<a href="#">c4rkqD_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of lacI family transcriptional regulator from2 arthrobacter sp. fb24, target efi-560007
40	<a href="#">c6ndiB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 2.60 angstrom resolution crystal structure of periplasmic binding and2 sugar binding domain of lacI family protein from klebsiella3 pneumoniae.
41	<a href="#">c2h0aA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcription regulator from2 thermus thermophilus
42	<a href="#">c4fe4C_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> xylose operon regulatory protein; <b>PDBTitle:</b> crystal structure of apo e. coli xylr
43	<a href="#">c3gybB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulators (lacI-family) <b>PDBTitle:</b> crystal structure of a lacI-family transcriptional2 regulatory protein from corynebacterium glutamicum
44	<a href="#">d1dbqa_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
45	<a href="#">c3ctpB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic binding protein/lacI transcriptional regulator; <b>PDBTitle:</b> crystal structure of periplasmic binding protein/lacI transcriptional2 regulator from alkaliphilus metalliredigens qymf complexed with d-3 xylulofuranose
46	<a href="#">c3clkB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcription regulator; <b>PDBTitle:</b> crystal structure of a transcription regulator from lactobacillus2 plantarum
47	<a href="#">d1jx6a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
48	<a href="#">c3jvdA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulators; <b>PDBTitle:</b> crystal structure of putative transcription regulation repressor (lacI2 family) from corynebacterium glutamicum
49	<a href="#">c3jy6B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of lacI transcriptional regulator from lactobacillus2 brevis
50	<a href="#">c4ry0A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable ribose abc transporter, substrate-binding protein; <b>PDBTitle:</b> crystal structure of ribose transporter solute binding protein2 rhe_pf00037 from rhizobium etli cfn 42, target efi-511357, in complex3 with d-ribose
51	<a href="#">c4rk0C_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> lacI family sugar-binding transcriptional regulator; <b>PDBTitle:</b> crystal structure of lacI family transcriptional regulator from2 enterococcus faecalis v583, target efi-512923, with bound ribose
52	<a href="#">c3tb6B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> arabinose metabolism transcriptional repressor; <b>PDBTitle:</b> structure of the effector-binding domain of arabinose repressor arar2 from bacillus subtilis

53	<a href="#">c3bilA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable lacI-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a probable lacI family transcriptional regulator2 from corynebacterium glutamicum
54	<a href="#">c3hs3A</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> ribose operon repressor; <b>PDBTitle:</b> crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
55	<a href="#">c3o74A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fructose transport system repressor frur; <b>PDBTitle:</b> crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
56	<a href="#">c2ioyB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic sugar-binding protein; <b>PDBTitle:</b> crystal structure of thermoanaerobacter tengcongensis ribose binding2 protein
57	<a href="#">c3g85A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (lacI family); <b>PDBTitle:</b> crystal structure of lacI family transcription regulator from2 clostridium acetobutylicum
58	<a href="#">c4irxA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter, periplasmic sugar-binding protein; <b>PDBTitle:</b> crystal structure of caulobacter myo-inositol binding protein bound to2 myo-inositol
59	<a href="#">c4ry8D</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> periplasmic binding protein; <b>PDBTitle:</b> crystal structure of 5-methylthioribose transporter solute binding2 protein tlet_1677 from thermotoga lettingae tmo target efi-511109 in3 complex with 5-methylthioribose
60	<a href="#">d2dria</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
61	<a href="#">c2fn9A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribose abc transporter, periplasmic ribose-binding protein; <b>PDBTitle:</b> thermotoga maritima ribose binding protein unliganded form
62	<a href="#">c4rweA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transport protein; <b>PDBTitle:</b> the crystal structure of a sugar-binding transport protein from2 yersinia pestis co92
63	<a href="#">c3l6uA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type sugar transport system periplasmic component; <b>PDBTitle:</b> crystal structure of abc-type sugar transport system, periplasmic2 component from exiguobacterium sibiricum
64	<a href="#">c5ulbA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar abc transporter; <b>PDBTitle:</b> crystal structure of sugar abc transporter from yersinia2 enterocolitica subsp. enterocolitica 8081
65	<a href="#">c4kq9A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribose abc transporter, substrate binding protein; <b>PDBTitle:</b> crystal structure of periplasmic ribose abc transporter from2 conexibacter woesei dsm 14684
66	<a href="#">c6gq0A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar binding protein; <b>PDBTitle:</b> crystal structure of ganp, a glucose-galactose binding protein from2 geobacillus stearothermophilus
67	<a href="#">c4rxmA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> possible sugar abc superfamily atp binding cassette <b>PDBTitle:</b> crystal structure of periplasmic abc transporter solute binding2 protein a7jw62 from manheimia haemolytica phl213, target efi-511105,3 in complex with myo-inositol
68	<a href="#">c4wutA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter substrate binding protein (ribose); <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis (avi_5133, target efi-511220)3 with bound d-fucose
69	<a href="#">c5dteD</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> monosaccharide-transporting atpase; <b>PDBTitle:</b> crystal structure of an abc transporter periplasmic solute binding2 protein (ipr025997) from actinobacillus succinogenes 130z(asuc_0081,3 target efi-511065) with bound d-allose
70	<a href="#">c4yv7A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/lacI transcriptional regulator; <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from mycobacterium smegmatis (msmei_3018, target efi-3_511327) with bound glycerol
71	<a href="#">d8abpa</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
72	<a href="#">c5hsgA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter, nucleotide binding/atpase <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein from2 klebsiella pneumoniae (kpn_01730, target efi-511059), apo open3 structure
73	<a href="#">c5dkvD</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> abc transporter substrate binding protein (ribose); <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein from2 agrobacterium vitis(avis_5339, target efi-511225) bound with alpha-d-3 tagatopyranose
74	<a href="#">c5ocpA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/lacI transcriptional regulator;

74	<a href="#">c3ucpA</a>	Alignment	not modelled	99.9	10	<b>PDBTitle:</b> the periplasmic binding protein component of the arabinose abc2 transporter from shewanella sp. ana-3 bound to alpha and beta-l-3 arabinofuranose <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator;
75	<a href="#">c4ry9A</a>	Alignment	not modelled	99.9	17	<b>PDBTitle:</b> crystal structure of carbohydrate transporter solute binding protein2 veis_2079 from vermiphobacter eiseniae ef01-2, target efi-511009,3 a complex with d-talitol <b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator;
76	<a href="#">c5hqjA</a>	Alignment	not modelled	99.9	17	<b>PDBTitle:</b> crystal structure of abc transporter solute binding protein b1g1h72 from burkholderia graminis c4d1m, target efi-511179, in complex with3 d-arabinose <b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-arabinose abc transporter, periplasmic l-arabinose-
77	<a href="#">c4kzkA</a>	Alignment	not modelled	99.9	16	<b>PDBTitle:</b> the structure of the periplasmic l-arabinose binding protein from2 burkholderia thailandensis
78	<a href="#">d1byka</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
79	<a href="#">c4y9tA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, solute binding protein; <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis s4 (avi_5305, target efi-511224)3 with bound alpha-d-glucosamine
80	<a href="#">d1guda</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
81	<a href="#">c4yleA</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator;
82	<a href="#">c3ma0A</a>	Alignment	not modelled	99.9	15	<b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from burkholderia multivorans (bmul_1631, target efi-3 511115) with an unknown ligand modelled as alpha-d-erythrofuranoose
83	<a href="#">c4jqoA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-xylose-binding periplasmic protein; <b>PDBTitle:</b> closed liganded crystal structure of xylose binding protein from2 escherichia coli
84	<a href="#">c4yo7A</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc ribose transporter, periplasmic solute-binding protein; <b>PDBTitle:</b> putative ribose abc transporter, periplasmic solute-binding protein2 from rhodobacter sphaeroides
85	<a href="#">c4rxtA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> solute binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter (sugar-binding protein); <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from bacillus halodurans c-125 (bh2323, target efi-3 511484) with bound myo-inositol
86	<a href="#">c3ksmA</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter;
87	<a href="#">c3e61A</a>	Alignment	not modelled	99.9	18	<b>PDBTitle:</b> crystal structure of carbohydrate transporter solute binding protein2 arad_9553 from agrobacterium radiobacter, target efi-511541, in3 complex with d-arabinose <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type sugar transport system, periplasmic component;
88	<a href="#">c4wt7B</a>	Alignment	not modelled	99.9	14	<b>PDBTitle:</b> crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional repressor of ribose operon;
89	<a href="#">c4rs3A</a>	Alignment	not modelled	99.9	16	<b>PDBTitle:</b> crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus <b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter substrate binding protein (ribose);
90	<a href="#">c5xsdA</a>	Alignment	not modelled	99.9	18	<b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis (avi_5165, target efi-511223)3 with bound allitol <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, carbohydrate uptake transporter-2 (cut2)
91	<a href="#">c3brsA</a>	Alignment	not modelled	99.9	12	<b>PDBTitle:</b> crystal structure of carbohydrate transporter a0qyb3 from2 mycobacterium smegmatis str. mc2 155, target efi-510969, in complex3 with xylitol <b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator;
92	<a href="#">c3l49D</a>	Alignment	not modelled	99.9	11	<b>PDBTitle:</b> xylfii-lytsn complex mutant - d103a <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator;
93	<a href="#">c5ix8A</a>	Alignment	not modelled	99.9	15	<b>PDBTitle:</b> crystal structure of sugar transporter from clostridium2 phytofermentans <b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> abc sugar (ribose) transporter, periplasmic substrate-
94	<a href="#">c3h75A</a>	Alignment	not modelled	99.9	16	<b>PDBTitle:</b> crystal structure of abc sugar transporter subunit from rhodobacter2 sphaeroides 2.4.1 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar abc transport system, substrate-binding <b>PDBTitle:</b> crystal structure of sugar abc transport system, substrate-binding2 protein from bordetella parapertussis 12822 <b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic sugar-binding domain protein;

94	<a href="#">c3173A</a>	Alignment	not modelled	99.9	10	<b>PDBTitle:</b> crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens <b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator;
95	<a href="#">c6hyhA</a>	Alignment	not modelled	99.9	16	<b>PDBTitle:</b> crystal structure of msmeg_1712 from mycobacterium smegmatis in2 complex with beta-d-fucofuranose <b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> monosaccharide abc transporter substrate-binding protein,
96	<a href="#">c4yhsA</a>	Alignment	not modelled	99.9	13	<b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from bradyrhizobium sp. btai1 (bbta_2440, target efi-3 511490) with bound bis-tris <b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> multiple sugar-binding periplasmic receptor chve;
97	<a href="#">c3uugB</a>	Alignment	not modelled	99.9	16	<b>PDBTitle:</b> crystal structure of the periplasmic sugar binding protein chve <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> twin-arginine translocation pathway signal protein;
98	<a href="#">c2rjoA</a>	Alignment	not modelled	99.9	17	<b>PDBTitle:</b> crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter periplasmic-binding protein ytfq;
99	<a href="#">c2vk2A</a>	Alignment	not modelled	99.9	15	<b>PDBTitle:</b> crystal structure of a galactofuranose binding protein <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter;
100	<a href="#">c4wwhA</a>	Alignment	not modelled	99.9	18	<b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from mycobacterium smegmatis (msmeg_1704, target efi-3 510967) with bound d-galactose <b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sugar abc transporter;
101	<a href="#">c3g1wB</a>	Alignment	not modelled	99.9	14	<b>PDBTitle:</b> crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans <b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
102	<a href="#">d1gcaa</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative periplasmic binding protein with substrate ribose;
103	<a href="#">c5braA</a>	Alignment	not modelled	99.9	16	<b>PDBTitle:</b> crystal structure of a putative periplasmic solute binding protein2 (ipr025997) from ochrobactrum anthropi atcc49188 (oant_2843, target3 efi-511085) <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator;
104	<a href="#">c4z0nA</a>	Alignment	not modelled	99.9	18	<b>PDBTitle:</b> crystal structure of a periplasmic solute binding protein (ipr025997)2 from streptobacillus moniliformis dsm-12112 (smon_0317, target efi-3 511281) with bound d-galactose <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator;
105	<a href="#">c4kqcA</a>	Alignment	not modelled	99.9	13	<b>PDBTitle:</b> abc transporter, lacI family transcriptional regulator from2 brachyspira murdochii <b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative lacI-family transcriptional regulator;
106	<a href="#">c3gbvB</a>	Alignment	not modelled	99.9	10	<b>PDBTitle:</b> crystal structure of a putative lacI transcriptional regulator from2 bacteroides fragilis <b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
107	<a href="#">d2fvya1</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> monosaccharide abc transporter substrate-binding protein,
108	<a href="#">c4ru1C</a>	Alignment	not modelled	99.9	16	<b>PDBTitle:</b> crystal structure of carbohydrate transporter acei_1806 from2 acidothermus cellulolyticus 11b, target efi-510965, in complex with3 myo-inositol <b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative solute-binding component of abc transporter;
109	<a href="#">c4ys6A</a>	Alignment	not modelled	99.9	15	<b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentans (cphy_1585, target efi-3 511156) with bound beta-d-glucose <b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sugar abc transporter, periplasmic sugar-binding protein;
110	<a href="#">c2qvcC</a>	Alignment	not modelled	99.9	20	<b>PDBTitle:</b> crystal structure of a periplasmic sugar abc transporter from2 thermotoga maritima <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein;
111	<a href="#">c2x7xA</a>	Alignment	not modelled	99.9	18	<b>PDBTitle:</b> fructose binding periplasmic domain of hybrid two component system2 bt1754 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> rhamnose abc transporter, periplasmic rhamnose-binding
112	<a href="#">c4kvfA</a>	Alignment	not modelled	99.9	14	<b>PDBTitle:</b> the crystal structure of a rhamnose abc transporter, periplasmic2 rhamnose-binding protein from kribbella flavida dsm 17836 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc sugar transporter, periplasmic sugar binding protein;
113	<a href="#">c3rotA</a>	Alignment	not modelled	99.9	19	<b>PDBTitle:</b> crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila <b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative lacI-type transcriptional regulator;
114	<a href="#">c3d02A</a>	Alignment	not modelled	99.9	13	<b>PDBTitle:</b> crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution <b>PDB header:</b> signaling protein

115	<a href="#">c3o1hB_</a>	Alignment	not modelled	99.9	11	<b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic protein tort; <b>PDBTitle:</b> crystal structure of the tors sensor domain - tort complex in the presence of tmao
116	<a href="#">c4pz0A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter, sugar-binding protein; <b>PDBTitle:</b> the crystal structure of a solute binding protein from bacillus2 anthracis str. ames in complex with quorum-sensing signal3 autoinducer-2 (ai-2)
117	<a href="#">c4rxuA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic sugar-binding protein; <b>PDBTitle:</b> crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
118	<a href="#">c6dspB_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> autoinducer 2-binding protein lsrB; <b>PDBTitle:</b> lsrB from clostridium saccharobutylicum in complex with ai-2
119	<a href="#">d1tjya_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
120	<a href="#">c4pe6B_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> solute-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative abc transporter; <b>PDBTitle:</b> crystal structure of abc transporter solute binding protein from2 thermobispora bispora dsm 43833