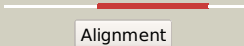
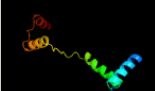
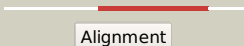

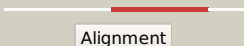
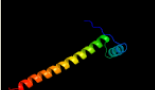
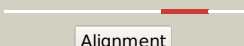
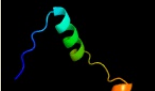



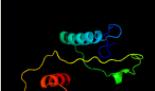
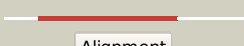
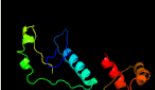





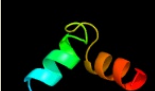



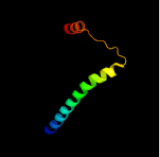
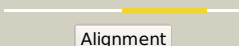

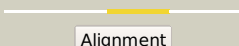
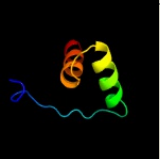
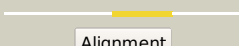
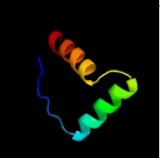
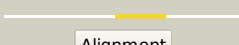
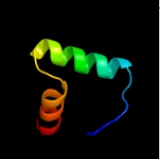
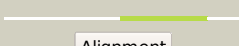

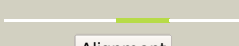

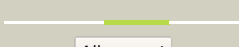
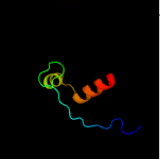
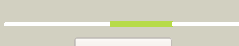
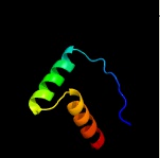
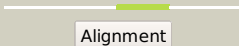
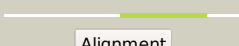
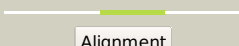



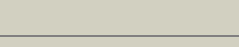


# Phyre2


Email	mdejesus@rockefeller.edu
Description	RVBD2803 (-) _3111832_3112299
Date	Wed Aug 7 12:50:46 BST 2019
Unique Job ID	202049d168948f0e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6gtsC_</a>	 Alignment		99.9	29	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> structure of the atat-atar complex bound dna
2	<a href="#">d1y9ba1</a>	 Alignment		99.9	31	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> VCA0319-like
3	<a href="#">c6ajnF_</a>	 Alignment		99.8	31	<b>PDB header:</b> toxin <b>Chain:</b> F; <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> crystal structure of atatr bound with accoa
4	<a href="#">c6gtrD_</a>	 Alignment		97.5	32	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> structure of the atat y144f mutant toxin bound to the c-terminus of2 the antitoxin atar and acetyl-coa
5	<a href="#">c6qeqD_</a>	 Alignment		95.7	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> pcff; <b>PDBTitle:</b> pcff from enterococcus faecalis pcf10
6	<a href="#">c6g1nB_</a>	 Alignment		95.4	13	<b>PDB header:</b> antitoxin <b>Chain:</b> B; <b>PDB Molecule:</b> antitoxin hicb; <b>PDBTitle:</b> crystal structure of the burkholderia pseudomallei antitoxin hicb
7	<a href="#">c4p7dA_</a>	 Alignment		94.5	15	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> antitoxin hicb3; <b>PDBTitle:</b> antitoxin hicb3 crystal structure
8	<a href="#">c2an7A_</a>	 Alignment		90.6	31	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein pard; <b>PDBTitle:</b> solution structure of the bacterial antidote pard
9	<a href="#">c2ba3A_</a>	 Alignment		84.4	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> nika; <b>PDBTitle:</b> nmr structure of nika n-terminal fragment
10	<a href="#">d1mnta_</a>	 Alignment		81.4	28	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
11	<a href="#">c1u9pA_</a>	 Alignment		79.6	11	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> parc; <b>PDBTitle:</b> permuted single-chain arc

12	<a href="#">c4mx6A_</a>	 Alignment		77.2	12	<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 from <i>Shewanella oneidensis</i> (so_3134), target efi-510275, with bound succinate
13	<a href="#">c4napD_</a>	 Alignment		76.7	20	<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 from <i>Desulfovibrio alaskensis</i> g20 (dde_0634), target efi-510102, with bound d-tryptophan
14	<a href="#">c3qogC_</a>	 Alignment		75.1	10	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> alginate and motility regulator z; <b>PDBTitle:</b> crystal structure of the transcription factor AmrZ in complex with the 18 base pair AmrZ1 binding site
15	<a href="#">c2k29A_</a>	 Alignment		74.6	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin relB; <b>PDBTitle:</b> structure of the dbd domain of <i>E. coli</i> antitoxin relB
16	<a href="#">d1b28a_</a>	 Alignment		71.0	20	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
17	<a href="#">c4pfiA_</a>	 Alignment		69.5	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter-dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from <i>Marinobacter aquaeolei</i> vt8 (maqu_2829, target efi-510133), apo open3 structure
18	<a href="#">d2bj7a1</a>	 Alignment		68.0	11	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
19	<a href="#">c5yrzC_</a>	 Alignment		67.9	15	<b>PDB header:</b> antitoxin/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hicb; <b>PDBTitle:</b> toxin-antitoxin complex from <i>Streptococcus pneumoniae</i>
20	<a href="#">d1myla_</a>	 Alignment		66.7	17	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
21	<a href="#">d1mylb_</a>	 Alignment	not modelled	66.2	19	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
22	<a href="#">c4p56C_</a>	 Alignment	not modelled	65.9	16	<b>PDB header:</b> solute-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative extracellular solute-binding protein; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from <i>Bordetella bronchiseptica</i> , target efi-510038 (bb2442), with bound (r)-mandelate and (s)-mandelate
23	<a href="#">c2k5jB_</a>	 Alignment	not modelled	65.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from <i>Shigella flexneri</i> serotype 5b (strain 8401). Northeast Structural Genomics Consortium target sft1
24	<a href="#">c2hpgB_</a>	 Alignment	not modelled	64.4	14	<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
25	<a href="#">c4q2uM_</a>	 Alignment	not modelled	62.7	16	<b>PDB header:</b> toxin/toxin repressor <b>Chain:</b> M: <b>PDB Molecule:</b> antitoxin dinj; <b>PDBTitle:</b> crystal structure of the <i>E. coli</i> dinj-yafq toxin-antitoxin complex
26	<a href="#">c4mncA_</a>	 Alignment	not modelled	62.2	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 from <i>Polaromonas</i> sp. js666 (bpro_4736), target efi-510156, with bound benzoyl formate, space group P21
27	<a href="#">c3fxbB_</a>	 Alignment	not modelled	57.0	21	<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 <b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> periplasmic substrate binding protein; <b>PDBTitle:</b> the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
28	<a href="#">c3gyyC_</a>	Alignment	not modelled	55.3	16	<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
29	<a href="#">c4o94B_</a>	Alignment	not modelled	55.3	12	<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
30	<a href="#">c2hzkB_</a>	Alignment	not modelled	53.9	16	<b>PDB header:</b> solute-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> c4-dicarboxylate transport system substrate-binding <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 sulfitebacter sp. nas-14.1, target efi-510292, with bound alpha-d-3 manuronate
31	<a href="#">c4ovpB_</a>	Alignment	not modelled	51.8	5	<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
32	<a href="#">c4n4uA_</a>	Alignment	not modelled	49.1	16	<b>PDB header:</b> transport <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic substrate binding protein; <b>PDBTitle:</b> high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata
33	<a href="#">c2vpnB_</a>	Alignment	not modelled	48.8	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative nickel-responsive regulator; <b>PDBTitle:</b> apo-nikr from helicobacter pylori in closed trans-2 conformation
34	<a href="#">c2ca9B_</a>	Alignment	not modelled	47.1	18	<b>PDB header:</b> solute-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_2138, target efi-510205) with3 bound glucuronate
35	<a href="#">c4x8rB_</a>	Alignment	not modelled	47.0	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
36	<a href="#">c3d3jA_</a>	Alignment	not modelled	46.4	22	<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
37	<a href="#">c4n5wB_</a>	Alignment	not modelled	45.8	4	<b>PDB header:</b> toxin/toxin inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin relb; <b>PDBTitle:</b> crystal structure of the intact e. coli relbe toxin-antitoxin complex
38	<a href="#">c4fxeB_</a>	Alignment	not modelled	44.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavo-hemoglobin; <b>PDBTitle:</b> x-ray structure of yeast flavo-hemoglobin in complex with econazole
39	<a href="#">c4g1bB_</a>	Alignment	not modelled	44.1	5	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
40	<a href="#">c3d3kD_</a>	Alignment	not modelled	44.0	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikr
41	<a href="#">c1q5vB_</a>	Alignment	not modelled	43.7	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikr-apo
42	<a href="#">c2bj3D_</a>	Alignment	not modelled	42.8	11	<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
43	<a href="#">c4pbqC_</a>	Alignment	not modelled	42.5	23	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
44	<a href="#">d2hzaa1</a>	Alignment	not modelled	40.9	13	<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 gos_1523157) in complex4 with co-crystallized 3-hydroxybenzoate
45	<a href="#">c5i7iB_</a>	Alignment	not modelled	39.1	25	<b>PDB header:</b> oxygen transport, oxygen storage <b>Chain:</b> C: <b>PDB Molecule:</b> hemoglobin-like flavoprotein; <b>PDBTitle:</b> crystal structure of acetate-bound hell's gate globin i
46	<a href="#">c3s1jC_</a>	Alignment	not modelled	38.6	10	<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
47	<a href="#">c4pe3A_</a>	Alignment	not modelled	38.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> abc transporter, solute-binding protein; <b>PDBTitle:</b> crystal structure of a periplasmic substrate binding protein in2 complex with lactate
48	<a href="#">c2zzxD_</a>	Alignment	not modelled	37.7	14	<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
49	<a href="#">c4p8bA_</a>	Alignment	not modelled	36.8	14	

						protein from2 ralstonia eutropha h16 (h16_a1328), target efi-510189, with bound3 (s)-2-hydroxy-2-methyl-3-oxobutanoate ((s)-2-acetolactate)
50	<a href="#">c4pddA</a>	 Alignment	not modelled	36.5	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 polaromonas sp js666 (bpro_0088, target efi-510167) bound to d-3 erythronate
51	<a href="#">c4mcoC</a>	 Alignment	not modelled	36.5	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
52	<a href="#">c4me7E</a>	 Alignment	not modelled	35.0	14	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> E: <b>PDB Molecule:</b> antitoxin endoai; <b>PDBTitle:</b> crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
53	<a href="#">c4pf8A</a>	 Alignment	not modelled	34.4	15	<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 sulfitebacter sp. nas-14.1 (target efi-510299) with bound beta-d-3 galacturonate
54	<a href="#">d1gvha1</a>	 Alignment	not modelled	33.8	9	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
55	<a href="#">c4petA</a>	 Alignment	not modelled	33.7	13	<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
56	<a href="#">c4pakA</a>	 Alignment	not modelled	33.3	21	<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
57	<a href="#">c2pfyA</a>	 Alignment	not modelled	33.2	23	<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
58	<a href="#">c6a6xC</a>	 Alignment	not modelled	32.2	25	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> antitoxin maze7; <b>PDBTitle:</b> the crystal structure of the mtb maze-mazf-mt9 complex
59	<a href="#">d1p94a</a>	 Alignment	not modelled	31.0	22	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
60	<a href="#">c4pfrA</a>	 Alignment	not modelled	30.7	12	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_3541, target efi-510203), apo open3 partially disordered
61	<a href="#">c3u65B</a>	 Alignment	not modelled	29.5	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> tp33 protein; <b>PDBTitle:</b> the crystal structure of tat-p(t) (tp0957)
62	<a href="#">c4yicA</a>	 Alignment	not modelled	29.4	14	<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
63	<a href="#">c4p1A</a>	 Alignment	not modelled	29.3	20	<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
64	<a href="#">d1cqxa1</a>	 Alignment	not modelled	28.7	9	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
65	<a href="#">c2kilA</a>	 Alignment	not modelled	28.5	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state
66	<a href="#">c5mnwA</a>	 Alignment	not modelled	28.3	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> guanylate cyclase soluble subunit beta-1; <b>PDBTitle:</b> solution structure of the cinaciguat bound human beta1 h-nox.
67	<a href="#">c4n6dA</a>	 Alignment	not modelled	26.7	9	<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 (desal_3247), target efi-510112,3 phased with i3c, open complex, c-terminus of symmetry mate bound in4 ligand binding site
68	<a href="#">c5im2A</a>	 Alignment	not modelled	26.3	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> twin-arginine translocation pathway signal; <b>PDBTitle:</b> crystal structure of a trap solute binding protein from rhodoferrax2 ferrireducens t118 (rfer_2570, target efi-510210) in complex with3 copurified benzoate
69	<a href="#">c2pfzA</a>	 Alignment	not modelled	25.5	16	<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
						<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp

70	<a href="#">c4xeqC</a>	Alignment	not modelled	25.2	9	subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from <i>Desulfovibrio vulgaris</i> (deval_0042, target efi-510114) bound to 3 copurified (r)-pantoic acid <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c4-dicarboxylate-binding protein;
71	<a href="#">c4pf6A</a>	Alignment	not modelled	24.7	25	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from <i>roseobacter denitrificans</i> (rd1_0742, target efi-510239) with bound 3-3 deoxy-d-manno-oct-2-ulosonic acid (kdo) <b>PDB header:</b> oxygen transport <b>Chain:</b> A: <b>PDB Molecule:</b> hemoglobin-like flavoprotein fused to roadblock/lc7 domain;
72	<a href="#">c3wfwA</a>	Alignment	not modelled	24.7	13	<b>PDBTitle:</b> crystal structure of the closed form of the hgb1's globin domain <b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
73	<a href="#">d1vhba</a>	Alignment	not modelled	24.1	4	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
74	<a href="#">c4n8gC</a>	Alignment	not modelled	23.8	25	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit;
75	<a href="#">c4ovqA</a>	Alignment	not modelled	23.1	20	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from <i>chromohalobacter salexigens</i> dsm 3043 (csal_0660), target efi-501075,3 with bound d-alanine-d-alanine <b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate abc transporter, substrate-binding <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from <i>roseobacter denitrificans</i> , target efi-510230, with bound beta-d-3 glucuronate
76	<a href="#">d2hzab1</a>	Alignment	not modelled	23.0	13	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
77	<a href="#">c4nguA</a>	Alignment	not modelled	23.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit;
78	<a href="#">c4n8yA</a>	Alignment	not modelled	22.9	20	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from <i>bradyrhizobium</i> sp. btai1 b (bbta_0128), target efi-5100563 (bbta_0128), complex with alpha/beta-d-galacturonate <b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> alr2278 protein;
79	<a href="#">c2o0cB</a>	Alignment	not modelled	18.8	9	<b>PDBTitle:</b> crystal structure of the h-nox domain from <i>Nostoc</i> sp. pcc 71202 complexed to no <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein bp1543;
80	<a href="#">c3kk4B</a>	Alignment	not modelled	18.4	24	<b>PDBTitle:</b> uncharacterized protein bp1543 from <i>Bordetella pertussis</i> tohama i <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function (duf416);
81	<a href="#">c3f7cA</a>	Alignment	not modelled	17.8	13	<b>PDBTitle:</b> crystal structure of a duf416 family protein (maqu_0942) from <i>Marinobacter aquaeolei</i> vt8 at 2.00 Å resolution <b>PDB header:</b> solute-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit;
82	<a href="#">c4ovsB</a>	Alignment	not modelled	17.5	11	<b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from <i>Sulfurospirillum deleyianum</i> dsm 6946 (sdel_0447), target efi-510309,3 with bound succinate <b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
83	<a href="#">d1myka</a>	Alignment	not modelled	17.4	18	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
84	<a href="#">d1bdta</a>	Alignment	not modelled	16.9	18	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
85	<a href="#">c5muul</a>	Alignment	not modelled	16.7	21	<b>PDB header:</b> virus <b>Chain:</b> I: <b>PDB Molecule:</b> major outer capsid protein; <b>PDBTitle:</b> dsrna bacteriophage phi6 nucleocapsid
86	<a href="#">d3e9va1</a>	Alignment	not modelled	16.7	16	<b>Fold:</b> BTG domain-like <b>Superfamily:</b> BTG domain-like <b>Family:</b> BTG domain-like
87	<a href="#">c2k6IA</a>	Alignment	not modelled	16.7	34	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;
88	<a href="#">c1cqxB</a>	Alignment	not modelled	16.5	9	<b>PDBTitle:</b> the solution structure of xacb0070 from <i>Xanthomonas axonopodis</i> pv citri reveals this new protein is a member of the rhh family of transcriptional repressors <b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> flavohemoprotein;
89	<a href="#">d1bazb</a>	Alignment	not modelled	16.4	18	<b>PDBTitle:</b> crystal structure of the flavohemoglobin from <i>Alcaligenes eutrophus</i> at 2.175 Å resolution <b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
90	<a href="#">c1gvhA</a>	Alignment	not modelled	15.9	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavohemoprotein;
91	<a href="#">c2wusR</a>	Alignment	not modelled	15.6	14	<b>PDBTitle:</b> the x-ray structure of ferric <i>Escherichia coli</i> 2 flavohemoglobin reveals an unsuspected geometry of the 3 distal heme pocket <b>PDB header:</b> structural protein <b>Chain:</b> R: <b>PDB Molecule:</b> putative uncharacterized protein;
92	<a href="#">d1v76a</a>	Alignment	not modelled	15.4	44	<b>PDBTitle:</b> bacterial actin mreB assembles in complex with cell shape protein rodZ <b>Fold:</b> Rof/RNase P subunit-like <b>Superfamily:</b> Rof/RNase P subunit-like <b>Family:</b> RNase P subunit p29-like

93	<a href="#">c2wy4A_</a>	Alignment	not modelled	15.2	11	<b>PDB header:</b> oxygen transport <b>Chain:</b> A: <b>PDB Molecule:</b> single domain haemoglobin; <b>PDBTitle:</b> structure of bacterial globin from campylobacter jejuni at2 1.35 a resolution
94	<a href="#">c4p47A_</a>	Alignment	not modelled	15.2	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 ochrobactrum anthropi (oant_4429), target efi-510151, c-terminus bound3 in ligand binding pocket
95	<a href="#">c5td3B_</a>	Alignment	not modelled	14.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> catechol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of catechol 1,2-dioxygenase from burkholderia2 vietnamiensis
96	<a href="#">c4nhbB_</a>	Alignment	not modelled	14.8	20	<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
97	<a href="#">c3b50A_</a>	Alignment	not modelled	14.4	9	<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.
98	<a href="#">d1baza_</a>	Alignment	not modelled	14.3	18	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
99	<a href="#">c2otoD_</a>	Alignment	not modelled	14.1	16	<b>PDB header:</b> surface active protein, toxin <b>Chain:</b> D: <b>PDB Molecule:</b> m protein; <b>PDBTitle:</b> n-terminal fragment of streptococcus pyogenes m1 protein