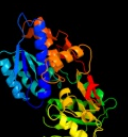
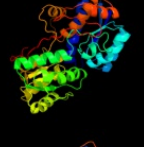
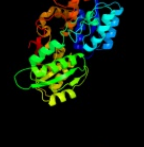
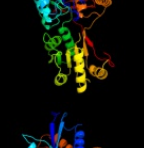
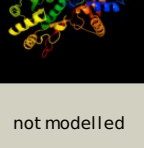


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2liva_	 Alignment		100.0	100	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
2	dlusga_	 Alignment		100.0	79	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
3	c3ip5A_	 Alignment		100.0	40	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein (amino acid); PDBTitle: structure of atu2422-gaba receptor in complex with alanine
4	c3i09A_	 Alignment		100.0	14	PDB header: transport protein Chain: A: PDB Molecule: periplasmic branched-chain amino acid-binding protein; PDBTitle: crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
5	c3hutA_	 Alignment		100.0	19	PDB header: transport protein Chain: A: PDB Molecule: putative branched-chain amino acid abc PDBTitle: crystal structure of a putative branched-chain amino acid2 abc transporter from rhodospirillum rubrum
6	c3h5lB_	 Alignment		100.0	19	PDB header: transport protein Chain: B: PDB Molecule: putative branched-chain amino acid abc PDBTitle: crystal structure of a putative branched-chain amino acid2 abc transporter from silicibacter pomeroyi
7	c3lkbB_	 Alignment		100.0	14	PDB header: transport protein Chain: B: PDB Molecule: probable branched-chain amino acid abc PDBTitle: crystal structure of a branched chain amino acid abc2 transporter from thermus thermophilus with bound valine
8	dlqo0a_	 Alignment		100.0	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
9	c3n0wA_	 Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: abc branched chain amino acid family transporter, PDBTitle: crystal structure of a branched chain amino acid abc transporter2 periplasmic ligand-binding protein (bx_c0949) from burkholderia3 xenovorans lb400 at 1.88 a resolution
10	c3t0nA_	 Alignment		100.0	18	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal; PDBTitle: crystal structure of twin-arginine translocation pathway signal from2 rhodopseudomonas palustris bisb5
11	c3i45A_	 Alignment		100.0	20	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of putative twin-arginine translocation pathway2 signal protein from rhodospirillum rubrum atcc 11170

12	c3n0xA_	Alignment		100.0	19	PDB header: transport protein Chain: A: PDB Molecule: possible substrate binding protein of abc transporter PDBTitle: crystal structure of an abc-type branched-chain amino acid transporter2 (rpa4397) from rhodopseudomonas palustris cga009 at 1.50 a resolution
13	c3td9A_	Alignment		100.0	23	PDB header: transport protein Chain: A: PDB Molecule: branched chain amino acid abc transporter, periplasmic PDBTitle: crystal structure of a leucine binding protein livk (tm1135) from2 thermotoga maritima msb8 at 1.90 a resolution
14	c3lopA_	Alignment		100.0	17	PDB header: substrate binding protein Chain: A: PDB Molecule: substrate binding periplasmic protein; PDBTitle: crystal structure of substrate-binding periplasmic protein2 (pbp) from ralstonia solanacearum
15	c3eafA_	Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
16	c3sg0A_	Alignment		100.0	17	PDB header: signaling protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
17	c3snrA_	Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
18	c1jdpA_	Alignment		100.0	15	PDB header: signaling protein Chain: A: PDB Molecule: atrial natriuretic peptide clearance receptor; PDBTitle: crystal structure of hormone/receptor complex
19	d1jdpA_	Alignment		100.0	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
20	c1yk1B_	Alignment		100.0	15	PDB header: hormone/growth factor receptor Chain: B: PDB Molecule: atrial natriuretic peptide clearance receptor; PDBTitle: structure of natriuretic peptide receptor-c complexed with brain2 natriuretic peptide
21	c3om1A_	Alignment	not modelled	100.0	12	PDB header: membrane protein Chain: A: PDB Molecule: glutamate receptor gluk5 (ka2); PDBTitle: crystal structure of the gluk5 (ka2) atd dimer at 1.7 angstrom2 resolution
22	d1ewka_	Alignment	not modelled	100.0	21	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
23	c3sm9A_	Alignment	not modelled	100.0	19	PDB header: signaling protein Chain: A: PDB Molecule: metabotropic glutamate receptor 3; PDBTitle: crystal structure of metabotropic glutamate receptor 3 precursor in2 presence of ly341495 antagonist
24	c3h6hB_	Alignment	not modelled	100.0	14	PDB header: membrane protein Chain: B: PDB Molecule: glutamate receptor, ionotropic kainate 2; PDBTitle: crystal structure of the glur6 amino terminal domain dimer assembly2 mpd form
25	c2e4zA_	Alignment	not modelled	100.0	18	PDB header: signaling protein Chain: A: PDB Molecule: metabotropic glutamate receptor 7; PDBTitle: crystal structure of the ligand-binding region of the group iii2 metabotropic glutamate receptor
26	d1dp4a_	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
27	c3sajB_	Alignment	not modelled	100.0	13	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor 1; PDBTitle: crystal structure of glutamate receptor glua1 amino terminal domain
28	c2e4wA_	Alignment	not modelled	100.0	18	PDB header: signaling protein Chain: A: PDB Molecule: metabotropic glutamate receptor 3; PDBTitle: crystal structure of the extracellular region of the group ii2 metabotropic glutamate receptor complexed with 1s,3s-acpd
						PDB header: transport protein

29	c3p3wC_	Alignment	not modelled	100.0	13	Chain: C: PDB Molecule: glutamate receptor 3; PDBTitle: structure of a dimeric glua3 n-terminal domain (ntd) at 4.2 a2 resolution
30	c3kg2A_	Alignment	not modelled	100.0	14	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775
31	c2wjxA_	Alignment	not modelled	100.0	13	PDB header: transport protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: crystal structure of the human ionotropic glutamate2 receptor glur2 atd region at 4.1 a resolution
32	d3ckma1	Alignment	not modelled	100.0	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
33	c3q41B_	Alignment	not modelled	100.0	12	PDB header: transport protein Chain: B: PDB Molecule: glutamate [nmda] receptor subunit zeta-1; PDBTitle: crystal structure of the glun1 n-terminal domain (ntd)
34	c3jpyA_	Alignment	not modelled	100.0	12	PDB header: transport protein Chain: A: PDB Molecule: glutamate [nmda] receptor subunit epsilon-2; PDBTitle: crystal structure of the zinc-bound amino terminal domain of the nmda2 receptor subunit nr2b
35	c3o1hB_	Alignment	not modelled	99.2	10	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic protein tort; PDBTitle: crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
36	c2rjoA_	Alignment	not modelled	99.2	11	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
37	c3brsA_	Alignment	not modelled	99.1	11	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
38	d8abpa_	Alignment	not modelled	99.1	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
39	d1jx6a_	Alignment	not modelled	99.0	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
40	c3ma0A_	Alignment	not modelled	99.0	12	PDB header: sugar binding protein Chain: A: PDB Molecule: d-xylose-binding periplasmic protein; PDBTitle: closed liganded crystal structure of xylose binding protein from2 escherichia coli
41	d1gcaa_	Alignment	not modelled	99.0	9	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
42	d1tjya_	Alignment	not modelled	99.0	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
43	d1guda_	Alignment	not modelled	98.9	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
44	c2qvcC_	Alignment	not modelled	98.9	12	PDB header: transport protein Chain: C: PDB Molecule: sugar abc transporter, periplasmic sugar-binding PDBTitle: crystal structure of a periplasmic sugar abc transporter2 from thermotoga maritima
45	d2fvya1	Alignment	not modelled	98.9	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
46	c3s99A_	Alignment	not modelled	98.9	9	PDB header: lipid binding protein Chain: A: PDB Molecule: basic membrane lipoprotein; PDBTitle: crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
47	c2vk2A_	Alignment	not modelled	98.9	13	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
48	c3ksmA_	Alignment	not modelled	98.9	16	PDB header: transport protein Chain: A: PDB Molecule: abc-type sugar transport system, periplasmic component; PDBTitle: crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
49	c2fqxA_	Alignment	not modelled	98.8	12	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
50	c2iksA_	Alignment	not modelled	98.8	10	PDB header: transcription Chain: A: PDB Molecule: dna-binding transcriptional dual regulator; PDBTitle: crystal structure of n-terminal truncated dna-binding transcriptional2 dual regulator from escherichia coli k12
51	c3h5oB_	Alignment	not modelled	98.8	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntnr; PDBTitle: the crystal structure of transcription regulator gntnr from2 chromobacterium violaceum
52	c3dbiA_	Alignment	not modelled	98.8	9	PDB header: transcription regulator Chain: A: PDB Molecule: sugar-binding transcriptional regulator, lacI family; PDBTitle: crystal structure of sugar-binding transcriptional regulator (lacI2 family) from escherichia coli complexed with phosphate
53	c3lftA_	Alignment	not modelled	98.7	9	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein;

53	c3h7A_	Alignment	not modelled	98.7	9	PDBTitle: the crystal structure of the abc domain in complex with l- trp from2 streptococcus pneumonia to 1.35a PDB header: transcription regulator
54	c3brqA_	Alignment	not modelled	98.7	10	Chain: A: PDB Molecule: hth-type transcriptional regulator ascg; PDBTitle: crystal structure of the escherichia coli transcriptional repressor2 ascg
55	c3d8uA_	Alignment	not modelled	98.7	11	PDB header: transcription regulator Chain: A: PDB Molecule: purr transcriptional regulator; PDBTitle: the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
56	c3h75A_	Alignment	not modelled	98.7	14	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic sugar-binding domain protein; PDBTitle: crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
57	c2hqbA_	Alignment	not modelled	98.6	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator of comk gene; PDBTitle: crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans
58	c3o74A_	Alignment	not modelled	98.5	11	PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
59	c3l6uA_	Alignment	not modelled	98.5	12	PDB header: transport protein Chain: A: PDB Molecule: abc-type sugar transport system periplasmic PDBTitle: crystal structure of abc-type sugar transport system,2 periplasmic component from exiguobacterium sibiricum
60	d2dria_	Alignment	not modelled	98.5	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
61	c2qh8A_	Alignment	not modelled	98.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved domain protein from vibrio2 cholerae o1 biovar eltor str. n16961
62	d1jyea_	Alignment	not modelled	98.5	7	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
63	c1jyeA_	Alignment	not modelled	98.5	7	PDB header: transcription Chain: A: PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
64	c3g1wB_	Alignment	not modelled	98.5	11	PDB header: transport protein Chain: B: PDB Molecule: sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans
65	c3rotA_	Alignment	not modelled	98.5	13	PDB header: transport protein Chain: A: PDB Molecule: abc sugar transporter, periplasmic sugar binding protein; PDBTitle: crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
66	c3e3mA_	Alignment	not modelled	98.4	10	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a lacI family transcriptional2 regulator from silicibacter pomeroyi
67	c3gv0A_	Alignment	not modelled	98.4	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI family transcription regulator from2 agrobacterium tumefaciens
68	c3hwcB_	Alignment	not modelled	98.4	11	PDB header: rna binding protein Chain: B: PDB Molecule: maltose operon transcriptional repressor; PDBTitle: crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus aureus
69	c3d02A_	Alignment	not modelled	98.3	9	PDB header: sugar binding protein Chain: A: PDB Molecule: putative lacI-type transcriptional regulator; PDBTitle: crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution
70	c2ioyB_	Alignment	not modelled	98.3	14	PDB header: sugar binding protein Chain: B: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
71	c3c3kA_	Alignment	not modelled	98.3	15	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
72	d1dbqa_	Alignment	not modelled	98.3	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
73	c2x7xA_	Alignment	not modelled	98.3	11	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component2 system bt1754
74	c3k4hA_	Alignment	not modelled	98.2	11	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator lacI from2 bacillus cereus subsp. cytotoxis nvh 391-98
75	c3k9cA_	Alignment	not modelled	98.2	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family protein; PDBTitle: crystal structure of lacI transcriptional regulator from rhodococcus2 species.
76	c3mizB_	Alignment	not modelled	98.2	16	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator protein, lacI PDBTitle: crystal structure of a putative transcriptional regulator2 protein, lacI family from rhizobium etli
						PDB header: transcription regulator Chain: B: PDB Molecule: putative lacI-family transcriptional

77	c3gbvB_	Alignment	not modelled	98.2	12	regulator; PDBTitle: crystal structure of a putative lacI transcriptional regulator from <i>Bacteroides fragilis</i>
78	c3ctpB_	Alignment	not modelled	98.2	13	PDB header: transcription regulator Chain: B: PDB Molecule: periplasmic binding protein/lacI transcriptional regulator; PDBTitle: crystal structure of periplasmic binding protein/lacI transcriptional2 regulator from <i>alkaliphilus metalliredigens</i> qymf complexed with d-3 xylulofuranose
79	c3bb1A_	Alignment	not modelled	98.2	9	PDB header: regulatory protein Chain: A: PDB Molecule: regulatory protein of lacI family; PDBTitle: crystal structure of a regulatory protein of lacI family from <i>2 chloroflexus aggregans</i>
80	c3qk7C_	Alignment	not modelled	98.1	11	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from <i>Yersinia pestis</i> biovar <i>microtus</i> str. 91001
81	d1t1fa_	Alignment	not modelled	98.1	7	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
82	c2qu7B_	Alignment	not modelled	98.1	11	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcription regulator2 from <i>Staphylococcus saprophyticus</i> subsp. <i>saprophyticus</i>
83	c2fn9A_	Alignment	not modelled	98.1	14	PDB header: sugar binding protein Chain: A: PDB Molecule: ribose abc transporter, periplasmic ribose-binding protein; PDBTitle: <i>thermotoga maritima</i> ribose binding protein unliganded form
84	c2rgyA_	Alignment	not modelled	98.0	9	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of transcriptional regulator of lacI family from <i>2 Burkholderia phyatum</i>
85	c3jy6B_	Alignment	not modelled	98.0	10	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI transcriptional regulator from <i>Lactobacillus2 brevis</i>
86	c3hs3A_	Alignment	not modelled	98.0	13	PDB header: transcription regulator Chain: A: PDB Molecule: ribose operon repressor; PDBTitle: crystal structure of periplasmic binding ribose operon2 repressor protein from <i>Lactobacillus acidophilus</i>
87	c3egcF_	Alignment	not modelled	97.9	10	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative ribose operon repressor; PDBTitle: crystal structure of a putative ribose operon repressor from <i>2 Burkholderia thailandensis</i>
88	c3l49D_	Alignment	not modelled	97.9	9	PDB header: transport protein Chain: D: PDB Molecule: abc sugar (ribose) transporter, periplasmic PDBTitle: crystal structure of abc sugar transporter subunit from <i>2 Rhodobacter sphaeroides 2.4.1</i>
89	c3jvdA_	Alignment	not modelled	97.9	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcription regulation repressor (lacI2 family) from <i>Corynebacterium glutamicum</i>
90	d2nzug1	Alignment	not modelled	97.9	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
91	c3bi1A_	Alignment	not modelled	97.8	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable lacI-family transcriptional regulator; PDBTitle: crystal structure of a probable lacI family transcriptional2 regulator from <i>Corynebacterium glutamicum</i>
92	c2o20H_	Alignment	not modelled	97.6	10	PDB header: transcription Chain: H: PDB Molecule: catabolite control protein a; PDBTitle: crystal structure of transcription regulator ccpa of <i>Lactococcus2 lactis</i>
93	c3gybB_	Alignment	not modelled	97.6	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulators (lacI-family) PDBTitle: crystal structure of a lacI-family transcriptional2 regulatory protein from <i>Corynebacterium glutamicum</i>
94	c3g85A_	Alignment	not modelled	97.5	9	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (lacI family); PDBTitle: crystal structure of lacI family transcription regulator from <i>2 Clostridium acetobutylicum</i>
95	c3clkB_	Alignment	not modelled	97.4	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from <i>Lactobacillus2 plantarum</i>
96	c3kkeA_	Alignment	not modelled	97.4	12	PDB header: transcription regulator Chain: A: PDB Molecule: lacI family transcriptional regulator; PDBTitle: crystal structure of a lacI family transcriptional regulator2 from <i>Mycobacterium smegmatis</i>
97	c3cs3A_	Alignment	not modelled	97.3	7	PDB header: transcription regulator Chain: A: PDB Molecule: sugar-binding transcriptional regulator, lacI family; PDBTitle: crystal structure of sugar-binding transcriptional regulator (lacI2 family) from <i>Enterococcus faecalis</i>
98	d1byka_	Alignment	not modelled	97.2	9	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
99	c3huuC_	Alignment	not modelled	97.1	9	PDB header: transcription regulator Chain: C: PDB Molecule: transcription regulator like protein; PDBTitle: crystal structure of transcription regulator like protein from <i>2 Staphylococcus haemolyticus</i>
100	c3qi7A_	Alignment	not modelled	96.9	14	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from <i>Clostridium difficile</i> 630 at 1.86 Å resolution
						PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transcriptional repressor of

101	c3e61A	Alignment	not modelled	96.9	14	ribose operon; PDBTitle: crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus
102	c2h0aA	Alignment	not modelled	96.4	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of probable transcription regulator from2 thermus thermophilus
103	c1zvva	Alignment	not modelled	96.4	12	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
104	c2dgdD	Alignment	not modelled	91.9	13	PDB header: lyase Chain: D: PDB Molecule: 223aa long hypothetical arylmalonate decarboxylase; PDBTitle: crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
105	c2xecD	Alignment	not modelled	90.3	15	PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to2 tris
106	c1bdhA	Alignment	not modelled	88.5	11	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
107	d1fuia2	Alignment	not modelled	88.2	14	Fold: Fucl/AraA N-terminal and middle domains Superfamily: Fucl/AraA N-terminal and middle domains Family: L-fucose isomerase, N-terminal and second domains
108	c3hl0B	Alignment	not modelled	86.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
109	c3nvaB	Alignment	not modelled	85.6	14	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
110	d7reqa2	Alignment	not modelled	85.3	9	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
111	d2ajta2	Alignment	not modelled	84.4	11	Fold: Fucl/AraA N-terminal and middle domains Superfamily: Fucl/AraA N-terminal and middle domains Family: AraA N-terminal and middle domain-like
112	c2jfoB	Alignment	not modelled	78.5	9	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
113	c2yxbA	Alignment	not modelled	78.2	10	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
114	d1xrsb1	Alignment	not modelled	78.2	10	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
115	c3kxD	Alignment	not modelled	76.8	16	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
116	d1mvoa	Alignment	not modelled	76.5	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
117	c2vlbC	Alignment	not modelled	75.6	15	PDB header: lyase Chain: C: PDB Molecule: arylmalonate decarboxylase; PDBTitle: structure of unliganded arylmalonate decarboxylase
118	c2qv7A	Alignment	not modelled	75.1	11	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
119	d2djia1	Alignment	not modelled	74.6	9	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
120	d1rrma	Alignment	not modelled	74.3	16	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase