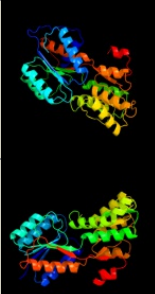
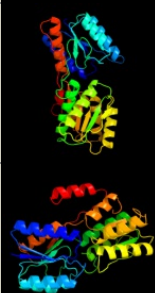
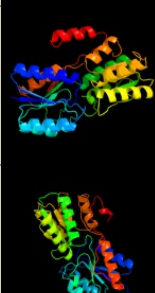
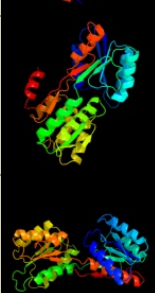


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rjoA_	 Alignment		100.0	17	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
2	dljx6a_	 Alignment		100.0	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
3	c3ma0A_	 Alignment		100.0	18	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
4	c3g1wB_	 Alignment		100.0	20	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
5	c2qvcC_	 Alignment		100.0	21	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
6	dl1tja_	 Alignment		100.0	20	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
7	c3ksmA_	 Alignment		100.0	19	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
8	c3o1hB_	 Alignment		100.0	15	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
9	c3d02A_	 Alignment		100.0	17	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
10	c2x7xA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component2 system bt1754
11	dlguda_	 Alignment		100.0	19	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like

12	c3gbvB_	Alignment		100.0	13	PDB header: transcription regulator Chain: B: PDB Molecule: putative lacI-family transcriptional regulator; PDBTitle: crystal structure of a putative lacI transcriptional regulator from2 bacteroides fragilis
13	c3l49D_	Alignment		100.0	18	PDB header: transport protein Chain: D: PDB Molecule: abc sugar (ribose) transporter, periplasmic PDBTitle: crystal structure of abc sugar transporter subunit from2 rhodobacter sphaeroides 2.4.1
14	c2fn9A_	Alignment		100.0	21	PDB header: sugar binding protein Chain: A: PDB Molecule: ribose abc transporter, periplasmic ribose-binding protein; PDBTitle: thermotoga maritima ribose binding protein unliganded form
15	d8abpa_	Alignment		100.0	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
16	dlgcaa_	Alignment		100.0	20	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
17	c3brsA_	Alignment		100.0	19	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/lacI transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
18	c3h75A_	Alignment		100.0	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
19	c3rota_	Alignment		100.0	17	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
20	d2fvya1	Alignment		100.0	20	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
21	c3l6uA_	Alignment	not modelled	100.0	15	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
22	c2vk2A_	Alignment	not modelled	100.0	18	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
23	c2ioyB_	Alignment	not modelled	100.0	21	PDB header: sugar binding protein Chain: B: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
24	d2nzug1	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
25	c3h5oB_	Alignment	not modelled	100.0	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
26	c2iksA_	Alignment	not modelled	100.0	16	PDB header: transcription regulator 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
27	c3c3kA_	Alignment	not modelled	100.0	14	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
28	d2dria_	Alignment	not modelled	100.0	18	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like

29	c3d8uA	Alignment	not modelled	100.0	12	PDB header: transcription regulator Chain: A: PDB Molecule: purrr transcriptional regulator; PDBTitle: the crystal structure of a purrr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
30	c3hwcB	Alignment	not modelled	100.0	15	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
31	c3e3mA	Alignment	not modelled	100.0	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
32	c3mizB	Alignment	not modelled	100.0	12	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
33	c3k9cA	Alignment	not modelled	100.0	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family protein; PDBTitle: crystal structure of laci transcriptional regulator from rhodococcus2 species.
34	c3o74A	Alignment	not modelled	100.0	12	PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
35	c3k4hA	Alignment	not modelled	100.0	13	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
36	c2rgyA	Alignment	not modelled	100.0	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of transcriptional regulator of laci family from2 burkholderia phymatum
37	c3dbiA	Alignment	not modelled	100.0	12	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
38	d1tifa	Alignment	not modelled	100.0	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
39	c3bblA	Alignment	not modelled	100.0	14	PDB header: regulatory protein Chain: A: PDB Molecule: regulatory protein of laci family; PDBTitle: crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
40	c3egcF	Alignment	not modelled	100.0	17	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative ribose operon repressor; PDBTitle: crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis
41	c3qk7C	Alignment	not modelled	100.0	11	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
42	c2o20H	Alignment	not modelled	100.0	14	PDB header: transcription Chain: H: PDB Molecule: catabolite control protein a; PDBTitle: crystal structure of transcription regulator ccpa of lactococcus2 lactis
43	c1jyeA	Alignment	not modelled	100.0	13	PDB header: transcription Chain: A: PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84I2 substitution
44	d1jyea	Alignment	not modelled	100.0	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
45	c3hs3A	Alignment	not modelled	100.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: ribose operon repressor; PDBTitle: crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
46	c3brqA	Alignment	not modelled	100.0	12	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator ascg; PDBTitle: crystal structure of the escherichia coli transcriptional repressor2 ascg
47	c3jy6B	Alignment	not modelled	100.0	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci transcriptional regulator from lactobacillus2 brevis
48	c2qu7B	Alignment	not modelled	100.0	14	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
49	c3ctpB	Alignment	not modelled	100.0	15	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 alkaliphilus metalliredigens qymf complexed with d-3 xylulofuranose
50	d1dbqa	Alignment	not modelled	100.0	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
51	c3kkeA	Alignment	not modelled	100.0	17	PDB header: transcription regulator Chain: A: PDB Molecule: laci family transcriptional regulator; PDBTitle: crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
52	c3gv0A	Alignment	not modelled	100.0	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
						PDB header: transcription regulator

53	c3g85A	Alignment	not modelled	100.0	15	Chain: A: PDB Molecule: transcriptional regulator (laci family); PDBTitle: crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
54	c1zvva	Alignment	not modelled	100.0	16	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
55	c3cs3A	Alignment	not modelled	100.0	12	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 enterococcus faecalis
56	c3huuC	Alignment	not modelled	100.0	12	PDB header: transcription regulator Chain: C: PDB Molecule: transcription regulator like protein; PDBTitle: crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
57	c3clkB	Alignment	not modelled	100.0	11	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
58	c3bilA	Alignment	not modelled	100.0	16	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 corynebacterium glutamicum
59	d1byka	Alignment	not modelled	100.0	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
60	c2h0aA	Alignment	not modelled	100.0	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of probable transcription regulator from2 thermus thermophilus
61	c3jvdA	Alignment	not modelled	100.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
62	c1bdhA	Alignment	not modelled	100.0	13	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
63	c3gybB	Alignment	not modelled	100.0	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulators (laci-family) PDBTitle: crystal structure of a laci-family transcriptional2 regulatory protein from corynebacterium glutamicum
64	c2qh8A	Alignment	not modelled	100.0	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
65	c3kxD	Alignment	not modelled	100.0	15	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
66	c3lftA	Alignment	not modelled	100.0	15	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the abc domain in complex with l-trp from2 streptococcus pneumonia to 1.35a
67	c3e61A	Alignment	not modelled	100.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transcriptional repressor of ribose operon; PDBTitle: crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus
68	c3h5tA	Alignment	not modelled	99.9	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a transcriptional regulator, laci2 family protein from corynebacterium glutamicum
69	c2hqbA	Alignment	not modelled	99.9	14	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
70	c2fqxA	Alignment	not modelled	99.9	14	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
71	c3s99A	Alignment	not modelled	99.8	11	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
72	c3i45A	Alignment	not modelled	99.0	15	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
73	c3eafA	Alignment	not modelled	98.9	9	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
74	c3t0nA	Alignment	not modelled	98.8	13	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
75	c3ip5A	Alignment	not modelled	98.8	12	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
76	c3i09A	Alignment	not modelled	98.8	11	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

77	d1qo0a_	Alignment	not modelled	98.8	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
78	c3h5lB_	Alignment	not modelled	98.8	12	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
79	c3sg0A_	Alignment	not modelled	98.7	15	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
80	c3n0wA_	Alignment	not modelled	98.7	13	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_e_c0949) from burkholderia3 xenovorans lb400 at 1.88 a resolution
81	c3lkbB_	Alignment	not modelled	98.7	12	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
82	c3snrA_	Alignment	not modelled	98.7	14	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
83	d2liva_	Alignment	not modelled	98.7	10	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
84	c3hutA_	Alignment	not modelled	98.6	10	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
85	c3td9A_	Alignment	not modelled	98.6	14	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
86	d1usga_	Alignment	not modelled	98.5	10	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
87	c3n0xA_	Alignment	not modelled	98.4	13	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
88	c1jdpA_	Alignment	not modelled	98.4	16	PDB header: signaling protein Chain: A: PDB Molecule: atrial natriuretic peptide clearance receptor; PDBTitle: crystal structure of hormone/receptor complex
89	d1jdpA_	Alignment	not modelled	98.4	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
90	c3lopA_	Alignment	not modelled	98.0	10	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
91	c1yk1B_	Alignment	not modelled	97.9	16	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
92	d1ewka_	Alignment	not modelled	97.4	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
93	c3qi7A_	Alignment	not modelled	97.2	10	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
94	c3h6hB_	Alignment	not modelled	97.2	11	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
95	c3q41B_	Alignment	not modelled	96.6	17	PDB header: transport protein Chain: B: PDB Molecule: glutamate [nmda] receptor subunit zeta-1; PDBTitle: crystal structure of the glun1 n-terminal domain (ntd)
96	c3sm9A_	Alignment	not modelled	96.5	12	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
97	d3ckma1	Alignment	not modelled	96.5	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
98	c3sajB_	Alignment	not modelled	96.0	8	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor 1; PDBTitle: crystal structure of glutamate receptor glua1 amino terminal domain
99	c3om1A_	Alignment	not modelled	96.0	13	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
100	d1dp4a_	Alignment	not modelled	95.6	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
101	c3wvE	Alignment	not modelled	94.7	15	PDB header: lyase Chain: F: PDB Molecule: 3-dehydroquinate dehydratase;

101	c2uyyl	Alignment	not modelled	94.7	10	PDBTitle: crystallographic structure of the typeii 3-dehydroquinase2 from thermus thermophilus PDB header: unknown function
102	c3u80A	Alignment	not modelled	94.1	11	Chain: A: PDB Molecule: 3-dehydroquinase dehydratase, type ii; PDBTitle: 1.60 angstrom resolution crystal structure of a 3-dehydroquinase2 dehydratase-like protein from bifidobacterium longum
103	c3kg2A	Alignment	not modelled	93.2	9	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
104	c3opyG	Alignment	not modelled	93.2	14	PDB header: transferase Chain: G: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
105	c2wjxA	Alignment	not modelled	93.0	8	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
106	d1gqoa	Alignment	not modelled	92.7	15	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinase dehydratase Family: Type II 3-dehydroquinase dehydratase
107	c3p3wC	Alignment	not modelled	92.7	7	PDB header: transport protein Chain: C: PDB Molecule: glutamate receptor 3; PDBTitle: structure of a dimeric glua3 n-terminal domain (ntd) at 4.2 a2 resolution
108	d1gtza	Alignment	not modelled	92.4	20	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinase dehydratase Family: Type II 3-dehydroquinase dehydratase
109	c3opyE	Alignment	not modelled	92.3	12	PDB header: transferase Chain: E: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
110	d2c4va1	Alignment	not modelled	92.1	22	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinase dehydratase Family: Type II 3-dehydroquinase dehydratase
111	c3lwzC	Alignment	not modelled	92.0	17	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinase dehydratase; PDBTitle: 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinase dehydratase (aroq) from yersinia pestis
112	c3n8kG	Alignment	not modelled	91.0	11	PDB header: lyase Chain: G: PDB Molecule: 3-dehydroquinase dehydratase; PDBTitle: type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
113	c2e4zA	Alignment	not modelled	90.7	15	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
114	d1h05a	Alignment	not modelled	90.7	11	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinase dehydratase Family: Type II 3-dehydroquinase dehydratase
115	d1uqra	Alignment	not modelled	90.6	17	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinase dehydratase Family: Type II 3-dehydroquinase dehydratase
116	c3kipU	Alignment	not modelled	90.5	18	PDB header: lyase Chain: U: PDB Molecule: 3-dehydroquinase, type ii; PDBTitle: crystal structure of type-ii 3-dehydroquinase from c. albicans
117	d2ajta2	Alignment	not modelled	90.5	8	Fold: Fucl/AraA N-terminal and middle domains Superfamily: Fucl/AraA N-terminal and middle domains Family: AraA N-terminal and middle domain-like
118	d1fuia2	Alignment	not modelled	89.7	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
119	c3o8nA	Alignment	not modelled	88.8	15	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
120	d1b0aa2	Alignment	not modelled	88.3	10	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase