



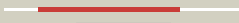

















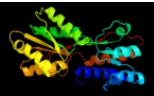



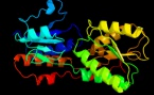


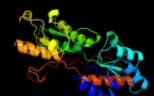
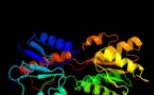


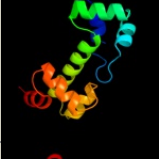

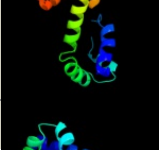


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h5oB_	 Alignment		100.0	21	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
2	c3qk7C_	 Alignment		100.0	19	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
3	d2nzug1	 Alignment		100.0	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
4	c2iksA_	 Alignment		100.0	16	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
5	c3k4hA_	 Alignment		100.0	19	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
6	c3c3kA_	 Alignment		100.0	19	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
7	c3dbiA_	 Alignment		100.0	17	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
8	c3e3mA_	 Alignment		100.0	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
9	c3k9cA_	 Alignment		100.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family protein; PDBTitle: crystal structure of laci transcriptional regulator from rhodococcus2 species.
10	c3gv0A_	 Alignment		100.0	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
11	c3d8uA_	 Alignment		100.0	15	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

12	c3hcwB_	Alignment		100.0	18	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
13	c3mizB_	Alignment		100.0	18	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator protein, laci PDBTitle: crystal structure of a putative transcriptional regulator2 protein, laci1 family from rhizobium etli
14	c3kkeA_	Alignment		100.0	19	PDB header: transcription regulator Chain: A: PDB Molecule: laci family transcriptional regulator; PDBTitle: crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
15	c3brqA_	Alignment		100.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator ascg; PDBTitle: crystal structure of the escherichia coli transcriptional repressor2 ascg
16	c3cs3A_	Alignment		100.0	15	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
17	c2rgyA_	Alignment		100.0	19	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of transcriptional regulator of laci family from2 burkholderia phymatum
18	c3clkB_	Alignment		100.0	18	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
19	c3bbIA_	Alignment		100.0	19	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
20	c3g85A_	Alignment		100.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (laci family); PDBTitle: crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
21	c3ctpB_	Alignment	not modelled	100.0	19	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
22	c3egcF_	Alignment	not modelled	100.0	16	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
23	d1tfa_	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
24	c2o20H_	Alignment	not modelled	100.0	18	PDB header: transcription Chain: H: PDB Molecule: catabolite control protein a; PDBTitle: crystal structure of transcription regulator ccpa of lactococcus2 lactis
25	c1zvVA_	Alignment	not modelled	100.0	18	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
26	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
27	c2h0aA_	Alignment	not modelled	100.0	23	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of probable transcription regulator from2 thermus thermophilus
28	c2ioyB_	Alignment	not modelled	100.0	15	PDB header: sugar binding protein Chain: B: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein

29	d1dbqa_	Alignment	not modelled	100.0	19	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
30	d1jyea_	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
31	c1jyeA_	Alignment	not modelled	100.0	16	PDB header: transcription Chain: A: PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84I2 substitution
32	d2dria_	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
33	c3jy6B_	Alignment	not modelled	100.0	17	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci transcriptional regulator from lactobacillus2 brevis
34	c3hs3A_	Alignment	not modelled	100.0	20	PDB header: transcription regulator Chain: A: PDB Molecule: ribose operon repressor; PDBTitle: crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
35	c3huuC_	Alignment	not modelled	100.0	21	PDB header: transcription regulator Chain: C: PDB Molecule: transcription regulator like protein; PDBTitle: crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
36	c3jvdA_	Alignment	not modelled	100.0	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
37	c3o74A_	Alignment	not modelled	100.0	10	PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
38	c3gybB_	Alignment	not modelled	100.0	22	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
39	c2fn9A_	Alignment	not modelled	100.0	17	PDB header: sugar binding protein Chain: A: PDB Molecule: ribose abc transporter, periplasmic ribose-binding protein; PDBTitle: thermotoga maritima ribose binding protein unliganded form
40	c3bi1A_	Alignment	not modelled	100.0	15	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
41	c3kxD_	Alignment	not modelled	100.0	13	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
42	d1jx6a_	Alignment	not modelled	100.0	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
43	c3l6uA_	Alignment	not modelled	100.0	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 exigubacterium sibiricum
44	d1byka_	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
45	c3h5tA_	Alignment	not modelled	100.0	18	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
46	d1guda_	Alignment	not modelled	100.0	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
47	d8abpa_	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
48	c3e61A_	Alignment	not modelled	100.0	17	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
49	c3ksmA_	Alignment	not modelled	100.0	17	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
50	c3brsA_	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
51	c1bdhA_	Alignment	not modelled	100.0	18	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
52	c3ma0A_	Alignment	not modelled	100.0	11	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
						PDB header: transport protein Chain: A: PDB Molecule: abc sugar transporter, periplasmic sugar

53	c3rotA_	Alignment	not modelled	100.0	14	binding protein; PDBTitle: crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
54	c3h75A_	Alignment	not modelled	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
55	c3g1wB_	Alignment	not modelled	100.0	15	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
56	c3l49D_	Alignment	not modelled	100.0	14	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
57	c2vk2A_	Alignment	not modelled	100.0	9	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
58	c2rjoA_	Alignment	not modelled	100.0	15	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
59	c3gbvB_	Alignment	not modelled	100.0	19	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
60	c3d02A_	Alignment	not modelled	100.0	11	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
61	d1gcaa_	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
62	c2x7xA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component2 system bt1754
63	c2qvcC_	Alignment	not modelled	100.0	16	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
64	d2fvya1	Alignment	not modelled	99.9	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
65	c3gbgA_	Alignment		99.9	18	PDB header: transcription regulator Chain: A: PDB Molecule: tcp pilus virulence regulatory protein; PDBTitle: crystal structure of toxT from vibrio cholerae o395
66	c3o1hB_	Alignment	not modelled	99.9	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
67	d1tjya_	Alignment	not modelled	99.9	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
68	c1d5yD_	Alignment		99.9	26	PDB header: transcription/dna Chain: D: PDB Molecule: rob transcription factor; PDBTitle: crystal structure of the e. coli rob transcription factor2 in complex with dna
69	c3oioA_	Alignment		99.9	28	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (arac-type dna-binding domain- PDBTitle: crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
70	c3oouA_	Alignment		99.9	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unknown function from listeria innocua
71	c2k9sA_	Alignment		99.9	27	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
						PDB header: transcription/dna

72	c1bl0A_	Alignment		99.9	21	Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
73	c3mn2B_	Alignment	not modelled	99.9	23	PDB header: transcription regulator Chain: B: PDB Molecule: probable arac family transcriptional regulator; PDBTitle: the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
74	c3mklB_	Alignment	not modelled	99.9	24	PDB header: transcription regulator Chain: B: PDB Molecule: hth-type transcriptional regulator gadx; PDBTitle: crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
75	c3lftA_	Alignment	not modelled	99.9	14	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
76	c2qh8A_	Alignment	not modelled	99.8	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
77	c2fqxA_	Alignment	not modelled	99.8	14	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
78	c3lsgD_	Alignment	not modelled	99.8	25	PDB header: transcription regulator Chain: D: PDB Molecule: two-component response regulator yesn; PDBTitle: the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
79	c2hqbA_	Alignment	not modelled	99.8	11	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
80	c3s99A_	Alignment	not modelled	99.3	12	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
81	d1bl0a2	Alignment	not modelled	99.3	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
82	d1d5ya2	Alignment	not modelled	99.3	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
83	d1bl0a1	Alignment	not modelled	99.0	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
84	d1d5ya1	Alignment	not modelled	99.0	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
85	c1zgwA_	Alignment	not modelled	98.9	18	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polypeptide; PDBTitle: nmr structure of e. coli ada protein in complex with dna
86	c3snrA_	Alignment	not modelled	98.7	9	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
87	c3i09A_	Alignment	not modelled	98.6	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
88	c3sg0A_	Alignment	not modelled	98.6	8	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
89	c3lopA_	Alignment	not modelled	98.5	14	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
90	c3t0nA_	Alignment	not modelled	98.5	12	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
91	d1qo0a_	Alignment	not modelled	98.5	14	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
92	d3ckma1	Alignment	not modelled	98.5	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
93	c3hutA_	Alignment	not modelled	98.5	18	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
94	c3ip5A_	Alignment	not modelled	98.5	11	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
95	c3qi7A_	Alignment	not modelled	98.3	15	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
						PDB header: transport protein

96	c3n0wA_	Alignment	not modelled	98.3	10	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
97	c3h5lB_	Alignment	not modelled	98.2	13	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
98	d2liva_	Alignment	not modelled	98.1	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
99	c3i45A_	Alignment	not modelled	98.1	10	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
100	d1jdpa_	Alignment	not modelled	98.0	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
101	c1jdpA_	Alignment	not modelled	98.0	12	PDB header: signaling protein Chain: A: PDB Molecule: atrial natriuretic peptide clearance receptor; PDBTitle: crystal structure of hormone/receptor complex
102	c3eafA_	Alignment	not modelled	97.9	8	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
103	d1usga_	Alignment	not modelled	97.9	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
104	c1yk1B_	Alignment	not modelled	97.8	12	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
105	c3lkbB_	Alignment	not modelled	97.8	11	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
106	c3n0xA_	Alignment	not modelled	97.5	18	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
107	c3td9A_	Alignment	not modelled	97.4	12	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
108	c3om1A_	Alignment	not modelled	97.2	11	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
109	c3q41B_	Alignment	not modelled	97.1	11	PDB header: transport protein Chain: B: PDB Molecule: glutamate [nmda] receptor subunit zeta-1; PDBTitle: crystal structure of the glun1 n-terminal domain (ntd)
110	c3kg2A_	Alignment	not modelled	96.9	12	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
111	c3sajB_	Alignment	not modelled	96.7	11	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor 1; PDBTitle: crystal structure of glutamate receptor glua1 amino terminal domain
112	c2wjxA_	Alignment	not modelled	96.2	12	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
113	c1zxxA_	Alignment	not modelled	96.1	17	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
114	d1ewka_	Alignment	not modelled	96.0	14	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
115	c3khtA_	Alignment	not modelled	95.9	15	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
116	d1dp4a_	Alignment	not modelled	95.8	10	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
117	c2e4wA_	Alignment	not modelled	95.7	11	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
118	c3h6hB_	Alignment	not modelled	95.6	7	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
119	d4pfka_	Alignment	not modelled	95.6	18	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
						Fold: Phosphofructokinase

120	d1pfka_	Alignment	not modelled	95.1	15	Superfamily: Phosphofructokinase Family: Phosphofructokinase
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