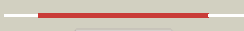
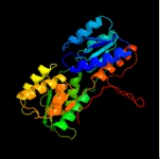
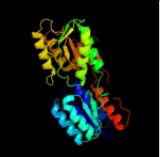
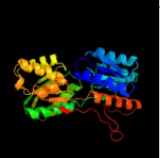
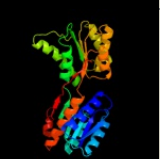
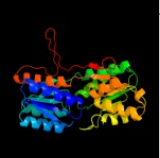


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ma0A_	 Alignment		100.0	100	PDB header: sugar binding protein Chain: A: PDB Molecule: d-xylose-binding periplasmic protein; PDBTitle: closed liganded crystal structure of xylose binding protein from2 escherichia coli
2	c2rjoA_	 Alignment		100.0	23	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
3	c3glwB_	 Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans
4	d1tjya_	 Alignment		100.0	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
5	c3d02A_	 Alignment		100.0	19	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
6	c3o1hB_	 Alignment		100.0	14	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
7	c2qvcC_	 Alignment		100.0	17	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
8	d1jx6a_	 Alignment		100.0	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
9	d1gcaa_	 Alignment		100.0	22	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
10	d2fvya1	 Alignment		100.0	21	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
11	c2x7xA_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component2 system bt1754

12	d8abpa_	Alignment		100.0	18	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
13	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
14	c3l49D_	Alignment		100.0	20	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
15	c3gbvB_	Alignment		100.0	12	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
16	c3h75A_	Alignment		100.0	17	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
17	c3l6uA_	Alignment		100.0	20	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
18	d1guda_	Alignment		100.0	21	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
19	c2vk2A_	Alignment		100.0	20	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
20	c2ioyB_	Alignment		100.0	26	PDB header: sugar binding protein Chain: B: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
21	c3brsA_	Alignment	not modelled	100.0	18	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
22	d2dria_	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	c3rotA_	Alignment	not modelled	100.0	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
24	c2fn9A_	Alignment	not modelled	100.0	22	PDB header: sugar binding protein Chain: A: PDB Molecule: ribose abc transporter, periplasmic ribose-binding protein; PDBTitle: thermotoga maritima ribose binding protein unliganded form
25	c3mizB_	Alignment	not modelled	100.0	14	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
26	c3h5oB_	Alignment	not modelled	100.0	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
27	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
						PDB header: transcription

28	c3e3mA	Alignment	not modelled	100.0	14	Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
29	c2iksA	Alignment	not modelled	100.0	13	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
30	c3d8uA	Alignment	not modelled	100.0	12	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
31	c3k4hA	Alignment	not modelled	100.0	15	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
32	c3o74A	Alignment	not modelled	100.0	15	PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
33	c3hcwB	Alignment	not modelled	100.0	9	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
34	c2rgyA	Alignment	not modelled	100.0	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of transcriptional regulator of laci family from2 burkholderia phymatum
35	c3dbiA	Alignment	not modelled	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 escherichia coli complexed with phosphate
36	c3c3kA	Alignment	not modelled	100.0	17	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
37	c3egcF	Alignment	not modelled	100.0	13	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
38	c3brqA	Alignment	not modelled	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
39	c3kkeA	Alignment	not modelled	100.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: laci family transcriptional regulator; PDBTitle: crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
40	c2qu7B	Alignment	not modelled	100.0	15	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator2 from staphylococcus saprophyticus subsp. saprophyticus
41	c3bblA	Alignment	not modelled	100.0	16	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
42	c3g85A	Alignment	not modelled	100.0	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (laci family); PDBTitle: crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
43	c1jyeA	Alignment	not modelled	100.0	23	PDB header: transcription Chain: A: PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
44	d1jyea	Alignment	not modelled	100.0	23	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	17	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	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
47	d1dbqa	Alignment	not modelled	100.0	18	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
48	c3gv0A	Alignment	not modelled	100.0	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
49	c3cs3A	Alignment	not modelled	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
50	d1tifa	Alignment	not modelled	100.0	21	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
51	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
52	c3gk7C	Alignment	not modelled	100.0	16	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators;

52	c3qk7C	Alignment	not modelled	100.0	10	PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001 PDB header: transcription regulator
53	c3k9cA	Alignment	not modelled	100.0	17	Chain: A: PDB Molecule: transcriptional regulator, laci family protein; PDBTitle: crystal structure of laci transcriptional regulator from rhodococcus2 species.
54	c3jy6B	Alignment	not modelled	100.0	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci transcriptional regulator from lactobacillus2 brevis
55	d1byka	Alignment	not modelled	100.0	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
56	c1zvva	Alignment	not modelled	100.0	17	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
57	c3huuC	Alignment	not modelled	100.0	9	PDB header: transcription regulator Chain: C: PDB Molecule: transcription regulator like protein; PDBTitle: crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
58	c3clkB	Alignment	not modelled	100.0	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
59	c3biIA	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
60	c3jvdA	Alignment	not modelled	100.0	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
61	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
62	c1bdhA	Alignment	not modelled	99.9	16	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
63	c3kxD	Alignment	not modelled	99.9	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
64	c3e61A	Alignment	not modelled	99.9	15	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
65	c3gybB	Alignment	not modelled	99.9	16	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
66	c2qh8A	Alignment	not modelled	99.9	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
67	c2hqba	Alignment	not modelled	99.9	12	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
68	c3lftA	Alignment	not modelled	99.9	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
69	c2fqxA	Alignment	not modelled	99.9	15	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
70	c3h5tA	Alignment	not modelled	99.9	15	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
71	c3s99A	Alignment	not modelled	99.8	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
72	c3i09A	Alignment	not modelled	98.8	13	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
73	c3snrA	Alignment	not modelled	98.6	10	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
74	c3sg0A	Alignment	not modelled	98.6	11	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
75	c3eafA	Alignment	not modelled	98.6	13	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
76	d2liva	Alignment	not modelled	98.5	9	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like

77	c3n0wA_	Alignment	not modelled	98.5	14	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
78	c3t0nA_	Alignment	not modelled	98.5	7	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
79	c3i45A_	Alignment	not modelled	98.4	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
80	d1usga_	Alignment	not modelled	98.4	9	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
81	c3ip5A_	Alignment	not modelled	98.4	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
82	c3lkbB_	Alignment	not modelled	98.4	7	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
83	c3td9A_	Alignment	not modelled	98.3	6	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
84	c3hutA_	Alignment	not modelled	98.3	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	d1qo0a_	Alignment	not modelled	98.2	10	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
86	c3lopA_	Alignment	not modelled	98.2	8	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
87	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
88	c3qi7A_	Alignment	not modelled	98.0	11	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
89	d3ckma1	Alignment	not modelled	97.9	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
90	d1jdpa_	Alignment	not modelled	97.8	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
91	c1jdpA_	Alignment	not modelled	97.8	11	PDB header: signaling protein Chain: A: PDB Molecule: atrial natriuretic peptide clearance receptor; PDBTitle: crystal structure of hormone/receptor complex
92	c3h6hB_	Alignment	not modelled	97.7	12	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
93	c3n0xA_	Alignment	not modelled	97.7	7	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
94	c3sajB_	Alignment	not modelled	97.3	6	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor 1; PDBTitle: crystal structure of glutamate receptor glua1 amino terminal domain
95	c3q41B_	Alignment	not modelled	97.0	13	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	d1ewka_	Alignment	not modelled	97.0	14	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
97	c1yk1B_	Alignment	not modelled	96.7	10	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
98	c2wjxA_	Alignment	not modelled	96.2	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
99	c3sm9A_	Alignment	not modelled	95.7	10	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
100	c3opyG_	Alignment	not modelled	95.4	15	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
101	c3kg2A_	Alignment	not modelled	94.5	7	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
102	c3opyE_	Alignment	not modelled	93.8	15	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
103	c3o8oC_	Alignment	not modelled	92.6	18	PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
104	c3p3wC_	Alignment	not modelled	92.5	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
105	d1dp4a_	Alignment	not modelled	91.9	10	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
106	d4pfka_	Alignment	not modelled	91.9	19	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
107	c2uygF_	Alignment	not modelled	91.8	13	PDB header: lyase Chain: F: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystallographic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
108	c3om1A_	Alignment	not modelled	90.1	8	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	c2e4zA_	Alignment	not modelled	89.6	14	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
110	d1c2ya_	Alignment	not modelled	87.4	7	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
111	c1zxxA_	Alignment	not modelled	86.1	19	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
112	d1h05a_	Alignment	not modelled	85.2	14	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase
113	d2c4va1	Alignment	not modelled	81.7	13	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase
114	c3opyB_	Alignment	not modelled	81.3	15	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
115	d1gqoa_	Alignment	not modelled	80.6	13	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase
116	c3n8kG_	Alignment	not modelled	80.6	14	PDB header: lyase Chain: G: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
117	c2obxH_	Alignment	not modelled	80.4	12	PDB header: transferase Chain: H: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase 1; PDBTitle: lumazine synthase ribh2 from mesorhizobium loti (gene ml17281, swiss-2 prot entry q986n2) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
118	d1rvv1_	Alignment	not modelled	80.0	13	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
119	d1gtza_	Alignment	not modelled	79.6	20	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase
120	d1nqua_	Alignment	not modelled	79.4	12	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase