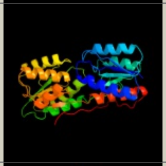
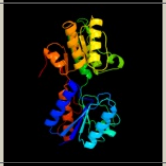
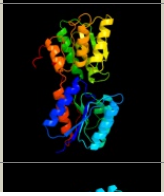
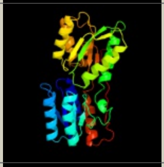
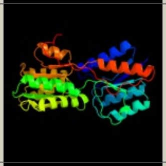
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P39265
Date	Thu Jan 5 11:58:38 GMT 2012
Unique Job ID	0851efbebc19f301

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1guda_	Alignment		100.0	100	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
2	c2rjoA_	Alignment		100.0	25	**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	c3ksmA_	Alignment		100.0	24	**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
4	d1tjya_	Alignment		100.0	19	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
5	d1jx6a_	Alignment		100.0	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
6	c3ma0A_	Alignment		100.0	20	**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
7	c3g1wB_	Alignment		100.0	23	**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
8	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
9	c2qvcC_	Alignment		100.0	24	**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
10	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
11	d1gcaa_	Alignment		100.0	21	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like

12	c3brsA_	Alignment		100.0	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein/laci transcriptional regulator; **PDBTitle:** crystal structure of sugar transporter from clostridium2 phytofermentans
13	c3h75A_	Alignment		100.0	21	**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
14	c2x7xA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** fructose binding periplasmic domain of hybrid two component2 system bt1754
15	c2vk2A_	Alignment		100.0	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq; **PDBTitle:** crystal structure of a galactofuranose binding protein
16	d8abpa_	Alignment		100.0	16	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
17	c2fn9A_	Alignment		100.0	27	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**ribose abc transporter, periplasmic ribose-binding protein; **PDBTitle:** thermotoga maritima ribose binding protein unliganded form
18	c3l6uA_	Alignment		100.0	24	**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
19	d2fvya1	Alignment		100.0	20	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
20	c2ioyB_	Alignment		100.0	36	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**periplasmic sugar-binding protein; **PDBTitle:** crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
21	c3gbvB_	Alignment	not modelled	100.0	17	**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
22	c3rotA_	Alignment	not modelled	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
23	c3h5oB_	Alignment	not modelled	100.0	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator gntr; **PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
24	d2dria_	Alignment	not modelled	100.0	34	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
25	c3l49D_	Alignment	not modelled	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
26	c2iksA_	Alignment	not modelled	100.0	15	**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
27	c3k4hA_	Alignment	not modelled	100.0	18	**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
28	d2nzug1	Alignment	not modelled	100.0	19	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I

						Family:L-arabinose binding protein-like
29	c3mizB_	Alignment	not modelled	100.0	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator protein, laci **PDBTitle:** crystal structure of a putative transcriptional regulator2 protein, lacl family from rhizobium etli
30	c2rgyA_	Alignment	not modelled	100.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of transcriptional regulator of laci family from2 burkhoderia phymatum
31	c3e3mA_	Alignment	not modelled	100.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
32	c3dbiA_	Alignment	not modelled	100.0	16	**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
33	c3d8uA_	Alignment	not modelled	100.0	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
34	c3c3kA_	Alignment	not modelled	100.0	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
35	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
36	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
37	c3egcF_	Alignment	not modelled	100.0	19	**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	c3hcwB_	Alignment	not modelled	100.0	10	**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 areus
39	c3ctpB_	Alignment	not modelled	100.0	18	**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
40	c3gv0A_	Alignment	not modelled	100.0	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
41	c3o74A_	Alignment	not modelled	100.0	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fructose transport system repressor frur; **PDBTitle:** crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
42	c3jy6B_	Alignment	not modelled	100.0	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci transcriptional regulator from lactobacillus2 brevis
43	c3qk7C_	Alignment	not modelled	100.0	16	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
44	d1tlfa_	Alignment	not modelled	100.0	17	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
45	d1jyea_	Alignment	not modelled	100.0	17	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
46	c1jyeA_	Alignment	not modelled	100.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lactose operon repressor; **PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
47	c2o20H_	Alignment	not modelled	100.0	17	**PDB header:**transcription **Chain:** H: **PDB Molecule:**catabolite control protein a; **PDBTitle:** crystal structure of transcription regulator ccpa of lactococcus2 lactis
48	c3bblA_	Alignment	not modelled	100.0	18	**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
49	d1dbqa_	Alignment	not modelled	100.0	17	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
50	c3g85A_	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 clostridium acetobutylicum
51	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.
52	c3clkB_	Alignment	not modelled	100.0	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcription regulator; **PDBTitle:** crystal structure of a transcription regulator from

						lactobacillus2 plantarum
53	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
54	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
55	c2qu7B_	Alignment	not modelled	100.0	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
56	c1zvvA_	Alignment	not modelled	100.0	19	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
57	c2h0aA_	Alignment	not modelled	100.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of probable transcription regulator from2 thermus thermophilus
58	d1byka_	Alignment	not modelled	100.0	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
59	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
60	c3bilA_	Alignment	not modelled	100.0	17	**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
61	c3gybB_	Alignment	not modelled	100.0	17	**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
62	c3jvdA_	Alignment	not modelled	100.0	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
63	c1bdhA_	Alignment	not modelled	100.0	16	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
64	c3kjxD_	Alignment	not modelled	100.0	17	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from silicibacter pomeroyi
65	c3e61A_	Alignment	not modelled	100.0	20	**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
66	c3h5tA_	Alignment	not modelled	99.9	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from corynebacterium glutamicum
67	c2qh8A_	Alignment	not modelled	99.9	14	**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
68	c3lftA_	Alignment	not modelled	99.9	16	**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	c2hqbA_	Alignment	not modelled	99.9	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
70	c2fqxA_	Alignment	not modelled	99.9	12	**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	c3sg0A_	Alignment	not modelled	98.9	14	**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
73	c3t0nA_	Alignment	not modelled	98.8	9	**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
74	c3i45A_	Alignment	not modelled	98.8	11	**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
75	d1qo0a_	Alignment	not modelled	98.8	10	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
76	c3i09A_	Alignment	not modelled	98.8	10	**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	c3n0wA_	Alignment	not modelled	98.7	7	**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 (bxe_c0949) from burkholderia3 xenovorans lb400 at 1.88 a resolution
78	d2liva_	Alignment	not modelled	98.7	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
79	c3lkbB_	Alignment	not modelled	98.7	9	**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
80	c3snrA_	Alignment	not modelled	98.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
81	c3hutA_	Alignment	not modelled	98.6	13	**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
82	c3h5lB_	Alignment	not modelled	98.6	9	**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
83	c3n0xA_	Alignment	not modelled	98.6	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
84	c3eafA_	Alignment	not modelled	98.5	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
85	c3ip5A_	Alignment	not modelled	98.5	13	**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
86	d1usga_	Alignment	not modelled	98.4	11	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
87	c1jdpA_	Alignment	not modelled	98.4	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**atrial natriuretic peptide clearance receptor; **PDBTitle:** crystal structure of hormone/receptor complex
88	d1jdpa_	Alignment	not modelled	98.4	11	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
89	c3lopA_	Alignment	not modelled	98.3	12	**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	c3td9A_	Alignment	not modelled	98.3	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
91	c3qi7A_	Alignment	not modelled	98.2	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
92	c1yk1B_	Alignment	not modelled	98.1	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
93	c3h6hB_	Alignment	not modelled	98.0	13	**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
94	d1ewka_	Alignment	not modelled	97.8	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
95	d3ckma1	Alignment	not modelled	97.7	11	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
96	d1dp4a_	Alignment	not modelled	97.5	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
97	c3sm9A_	Alignment	not modelled	97.5	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
98	c3om1A_	Alignment	not modelled	97.1	9	**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
99	c3q41B_	Alignment	not modelled	96.8	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)
100	c3sajB_	Alignment	not modelled	96.2	6	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate receptor 1; **PDBTitle:** crystal structure of glutamate receptor glua1 amino terminal domain

101	c3p3wC_	Alignment	not modelled	96.1	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
102	c2wjxA_	Alignment	not modelled	95.3	6	**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
103	d1o4va_	Alignment	not modelled	94.7	13	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
104	c3lp6D_	Alignment	not modelled	94.5	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
105	c2f59B_	Alignment	not modelled	94.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
106	d4pfka_	Alignment	not modelled	94.1	19	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
107	c3opyG_	Alignment	not modelled	94.1	12	**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
108	c2e4zA_	Alignment	not modelled	94.0	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
109	c1zxxA_	Alignment	not modelled	93.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase; **PDBTitle:** the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
110	c2fw9A_	Alignment	not modelled	92.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
111	c3opyE_	Alignment	not modelled	92.7	11	**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
112	c2uygF_	Alignment	not modelled	92.7	14	**PDB header:**lyase **Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystallographic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
113	c2e4wA_	Alignment	not modelled	92.5	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
114	d1u11a_	Alignment	not modelled	92.4	12	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
115	c3kg2A_	Alignment	not modelled	91.8	5	**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
116	c1vcnA_	Alignment	not modelled	91.4	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
117	c3orsD_	Alignment	not modelled	90.7	11	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
118	c3nvaB_	Alignment	not modelled	90.7	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
119	c1w19E_	Alignment	not modelled	89.7	12	**PDB header:**transferase **Chain:** E: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase; **PDBTitle:** lumazine synthase from mycobacterium tuberculosis bound to2 3-(1,3,7-trihydro-9-d-ribityl-2,6,8-purinetrione-7-yl)3 propane 1-phosphate
120	c3o8oC_	Alignment	not modelled	89.6	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**6-phosphofructokinase subunit alpha; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae