Phyre^2

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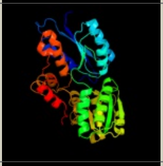
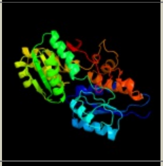
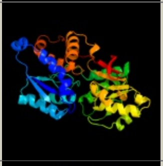
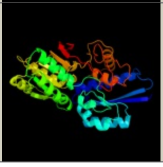
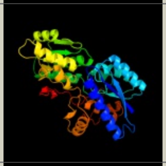
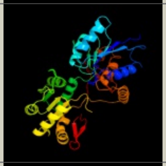
Description	P45464
Date	Thu Jan 5 12:02:41 GMT 2012
Unique Job ID	9aa65b035587d68c

Detailed template information

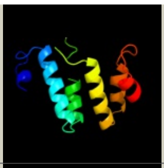
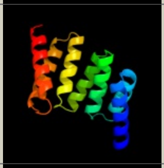
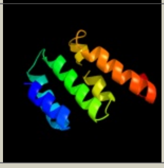
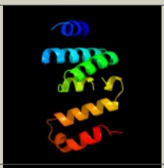
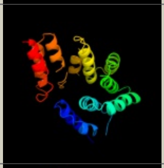
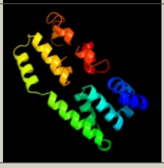
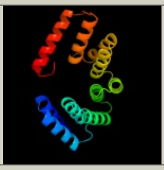
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3ckma1	Alignment		100.0	38	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
2	d1qo0a_	Alignment		100.0	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
3	c3hutA_	Alignment		100.0	21	**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
4	c3i09A_	Alignment		100.0	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic branched-chain amino acid-binding protein; **PDBTitle:** crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
5	c3t0nA_	Alignment		100.0	15	**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
6	d2liva_	Alignment		100.0	15	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
7	c3snrA_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
8	c3td9A_	Alignment		100.0	18	**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
9	c3n0wA_	Alignment		100.0	15	**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
10	c3n0xA_	Alignment		100.0	17	**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
11	c3lkbB_	Alignment		100.0	13	**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

12	d1usga_	Alignment		100.0	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
13	c3h5lB_	Alignment		100.0	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
14	c3i45A_	Alignment		100.0	14	**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
15	c3ip5A_	Alignment		100.0	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
16	c3sg0A_	Alignment		100.0	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
17	c3lopA_	Alignment		100.0	16	**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
18	c3eafA_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein; **PDBTitle:** crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
19	d1jdpa_	Alignment		100.0	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
20	c1jdpA_	Alignment		100.0	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**atrial natriuretic peptide clearance receptor; **PDBTitle:** crystal structure of hormone/receptor complex
21	c1yk1B_	Alignment	not modelled	100.0	11	**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
22	c3om1A_	Alignment	not modelled	100.0	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate receptor gluk5 (ka2); **PDBTitle:** crystal structure of the gluk5 (ka2) atd dimer at 1.7 angstrom2 resolution
23	d1dp4a_	Alignment	not modelled	100.0	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
24	c3h6hB_	Alignment	not modelled	100.0	10	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glutamate receptor, ionotropic kainate 2; **PDBTitle:** crystal structure of the glur6 amino terminal domain dimer assembly2 mpd form
25	c3sm9A_	Alignment	not modelled	100.0	16	**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
26	d1ewka_	Alignment	not modelled	100.0	12	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
27	c2e4zA_	Alignment	not modelled	100.0	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
28	c3sajB_	Alignment	not modelled	100.0	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate receptor 1; **PDBTitle:** crystal structure of glutamate receptor glua1 amino terminal domain

29	c3kg2A_	Alignment	not modelled	100.0	16	**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
30	c3p3wC_	Alignment	not modelled	100.0	12	**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
31	c2e4wA_	Alignment	not modelled	100.0	17	**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
32	c2wjxA_	Alignment	not modelled	99.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glutamate receptor 2; **PDBTitle:** crystal structure of the human ionotropic glutamate2 receptor glur2 atd region at 4.1 a resolution
33	c3q41B_	Alignment	not modelled	99.9	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate [nmda] receptor subunit zeta-1; **PDBTitle:** crystal structure of the glun1 n-terminal domain (ntd)
34	c3jpyA_	Alignment	not modelled	99.7	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glutamate [nmda] receptor subunit epsilon-2; **PDBTitle:** crystal structure of the zinc-bound amino terminal domain of the nmda2 receptor subunit nr2b
35	c2iksA_	Alignment	not modelled	98.6	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
36	c3h5oB_	Alignment	not modelled	98.5	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator gntr; **PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
37	c3mizB_	Alignment	not modelled	98.5	14	**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
38	c3g85A_	Alignment	not modelled	98.4	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (laci family); **PDBTitle:** crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
39	c3d8uA_	Alignment	not modelled	98.4	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
40	c3c3kA_	Alignment	not modelled	98.4	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
41	c3brqA_	Alignment	not modelled	98.4	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator ascg; **PDBTitle:** crystal structure of the escherichia coli transcriptional repressor2 ascg
42	c3dbiA_	Alignment	not modelled	98.3	11	**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
43	c2rjoA_	Alignment	not modelled	98.3	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
44	c3gv0A_	Alignment	not modelled	98.3	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
45	c3e3mA_	Alignment	not modelled	98.3	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
46	c3k4hA_	Alignment	not modelled	98.3	10	**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
47	c3k9cA_	Alignment	not modelled	98.3	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family protein; **PDBTitle:** crystal structure of laci transcriptional regulator from rhodococcus2 species.
48	c3qk7C_	Alignment	not modelled	98.3	15	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
49	d1jx6a_	Alignment	not modelled	98.3	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
50	c3hcwB_	Alignment	not modelled	98.3	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 areus
51	c2rgyA_	Alignment	not modelled	98.3	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of transcriptional regulator of laci family from2 burkhoderia phymatum
52	d1tjya_	Alignment	not modelled	98.1	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like

53	c3ksmA_	Alignment	not modelled	98.1	14	**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
54	c3o1hB_	Alignment	not modelled	98.0	16	**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
55	d2nzug1	Alignment	not modelled	98.0	10	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
56	c2qu7B_	Alignment	not modelled	98.0	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
57	c3bblA_	Alignment	not modelled	97.9	9	**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
58	c3cs3A_	Alignment	not modelled	97.9	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 enterococcus faecalis
59	c3egcF_	Alignment	not modelled	97.9	15	**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
60	d1gcaa_	Alignment	not modelled	97.8	16	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
61	c3h75A_	Alignment	not modelled	97.8	10	**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
62	c2fqxA_	Alignment	not modelled	97.6	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**membrane lipoprotein tmpc; **PDBTitle:** pnra from treponema pallidum complexed with guanosine
63	c2ioyB_	Alignment	not modelled	97.6	17	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**periplasmic sugar-binding protein; **PDBTitle:** crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
64	c3lftA_	Alignment	not modelled	97.6	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
65	c3jy6B_	Alignment	not modelled	97.6	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci transcriptional regulator from lactobacillus2 brevis
66	c2h0aA_	Alignment	not modelled	97.6	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of probable transcription regulator from2 thermus thermophilus
67	d1jyea_	Alignment	not modelled	97.5	12	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
68	c1jyeA_	Alignment	not modelled	97.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lactose operon repressor; **PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
69	c2o20H_	Alignment	not modelled	97.5	9	**PDB header:**transcription **Chain:** H: **PDB Molecule:**catabolite control protein a; **PDBTitle:** crystal structure of transcription regulator ccpa of lactococcus2 lactis
70	c3ma0A_	Alignment	not modelled	97.5	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
71	d1guda_	Alignment	not modelled	97.5	15	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
72	c2vk2A_	Alignment	not modelled	97.5	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq; **PDBTitle:** crystal structure of a galactofuranose binding protein
73	c3gybB_	Alignment	not modelled	97.5	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
74	c3brsA_	Alignment	not modelled	97.4	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein/laci transcriptional regulator; **PDBTitle:** crystal structure of sugar transporter from clostridium2 phytofermentans
75	c3kkeA_	Alignment	not modelled	97.4	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
76	c3jvdA_	Alignment	not modelled	97.3	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
77	c2fn9A_	Alignment	not modelled	97.3	11	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**ribose abc transporter, periplasmic ribose-binding protein; **PDBTitle:** thermotoga maritima ribose binding protein unliganded

						form
78	c3clkB_	Alignment	not modelled	97.2	6	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcription regulator; **PDBTitle:** crystal structure of a transcription regulator from lactobacillus2 plantarum
79	d2dria_	Alignment	not modelled	97.2	16	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
80	c3d02A_	Alignment	not modelled	97.2	13	**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
81	c2qvcC_	Alignment	not modelled	97.1	13	**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
82	c1zvvA_	Alignment	not modelled	97.1	12	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
83	c3ctpB_	Alignment	not modelled	97.0	12	**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
84	d8abpa_	Alignment	not modelled	97.0	8	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
85	c2hqbA_	Alignment	not modelled	96.8	10	**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
86	c2dgdD_	Alignment	not modelled	96.7	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**223aa long hypothetical arylmalonate decarboxylase; **PDBTitle:** crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
87	c2xecD_	Alignment	not modelled	96.7	13	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
88	c2qh8A_	Alignment	not modelled	96.7	12	**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
89	d1byka_	Alignment	not modelled	96.7	15	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
90	c3bilA_	Alignment	not modelled	96.6	13	**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
91	c3g1wB_	Alignment	not modelled	96.5	7	**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
92	c2x7xA_	Alignment	not modelled	96.5	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** fructose binding periplasmic domain of hybrid two component2 system bt1754
93	d2fvya1	Alignment	not modelled	96.0	17	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
94	c3l6uA_	Alignment	not modelled	95.9	10	**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
95	c3s99A_	Alignment	not modelled	95.5	8	**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
96	c2vlbC_	Alignment	not modelled	95.4	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**arylmalonate decarboxylase; **PDBTitle:** structure of unliganded arylmalonate decarboxylase
97	d1dbqa_	Alignment	not modelled	95.3	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
98	c3o74A_	Alignment	not modelled	95.3	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fructose transport system repressor frur; **PDBTitle:** crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
99	c3e61A_	Alignment	not modelled	94.3	12	**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

100	c3fflC_	Alignment		93.2	13	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**anaphase-promoting complex subunit 7; **PDBTitle:** crystal structure of the n-terminal domain of anaphase-2 promoting complex subunit 7
101	c2xcbA_	Alignment		93.1	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**regulatory protein pcrh; **PDBTitle:** crystal structure of pcrh in complex with the chaperone2 binding region of popd
102	c2kc7A_	Alignment		92.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bfr218_protein; **PDBTitle:** solution nmr structure of bacteroides fragilis protein2 bf1650. northeast structural genomics consortium target3 bfr218
103	d1tlfa_	Alignment	not modelled	92.5	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
104	c3rotA_	Alignment	not modelled	92.4	11	**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
105	c3kjxD_	Alignment	not modelled	92.3	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
106	c3hs3A_	Alignment	not modelled	91.7	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**ribose operon repressor; **PDBTitle:** crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
107	c3k9iA_	Alignment		91.5	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bh0479 protein; **PDBTitle:** crystal structure of putative protein binding protein (np_241345.1)2 from bacillus halodurans at 2.71 a resolution
108	c3hymB_	Alignment		91.1	5	**PDB header:**cell cycle, ligase **Chain:** B: **PDB Molecule:**cell division cycle protein 16 homolog; **PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
109	c2r5sB_	Alignment		91.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp0806; **PDBTitle:** the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633
110	c2xevB_	Alignment	not modelled	90.4	12	**PDB header:**metal binding **Chain:** B: **PDB Molecule:**ybgf; **PDBTitle:** crystal structure of the tpr domain of xanthomonas2 campestris ybgf
111	c3pe3D_	Alignment		89.3	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
112	c3l49D_	Alignment	not modelled	88.2	8	**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
113	c3gbvB_	Alignment	not modelled	88.2	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
114	c3huuC_	Alignment	not modelled	87.9	11	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcription regulator like protein; **PDBTitle:** crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
115	c2xpiA_	Alignment	not modelled	87.8	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**anaphase-promoting complex subunit cut9; **PDBTitle:** crystal structure of apc/c hetero-tetramer cut9-hcn1
116	c2dbaA_	Alignment	not modelled	86.7	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**smooth muscle cell associated protein-1, isoform **PDBTitle:** the solution structure of the tetratrico peptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
117	c3urzB_	Alignment	not modelled	85.5	11	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein (bacova_03105) from2 bacteroides ovatus atcc 8483 at 2.19 a

						resolution
118	d1zbpa1	Alignment	not modelled	85.2	19	**Fold:**ImpE-like **Superfamily:**ImpE-like **Family:**ImpE-like
119	d1w3ba_	Alignment	not modelled	85.2	12	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
120	c3mv3B_	Alignment	not modelled	84.7	11	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**coatomer subunit epsilon; **PDBTitle:** crystal structure of a-cop in complex with e-cop