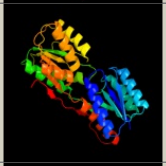
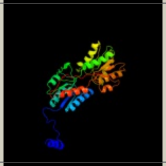
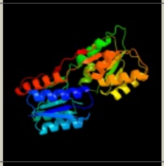
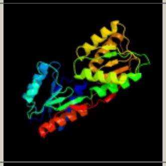
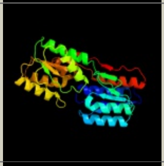
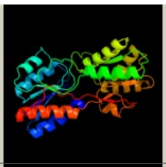
# Phyre2

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P02925 |
| Date | Thu Jan 5 10:57:39 GMT 2012 |
| Unique Job ID | a71e0804b44fd1c6 |

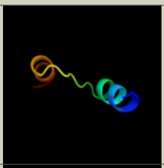
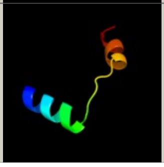
Detailed template information

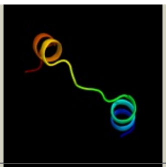
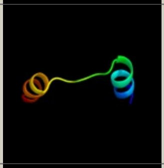
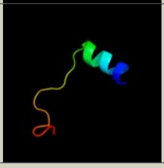
| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2dria_ | Alignment |  | 100.0 | 100 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 2 | c2ioyB_ | Alignment |  | 100.0 | 57 | **PDB header:**sugar binding protein<br>**Chain:** B: **PDB Molecule:**periplasmic sugar-binding protein;<br>**PDBTitle:** crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein |
| 3 | c1zvvA_ | Alignment |  | 100.0 | 16 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator;<br>**PDBTitle:** crystal structure of a ccpa-crh-dna complex |
| 4 | c3l6uA_ | Alignment |  | 100.0 | 24 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**abc-type sugar transport system periplasmic<br>**PDBTitle:** crystal structure of abc-type sugar transport system,2 periplasmic component from exiguobacterium sibiricum |
| 5 | c2fn9A_ | Alignment |  | 100.0 | 40 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**ribose abc transporter, periplasmic ribose-binding protein;<br>**PDBTitle:** thermotoga maritima ribose binding protein unliganded form |
| 6 | d1jx6a_ | Alignment |  | 100.0 | 17 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 7 | c2iksA_ | Alignment |  | 100.0 | 16 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**dna-binding transcriptional dual regulator;<br>**PDBTitle:** crystal structure of n-terminal truncated dna-binding transcriptional2 dual regulator from escherichia coli k12 |
| 8 | c3l49D_ | Alignment |  | 100.0 | 22 | **PDB header:**transport protein<br>**Chain:** D: **PDB Molecule:**abc sugar (ribose) transporter, periplasmic<br>**PDBTitle:** crystal structure of abc sugar transporter subunit from2 rhodobacter sphaeroides 2.4.1 |
| 9 | c3c3kA_ | Alignment |  | 100.0 | 20 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**alanine racemase;<br>**PDBTitle:** crystal structure of an uncharacterized protein from actinobacillus2 succinogenes |
| 10 | c3h5oB_ | Alignment |  | 100.0 | 19 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**transcriptional regulator gntr;<br>**PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum |
| 11 | c3k4hA_ | Alignment |  | 100.0 | 17 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**putative transcriptional regulator;<br>**PDBTitle:** crystal structure of putative transcriptional regulator laci from2 bacillus cereus subsp. cytotoxis nvh 391-98 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | c3e3mA_ | Alignment |  | 100.0 | 16 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, laci family;<br>**PDBTitle:** crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi |
| 13 | d2nzug1 | Alignment |  | 100.0 | 16 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 14 | c3dbiA_ | Alignment |  | 100.0 | 19 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family;<br>**PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from escherichia coli complexed with phosphate |
| 15 | c3mizB_ | Alignment |  | 100.0 | 16 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**putative transcriptional regulator protein, laci<br>**PDBTitle:** crystal structure of a putative transcriptional regulator2 protein, lacI family from rhizobium etli |
| 16 | c3kjxD_ | Alignment |  | 100.0 | 18 | **PDB header:**transcription regulator<br>**Chain:** D: **PDB Molecule:**transcriptional regulator, laci family;<br>**PDBTitle:** crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi |
| 17 | d1tlfa_ | Alignment |  | 100.0 | 21 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 18 | c3egcF_ | Alignment |  | 100.0 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** F: **PDB Molecule:**putative ribose operon repressor;<br>**PDBTitle:** crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis |
| 19 | c1jyeA_ | Alignment |  | 100.0 | 21 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**lactose operon repressor;<br>**PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution |
| 20 | d1jyea_ | Alignment |  | 100.0 | 21 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 21 | c3ctpB_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**periplasmic binding protein/laci transcriptional regulator;<br>**PDBTitle:** crystal structure of periplasmic binding protein/laci transcriptional2 regulator from alkaliphilus metalliredigens qymf complexed with d-3 xylulofuranose |
| 22 | c3cs3A_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family;<br>**PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis |
| 23 | c1bdhA_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**protein (purine repressor);<br>**PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex |
| 24 | c3d8uA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**purr transcriptional regulator;<br>**PDBTitle:** the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633 |
| 25 | c3brsA_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**periplasmic binding protein/laci transcriptional regulator;<br>**PDBTitle:** crystal structure of sugar transporter from clostridium2 phytofermentans |
| 26 | c3brqA_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**hth-type transcriptional regulator ascg;<br>**PDBTitle:** crystal structure of the escherichia coli transcriptional repressor2 ascg |
| 27 | c2rgyA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, laci family;<br>**PDBTitle:** crystal structure of transcriptional regulator of laci family from2 burkhoderia phymatum |

| | | | | | | |
|---|---|---|---|---|---|---|
| 28 | c3kkeA_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**laci family transcriptional regulator;<br>**PDBTitle:** crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis |
| 29 | c3ma0A_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**d-xylose-binding periplasmic protein;<br>**PDBTitle:** closed liganded crystal structure of xylose binding protein from2 escherichia coli |
| 30 | c3hcwB_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**rna binding protein<br>**Chain:** B: **PDB Molecule:**maltose operon transcriptional repressor;<br>**PDBTitle:** crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus areus |
| 31 | c2rjoA_ | Alignment | not modelled | 100.0 | 26 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein;<br>**PDBTitle:** crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans |
| 32 | c3ksmA_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**abc-type sugar transport system, periplasmic component;<br>**PDBTitle:** crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis |
| 33 | c3o74A_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**fructose transport system repressor frur;<br>**PDBTitle:** crystal structure of cra transcriptional dual regulator from2 pseudomonas putida |
| 34 | c2o20H_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**transcription<br>**Chain:** H: **PDB Molecule:**catabolite control protein a;<br>**PDBTitle:** crystal structure of transcription regulator ccpa of lactococcus2 lactis |
| 35 | d1guda_ | Alignment | not modelled | 100.0 | 35 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 36 | d1dbqa_ | Alignment | not modelled | 100.0 | 22 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 37 | c3g85A_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator (laci family);<br>**PDBTitle:** crystal structure of laci family transcription regulator from2 clostridium acetobutylicum |
| 38 | c3qk7C_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**transcription regulator<br>**Chain:** C: **PDB Molecule:**transcriptional regulators;<br>**PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001 |
| 39 | c3k9cA_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, laci family protein;<br>**PDBTitle:** crystal structure of laci transcriptional regulator from rhodococcus2 species. |
| 40 | c3gv0A_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, laci family;<br>**PDBTitle:** crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens |
| 41 | c3hs3A_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**ribose operon repressor;<br>**PDBTitle:** crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus |
| 42 | d1gcaa_ | Alignment | not modelled | 100.0 | 25 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 43 | c3bblA_ | Alignment | not modelled | 100.0 | 13 | **PDB header:**regulatory protein<br>**Chain:** A: **PDB Molecule:**regulatory protein of laci family;<br>**PDBTitle:** crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans |
| 44 | c3g1wB_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**sugar abc transporter;<br>**PDBTitle:** crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans |
| 45 | c3jy6B_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**transcriptional regulator, laci family;<br>**PDBTitle:** crystal structure of laci transcriptional regulator from lactobacillus2 brevis |
| 46 | c2qvcC_ | Alignment | not modelled | 100.0 | 25 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**sugar abc transporter, periplasmic sugar-binding<br>**PDBTitle:** crystal structure of a periplasmic sugar abc transporter2 from thermotoga maritima |
| 47 | c3gbvB_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**putative laci-family transcriptional regulator;<br>**PDBTitle:** crystal structure of a putative laci transcriptional regulator from2 bacteroides fragilis |
| 48 | d8abpa_ | Alignment | not modelled | 100.0 | 20 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 49 | c2qu7B_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**putative transcriptional regulator;<br>**PDBTitle:** crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus |
| 50 | d2fvya1 | Alignment | not modelled | 100.0 | 25 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 51 | c3o1hB_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**periplasmic protein tort;<br>**PDBTitle:** crystal structure of the tors sensor domain - tort complex in the2 presence of tmao |
| 52 | c2h0aA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulator; |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 52 | c2h0aA_ | Alignment | not modelled | 100.0 | 21 | **PDBTitle:** crystal structure of probable transcription regulator from2 thermus thermophilus |
| 53 | c3huuC_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**transcription regulator<br>**Chain:** C: **PDB Molecule:**transcription regulator like protein;<br>**PDBTitle:** crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus |
| 54 | d1byka_ | Alignment | not modelled | 100.0 | 16 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 55 | c3bilA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**probable laci-family transcriptional regulator;<br>**PDBTitle:** crystal structure of a probable laci family transcriptional2 regulator from corynebacterium glutamicum |
| 56 | c3d02A_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**putative laci-type transcriptional regulator;<br>**PDBTitle:** crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution |
| 57 | c2x7xA_ | Alignment | not modelled | 100.0 | 26 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor protein;<br>**PDBTitle:** fructose binding periplasmic domain of hybrid two component2 system bt1754 |
| 58 | c3clkB_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**transcription regulator;<br>**PDBTitle:** crystal structure of a transcription regulator from lactobacillus2 plantarum |
| 59 | c3jvdA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulators;<br>**PDBTitle:** crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum |
| 60 | d1tjya_ | Alignment | not modelled | 100.0 | 19 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 61 | c3gybB_ | Alignment | not modelled | 100.0 | 24 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**transcriptional regulators (laci-family<br>**PDBTitle:** crystal structure of a laci-family transcriptional2 regulatory protein from corynebacterium glutamicum |
| 62 | c3h5tA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, laci family;<br>**PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from corynebacterium glutamicum |
| 63 | c3rotA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**abc sugar transporter, periplasmic sugar binding protein;<br>**PDBTitle:** crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila |
| 64 | c2vk2A_ | Alignment | not modelled | 100.0 | 25 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq;<br>**PDBTitle:** crystal structure of a galactofuranose binding protein |
| 65 | c3h75A_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**periplasmic sugar-binding domain protein;<br>**PDBTitle:** crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens |
| 66 | c3e61A_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative transcriptional repressor of ribose operon;<br>**PDBTitle:** crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus |
| 67 | c2hqbA_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional activator of comk gene;<br>**PDBTitle:** crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans |
| 68 | c3lftA_ | Alignment | not modelled | 99.8 | 14 | **PDB header:**structure genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** the crystal structure of the abc domain in complex with l-trp from2 streptococcus pneumonia to 1.35a |
| 69 | c2qh8A_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of conserved domain protein from vibrio2 cholerae o1 biovar eltor str. n16961 |
| 70 | c2fqxA_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**membrane lipoprotein tmpc;<br>**PDBTitle:** pnra from treponema pallidum complexed with guanosine |
| 71 | c3s99A_ | Alignment | not modelled | 99.5 | 12 | **PDB header:**lipid binding protein<br>**Chain:** A: **PDB Molecule:**basic membrane lipoprotein;<br>**PDBTitle:** crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak |
| 72 | c3sg0A_ | Alignment | not modelled | 98.6 | 16 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor;<br>**PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2 |
| 73 | c3i09A_ | Alignment | not modelled | 98.5 | 15 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**periplasmic branched-chain amino acid-binding protein;<br>**PDBTitle:** crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution |
| 74 | c3hutA_ | Alignment | not modelled | 98.5 | 13 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**putative branched-chain amino acid abc<br>**PDBTitle:** crystal structure of a putative branched-chain amino acid2 abc transporter from rhodospirillum rubrum |
| 75 | c3snrA_ | Alignment | not modelled | 98.4 | 14 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor;<br>**PDBTitle:** rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris. |
|  |  |  |  |  |  | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**abc branched chain amino acid family |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 76 | c3n0wA_ | Alignment | not modelled | 98.3 | 10 | transporter,<br>**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 |
| 77 | c3t0nA_ | Alignment | not modelled | 98.3 | 17 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal;<br>**PDBTitle:** crystal structure of twin-arginine translocation pathway signal from2 rhodopseudomonas palustris bisb5 |
| 78 | d1qo0a_ | Alignment | not modelled | 98.2 | 13 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 79 | c3lopA_ | Alignment | not modelled | 98.1 | 15 | **PDB header:**substrate binding protein<br>**Chain:** A: **PDB Molecule:**substrate binding periplasmic protein;<br>**PDBTitle:** crystal structure of substrate-binding periplasmic protein2 (pbp) from ralstonia solanacearum |
| 80 | d3ckma1 | Alignment | not modelled | 98.1 | 9 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 81 | c3qi7A_ | Alignment | not modelled | 98.0 | 12 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**putative transcriptional regulator;<br>**PDBTitle:** crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution |
| 82 | c3i45A_ | Alignment | not modelled | 98.0 | 13 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein;<br>**PDBTitle:** crystal structure of putative twin-arginine translocation pathway2 signal protein from rhodospirillum rubrum atcc 11170 |
| 83 | d2liva_ | Alignment | not modelled | 98.0 | 16 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 84 | c3h5lB_ | Alignment | not modelled | 97.9 | 12 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**putative branched-chain amino acid abc<br>**PDBTitle:** crystal structure of a putative branched-chain amino acid2 abc transporter from silicibacter pomeroyi |
| 85 | c3ip5A_ | Alignment | not modelled | 97.9 | 16 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein (amino acid);<br>**PDBTitle:** structure of atu2422-gaba receptor in complex with alanine |
| 86 | c3n0xA_ | Alignment | not modelled | 97.8 | 16 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**possible substrate binding protein of abc transporter<br>**PDBTitle:** crystal structure of an abc-type branched-chain amino acid transporter2 (rpa4397) from rhodopseudomonas palustris cga009 at 1.50 a resolution |
| 87 | c3eafA_ | Alignment | not modelled | 97.6 | 12 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein;<br>**PDBTitle:** crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix |
| 88 | d1usga_ | Alignment | not modelled | 97.6 | 16 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 89 | c3td9A_ | Alignment | not modelled | 97.6 | 13 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**branched chain amino acid abc transporter, periplasmic<br>**PDBTitle:** crystal structure of a leucine binding protein livk (tm1135) from2 thermotoga maritima msb8 at 1.90 a resolution |
| 90 | c3lkbB_ | Alignment | not modelled | 97.6 | 12 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**probable branched-chain amino acid abc<br>**PDBTitle:** crystal structure of a branched chain amino acid abc2 transporter from thermus thermophilus with bound valine |
| 91 | d1jdpa_ | Alignment | not modelled | 97.2 | 9 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 92 | c1jdpA_ | Alignment | not modelled | 97.2 | 9 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**atrial natriuretic peptide clearance receptor;<br>**PDBTitle:** crystal structure of hormone/receptor complex |
| 93 | c3q41B_ | Alignment | not modelled | 97.2 | 11 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**glutamate [nmda] receptor subunit zeta-1;<br>**PDBTitle:** crystal structure of the glun1 n-terminal domain (ntd) |
| 94 | c3sajB_ | Alignment | not modelled | 97.0 | 9 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**glutamate receptor 1;<br>**PDBTitle:** crystal structure of glutamate receptor glua1 amino terminal domain |
| 95 | c3sm9A_ | Alignment | not modelled | 96.9 | 14 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**metabotropic glutamate receptor 3;<br>**PDBTitle:** crystal structure of metabotropic glutamate receptor 3 precursor in2 presence of ly341495 antagonist |
| 96 | d2hsga1 | Alignment |  | 96.8 | 16 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 97 | d1qpza1 | Alignment |  | 96.8 | 8 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |

| | | | | | | |
|---|---|---|---|---|---|---|
| 98 | d1efaa1 | Alignment |  | 96.7 | 12 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 99 | d2bjca1 | Alignment |  | 96.7 | 12 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 100 | d1uxda_ | Alignment |  | 96.5 | 12 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 101 | c1yk1B_ | Alignment | not modelled | 96.2 | 10 | **PDB header:**hormone/growth factor receptor<br>**Chain:** B: **PDB Molecule:**atrial natriuretic peptide clearance receptor;<br>**PDBTitle:** structure of natriuretic peptide receptor-c complexed with brain2 natriuretic peptide |
| 102 | c3h6hB_ | Alignment | not modelled | 96.0 | 13 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**glutamate receptor, ionotropic kainate 2;<br>**PDBTitle:** crystal structure of the glur6 amino terminal domain dimer assembly2 mpd form |
| 103 | d1dp4a_ | Alignment | not modelled | 94.7 | 12 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 104 | d1ewka_ | Alignment | not modelled | 94.4 | 15 | **Fold:**Periplasmic binding protein-like I<br>**Superfamily:**Periplasmic binding protein-like I<br>**Family:**L-arabinose binding protein-like |
| 105 | c3p3wC_ | Alignment | not modelled | 93.5 | 8 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**glutamate receptor 3;<br>**PDBTitle:** structure of a dimeric glua3 n-terminal domain (ntd) at 4.2 a2 resolution |
| 106 | d1uxca_ | Alignment | not modelled | 91.7 | 13 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 107 | c2e4wA_ | Alignment | not modelled | 90.5 | 12 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**metabotropic glutamate receptor 3;<br>**PDBTitle:** crystal structure of the extracellular region of the group ii2 metabotropic glutamate receptor complexed with 1s,3s-acpd |
| 108 | d1lcda_ | Alignment | not modelled | 90.2 | 6 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 109 | c3om1A_ | Alignment | not modelled | 89.9 | 9 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**glutamate receptor gluk5 (ka2);<br>**PDBTitle:** crystal structure of the gluk5 (ka2) atd dimer at 1.7 angstrom2 resolution |
| 110 | c2e4zA_ | Alignment | not modelled | 88.2 | 16 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**metabotropic glutamate receptor 7;<br>**PDBTitle:** crystal structure of the ligand-binding region of the group iii2 metabotropic glutamate receptor |
| 111 | c2l8nA_ | Alignment | not modelled | 87.3 | 6 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional repressor cytr;<br>**PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna |
| 112 | c2lcvA_ | Alignment | not modelled | 86.6 | 7 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr;<br>**PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation |
| 113 | c2f59B_ | Alignment | not modelled | 85.1 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1;<br>**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 |
| 114 | c3kg2A_ | Alignment | not modelled | 85.0 | 9 | **PDB header:**membrane protein, transport protein<br>**Chain:** A: **PDB Molecule:**glutamate receptor 2;<br>**PDBTitle:** ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775 |
| 115 | c3mk3L_ | Alignment | not modelled | 84.9 | 16 | **PDB header:**transferase<br>**Chain:** L: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase;<br>**PDBTitle:** crystal structure of lumazine synthase from salmonella typhimurium lt2 |
| 116 | d1di0a_ | Alignment | not modelled | 84.8 | 8 | **Fold:**Lumazine synthase<br>**Superfamily:**Lumazine synthase<br>**Family:**Lumazine synthase |
| 117 | d1c2ya_ | Alignment | not modelled | 84.5 | 13 | **Fold:**Lumazine synthase<br>**Superfamily:**Lumazine synthase<br>**Family:**Lumazine synthase |
| 118 | d1rvv1_ | Alignment | not modelled | 84.3 | 13 | **Fold:**Lumazine synthase<br>**Superfamily:**Lumazine synthase<br>**Family:**Lumazine synthase |
| 119 | d1nqua_ | Alignment | not modelled | 83.6 | 10 | **Fold:**Lumazine synthase<br>**Superfamily:**Lumazine synthase<br>**Family:**Lumazine synthase |
| 120 | c2obxH_ | Alignment | not modelled | 82.5 | 15 | **PDB header:**transferase<br>**Chain:** H: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; |

| | | | | | | |
|---|---|---|---|---|---|---|
| 120 | c2obxH_ | Alignment | not modelled | 82.5 | 15 | **PDBTitle:** lumazine synthase ribh2 from mesorhizobium loti (gene mll7281, swiss-2 prot entry q986n2) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione |