










Phyre2

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| Description | multi-dom |
| Date | Sun Sep 7 16:46:09 BST 2014 |
| Unique Job ID | 7563ce6b200bdd4e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c4h1gA_ |  Alignment |  | 100.0 | 100 | PDB header: motor protein Chain: A: PDB Molecule: maltose binding protein-cakar3 motor domain fusion protein; PDBTitle: structure of candida albicans kar3 motor domain fused to maltose-2 binding protein |
| 2 | c3f5fA_ |  Alignment |  | 100.0 | 99 | PDB header: transport, transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein, heparan PDBTitle: crystal structure of heparan sulfate 2-o-sulfotransferase2 from gallus gallus as a maltose binding protein fusion. |
| 3 | c3ob4A_ |  Alignment |  | 100.0 | 98 | PDB header: allergen Chain: A: PDB Molecule: maltose abc transporter periplasmic protein, arah 2; PDBTitle: mbp-fusion protein of the major peanut allergen ara h 2 |
| 4 | c3h4zC_ |  Alignment |  | 100.0 | 95 | PDB header: allergen Chain: C: PDB Molecule: maltose-binding periplasmic protein fused with allergen PDBTitle: crystal structure of an mbp-der p 7 fusion protein |
| 5 | c3dm0A_ |  Alignment |  | 100.0 | 99 | PDB header: sugar binding protein,signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein fused with PDBTitle: maltose binding protein fusion with rack1 from a. thaliana |
| 6 | c4egcA_ |  Alignment |  | 100.0 | 88 | PDB header: transcription/hydrolase Chain: A: PDB Molecule: maltose-binding periplasmic protein, homeobox protein six1 PDBTitle: crystal structure of mbp-fused human six1 bound to human eya2 eya2 domain |
| 7 | c4kegA_ |  Alignment |  | 100.0 | 91 | PDB header: lipid binding protein Chain: A: PDB Molecule: maltose-binding periplasmic/palate lung and nasal PDBTitle: crystal structure of mbp fused human splunc1 |
| 8 | c4bl9D_ |  Alignment |  | 100.0 | 100 | PDB header: signaling protein Chain: D: PDB Molecule: maltose-binding periplasmic protein, suppressor of fused PDBTitle: crystal structure of full-length human suppressor of fused (2 sufu) mutant lacking a regulatory subdomain (crystal form i) |
| 9 | c3py7A_ |  Alignment |  | 100.0 | 98 | PDB header: viral protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,paxillin ld1,protein e6 PDBTitle: crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution |
| 10 | c3o3uN_ |  Alignment |  | 100.0 | 100 | PDB header: transport protein, signaling protein Chain: N: PDB Molecule: maltose-binding periplasmic protein, advanced glycosylation PDBTitle: crystal structure of human receptor for advanced glycation endproducts2 (rage) |
| 11 | c1hsjA_ |  Alignment |  | 100.0 | 93 | PDB header: transcription/sugar binding protein Chain: A: PDB Molecule: fusion protein consisting of staphylococcus PDBTitle: sarr mbp fusion structure |

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|----|------------------------|-----------|---|-------|-----|---|
| 12 | c3mp6A | Alignment |  | 100.0 | 99 | PDB header: histone binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, linker, saga- PDBTitle: complex structure of sgf29 and dimethylated h3k4 |
| 13 | c3d4cA | Alignment |  | 100.0 | 100 | PDB header: cell adhesion Chain: A: PDB Molecule: maltose-binding periplasmic protein, linker, zona pellucida PDBTitle: zp-n domain of mammalian sperm receptor zp3 (crystal form i) |
| 14 | c2nvuB | Alignment |  | 100.0 | 75 | PDB header: protein turnover, ligase Chain: B: PDB Molecule: maltose binding protein/nedd8-activating enzyme PDBTitle: structure of appbp1-uba3-nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex |
| 15 | c4edqA | Alignment |  | 100.0 | 100 | PDB header: transport protein/contractile protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,myosin-binding protein PDBTitle: mbp-fusion protein of myosin-binding protein c residues 149-269 |
| 16 | c3vd8A | Alignment |  | 100.0 | 95 | PDB header: sugar binding protein,signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, interferon-inducible PDBTitle: crystal structure of human aim2 pyd domain with mbp fusion |
| 17 | c4kv3A | Alignment |  | 100.0 | 100 | PDB header: protein transport Chain: A: PDB Molecule: chimera fusion protein of esx-1 secretion system protein PDBTitle: ubiquitin-like domain of the mycobacterium tuberculosis type vii2 secretion system protein eccd1 as maltose-binding protein fusion |
| 18 | c3c4mA | Alignment |  | 100.0 | 96 | PDB header: membrane protein Chain: A: PDB Molecule: fusion protein of maltose-binding periplasmic protein and PDBTitle: structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r) |
| 19 | c4ozqA | Alignment |  | 100.0 | 100 | PDB header: motor protein Chain: A: PDB Molecule: chimera of maltose-binding periplasmic protein and kinesin PDBTitle: crystal structure of the mouse kif14 motor domain |
| 20 | c4logA | Alignment |  | 100.0 | 99 | PDB header: transcription Chain: A: PDB Molecule: maltose abc transporter periplasmic protein and nr2e3 PDBTitle: the crystal structure of the orphan nuclear receptor pnr ligand2 binding domain fused with mbp |
| 21 | c4pqqA | Alignment | not modelled | 100.0 | 99 | PDB header: dna binding protein Chain: A: PDB Molecule: maltose abc transporter periplasmic protein, truncated PDBTitle: c-terminal domain of dna binding protein |
| 22 | c1r6zA | Alignment | not modelled | 100.0 | 99 | PDB header: gene regulation Chain: A: PDB Molecule: chimera of maltose-binding periplasmic protein and PDBTitle: the crystal structure of the argonaute2 paz domain (as a mbp fusion) |
| 23 | c4ifpC | Alignment | not modelled | 100.0 | 99 | PDB header: immune system Chain: C: PDB Molecule: maltose-binding periplasmic protein, nacht, lrr and pyd PDBTitle: x-ray crystal structure of human nlrp1 card domain |
| 24 | c3oaiB | Alignment | not modelled | 100.0 | 99 | PDB header: membrane protein, cell adhesion Chain: B: PDB Molecule: maltose-binding periplasmic protein, myelin protein p0; PDBTitle: crystal structure of the extra-cellular domain of human myelin protein2 zero |
| 25 | c4b3nA | Alignment | not modelled | 100.0 | 97 | PDB header: sugar binding protein/ligase Chain: A: PDB Molecule: maltose-binding periplasmic protein, tripartite PDBTitle: crystal structure of rhesus trim5alpha pry/spry domain |
| 26 | c3waiA | Alignment | not modelled | 100.0 | 99 | PDB header: transferase, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, transmembrane PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion |
| 27 | c3osqA | Alignment | not modelled | 100.0 | 100 | PDB header: fluorescent protein, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, green fluorescent PDBTitle: maltose-bound maltose sensor engineered by insertion of |

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|----|-------------------------|-----------|--------------|-------|-----|--|
| | | | | | | circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 175 |
| 28 | c2vqgA_ | Alignment | not modelled | 100.0 | 98 | PDB header: immune system/transport Chain: A: PDB Molecule: maltose-binding periplasmic protein, PDBTitle: crystal structure of human ips-1 card |
| 29 | c4my2A_ | Alignment | not modelled | 100.0 | 98 | PDB header: signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, norrin fusion protein; PDBTitle: crystal structure of norrin in fusion with maltose binding protein |
| 30 | c1y4cA_ | Alignment | not modelled | 100.0 | 98 | PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp |
| 31 | c3csgA_ | Alignment | not modelled | 100.0 | 98 | PDB header: de novo protein, sugar binding protein Chain: A: PDB Molecule: maltose-binding protein monobody ys1 fusion; PDBTitle: crystal structure of monobody ys1(mbp-74)/maltose binding2 protein fusion complex |
| 32 | c3osrA_ | Alignment | not modelled | 100.0 | 100 | PDB header: fluorescent protein, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, green fluorescent PDBTitle: maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 311 |
| 33 | c4exkA_ | Alignment | not modelled | 100.0 | 98 | PDB header: transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, uncharacterized PDBTitle: a chimera protein containing mbp fused to the c-terminal domain of the2 uncharacterized protein stm14_2015 from salmonella enterica |
| 34 | c3a3cA_ | Alignment | not modelled | 100.0 | 95 | PDB header: protein transport Chain: A: PDB Molecule: maltose-binding periplasmic protein, linker, mitochondrial PDBTitle: crystal structure of tim40/mia40 fusing mbp, c296s and c298s mutant |
| 35 | c3ehuA_ | Alignment | not modelled | 100.0 | 98 | PDB header: membrane protein Chain: A: PDB Molecule: fusion protein of crfr1 extracellular domain and mbp; PDBTitle: crystal structure of the extracellular domain of human corticotropin2 releasing factor receptor type 1 (crfr1) in complex with crf |
| 36 | c1mg1A_ | Alignment | not modelled | 100.0 | 100 | PDB header: viral protein Chain: A: PDB Molecule: protein (htlv-1 gp21 ectodomain/maltose- binding protein PDBTitle: htlv-1 gp21 ectodomain/maltose-binding protein chimera |
| 37 | c4dxkB_ | Alignment | not modelled | 100.0 | 90 | PDB header: sugar binding protein, hydrolase Chain: B: PDB Molecule: maltose-binding periplasmic protein, beta- lactamase tem PDBTitle: 2.29a structure of the engineered mbp tem-1 fusion protein rg13 in2 complex with zinc, p1 space group |
| 38 | c1mh3A_ | Alignment | not modelled | 100.0 | 99 | PDB header: sugar binding, dna binding protein Chain: A: PDB Molecule: maltose binding-a1 homeodomain protein chimera; PDBTitle: maltose binding-a1 homeodomain protein chimera, crystal2 form i |
| 39 | c1svxB_ | Alignment | not modelled | 100.0 | 98 | PDB header: de novo protein/sugar binding protein Chain: B: PDB Molecule: maltose-binding periplasmic protein; PDBTitle: crystal structure of a designed selected ankyrin repeat2 protein in complex with the maltose binding protein |
| 40 | c3iouB_ | Alignment | not modelled | 100.0 | 100 | PDB header: signaling protein Chain: B: PDB Molecule: maltose-binding protein, huntingtin fusion PDBTitle: huntingtin amino-terminal region with 17 gln residues -2 crystal c94 |
| 41 | d1laxa_ | Alignment | not modelled | 100.0 | 98 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 42 | c2zykA_ | Alignment | not modelled | 100.0 | 29 | PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin |
| 43 | c4hs7A_ | Alignment | not modelled | 100.0 | 28 | PDB header: solute-binding protein Chain: A: PDB Molecule: bacterial extracellular solute-binding protein, putative; PDBTitle: 2.6 angstrom structure of the extracellular solute-binding protein2 from staphylococcus aureus in complex with peg. |
| 44 | c2fncA_ | Alignment | not modelled | 100.0 | 33 | PDB header: sugar binding protein Chain: A: PDB Molecule: maltose abc transporter, periplasmic maltose-binding PDBTitle: thermotoga maritima maltotriose binding protein bound with2 maltotriose. |
| 45 | d1elja_ | Alignment | not modelled | 100.0 | 27 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 46 | c2gh9A_ | Alignment | not modelled | 100.0 | 29 | PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose |
| 47 | c2xd3A_ | Alignment | not modelled | 100.0 | 28 | PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: the crystal structure of malx from streptococcus pneumoniae2 in complex with maltopentaose. |
| 48 | d1eu8a_ | Alignment | not modelled | 100.0 | 24 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 49 | c3k02A_ | Alignment | not modelled | 100.0 | 23 | PDB header: transport protein Chain: A: PDB Molecule: acarbose/maltose binding protein gach; PDBTitle: crystal structures of the gach receptor of streptomyces glaucescens2 gla.o in the unliganded form and in complex with acarbose and an3 acarbose homolog. comparison with acarbose- |

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| | | | | | | loaded maltose binding4 protein of salmonella typhimurium. PDB header: sugar binding protein Chain: B: PDB Molecule: abc transporter sugar binding protein; PDBTitle: the structure of the sugar-binding protein male from the phytopathogen2 xanthomonas citri |
| 50 | c3uorB_ | Alignment | not modelled | 100.0 | 22 | PDB header: sugar binding protein Chain: B: PDB Molecule: galacto-n-biose/lacto-n-biose i transporter substrate- PDBTitle: the galacto-n-biose-/lacto-n-biose i-binding protein (gl-bp) of the2 abc transporter from bifidobacterium longum in complex with lacto-n-3 tetraose |
| 51 | c2z8fB_ | Alignment | not modelled | 100.0 | 18 | PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: crystal structure of sugar transporter achI_0255 from arthrobacter2 chlorophenolicus a6, target efi-510633, with bound laminaribiose |
| 52 | c4r2fA_ | Alignment | not modelled | 100.0 | 15 | PDB header: maltose-binding protein Chain: A: PDB Molecule: maltose-binding protein; PDBTitle: x-ray structures of the maltose-maltodextrin binding2 protein of the thermoacidophilic bacterium alicyclobacillus3 acidocaldarius |
| 53 | c1ursa_ | Alignment | not modelled | 100.0 | 28 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 54 | d1ursa_ | Alignment | not modelled | 100.0 | 28 | PDB header: transport protein Chain: C: PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus |
| 55 | c4g68C_ | Alignment | not modelled | 100.0 | 20 | PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus |
| 56 | c4g68A_ | Alignment | not modelled | 100.0 | 20 | PDB header: diester-binding protein Chain: A: PDB Molecule: sn-glycerol-3-phosphate-binding periplasmic protein ugpb; PDBTitle: substrate bound sn-glycerol-3-phosphate binding periplasmic protein2 ugpb from escherichia coli |
| 57 | c4aq4A_ | Alignment | not modelled | 100.0 | 17 | PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: extracellular solute-binding protein family 1 from alicyclobacillus2 acidocaldarius subsp. acidocaldarius dsm 446 |
| 58 | c4ovjA_ | Alignment | not modelled | 100.0 | 14 | PDB header: sugar binding protein Chain: A: PDB Molecule: sn-glycerol-3-phosphate abc transporter substrate-binding PDBTitle: crystal structure of mycobacterium tuberculosis ugpb |
| 59 | c4mfiA_ | Alignment | not modelled | 100.0 | 17 | PDB header: sugar-binding protein Chain: A: PDB Molecule: abc type periplasmic sugar-binding protein; PDBTitle: structure of a periplasmic oligogalacturonide binding2 protein from yersinia enterocolitica |
| 60 | c2uvqA_ | Alignment | not modelled | 100.0 | 17 | PDB header: sugar binding protein Chain: A: PDB Molecule: abc transporter binding protein acbh; PDBTitle: crystal structures and biochemical characterization of the bacterial2 solute receptor acbh reveal an unprecedented exclusive substrate3 preference for b-d-galactopyranose |
| 61 | c3oo6A_ | Alignment | not modelled | 100.0 | 16 | PDB header: unknown function Chain: C: PDB Molecule: lmo0859 protein; PDBTitle: 2.1 angstrom resolution crystal structure of uncharacterized protein2 lmo0859 from listeria monocytogenes egd-e |
| 62 | c4gqoC_ | Alignment | not modelled | 100.0 | 18 | PDB header: transport protein Chain: A: PDB Molecule: xos binding protein; PDBTitle: structure of the xylo-oligosaccharide specific solute2 binding protein from bifidobacterium animalis subsp.3 lactis bl-04 in complex with xylo-tetraose |
| 63 | c3zkkA_ | Alignment | not modelled | 100.0 | 18 | PDB header: transport protein Chain: B: PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: crystal structure of sugar transporter oant_3817 from ochrobactrum2 anthropi, target efi-510558, with bound glucose |
| 64 | c4r2bB_ | Alignment | not modelled | 100.0 | 16 | PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar-binding lipoprotein; PDBTitle: crystal structure of bxle from streptomyces thermoviolaceus opc-520 |
| 65 | c3vxbA_ | Alignment | not modelled | 100.0 | 18 | PDB header: transport protein Chain: B: PDB Molecule: extracellular solute-binding protein, family 1; PDBTitle: the structure of a family 1 extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis |
| 66 | c3qufB_ | Alignment | not modelled | 100.0 | 20 | PDB header: sugar binding protein Chain: D: PDB Molecule: glucose-binding protein; PDBTitle: thermus thermophilus glucose/galactose binding protein2 bound with galactose |
| 67 | c2b3fD_ | Alignment | not modelled | 100.0 | 18 | PDB header: transport protein Chain: C: PDB Molecule: probable secreted solute-binding lipoprotein; PDBTitle: crystal structure of probable secreted solute-binding2 lipoprotein from streptomyces coelicolor |
| 68 | c3i3vC_ | Alignment | not modelled | 100.0 | 15 | PDB header: sugar-binding protein Chain: A: PDB Molecule: probable sugar abc transporter, sugar-binding PDBTitle: structure of a streptococcus pneumoniae solute-binding2 protein in complex with the blood group a-trisaccharide. |
| 69 | c2w7yA_ | Alignment | not modelled | 100.0 | 16 | PDB header: sugar binding protein Chain: B: PDB Molecule: sugar abc transporter, sugar-binding protein; PDBTitle: crystal structure of rafe from streptococcus pneumoniae complexed with2 raffinose |
| 70 | c2i58B_ | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: thiamine pyridinylase i; |
| 71 | c1kvcA_ | Alignment | not modelled | 100.0 | 14 | |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 71 | c4ky3A | Alignment | not modelled | 100.0 | 14 | PDBTitle: clostridium botulinum thiaminase i in complex with thiamin |
| 72 | d3thia | Alignment | not modelled | 100.0 | 15 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 73 | d1j1na | Alignment | not modelled | 100.0 | 17 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 74 | d1y3na1 | Alignment | not modelled | 100.0 | 17 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 75 | c4hcwC | Alignment | not modelled | 100.0 | 11 | PDB header: transferase Chain: C: PDB Molecule: thiaminase-i; PDBTitle: structure of a eukaryotic thiaminase-i |
| 76 | c3tttB | Alignment | not modelled | 100.0 | 14 | PDB header: transport protein Chain: B: PDB Molecule: polyamine transport protein; PDBTitle: crystal structure of apo-spue |
| 77 | c3ttkA | Alignment | not modelled | 100.0 | 17 | PDB header: transport protein Chain: A: PDB Molecule: polyamine transport protein; PDBTitle: crystal structure of apo-spud |
| 78 | c4eqbA | Alignment | not modelled | 100.0 | 18 | PDB header: transport protein Chain: A: PDB Molecule: spermidine/putrescine abc superfamily atp binding cassette PDBTitle: 1.5 angstrom crystal structure of spermidine/putrescine abc2 transporter substrate-binding protein potd from streptococcus3 pneumoniae strain canada mdr_19a in complex with calcium and hepes |
| 79 | c2v84A | Alignment | not modelled | 100.0 | 15 | PDB header: transport protein Chain: A: PDB Molecule: spermidine/putrescine abc transporter, periplasmic PDBTitle: crystal structure of the tp0655 (tppotd) lipoprotein of2 treponema pallidum |
| 80 | d1a99a | Alignment | not modelled | 100.0 | 18 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 81 | d1pota | Alignment | not modelled | 100.0 | 17 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 82 | c4eq7B | Alignment | not modelled | 100.0 | 17 | PDB header: transport protein Chain: B: PDB Molecule: abc transporter, substrate binding protein (polyamine); PDBTitle: structure of atu4243-gaba receptor |
| 83 | c4i1dB | Alignment | not modelled | 100.0 | 14 | PDB header: transport protein Chain: B: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: the crystal structure of an abc transporter substrate-binding protein2 from bradyrhizobium japonicum usda 110 |
| 84 | c4gl0A | Alignment | not modelled | 100.0 | 18 | PDB header: transport protein Chain: A: PDB Molecule: lmo0810 protein; PDBTitle: putative spermidine/putrescine abc transporter from listeria2 monocytogenes |
| 85 | c3ombA | Alignment | not modelled | 100.0 | 21 | PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein, family 1; PDBTitle: crystal structure of extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis |
| 86 | c3rpwA | Alignment | not modelled | 100.0 | 20 | PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: the crystal structure of an abc transporter from rhodopseudomonas2 palustris cga009 |
| 87 | c3c9hB | Alignment | not modelled | 100.0 | 15 | PDB header: transport protein Chain: B: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of the substrate binding protein of the abc2 transporter from agrobacterium tumefaciens |
| 88 | c4edpA | Alignment | not modelled | 100.0 | 19 | PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate-binding protein; PDBTitle: 1.85 angstrom resolution crystal structure of an abc transporter from2 clostridium perfringens atcc 13124 |
| 89 | d1y4ta | Alignment | not modelled | 100.0 | 20 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 90 | c3pu5A | Alignment | not modelled | 100.0 | 16 | PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein; PDBTitle: the crystal structure of a putative extracellular solute-binding2 protein from bordetella parapertussis |
| 91 | c2pt1A | Alignment | not modelled | 100.0 | 17 | PDB header: metal transport Chain: A: PDB Molecule: iron transport protein; PDBTitle: futa1 synechocystis pcc 6803 |
| 92 | d1q35a | Alignment | not modelled | 100.0 | 17 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 93 | c4eloD | Alignment | not modelled | 100.0 | 18 | PDB header: metal transport Chain: D: PDB Molecule: iron abc transporter, periplasmic iron-binding protein; PDBTitle: ferric binding protein in apo form 1 |
| 94 | d1xvxa | Alignment | not modelled | 100.0 | 20 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 95 | d1xc1a | Alignment | not modelled | 100.0 | 16 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 96 | c2vozA | Alignment | not modelled | 100.0 | 16 | PDB header: metal-binding protein Chain: A: PDB Molecule: periplasmic iron-binding protein; PDBTitle: apo futa2 from synechocystis pcc6803 |

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| 97 | d1nnfa_ | Alignment | not modelled | 100.0 | 21 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 98 | d1y9ua_ | Alignment | not modelled | 100.0 | 17 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 99 | c2qrvD_ | Alignment | not modelled | 100.0 | 15 | PDB header: transport protein Chain: D: PDB Molecule: thiamine-binding periplasmic protein; PDBTitle: periplasmic thiamin binding protein |
| 100 | d1xvya_ | Alignment | not modelled | 100.0 | 21 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 101 | d2onsa1 | Alignment | not modelled | 99.9 | 13 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 102 | c3cfxA_ | Alignment | not modelled | 99.9 | 12 | PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein ma_0280; PDBTitle: crystal structure of m. acetivorans periplasmic binding protein2 moda/wtpa with bound tungstate |
| 103 | c3cfzA_ | Alignment | not modelled | 99.9 | 12 | PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein mj1186; PDBTitle: crystal structure of m. jannaschii periplasmic binding2 protein moda/wtpa with bound tungstate |
| 104 | c3k6wA_ | Alignment | not modelled | 99.9 | 11 | PDB header: transport protein Chain: A: PDB Molecule: solute-binding protein ma_0280; PDBTitle: apo and ligand bound structures of moda from the archaeon2 methanosarcina acetivorans |
| 105 | c3cg1A_ | Alignment | not modelled | 99.9 | 15 | PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein pf0080; PDBTitle: crystal structure of p. furiosus periplasmic binding protein2 moda/wtpa with bound tungstate |
| 106 | c3cg3A_ | Alignment | not modelled | 99.8 | 14 | PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein ph0151; PDBTitle: crystal structure of p. horikoshii periplasmic binding2 protein moda/wtpa with bound tungstate |
| 107 | d1sbpa_ | Alignment | not modelled | 99.7 | 15 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 108 | d1atga_ | Alignment | not modelled | 99.7 | 13 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 109 | d1amfa_ | Alignment | not modelled | 99.6 | 18 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 110 | c2h5yC_ | Alignment | not modelled | 99.6 | 18 | PDB header: metal transport Chain: C: PDB Molecule: molybdate-binding periplasmic protein; PDBTitle: crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate |
| 111 | c4kd5A_ | Alignment | not modelled | 99.5 | 18 | PDB header: transport protein Chain: A: PDB Molecule: abc-type transport system, molybdenum-specific PDBTitle: substrate binding domain of putative molybdenum abc transporter from2 clostridium difficile |
| 112 | c4jwoA_ | Alignment | not modelled | 99.4 | 14 | PDB header: phosphate binding protein Chain: A: PDB Molecule: phosphate binding protein; PDBTitle: the crystal structure of a possible phosphate binding protein from2 planctomyces limnophilus dsm 3776 |
| 113 | c3fj7A_ | Alignment | not modelled | 99.4 | 17 | PDB header: protein binding Chain: A: PDB Molecule: major antigenic peptide peb3; PDBTitle: crystal structure of l-phospholactate bound peb3 |
| 114 | c4jb7A_ | Alignment | not modelled | 99.3 | 13 | PDB header: cell invasion Chain: A: PDB Molecule: accessory colonization factor acfc; PDBTitle: 1.42 angstrom resolution crystal structure of accessory colonization2 factor acfc (acfc) in complex with d-aspartic acid |
| 115 | c3lr1A_ | Alignment | not modelled | 99.3 | 15 | PDB header: transport protein Chain: A: PDB Molecule: tungstate abc transporter, periplasmic tungstate- PDBTitle: the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens |
| 116 | c3muqB_ | Alignment | not modelled | 99.0 | 18 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633 |
| 117 | c3kn3C_ | Alignment | not modelled | 99.0 | 11 | PDB header: transcription Chain: C: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinella succinogenes |
| 118 | c4gd5B_ | Alignment | not modelled | 98.7 | 18 | PDB header: transport protein Chain: B: PDB Molecule: phosphate abc transporter, phosphate-binding protein; PDBTitle: x-ray crystal structure of a putative phosphate abc transporter2 substrate-binding protein with bound phosphate from clostridium3 perfringens |
| 119 | c1twyG_ | Alignment | not modelled | 98.7 | 12 | PDB header: structural genomics, unknown function Chain: G: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae |
| 120 | d1twya_ | Alignment | not modelled | 98.7 | 12 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |