





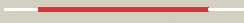





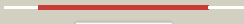



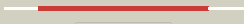







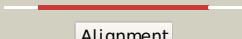




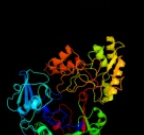











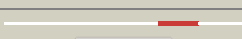
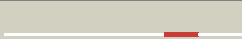


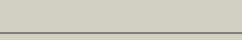

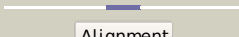


| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d1uqwa_ |  Alignment |  | 100.0 | 98 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 2 | d1dpea_ |  Alignment |  | 100.0 | 27 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 3 | c3tpaA_ |  Alignment |  | 100.0 | 26 | PDB header: heme binding protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: structure of hbpa2 from haemophilus parasuis |
| 4 | c3m8uA_ |  Alignment |  | 100.0 | 28 | PDB header: transport protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg) |
| 5 | c3o9pA_ |  Alignment |  | 100.0 | 20 | PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: periplasmic murein peptide-binding protein; PDBTitle: the structure of the escherichia coli murein tripeptide binding2 protein mppa |
| 6 | c2wokA_ |  Alignment |  | 100.0 | 22 | PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: clavulanic acid biosynthesis oligopeptide PDBTitle: clavulanic acid biosynthesis oligopeptide2 binding protein 2 complexed with bradykinin |
| 7 | d1jeta_ |  Alignment |  | 100.0 | 22 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 8 | d1zlqa1 |  Alignment |  | 100.0 | 22 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 9 | d1xoca1 |  Alignment |  | 100.0 | 24 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 10 | c3t66A_ |  Alignment |  | 100.0 | 25 | PDB header: transport protein Chain: A: PDB Molecule: nickel abc transporter (nickel-binding protein); PDBTitle: crystal structure of nickel abc transporter from bacillus halodurans |
| 11 | c3rqta_ |  Alignment |  | 100.0 | 21 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of the complex of ligand binding2 component of abc-type import system from staphylococcus aureus with3 nickel and two histidines |

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|----|--------------------------|---|---|-------|----|---|
| 12 | c1ztyA_ |  Alignment |  | 100.0 | 20 | PDB header: sugar binding protein, signaling protein Chain: A: PDB Molecule: chitin oligosaccharide binding protein; PDBTitle: crystal structure of the chitin oligosaccharide binding2 protein |
| 13 | c2o7jA_ |  Alignment |  | 100.0 | 21 | PDB header: sugar binding protein Chain: A: PDB Molecule: oligopeptide abc transporter, periplasmic PDBTitle: the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaoase |
| 14 | c2grvC_ |  Alignment |  | 100.0 | 18 | PDB header: biosynthetic protein Chain: C: PDB Molecule: lpqw; PDBTitle: crystal structure of lpqw |
| 15 | c3ftoA_ |  Alignment |  | 100.0 | 20 | PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide-binding protein oppa; PDBTitle: crystal structure of oppa in a open conformation |
| 16 | c3ry3B_ |  Alignment |  | 100.0 | 22 | PDB header: transport protein Chain: B: PDB Molecule: putative solute-binding protein; PDBTitle: putative solute-binding protein from yersinia pestis. |
| 17 | d1vr5a1 |  Alignment |  | 100.0 | 22 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 18 | c2d5wA_ |  Alignment |  | 100.0 | 16 | PDB header: peptide binding protein Chain: A: PDB Molecule: peptide abc transporter, peptide-binding protein; PDBTitle: the crystal structure of oligopeptide binding protein from thermus2 thermophilus hb8 complexed with pentapeptide |
| 19 | c3lrvuB_ |  Alignment |  | 100.0 | 22 | PDB header: transport protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi |
| 20 | c3pamB_ |  Alignment |  | 100.0 | 20 | PDB header: transport protein Chain: B: PDB Molecule: transmembrane protein; PDBTitle: crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1 |
| 21 | c3o6pA_ |  Alignment | not modelled | 100.0 | 27 | PDB header: protein binding Chain: A: PDB Molecule: peptide abc transporter, peptide-binding protein; PDBTitle: crystal structure of peptide abc transporter, peptide-binding protein |
| 22 | c3chgB_ |  Alignment | not modelled | 92.5 | 14 | PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa |
| 23 | c3tmgA_ |  Alignment | not modelled | 91.5 | 7 | PDB header: transport protein Chain: A: PDB Molecule: glycine betaine, l-proline abc transporter, PDBTitle: crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi |
| 24 | c3l6ga_ |  Alignment | not modelled | 91.0 | 13 | PDB header: glycine betaine-binding protein Chain: A: PDB Molecule: betaine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcal opuac in its open conformation |
| 25 | c2rejA_ |  Alignment | not modelled | 88.3 | 12 | PDB header: choline-binding protein Chain: A: PDB Molecule: putative glycine betaine abc transporter protein; PDBTitle: abc-transporter choline binding protein in unliganded semi-2 closed conformation |
| 26 | c3r6uA_ |  Alignment | not modelled | 72.9 | 8 | PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis |
| 27 | d1e5da1 |  Alignment | not modelled | 70.5 | 7 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related |

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|----|-------------------------|-----------|--------------|------|----|--|
| 28 | dlycga1 | Alignment | not modelled | 69.2 | 12 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related |
| 29 | dlja1a2 | Alignment | not modelled | 60.3 | 10 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like |
| 30 | dlr9la_ | Alignment | not modelled | 60.3 | 10 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 31 | dlb1ca_ | Alignment | not modelled | 58.9 | 12 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like |
| 32 | dlxs5a_ | Alignment | not modelled | 58.5 | 7 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 33 | c3f6sl_ | Alignment | not modelled | 55.8 | 8 | PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers |
| 34 | c3fniA_ | Alignment | not modelled | 54.1 | 10 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (al13895) from nostoc2 sp., northeast structural genomics consortium target nsr431a |
| 35 | c3hlyA_ | Alignment | not modelled | 51.9 | 15 | PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from2 synechococcus sp q5nzp6_synp6 protein. northeast structural3 genomics consortium target snr135d. |
| 36 | c2ek8A_ | Alignment | not modelled | 47.9 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: aminopeptidase from aneurinibacillus sp. strain am-1 |
| 37 | c3un6A_ | Alignment | not modelled | 47.1 | 13 | PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein saouhsc_00137; PDBTitle: 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound |
| 38 | c3gxaA_ | Alignment | not modelled | 46.2 | 10 | PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946 |
| 39 | dlf4pa_ | Alignment | not modelled | 44.2 | 8 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related |
| 40 | c3k2dA_ | Alignment | not modelled | 43.7 | 12 | PDB header: immune system Chain: A: PDB Molecule: abc-type metal ion transport system, periplasmic component; PDBTitle: crystal structure of immunogenic lipoprotein a from vibrio vulnificus |
| 41 | c3hn0A_ | Alignment | not modelled | 43.5 | 21 | PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein; PDBTitle: crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution |
| 42 | c1bvyF_ | Alignment | not modelled | 43.4 | 18 | PDB header: oxidoreductase Chain: F: PDB Molecule: protein (cytochrome p450 bm-3); PDBTitle: complex of the heme and fmN-binding domains of the2 cytochrome p450(bm-3) |
| 43 | dlbvyf_ | Alignment | not modelled | 43.4 | 18 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related |
| 44 | c3ir1F_ | Alignment | not modelled | 42.8 | 10 | PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis |
| 45 | dlsw5a_ | Alignment | not modelled | 42.5 | 11 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 46 | c2zykA_ | Alignment | not modelled | 42.4 | 9 | PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin |
| 47 | c3pppA_ | Alignment | not modelled | 39.9 | 12 | PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline-binding protein; PDBTitle: structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc |
| 48 | c3tqwA_ | Alignment | not modelled | 39.0 | 11 | PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii |
| 49 | d5nula_ | Alignment | not modelled | 38.1 | 6 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related |
| 50 | c3nohA_ | Alignment | not modelled | 37.8 | 16 | PDB header: peptide binding protein Chain: A: PDB Molecule: putative peptide binding protein; PDBTitle: crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution |
| 51 | c2o1mB_ | Alignment | not modelled | 36.3 | 11 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable amino-acid abc transporter PDBTitle: crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytnk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572 |
| 52 | c2hnbA_ | Alignment | not modelled | 34.3 | 19 | PDB header: electron transport Chain: A: PDB Molecule: protein mioc; |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: solution structure of a bacterial holo-flavodoxin |
| 53 | c3d7nA | Alignment | not modelled | 33.0 | 7 | PDB header: electron transport Chain: A: PDB Molecule: flavodoxin, wrba-like protein; PDBTitle: the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens |
| 54 | c3guxA | Alignment | not modelled | 32.1 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: putative zn-dependent exopeptidase; PDBTitle: crystal structure of a putative zn-dependent exopeptidase (bv_u_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution |
| 55 | c1j9zB | Alignment | not modelled | 31.9 | 11 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-cytochrome p450 reductase; PDBTitle: cypor-w677g |
| 56 | d1vmea1 | Alignment | not modelled | 30.8 | 15 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related |
| 57 | d1ydga | Alignment | not modelled | 28.8 | 8 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like |
| 58 | c3ix1B | Alignment | not modelled | 28.5 | 13 | PDB header: biosynthetic protein Chain: B: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans |
| 59 | c3ix1A | Alignment | not modelled | 28.5 | 13 | PDB header: biosynthetic protein Chain: A: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans |
| 60 | d2fz5a1 | Alignment | not modelled | 28.4 | 9 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related |
| 61 | d1g7da | Alignment | not modelled | 26.3 | 16 | Fold: ERP29 C domain-like Superfamily: ERP29 C domain-like Family: ERP29 C domain-like |
| 62 | d2arka1 | Alignment | not modelled | 25.6 | 12 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like |
| 63 | d2vv5a2 | Alignment | not modelled | 24.0 | 15 | Fold: Ferredoxin-like Superfamily: Mechanosensitive channel protein MscS (YggB), C-terminal domain Family: Mechanosensitive channel protein MscS (YggB), C-terminal domain |
| 64 | c2x26A | Alignment | not modelled | 23.7 | 10 | PDB header: transport protein Chain: A: PDB Molecule: periplasmic aliphatic sulphonates-binding protein; PDBTitle: crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli |
| 65 | c3oo6A | Alignment | not modelled | 23.2 | 11 | 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 |
| 66 | c3ombA | Alignment | not modelled | 23.1 | 10 | 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 |
| 67 | c2f06B | Alignment | not modelled | 22.3 | 20 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron |
| 68 | d2a5la1 | Alignment | not modelled | 22.2 | 14 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like |
| 69 | c3iibA | Alignment | not modelled | 21.3 | 6 | PDB header: hydrolase Chain: A: PDB Molecule: peptidase m28; PDBTitle: crystal structure of peptidase m28 precursor (yp_926796.1) from2 shewanella amazonensis sb2b at 1.70 a resolution |
| 70 | c1xt8B | Alignment | not modelled | 20.9 | 14 | PDB header: transport protein Chain: B: PDB Molecule: putative amino-acid transporter periplasmic solute-binding PDBTitle: crystal structure of cysteine-binding protein from campylobacter2 jejuni at 2.0 a resolution |
| 71 | d1uwda | Alignment | not modelled | 20.5 | 14 | Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like |
| 72 | c3t6mA | Alignment | not modelled | 20.3 | 6 | PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of the catalytic domain of dape protein from2 v.cholerea in the zn bound form |
| 73 | c3nbmA | Alignment | not modelled | 20.2 | 5 | PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae. |
| 74 | c1ychD | Alignment | not modelled | 20.1 | 7 | PDB header: oxidoreductase Chain: D: PDB Molecule: nitric oxide reductase; PDBTitle: x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase |
| 75 | c3kbrA | Alignment | not modelled | 19.6 | 8 | PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01 |

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|----|-------------------------|---|--------------|------|----|---|
| 76 | c3e4rA |  Alignment | not modelled | 19.2 | 11 | PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein; PDBTitle: crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes |
| 77 | c2l2qA |  Alignment | not modelled | 18.9 | 11 | PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi |
| 78 | c2x7vA |  Alignment | not modelled | 18.3 | 6 | PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc |
| 79 | c2q9uB |  Alignment | not modelled | 18.2 | 6 | PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis |
| 80 | d1iiba |  Alignment | not modelled | 17.6 | 10 | Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit |
| 81 | c2wteB |  Alignment | not modelled | 16.7 | 9 | PDB header: antiviral protein Chain: B: PDB Molecule: csa3; PDBTitle: the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution. |
| 82 | c3a9lB |  Alignment | not modelled | 16.6 | 20 | PDB header: hydrolase Chain: B: PDB Molecule: poly-gamma-glutamate hydrolase; PDBTitle: structure of bacteriophage poly-gamma-glutamate hydrolase |
| 83 | d1vgya1 |  Alignment | not modelled | 16.0 | 9 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 84 | d2p0la1 |  Alignment | not modelled | 15.7 | 13 | Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like |
| 85 | c1p99A |  Alignment | not modelled | 15.7 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus2 aureus |
| 86 | d1p99a |  Alignment | not modelled | 15.7 | 13 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 87 | d1ykga1 |  Alignment | not modelled | 15.2 | 16 | Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like |
| 88 | c2ylnA |  Alignment | not modelled | 15.1 | 18 | PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter, periplasmic binding protein, PDBTitle: crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation |
| 89 | c2uvga |  Alignment | not modelled | 14.9 | 6 | 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 |
| 90 | c2zkiH |  Alignment | not modelled | 14.9 | 3 | PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872) |
| 91 | c3tc8A |  Alignment | not modelled | 14.7 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a hypothetical zn-dependent exopeptidase2 (bdi_3547) from parabacteroides distansonis atcc 8503 at 1.06 a3 resolution |
| 92 | c2gh9A |  Alignment | not modelled | 14.6 | 10 | PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose |
| 93 | c3i6vA |  Alignment | not modelled | 14.3 | 15 | PDB header: transport protein Chain: A: PDB Molecule: periplasmic his/glu/gln/arg/opine family-binding protein; PDBTitle: crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine |
| 94 | c3r39A |  Alignment | not modelled | 13.9 | 18 | PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica |
| 95 | c2v25B |  Alignment | not modelled | 13.7 | 8 | PDB header: receptor Chain: B: PDB Molecule: major cell-binding factor; PDBTitle: structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate |
| 96 | d2q02a1 |  Alignment | not modelled | 13.6 | 10 | Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lolI-like |
| 97 | c3n5fB |  Alignment | not modelled | 13.6 | 4 | PDB header: hydrolase Chain: B: PDB Molecule: n-carbamoyl-l-amino acid hydrolase; PDBTitle: crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43 |
| 98 | c3kzgB |  Alignment | not modelled | 13.3 | 7 | PDB header: transport protein Chain: B: PDB Molecule: arginine 3rd transport system periplasmic binding PDBTitle: crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila |
| 99 | c3hr4C |  Alignment | not modelled | 13.3 | 10 | PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex |

