


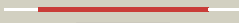
















Phyre2

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 Description RVBD3044_(fecB)_3405147_3406226
 Date Thu Aug 8 16:20:21 BST 2019
 Unique Job ID e552df54ab345190

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c3eiwA_ |  Alignment |  | 100.0 | 18 | PDB header: transport protein Chain: A: PDB Molecule: htsa protein; PDBTitle: crystal structure of staphylococcus aureus lipoprotein, htsa |
| 2 | c3tnyA_ |  Alignment |  | 100.0 | 24 | PDB header: metal transport Chain: A: PDB Molecule: fyfiy (abc transport system substrate-binding protein); PDBTitle: structure of yfiy from bacillus cereus bound to the siderophore iron2 (iii) schizokinen |
| 3 | c4hn9B_ |  Alignment |  | 100.0 | 14 | PDB header: transport protein Chain: B: PDB Molecule: iron complex transport system substrate-binding protein; PDBTitle: crystal structure of iron abc transporter solute-binding protein from2 eubacterium eligens |
| 4 | c3gfvA_ |  Alignment |  | 100.0 | 14 | PDB header: transport protein Chain: A: PDB Molecule: uncharacterized abc transporter solute-binding protein PDBTitle: crystal structure of petrobactin-binding protein yclq from bacillu2 subtilis |
| 5 | c3pshA_ |  Alignment |  | 100.0 | 13 | PDB header: metal transport Chain: A: PDB Molecule: protein hi_1472; PDBTitle: classification of a haemophilus influenzae abc transporter hi1470/712 through its cognate molybdate periplasmic binding protein mola (mola3 bound to molybdate) |
| 6 | c5az3A_ |  Alignment |  | 100.0 | 13 | PDB header: transport protein Chain: A: PDB Molecule: abc-type transporter, periplasmic component; PDBTitle: crystal structure of heme binding protein hmut |
| 7 | c4ovkA_ |  Alignment |  | 100.0 | 16 | PDB header: solute-binding protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of periplasmic solute binding protein from2 veillonella parvula dsm 2008 |
| 8 | c3tefA_ |  Alignment |  | 100.0 | 18 | PDB header: transport protein Chain: A: PDB Molecule: iron(iii) abc transporter, periplasmic iron-compound- PDBTitle: crystal structure of the periplasmic catecholate-siderophore binding2 protein vctp from vibrio cholerae |
| 9 | d2chua1 |  Alignment |  | 100.0 | 20 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TM0189-like |
| 10 | c3r5tA_ |  Alignment |  | 100.0 | 19 | PDB header: metal transport Chain: A: PDB Molecule: ferric vibriobactin abc transporter, periplasmic ferric PDBTitle: crystal structure of holo-viup |
| 11 | c3tlkB_ |  Alignment |  | 100.0 | 17 | PDB header: metal transport Chain: B: PDB Molecule: ferrienterobactin-binding periplasmic protein; PDBTitle: crystal structure of holo fepb |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c3be5D_ | Alignment | | 100.0 | 20 | PDB header: metal transport Chain: D: PDB Molecule: putative iron compound-binding protein of abc transporter PDBTitle: crystal structure of fite (crystal form 1), a group iii periplasmic2 siderophore binding protein |
| 13 | c4jccA_ | Alignment | | 100.0 | 20 | PDB header: transport protein Chain: A: PDB Molecule: iron-compound abc transporter, iron-compound-binding PDBTitle: crystal structure of iron uptake abc transporter substrate-binding2 protein piva from streptococcus pneumoniae canada mdr_19a |
| 14 | c5cr9A_ | Alignment | | 100.0 | 16 | PDB header: transport protein Chain: A: PDB Molecule: abc-type fe3+-hydroxamate transport system, periplasmic PDBTitle: crystal structure of abc-type fe3+-hydroxamate transport system from2 saccharomonospora viridis dsm 43017 |
| 15 | c6mf1A_ | Alignment | | 100.0 | 19 | PDB header: metal transport Chain: A: PDB Molecule: baub; PDBTitle: structure of siderophore binding protein baub bound to a complex2 between two molecules of acinetobactin and ferric iron. |
| 16 | c6allB_ | Alignment | | 100.0 | 18 | PDB header: metal transport Chain: B: PDB Molecule: fe(3+)-citrate-binding protein yfmc; PDBTitle: crystal structure of a predicted ferric/iron (iii) hydroxamate2 siderophore substrate binding protein from bacillus anthracis |
| 17 | c2phzA_ | Alignment | | 100.0 | 14 | PDB header: transport protein Chain: A: PDB Molecule: iron-uptake system-binding protein; PDBTitle: crystal structure of iron-uptake system-binding protein feua from2 bacillus subtilis. northeast structural genomics target sr580. |
| 18 | d2phza1 | Alignment | | 100.0 | 14 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TM0189-like |
| 19 | c4n01B_ | Alignment | | 100.0 | 12 | PDB header: transport protein Chain: B: PDB Molecule: periplasmic binding protein; PDBTitle: the crystal structure of a periplasmic binding protein from2 veillonella parvula dsm 2008 |
| 20 | c4pagA_ | Alignment | | 100.0 | 15 | PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: abc transporter solute binding protein from sulfurospirillum2 deleyianum dsm 6946 |
| 21 | c5gj3A_ | Alignment | not modelled | 100.0 | 18 | PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: periplasmic heme-binding protein rhut from roseiflexus sp. rs-1 in2 two-heme bound form (holo-2) |
| 22 | c6b2xB_ | Alignment | not modelled | 100.0 | 15 | PDB header: metal transport Chain: B: PDB Molecule: solute-binding periplasmic protein of iron/siderophore abc PDBTitle: apo yiuA crystal form 1 |
| 23 | c4mx8C_ | Alignment | not modelled | 100.0 | 23 | PDB header: solute-binding protein Chain: C: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of troa-like periplasmic binding protein2 peripla_bp_2 from xylanimonas cellulositytica |
| 24 | c4mlzB_ | Alignment | not modelled | 100.0 | 18 | PDB header: solute binding protein Chain: B: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of periplasmic binding protein from jonesia2 denitrificans |
| 25 | c4ljsA_ | Alignment | not modelled | 100.0 | 17 | PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: the crystal structure of a periplasmic binding protein from2 veillonella parvula dsm 2008 |
| 26 | c5dh0B_ | Alignment | not modelled | 100.0 | 20 | PDB header: protein binding Chain: B: PDB Molecule: siderophore periplasmic binding protein; PDBTitle: structure of the siderophore periplasmic binding protein from the2 fuscachelin gene cluster of thermobifida fusca in p41 |
| 27 | c5flyB_ | Alignment | not modelled | 100.0 | 19 | PDB header: metal transport Chain: B: PDB Molecule: ferrichrome-binding periplasmic protein; PDBTitle: the fhud protein from s.pseudintermedius |
| 28 | c4b8yA_ | Alignment | not modelled | 100.0 | 18 | PDB header: transport protein/siderophore Chain: A: PDB Molecule: fhud2; PDBTitle: ferrichrome-bound fhud2 |
| | | | | | | PDB header: solute-binding protein Chain: B: PDB Molecule: iron complex transporter substrate- |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 29 | c4pm4B_ | Alignment | not modelled | 100.0 | 16 | binding protein; PDBTitle: structure of a putative periplasmic iron siderophore binding protein2 (rv0265c) from mycobacterium tuberculosis h37rv |
| 30 | c4h59A_ | Alignment | not modelled | 100.0 | 17 | PDB header: transport protein Chain: A: PDB Molecule: iron-compound abc transporter, iron compound-binding PDBTitle: crystal structure of iron uptake abc transporter substrate-binding2 protein p1aa from streptococcus pneumoniae canada mdr_19a bound to3 bis-tris propane |
| 31 | c4mo9A_ | Alignment | not modelled | 100.0 | 15 | PDB header: solute-binding protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of troa-like periplasmic binding protein fepb from2 veillonella parvula |
| 32 | c5khlB_ | Alignment | not modelled | 100.0 | 16 | PDB header: transport protein Chain: B: PDB Molecule: hemin abc transporter, periplasmic hemin-binding protein PDBTitle: crystal structure of periplasmic heme binding protein hutb of vibrio2 cholerae |
| 33 | c2r79A_ | Alignment | not modelled | 100.0 | 22 | PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of a periplasmic heme binding protein from2 pseudomonas aeruginosa |
| 34 | c5joqA_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: lmo2184 protein; PDBTitle: crystal structure of an abc transporter substrate-binding protein from2 listeria monocytogenes egd-e |
| 35 | c4mdyA_ | Alignment | not modelled | 100.0 | 18 | PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of periplasmic solute binding protein from2 mycobacterium smegmatis str. mc2 155 |
| 36 | c5yscA_ | Alignment | not modelled | 100.0 | 17 | PDB header: transport protein Chain: A: PDB Molecule: vitamin b12-binding protein; PDBTitle: crystal structure of periplasmic vitamin b12 binding protein btuf of2 vibrio cholerae |
| 37 | c4inpA_ | Alignment | not modelled | 100.0 | 10 | PDB header: transport protein Chain: A: PDB Molecule: iron (iii) abc transporter, periplasmic iron-binding PDBTitle: the crystal structure of helicobacter pylori ceue (hp1561) with ni(ii)2 bound |
| 38 | c4m7oA_ | Alignment | not modelled | 100.0 | 14 | PDB header: iron binding protein Chain: A: PDB Molecule: iron-binding protein; PDBTitle: the crystal structure of a possible an iron-binding (periplasmic2 solute-binding) protein from staphylococcus epidermidis atcc 12228. |
| 39 | c3mwgA_ | Alignment | not modelled | 100.0 | 22 | PDB header: transport protein Chain: A: PDB Molecule: iron-regulated abc transporter siderophore-binding protein PDBTitle: crystal structure of staphylococcus aureus sira |
| 40 | c3md9A_ | Alignment | not modelled | 100.0 | 19 | PDB header: transport protein Chain: A: PDB Molecule: hemin-binding periplasmic protein hmut; PDBTitle: structure of apo form of a periplasmic heme binding protein |
| 41 | c2x4lA_ | Alignment | not modelled | 100.0 | 13 | PDB header: transport Chain: A: PDB Molecule: ferric-siderophore receptor protein; PDBTitle: crystal structure of dese, a ferric-siderophore receptor protein from2 streptomyces coelicolor |
| 42 | c2r7aC_ | Alignment | not modelled | 100.0 | 19 | PDB header: transport protein Chain: C: PDB Molecule: bacterial heme binding protein; PDBTitle: crystal structure of a periplasmic heme binding protein from shigella2 dysenteriae |
| 43 | c5b58T_ | Alignment | not modelled | 100.0 | 22 | PDB header: metal binding protein Chain: T: PDB Molecule: putative hemin transport system, substrate-binding protein; PDBTitle: inward-facing conformation of abc heme importer bhuuv in complex with2 periplasmic heme binding protein bhut from burkholderia cenocepacia |
| 44 | c2q8pA_ | Alignment | not modelled | 100.0 | 13 | PDB header: metal transport Chain: A: PDB Molecule: iron-regulated surface determinant e; PDBTitle: crystal structure of selenomethionine labelled s. aureus isde2 complexed with heme |
| 45 | d1esza_ | Alignment | not modelled | 100.0 | 19 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Periplasmic ferric siderophore binding protein FhuD |
| 46 | c5ggxD_ | Alignment | not modelled | 100.0 | 21 | PDB header: transport protein Chain: D: PDB Molecule: iron(iii) abc transporter, periplasmic iron-compound- PDBTitle: crystal structure of fe3+ - desferal bound siderophore binding protein2 fhud from vibrio cholerae |
| 47 | c3g9qA_ | Alignment | not modelled | 100.0 | 16 | PDB header: transport protein Chain: A: PDB Molecule: ferrichrome-binding protein; PDBTitle: crystal structure of the fhud fold-family bsu3320, a periplasmic2 binding protein component of a fep/fec-like ferrichrome abc3 transporter from bacillus subtilis. northeast structural genomics4 consortium target sr577a |
| 48 | d2etva1 | Alignment | not modelled | 100.0 | 11 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TM0189-like |
| 49 | d1n2za_ | Alignment | not modelled | 100.0 | 15 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like |
| 50 | c5n6yD_ | Alignment | not modelled | 93.7 | 11 | PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase vanadium-iron protein alpha chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase |
| 51 | c3aerC_ | Alignment | not modelled | 92.7 | 12 | PDB header: oxidoreductase Chain: C: PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark |
| | | | | | | PDB header: oxidoreductase Chain: C: PDB Molecule: light-independent protochlorophyllide |

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|----|-------------------------|-----------|--------------|------|----|--|
| 52 | c2ynmC_ | Alignment | not modelled | 92.7 | 11 | reductase subunit n; PDBTitle: structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a |
| 53 | d1m1na_ | Alignment | not modelled | 90.9 | 9 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein |
| 54 | d1qh8a_ | Alignment | not modelled | 89.4 | 14 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein |
| 55 | c3pdiG_ | Alignment | not modelled | 82.2 | 13 | PDB header: protein binding Chain: G: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nife; PDBTitle: precursor bound nifen |
| 56 | d1qh8b_ | Alignment | not modelled | 77.9 | 16 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein |
| 57 | c2ynmD_ | Alignment | not modelled | 72.2 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a |
| 58 | d1m1nb_ | Alignment | not modelled | 66.6 | 15 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein |
| 59 | c4rvqA_ | Alignment | not modelled | 60.5 | 14 | PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp |
| 60 | c5kojD_ | Alignment | not modelled | 58.4 | 18 | PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase femo beta subunit protein nifk; PDBTitle: nitrogenase mofep protein in the ids oxidized state |
| 61 | d1miob_ | Alignment | not modelled | 57.7 | 13 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein |
| 62 | c3aerB_ | Alignment | not modelled | 56.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark |
| 63 | d1mioa_ | Alignment | not modelled | 53.1 | 6 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein |
| 64 | c5jm0A_ | Alignment | not modelled | 47.3 | 9 | PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase,alpha-mannosidase,alpha-mannosidase; PDBTitle: structure of the s. cerevisiae alpha-mannosidase 1 |
| 65 | c5vytD_ | Alignment | not modelled | 47.1 | 15 | PDB header: transferase Chain: D: PDB Molecule: gdp-mannose 4,6-dehydratase / gdp-4-amino-4,6-dideoxy-d- PDBTitle: crystal structure of the wbkc n-formyltransferase (f142a variant) from2 brucella melitensis |
| 66 | c3ndjA_ | Alignment | not modelled | 45.4 | 15 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product |
| 67 | d1q3qa2 | Alignment | not modelled | 43.3 | 16 | Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain |
| 68 | c3pdiB_ | Alignment | not modelled | 36.4 | 10 | PDB header: protein binding Chain: B: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nifn; PDBTitle: precursor bound nifen |
| 69 | c2r8rB_ | Alignment | not modelled | 35.9 | 28 | PDB header: transferase Chain: B: PDB Molecule: sensor protein; PDBTitle: crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000 |
| 70 | d1gmla_ | Alignment | not modelled | 35.8 | 18 | Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain |
| 71 | c3woaA_ | Alignment | not modelled | 35.4 | 13 | PDB header: dna binding protein, sugar binding prote Chain: A: PDB Molecule: repressor protein ci, maltose-binding periplasmic protein; PDBTitle: crystal structure of lambda repressor (1-45) fused with maltose-2 binding protein |
| 72 | d1assa_ | Alignment | not modelled | 31.5 | 16 | Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain |
| 73 | d1a6db2 | Alignment | not modelled | 30.1 | 10 | Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain |
| 74 | d7reqa2 | Alignment | not modelled | 30.0 | 13 | Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain |
| 75 | c2xdqA_ | Alignment | not modelled | 26.9 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: dark operative protochlorophyllide oxidoreductase (chl-chlb)2 complex Fold: Aminoacid dehydrogenase-like, N-terminal domain |

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|----|-------------------------|-----------|--------------|------|----|---|
| 76 | d1edza2 | Alignment | not modelled | 22.0 | 7 | Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase |
| 77 | c5ghrA | Alignment | not modelled | 21.9 | 15 | PDB header: dna binding protein/replication Chain: A: PDB Molecule: ssdna-specific exonuclease; PDBTitle: dna replication protein |
| 78 | d1a9xb2 | Alignment | not modelled | 21.8 | 26 | Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT) |
| 79 | d1ccwa | Alignment | not modelled | 20.2 | 16 | Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain |
| 80 | d1a4ia2 | Alignment | not modelled | 18.4 | 9 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase |
| 81 | c4hh3C | Alignment | not modelled | 18.0 | 12 | PDB header: flavoprotein/transcription Chain: C: PDB Molecule: appa protein; PDBTitle: structure of the appa-ppsr2 core complex from rb. sphaeroides |
| 82 | c5ghrC | Alignment | not modelled | 17.6 | 16 | PDB header: dna binding protein/replication Chain: C: PDB Molecule: ssdna-specific exonuclease; PDBTitle: dna replication protein |
| 83 | c6aqeB | Alignment | not modelled | 15.8 | 17 | PDB header: transferase Chain: B: PDB Molecule: molecule a; PDBTitle: crystal structure of ppk2 in complex with mg atp |
| 84 | c5kzoA | Alignment | not modelled | 15.6 | 44 | PDB header: transcription Chain: A: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: notch1 transmembrane and associated juxtamembrane segment |
| 85 | c1a4iB | Alignment | not modelled | 15.5 | 9 | PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase |
| 86 | c6dspB | Alignment | not modelled | 14.7 | 12 | PDB header: signaling protein Chain: B: PDB Molecule: autoinducer 2-binding protein lsrb; PDBTitle: lsrb from clostridium saccharobutylicum in complex with ai-2 |
| 87 | c5n6yE | Alignment | not modelled | 14.3 | 9 | PDB header: oxidoreductase Chain: E: PDB Molecule: nitrogenase vanadium-iron protein beta chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase |
| 88 | d1q7ea | Alignment | not modelled | 13.7 | 11 | Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF) |
| 89 | c5o4jC | Alignment | not modelled | 13.5 | 19 | PDB header: transferase Chain: C: PDB Molecule: hcg; PDBTitle: hcg from methanococcus maripaludis cocrystallized with sah and2 pyridinol |
| 90 | c2gm2A | Alignment | not modelled | 13.1 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35 |
| 91 | c4yegA | Alignment | not modelled | 12.8 | 6 | PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase 2; PDBTitle: characterisation of polyphosphate kinase 2 from the intracellular2 pathogen francisella tularensis |
| 92 | c3czqA | Alignment | not modelled | 12.8 | 8 | PDB header: transferase Chain: A: PDB Molecule: putative polyphosphate kinase 2; PDBTitle: crystal structure of putative polyphosphate kinase 2 from2 sinorhizobium meliloti |
| 93 | c4oxqB | Alignment | not modelled | 11.4 | 10 | PDB header: metal binding protein Chain: B: PDB Molecule: manganese abc transporter, periplasmic-binding protein PDBTitle: structure of staphylococcus pseudintermedius metal-binding protein2 sita in complex with zinc |
| 94 | c4u7pA | Alignment | not modelled | 11.3 | 20 | PDB header: transferase/transferase regulator Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: crystal structure of dnmt3a-dnmt3l complex |
| 95 | c4k40B | Alignment | not modelled | 11.1 | 31 | PDB header: hydrolase Chain: B: PDB Molecule: gdsl-like lipase/acylhydrolase family protein; PDBTitle: peptidoglycan o-acetylerase in action, 0 min |
| 96 | c5d5oE | Alignment | not modelled | 11.0 | 34 | PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein mj0489; PDBTitle: hcg from methanocaldococcus jannaschii |
| 97 | c2z4dA | Alignment | not modelled | 10.9 | 20 | PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn13; PDBTitle: nmr structures of yeast proteasome component rpn13 |
| 98 | c3dcjA | Alignment | not modelled | 10.8 | 24 | PDB header: transferase Chain: A: PDB Molecule: probable 5'-phosphoribosylglycinamide formyltransferase PDBTitle: crystal structure of glycinamide formyltransferase (purn) from2 mycobacterium tuberculosis in complex with 5-methyl-5,6,7,8-3 tetrahydrofolic acid derivative |
| 99 | c3obiC | Alignment | not modelled | 10.4 | 19 | PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodospseudomonas palustris cga009 at 1.95 a resolution |