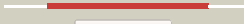



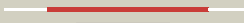












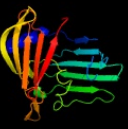



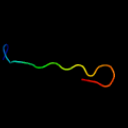


Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2945c_(lppX)_3290634_3291335 |
| Date | Thu Aug 8 16:20:10 BST 2019 |
| Unique Job ID | 9a24cbbb8eb3ff28 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d2byoa1 |  Alignment |  | 100.0 | 93 | Fold: LoIA-like prokaryotic lipoproteins and lipoprotein localization factors Superfamily: Prokaryotic lipoproteins and lipoprotein localization factors Family: LppX-like |
| 2 | c3mhaB |  Alignment |  | 100.0 | 32 | PDB header: lipid binding protein Chain: B: PDB Molecule: lipoprotein lprg; PDBTitle: crystal structure of lprg from mycobacterium tuberculosis bound to pim |
| 3 | c4qa8A |  Alignment |  | 100.0 | 31 | PDB header: lipid transport Chain: A: PDB Molecule: putative lipoprotein lprf; PDBTitle: crystal structure of lprf from mycobacterium bovis |
| 4 | c3buuB |  Alignment |  | 97.8 | 15 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized lola superfamily protein ne2245; PDBTitle: crystal structure of lola superfamily protein ne2245 from2 nitrosomonas europaea |
| 5 | c4mxtA |  Alignment |  | 97.1 | 14 | PDB header: protein transport Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an outer-membrane lipoprotein carrier protein2 (bacuni_04723) from bacteroides uniformis atcc 8492 at 1.40 a3 resolution |
| 6 | c6in8A |  Alignment |  | 96.2 | 9 | PDB header: membrane protein Chain: A: PDB Molecule: sigma factor alga regulatory protein mucb; PDBTitle: crystal structure of mucb |
| 7 | c2v43A |  Alignment |  | 94.2 | 15 | PDB header: regulator Chain: A: PDB Molecule: sigma-e factor regulatory protein rseb; PDBTitle: crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli |
| 8 | c4z48B |  Alignment |  | 90.1 | 22 | PDB header: structural biology, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf1329 family protein (despig_00262) from2 desulfovibrio piger atcc 29098 at 1.75 a resolution |
| 9 | c3bk5A |  Alignment |  | 82.7 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative outer membrane lipoprotein-sorting protein; PDBTitle: crystal structure of putative outer membrane lipoprotein-sorting2 protein domain from vibrio parahaemolyticus |
| 10 | c3woaA |  Alignment |  | 76.5 | 7 | 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 |
| 11 | c4mjsQ |  Alignment |  | 49.3 | 25 | PDB header: transferase/protein binding Chain: Q: PDB Molecule: protein kinase c zeta type; PDBTitle: crystal structure of a pb1 complex |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c2w7qB_ | Alignment | | 45.9 | 10 | PDB header: protein transport Chain: B: PDB Molecule: outer-membrane lipoprotein carrier protein; PDBTitle: structure of pseudomonas aeruginosa lola |
| 13 | c6mitC_ | Alignment | | 21.0 | 30 | PDB header: lipid transport Chain: C: PDB Molecule: lipopolysaccharide export system protein lptc; PDBTitle: lptbfgc from enterobacter cloacae |
| 14 | c5b3zB_ | Alignment | | 16.3 | 15 | PDB header: isomerase,sugar binding protein Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase nima-interacting 1, PDBTitle: crystal structure of hpin1 ww domain (5-39) fused with maltose-binding2 protein |
| 15 | c5az3A_ | Alignment | | 16.0 | 15 | PDB header: transport protein Chain: A: PDB Molecule: abc-type transporter, periplasmic component; PDBTitle: crystal structure of heme binding protein hmut |
| 16 | c3p8dB_ | Alignment | | 15.0 | 9 | PDB header: protein binding Chain: B: PDB Molecule: medulloblastoma antigen mu-mb-50.72; PDBTitle: crystal structure of the second tudor domain of human phf20 (homodimer2 form) |
| 17 | c2ldmA_ | Alignment | | 14.5 | 9 | PDB header: transcription/protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of human phf20 tudor2 domain bound to a p53 segment2 containing a dimethyllysine analog p53k370me2 |
| 18 | c4zv4C_ | Alignment | | 12.9 | 44 | PDB header: translation Chain: C: PDB Molecule: tse6; PDBTitle: structure of tse6 in complex with ef-tu |
| 19 | d2hqxa1 | Alignment | | 11.1 | 12 | Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain |
| 20 | c2hqxB_ | Alignment | | 11.1 | 12 | PDB header: transcription Chain: B: PDB Molecule: p100 co-activator tudor domain; PDBTitle: crystal structure of human p100 tudor domain conserved2 region |
| 21 | d1wmxa_ | Alignment | not modelled | 8.9 | 32 | Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 30 carbohydrate binding module, CBM30 (PKD repeat) |
| 22 | c5o60Y_ | Alignment | not modelled | 8.8 | 16 | PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l28; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis |
| 23 | c2equA_ | Alignment | not modelled | 7.9 | 6 | PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1 |
| 24 | c6gwjD_ | Alignment | not modelled | 7.6 | 19 | PDB header: rna binding protein Chain: D: PDB Molecule: ekc/keops complex subunit gon7; PDBTitle: protein complex |
| 25 | c2e76D_ | Alignment | not modelled | 7.5 | 4 | PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus |
| 26 | c3qiiA_ | Alignment | not modelled | 6.9 | 9 | PDB header: transcription regulator Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 2 of human phd finger protein 20 |
| 27 | c2k9yB_ | Alignment | not modelled | 6.5 | 40 | PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0 |
| 28 | c2k9yA_ | Alignment | not modelled | 6.5 | 40 | PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0 |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|---|
| 29 | c1nbjA_ | Alignment | not modelled | 6.5 | 38 | PDB header: plant protein Chain: A: PDB Molecule: cycloviolacin o1; PDBTitle: high-resolution solution structure of cycloviolacin o1 |
| 30 | d1nbja_ | Alignment | not modelled | 6.5 | 38 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Cycloviolacin |
| 31 | d1r17a1 | Alignment | not modelled | 6.5 | 15 | Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Fibrinogen-binding domain |
| 32 | c2lojA_ | Alignment | not modelled | 6.2 | 25 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: solution nmr structure of tstm1273 from salmonella typhimurium lt2,2 nesg target stt322, csgid target idp01027 and omsp target tstm1273 |
| 33 | c1vb8A_ | Alignment | not modelled | 6.0 | 38 | PDB header: plant protein Chain: A: PDB Molecule: viola hederacea root peptide 1; PDBTitle: solution structure of vhr1, the first cyclotide from root2 tissue |
| 34 | d1vb8a_ | Alignment | not modelled | 6.0 | 38 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Cycloviolacin |
| 35 | c4e6nB_ | Alignment | not modelled | 5.9 | 25 | PDB header: protein binding Chain: B: PDB Molecule: methyltransferase type 12; PDBTitle: crystal structure of bacterial pnkp-c/hen1-n heterodimer |
| 36 | c2jraB_ | Alignment | not modelled | 5.4 | 15 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein rpa2121; PDBTitle: a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6 |
| 37 | c4q5wB_ | Alignment | not modelled | 5.4 | 15 | PDB header: transcription Chain: B: PDB Molecule: maternal protein tudor; PDBTitle: crystal structure of extended-tudor 9 of drosophila melanogaster |