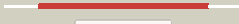



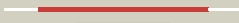
















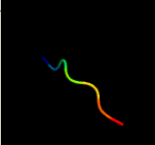
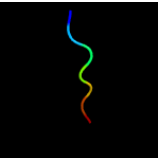

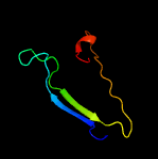
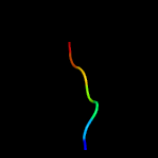
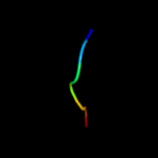
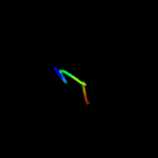


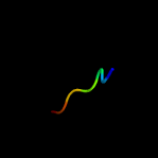


Phyre2

| | |
|------------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2204c (-)_2468939_2469295 |
| Date | Mon Aug 5 13:25:33 BST 2019 |
| Unique Job ID | 31fb4182cb504cc9 |

Detailed template
information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c2d2aA_ |  Alignment |  | 100.0 | 32 | PDB header: metal transport Chain: A: PDB Molecule: sufa protein; PDBTitle: crystal structure of escherichia coli sufa involved in biosynthesis of2 iron-sulfur clusters |
| 2 | c2apnA_ |  Alignment |  | 100.0 | 43 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hi1723; PDBTitle: hi1723 solution structure |
| 3 | c1x0gA_ |  Alignment |  | 100.0 | 32 | PDB header: metal binding protein Chain: A: PDB Molecule: isca; PDBTitle: crystal structure of isca with the [2fe-2s] cluster |
| 4 | c2k4zA_ |  Alignment |  | 100.0 | 23 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dsrr; PDBTitle: solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5 |
| 5 | d1s98a_ |  Alignment |  | 100.0 | 33 | Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain |
| 6 | d1nwba_ |  Alignment |  | 100.0 | 37 | Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain |
| 7 | d2p2ea1 |  Alignment |  | 98.1 | 16 | Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain |
| 8 | c2qgoA_ |  Alignment |  | 97.9 | 14 | PDB header: biosynthetic protein Chain: A: PDB Molecule: putative fe-s biosynthesis protein; PDBTitle: crystal structure of a putative fe-s biosynthesis protein from2 lactobacillus acidophilus |
| 9 | d1sp2a_ |  Alignment |  | 17.4 | 50 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 10 | c2x5hD_ |  Alignment |  | 16.2 | 18 | PDB header: viral protein Chain: D: PDB Molecule: orf 131; PDBTitle: crystal structure of the orf131 l26m l51m double mutant2 from sulfobolus islandicus rudivirus 1 |
| 11 | d1zfdA_ |  Alignment |  | 16.0 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|---|
| 12 | d1a1ia1 | Alignment |  | 13.9 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 13 | c2ab3A | Alignment |  | 13.8 | 83 | PDB header: rna binding protein Chain: A: PDB Molecule: znf29; PDBTitle: solution structures and characterization of hiv rre iib rna2 targeting zinc finger proteins |
| 14 | c6bzsA | Alignment |  | 13.7 | 13 | PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd1 in apo state |
| 15 | d1aaya1 | Alignment |  | 13.3 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 16 | d1a1ga1 | Alignment |  | 12.9 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 17 | d1ubdc3 | Alignment |  | 12.8 | 43 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 18 | c1gxsC | Alignment |  | 12.6 | 19 | PDB header: lyase Chain: C: PDB Molecule: p-(s)-hydroxymandelonitrile lyase chain a; PDBTitle: crystal structure of hydroxynitrile lyase from sorghum2 bicolor in complex with inhibitor benzoic acid: a novel3 cyanogenic enzyme |
| 19 | d1u86a1 | Alignment |  | 12.3 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 20 | d1a1ha1 | Alignment |  | 12.2 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 21 | c4imhA | Alignment | not modelled | 12.1 | 20 | PDB header: metal transport, transport protein Chain: A: PDB Molecule: hemin degrading factor; PDBTitle: crystal structure of cytoplasmic heme binding protein, phus, from2 pseudomonas aeruginosa |
| 22 | d2hq2a1 | Alignment | not modelled | 12.0 | 23 | Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/ChuS-like |
| 23 | d1f2ig1 | Alignment | not modelled | 11.6 | 38 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 24 | d1tf3a2 | Alignment | not modelled | 11.1 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 25 | c2kvfA | Alignment | not modelled | 11.1 | 30 | PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 32; PDBTitle: structure of the three-cys2his2 domain of mouse testis zinc2 finger protein |
| 26 | d2glia3 | Alignment | not modelled | 10.8 | 21 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 27 | c4z4pA | Alignment | not modelled | 10.4 | 32 | PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase 2d; PDBTitle: structure of the ml14 set domain |
| 28 | d2j0pa1 | Alignment | not modelled | 10.1 | 20 | Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/ChuS-like |
| | | | | | | PDB header: hydrolase |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c4ox3A | Alignment | not modelled | 10.0 | 18 | Chain: A: PDB Molecule: putative carboxypeptidase yodj; PDBTitle: structure of the ldcb ld-carboxypeptidase reveals the molecular basis2 of peptidoglycan recognition |
| 30 | d2cy5a1 | Alignment | not modelled | 9.9 | 22 | Fold: PH domain-like barrel Superfamily: PH domain-like Family: Phosphotyrosine-binding domain (PTB) |
| 31 | c3tsjA | Alignment | not modelled | 9.8 | 18 | PDB header: allergen, oxidoreductase Chain: A: PDB Molecule: pollen allergen phi p 4; PDBTitle: crystal structure of phi p 4, a grass pollen allergen with glucose2 dehydrogenase activity |
| 32 | d2yt9a1 | Alignment | not modelled | 9.6 | 43 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 33 | c6n2gC | Alignment | not modelled | 9.1 | 10 | PDB header: chaperone Chain: C: PDB Molecule: nucleosome assembly protein; PDBTitle: crystal structure of caenorhabditis elegans nap1 |
| 34 | d1ncsa | Alignment | not modelled | 8.7 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 35 | d2dlka2 | Alignment | not modelled | 8.5 | 86 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 36 | c3qkgA | Alignment | not modelled | 8.4 | 15 | PDB header: immune system Chain: A: PDB Molecule: protein ambp; PDBTitle: crystal structure of alpha-1-microglobulin at 2.3 a resolution |
| 37 | c2kdxA | Alignment | not modelled | 8.4 | 18 | PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein |
| 38 | d1x6ea2 | Alignment | not modelled | 8.1 | 50 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 39 | c5b3hC | Alignment | not modelled | 8.0 | 50 | PDB header: transcription Chain: C: PDB Molecule: zinc finger protein jackdaw; PDBTitle: the crystal structure of the jackdaw/idd10 bound to the heterodimeric2 shr-scr complex |
| 40 | c3pm7A | Alignment | not modelled | 8.0 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ef_3132 protein from enterococcus faecalis at the2 resolution 2a, northeast structural genomics consortium target efr184 |
| 41 | d2a2ua | Alignment | not modelled | 8.0 | 15 | Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like |
| 42 | c2nq2C | Alignment | not modelled | 7.8 | 11 | PDB header: metal transport Chain: C: PDB Molecule: hypothetical abc transporter atp-binding protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter. |
| 43 | c5zet2 | Alignment | not modelled | 7.7 | 71 | PDB header: ribosome Chain: 2: PDB Molecule: 50s ribosomal protein l31; PDBTitle: m. smegmatis p/p state 50s ribosomal subunit |
| 44 | c1bcrA | Alignment | not modelled | 7.6 | 21 | PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine carboxypeptidase ii; PDBTitle: complex of the wheat serine carboxypeptidase, cpdw-ii, with the2 microbial peptide aldehyde inhibitor, antipain, and arginine at room3 temperature |
| 45 | c4az3A | Alignment | not modelled | 7.5 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: lysosomal protective protein 32 kda chain; PDBTitle: crystal structure of cathepsin a, complexed with 15a |
| 46 | c2wh44 | Alignment | not modelled | 7.5 | 60 | PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome |
| 47 | c5gplA | Alignment | not modelled | 7.3 | 19 | PDB header: chaperone Chain: A: PDB Molecule: putative nucleosome assembly protein c36b7.08c; PDBTitle: crystal structure of ccp1 |
| 48 | d1vsra | Alignment | not modelled | 7.2 | 10 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease |
| 49 | c2l3aA | Alignment | not modelled | 7.1 | 7 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of homodimer protein sp_0782 (7-79) from2 streptococcus pneumoniae northeast structural genomics consortium3 target spr104 . |
| 50 | c1znmA | Alignment | not modelled | 7.1 | 43 | PDB header: zinc finger Chain: A: PDB Molecule: yy1; PDBTitle: a zinc finger with an artificial beta-turn, original sequence taken2 from the third zinc finger domain of the human transcriptional3 repressor protein yy1 (ying and yang 1, a delta transcription4 factor), nmr, 34 structures |
| 51 | c3a44D | Alignment | not modelled | 7.0 | 17 | PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form |
| 52 | c3c3jA | Alignment | not modelled | 6.8 | 25 | PDB header: isomerase Chain: A: PDB Molecule: putative tagatose-6-phosphate ketose/aldose isomerase; PDBTitle: crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli |
| 53 | c3f1f4 | Alignment | not modelled | 6.8 | 60 | PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: crystal structure of a translation termination complex formed with2 release factor rf2. this file contains the 50s subunit of |

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|----|-------------------------|-----------|--------------|-----|----|--|
| | | | | | | one 70s3 ribosome. the entire crystal structure contains two 70s ribosomes as4 described in remark 400. |
| 54 | c5ghrA_ | Alignment | not modelled | 6.8 | 23 | PDB header: dna binding protein/replication Chain: A: PDB Molecule: ssdna-specific exonuclease; PDBTitle: dna replication protein |
| 55 | d1jzua_ | Alignment | not modelled | 6.7 | 18 | Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like |
| 56 | c2yuja_ | Alignment | not modelled | 6.7 | 20 | PDB header: protein binding Chain: A: PDB Molecule: ubiquitin fusion degradation 1-like; PDBTitle: solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1 |
| 57 | c1va1A_ | Alignment | not modelled | 6.7 | 29 | PDB header: transcription Chain: A: PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1) |
| 58 | c4lrvL_ | Alignment | not modelled | 6.6 | 21 | PDB header: dna binding protein Chain: L: PDB Molecule: dna sulfur modification protein dnde; PDBTitle: crystal structure of dnde from escherichia coli b7a involved in dna2_phosphorothioation modification |
| 59 | c5o60g_ | Alignment | not modelled | 6.6 | 71 | PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis |
| 60 | c3h5ja_ | Alignment | not modelled | 6.5 | 40 | PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis |
| 61 | c6avjB_ | Alignment | not modelled | 6.3 | 15 | PDB header: metal binding protein Chain: B: PDB Molecule: cdgsh iron-sulfur domain-containing protein 3, PDBTitle: crystal structure of human mitochondrial inner neet protein (mint)2 /cisd3 |
| 62 | c3a0rA_ | Alignment | not modelled | 6.2 | 14 | PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360) |
| 63 | c3q3wB_ | Alignment | not modelled | 6.2 | 40 | PDB header: transferase Chain: B: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: isopropylmalate isomerase small subunit from campylobacter jejuni. |
| 64 | c2hcuA_ | Alignment | not modelled | 6.2 | 40 | PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: crystal structure of smu.1381 (or leud) from streptococcus mutans |
| 65 | c1t2ya_ | Alignment | not modelled | 6.0 | 36 | PDB header: metal binding protein Chain: A: PDB Molecule: metallothionein; PDBTitle: nmr solution structure of the protein part of cu6-2 neurospora crassa mt |
| 66 | d2cota1 | Alignment | not modelled | 6.0 | 50 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 67 | d1r44a_ | Alignment | not modelled | 5.9 | 12 | Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanX-like |
| 68 | d1znda1 | Alignment | not modelled | 5.9 | 12 | Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like |
| 69 | c3odpA_ | Alignment | not modelled | 5.8 | 25 | PDB header: isomerase Chain: A: PDB Molecule: putative tagatose-6-phosphate ketose/aldose isomerase; PDBTitle: crystal structure of a putative tagatose-6-phosphate ketose/aldose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution |
| 70 | d1gq2a2 | Alignment | not modelled | 5.8 | 14 | Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain |
| 71 | c2j034_ | Alignment | not modelled | 5.6 | 43 | PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii. |
| 72 | d2j0141 | Alignment | not modelled | 5.6 | 43 | Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p |
| 73 | d2h85a2 | Alignment | not modelled | 5.6 | 29 | Fold: EndoU-like Superfamily: EndoU-like Family: Nsp15 C-terminal domain-like |
| 74 | d1vmha_ | Alignment | not modelled | 5.5 | 14 | Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like |
| 75 | d1wmia1 | Alignment | not modelled | 5.5 | 20 | Fold: RelE-like Superfamily: RelE-like Family: RelE-like |
| 76 | c6b3qa_ | Alignment | not modelled | 5.5 | 75 | PDB header: hydrolase/hormone Chain: A: PDB Molecule: insulin-degrading enzyme; PDBTitle: cryo-em structure of human insulin degrading enzyme in complex with2 insulin |
| 77 | c3hlza_ | Alignment | not modelled | 5.4 | 22 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bt_1490; PDBTitle: crystal structure of bt_1490 (np_810393.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.50 a resolution |
| | | | | | | Fold: alpha/beta-Hydrolases |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|---|
| 78 | d1ivya_ | Alignment | not modelled | 5.4 | 16 | Superfamily: alpha/beta-Hydrolases Family: Serine carboxypeptidase-like |
| 79 | c5hnmC_ | Alignment | not modelled | 5.4 | 16 | PDB header: hydrolase Chain: C: PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: crystal structure of vancomycin resistance d,d-pentapeptidase van2 e175a mutant from vanb-type resistance cassette in complex with3 zn(ii) |
| 80 | d2cota2 | Alignment | not modelled | 5.3 | 67 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 81 | c4f7uP_ | Alignment | not modelled | 5.3 | 11 | PDB header: splicing Chain: P: PDB Molecule: methylosome subunit picln; PDBTitle: the 6s snrnp assembly intermediate |
| 82 | c3vbaE_ | Alignment | not modelled | 5.3 | 60 | PDB header: lyase Chain: E: PDB Molecule: isopropylmalate/citramalate isomerase small subunit; PDBTitle: crystal structure of methanogen 3-isopropylmalate isomerase small2 subunit |
| 83 | d1jj7a_ | Alignment | not modelled | 5.3 | 16 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 84 | d2ayua1 | Alignment | not modelled | 5.2 | 16 | Fold: NAP-like Superfamily: NAP-like Family: NAP-like |
| 85 | c2ayuA_ | Alignment | not modelled | 5.2 | 16 | PDB header: chaperone Chain: A: PDB Molecule: nucleosome assembly protein; PDBTitle: the structure of nucleosome assembly protein suggests a mechanism for2 histone binding and shuttling |
| 86 | d2jn4a1 | Alignment | not modelled | 5.2 | 12 | Fold: NifT/FixU barrel-like Superfamily: NifT/FixU-like Family: NifT/FixU |
| 87 | c2jn4A_ | Alignment | not modelled | 5.2 | 12 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein fixu, nift; PDBTitle: solution nmr structure of protein rp4601 from rhodospseudomonas2 palustris. northeast structural genomics consortium target rpt2;3 ontario center for structural proteomics target rp4601. |
| 88 | d1p4xa1 | Alignment | not modelled | 5.2 | 11 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 89 | c5vbnB_ | Alignment | not modelled | 5.1 | 19 | PDB header: transferase Chain: B: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: crystal structure of human dna polymerase epsilon b-subunit in complex2 with c-terminal domain of catalytic subunit |