

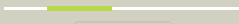


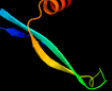

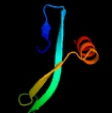

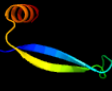

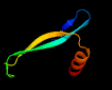

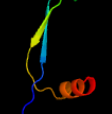



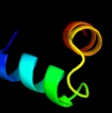

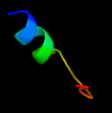




Phyre2

| | |
|------------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2256c (-)_2529351_2529884 |
| Date | Mon Aug 5 13:25:39 BST 2019 |
| Unique Job ID | daf675633bb9b93c |

Detailed template
information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c4el8A_ |  Alignment |  | 67.2 | 36 | PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 48; PDBTitle: the unliganded structure of c.cescii cela gh48 module |
| 2 | d1l1ya_ |  Alignment |  | 62.8 | 29 | Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain |
| 3 | c1l2aD_ |  Alignment |  | 62.8 | 29 | PDB header: hydrolase Chain: D: PDB Molecule: cellobiohydrolase; PDBTitle: the crystal structure and catalytic mechanism of 2 cellobiohydrolase cels, the major enzymatic component of 3 the clostridium thermocellum cellulosome |
| 4 | d1g9ga_ |  Alignment |  | 59.2 | 24 | Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain |
| 5 | c4kkkA_ |  Alignment |  | 49.4 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: exoglucanase s; PDBTitle: complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose |
| 6 | c4fusA_ |  Alignment |  | 45.1 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: rtx toxins and related ca2+-binding protein; PDBTitle: the x-ray structure of hahella chejuensis family 48 glycosyl hydrolase |
| 7 | c5bv9A_ |  Alignment |  | 45.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of bacillus pumilus gh48 in complex with cellobiose |
| 8 | c4jiiA_ |  Alignment |  | 44.3 | 29 | PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of t. fusca gh48 d224n mutant |
| 9 | d1wglA_ |  Alignment |  | 22.9 | 15 | Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain |
| 10 | d1isia_ |  Alignment |  | 21.6 | 44 | Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: ADP ribosyl cyclase-like |
| 11 | c5vztB_ |  Alignment |  | 21.2 | 23 | PDB header: cell cycle Chain: B: PDB Molecule: f-box only protein 31; PDBTitle: crystal structure of the skp1-fbxo31 complex |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c2wjyA_ | Alignment | | 20.2 | 46 | PDB header: hydrolase Chain: A; PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form |
| 13 | c2eg9B_ | Alignment | | 19.8 | 38 | PDB header: hydrolase Chain: B; PDB Molecule: adp-ribosyl cyclase 1; PDBTitle: crystal structure of the truncated extracellular domain of2 mouse cd38 |
| 14 | d1r12a_ | Alignment | | 18.2 | 31 | Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: ADP ribosyl cyclase-like |
| 15 | c3ideD_ | Alignment | | 17.5 | 17 | PDB header: virus like particle Chain: D; PDB Molecule: capsid protein vp2; PDBTitle: structure of ipnv subviral particle |
| 16 | c2df7H_ | Alignment | | 16.6 | 21 | PDB header: virus like particle Chain: H; PDB Molecule: structural polyprotein vp2; PDBTitle: crystal structure of infectious bursal disease virus vp2 subviral2 particle |
| 17 | d2df7a1 | Alignment | | 16.0 | 21 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Birnaviridae-like VP |
| 18 | c2i5gB_ | Alignment | | 15.2 | 36 | PDB header: hydrolase Chain: B; PDB Molecule: amidohydrolase; PDBTitle: crystal strcuture of amidohydrolase from pseudomonas aeruginosa |
| 19 | c2xz1A_ | Alignment | | 14.8 | 50 | PDB header: hydrolase/rna Chain: A; PDB Molecule: atp-dependent helicase nam7; PDBTitle: upf1-rna complex |
| 20 | c5ijpB_ | Alignment | | 14.7 | 26 | PDB header: ligase Chain: B; PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6 |
| 21 | c3b40A_ | Alignment | not modelled | 14.7 | 29 | PDB header: hydrolase Chain: A; PDB Molecule: probable dipeptidase; PDBTitle: crystal structure of the probable dipeptidase pvdm from pseudomonas2 aeruginosa |
| 22 | d1yl7a2 | Alignment | not modelled | 14.2 | 19 | Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like |
| 23 | d2ef1a1 | Alignment | not modelled | 14.2 | 31 | Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: ADP ribosyl cyclase-like |
| 24 | c2jy5A_ | Alignment | not modelled | 14.2 | 11 | PDB header: signaling protein Chain: A; PDB Molecule: ubiquilin-1; PDBTitle: nmr structure of ubiquilin 1 uba domain |
| 25 | c5bniA_ | Alignment | not modelled | 14.1 | 31 | PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: porcine cd38 complexed with complexed with a covalent intermediate,2 ribo-f-ribose-5'-phosphate |
| 26 | c1rqra_ | Alignment | not modelled | 13.3 | 31 | PDB header: transferase Chain: A; PDB Molecule: 5'-fluoro-5'-deoxyadenosine synthase; PDBTitle: crystal structure and mechanism of a bacterial fluorinating enzyme,2 product complex |
| 27 | d1veja1 | Alignment | not modelled | 13.3 | 12 | Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain |
| 28 | d1mw7a_ | Alignment | not modelled | 13.2 | 16 | Fold: YebC-like Superfamily: YebC-like Family: YebC-like |
| 29 | c3rbyB_ | Alignment | not modelled | 13.1 | 18 | PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein ylr301w; PDBTitle: crystal structure of uncharacterized protein ylr301w |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | from2 saccharomyces cerevisiae |
| 30 | c6a7vU_ | Alignment | not modelled | 13.0 | 20 | PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex |
| 31 | c3ghhA_ | Alignment | not modelled | 12.7 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: ecto-nad+ glycohydrolase (cd38 molecule); PDBTitle: structural insights into the catalytic mechanism of cd38: evidence for2 a conformationally flexible covalent enzyme-substrate complex. |
| 32 | c5mrvB_ | Alignment | not modelled | 12.3 | 23 | PDB header: hydrolase Chain: B: PDB Molecule: carboxypeptidase o; PDBTitle: crystal structure of human carboxypeptidase o in complex with nvci |
| 33 | d1lfpA_ | Alignment | not modelled | 12.2 | 18 | Fold: YebC-like Superfamily: YebC-like Family: YebC-like |
| 34 | c1s21A_ | Alignment | not modelled | 11.5 | 29 | PDB header: chaperone Chain: A: PDB Molecule: orf2; PDBTitle: crystal structure of avrpphf orf2, a type iii effector from p.2 syringae |
| 35 | d1s21a_ | Alignment | not modelled | 11.5 | 29 | Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: AvrPphF ORF2, a type III effector |
| 36 | c5fu4B_ | Alignment | not modelled | 11.5 | 38 | PDB header: sugar binding protein Chain: B: PDB Molecule: cbm74-rfgh5; PDBTitle: the complexity of the ruminococcus flavefaciens cellulosome reflects2 an expansion in glycan recognition |
| 37 | c4gr5B_ | Alignment | not modelled | 11.3 | 30 | PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp |
| 38 | c3lu2B_ | Alignment | not modelled | 11.3 | 27 | PDB header: hydrolase Chain: B: PDB Molecule: lmo2462 protein; PDBTitle: structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase |
| 39 | d1j5pa3 | Alignment | not modelled | 11.2 | 7 | Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like |
| 40 | d2imha1 | Alignment | not modelled | 10.8 | 23 | Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: SPO2555-like |
| 41 | d1zvpa2 | Alignment | not modelled | 10.7 | 11 | Fold: Ferredoxin-like Superfamily: ACT-like Family: VC0802-like |
| 42 | d1gff2_ | Alignment | not modelled | 10.4 | 24 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP |
| 43 | d2axpa1 | Alignment | not modelled | 10.1 | 35 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 44 | c5z2fA_ | Alignment | not modelled | 10.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: nadph/pda bound dihydrodipicolinate reductase from paenisporsarcina2 sp. tg-14 |
| 45 | d1vmaa1 | Alignment | not modelled | 9.9 | 17 | Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins |
| 46 | d1zhva2 | Alignment | not modelled | 9.7 | 11 | Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like |
| 47 | d1nera_ | Alignment | not modelled | 9.7 | 26 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 48 | c2ragB_ | Alignment | not modelled | 9.4 | 36 | PDB header: hydrolase Chain: B: PDB Molecule: dipeptidase; PDBTitle: crystal structure of aminohydrolase from caulobacter crescentus |
| 49 | c3fdgA_ | Alignment | not modelled | 9.0 | 36 | PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase ac. metallo peptidase. merops family m19; PDBTitle: the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19 |
| 50 | c5jipC_ | Alignment | not modelled | 8.8 | 26 | PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6 |
| 51 | d1m06g_ | Alignment | not modelled | 8.7 | 27 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP |
| 52 | c2dhyA_ | Alignment | not modelled | 8.5 | 12 | PDB header: immune system Chain: A: PDB Molecule: cue domain-containing protein 1; PDBTitle: solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1) |
| 53 | c3n70F_ | Alignment | not modelled | 8.4 | 37 | PDB header: transport protein Chain: F: PDB Molecule: transport activator; PDBTitle: the crystal structure of the p-loop ntpase domain of the sigma-542 transport activator from e. coli to 2.8a |
| 54 | c3esmA_ | Alignment | not modelled | 8.1 | 20 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from nocardia2 farcinica reveals an immunoglobulin-like fold |
| | | | | | | Fold: DHS-like NAD/FAD-binding domain |

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|----|-------------------------|-----------|--------------|-----|----|---|
| 55 | d1j8fa_ | Alignment | not modelled | 7.6 | 35 | Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators |
| 56 | d1h41a2 | Alignment | not modelled | 7.6 | 17 | Fold: Zincin-like Superfamily: beta-N-acetylhexosaminidase-like domain Family: alpha-D-glucuronidase, N-terminal domain |
| 57 | c5ns5A_ | Alignment | not modelled | 7.5 | 36 | PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase glij; PDBTitle: cys-gly dipeptidase glij in complex with cu2+ and zn2+ |
| 58 | c2cwbA_ | Alignment | not modelled | 7.1 | 8 | PDB header: protein binding Chain: A: PDB Molecule: chimera of immunoglobulin g binding protein g PDBTitle: solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin |
| 59 | d1rqpa2 | Alignment | not modelled | 7.1 | 26 | Fold: Bacterial fluorinating enzyme, N-terminal domain Superfamily: Bacterial fluorinating enzyme, N-terminal domain Family: Bacterial fluorinating enzyme, N-terminal domain |
| 60 | d1t1ja_ | Alignment | not modelled | 6.9 | 20 | Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: Hypothetical protein PA1492 |
| 61 | c4yxpA_ | Alignment | not modelled | 6.9 | 13 | PDB header: viral protein Chain: A: PDB Molecule: mrna export factor; PDBTitle: the structure of the folded domain of the signature multifunctional2 protein icp27 from herpes simplex virus-1 reveals an intertwined3 dimer. |
| 62 | d2piaa2 | Alignment | not modelled | 6.4 | 21 | Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like |
| 63 | c5i2cA_ | Alignment | not modelled | 6.2 | 14 | PDB header: signaling protein Chain: A: PDB Molecule: gats-like protein 3; PDBTitle: arginine-bound castor1 from homo sapiens |
| 64 | c5ohgl_ | Alignment | not modelled | 6.2 | 40 | PDB header: lyase Chain: J: PDB Molecule: ribonuclease e; PDBTitle: enolase in complex with rnase e |
| 65 | d2bwba1 | Alignment | not modelled | 6.1 | 23 | Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain |
| 66 | c6ozvA_ | Alignment | not modelled | 6.1 | 33 | PDB header: biosynthetic protein Chain: A: PDB Molecule: txo1; PDBTitle: the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp |
| 67 | c3itcA_ | Alignment | not modelled | 5.9 | 50 | PDB header: hydrolase Chain: A: PDB Molecule: renal dipeptidase; PDBTitle: crystal structure of sco3058 with bound citrate and glycerol |
| 68 | d1wiva_ | Alignment | not modelled | 5.8 | 15 | Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain |
| 69 | d1twda_ | Alignment | not modelled | 5.6 | 22 | Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like |
| 70 | c2vsaA_ | Alignment | not modelled | 5.5 | 24 | PDB header: toxin Chain: A: PDB Molecule: mosquitocidal toxin; PDBTitle: structure and mode of action of a mosquitocidal holotoxin |
| 71 | d2ns0a1 | Alignment | not modelled | 5.4 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like |
| 72 | d1itua_ | Alignment | not modelled | 5.3 | 36 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Renal dipeptidase |
| 73 | c1zhvA_ | Alignment | not modelled | 5.3 | 11 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu0741; PDBTitle: x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8. |
| 74 | d1b7go1 | Alignment | not modelled | 5.2 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 75 | c2b44A_ | Alignment | not modelled | 5.1 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form |
| 76 | c5y7dA_ | Alignment | not modelled | 5.1 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: protein cxorf40a; PDBTitle: crystal structure of human endothelial-overexpressed lps associated2 factor 1 |