




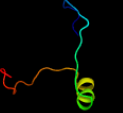

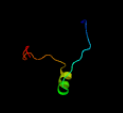

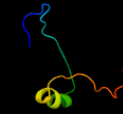

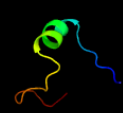
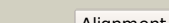

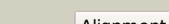


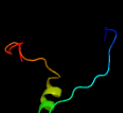
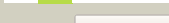


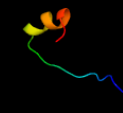



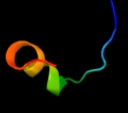

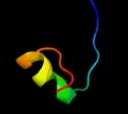
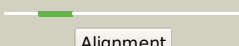
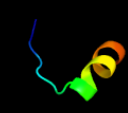
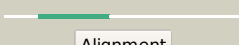
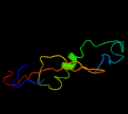
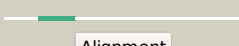
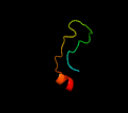






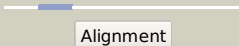



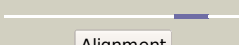





Phyre2

| | |
|------------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0059 (-)_63197_63889 |
| Date | Tue Jul 23 14:50:09 BST 2019 |
| Unique Job ID | 5a007523a0c69c00 |

Detailed template
information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | d1wfxa_ |  Alignment |  | 95.8 | 19 | Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: Tpt1/KptA |
| 2 | c6edeA_ |  Alignment |  | 95.7 | 19 | PDB header: transferase Chain: A: PDB Molecule: probable rna 2'-phosphotransferase; PDBTitle: trna 2'-phosphotransferase |
| 3 | d1gs0a2 |  Alignment |  | 90.4 | 23 | Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: Poly(ADP-ribose) polymerase, C-terminal domain |
| 4 | c2paxA_ |  Alignment |  | 87.8 | 22 | PDB header: transferase Chain: A: PDB Molecule: poly(adp-ribose) polymerase; PDBTitle: the catalytic fragment of poly(adp-ribose) polymerase2 complexed with 4-amino-1,8-naphthalimide |
| 5 | c1gs0B_ |  Alignment |  | 87.4 | 23 | PDB header: transferase Chain: B: PDB Molecule: poly (adp-ribose) polymerase-2; PDBTitle: crystal structure of the catalytic fragment of murine poly2 (adp-ribose) polymerase-2 |
| 6 | d2rd6a2 |  Alignment |  | 84.5 | 27 | Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: Poly(ADP-ribose) polymerase, C-terminal domain |
| 7 | c3c4hA_ |  Alignment |  | 81.5 | 24 | PDB header: transferase Chain: A: PDB Molecule: poly(adp-ribose) polymerase 3; PDBTitle: human poly(adp-ribose) polymerase 3, catalytic fragment in complex2 with an inhibitor dr2313 |
| 8 | c4dqyF_ |  Alignment |  | 81.4 | 22 | PDB header: transferase/dna Chain: F: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: structure of human parp-1 bound to a dna double strand break |
| 9 | d1efya2 |  Alignment |  | 79.8 | 22 | Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: Poly(ADP-ribose) polymerase, C-terminal domain |
| 10 | c2x5yA_ |  Alignment |  | 66.6 | 11 | PDB header: immune system Chain: A: PDB Molecule: zinc finger ccch-type antiviral protein 1; PDBTitle: human zc3hav1 (artd13), c-terminal domain |
| 11 | c3goyD_ |  Alignment |  | 62.8 | 22 | PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: poly [adp-ribose] polymerase 14; PDBTitle: crystal structure of human poly(adp-ribose) polymerase 14, catalytic2 fragment in complex with an inhibitor 3-aminobenzamide |

| | | | | | | |
|----|-------------------------|---|---|------|----|--|
| 12 | c3bjjA |  Alignment |  | 58.8 | 26 | PDB header: transferase Chain: A; PDB Molecule: poly(adp-ribose) polymerase 15; PDBTitle: crystal structure of human poly(adp-ribose) polymerase 15, catalytic2 fragment |
| 13 | c5ngoA |  Alignment |  | 58.3 | 16 | PDB header: plant protein Chain: A; PDB Molecule: inactive poly [adp-ribose] polymerase rcd1; PDBTitle: crystal structure of the parp domain of arabidopsis radical-induced2 cell death1 |
| 14 | c3hkvA |  Alignment |  | 55.2 | 27 | PDB header: transferase Chain: A; PDB Molecule: poly [adp-ribose] polymerase 10; PDBTitle: human poly(adp-ribose) polymerase 10, catalytic fragment in complex2 with an inhibitor 3-aminobenzamide |
| 15 | c2pqfF |  Alignment |  | 52.8 | 21 | PDB header: transferase Chain: F; PDB Molecule: poly [adp-ribose] polymerase 12; PDBTitle: human poly(adp-ribose) polymerase 12, catalytic fragment in complex2 with an inhibitor 3-aminobenzoic acid |
| 16 | c1s1lL |  Alignment |  | 46.8 | 19 | PDB header: ribosome Chain: L; PDB Molecule: 60s ribosomal protein l15-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1l, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h. |
| 17 | c3j39N |  Alignment |  | 41.9 | 31 | PDB header: ribosome Chain: N; PDB Molecule: 60s ribosomal protein l15; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins |
| 18 | d2o0qa1 |  Alignment |  | 35.6 | 11 | Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: CC0527-like |
| 19 | c3zf7Q |  Alignment |  | 31.0 | 31 | PDB header: ribosome Chain: Q; PDB Molecule: ribosomal protein l15; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 20 | c3mhkA |  Alignment |  | 27.6 | 23 | PDB header: transferase Chain: A; PDB Molecule: tankyrase-2; PDBTitle: human tankyrase 2 - catalytic parp domain in complex with 2-(2-2 pyridyl)-7,8-dihydro-5h-thiino[4,3-d]pyrimidin-4-ol |
| 21 | c6j7jA |  Alignment | not modelled | 20.3 | 22 | PDB header: transferase Chain: A; PDB Molecule: pseudomonas aeruginosa earp; PDBTitle: crystal structure of pseudomonas aeruginosa earp |
| 22 | d1vf5b |  Alignment | not modelled | 19.8 | 23 | Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 23 | d1lt3a |  Alignment | not modelled | 18.0 | 18 | Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: ADP-ribosylating toxins |
| 24 | d2a5db1 |  Alignment | not modelled | 17.3 | 12 | Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: ADP-ribosylating toxins |
| 25 | d1q90d |  Alignment | not modelled | 15.3 | 23 | Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 26 | c1tiiA |  Alignment | not modelled | 15.1 | 18 | PDB header: enterotoxin Chain: A; PDB Molecule: heat labile enterotoxin type iib; PDBTitle: escherichia coli heat labile enterotoxin type iib |
| 27 | c4z9dA |  Alignment | not modelled | 14.7 | 21 | PDB header: transferase Chain: A; PDB Molecule: pertussis toxin-like subunit arta; PDBTitle: ecplta |
| | |  | | | | Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 28 | d2e74b1 | Alignment | not modelled | 14.4 | 23 | Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 29 | c4n7vB | Alignment | not modelled | 14.1 | 28 | PDB header: cell cycle Chain: B: PDB Molecule: serine/threonine-protein kinase plk4; PDBTitle: crystal structure of human plk4 cryptic polo box (cpb) in complex with2 a cep152 n-terminal fragment |
| 30 | c5d0qC | Alignment | not modelled | 12.8 | 15 | PDB header: protein transport Chain: C: PDB Molecule: outer membrane protein assembly factor bamc; PDBTitle: bamacde complex, outer membrane beta-barrel assembly machinery (bam)2 complex |
| 31 | d1s5da | Alignment | not modelled | 12.5 | 18 | Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: ADP-ribosylating toxins |
| 32 | d1lvaa3 | Alignment | not modelled | 11.1 | 11 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB |
| 33 | c4qo6A | Alignment | not modelled | 9.9 | 15 | PDB header: structural protein Chain: A: PDB Molecule: adenylate cyclase-like protein; PDBTitle: structural studies of cdsd, a structural protein of the type iii2 secretion system (tts) of chlamydia trachomatis |
| 34 | c3cwbC | Alignment | not modelled | 9.7 | 24 | PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome b; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d |
| 35 | d1gmnbl | Alignment | not modelled | 9.6 | 31 | Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Hairpin loop containing domain |
| 36 | c3nffD | Alignment | not modelled | 9.2 | 14 | PDB header: transcription Chain: D: PDB Molecule: rna polymerase i subunit a34.5; PDBTitle: crystal structure of extended dimerization module of rna polymerase i2 subcomplex a49/a34.5 |
| 37 | d1ffki | Alignment | not modelled | 9.1 | 38 | Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e |
| 38 | c3cx5N | Alignment | not modelled | 8.8 | 19 | PDB header: oxidoreductase Chain: N: PDB Molecule: cytochrome b; PDBTitle: structure of complex iii with bound cytochrome c in reduced state and2 definition of a minimal core interface for electron transfer. |
| 39 | c1b8xA | Alignment | not modelled | 8.7 | 37 | PDB header: signal protein Chain: A: PDB Molecule: protein (aml-1b); PDBTitle: glutathione s-transferase fused with the nuclear matrix targeting2 signal of the transcription factor aml-1 |
| 40 | c2rf5A | Alignment | not modelled | 8.6 | 29 | PDB header: transferase Chain: A: PDB Molecule: tankyrase-1; PDBTitle: crystal structure of human tankyrase 1- catalytic parp domain |
| 41 | c4f0dB | Alignment | not modelled | 8.3 | 22 | PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: poly [adp-ribose] polymerase 16; PDBTitle: human artd15/parp16 in complex with 3-aminobenzamide |
| 42 | c3iz5P | Alignment | not modelled | 7.8 | 31 | PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l15 (l15e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 43 | c2qjkM | Alignment | not modelled | 7.7 | 14 | PDB header: electron transport Chain: M: PDB Molecule: cytochrome b; PDBTitle: crystal structure analysis of mutant rhodobacter2 sphaeroides bc1 with stigmatellin and antimycin |
| 44 | c3ecsD | Alignment | not modelled | 7.6 | 15 | PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha |
| 45 | c4hl5A | Alignment | not modelled | 7.5 | 24 | PDB header: transferase Chain: A: PDB Molecule: tankyrase-2; PDBTitle: complex structure of human tankyrase 2 with 7-hydroxy -4'-2 methoxyflavone |
| 46 | c2jz5A | Alignment | not modelled | 7.1 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vpa0419; PDBTitle: nmr solution structure of protein vpa0419 from vibrio2 parahaemolyticus. northeast structural genomics target3 vpr68 |
| 47 | c5dazA | Alignment | not modelled | 6.7 | 23 | PDB header: transferase Chain: A: PDB Molecule: scabin; PDBTitle: crystal structure of scabin, a mono-adp-ribosyltransferase from2 streptomyces scabies |
| 48 | c6blhG | Alignment | not modelled | 6.6 | 23 | PDB header: viral protein/immune system Chain: G: PDB Molecule: major surface glycoprotein g; PDBTitle: rsv g central conserved region bound to fab cb017.5 |
| 49 | c4a1cL | Alignment | not modelled | 6.0 | 28 | PDB header: ribosome Chain: L: PDB Molecule: ribosomal protein l15; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4. |
| 50 | c4g7nB | Alignment | not modelled | 6.0 | 36 | PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase plk4; PDBTitle: the structure of the plk4 cryptic polo box reveals two tandem polo2 boxes required for centriole duplication |
| 51 | c6bliF | Alignment | not modelled | 5.9 | 27 | PDB header: viral protein/immune system Chain: F: PDB Molecule: major surface glycoprotein g; PDBTitle: rsv g peptide bound to fab cb002.5 |
| 52 | d1d0na5 | Alignment | not modelled | 5.7 | 10 | Fold: Gelsolin-like Superfamily: Actin depolymerizing proteins Family: Gelsolin-like |
| | | | | | | PDB header: cell adhesion Chain: A: PDB Molecule: toxin coregulated pilus biosynthesis |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|--|
| 53 | c3oc5A_ | Alignment | not modelled | 5.7 | 13 | protein f; PDBTitle: crystal structure of the vibrio cholerae secreted colonization factor2 tcpf |
| 54 | c6bli_ | Alignment | not modelled | 5.5 | 27 | PDB header: viral protein/immune system Chain: I; PDB Molecule: major surface glycoprotein g; PDBTitle: rsv g peptide bound to fab cb002.5 |
| 55 | d1bg5a1 | Alignment | not modelled | 5.4 | 35 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 56 | c1xmaA_ | Alignment | not modelled | 5.3 | 22 | PDB header: transcription Chain: A; PDB Molecule: predicted transcriptional regulator; PDBTitle: structure of a transcriptional regulator from clostridium thermocellum2 cth-833 |
| 57 | d1xmaa_ | Alignment | not modelled | 5.3 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like |