

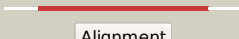

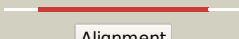

















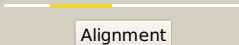

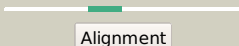

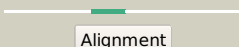

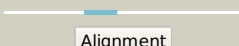

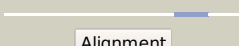
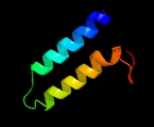
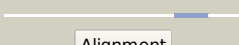

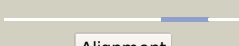
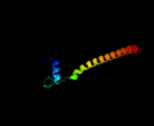







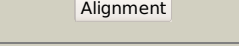
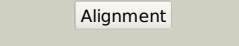


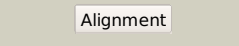
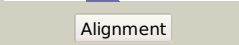


Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2761c_(hsdS)_3071556_3072650 |
| Date | Wed Aug 7 12:50:42 BST 2019 |
| Unique Job ID | 0de8c16813d1e0b2 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c1yf2A_ |  Alignment |  | 100.0 | 16 | PDB header: hydrolase regulator Chain: A: PDB Molecule: type i restriction-modification enzyme, s subunit; PDBTitle: three-dimensional structure of dna sequence specificity (s) subunit of2 a type i restriction-modification enzyme and its functional3 implications |
| 2 | c1ydxA_ |  Alignment |  | 100.0 | 16 | PDB header: dna binding protein Chain: A: PDB Molecule: type i restriction enzyme specificity protein mg438; PDBTitle: crystal structure of type-i restriction-modification system s subunit2 from m. genitalium |
| 3 | c2y7cA_ |  Alignment |  | 100.0 | 10 | PDB header: transferase Chain: A: PDB Molecule: type-1 restriction enzyme ecoki specificity protein; PDBTitle: atomic model of the ocr-bound methylase complex from the type i2 restriction-modification enzyme ecoki (m2s1). based on fitting into3 em map 1534. |
| 4 | c3okgB_ |  Alignment |  | 100.0 | 12 | PDB header: dna binding protein Chain: B: PDB Molecule: restriction endonuclease s subunits; PDBTitle: crystal structure of hsdS subunit from thermoanaerobacter2 tengcongensis |
| 5 | d1ydx2 |  Alignment |  | 100.0 | 18 | Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain |
| 6 | d1yf2a2 |  Alignment |  | 99.9 | 16 | Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain |
| 7 | d1ydx1 |  Alignment |  | 99.9 | 19 | Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain |
| 8 | d1yf2a1 |  Alignment |  | 99.9 | 17 | Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain |
| 9 | c1aqjB_ |  Alignment |  | 97.1 | 13 | PDB header: methyltransferase Chain: B: PDB Molecule: adenine-n6-dna-methyltransferase taqi; PDBTitle: structure of adenine-n6-dna-methyltransferase taqi |
| 10 | c1g38A_ |  Alignment |  | 96.8 | 13 | PDB header: transferase/dna Chain: A: PDB Molecule: modification methylase taqi; PDBTitle: adenine-specific methyltransferase m. taq i/dna complex |
| 11 | c3s1sA_ |  Alignment |  | 93.3 | 13 | PDB header: hydrolase, transferase Chain: A: PDB Molecule: restriction endonuclease bpusi; PDBTitle: characterization and crystal structure of the type iig restriction2 endonuclease bpusi |

| | | | | | | |
|----|-------------------------|---|---|------|----|---|
| 12 | c5hr4J_ |  Alignment |  | 76.3 | 13 | PDB header: hydrolase/dna Chain: J; PDB Molecule: mmei; PDBTitle: structure of type iii restriction-modification enzyme mmei in complex2 with dna has implications for engineering of new specificities |
| 13 | c3bc1F_ |  Alignment |  | 49.9 | 12 | PDB header: signaling protein/transport protein Chain: F; PDB Molecule: synaptotagmin-like protein 2; PDBTitle: crystal structure of the complex rab27a-slp2a |
| 14 | d1zkea1 |  Alignment |  | 41.9 | 7 | Fold: ROP-like Superfamily: HP1531-like Family: HP1531-like |
| 15 | c5ihfA_ |  Alignment |  | 32.3 | 20 | PDB header: unknown function Chain: A; PDB Molecule: virg-like protein; PDBTitle: salmonella typhimurium virg-like (stv) protein |
| 16 | c4jkvA_ |  Alignment |  | 26.7 | 20 | PDB header: membrane protein Chain: A; PDB Molecule: soluble cytochrome b562, smoothed homolog; PDBTitle: structure of the human smoothed 7tm receptor in complex with an2 antitumor agent |
| 17 | c4ug1A_ |  Alignment |  | 25.1 | 11 | PDB header: cell cycle Chain: A; PDB Molecule: cell cycle protein gpsb; PDBTitle: gpsb n-terminal domain |
| 18 | c6d80A_ |  Alignment |  | 23.6 | 6 | PDB header: transport protein Chain: A; PDB Molecule: mitochondrial calcium uniporter; PDBTitle: cryo-em structure of the mitochondrial calcium uniporter from n.2 fischeri bound to saposin |
| 19 | c2lqtA_ |  Alignment |  | 22.5 | 22 | PDB header: unknown function Chain: A; PDB Molecule: coiled-coil-helix-coiled-coil-helix domain-containing PDBTitle: solution structure of chcd7 |
| 20 | d2ih2a2 |  Alignment |  | 21.5 | 14 | Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: TaqI C-terminal domain-like |
| 21 | c6j5id_ |  Alignment | not modelled | 16.8 | 18 | PDB header: membrane protein Chain: D; PDB Molecule: atp synthase subunit beta; PDBTitle: cryo-em structure of the mammalian dp-state atp synthase |
| 22 | c6roiA_ |  Alignment | not modelled | 16.4 | 18 | PDB header: lipid transport Chain: A; PDB Molecule: probable phospholipid-transporting atpase drs2; PDBTitle: cryo-em structure of the partially activated drs2p-cdc50p |
| 23 | c3vhlA_ |  Alignment | not modelled | 16.2 | 16 | PDB header: signaling protein Chain: A; PDB Molecule: dedicator of cytokinesis protein 8; PDBTitle: crystal structure of the dhr-2 domain of dock8 in complex with cdc422 (t17n mutant) |
| 24 | c4zrkH_ |  Alignment | not modelled | 16.1 | 42 | PDB header: signaling protein/transferase Chain: H; PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex |
| 25 | c4zrkF_ |  Alignment | not modelled | 16.1 | 42 | PDB header: signaling protein/transferase Chain: F; PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex |
| 26 | c4zrkE_ |  Alignment | not modelled | 16.1 | 42 | PDB header: signaling protein/transferase Chain: E; PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex |
| 27 | c4zrkG_ |  Alignment | not modelled | 15.9 | 42 | PDB header: signaling protein/transferase Chain: G; PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex |
| 28 | c2ke4A_ |  Alignment | not modelled | 15.3 | 12 | PDB header: membrane protein Chain: A; PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cip4 |
| 29 | c5frgA_ |  Alignment | not modelled | 15.2 | 7 | PDB header: protein binding Chain: A; PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1 |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 30 | d1y71a1 | Alignment | not modelled | 14.4 | 15 | Fold: SH3-like barrel Superfamily: Kinase-associated protein B-like Family: Kinase-associated protein B-like |
| 31 | c2jufA | Alignment | not modelled | 14.4 | 16 | PDB header: gene regulation Chain: A: PDB Molecule: p53-associated parkin-like cytoplasmic protein; PDBTitle: nmr solution structure of parc cph domain. nesg target2 hr3443b/sgc-toronto |
| 32 | c4f8cC | Alignment | not modelled | 14.4 | 9 | PDB header: cell cycle/protein binding Chain: C: PDB Molecule: cycle inhibiting factor; PDBTitle: structure of the cif:nedd8 complex - yersinia pseudotuberculosis cycle2 inhibiting factor in complex with human nedd8 |
| 33 | c2gd3A | Alignment | not modelled | 13.1 | 42 | PDB header: unknown function Chain: A: PDB Molecule: humanin; PDBTitle: nmr structure of s14g-humanin in 30% tfe solution |
| 34 | c2wukD | Alignment | not modelled | 12.6 | 9 | PDB header: cell cycle Chain: D: PDB Molecule: septum site-determining protein diviva; PDBTitle: diviva n-terminal domain, f17a mutant |
| 35 | c6cfzC | Alignment | not modelled | 12.6 | 35 | PDB header: nuclear protein Chain: C: PDB Molecule: dad2; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface |
| 36 | c3mudA | Alignment | not modelled | 12.3 | 14 | PDB header: contractile protein Chain: A: PDB Molecule: dna repair protein xrcc4,tropomyosin alpha-1 chain; PDBTitle: structure of the tropomyosin overlap complex from chicken smooth2 muscle |
| 37 | c5zx8A | Alignment | not modelled | 12.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from thermophilus |
| 38 | c3ghgK | Alignment | not modelled | 11.9 | 8 | PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen |
| 39 | d2jnga1 | Alignment | not modelled | 11.9 | 16 | Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: CPH domain |
| 40 | c5xauC | Alignment | not modelled | 11.5 | 19 | PDB header: cell adhesion Chain: C: PDB Molecule: laminin subunit gamma-1; PDBTitle: crystal structure of integrin binding fragment of laminin-511 |
| 41 | c2xvsA | Alignment | not modelled | 10.9 | 8 | PDB header: antitumor protein Chain: A: PDB Molecule: tetratricopeptide repeat protein 5; PDBTitle: crystal structure of human ttc5 (strap) c-terminal ob2 domain |
| 42 | c2wmoA | Alignment | not modelled | 10.9 | 24 | PDB header: cell cycle Chain: A: PDB Molecule: dedicator of cytokinesis protein 9; PDBTitle: structure of the complex between dock9 and cdc42. |
| 43 | c2owvB | Alignment | not modelled | 10.7 | 13 | PDB header: dna binding protein Chain: B: PDB Molecule: recombination-associated protein rdgc; PDBTitle: the recombination-associated protein rdgc adopts a novel toroidal2 architecture for dna binding |
| 44 | c2hjqa | Alignment | not modelled | 10.6 | 10 | PDB header: structural genomics Chain: A: PDB Molecule: hypothetical protein yqbf; PDBTitle: nmr structure of bacillus subtilis protein yqbf, northeast2 structural genomics target sr449 |
| 45 | d2nrka1 | Alignment | not modelled | 10.4 | 8 | Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: GrpB-like |
| 46 | c4ylyB | Alignment | not modelled | 10.2 | 14 | PDB header: hydrolase Chain: B: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from a gram-positive2 bacterium, staphylococcus aureus at 2.25 angstrom resolution |
| 47 | c6gqaD | Alignment | not modelled | 10.0 | 6 | PDB header: cell cycle Chain: D: PDB Molecule: cell cycle protein gpsb; PDBTitle: cell division regulator s. pneumoniae gpsb |
| 48 | c3kxeD | Alignment | not modelled | 9.2 | 21 | PDB header: protein binding Chain: D: PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex |
| 49 | c2l5gB | Alignment | not modelled | 8.7 | 10 | PDB header: transcription regulator Chain: B: PDB Molecule: putative uncharacterized protein ncor2; PDBTitle: co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207 |
| 50 | c3plwA | Alignment | not modelled | 8.5 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage |
| 51 | c5td8B | Alignment | not modelled | 8.3 | 12 | PDB header: replication Chain: B: PDB Molecule: kinetochore protein nuf2; PDBTitle: crystal structure of an extended dwarf ndc80 complex |
| 52 | c3zifP | Alignment | not modelled | 7.5 | 10 | PDB header: virus Chain: P: PDB Molecule: pix; PDBTitle: cryo-em structures of two intermediates provide insight into2 adenovirus assembly and disassembly |
| 53 | c4ct4C | Alignment | not modelled | 7.3 | 7 | PDB header: rna binding protein Chain: C: PDB Molecule: ccr4-not transcription complex subunit 1; PDBTitle: cnot1 mif4g domain - ddx6 complex |
| 54 | c4q55B | Alignment | not modelled | 7.3 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from a gram-positive2 bacterium, streptococcus pyogenes at 2.19a resolution shows the3 closed structure of the substrate binding cleft |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|--|
| 55 | c3q4fG_ | Alignment | not modelled | 7.3 | 17 | PDB header: dna binding protein/protein binding Chain: G; PDB Molecule: dna repair protein xrcc4; PDBTitle: crystal structure of xrcc4/xlf-cernunnos complex |
| 56 | c4hpgE_ | Alignment | not modelled | 7.3 | 22 | PDB header: protein transport Chain: E; PDB Molecule: atg31; PDBTitle: crystal structure of the atg17-atg31-atg29 complex |
| 57 | c2lvqA_ | Alignment | not modelled | 7.2 | 12 | PDB header: membrane protein Chain: A; PDB Molecule: non-structural protein 4b; PDBTitle: nmr structure of hcv non-structural protein ab, ns4b(1-40) |
| 58 | c3cqxD_ | Alignment | not modelled | 6.8 | 24 | PDB header: chaperone Chain: D; PDB Molecule: bag family molecular chaperone regulator 2; PDBTitle: chaperone complex |
| 59 | c5kb0A_ | Alignment | not modelled | 6.8 | 19 | PDB header: de novo protein Chain: A; PDB Molecule: pb(ii)zn(ii)(grand coil ser-l16c130h)3+; PDBTitle: crystal structure of a tris-thiolate pb(ii) complex in a de novo2 three-stranded coiled coil peptide |
| 60 | d1q08a_ | Alignment | not modelled | 6.8 | 14 | Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators |
| 61 | d1vf6a_ | Alignment | not modelled | 6.7 | 10 | Fold: L27 domain Superfamily: L27 domain Family: L27 domain |
| 62 | c4pn8A_ | Alignment | not modelled | 6.7 | 14 | PDB header: de novo protein Chain: A; PDB Molecule: cc-pent; PDBTitle: a de novo designed pentameric coiled coil cc-pent. |
| 63 | c4pn8H_ | Alignment | not modelled | 6.7 | 14 | PDB header: de novo protein Chain: H; PDB Molecule: cc-pent; PDBTitle: a de novo designed pentameric coiled coil cc-pent. |
| 64 | c4pn8D_ | Alignment | not modelled | 6.7 | 14 | PDB header: de novo protein Chain: D; PDB Molecule: cc-pent; PDBTitle: a de novo designed pentameric coiled coil cc-pent. |
| 65 | c4pn8C_ | Alignment | not modelled | 6.7 | 14 | PDB header: de novo protein Chain: C; PDB Molecule: cc-pent; PDBTitle: a de novo designed pentameric coiled coil cc-pent. |
| 66 | c4pn8B_ | Alignment | not modelled | 6.7 | 14 | PDB header: de novo protein Chain: B; PDB Molecule: cc-pent; PDBTitle: a de novo designed pentameric coiled coil cc-pent. |
| 67 | c4pn8J_ | Alignment | not modelled | 6.7 | 14 | PDB header: de novo protein Chain: J; PDB Molecule: cc-pent; PDBTitle: a de novo designed pentameric coiled coil cc-pent. |
| 68 | c4pn8E_ | Alignment | not modelled | 6.7 | 14 | PDB header: de novo protein Chain: E; PDB Molecule: cc-pent; PDBTitle: a de novo designed pentameric coiled coil cc-pent. |
| 69 | c4pn8G_ | Alignment | not modelled | 6.7 | 14 | PDB header: de novo protein Chain: G; PDB Molecule: cc-pent; PDBTitle: a de novo designed pentameric coiled coil cc-pent. |
| 70 | c4pn8F_ | Alignment | not modelled | 6.7 | 14 | PDB header: de novo protein Chain: F; PDB Molecule: cc-pent; PDBTitle: a de novo designed pentameric coiled coil cc-pent. |
| 71 | d2clyb1 | Alignment | not modelled | 6.6 | 6 | Fold: ATP synthase D chain-like Superfamily: ATP synthase D chain-like Family: ATP synthase D chain-like |
| 72 | c1vf6B_ | Alignment | not modelled | 6.4 | 10 | PDB header: protein binding/protein transport Chain: B; PDB Molecule: pals1-associated tight junction protein; PDBTitle: 2.1 angstrom crystal structure of the pals-1-l27n and patj l272 heterodimer complex |
| 73 | c4me1B_ | Alignment | not modelled | 6.3 | 17 | PDB header: hydrolase Chain: B; PDB Molecule: ubiquitin carboxyl-terminal hydrolase 11; PDBTitle: crystal structure of the human usp11 dusp-ubl domains |
| 74 | d1o5ha_ | Alignment | not modelled | 6.3 | 15 | Fold: Methenyltetrahydrofolate cyclohydrolase-like Superfamily: Methenyltetrahydrofolate cyclohydrolase-like Family: Methenyltetrahydrofolate cyclohydrolase-like |
| 75 | c3v21A_ | Alignment | not modelled | 5.8 | 16 | PDB header: hydrolase Chain: A; PDB Molecule: peptidyl-trna hydrolase; PDBTitle: structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis |
| 76 | c1ei3E_ | Alignment | not modelled | 5.8 | 9 | PDB header: blood clotting Chain: E; PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen |
| 77 | c5gmkT_ | Alignment | not modelled | 5.6 | 13 | PDB header: rna binding protein/rna Chain: T; PDB Molecule: pre-mrna-splicing factor bud31; PDBTitle: cryo-em structure of the catalytic step i spliceosome (c complex) at2 3.4 angstrom resolution |
| 78 | c5gnaB_ | Alignment | not modelled | 5.6 | 17 | PDB header: gene regulation Chain: B; PDB Molecule: flagellar hook-associated protein 2; PDBTitle: crystal structure of flagellin assembly related protein |
| 79 | c2e6iA_ | Alignment | not modelled | 5.5 | 20 | PDB header: transferase Chain: A; PDB Molecule: tyrosine-protein kinase itk/tsk; PDBTitle: solution structure of the btk motif of tyrosine-protein2 kinase itk from human |
| 80 | c3pp5A_ | Alignment | not modelled | 5.5 | 16 | PDB header: structural protein Chain: A; PDB Molecule: brk1; PDBTitle: high-resolution structure of the trimeric scar/wave complex precursor2 brk1 |
| 81 | c2l21A_ | Alignment | not modelled | 5.5 | 12 | PDB header: transferase Chain: A; PDB Molecule: transcriptional repressor p66-alpha; PDBTitle: solution structure of the coiled-coil complex between mbd2 and2 p66alpha |
| | | | | | | PDB header: structural genomics, unknown function |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|--|
| 82 | c3njcA_ | Alignment | not modelled | 5.5 | 23 | Chain: A: PDB Molecule: yslb protein; PDBTitle: crystal structure of the yslb protein from bacillus subtilis.2 northeast structural genomics consortium target sr460. |
| 83 | c2yinB_ | Alignment | not modelled | 5.3 | 19 | PDB header: apoptosis Chain: B: PDB Molecule: dedicator of cytokinesis protein 2; PDBTitle: structure of the complex between dock2 and rac1. |
| 84 | c2clyE_ | Alignment | not modelled | 5.3 | 6 | PDB header: hydrolase Chain: E: PDB Molecule: atp synthase d chain, mitochondrial; PDBTitle: subcomplex of the stator of bovine mitochondrial atp synthase |
| 85 | c6dnfA_ | Alignment | not modelled | 5.3 | 6 | PDB header: membrane protein Chain: A: PDB Molecule: mitochondrial calcium uniporter mcu; PDBTitle: cryo-em structure of the mitochondrial calcium uniporter mcu from the2 fungus cyphellophora europaea |
| 86 | c3p8cE_ | Alignment | not modelled | 5.3 | 26 | PDB header: protein binding Chain: E: PDB Molecule: probable protein brick1; PDBTitle: structure and control of the actin regulatory wave complex |
| 87 | d1t3ua_ | Alignment | not modelled | 5.2 | 19 | Fold: Cell division protein ZapA-like Superfamily: Cell division protein ZapA-like Family: Cell division protein ZapA-like |
| 88 | c3zeyZ_ | Alignment | not modelled | 5.1 | 33 | PDB header: ribosome Chain: Z: PDB Molecule: 40s ribosomal protein s33, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 89 | c1t6fA_ | Alignment | not modelled | 5.1 | 9 | PDB header: cell cycle Chain: A: PDB Molecule: geminin; PDBTitle: crystal structure of the coiled-coil dimerization motif of2 geminin |
| 90 | c4ypiG_ | Alignment | not modelled | 5.1 | 23 | PDB header: rna binding protein Chain: G: PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of ebola virus nucleoprotein n-terminal fragment bound to a2 peptide derived from ebola vp35 |
| 91 | c4ypiF_ | Alignment | not modelled | 5.1 | 23 | PDB header: rna binding protein Chain: F: PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of ebola virus nucleoprotein n-terminal fragment bound to a2 peptide derived from ebola vp35 |