
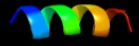
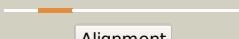

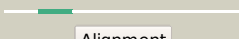


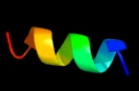



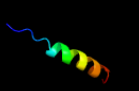




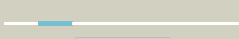
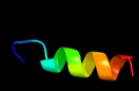

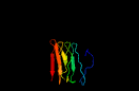




Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0314c_(-)_382879_383541 |
| Date | Tue Jul 23 14:50:38 BST 2019 |
| Unique Job ID | 98edd3bfcf979b8b |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c1zxaB_ |  Alignment |  | 89.9 | 50 | PDB header: transferase Chain: B: PDB Molecule: cgmp-dependent protein kinase 1, alpha isozyme; PDBTitle: solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia |
| 2 | c4r4mB_ |  Alignment |  | 88.9 | 50 | PDB header: dna binding protein Chain: B: PDB Molecule: cgmp-dependent protein kinase 1; PDBTitle: crystal structure of c42l cgmp dependent protein kinase i alpha (pkgi2 alpha) leucine zipper |
| 3 | c5ua4B_ |  Alignment |  | 49.2 | 43 | PDB header: apoptosis Chain: B: PDB Molecule: bh3-interacting domain death agonist; PDBTitle: crystal structure of a179l:bid bh3 complex |
| 4 | d2csga1 |  Alignment |  | 43.7 | 46 | Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: YbiU-like |
| 5 | d1grja1 |  Alignment |  | 37.0 | 42 | Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain |
| 6 | c4xa6C_ |  Alignment |  | 35.5 | 41 | PDB header: motor protein Chain: C: PDB Molecule: gp7-myh7(1777-1855)-eb1 chimera protein; PDBTitle: crystal structure of the coiled-coil surrounding skip 4 of myh7 |
| 7 | d2f23a1 |  Alignment |  | 35.0 | 58 | Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain |
| 8 | c1x37A_ |  Alignment |  | 34.2 | 56 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease la 1; PDBTitle: structure of bacillus subtilis lon protease ssd domain |
| 9 | d1qzma_ |  Alignment |  | 30.4 | 44 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain |
| 10 | c3ljyA_ |  Alignment |  | 29.9 | 14 | PDB header: cell adhesion Chain: A: PDB Molecule: putative adhesin; PDBTitle: crystal structure of putative adhesin (yp_001304413.1) from 2 parabacteroides distazonis atcc 8503 at 2.4Å a resolution |
| 11 | c4xa6B_ |  Alignment |  | 29.9 | 53 | PDB header: motor protein Chain: B: PDB Molecule: gp7-myh7(1777-1855)-eb1 chimera protein; PDBTitle: crystal structure of the coiled-coil surrounding skip 4 of myh7 |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c4ll7C_ | Alignment | | 28.4 | 16 | PDB header: transport protein Chain: C: PDB Molecule: swi5-dependent ho expression protein 3; PDBTitle: structure of she3p amino terminus. |
| 13 | c2yonA_ | Alignment | | 28.1 | 50 | PDB header: signaling protein Chain: A: PDB Molecule: sensory box protein; PDBTitle: solution nmr structure of the c-terminal extension of two bacterial2 light, oxygen, voltage (lov) photoreceptor proteins from3 pseudomonas putida |
| 14 | c3b0zA_ | Alignment | | 25.3 | 39 | PDB header: protein transport Chain: A: PDB Molecule: flagellar biosynthetic protein flhb; PDBTitle: crystal structure of cytoplasmic domain of flhb from salmonella2 typhimurium |
| 15 | c3cf4A_ | Alignment | | 25.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: acetyl-coa decarboxylase/synthase alpha subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex |
| 16 | c5j0kA_ | Alignment | | 24.3 | 70 | PDB header: de novo protein Chain: A: PDB Molecule: designed protein 2l4hc2_23; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity |
| 17 | c2dbiA_ | Alignment | | 23.5 | 30 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ybiu; PDBTitle: crystal structure of a hypothetical protein jw0805 from2 escherichia coli |
| 18 | c4gitA_ | Alignment | | 23.2 | 44 | PDB header: hydrolase Chain: A: PDB Molecule: lon protease; PDBTitle: crystal structure of alpha sub-domain of lon protease from2 brevicacillus thermoruber |
| 19 | c6hwhX_ | Alignment | | 22.7 | 38 | PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis |
| 20 | c3x37A_ | Alignment | | 22.0 | 40 | PDB header: replication regulator Chain: A: PDB Molecule: zyro0c14696p; PDBTitle: crystal structure of the n-terminal domain of sld7 in complex with2 sld3 |
| 21 | d1ukfa_ | Alignment | not modelled | 21.5 | 32 | Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Avirulence protein Avrpph3 |
| 22 | c3ci9B_ | Alignment | not modelled | 19.1 | 47 | PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1 |
| 23 | c5ymaA_ | Alignment | not modelled | 18.9 | 55 | PDB header: ribosomal protein Chain: A: PDB Molecule: putative rrna processing protein; PDBTitle: crystal structure of ribosome assembly factor efg1 |
| 24 | c5fiyE_ | Alignment | not modelled | 18.7 | 42 | PDB header: apoptosis Chain: E: PDB Molecule: prkc apoptosis wt1 regulator protein; PDBTitle: crystal structure of coiled coil domain of pawr |
| 25 | c2ml9A_ | Alignment | not modelled | 18.3 | 22 | PDB header: membrane protein Chain: A: PDB Molecule: yop proteins translocation protein u; PDBTitle: solution structure of yscucln in a micellar complex with sds |
| 26 | c6b87C_ | Alignment | not modelled | 18.3 | 88 | PDB header: membrane protein Chain: C: PDB Molecule: tmhc2_e; PDBTitle: crystal structure of transmembrane protein tmhc2_e |
| 27 | c5mc9B_ | Alignment | not modelled | 17.9 | 29 | PDB header: cell adhesion Chain: B: PDB Molecule: laminin subunit beta-1; PDBTitle: crystal structure of the heterotrimeric integrin-binding region of2 laminin-111 |
| 28 | c1gthD_ | Alignment | not modelled | 17.7 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil |
| 29 | c1grjA_ | Alignment | not modelled | 17.5 | 42 | PDB header: transcription regulation Chain: A: PDB Molecule: grea protein; |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: grea transcript cleavage factor from escherichia coli |
| 30 | c4fi5A_ | Alignment | not modelled | 16.9 | 57 | PDB header: viral protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: crystal structure of the n-terminal domain of hantaan virus strain 76-2 118 nucleoprotein |
| 31 | c2p4vA_ | Alignment | not modelled | 16.8 | 25 | PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution |
| 32 | c2etnA_ | Alignment | not modelled | 16.8 | 58 | PDB header: transcription Chain: A: PDB Molecule: anti-cleavage anti-grea transcription factor PDBTitle: crystal structure of thermus aquaticus gfh1 |
| 33 | c4i0oA_ | Alignment | not modelled | 16.2 | 44 | PDB header: structural protein Chain: A: PDB Molecule: protein elys; PDBTitle: nucleoporin elys (aa1-494), mus musculus |
| 34 | d1k4za_ | Alignment | not modelled | 15.4 | 16 | Fold: Single-stranded right-handed beta-helix Superfamily: C-terminal domain of adenylyl cyclase associated protein Family: C-terminal domain of adenylyl cyclase associated protein |
| 35 | c1wt6B_ | Alignment | not modelled | 14.9 | 40 | PDB header: transferase Chain: B: PDB Molecule: myotonin-protein kinase; PDBTitle: coiled-coil domain of dmpk |
| 36 | d1v29a_ | Alignment | not modelled | 14.0 | 33 | Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain |
| 37 | c3s7xC_ | Alignment | not modelled | 13.9 | 33 | PDB header: viral protein Chain: C: PDB Molecule: major capsid protein vp1; PDBTitle: unassembled washington university polyomavirus vp1 pentamer r198k2 mutant |
| 38 | d1up8a_ | Alignment | not modelled | 12.6 | 25 | Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase) |
| 39 | c3jx8B_ | Alignment | not modelled | 12.6 | 15 | PDB header: cell adhesion Chain: B: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of putative lipid binding protein (yp_001304415.1)2 from parabacteroides distasonis atcc 8503 at 2.16 a resolution |
| 40 | c4pcgD_ | Alignment | not modelled | 12.0 | 33 | PDB header: viral protein Chain: D: PDB Molecule: vp1; PDBTitle: structure of human polyomavirus 6 (hpyv6) vp1 pentamer |
| 41 | c6dmxF_ | Alignment | not modelled | 11.7 | 64 | PDB header: transcription Chain: F: PDB Molecule: transcriptional activator myb; PDBTitle: hbz56 in complex with kix and c-myb |
| 42 | c4pchE_ | Alignment | not modelled | 11.5 | 33 | PDB header: viral protein Chain: E: PDB Molecule: vp1; PDBTitle: structure of human polyomavirus 7 (hpyv7) vp1 pentamer |
| 43 | c3bc1F_ | Alignment | not modelled | 10.7 | 25 | PDB header: signaling protein/transport protein Chain: F: PDB Molecule: synaptotagmin-like protein 2; PDBTitle: crystal structure of the complex rab27a-slp2a |
| 44 | c5grqC_ | Alignment | not modelled | 10.1 | 50 | PDB header: hydrolase Chain: C: PDB Molecule: transcriptional regulator atrx; PDBTitle: crystal structure of dhb domain of daxx in complex with an atrx2 peptide |
| 45 | c3sulA_ | Alignment | not modelled | 9.9 | 36 | PDB header: unknown function Chain: A: PDB Molecule: cerato-platanin-like protein; PDBTitle: crystal structure of cerato-platanin 3 from m. pernicioso (mpcp3) |
| 46 | c4mbyB_ | Alignment | not modelled | 9.6 | 33 | PDB header: viral protein Chain: B: PDB Molecule: major capsid protein vp1; PDBTitle: structure of b-lymphotropic polyomavirus vp1 in complex with 3'-2 sialyllactose |
| 47 | c3bwrC_ | Alignment | not modelled | 9.6 | 33 | PDB header: viral protein Chain: C: PDB Molecule: capsid protein vp1; PDBTitle: sv40 vp1 pentamer in complex with gm1 oligosaccharide |
| 48 | c3m0dC_ | Alignment | not modelled | 9.6 | 45 | PDB header: signaling protein Chain: C: PDB Molecule: tnf receptor-associated factor 1; PDBTitle: crystal structure of the traf1:traf2:ciap2 complex |
| 49 | d2qtva4 | Alignment | not modelled | 9.6 | 35 | Fold: Gelsolin-like Superfamily: C-terminal, gelsolin-like domain of Sec23/24 Family: C-terminal, gelsolin-like domain of Sec23/24 |
| 50 | d1tg7a1 | Alignment | not modelled | 9.3 | 18 | Fold: Beta-galactosidase LacA, domain 3 Superfamily: Beta-galactosidase LacA, domain 3 Family: Beta-galactosidase LacA, domain 3 |
| 51 | d1qhba_ | Alignment | not modelled | 9.1 | 32 | Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase) |
| 52 | c5svhB_ | Alignment | not modelled | 8.9 | 64 | PDB header: transcription Chain: B: PDB Molecule: mll/c-myb chimera; PDBTitle: crystal structure of the kix domain of cbp in complex with a mll/c-myb2 chimera |
| 53 | c5grqD_ | Alignment | not modelled | 8.8 | 50 | PDB header: hydrolase Chain: D: PDB Molecule: transcriptional regulator atrx; PDBTitle: crystal structure of dhb domain of daxx in complex with an atrx2 peptide |
| 54 | c5f5tD_ | Alignment | not modelled | 8.8 | 63 | PDB header: splicing Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the prp38-mfap1 complex of chaetomium2 thermophilum |
| 55 | d1vpsa_ | Alignment | not modelled | 8.8 | 25 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group I dsDNA viruses Family: Papovaviridae-like VP |

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|----|-------------------------|-----------|--------------|-----|----|---|
| 56 | c4bpsA | Alignment | not modelled | 8.7 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: fkbo; PDBTitle: crystal structure of chorismatase at 1.08 angstrom resolution. |
| 57 | c2yomA | Alignment | not modelled | 8.7 | 64 | PDB header: signaling protein Chain: A: PDB Molecule: sensory box protein; PDBTitle: solution nmr structure of the c-terminal extension of two bacterial2 light, oxygen, voltage (lov) photoreceptor proteins from3 pseudomonas putida |
| 58 | c6dmxH | Alignment | not modelled | 8.4 | 47 | PDB header: transcription Chain: H: PDB Molecule: transcriptional activator myb; PDBTitle: hbz56 in complex with kix and c-myb |
| 59 | c6dnqA | Alignment | not modelled | 8.4 | 47 | PDB header: transcription Chain: A: PDB Molecule: transcriptional activator myb; PDBTitle: hbz77 in complex with kix and c-myb |
| 60 | c3lfhF | Alignment | not modelled | 8.3 | 19 | PDB header: transferase Chain: F: PDB Molecule: phosphotransferase system, mannose/fructose-specific PDBTitle: crystal structure of manxa from thermoanaerobacter tengcongensis |
| 61 | c2m0dA | Alignment | not modelled | 8.3 | 38 | PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 5 |
| 62 | d1t3la1 | Alignment | not modelled | 8.3 | 62 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 63 | d1to3a | Alignment | not modelled | 8.3 | 10 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 64 | c4pasB | Alignment | not modelled | 8.1 | 50 | PDB header: signaling protein Chain: B: PDB Molecule: gamma-aminobutyric acid type b receptor subunit 2; PDBTitle: heterodimeric coiled-coil structure of human gaba(b) receptor |
| 65 | c4u62D | Alignment | not modelled | 7.9 | 25 | PDB header: viral protein Chain: D: PDB Molecule: structural protein vp1; PDBTitle: trichodysplasia spinulosa-associated polyomavirus (tspyv) vp1 in2 complex with 3'-sialyllactose |
| 66 | c4q16C | Alignment | not modelled | 7.8 | 24 | PDB header: ligase Chain: C: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad+ synthetase from deinococcus radiodurans |
| 67 | d1tuva | Alignment | not modelled | 7.8 | 14 | Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like |
| 68 | c2ergA | Alignment | not modelled | 7.6 | 46 | PDB header: transcription activator/dna Chain: A: PDB Molecule: regulatory protein leu3; PDBTitle: crystal structure of leu3 dna-binding domain with a single2 h50c mutation complexed with a 15mer dna duplex |
| 69 | c4fmiN | Alignment | not modelled | 7.4 | 25 | PDB header: viral protein Chain: N: PDB Molecule: vp1; PDBTitle: merkel cell polyomavirus vp1 in complex with 3'-sialyllactosamine |
| 70 | c3d9xA | Alignment | not modelled | 7.0 | 15 | PDB header: cell adhesion Chain: A: PDB Molecule: adhesin a; PDBTitle: structure of the head of the bartonella adhesin bada |
| 71 | d2b9da1 | Alignment | not modelled | 7.0 | 32 | Fold: E7 C-terminal domain-like Superfamily: E7 C-terminal domain-like Family: E7 C-terminal domain-like |
| 72 | c6odmK | Alignment | not modelled | 6.9 | 45 | PDB header: viral protein Chain: K: PDB Molecule: capsid vertex component 2; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit |
| 73 | c3k81D | Alignment | not modelled | 6.8 | 27 | PDB header: immune system, rna binding protein Chain: D: PDB Molecule: mp18 rna editing complex protein; PDBTitle: structure of the central interaction protein from the trypanosoma2 brucei editosome in complex with single domain antibodies |
| 74 | d1zela1 | Alignment | not modelled | 6.8 | 64 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rv2827c N-terminal domain-like |
| 75 | c1hwtC | Alignment | not modelled | 6.4 | 31 | PDB header: gene regulation/dna Chain: C: PDB Molecule: protein (heme activator protein); PDBTitle: structure of a hap1/dna complex reveals dramatically2 asymmetric dna binding by a homodimeric protein |
| 76 | c4k83A | Alignment | not modelled | 6.3 | 43 | PDB header: structural protein Chain: A: PDB Molecule: lv-ranaspumin (lv-rsn-1); PDBTitle: crystal structure of lv-ranaspumin (lv-rsn-1) from the foam nest of2 leptodactylus vastus, orthorhombic crystal form |
| 77 | c3oggA | Alignment | not modelled | 6.2 | 22 | PDB header: toxin Chain: A: PDB Molecule: botulinum neurotoxin type d; PDBTitle: crystal structure of the receptor binding domain of botulinum2 neurotoxin d |
| 78 | c3m06F | Alignment | not modelled | 6.2 | 27 | PDB header: protein binding Chain: F: PDB Molecule: tnf receptor-associated factor 2; PDBTitle: crystal structure of traf2 |
| 79 | d1k8fa | Alignment | not modelled | 6.1 | 20 | Fold: Single-stranded right-handed beta-helix Superfamily: C-terminal domain of adenylylcyase associated protein Family: C-terminal domain of adenylylcyase associated protein |
| 80 | c5tdwA | Alignment | not modelled | 6.1 | 31 | PDB header: transcription Chain: A: PDB Molecule: set domain-containing protein 3; PDBTitle: set3 phd finger in complex with histone h3k4me3 |
| | | | | | | PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 81 | c3k2gA_ | Alignment | not modelled | 6.0 | 34 | phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from <i>2</i> rhodobacter sphaeroides |
| 82 | d1zl0a2 | Alignment | not modelled | 5.9 | 19 | Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like |
| 83 | c5lpcA_ | Alignment | not modelled | 5.9 | 28 | PDB header: oxidoreductase Chain: A; PDB Molecule: vanadium-dependent bromoperoxidase; PDBTitle: crystal structure of vanadium-dependent haloperoxidase from <i>a. marina</i> |
| 84 | c2cwoD_ | Alignment | not modelled | 5.8 | 32 | PDB header: rna binding protein Chain: D; PDB Molecule: rna silencing suppressor; PDBTitle: crystal structure of rna silencing suppressor p21 from beet yellows2 virus |
| 85 | d1vk3a2 | Alignment | not modelled | 5.7 | 10 | Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like |
| 86 | c4l3rB_ | Alignment | not modelled | 5.6 | 17 | PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4847 family protein (bacegg_01241) from <i>2</i> bacteroides eggerthii dsm 20697 at 2.23 a resolution |
| 87 | c5uyoA_ | Alignment | not modelled | 5.4 | 54 | PDB header: de novo protein Chain: A; PDB Molecule: heeh_rd4_0097; PDBTitle: solution nmr structure of the de novo mini protein heeh_rd4_0097 |
| 88 | d1foka3 | Alignment | not modelled | 5.3 | 40 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Restriction endonuclease FokI, N-terminal (recognition) domain |
| 89 | c4ds7E_ | Alignment | not modelled | 5.2 | 21 | PDB header: protein binding Chain: E; PDB Molecule: spindle pole body component 110; PDBTitle: crystal structure of yeast calmodulin bound to the c-terminal fragment2 of spindle pole body protein spc110 |
| 90 | d2foka3 | Alignment | not modelled | 5.2 | 40 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Restriction endonuclease FokI, N-terminal (recognition) domain |
| 91 | d1sva1_ | Alignment | not modelled | 5.2 | 30 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group I dsDNA viruses Family: Papovaviridae-like VP |