

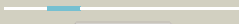








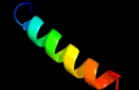
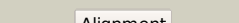


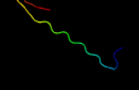

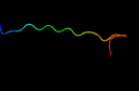

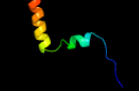


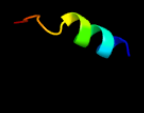


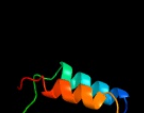







Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3092c_(-)_3460811_3461731 |
| Date | Thu Aug 8 16:20:27 BST 2019 |
| Unique Job ID | b527800cb1fa019a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c5wwoB_ |  Alignment |  | 40.8 | 27 | PDB header: rna binding protein Chain: B; PDB Molecule: essential nuclear protein 1; PDBTitle: crystal structure of enp1 |
| 2 | d2enda_ |  Alignment |  | 37.0 | 35 | Fold: T4 endonuclease V Superfamily: T4 endonuclease V Family: T4 endonuclease V |
| 3 | c2l9uB_ |  Alignment |  | 36.5 | 41 | PDB header: membrane protein Chain: B; PDB Molecule: receptor tyrosine-protein kinase erbB-3; PDBTitle: spatial structure of dimeric erbB3 transmembrane domain |
| 4 | c2l9uA_ |  Alignment |  | 36.5 | 41 | PDB header: membrane protein Chain: A; PDB Molecule: receptor tyrosine-protein kinase erbB-3; PDBTitle: spatial structure of dimeric erbB3 transmembrane domain |
| 5 | c4cv5D_ |  Alignment |  | 27.3 | 21 | PDB header: cell cycle Chain: D; PDB Molecule: protein caf40; PDBTitle: yeast not1 cn9bd-caf40 complex |
| 6 | c5doqC_ |  Alignment |  | 21.9 | 48 | PDB header: oxidoreductase Chain: C; PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans |
| 7 | c5lr6C_ |  Alignment |  | 21.9 | 48 | PDB header: oxidoreductase Chain: C; PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans |
| 8 | c5tvoB_ |  Alignment |  | 20.2 | 25 | PDB header: lyase Chain: B; PDB Molecule: s-adenosylmethionine decarboxylase proenzyme; PDBTitle: crystal structure of trypanosoma brucei adometdc-delta26 monomer |
| 9 | c5tvfC_ |  Alignment |  | 18.5 | 30 | PDB header: lyase Chain: C; PDB Molecule: s-adenosylmethionine decarboxylase beta chain; PDBTitle: crystal structure of trypanosoma brucei adometdc/prozyme heterodimer2 in complex with inhibitor cgp 40215 |
| 10 | c2voyB_ |  Alignment |  | 16.5 | 22 | PDB header: hydrolase Chain: B; PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus |
| 11 | c4r0cB_ |  Alignment |  | 16.4 | 17 | PDB header: membrane protein Chain: B; PDB Molecule: abgt putative transporter family; PDBTitle: crystal structure of the alcanivorax borkumensis ydah transporter2 reveals an unusual topology |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|--|
| 12 | d1nexa2 | Alignment |  | 16.2 | 19 | Fold: POZ domain Superfamily: POZ domain Family: BTB/POZ domain |
| 13 | c4gl6B | Alignment |  | 15.6 | 17 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf5037 family protein (rumgna_01148) from <i>2 ruminococcus gnavus</i> atcc 29149 at 2.55 a resolution |
| 14 | c1i7mD | Alignment |  | 15.0 | 44 | PDB header: lyase Chain: D: PDB Molecule: s-adenosylmethionine decarboxylase beta chain; PDBTitle: human s-adenosylmethionine decarboxylase with covalently bound 2 pyruvoyl group and complexed with 4-amidinoindan-1-one-2'-3 amidinohydrazone |
| 15 | c6g4ww | Alignment |  | 14.0 | 24 | PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s15a; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a |
| 16 | c4zr0A | Alignment |  | 13.5 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: ceramide very long chain fatty acid hydroxylase scs7; PDBTitle: full length scs7p (only hydroxylase domain visible) |
| 17 | c1w8xP | Alignment |  | 12.5 | 60 | PDB header: virus Chain: P: PDB Molecule: protein p16; PDBTitle: structural analysis of prd1 |
| 18 | d2c9wc1 | Alignment |  | 10.4 | 18 | Fold: POZ domain Superfamily: POZ domain Family: BTB/POZ domain |
| 19 | c5j6vA | Alignment |  | 9.9 | 36 | PDB header: antimicrobial protein Chain: A: PDB Molecule: hylin-d; PDBTitle: nmr structures of hylin-a1 analogs: hylin-d |
| 20 | c5j6wA | Alignment |  | 9.5 | 36 | PDB header: antimicrobial protein Chain: A: PDB Molecule: hylin-k; PDBTitle: nmr structures of hylin-a1 analogs: hylin-k |
| 21 | d1kf6d | Alignment | not modelled | 8.6 | 20 | Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD) |
| 22 | c6ig0H | Alignment | not modelled | 8.6 | 50 | PDB header: rna binding protein Chain: H: PDB Molecule: type iii-a crisper-associated ramp protein csm5; PDBTitle: type iii-a csm complex, cryo-em structure of csm-ctr1, atp bound |
| 23 | d1urfa | Alignment | not modelled | 7.3 | 19 | Fold: Long alpha-hairpin Superfamily: HR1 repeat Family: HR1 repeat |
| 24 | c6musF | Alignment | not modelled | 7.3 | 50 | PDB header: rna binding protein/rna Chain: F: PDB Molecule: uncharacterized protein csm5; PDBTitle: cryo-em structure of larger csm-crrna-target rna ternary complex in 2 type iii-a crisper-cas system |
| 25 | c5lqzW | Alignment | not modelled | 6.6 | 12 | PDB header: hydrolase Chain: W: PDB Molecule: atp synthase subunit d; PDBTitle: structure of f-atpase from <i>pichia angusta</i> , state1 |
| 26 | c5lqxW | Alignment | not modelled | 6.6 | 12 | PDB header: hydrolase Chain: W: PDB Molecule: atp synthase subunit d; PDBTitle: structure of f-atpase from <i>pichia angusta</i> , state3 |
| 27 | c5lqyW | Alignment | not modelled | 6.6 | 12 | PDB header: hydrolase Chain: W: PDB Molecule: atp synthase subunit d; PDBTitle: structure of f-atpase from <i>pichia angusta</i> , in state2 |
| 28 | c2zjsE | Alignment | not modelled | 6.5 | 23 | PDB header: protein transport/immune system Chain: E: PDB Molecule: preprotein translocase sece subunit; PDBTitle: crystal structure of sece translocon from <i>thermus thermophilus</i> with a2 fab fragment |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|--|
| 29 | c2zqpE_ | Alignment | not modelled | 6.5 | 23 | PDB header: protein transport Chain: E; PDB Molecule: preprotein translocase sece subunit; PDBTitle: crystal structure of secey translocon from thermus2 thermophilus |
| 30 | c1msvB_ | Alignment | not modelled | 6.4 | 44 | PDB header: lyase Chain: B; PDB Molecule: s-adenosylmethionine decarboxylase proenzyme; PDBTitle: the s68a s-adenosylmethionine decarboxylase proenzyme2 processing mutant. |
| 31 | c5gtuB_ | Alignment | not modelled | 6.4 | 57 | PDB header: hydrolase Chain: B; PDB Molecule: tbcl1 domain family member 5; PDBTitle: structural and mechanistic insights into regulation of the retromer2 coat by tbcl1d5 |
| 32 | d1fs1b2 | Alignment | not modelled | 6.3 | 23 | Fold: POZ domain Superfamily: POZ domain Family: BTB/POZ domain |
| 33 | d1j10a_ | Alignment | not modelled | 6.1 | 44 | Fold: S-adenosylmethionine decarboxylase Superfamily: S-adenosylmethionine decarboxylase Family: S-adenosylmethionine decarboxylase |
| 34 | c4px7A_ | Alignment | not modelled | 6.0 | 17 | PDB header: hydrolase Chain: A; PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pgpb |
| 35 | d1lgha_ | Alignment | not modelled | 5.8 | 36 | Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits |
| 36 | c4fe1l_ | Alignment | not modelled | 5.8 | 33 | PDB header: photosynthesis Chain: I; PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: improving the accuracy of macromolecular structure refinement at 7 a2 resolution |
| 37 | d1jb0i_ | Alignment | not modelled | 5.8 | 33 | Fold: Single transmembrane helix Superfamily: Subunit VIII of photosystem I reaction centre, PsaI Family: Subunit VIII of photosystem I reaction centre, PsaI |
| 38 | c5wujA_ | Alignment | not modelled | 5.6 | 22 | PDB header: motor protein Chain: A; PDB Molecule: flagellar m-ring protein; PDBTitle: crystal structure of flif-flig complex from h. pylori |
| 39 | c2m55B_ | Alignment | not modelled | 5.6 | 33 | PDB header: calcium binding protein/protein fibril Chain: B; PDB Molecule: alpha-synuclein; PDBTitle: nmr structure of the complex of an n-terminally acetylated alpha-2 synuclein peptide with calmodulin |
| 40 | c6bcdB_ | Alignment | not modelled | 5.5 | 23 | PDB header: replication Chain: B; PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: crystal structure of rev7-k44a/r124a/a135d in complex with rev3-rbm22 (residues 1988-2014) |
| 41 | d2bapa1 | Alignment | not modelled | 5.4 | 18 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Diap1 N-terminal region-like |
| 42 | c5w71A_ | Alignment | not modelled | 5.3 | 15 | PDB header: membrane protein Chain: A; PDB Molecule: n,n'-diacetylbacliosaminyl-1-phosphate transferase; PDBTitle: structure of campylobacter concisus pglc i57m/q175m variant |
| 43 | c6bc8B_ | Alignment | not modelled | 5.2 | 23 | PDB header: replication Chain: B; PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: crystal structure of rev7-r124a/rev3-rbm2 (residues 1988-2014) complex |