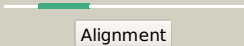

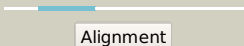
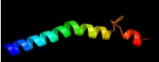
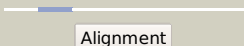
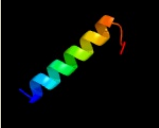
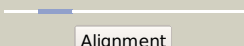
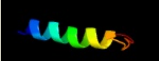
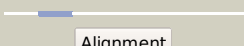

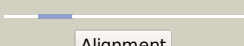
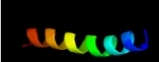
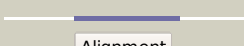
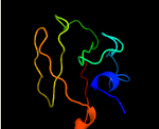
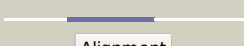









Phyre2

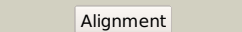
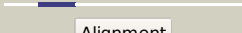
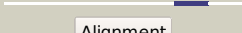
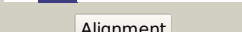
| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1382_(-)_1555483_1555980 |
| Date | Wed Jul 31 22:05:48 BST 2019 |
| Unique Job ID | 2aa613a7123708c7 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d2oara1 |  Alignment |  | 48.4 | 18 | Fold: Gated mechanosensitive channel Superfamily: Gated mechanosensitive channel Family: Gated mechanosensitive channel |
| 2 | c2oarA |  Alignment |  | 31.2 | 18 | PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl) |
| 3 | c6adqP |  Alignment |  | 26.2 | 46 | PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciiv2civ2sod2 from mycobacterium smegmatis |
| 4 | c2micB |  Alignment |  | 22.9 | 31 | PDB header: membrane protein Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles |
| 5 | c2micA |  Alignment |  | 22.9 | 31 | PDB header: membrane protein Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles |
| 6 | c4cdiC |  Alignment |  | 22.6 | 28 | PDB header: membrane protein Chain: C: PDB Molecule: predicted protein; PDBTitle: crystal structure of acrb-acrz complex |
| 7 | c2grxB |  Alignment |  | 18.7 | 16 | PDB header: metal transport Chain: B: PDB Molecule: ferrichrome-iron receptor; PDBTitle: crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome |
| 8 | c3ts3D |  Alignment |  | 17.8 | 30 | PDB header: viral protein Chain: D: PDB Molecule: capsid polyprotein; PDBTitle: crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution |
| 9 | c2lowA |  Alignment |  | 15.8 | 16 | PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip |
| 10 | c2lp1A |  Alignment |  | 15.1 | 19 | PDB header: membrane protein Chain: A: PDB Molecule: c99; PDBTitle: the solution nmr structure of the transmembrane c-terminal domain of2 the amyloid precursor protein (c99) |
| 11 | c3hzqA |  Alignment |  | 14.8 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of a tetrameric mscl in an expanded intermediate state |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c2xfvB_ | Alignment | | 14.2 | 33 | PDB header: cell-cycle Chain: B: PDB Molecule: regulatory protein swi6; PDBTitle: structure of the amino-terminal domain from the cell-cycle2 regulator swi6 |
| 13 | d1eyqa_ | Alignment | | 14.2 | 20 | Fold: Chalcone isomerase Superfamily: Chalcone isomerase Family: Chalcone isomerase |
| 14 | c3t2dA_ | Alignment | | 13.4 | 12 | PDB header: lyase, hydrolase Chain: A: PDB Molecule: fructose-1,6-bisphosphate aldolase/phosphatase; PDBTitle: fructose-1,6-bisphosphate aldolase/phosphatase from thermoproteus2 neutrophilus, fbp-bound form |
| 15 | c4doiB_ | Alignment | | 13.1 | 20 | PDB header: isomerase Chain: B: PDB Molecule: chalcone--flavonone isomerase 1; PDBTitle: crystal structure of arabidopsis thaliana chalcone isomerase at3g551202 (atchi) |
| 16 | c5yx4A_ | Alignment | | 12.7 | 15 | PDB header: isomerase Chain: A: PDB Molecule: chalcone-flavonone isomerase family protein; PDBTitle: isoliquiritigenin-complexed chalcone isomerase (s189a) from the2 antarctic vascular plant deschampsia antarctica (dachi1) |
| 17 | c4doka_ | Alignment | | 12.4 | 10 | PDB header: isomerase Chain: A: PDB Molecule: similarity to chalcone-flavonone isomerase; PDBTitle: crystal structure of arabidopsis thaliana chalcone-isomerase like2 protein at5g05270 (atchil) |
| 18 | d2ix0a3 | Alignment | | 11.7 | 26 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 19 | d1a62a2 | Alignment | | 11.3 | 24 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 20 | d2ix0a2 | Alignment | | 10.9 | 15 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 21 | d1qb5d_ | Alignment | not modelled | 10.7 | 36 | Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits |
| 22 | c5wl4D_ | Alignment | not modelled | 10.3 | 20 | PDB header: isomerase Chain: D: PDB Molecule: engineered chalcone isomerase ancr3; PDBTitle: crystal structure of chalcone isomerase engineered from ancestral2 inference (ancr3) |
| 23 | d1ea0a3 | Alignment | not modelled | 10.0 | 21 | Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases |
| 24 | d1f7ra_ | Alignment | not modelled | 9.2 | 18 | Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like |
| 25 | c3mk7F_ | Alignment | not modelled | 9.0 | 8 | PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase |
| 26 | c3ixzB_ | Alignment | not modelled | 8.9 | 25 | PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride |
| 27 | c3d0fA_ | Alignment | not modelled | 8.7 | 16 | PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718 |
| 28 | c2lioA_ | Alignment | not modelled | 8.3 | 25 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of bfr322 from bacteroides fragilis, |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|--|
| | | | | | | northeast2 structural genomics consortium target bfr322 |
| 29 | d1by5a_ | Alignment | not modelled | 8.2 | 16 | Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel |
| 30 | c1n62E_ | Alignment | not modelled | 8.0 | 8 | PDB header: oxidoreductase Chain: E: PDB Molecule: carbon monoxide dehydrogenase large chain; PDBTitle: crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state |
| 31 | c4dooA_ | Alignment | not modelled | 7.8 | 25 | PDB header: isomerase Chain: A: PDB Molecule: chalcone-flavanone isomerase family protein; PDBTitle: crystal structure of arabidopsis thaliana fatty-acid binding protein2 at3g63170 (atfap1) |
| 32 | d2pila_ | Alignment | not modelled | 7.6 | 16 | Fold: Pili subunits Superfamily: Pili subunits Family: Pilin |
| 33 | d2gcla1 | Alignment | not modelled | 7.4 | 17 | Fold: PH domain-like barrel Superfamily: PH domain-like Family: SSRP1-like |
| 34 | d1f7da_ | Alignment | not modelled | 7.4 | 16 | Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like |
| 35 | c2mkaA_ | Alignment | not modelled | 7.3 | 26 | PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state |
| 36 | c2mk9A_ | Alignment | not modelled | 7.3 | 26 | PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the dimeric transmembrane domain of toll-like2 receptor 3 |
| 37 | c2mkaC_ | Alignment | not modelled | 7.3 | 26 | PDB header: immune system Chain: C: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state |
| 38 | c2mk9B_ | Alignment | not modelled | 7.3 | 26 | PDB header: immune system Chain: B: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the dimeric transmembrane domain of toll-like2 receptor 3 |
| 39 | c2mkaB_ | Alignment | not modelled | 7.3 | 26 | PDB header: immune system Chain: B: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state |
| 40 | d1oqwa_ | Alignment | not modelled | 7.1 | 22 | Fold: Pili subunits Superfamily: Pili subunits Family: Pilin |
| 41 | c3ssmB_ | Alignment | not modelled | 6.9 | 36 | PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 1 |
| 42 | d1duna_ | Alignment | not modelled | 6.8 | 15 | Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like |
| 43 | c2l6wA_ | Alignment | not modelled | 6.5 | 29 | PDB header: membrane protein Chain: A: PDB Molecule: beta-type platelet-derived growth factor receptor; PDBTitle: pdgfr beta-tm |
| 44 | c2l6wB_ | Alignment | not modelled | 6.5 | 29 | PDB header: membrane protein Chain: B: PDB Molecule: beta-type platelet-derived growth factor receptor; PDBTitle: pdgfr beta-tm |
| 45 | c2rddB_ | Alignment | not modelled | 6.4 | 17 | PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix. |
| 46 | d1mrza1 | Alignment | not modelled | 6.4 | 23 | Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like |
| 47 | c2mkvA_ | Alignment | not modelled | 6.3 | 18 | PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles |
| 48 | c3wmmP_ | Alignment | not modelled | 6.3 | 25 | PDB header: photosynthesis Chain: P: PDB Molecule: lh1 beta polypeptide; PDBTitle: crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form |
| 49 | c4dola_ | Alignment | not modelled | 6.1 | 30 | PDB header: isomerase Chain: A: PDB Molecule: at1g53520; PDBTitle: crystal structure of arabidopsis thaliana fatty-acid binding protein2 at1g53520 (atfap3) |
| 50 | d1ofda3 | Alignment | not modelled | 6.1 | 25 | Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases |
| 51 | c2e12B_ | Alignment | not modelled | 6.0 | 29 | PDB header: translation Chain: B: PDB Molecule: hypothetical protein xcc3642; PDBTitle: the crystal structure of xc5848 from xanthomonas campestris2 adopting a novel variant of sm-like motif |
| 52 | c2vdcF_ | Alignment | not modelled | 5.8 | 21 | PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadh] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications. |
| 53 | c5h7yB_ | Alignment | not modelled | 5.7 | 33 | PDB header: hydrolase inhibitor/peptide Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: structure of immunity protein tplei of t6ss from pseudomonas2 aeruginosa complexed with "I" peptide |

| | | | | | | |
|----|-------------------------|---|--------------|-----|----|---|
| 54 | c1wa7B_ |  Alignment | not modelled | 5.7 | 25 | PDB header: sh3 domain Chain: B: PDB Molecule: hypothetical 28.7 kda protein in dhfr 3'region PDBTitle: sh3 domain of human lyn tyrosine kinase in complex with a2 herpesviral ligand |
| 55 | c6fkip_ |  Alignment | not modelled | 5.5 | 7 | PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3 |
| 56 | d2pwaa1 |  Alignment | not modelled | 5.5 | 36 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 57 | c5wdaL_ |  Alignment | not modelled | 5.5 | 20 | PDB header: protein transport Chain: L: PDB Molecule: general secretion pathway protein g; PDBTitle: structure of the pulg pseudopilus |