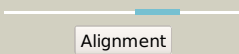
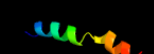
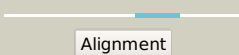
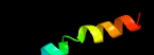
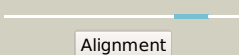



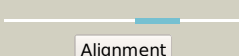

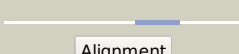

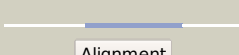

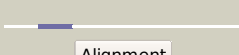

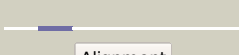







Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1824 (-) _2070661_2071026 |
| Date | Fri Aug 2 13:30:43 BST 2019 |
| Unique Job ID | e0ecefbf1fce95ee |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c2ka1B_ |  Alignment |  | 35.0 | 38 | PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles |
| 2 | c2ka2A_ |  Alignment |  | 35.0 | 38 | PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints |
| 3 | d1hula_ |  Alignment |  | 30.3 | 23 | Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines |
| 4 | c2ka1A_ |  Alignment |  | 30.3 | 38 | PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles |
| 5 | c2ka2B_ |  Alignment |  | 30.3 | 38 | PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints |
| 6 | c2j5dA_ |  Alignment |  | 26.3 | 38 | PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting protein 3; PDBTitle: nmr structure of bnip3 transmembrane domain in lipid bicelles |
| 7 | c3t6gB_ |  Alignment |  | 23.6 | 26 | PDB header: signaling protein, cell adhesion Chain: B: PDB Molecule: breast cancer anti-estrogen resistance protein 1; PDBTitle: structure of the complex between nsp3 (shep1) and p130cas |
| 8 | c6ijoI_ |  Alignment |  | 19.6 | 21 | PDB header: photosynthesis Chain: I: PDB Molecule: psai; PDBTitle: photosystem i of chlamydomonas reinhardtii |
| 9 | c6jo5I_ |  Alignment |  | 18.2 | 21 | PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: structure of the green algal photosystem i supercomplex with light-2 harvesting complex i |
| 10 | c6igzI_ |  Alignment |  | 17.6 | 18 | PDB header: plant protein Chain: I: PDB Molecule: psai; PDBTitle: structure of psi-lhci |
| 11 | c4i7zE_ |  Alignment |  | 17.1 | 44 | PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of cytochrome b6f in dopg, with disordered rieske2 iron-sulfur protein soluble domain |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 12 | c4pv1E_ | Alignment | | 17.1 | 44 | PDB header: electron transport/inhibitor Chain: E; PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: cytochrome b6f structure from m. lamosus with the quinone analog2 inhibitor stigmatellin |
| 13 | c3q4nA_ | Alignment | | 15.6 | 16 | PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein mj0754; PDBTitle: crystal structure of hypothetical protein mj0754 from methanococcus2 jannaschii dsm 2661 |
| 14 | d2e74e1 | Alignment | | 14.6 | 44 | Fold: Single transmembrane helix Superfamily: PetL subunit of the cytochrome b6f complex Family: PetL subunit of the cytochrome b6f complex |
| 15 | c2e75E_ | Alignment | | 14.6 | 44 | PDB header: photosynthesis Chain: E; PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.lamosus |
| 16 | c1vf5R_ | Alignment | | 14.6 | 44 | PDB header: photosynthesis Chain: R; PDB Molecule: protein pet I; PDBTitle: crystal structure of cytochrome b6f complex from m.lamosus |
| 17 | c2e76E_ | Alignment | | 14.6 | 44 | PDB header: photosynthesis Chain: E; PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.lamosus |
| 18 | c4h0IE_ | Alignment | | 14.6 | 44 | PDB header: photosynthesis Chain: E; PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: cytochrome b6f complex crystal structure from mastigocladus lamosus2 with n-side inhibitor nqno |
| 19 | c4h13E_ | Alignment | | 14.6 | 44 | PDB header: photosynthesis Chain: E; PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from mastigocladus2 lamosus with tds |
| 20 | c2e74E_ | Alignment | | 14.6 | 44 | PDB header: photosynthesis Chain: E; PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from m.lamosus |
| 21 | c1vf5E_ | Alignment | not modelled | 13.6 | 39 | PDB header: photosynthesis Chain: E; PDB Molecule: protein pet I; PDBTitle: crystal structure of cytochrome b6f complex from m.lamosus |
| 22 | c2lowA_ | Alignment | not modelled | 13.6 | 29 | PDB header: membrane protein Chain: A; PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip |
| 23 | c2n6uA_ | Alignment | not modelled | 11.5 | 54 | PDB header: unknown function Chain: A; PDB Molecule: astexin2-dc4; PDBTitle: solution study of astexin2-dc4 |
| 24 | d1u61a_ | Alignment | not modelled | 11.0 | 33 | Fold: RNase III domain-like Superfamily: RNase III domain-like Family: RNase III catalytic domain-like |
| 25 | d1ciya3 | Alignment | not modelled | 10.5 | 10 | Fold: Toxins' membrane translocation domains Superfamily: delta-Endotoxin (insecticide), N-terminal domain Family: delta-Endotoxin (insecticide), N-terminal domain |
| 26 | c5wudA_ | Alignment | not modelled | 10.4 | 23 | PDB header: membrane protein Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: structural basis for conductance through tric cation channels |
| 27 | c3thgA_ | Alignment | not modelled | 10.2 | 62 | PDB header: protein binding Chain: A; PDB Molecule: ribulose bisphosphate carboxylase/oxygenase activase 1, PDBTitle: crystal structure of the creosote rubisco activase c-domain |
| 28 | c3jrza_ | Alignment | not modelled | 10.0 | 31 | PDB header: toxin Chain: A; PDB Molecule: ccdb; PDBTitle: ccdbvfi-formii-ph5.6 |
| | | | | | | PDB header: structural genomics, unknown function |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|--|
| 29 | c2gslE_ | Alignment | not modelled | 9.8 | 22 | Chain: E; PDB Molecule: hypothetical protein; PDBTitle: x-ray crystal structure of protein fn1578 from fusobacterium2 nucleatum. northeast structural genomics consortium target nr1. |
| 30 | c1wyyB_ | Alignment | not modelled | 7.9 | 29 | PDB header: viral protein Chain: B; PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein |
| 31 | c2mgyA_ | Alignment | not modelled | 7.5 | 11 | PDB header: membrane protein Chain: A; PDB Molecule: translocator protein; PDBTitle: solution structure of the mitochondrial translocator protein (tspo) in2 complex with its high-affinity ligand pk11195 |
| 32 | c5dn6X_ | Alignment | not modelled | 7.5 | 33 | PDB header: hydrolase Chain: X; PDB Molecule: atp synthase subunit a,atp synthase subunit a; PDBTitle: atp synthase from paracoccus denitrificans |
| 33 | d1t07a_ | Alignment | not modelled | 7.4 | 27 | Fold: YggX-like Superfamily: YggX-like Family: YggX-like |
| 34 | c1x3oA_ | Alignment | not modelled | 7.2 | 22 | PDB header: lipid transport Chain: A; PDB Molecule: acyl carrier protein; PDBTitle: crystal structure of the acyl carrier protein from thermus2 thermophilus hb8 |
| 35 | d1xs8a_ | Alignment | not modelled | 6.9 | 36 | Fold: YggX-like Superfamily: YggX-like Family: YggX-like |
| 36 | c2ju2A_ | Alignment | not modelled | 6.7 | 17 | PDB header: transferase Chain: A; PDB Molecule: erythronolide synthase; PDBTitle: minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs) |
| 37 | c2gpvH_ | Alignment | not modelled | 6.3 | 44 | PDB header: transcription Chain: H; PDB Molecule: nuclear receptor corepressor 2; PDBTitle: estrogen related receptor-gamma ligand binding domain complexed with2 4-hydroxy-tamoxifen and a smrt peptide |
| 38 | c2gpvG_ | Alignment | not modelled | 6.3 | 44 | PDB header: transcription Chain: G; PDB Molecule: nuclear receptor corepressor 2; PDBTitle: estrogen related receptor-gamma ligand binding domain complexed with2 4-hydroxy-tamoxifen and a smrt peptide |
| 39 | c2gpvI_ | Alignment | not modelled | 6.3 | 44 | PDB header: transcription Chain: I; PDB Molecule: nuclear receptor corepressor 2; PDBTitle: estrogen related receptor-gamma ligand binding domain complexed with2 4-hydroxy-tamoxifen and a smrt peptide |
| 40 | c2mzyA_ | Alignment | not modelled | 5.8 | 27 | PDB header: iron binding protein Chain: A; PDB Molecule: probable fe(2+)-trafficking protein; PDBTitle: 1h, 13c, and 15n chemical shift assignments and structure of probable2 fe(2+)-trafficking protein from burkholderia pseudomallei 1710b. |
| 41 | c2lezA_ | Alignment | not modelled | 5.6 | 25 | PDB header: signaling protein Chain: A; PDB Molecule: secreted effector protein pipb2; PDBTitle: solution nmr structure of n-terminal domain of salmonella effector2 protein pipb2. northeast structural genomics consortium (nsg) target3 stt318a |
| 42 | c5zjil_ | Alignment | not modelled | 5.3 | 15 | PDB header: membrane protein Chain: I; PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: structure of photosystem i supercomplex with light-harvesting2 complexes i and ii |