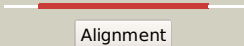
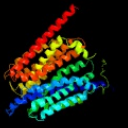
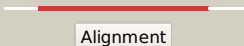

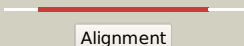







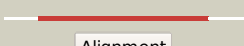
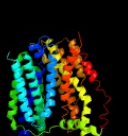










Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2508c_(-)_2823266_2824603 |
| Date | Wed Aug 7 12:50:14 BST 2019 |
| Unique Job ID | d1c0c8257f51c1d8 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | d1pw4a_ |  Alignment |  | 100.0 | 13 | Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter |
| 2 | c3wdoA_ |  Alignment |  | 100.0 | 14 | PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter |
| 3 | c4j05A_ |  Alignment |  | 100.0 | 13 | PDB header: transport protein Chain: A: PDB Molecule: phosphate transporter; PDBTitle: crystal structure of a eukaryotic phosphate transporter |
| 4 | d1pv7a_ |  Alignment |  | 100.0 | 10 | Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter |
| 5 | c1pv7B_ |  Alignment |  | 100.0 | 10 | PDB header: transport protein Chain: B: PDB Molecule: lactose permease; PDBTitle: crystal structure of lactose permease with tdg |
| 6 | c6e9oA_ |  Alignment |  | 100.0 | 11 | PDB header: membrane protein Chain: A: PDB Molecule: d-galactonate transport; PDBTitle: e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form |
| 7 | c4cl5B_ |  Alignment |  | 100.0 | 11 | PDB header: transport protein Chain: B: PDB Molecule: nitrate transporter 1.1; PDBTitle: crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate. |
| 8 | c6g9xB_ |  Alignment |  | 100.0 | 15 | PDB header: membrane protein Chain: B: PDB Molecule: major facilitator superfamily mfs_1; PDBTitle: crystal structure of a mfs transporter at 2.54 angstroem resolution |
| 9 | c5c65A_ |  Alignment |  | 100.0 | 10 | PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: structure of the human glucose transporter glut3 / slc2a3 |
| 10 | c6h7dA_ |  Alignment |  | 100.0 | 10 | PDB header: membrane protein Chain: A: PDB Molecule: sugar transport protein 10; PDBTitle: crystal structure of a. thaliana sugar transport protein 10 in complex2 with glucose in the outward occluded state |
| 11 | c4ldsB_ |  Alignment |  | 100.0 | 12 | PDB header: transport protein, membrane protein Chain: B: PDB Molecule: bicyclomycin resistance protein tcab; PDBTitle: the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | c5aynA_ | Alignment | | 100.0 | 13 | PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 39 (iron-regulated transporter); PDBTitle: crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state |
| 13 | c4ybgB_ | Alignment | | 100.0 | 10 | PDB header: transport protein/immune system Chain: B: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: rat glut5 with fv in the outward-open form |
| 14 | c4iu8A_ | Alignment | | 100.0 | 10 | PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative) |
| 15 | c4w6vA_ | Alignment | | 99.9 | 10 | PDB header: transport protein Chain: A: PDB Molecule: di-/tripeptide transporter; PDBTitle: crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution |
| 16 | c4zp0A_ | Alignment | | 99.9 | 13 | PDB header: transport protein Chain: A: PDB Molecule: multidrug transporter mdfa; PDBTitle: crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate |
| 17 | c3o7pA_ | Alignment | | 99.9 | 10 | PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a) |
| 18 | c5aymA_ | Alignment | | 99.9 | 12 | PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 39 (iron-regulated transporter); PDBTitle: crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron |
| 19 | c4gbzA_ | Alignment | | 99.9 | 14 | PDB header: transport protein Chain: A: PDB Molecule: d-xylose-proton symporter; PDBTitle: the structure of the mfs (major facilitator superfamily) proton:xylose2 symporter xyle bound to d-glucose |
| 20 | c6ei3A_ | Alignment | | 99.9 | 9 | PDB header: membrane protein Chain: A: PDB Molecule: proton-dependent oligopeptide transporter family protein; PDBTitle: crystal structure of auto inhibited pot family peptide transporter |
| 21 | c6gs7A_ | Alignment | not modelled | 99.9 | 10 | PDB header: membrane protein Chain: A: PDB Molecule: dipeptide and tripeptide permease a; PDBTitle: crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer |
| 22 | c4ikyA_ | Alignment | not modelled | 99.9 | 12 | PDB header: transport protein Chain: A: PDB Molecule: di-/tripeptide abc transporter (permease); PDBTitle: crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate |
| 23 | c4iu9A_ | Alignment | not modelled | 99.9 | 14 | PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter |
| 24 | c6exsA_ | Alignment | not modelled | 99.9 | 10 | PDB header: membrane protein Chain: A: PDB Molecule: peptide abc transporter permease; PDBTitle: crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide. |
| 25 | c4pypA_ | Alignment | not modelled | 99.9 | 10 | PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: crystal structure of the human glucose transporter glut1 |
| 26 | c2gfpA_ | Alignment | not modelled | 99.9 | 15 | PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli |
| 27 | c4apsB_ | Alignment | not modelled | 99.9 | 8 | PDB header: transport protein Chain: B: PDB Molecule: di- or tripeptide h+ symporter; PDBTitle: crystal structure of a pot family peptide transporter in an inward2 open conformation. |
| 28 | c2xutC_ | Alignment | not modelled | 99.9 | 8 | PDB header: transport protein Chain: C: PDB Molecule: proton/peptide symporter family protein; PDBTitle: crystal structure of a proton dependent oligopeptide (pot) family2 transporter. |
| 29 | c4lanB_ | Alignment | not modelled | 99.9 | 11 | PDB header: membrane protein, transport protein Chain: B: PDB Molecule: proton:oligopeptide symporter pot family; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c4repB_ | Alignment | not modelled | 99.9 | 11 | PDBTitle: structural insights into substrate recognition in proton dependent2 oligopeptide transporters |
| 30 | c4q65A_ | Alignment | not modelled | 99.9 | 10 | PDB header: transport protein Chain: A: PDB Molecule: dipeptide permease d; PDBTitle: structure of the e. coli peptide transporter ybgh |
| 31 | c4m64D_ | Alignment | not modelled | 99.9 | 11 | PDB header: transport protein Chain: D: PDB Molecule: melibiose carrier protein; PDBTitle: 3d crystal structure of na+/melibiose symporter of salmonella2 typhimurium |
| 32 | c6ob7A_ | Alignment | not modelled | 99.6 | 13 | PDB header: transport protein Chain: A: PDB Molecule: equilibrative nucleoside transporter 1; PDBTitle: human equilibrative nucleoside transporter-1, dilazep bound |
| 33 | c2g9pA_ | Alignment | not modelled | 18.0 | 14 | PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide latarcin 2a; PDBTitle: nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom |
| 34 | c3b9yA_ | Alignment | not modelled | 12.5 | 11 | PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein |
| 35 | c2jo1A_ | Alignment | not modelled | 8.7 | 14 | PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles |
| 36 | c2kluA_ | Alignment | not modelled | 7.4 | 19 | PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4 |
| 37 | d1rh1a2 | Alignment | not modelled | 7.3 | 23 | Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin |
| 38 | c4djiA_ | Alignment | not modelled | 6.8 | 10 | PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc |
| 39 | c5by3A_ | Alignment | not modelled | 6.1 | 19 | PDB header: sugar binding protein Chain: A: PDB Molecule: btgh115a; PDBTitle: a novel family gh115 4-o-methyl-alpha-glucuronidase, btgh115a, with2 specificity for decorated arabinogalactans |
| 40 | c2rddB_ | Alignment | not modelled | 6.0 | 6 | 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. |
| 41 | c2jp3A_ | Alignment | not modelled | 6.0 | 19 | PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles |