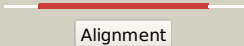









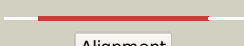












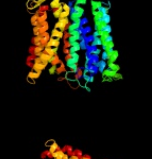
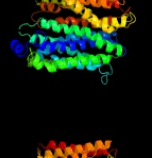
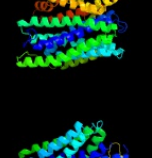
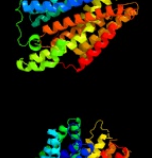
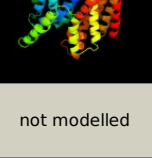


Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0261c_(narK3)_312759_314168 |
| Date | Tue Jul 23 14:50:32 BST 2019 |
| Unique Job ID | 39d04aed8f6092bb |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4iu8A_ |  Alignment |  | 100.0 | 27 | PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative) |
| 2 | c4iu9A_ |  Alignment |  | 100.0 | 30 | PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter |
| 3 | d1pw4a_ |  Alignment |  | 100.0 | 10 | Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter |
| 4 | 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 |
| 5 | c3wdoA_ |  Alignment |  | 100.0 | 13 | PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter |
| 6 | c4ldsB_ |  Alignment |  | 100.0 | 13 | PDB header: transport protein, membrane protein Chain: B: PDB Molecule: bicyclomycin resistance protein tcb; PDBTitle: the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis |
| 7 | c6g9xB_ |  Alignment |  | 100.0 | 16 | PDB header: membrane protein Chain: B: PDB Molecule: major facilitator superfamily mfs_1; PDBTitle: crystal structure of a mfs transporter at 2.54 angstrom resolution |
| 8 | c6h7dA_ |  Alignment |  | 100.0 | 11 | 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 |
| 9 | c3o7pA_ |  Alignment |  | 100.0 | 11 | PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a) |
| 10 | c5c65A_ |  Alignment |  | 100.0 | 12 | PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: structure of the human glucose transporter glut3 / slc2a3 |
| 11 | c4cl5B_ |  Alignment |  | 100.0 | 12 | 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. |

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|----|-------------------------|-----------|---|-------|----|--|
| 12 | c4ybqB_ | Alignment |  | 100.0 | 12 | 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 |
| 13 | c6gs7A_ | Alignment |  | 100.0 | 12 | PDB header: membrane protein Chain: A: PDB Molecule: dipeptide and tripeptide permease a; PDBTitle: crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer |
| 14 | c4j05A_ | Alignment |  | 100.0 | 11 | PDB header: transport protein Chain: A: PDB Molecule: phosphate transporter; PDBTitle: crystal structure of a eukaryotic phosphate transporter |
| 15 | c4zp0A_ | Alignment |  | 100.0 | 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 |
| 16 | c6exsA_ | Alignment |  | 100.0 | 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. |
| 17 | c4ikyA_ | Alignment |  | 100.0 | 13 | 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 |
| 18 | c4w6vA_ | Alignment |  | 100.0 | 13 | 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 |
| 19 | c6ei3A_ | Alignment |  | 100.0 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: proton-dependent oligopeptide transporter family protein; PDBTitle: crystal structure of auto inhibited pot family peptide transporter |
| 20 | c4apsB_ | Alignment |  | 100.0 | 11 | 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. |
| 21 | d1pv7a_ | Alignment | not modelled | 100.0 | 12 | Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter |
| 22 | c1pv7B_ | Alignment | not modelled | 100.0 | 12 | PDB header: transport protein Chain: B: PDB Molecule: lactose permease; PDBTitle: crystal structure of lactose permease with tdg |
| 23 | c4pypA_ | Alignment | not modelled | 100.0 | 13 | PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: crystal structure of the human glucose transporter glut1 |
| 24 | c4q65A_ | Alignment | not modelled | 100.0 | 12 | PDB header: transport protein Chain: A: PDB Molecule: dipeptide permease d; PDBTitle: structure of the e. coli peptide transporter ybgh |
| 25 | c4gbzA_ | Alignment | not modelled | 100.0 | 12 | 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 |
| 26 | c4lepB_ | Alignment | not modelled | 100.0 | 12 | PDB header: membrane protein, transport protein Chain: B: PDB Molecule: proton:oligopeptide symporter pot family; PDBTitle: structural insights into substrate recognition in proton dependent2 oligopeptide transporters |
| 27 | c2gfpA_ | Alignment | not modelled | 100.0 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli |
| 28 | c2xutC_ | Alignment | not modelled | 100.0 | 14 | PDB header: transport protein Chain: C: PDB Molecule: proton/peptide symporter family protein; PDBTitle: crystal structure of a proton dependent oligopeptide (pot) family2 transporter. PDB header: transport protein |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c5aynA_ | Alignment | not modelled | 99.9 | 9 | 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 |
| 30 | c5aymA_ | Alignment | not modelled | 99.9 | 8 | 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 |
| 31 | c4m64D_ | Alignment | not modelled | 99.8 | 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 | 99.5 | 10 | PDB header: transport protein Chain: A: PDB Molecule: equilibrative nucleoside transporter 1; PDBTitle: human equilibrative nucleoside transporter-1, dilazep bound |
| 33 | c3b9yA_ | Alignment | not modelled | 70.8 | 12 | PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein |
| 34 | c3hd6A_ | Alignment | not modelled | 42.8 | 7 | PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg |
| 35 | c3mp6A_ | Alignment | not modelled | 41.8 | 27 | PDB header: histone binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,linker,saga-associated PDBTitle: complex structure of sgf29 and dimethylated h3k4 |
| 36 | c6eu6A_ | Alignment | not modelled | 27.6 | 11 | PDB header: membrane protein Chain: A: PDB Molecule: ammonium transporter; PDBTitle: sensor amt protein |
| 37 | c2rddB_ | Alignment | not modelled | 20.6 | 11 | 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. |
| 38 | c2gleA_ | Alignment | not modelled | 17.1 | 20 | PDB header: protein binding Chain: A: PDB Molecule: neurabin-1; PDBTitle: solution structure of neurabin sam domain |
| 39 | c2l92A_ | Alignment | not modelled | 16.5 | 24 | PDB header: dna binding protein Chain: A: PDB Molecule: histone family protein nucleoid-structuring protein h-ns; PDBTitle: solution structure of the c-terminal domain of h-ns like protein bv3f |
| 40 | c5aezA_ | Alignment | not modelled | 15.4 | 10 | PDB header: membrane protein Chain: A: PDB Molecule: mep2; PDBTitle: crystal structure of candida albicans mep2 |
| 41 | c6hwhB_ | Alignment | not modelled | 13.9 | 11 | PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis |
| 42 | c3qngD_ | Alignment | not modelled | 13.5 | 18 | PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system |
| 43 | c6bx3N_ | Alignment | not modelled | 10.7 | 31 | PDB header: gene regulation/transferase Chain: N: PDB Molecule: compass component sdc1; PDBTitle: structure of histone h3k4 methyltransferase |
| 44 | c2k04D_ | Alignment | not modelled | 10.5 | 25 | PDB header: cytokine Chain: D: PDB Molecule: c-x-c chemokine receptor type 4; PDBTitle: structure of sdf1 in complex with the cxcr4 n-terminus containing no2 sulfotyrosines |
| 45 | c2g9pA_ | Alignment | not modelled | 10.4 | 21 | 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 |
| 46 | c2e8pA_ | Alignment | not modelled | 10.3 | 15 | PDB header: signaling protein Chain: A: PDB Molecule: elf3 protein; PDBTitle: solution structure of the n-terminal sam-domain of e74-like2 factor 3 |
| 47 | c5aexB_ | Alignment | not modelled | 9.9 | 12 | PDB header: membrane protein Chain: B: PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2 |
| 48 | c6oh2A_ | Alignment | not modelled | 9.7 | 10 | PDB header: transport protein Chain: A: PDB Molecule: cmp-sialic acid transporter; PDBTitle: x-ray crystal structure of the mouse cmp-sialic acid transporter in2 complex with cmp, by lipidic cubic phase |
| 49 | c5a4hA_ | Alignment | not modelled | 9.6 | 33 | PDB header: transferase Chain: A: PDB Molecule: 1-acylglycerol-3-phosphate o-acyltransferase abhd5; PDBTitle: solution structure of the lipid droplet anchoring peptide2 of cgi-58 bound to dpc micelles |
| 50 | c6chgE_ | Alignment | not modelled | 8.6 | 31 | PDB header: transferase Chain: E: PDB Molecule: klla0e03521p; PDBTitle: crystal structure of the yeast compass catalytic module |
| 51 | d2z15a1 | Alignment | not modelled | 8.4 | 36 | Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like |
| 52 | c6r8fG_ | Alignment | not modelled | 8.3 | 22 | PDB header: signaling protein Chain: G: PDB Molecule: brisc and brca1-a complex member 2,brcc45 (bre, brisc and PDBTitle: cryo-em structure of the human brisc-shmt2 complex |
| 53 | c6r8fE_ | Alignment | not modelled | 8.3 | 22 | PDB header: signaling protein Chain: E: PDB Molecule: brisc and brca1-a complex member 2,brcc45 (bre, brisc and |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|---|
| | | | | | | PDBTitle: cryo-em structure of the human brisc-shmt2 complex |
| 54 | d3e9va1 | Alignment | not modelled | 8.3 | 36 | Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like |
| 55 | c2kjeB | Alignment | not modelled | 8.2 | 50 | PDB header: transcription Chain: B: PDB Molecule: early e1a 32 kda protein; PDBTitle: nmr structure of cbp taz2 and adenoviral e1a complex |
| 56 | c2nuuF | Alignment | not modelled | 7.7 | 12 | PDB header: transport protein/signaling protein Chain: F: PDB Molecule: ammonia channel; PDBTitle: regulating the escherichia coli ammonia channel: the crystal structure2 of the amtb-glnk complex |
| 57 | c5td6A | Alignment | not modelled | 7.3 | 21 | PDB header: rna binding protein Chain: A: PDB Molecule: fog-3 protein; PDBTitle: c. elegans fog-3 btg/tob domain - h47n, c117a |
| 58 | c4mhyB | Alignment | not modelled | 7.3 | 18 | PDB header: transcription Chain: B: PDB Molecule: protein c-ets-2; PDBTitle: crystal structure of the pnt domain of human ets2 |
| 59 | c3hftA | Alignment | not modelled | 7.2 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: wbms, polysaccharide deacetylase involved in o-antigen PDBTitle: crystal structure of a putative polysaccharide deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution |
| 60 | d1sv0c | Alignment | not modelled | 7.2 | 27 | Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain |
| 61 | d1sxda | Alignment | not modelled | 7.1 | 27 | Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain |
| 62 | d1sv0a | Alignment | not modelled | 6.7 | 27 | Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain |
| 63 | c5t86A | Alignment | not modelled | 6.7 | 38 | PDB header: toxin Chain: A: PDB Molecule: cdia toxin; PDBTitle: crystal structure of cdi complex from e. coli a0 34/86 |
| 64 | c4od5C | Alignment | not modelled | 6.7 | 13 | PDB header: transferase Chain: C: PDB Molecule: 4-hydroxybenzoate octaprenyltransferase; PDBTitle: substrate-bound structure of a ubia homolog from aeropyrum pernix k1 |
| 65 | c3lgeF | Alignment | not modelled | 6.5 | 43 | PDB header: lyase/protein binding Chain: F: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex |
| 66 | c3lgeG | Alignment | not modelled | 6.5 | 43 | PDB header: lyase/protein binding Chain: G: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex |
| 67 | c2zxeG | Alignment | not modelled | 6.4 | 13 | PDB header: hydrolase/transport protein Chain: G: PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state |
| 68 | c3o6xC | Alignment | not modelled | 6.3 | 13 | PDB header: ligase Chain: C: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis |
| 69 | d1ji7a | Alignment | not modelled | 6.1 | 9 | Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain |
| 70 | c3jcuZ | Alignment | not modelled | 5.9 | 13 | PDB header: membrane protein Chain: Z: PDB Molecule: photosystem ii reaction center protein z; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution |
| 71 | c2dkxA | Alignment | not modelled | 5.9 | 27 | PDB header: signaling protein Chain: A: PDB Molecule: sam pointed domain-containing ets transcription PDBTitle: solution structure of the sam_pnt-domain of ets2 transcription factor pdef (prostate ets) |
| 72 | c6hwhX | Alignment | not modelled | 5.9 | 10 | PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis |
| 73 | c2o8kA | Alignment | not modelled | 5.8 | 19 | PDB header: transcription/dna Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: nmr structure of the sigma-54 rpon domain bound to the-242 promoter element |
| 74 | c4ev6E | Alignment | not modelled | 5.8 | 25 | PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii |
| 75 | c5gyqA | Alignment | not modelled | 5.7 | 31 | PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein; PDBTitle: putative receptor-binding domain of bat-derived coronavirus hku9 spike2 protein |
| 76 | c2bbjB | Alignment | not modelled | 5.7 | 7 | PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter |
| 77 | d1bqva | Alignment | not modelled | 5.7 | 27 | Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain |
| 78 | c2jr1A | Alignment | not modelled | 5.7 | 16 | PDB header: dna binding protein Chain: A: PDB Molecule: virulence regulator; PDBTitle: solution structure of the dna binding domain of a nucleoid-associated2 protein, h-ns, from the phytopathogen xylella fastidiosa. |
| | | | | | | PDB header: membrane protein/metal transport |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 79 | c4k1cA_ | Alignment | not modelled | 5.6 | 11 | Chain: A: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger |
| 80 | c2m0oA_ | Alignment | not modelled | 5.6 | 24 | PDB header: peptide binding protein Chain: A: PDB Molecule: phd finger protein 1; PDBTitle: the solution structure of human phf1 in complex with h3k36me3 |
| 81 | c2nudD_ | Alignment | not modelled | 5.4 | 43 | PDB header: toxin/protein binding Chain: D: PDB Molecule: rpm1-interacting protein 4; PDBTitle: the structure of the type iii effector avrb complexed with2 a high-affinity rin4 peptide |
| 82 | c2nudC_ | Alignment | not modelled | 5.4 | 43 | PDB header: toxin/protein binding Chain: C: PDB Molecule: rpm1-interacting protein 4; PDBTitle: the structure of the type iii effector avrb complexed with2 a high-affinity rin4 peptide |
| 83 | c5u6fA_ | Alignment | not modelled | 5.3 | 30 | PDB header: cell adhesion Chain: A: PDB Molecule: lpxtg-motif cell wall anchor domain protein; PDBTitle: bacterial adhesin from mobiluncus mulieris containing intramolecular2 disulfide, isopeptide, and ester bond cross-links (space group p21) |
| 84 | c5m73H_ | Alignment | not modelled | 5.1 | 30 | PDB header: rna binding protein Chain: H: PDB Molecule: signal recognition particle subunit srp72; PDBTitle: structure of the human srp s domain with srp72 rna-binding domain |
| 85 | c6gjeA_ | Alignment | not modelled | 5.0 | 11 | PDB header: protein transport Chain: A: PDB Molecule: protein amnionless; PDBTitle: structure of the amnionless(20-357)-cubilin(36-135) complex |