






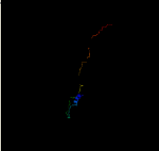

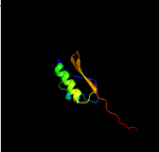

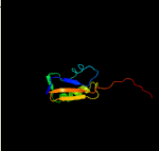

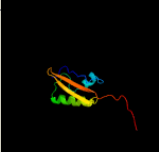

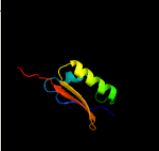

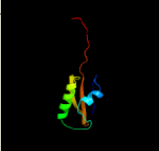
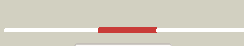



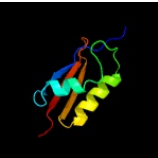

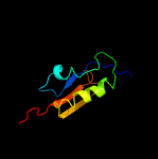


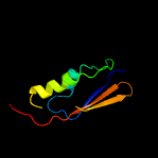
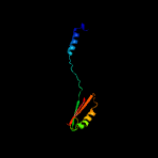
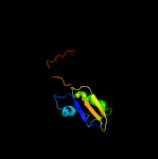





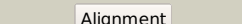
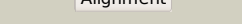

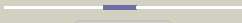
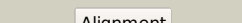

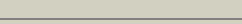

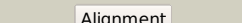
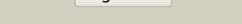

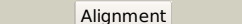
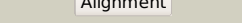
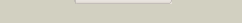

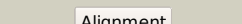
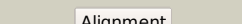
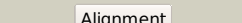
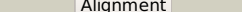
Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2151c_(ftsQ)_2409705_2410649 |
| Date | Mon Aug 5 13:25:27 BST 2019 |
| Unique Job ID | f34ab66aea054e57 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c2vh1A_ |  Alignment |  | 100.0 | 15 | PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsq; PDBTitle: crystal structure of bacterial cell division protein ftsq from e.coli |
| 2 | c2vh2A_ |  Alignment |  | 100.0 | 17 | PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsq; PDBTitle: crystal structure of cell division protein ftsq from yersinia2 enterecolitica |
| 3 | c2aljA_ |  Alignment |  | 99.0 | 13 | PDB header: cell cycle Chain: A: PDB Molecule: cell-division initiation protein; PDBTitle: structure of the cis conformer of the major extracytoplasmic2 domain of the bacterial cell division protein divib from3 geobacillus stearothermophilus |
| 4 | c3j00Z_ |  Alignment |  | 98.8 | 12 | PDB header: ribosome/ribosomal protein Chain: Z: PDB Molecule: cell division protein ftsq; PDBTitle: structure of the ribosome-secye complex in the membrane environment |
| 5 | c2qczA_ |  Alignment |  | 97.6 | 19 | PDB header: membrane protein, protein transport Chain: A: PDB Molecule: outer membrane protein assembly factor yaet; PDBTitle: structure of n-terminal domain of e. coli yaet |
| 6 | c4k3bA_ |  Alignment |  | 97.4 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein assembly factor bama; PDBTitle: the crystal structure of bama from neisseria gonorrhoeae |
| 7 | c3efcA_ |  Alignment |  | 97.2 | 19 | PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein assembly factor yaet; PDBTitle: crystal structure of yaet periplasmic domain |
| 8 | c4c4vA_ |  Alignment |  | 96.8 | 15 | PDB header: protein transport Chain: A: PDB Molecule: outer membrane protein assembly factor bama; PDBTitle: structure of the outer membrane protein insertase bama with one2 potra domain. |
| 9 | c5ekqA_ |  Alignment |  | 96.4 | 21 | PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein assembly factor bama; PDBTitle: the structure of the bamacde subcomplex from e. coli |
| 10 | c2v9hA_ |  Alignment |  | 96.1 | 19 | PDB header: protein-binding Chain: A: PDB Molecule: outer membrane protein assembly factor yaet; PDBTitle: solution structure of an escherichia coli yaet tandem potra2 domain |
| 11 | c2x8xX_ |  Alignment |  | 95.4 | 22 | PDB header: chaperone Chain: X: PDB Molecule: tlr1789 protein; PDBTitle: structure of the n-terminal domain of omp85 from the2 thermophilic cyanobacterium thermosynechococcus elongatus |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|---|
| 12 | c4c00A_ | Alignment |  | 94.8 | 13 | PDB header: transport protein Chain: A: PDB Molecule: translocation and assembly module tama; PDBTitle: crystal structure of tama from e. coli |
| 13 | c3og5A_ | Alignment |  | 94.5 | 15 | PDB header: protein binding Chain: A: PDB Molecule: outer membrane protein assembly complex, yaet protein; PDBTitle: crystal structure of bama potra45 tandem |
| 14 | c4k3cA_ | Alignment |  | 93.4 | 12 | PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein assembly factor bama; PDBTitle: the crystal structure of bama from haemophilus ducreyi lacking potra2 domains 1-3 |
| 15 | c2mhjA_ | Alignment |  | 93.1 | 15 | PDB header: protein transport Chain: A: PDB Molecule: tps4 protein; PDBTitle: solution structure of tps4 n-terminal potra domain from pseudomonas2 aeruginosa |
| 16 | c3mc8A_ | Alignment |  | 87.1 | 14 | PDB header: membrane protein Chain: A: PDB Molecule: alr2269 protein; PDBTitle: potra1-3 of the periplasmic domain of omp85 from anabaena |
| 17 | c5efrA_ | Alignment |  | 79.1 | 14 | PDB header: cell adhesion Chain: A: PDB Molecule: bama-bamd fusion protein; PDBTitle: crystal structure of a bama-bamd fusion |
| 18 | c5lq3F_ | Alignment |  | 77.5 | 8 | PDB header: transport protein Chain: F: PDB Molecule: cmcb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmcb |
| 19 | c4pk1A_ | Alignment |  | 76.5 | 19 | PDB header: protein binding Chain: A: PDB Molecule: chimera protein of outer membrane protein assembly factors PDBTitle: structure of bamb fused to a bama potra domain fragment |
| 20 | c2qdzA_ | Alignment |  | 73.3 | 4 | PDB header: protein transport Chain: A: PDB Molecule: tps2 transporter fhac; PDBTitle: structure of the membrane protein fhac: a member of the omp85/tps2 transporter family |
| 21 | c5uayA_ | Alignment | not modelled | 73.0 | 8 | PDB header: membrane protein Chain: A: PDB Molecule: protein toc75-3, chloroplastic; PDBTitle: the structure of the arabidopsis thaliana toc75 potra domains |
| 22 | c4mt1A_ | Alignment | not modelled | 72.3 | 10 | PDB header: membrane protein, transport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump |
| 23 | c6f0kA_ | Alignment | not modelled | 56.8 | 26 | PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii |
| 24 | c2v50A_ | Alignment | not modelled | 54.7 | 19 | PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein mexb; PDBTitle: the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb |
| 25 | c2rjbD_ | Alignment | not modelled | 49.1 | 22 | PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein ydcj (sf1787) from 2 shigella flexneri which includes domain duf1338. northeast structural3 genomics consortium target sfr276 |
| 26 | c6csxA_ | Alignment | not modelled | 47.4 | 15 | PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb; PDBTitle: single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom |
| 27 | c6owsB_ | Alignment | not modelled | 47.0 | 13 | PDB header: membrane protein Chain: B: PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump |
| 28 | c4k0eA_ | Alignment | not modelled | 34.1 | 15 | PDB header: transport protein Chain: A: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, |

| | | | | | | |
|----|-------------------------|---|--------------|------|----|--|
| | | | | | | crystal form ii |
| 29 | c2lnaA |  Alignment | not modelled | 26.7 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: solution nmr structure of the mitochondrial inner membrane domain2 (residues 164-251), fts_h_ext, from the paraplegin-like protein afg3l23 from homo sapiens, northeast structural genomics consortium target4 hr6741a |
| 30 | c6fosD |  Alignment | not modelled | 26.5 | 25 | PDB header: photosynthesis Chain: D: PDB Molecule: photosystem i p700 chlorophyll a apoprotein a2; PDBTitle: cyanidioschyzon merolae photosystem i |
| 31 | c3hd7A |  Alignment | not modelled | 24.9 | 13 | PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1 |
| 32 | c1oy8A |  Alignment | not modelled | 23.5 | 17 | PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump |
| 33 | c2cghB |  Alignment | not modelled | 22.1 | 17 | PDB header: ligase Chain: B: PDB Molecule: biotin ligase; PDBTitle: crystal structure of biotin ligase from mycobacterium tuberculosis |
| 34 | c6btmA |  Alignment | not modelled | 19.0 | 9 | PDB header: membrane protein Chain: A: PDB Molecule: alternative complex iii subunit a; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type) |
| 35 | d2hkja1 |  Alignment | not modelled | 18.5 | 16 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain |
| 36 | c2gamA |  Alignment | not modelled | 17.8 | 11 | PDB header: transferase Chain: A: PDB Molecule: beta-1,6-n-acetylglucosaminyltransferase; PDBTitle: x-ray crystal structure of murine leukocyte-type core 2 b1,6-n-2 acetylglucosaminyltransferase (c2gnt-1) in complex with galb1,3galnac |
| 37 | d1ee8a1 |  Alignment | not modelled | 17.1 | 24 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins |
| 38 | c2kogA |  Alignment | not modelled | 16.0 | 15 | PDB header: membrane protein Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: lipid-bound synaptobrevin solution nmr structure |
| 39 | c2mpnB |  Alignment | not modelled | 15.7 | 15 | PDB header: membrane protein Chain: B: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli |
| 40 | c2mpnA |  Alignment | not modelled | 15.7 | 15 | PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli |
| 41 | d1tdza1 |  Alignment | not modelled | 15.0 | 21 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins |
| 42 | d1r2za1 |  Alignment | not modelled | 14.4 | 17 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins |
| 43 | d1k82a1 |  Alignment | not modelled | 14.0 | 21 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins |
| 44 | c3k07A |  Alignment | not modelled | 13.2 | 13 | PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa |
| 45 | c5t4oj |  Alignment | not modelled | 11.6 | 19 | PDB header: hydrolase Chain: J: PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1 |
| 46 | c4k0eC |  Alignment | not modelled | 11.1 | 15 | PDB header: transport protein Chain: C: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii |
| 47 | d1jb0d |  Alignment | not modelled | 10.8 | 22 | Fold: Photosystem I subunit Psd Superfamily: Photosystem I subunit Psd Family: Photosystem I subunit Psd |
| 48 | d1uwda |  Alignment | not modelled | 10.5 | 18 | Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like |
| 49 | c2y9jt |  Alignment | not modelled | 10.3 | 35 | PDB header: protein transport Chain: T: PDB Molecule: protein prgh; PDBTitle: three-dimensional model of salmonella's needle complex at subnanometer2 resolution |
| 50 | c6mk7A | Alignment | not modelled | 9.9 | 17 | PDB header: membrane protein Chain: A: PDB Molecule: cell division protein ftsx; PDBTitle: solution structure of the large extracellular loop of ftsx in2 streptococcus pneumoniae |
| 51 | c5irdA | Alignment | not modelled | 9.9 | 18 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of rv1466 from mycobacterium tuberculosis, a2 protein associated with [fe-s] complex assembly and repair - seattle3 structural genomics center for infectious disease target4 mytud.17486.a |
| 52 | d1k3xa1 | Alignment | not modelled | 9.9 | 14 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins |
| 53 | c2eq8C | Alignment | not modelled | 9.7 | 25 | PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide |

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|----|-------------------------|-----------|--------------|-----|----|--|
| | | | | | | PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdp |
| 54 | c3twkB_ | Alignment | not modelled | 9.7 | 30 | PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg |
| 55 | c4babC_ | Alignment | not modelled | 9.2 | 19 | PDB header: lyase Chain: C: PDB Molecule: phenylalanine aminomutase; PDBTitle: redesign of a phenylalanine aminomutase into a beta-phenylalanine2 ammonia lyase |
| 56 | c5t3bB_ | Alignment | not modelled | 8.0 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase; PDBTitle: crystal structure of bpgH50 |
| 57 | c6fkip_ | Alignment | not modelled | 8.0 | 15 | PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3 |
| 58 | c1ee8A_ | Alignment | not modelled | 7.8 | 24 | PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8 |
| 59 | c5c5hA_ | Alignment | not modelled | 7.3 | 17 | PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: r195k e. coli mene with bound osb-ams |
| 60 | d2ajta1 | Alignment | not modelled | 7.3 | 21 | Fold: Reductase/isomerase/elongation factor common domain Superfamily: Fucl/AraA C-terminal domain-like Family: AraA C-terminal domain-like |
| 61 | c1yj7A_ | Alignment | not modelled | 7.2 | 17 | PDB header: protein transport Chain: A: PDB Molecule: escj; PDBTitle: crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj |
| 62 | d2cu6a1 | Alignment | not modelled | 6.9 | 18 | Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like |
| 63 | c3lnoA_ | Alignment | not modelled | 6.6 | 12 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of domain of unknown function duf59 from2 bacillus anthracis |
| 64 | c4bq3A_ | Alignment | not modelled | 6.2 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: b-agarase; PDBTitle: structural analysis of an exo-beta-agarase |
| 65 | c5z6pB_ | Alignment | not modelled | 6.2 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: b-agarase; PDBTitle: the crystal structure of an agarase, agwh50c |
| 66 | c1k82D_ | Alignment | not modelled | 6.2 | 21 | PDB header: hydrolase/dna Chain: D: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna |
| 67 | d3duea1 | Alignment | not modelled | 6.1 | 15 | Fold: BLIP-like Superfamily: BT0923-like Family: BT0923-like |
| 68 | c4d56A_ | Alignment | not modelled | 5.8 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains |
| 69 | c5wmmA_ | Alignment | not modelled | 5.7 | 17 | PDB header: biosynthetic protein Chain: A: PDB Molecule: nrps; PDBTitle: crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios |
| 70 | d1smpi_ | Alignment | not modelled | 5.7 | 37 | Fold: Streptavidin-like Superfamily: beta-Barrel protease inhibitors Family: Metalloprotease inhibitor |
| 71 | c6bzsa_ | Alignment | not modelled | 5.7 | 24 | PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd1 in apo state |
| 72 | c5v6fA_ | Alignment | not modelled | 5.5 | 38 | PDB header: sugar binding protein Chain: A: PDB Molecule: hemolysin-related protein; PDBTitle: crystal structure of the second beta-prism domain of rbmc from v.2 cholerae bound to mannantriose |
| 73 | c3a46B_ | Alignment | not modelled | 5.5 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of mvnei1/thf complex |
| 74 | c2f5qA_ | Alignment | not modelled | 5.5 | 17 | PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2 |
| 75 | c3r85H_ | Alignment | not modelled | 5.2 | 33 | PDB header: apoptosis Chain: H: PDB Molecule: heme-binding protein 2; PDBTitle: crystal structure of human soul bh3 domain in complex with bcl-xl |
| 76 | c3r85E_ | Alignment | not modelled | 5.2 | 33 | PDB header: apoptosis Chain: E: PDB Molecule: heme-binding protein 2; PDBTitle: crystal structure of human soul bh3 domain in complex with bcl-xl |
| 77 | c3r85G_ | Alignment | not modelled | 5.2 | 33 | PDB header: apoptosis Chain: G: PDB Molecule: heme-binding protein 2; PDBTitle: crystal structure of human soul bh3 domain in complex with bcl-xl |
| 78 | c3l8cA_ | Alignment | not modelled | 5.2 | 23 | PDB header: ligase Chain: A: PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 1; PDBTitle: structure of probable d-alanine--poly(phosphoribitol) ligase subunit-12 from streptococcus pyogenes |