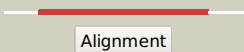

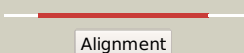

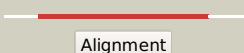
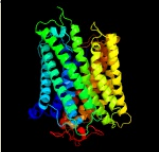
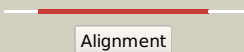


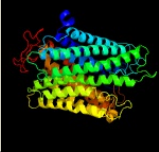
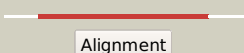

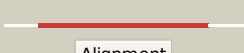




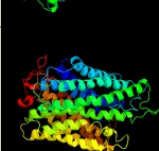

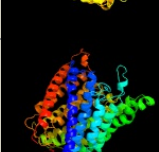
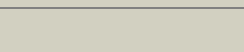



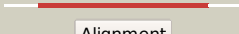

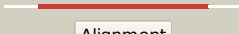








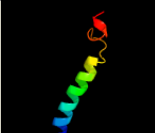

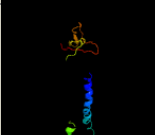
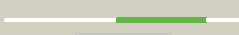

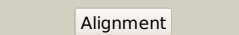
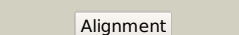
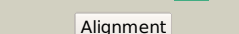


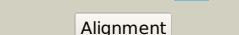
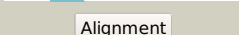
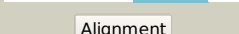


Phyre2

| | |
|---------------|--------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3043c_ctaD_3403211_3404932 |
| Date | Thu Aug 8 16:20:21 BST 2019 |
| Unique Job ID | f79bcf47bdfeaf9a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 | c6hwhQ_ |  Alignment |  | 100.0 | 86 | PDB header: electron transport Chain: Q: PDB Molecule: cytochrome c oxidase subunit 1; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis |
| 2 | c1m56G_ |  Alignment |  | 100.0 | 47 | PDB header: oxidoreductase Chain: G: PDB Molecule: cytochrome c oxidase; PDBTitle: structure of cytochrome c oxidase from rhodospirillum rubrum |
| 3 | d3dtua1 |  Alignment |  | 100.0 | 47 | Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like |
| 4 | c2yevA_ |  Alignment |  | 100.0 | 44 | PDB header: electron transport Chain: A: PDB Molecule: cytochrome c oxidase polypeptide i+iii; PDBTitle: structure of caa3-type cytochrome oxidase |
| 5 | c6hu9m_ |  Alignment |  | 100.0 | 41 | PDB header: oxidoreductase/electron transport Chain: M: PDB Molecule: cytochrome b-c1 complex subunit 2, mitochondrial; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae |
| 6 | d1v54a_ |  Alignment |  | 100.0 | 41 | Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like |
| 7 | d1ar1a_ |  Alignment |  | 100.0 | 47 | Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like |
| 8 | d1ffta_ |  Alignment |  | 100.0 | 46 | Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like |
| 9 | c1fftF_ |  Alignment |  | 100.0 | 46 | PDB header: oxidoreductase Chain: F: PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli |
| 10 | c3eh4A_ |  Alignment |  | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c oxidase subunit 1; PDBTitle: structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus |
| 11 | d1xmea1 |  Alignment |  | 100.0 | 21 | Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like |

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|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|-------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | c3mk7K_ |  Alignment |  | 100.0 | 17 | PDB header: oxidoreductase Chain: K: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit n; PDBTitle: the structure of cbb3 cytochrome oxidase |
| 13 | c3o0rB_ |  Alignment |  | 100.0 | 16 | PDB header: immune system/oxidoreductase Chain: B: PDB Molecule: nitric oxide reductase subunit b; PDBTitle: crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment |
| 14 | c4xydA_ |  Alignment |  | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide reductase subunit b; PDBTitle: nitric oxide reductase from roseobacter denitrificans (rdnor) |
| 15 | c3aygA_ |  Alignment |  | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: nitric oxide reductase; PDBTitle: crystal structure of nitric oxide reductase complex with hqno |
| 16 | c6elhA_ |  Alignment |  | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide reductase; PDBTitle: low resolution structure of neisseria meningitidis qnor |
| 17 | c5ir6A_ |  Alignment |  | 81.5 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: bd-type quinol oxidase subunit i; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans |
| 18 | c5z62N_ |  Alignment |  | 56.7 | 28 | PDB header: electron transport Chain: N: PDB Molecule: cytochrome c oxidase subunit ndufa4; PDBTitle: structure of human cytochrome c oxidase |
| 19 | c1fftG_ |  Alignment |  | 50.3 | 12 | PDB header: oxidoreductase Chain: G: PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli |
| 20 | c6g7oA_ |  Alignment |  | 50.2 | 16 | PDB header: membrane protein Chain: A: PDB Molecule: alkaline ceramidase 3,soluble cytochrome b562; PDBTitle: crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution |
| 21 | c5xgrF_ |  Alignment | not modelled | 46.4 | 40 | PDB header: viral protein Chain: F: PDB Molecule: spike protein s1; PDBTitle: structure of the s1 subunit c-terminal domain from bat-derived2 coronavirus hku5 spike protein |
| 22 | c6eznH_ |  Alignment | not modelled | 44.6 | 14 | PDB header: membrane protein Chain: H: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex |
| 23 | c4qzvB_ |  Alignment | not modelled | 44.1 | 27 | PDB header: hydrolase/viral protein Chain: B: PDB Molecule: spike protein s1; PDBTitle: bat-derived coronavirus hku4 uses mers-cov receptor human cd26 for2 cell entry |
| 24 | c6humO_ |  Alignment | not modelled | 41.3 | 23 | PDB header: proton transport Chain: O: PDB Molecule: nad(p)h-quinone oxidoreductase subunit o; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus |
| 25 | c2yevB_ |  Alignment | not modelled | 39.6 | 14 | PDB header: electron transport Chain: B: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of caa3-type cytochrome oxidase |
| 26 | c4kqzA_ |  Alignment | not modelled | 38.6 | 27 | PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: structure of the receptor binding domain (rbd) of mers-cov spike |
| 27 | d1rzhh2 |  Alignment | not modelled | 31.5 | 44 | Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region |
| 28 | c5zlgA_ |  Alignment | not modelled | 30.7 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b reductase 1; PDBTitle: human duodenal cytochrome b (dctyb) in zinc ion and |

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|----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | | | | | | ascorbate bound2 form |
| 29 | c6f0kF_ | Alignment | not modelled | 30.5 | 16 | PDB header: membrane protein Chain: F: PDB Molecule: actf; PDBTitle: alternative complex iii |
| 30 | d1fftb2 | Alignment | not modelled | 30.5 | 10 | Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region |
| 31 | c3ke2A_ | Alignment | not modelled | 28.7 | 57 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yp_928783.1; PDBTitle: crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution |
| 32 | c3scie_ | Alignment | not modelled | 27.2 | 14 | PDB header: hydrolase/viral protein Chain: E: PDB Molecule: spike glycoprotein; PDBTitle: crystal structure of spike protein receptor-binding domain from a2 predicted sars coronavirus human strain complexed with human receptor3 ace2 |
| 33 | d1eysl_ | Alignment | not modelled | 26.9 | 13 | Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits |
| 34 | d2ghvc1 | Alignment | not modelled | 26.7 | 13 | Fold: SARS receptor-binding domain-like Superfamily: SARS receptor-binding domain-like Family: SARS receptor-binding domain-like |
| 35 | d1ufaa1 | Alignment | not modelled | 26.5 | 20 | Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: AmyC C-terminal domain-like |
| 36 | d1l9bh2 | Alignment | not modelled | 25.8 | 43 | Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region |
| 37 | c5kwbA_ | Alignment | not modelled | 25.5 | 20 | PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein; PDBTitle: crystal structure of the receptor binding domain of the spike2 glycoprotein of human betacoronavirus hku1 (hku1 1a-ctd, 1.93 angstrom, molecular replacement) |
| 38 | d2b5dx1 | Alignment | not modelled | 24.8 | 17 | Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: AmyC C-terminal domain-like |
| 39 | d1y5ic1 | Alignment | not modelled | 24.6 | 18 | Fold: Heme-binding four-helical bundle Superfamily: Respiratory nitrate reductase 1 gamma chain Family: Respiratory nitrate reductase 1 gamma chain |
| 40 | c3j2lg_ | Alignment | not modelled | 24.3 | 25 | PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l7ae; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins) |
| 41 | d2rcrh2 | Alignment | not modelled | 23.8 | 43 | Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region |
| 42 | c3up6A_ | Alignment | not modelled | 23.5 | 23 | PDB header: cell adhesion Chain: A: PDB Molecule: hypothetical protein bacova_04078; PDBTitle: crystal structure of a putative cell adhesion protein (bacova_04078)2 from bacteroides ovatus atcc 8483 at 2.80 a resolution |
| 43 | c6abfC_ | Alignment | not modelled | 23.5 | 20 | PDB header: viral protein/rna Chain: C: PDB Molecule: polymerase pb2; PDBTitle: structure of influenza d virus polymerase bound to vrna promoter in2 mode b conformation (class b1) |
| 44 | c3p4hA_ | Alignment | not modelled | 23.2 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna ligase, n-terminal domain protein; PDBTitle: structures of archaeal members of the ligd 3'-phosphoesterase dna2 repair enzyme superfamily |
| 45 | c5vrhA_ | Alignment | not modelled | 22.7 | 11 | PDB header: transferase Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: apolipoprotein n-acyltransferase c387s active site mutant |
| 46 | c6hwhL_ | Alignment | not modelled | 22.6 | 11 | PDB header: electron transport Chain: L: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis |
| 47 | c2kxqB_ | Alignment | not modelled | 22.4 | 33 | PDB header: protein binding Chain: B: PDB Molecule: smad7 py motif containing peptide; PDBTitle: solution structure of smurf2 ww2 and ww3 bound to smad7 py motif2 containing peptide |
| 48 | c2djyB_ | Alignment | not modelled | 22.4 | 33 | PDB header: ligase/signaling protein Chain: B: PDB Molecule: mothers against decapentaplegic homolog 7; PDBTitle: solution structure of smurf2 ww3 domain-smad7 py peptide2 complex |
| 49 | d1xmeb2 | Alignment | not modelled | 22.4 | 29 | Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region |
| 50 | c6humG_ | Alignment | not modelled | 22.4 | 23 | PDB header: proton transport Chain: G: PDB Molecule: nadh dehydrogenase subunit 6; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus |
| 51 | c5zjio_ | Alignment | not modelled | 22.4 | 29 | PDB header: membrane protein Chain: O: PDB Molecule: 16kda membrane protein; PDBTitle: structure of photosystem i supercomplex with light-harvesting2 complexes i and ii |
| 52 | d2gl5a2 | Alignment | not modelled | 22.3 | 12 | Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like |

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|----|-------------------------|-----------|--------------|------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 53 | c5x5fC | Alignment | not modelled | 22.3 | 27 | PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2 |
| 54 | c6nbxG | Alignment | not modelled | 22.2 | 23 | PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2) |
| 55 | c6roiC | Alignment | not modelled | 22.0 | 14 | PDB header: lipid transport Chain: C: PDB Molecule: cell division control protein 50; PDBTitle: cryo-em structure of the partially activated drs2p-cdc50p |
| 56 | d1l2wi | Alignment | not modelled | 22.0 | 20 | Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone |
| 57 | c5is0E | Alignment | not modelled | 21.9 | 8 | PDB header: transport protein Chain: E: PDB Molecule: transient receptor potential cation channel subfamily v PDBTitle: structure of trpv1 in complex with capsazepine, determined in lipid2 nanodisc |
| 58 | d2djia3 | Alignment | not modelled | 21.8 | 13 | Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module |
| 59 | c3rkoF | Alignment | not modelled | 21.8 | 15 | PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 60 | c6gcs6 | Alignment | not modelled | 21.4 | 16 | PDB header: oxidoreductase Chain: 6: PDB Molecule: nd6 subunit (nu6m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica |
| 61 | d1n7za | Alignment | not modelled | 21.3 | 25 | Fold: Baseplate structural protein gp8 Superfamily: Baseplate structural protein gp8 Family: Baseplate structural protein gp8 |
| 62 | c5zz9E | Alignment | not modelled | 20.8 | 71 | PDB header: protein binding Chain: E: PDB Molecule: peptide from drebrin; PDBTitle: crystal structure of homer2 evh1/drebrin ppxxf complex |
| 63 | c3p43A | Alignment | not modelled | 20.4 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and activities of archaeal members of the ligd 3'2 phosphoesterase dna repair enzyme superfamily |
| 64 | c5i6xA | Alignment | not modelled | 20.0 | 12 | PDB header: membrane protein Chain: A: PDB Molecule: sodium-dependent serotonin transporter; PDBTitle: x-ray structure of the ts3 human serotonin transporter complexed with2 paroxetine at the central site |
| 65 | c4fxwB | Alignment | not modelled | 20.0 | 38 | PDB header: protein binding Chain: B: PDB Molecule: splicing factor 1; PDBTitle: structure of phosphorylated sf1 complex with u2af65-uhm domain |
| 66 | c5y88S | Alignment | not modelled | 19.9 | 33 | PDB header: splicing Chain: S: PDB Molecule: pre-mrna-processing factor 17; PDBTitle: cryo-em structure of the intron-lariat spliceosome ready for2 disassembly from s.cerevisiae at 3.5 angstrom |
| 67 | c5dmpA | Alignment | not modelled | 19.9 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the archaeal nhej phosphoesterase from methanocella2 paludicola. |
| 68 | c3n9dA | Alignment | not modelled | 19.3 | 11 | PDB header: ligase Chain: A: PDB Molecule: probable atp-dependent dna ligase; PDBTitle: monoclinic structure of p. aeruginosa ligd phosphoesterase domain |
| 69 | c5xu1M | Alignment | not modelled | 19.2 | 21 | PDB header: transport protein Chain: M: PDB Molecule: abc transporter permeae; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6 |
| 70 | c2kncB | Alignment | not modelled | 18.9 | 17 | PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex |
| 71 | c3mk7F | Alignment | not modelled | 18.7 | 20 | PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase |
| 72 | c2m09A | Alignment | not modelled | 18.7 | 27 | PDB header: transcription Chain: A: PDB Molecule: splicing factor 1; PDBTitle: structure, phosphorylation and u2af65 binding of the nterminal domain2 of splicing factor 1 during 3 splice site recognition |
| 73 | c5c8jj | Alignment | not modelled | 18.6 | 23 | PDB header: membrane protein Chain: J: PDB Molecule: protein mj0480; PDBTitle: a yidc-like protein in the archaeal plasma membrane |
| 74 | c5hypB | Alignment | not modelled | 18.4 | 36 | PDB header: immune system Chain: B: PDB Molecule: m28 protein; PDBTitle: structure of human c4b-binding protein alpha cain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m283 protein |
| 75 | c2n1pA | Alignment | not modelled | 18.3 | 18 | PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 5b, ns5b; PDBTitle: structure of the c-terminal membrane domain of hcv ns5b protein |
| 76 | c5cmyB | Alignment | not modelled | 18.3 | 27 | PDB header: protein transport Chain: B: PDB Molecule: epsin-5; PDBTitle: crystal structure of yeast ent5 n-terminal domain-native |
| 77 | c2kxaA | Alignment | not modelled | 18.2 | 32 | PDB header: viral protein, immune system Chain: A: PDB Molecule: haemagglutinin ha2 chain peptide; PDBTitle: the hemagglutinin fusion peptide (h1 subtype) at ph 7.4 |
| 78 | c2kgnA | Alignment | not modelled | 18.0 | 25 | PDB header: signaling protein Chain: A: PDB Molecule: protein ste5; PDBTitle: solution structure of ste5pm24 in the zwitterionic dpc2 micelle |

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|----|-------------------------|-----------|--------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 79 | d1eysh2 | Alignment | not modelled | 18.0 | 28 | Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region |
| 80 | c6bdtC_ | Alignment | not modelled | 18.0 | 21 | PDB header: hydrolase Chain: C: PDB Molecule: calpain-3; PDBTitle: crystal structure of human calpain-3 protease core mutant-c129s |
| 81 | d2odgc1 | Alignment | not modelled | 18.0 | 26 | Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain |
| 82 | d1ehkb2 | Alignment | not modelled | 17.8 | 30 | Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region |
| 83 | d1kp0a1 | Alignment | not modelled | 17.8 | 25 | Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain |
| 84 | d2axtc1 | Alignment | not modelled | 17.7 | 15 | Fold: Photosystem II antenna protein-like Superfamily: Photosystem II antenna protein-like Family: Photosystem II antenna protein-like |
| 85 | c2axtc_ | Alignment | not modelled | 17.7 | 15 | PDB header: electron transport Chain: C: PDB Molecule: photosystem ii cp43 protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus |
| 86 | c2m0gA_ | Alignment | not modelled | 17.7 | 38 | PDB header: splicing Chain: A: PDB Molecule: splicing factor 1; PDBTitle: structure, phosphorylation and u2af65 binding of the nterminal domain2 of splicing factor 1 during 3 splice site recognition |
| 87 | c2rmzA_ | Alignment | not modelled | 17.7 | 17 | PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment |
| 88 | c2khfA_ | Alignment | not modelled | 17.7 | 44 | PDB header: antimicrobial protein Chain: A: PDB Molecule: plnj; PDBTitle: plantaricin j in dpc-micelles |
| 89 | c2khgA_ | Alignment | not modelled | 17.7 | 44 | PDB header: antimicrobial protein Chain: A: PDB Molecule: plnj; PDBTitle: plantaricin j in tfe |
| 90 | c4ct4C_ | Alignment | not modelled | 17.5 | 30 | PDB header: rna binding protein Chain: C: PDB Molecule: ccr4-not transcription complex subunit 1; PDBTitle: cnot1 mif4g domain - ddx6 complex |
| 91 | c1k6nH_ | Alignment | not modelled | 17.4 | 25 | PDB header: photosynthesis Chain: H: PDB Molecule: photosynthetic reaction center h subunit; PDBTitle: e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides |
| 92 | c2k4fA_ | Alignment | not modelled | 17.2 | 29 | PDB header: immune system, signaling protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd3 epsilon chain; PDBTitle: mouse cd3epsilon cytoplasmic tail |
| 93 | c6bmsA_ | Alignment | not modelled | 17.2 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: palmitoyltransferase; PDBTitle: palmitoyltransferase structure |
| 94 | c5n9yB_ | Alignment | not modelled | 16.9 | 6 | PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb |
| 95 | c6hu9u_ | Alignment | not modelled | 16.9 | 19 | PDB header: oxidoreductase/electron transport Chain: U: PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae |
| 96 | c3chxG_ | Alignment | not modelled | 16.9 | 23 | PDB header: membrane protein Chain: G: PDB Molecule: pmoc; PDBTitle: crystal structure of methylosinus trichosporium ob3b particulate2 methane monooxygenase (pmmo) |
| 97 | c5ldda_ | Alignment | not modelled | 16.8 | 17 | PDB header: protein transport Chain: A: PDB Molecule: mon1; PDBTitle: crystal structure of the heterodimeric gef mon1-ccz1 in complex with2 ypt7 |
| 98 | c4b8cH_ | Alignment | not modelled | 16.7 | 19 | PDB header: hydrolase/cell cycle Chain: H: PDB Molecule: general negative regulator of transcription subunit 1; PDBTitle: nuclease module of the yeast ccr4-not complex |
| 99 | c3jclC_ | Alignment | not modelled | 16.4 | 30 | PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer |