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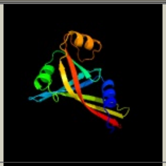
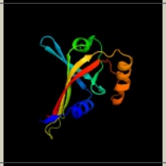
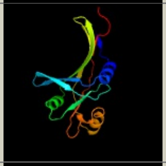
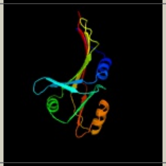
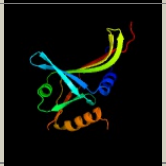
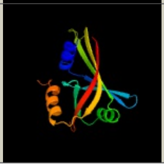
|---|---|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0080_(-)_89019_89477 |
| Date | Tue Jul 23 14:50:11 BST 2019 |
| Unique Job ID | 4a1a7350b49e5194 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3fkhB_ | Alignment |  | 100.0 | 33 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative pyridoxamine 5'-phosphate oxidase;<br>**PDBTitle:** crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution |
| 2 | c6rk0A_ | Alignment |  | 100.0 | 14 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** structure of the flavocytochrome anf3 from azotobacter vinelandii |
| 3 | c3u0iA_ | Alignment |  | 100.0 | 15 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**probable fad-binding, putative uncharacterized protein;<br>**PDBTitle:** crystal structure of a probable fad-binding, putative uncharacterized2 protein from brucella melitensis |
| 4 | c6eciQ_ | Alignment |  | 100.0 | 35 | **PDB header:**fad-binding protein<br>**Chain:** Q: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related, fmn-binding<br>**PDBTitle:** structure of the fad binding protein msmeg_5243 from mycobacterium2 smegmatis |
| 5 | c3cp3A_ | Alignment |  | 100.0 | 31 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae |
| 6 | d2hq9a1 | Alignment |  | 100.0 | 23 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 7 | d2fura1 | Alignment |  | 100.0 | 13 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 8 | d2vpaa1 | Alignment |  | 100.0 | 18 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 9 | d2fg9a1 | Alignment |  | 100.0 | 11 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 10 | c4ybnB_ | Alignment |  | 100.0 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**flavin-nucleotide-binding protein;<br>**PDBTitle:** structure of the fad and heme binding protein msmeg_4975 from2 mycobacterium smegmatis |
| 11 | d2htia1 | Alignment |  | 100.0 | 15 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |

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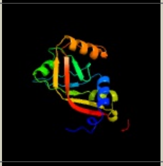
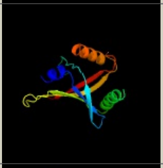
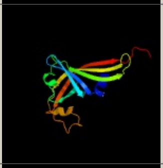
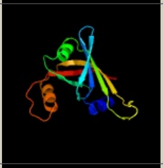
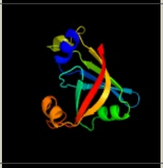
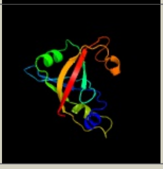
| 12 | c2htiA_ | Alignment |  | 100.0 | 15 | **PDB header:**fmn-binding protein<br>**Chain:** A: **PDB Molecule:**bh0577 protein;<br>**PDBTitle:** crystal structure of a flavin-nucleotide-binding protein (bh_0577)2 from bacillus halodurans at 2.50 a resolution |
| 13 | d1rfea_ | Alignment |  | 99.9 | 17 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 14 | c4zkyB_ | Alignment |  | 99.9 | 21 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**pyridoxamine 5-phosphate oxidase;<br>**PDBTitle:** structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis |
| 15 | c3f7eB_ | Alignment |  | 99.9 | 13 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related, fmn-<br>**PDBTitle:** msmeg_3380 f420 reductase |
| 16 | c2ol5B_ | Alignment |  | 99.9 | 11 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**pai 2 protein;<br>**PDBTitle:** crystal structure of a protease synthase and sporulation negative2 regulatory protein pai 2 from bacillus stearothermophilus |
| 17 | c3db0B_ | Alignment |  | 99.9 | 17 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**lin2891 protein;<br>**PDBTitle:** crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution |
| 18 | c3ec6A_ | Alignment |  | 99.9 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**general stress protein 26;<br>**PDBTitle:** crystal structure of the general stress protein 26 from bacillus2 anthracis str. sterne |
| 19 | d2asfa1 | Alignment |  | 99.8 | 20 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 20 | d2i02a1 | Alignment |  | 99.8 | 14 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 21 | c3tgvD_ | Alignment | not modelled | 99.8 | 8 | **PDB header:**heme binding protein<br>**Chain:** D: **PDB Molecule:**heme-binding protein hutz;<br>**PDBTitle:** crystal structure of hutz,the heme storsge protein from vibrio2 cholerae |
| 22 | c2re7A_ | Alignment | not modelled | 99.8 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a pyridoxamine 5'-phosphate oxidase related2 protein (psyc_0186) from psychrobacter arcticus 273-4 at 2.50 a3 resolution |
| 23 | d1w9aa_ | Alignment | not modelled | 99.8 | 15 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 24 | c2iabB_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** crystal structure of a protein with fmn-binding split barrel fold2 (np_828636.1) from streptomyces avermitilis at 2.00 a resolution |
| 25 | d2fhqa1 | Alignment | not modelled | 99.7 | 17 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 26 | c2ig6B_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nimc/nima family protein;<br>**PDBTitle:** crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution |
| 27 | d2hq7a1 | Alignment | not modelled | 99.7 | 14 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 28 | d1vl7a_ | Alignment | not modelled | 99.7 | 7 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |

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| 29 | c3u34D_ | Alignment | not modelled | 99.6 | 12 | **PDB header:**protein binding<br>**Chain:** D: **PDB Molecule:**general stress protein;<br>**PDBTitle:** crystal structure of the general stress fmn/fad binding protein from2 the phytopathogen xanthomonas citri |
| 30 | c3dmbA_ | Alignment | not modelled | 99.6 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative general stress protein 26 with a pnp-oxidase like<br>**PDBTitle:** crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution |
| 31 | c2hhzA_ | Alignment | not modelled | 99.6 | 10 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related;<br>**PDBTitle:** crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution |
| 32 | d2arza1 | Alignment | not modelled | 99.6 | 13 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 33 | c5escD_ | Alignment | not modelled | 99.6 | 13 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**hupz;<br>**PDBTitle:** crystal structure of group a streptococcus hupz |
| 34 | c2htdB_ | Alignment | not modelled | 99.6 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**predicted flavin-nucleotide-binding protein from cog3576<br>**PDBTitle:** crystal structure of a putative pyridoxamine 5'-phosphate oxidase2 (ldb0262) from lactobacillus delbrueckii subsp. at 1.60 a resolution |
| 35 | c5bncB_ | Alignment | not modelled | 99.5 | 17 | **PDB header:**heme binding protein<br>**Chain:** B: **PDB Molecule:**heme binding protein msmeg_6519;<br>**PDBTitle:** structure of heme binding protein msmeg_6519 from mycobacterium2 smegmatis |
| 36 | c3gasA_ | Alignment | not modelled | 99.5 | 7 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**heme oxygenase;<br>**PDBTitle:** crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme |
| 37 | c3dnhB_ | Alignment | not modelled | 99.5 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein atu2129;<br>**PDBTitle:** the crystal structure of the protein atu2129 (unknown function) from2 agrobacterium tumefaciens str. c58 |
| 38 | c2q9kA_ | Alignment | not modelled | 99.5 | 7 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution |
| 39 | c2qeaB_ | Alignment | not modelled | 99.4 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative general stress protein 26;<br>**PDBTitle:** crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution |
| 40 | d1flma_ | Alignment | not modelled | 99.4 | 11 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 41 | d1ty9a_ | Alignment | not modelled | 99.3 | 20 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 42 | d1t9ma_ | Alignment | not modelled | 99.2 | 18 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 43 | d2a2ja1 | Alignment | not modelled | 99.2 | 21 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 44 | d1dnla_ | Alignment | not modelled | 99.2 | 17 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 45 | c2ou5B_ | Alignment | not modelled | 99.1 | 12 | **PDB header:**flavoprotein<br>**Chain:** B: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related, fmn-binding;<br>**PDBTitle:** crystal structure of a pyridoxamine 5'-phosphate oxidase-related fmn-2 binding protein (jann_0254) from jannaschia sp. ccs1 at 1.60 a3 resolution |
| 46 | c2a2jA_ | Alignment | not modelled | 99.1 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase;<br>**PDBTitle:** crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis |
| 47 | c4hmwB_ | Alignment | not modelled | 99.1 | 18 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase;<br>**PDBTitle:** crystal structure of phzg from burkholderia lata 383 |
| 48 | d1nrga_ | Alignment | not modelled | 99.1 | 13 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 49 | c1nrgA_ | Alignment | not modelled | 99.1 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**pyridoxine 5'-phosphate oxidase;<br>**PDBTitle:** structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase |
| 50 | d1xhna1 | Alignment | not modelled | 99.0 | 13 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| 51 | c4n7rD_ | Alignment | not modelled | 98.8 | 14 | **PDB header:**oxidoreductase/protein binding<br>**Chain:** D: **PDB Molecule:**genomic dna, chromosome 3, p1 clone: mxl8;<br>**PDBTitle:** crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein |
| 52 | d1ci0a_ | Alignment | not modelled | 98.4 | 14 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**PNP-oxidase like |
| | | | | | | **PDB header:**flavoprotein |

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| 53 | c2i51B_ | Alignment | not modelled | 98.4 | 16 | **Chain:** B: **PDB Molecule:**uncharacterized conserved protein of cog5135;<br>**PDBTitle:** crystal structure of a pyridoxamine 5'-phosphate oxidase-related, fmn2 binding protein (npun_f5749) from nostoc punctiforme pcc 73102 at3 1.40 a resolution |
| 54 | c3ba3A_ | Alignment | not modelled | 97.8 | 6 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-like protein;<br>**PDBTitle:** crystal structure of pyridoxamine 5'-phosphate oxidase-like protein2 (np_783940.1) from lactobacillus plantarum at 1.55 a resolution |
| 55 | c3r5yC_ | Alignment | not modelled | 97.5 | 22 | **PDB header:**unknown function<br>**Chain:** C: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420 |
| 56 | c3r5zB_ | Alignment | not modelled | 97.4 | 18 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420 |
| 57 | c3r5wO_ | Alignment | not modelled | 97.3 | 20 | **PDB header:**oxidoreductase<br>**Chain:** O: **PDB Molecule:**deazaflavin-dependent nitroreductase;<br>**PDBTitle:** structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420 |
| 58 | c4y9iA_ | Alignment | not modelled | 96.9 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**mycobacterium tuberculosis paralogous family 11;<br>**PDBTitle:** structure of f420-h2 dependent reductase (fdr-a) msmeg_2027 |
| 59 | c3h96B_ | Alignment | not modelled | 96.8 | 19 | **PDB header:**flavoprotein<br>**Chain:** B: **PDB Molecule:**f420-h2 dependent reductase a;<br>**PDBTitle:** msmeg_3358 f420 reductase |
| 60 | d2ptfa1 | Alignment | not modelled | 87.5 | 15 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**MTH863-like |
| 61 | c3e4vA_ | Alignment | not modelled | 82.3 | 15 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**nadh:fmn oxidoreductase like protein;<br>**PDBTitle:** crystal structure of nadh:fmn oxidoreductase like protein in complex2 with fmn (yp_544701.1) from methylobacillus flagellatus kt at 1.40 a3 resolution |
| 62 | d2nr4a1 | Alignment | not modelled | 82.0 | 16 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**MTH863-like |
| 63 | c3hmzA_ | Alignment | not modelled | 79.2 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**flavin reductase domain protein, fmn-binding;<br>**PDBTitle:** crystal structure of a fmn-binding domain of flavin reductases-like2 enzyme (sbal_0626) from shewanella baltica os155 at 1.50 a resolution |
| 64 | c3fgeA_ | Alignment | not modelled | 79.0 | 9 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative flavin reductase with split barrel domain;<br>**PDBTitle:** crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution |
| 65 | c2ptfB_ | Alignment | not modelled | 74.3 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein mth_863;<br>**PDBTitle:** crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn |
| 66 | d1ejea_ | Alignment | not modelled | 69.3 | 12 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**NADH:FMN oxidoreductase-like |
| 67 | c3b5mD_ | Alignment | not modelled | 58.9 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica |
| 68 | c4z85A_ | Alignment | not modelled | 51.7 | 10 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-nitrobenzoate nitroreductase;<br>**PDBTitle:** crystal structur of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa |
| 69 | d2imla1 | Alignment | not modelled | 47.1 | 8 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**MTH863-like |
| 70 | c3pftA_ | Alignment | not modelled | 41.3 | 9 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**flavin reductase;<br>**PDBTitle:** crystal structure of untagged c54a mutant flavin reductase (dszd) in2 complex with fmn from mycobacterium goodii |
| 71 | c3bpkB_ | Alignment | not modelled | 32.6 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase component b;<br>**PDBTitle:** crystal structure of nitrilotriacetate monooxygenase component b from2 bacillus cereus |
| 72 | c4fmoB_ | Alignment | not modelled | 29.2 | 13 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**dna mismatch repair protein pms1;<br>**PDBTitle:** structure of the c-terminal domain of the saccharomyces cerevisiae2 mutl alpha (mlh1/pms1) heterodimer bound to a fragment of exo1 |
| 73 | c2xi5D_ | Alignment | not modelled | 27.0 | 26 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**rna polymerase l;<br>**PDBTitle:** n-terminal endonuclease domain of la crosse virus l-protein |
| 74 | c2xi7B_ | Alignment | not modelled | 26.9 | 26 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**rna polymerase l;<br>**PDBTitle:** n-terminal endonuclease domain of la crosse virus l-protein |
| 75 | c2r6vA_ | Alignment | not modelled | 22.4 | 14 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**uncharacterized protein ph0856;<br>**PDBTitle:** crystal structure of fmn-binding protein (np_142786.1) from pyrococcus2 horikoshii at 1.35 a resolution |
| | | | | | | **PDB header:**dna binding protein/dna |

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| 76 | c3brgC_ | Alignment | not modelled | 20.6 | 29 | **Chain:** C: **PDB Molecule:**recombining binding protein suppressor of hairless;<br>**PDBTitle:** csl (rbp-jk) bound to dna |
| 77 | c2zkru_ | Alignment | not modelled | 17.8 | 10 | **PDB header:**ribosomal protein/rna<br>**Chain:** U: **PDB Molecule:**rna expansion segment es41;<br>**PDBTitle:** structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 78 | c3ccjU_ | Alignment | not modelled | 17.7 | 10 | **PDB header:**ribosome<br>**Chain:** U: **PDB Molecule:**50s ribosomal protein l24e;<br>**PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u |
| 79 | d1vqou1 | Alignment | not modelled | 16.6 | 10 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**Ribosomal protein L24e |
| 80 | c3j21V_ | Alignment | not modelled | 16.4 | 14 | **PDB header:**ribosome<br>**Chain:** V: **PDB Molecule:**50s ribosomal protein l24e;<br>**PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins) |
| 81 | c4a1eT_ | Alignment | not modelled | 15.3 | 21 | **PDB header:**ribosome<br>**Chain:** T: **PDB Molecule:**rpl24;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1 |
| 82 | c3iz5Z_ | Alignment | not modelled | 15.1 | 14 | **PDB header:**ribosome<br>**Chain:** Z: **PDB Molecule:**60s ribosomal protein l24 (l24e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 83 | c4ukjN_ | Alignment | not modelled | 15.0 | 7 | **PDB header:**ribosome<br>**Chain:** N: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of blasticidin s bound to the yeast 80s ribosome |
| 84 | c4uloO_ | Alignment | not modelled | 14.8 | 7 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of phyllanthoside bound to the yeast 80s ribosome |
| 85 | c4uldO_ | Alignment | not modelled | 14.8 | 7 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of nagilactone c bound to the yeast 80s ribosome |
| 86 | c3j39W_ | Alignment | not modelled | 14.7 | 10 | **PDB header:**ribosome<br>**Chain:** W: **PDB Molecule:**60s ribosomal protein l24;<br>**PDBTitle:** structure of the d. melanogaster 60s ribosomal proteins |
| 87 | c4ukyO_ | Alignment | not modelled | 14.0 | 7 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of edeine bound to the yeast 80s ribosome |
| 88 | c4ukeO_ | Alignment | not modelled | 14.0 | 7 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of cycloheximide bound to the yeast 80s ribosome |
| 89 | c4b6aW_ | Alignment | not modelled | 14.0 | 7 | **PDB header:**ribosome<br>**Chain:** W: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1 |
| 90 | c4byuW_ | Alignment | not modelled | 14.0 | 7 | **PDB header:**ribosome<br>**Chain:** W: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** cryo-em reconstruction of the 80s-eif5b-met-itrnamet2 eukaryotic translation initiation complex |
| 91 | c4bynW_ | Alignment | not modelled | 14.0 | 7 | **PDB header:**ribosome<br>**Chain:** W: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** cryo-em reconstruction of the 80s-eif5b-met-itrnamet eukaryotic2 translation initiation complex |
| 92 | c3u5iW_ | Alignment | not modelled | 14.0 | 7 | **PDB header:**ribosome<br>**Chain:** W: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome b |
| 93 | c4ujoO_ | Alignment | not modelled | 13.8 | 7 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of lycorine bound to the yeast 80s ribosome |
| 94 | c4ukoN_ | Alignment | not modelled | 13.8 | 7 | **PDB header:**ribosome<br>**Chain:** N: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of cryptopleurine bound to the yeast 80s ribosome |
| 95 | c4ujjO_ | Alignment | not modelled | 13.8 | 7 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of narciclasine bound to the yeast 80s ribosome |
| 96 | c4ul3O_ | Alignment | not modelled | 13.8 | 7 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of geneticin bound to the yeast 80s ribosome |
| 97 | c4ul8O_ | Alignment | not modelled | 13.8 | 7 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of homoharringtonine bound to the yeast 80s ribosome |
| 98 | c4uk3O_ | Alignment | not modelled | 13.8 | 7 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of anisomycin bound to the yeast 80s ribosome |
| 99 | c4ultN_ | Alignment | not modelled | 13.8 | 7 | **PDB header:**ribosome<br>**Chain:** N: **PDB Molecule:**60s ribosomal protein l24-a;<br>**PDBTitle:** crystal structure of verrucarin bound to the yeast 80s ribosome |