**A. thaliana**

In the table presented all plant/algae/ full ribosome (2 subunits) models in PDB.

The model for 80S ribosome from *A. thaliana* is absent.

Here (<https://www.mdpi.com/1422-0067/22/11/6160>) and here (<https://doi.org/10.1093/nar/gkad827>) as model for *A. thaliana* was used 4V7E. I used the same model.

mRNA from 4V7E (mRNA output files numeration from A to E site)

Peptide from 6R6G (peptide output files numeration from PTC to exit tunnel)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Title | PDB | Organism(s): | Quality: | | | | | |
| Resolution: | Modelled Residue Count: | Unique protein chains: | Rama: | Sidechain: | RNA: |
| Structure of the plant mitochondrial ribosome | 6XYW | *A. thaliana* | 3.86 Å  (Cryo) | 16,740 | 86 | 0.3 % | 0.9 % | 0.36 |
| Structure of the actively translating plant 80S ribosome at 2.2 Å resolution | 8B2L | *N. tabacum* | 2.2 Å  (Cryo) | 16,485 | 76 | 0.0 % | 3.2 % | 0.62 |
| Specific features and methylation sites of a plant 80S ribosome | 7QIZ | *S. lycopersicum* | 2.38 Å  (Cryo) | 15,945 | 73 | 0.0 % | 0.2 % | 0.66 |
| Structure of the 70S chloroplast ribosome | 5MMM | *S. oleracea* | 3.4 Å  (Cryo) | 11,345 | 56 | 0.3 % | 8.5 % | 0.44 |
| Structure of the 70S chloroplast ribosome from spinach | 5X8P | *S. oleracea* | 3.4 Å  (Cryo) | 10,831 | 54 | 0.6 % | 0.8 % | 0.51 |
| Structure of the chloroplast ribosome with chl-RRF and hibernation-promoting factor | 6ERI | *S. oleracea* | 3.0 Å  (Cryo) | 10,749 | 53 | 0.0 % | 1.1 % | 0.66 |
| Cryo-EM structure of the spinach chloroplast ribosome reveals the location of plastid-specific ribosomal proteins and extensions | 5MLC | *S. oleracea* | 3.6 Å  (Cryo) | 6,385 | 29 | 3.0 % | 6.9 % | 0.39 |
| Model of the small subunit RNA based on a 5.5 A cryo-EM map of Triticum aestivum translating 80S ribosome | 4V7E | *Triticum aestivum* | 5.5 Å  (Cryo) | 17,350 | 80 | 8.1 % | 4.5 % | 0.46 |
| Cryo-EM structure of the highly atypical cytoplasmic ribosome of Euglena gracilis | 6ZJ3 | *Euglena gracilis* | 3.15 Å  (Cryo) | 17,647 | 78 | 0.0 % | 0.4 % | 0.51 |
| Structure of the mitochondrial ribosome from Polytomella magna | 8A22 | *Polytomella magna* | 2.91 Å  (Cryo) | 20,242 | 104 | 0.0 % | 0.6 % | 0.57 |
| Structure of the mitochondrial ribosome from Polytomella magna with tRNA bound to the P site | 8APN | *Polytomella magna* | 3.10 Å  (Cryo) | 20,329 | 106 | 0.0 % | 0.5 % | 0.58 |
| Structure of the mitochondrial ribosome from Polytomella magna with tRNAs bound to the A and P sites | 8APO | *Polytomella magna* | 3.20 Å  (Cryo) | 20,295 | 104 | 0.0 % | 0.5 % | 0.58 |
| Ribosome subunit structures | | | | | | | | |
| Large subunit of the Chlamydomonas reinhardtii mitoribosome | 7PKT | *Chlamydomonas reinhardtii* | 3 Å  (Cryo) |  | 45 |  |  |  |
| Small subunit of the Chlamydomonas reinhardtii mitoribosome | 7PKQ | *Chlamydomonas reinhardtii* | 4.2 Å  (Cryo) |  | 38 |  |  |  |
| Cryo-EM structure of the plant 60S subunit | 8AZW | *Nicotiana tabacum* | 2.14 Å  (Cryo) |  | 43 |  |  |  |
| Specific features and methylation sites of a plant ribosome. 60S ribosomal subunit | 7QIW | *Solanum lycopersicum* | 2.35 Å  (Cryo) |  | 41 |  |  |  |
| Cryo-EM structure of the plant 40S subunit | 8AUV | *Nicotiana tabacum* | 2.38 Å  (Cryo) |  | 33 |  |  |  |
| Structure of the 50S large subunit of chloroplast ribosome from spinach | 5X8T | *S. oleracea* | 3.30 Å  (Cryo) |  | 29 |  |  |  |
| Structure of the large subunit of the chloro-ribosome | 5H1S | *S. oleracea* | 3.5 Å  (Cryo) |  | 29 |  |  |  |
| Structure of the small subunit of the chloroplast ribosome | 5MMJ | *S. oleracea* | 3.6 Å  (Cryo) |  | 26 |  |  |  |
| Specific features and methylation sites of a plant ribosome. 40S body ribosomal subunit | 7QIX | *Solanum lycopersicum* | 2.53 Å  (Cryo) |  | 21 |  |  |  |
| Structure of the 30S small subunit of chloroplast ribosome from spinach | 5X8R | *S. oleracea* | 3.7 Å  (Cryo) |  | 25 |  |  |  |