***H. sapiens***

In the table presented some *H. sapiens* ribosome (2 subunits) models in PDB.

mRNA from 6y0g (mRNA output files numeration from A to E site)

Information for compare: 6y0g-assembly1.cif #1/A4 U 47 P atom position (used in *H. sapiens)* is closest to position 8ccs.cif #5/Dd G 21 P (used in *S. cerevisiae)*

Peptide from 7qwq (peptide output files numeration from PTC to exit tunnel)

A diagram of a protein cycle

Description automatically generated with medium confidence

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Title | PDB | Organism(s): | Quality: | | | | | |
| Resolution: | Modelled Residue Count: | Unique protein chains: | Rama: | Sidechain: | RNA: |
| Terminating ribosome with SRI-41315 | 8SCB | *H. sapiens* | 2.50 Å | 18,101 | 80 | 0.1 % | 5.1 % | 0.5 |
| Structure of the Human cytoplasmic Ribosome with human tRNA Asp(ManQ34) and mRNA(GAU) | 8JDK | *H. sapiens* | 2.26 Å | 16,691 | 73 | 0.1 % | 3.3 % | 0.56 |
| mRNA decoding in human is kinetically and structurally distinct from bacteria (IC state) | 8G5Y | *H. sapiens* | 2.29 Å | 17,564 | 77 | 0.1 % | 5.0 % | 0.56 |
| High resolution cry-EM structure of the human 80S ribosome from SNORD127+/- Kasumi-1 cells | 7XNY | *H. sapiens* | 2.50 Å | 17,205 | 75 | 0.1 % | 4.7 % | 0.55 |
| Ternary complex of ribosome nascent chain with SRP and NAC | 7QWQ | *H. sapiens* | 2.83 Å | 11,304 | 48 | 0 | 0.2 % | 0.57 |
| Structure of human ribosome in classical-PRE state | 6Y0G | *H. sapiens* | 3.20 Å | 17,127 | 76 | 0.1 % | 0.6 % | 0.46 |
| Structure of human ribosome in hybrid-PRE state | 6Y57 | *H. sapiens* | 3.50 Å | 16,722 | 75 | 0.2 % | 0.8 % | 0.46 |
| Structure of human ribosome in POST state | 6Y2L | *H. sapiens* | 3.00 Å | 16,811 | 74 | 0.2 % | 0.3 % | 0.49 |
| Cryo-EM structure of human 80S ribosomes bound to EBP1, eEF2 and SERBP1 | 6Z6M | *H. sapiens* | 3.10 Å | 18,822 | 79 | 0.2 % | 0.8 % | 0.49 |