

RCSB Title	Accession codes: SSU, LSU	Ribosomal composition	rotation state	mRNA	tRNA	other ligands	Res. (Å)	Refinement Parameters	Organism	Phylogenetic Domain	Ref	PubMed ID
Structure of the large ribosomal subunit from human mitochondria	3J7Y	LSU	NA	N	N	N	3.4	NA	<i>Homo sapiens</i>	Mitochondrial	[1]	25278503
39S large subunit of the porcine mitochondrial ribosome	4CE4	LSU	NA	N	N	N	4.9	NA	<i>Sus scrofa</i>	Mitochondrial	[2]	24362565
Cryo-EM structure of the small subunit of the mammalian mitochondrial ribosome.	3J6V	SSU	NA	N	N	N	7	NA	<i>Bos taurus</i>	Mitochondrial	[3]	24799711
Structure of the yeast mitochondrial large ribosomal subunit.	1VW3	LSU	NA	N	N	N	3.2	NA	<i>Saccharomyces cerevisiae</i>	Mitochondrial	[4]	24675956
The re-refined crystal structure of the Haloarcula marismortui large ribosomal subunit at 2.4 Angstrom resolution: more complete structure of the L7/L12 and L1 stalk, L5 and LX proteins	4HUB	LSU	NA	N	none	none	2.4	R-Value: 0.166 (obs.) R-Free: 0.206	<i>Haloarcula marismortui</i>	Archaea	[5]	23695244
Control of ribosomal subunit rotation by elongation factor G	4KIX 4KIY	SSU/LSU	ratcheted	N	none	EFG, viomycin	2.9	R-Value: 0.223 (work) R-Free: 0.271	<i>Escherichia coli</i>	Bacteria	[6]	23812721
Structure of the <i>Thermus thermophilus</i> 70S ribosome complexed with mRNA, tRNA and paromomycin	2J00 2J01	SSU/LSU	non-ratcheted	Y	A(ASL [%]), P, E	paromomycin	2.8	R-Value: 0.271 (obs.) R-Free: 0.313	<i>Thermus thermophilus</i>	Bacteria	[7]	16959973
The structure of the ribosome with Elongation Factor G trapped in the post-translocational state	2WR1 2WRJ 2WRK 2WRL	SSU/LSU	non-ratcheted	Y	P, E	EFG-fusidic acid	3.60	R-Value: 0.227 (obs.) R-Free: 0.260	<i>Thermus thermophilus</i>	Bacteria	[8]	19833919
Structure of the <i>Thermus thermophilus</i> 70S ribosome in complex with mRNA, paromomycin, acylated A- and P-site tRNAs, and E-site tRNA	2WDK 2WDL	SSU/LSU	non-ratcheted	Y	aa-A ⁸ ,aa-P ⁸ ,E	paromomycin	3.5	R-Value: 0.208 (obs.) R-Free: 0.256	<i>Thermus thermophilus</i>	Bacteria	[9]	19363482
Crystal structure of the ribosome bound to elongation factor G in the guanosine triphosphatase state	4JUW 4JUX	SSU/LSU	ratcheted	Y	P/E hybrid state tRNA	EF-G, GDPCP	2.86	R-Value: 0.220 (obs.) R-Free: 0.250	<i>Thermus thermophilus</i>	Bacteria	[10]	19363482
The structure of the eukaryotic ribosome at 3.0 a resolution	3USB 3USC 3USD 3USE	SSU/LSU	ratcheted	N	none	none	3.0	R-Value: 0.182 (obs.) R-Free: 0.228	<i>Saccharomyces cerevisiae</i>	Eucarya	[11]	22096102

% A(ASL) = A-site anticodon stem loop⁷.

& aa = aminoacylated