

### Ribosome Structure & Synthesis

Structure	Synthesis
Large ribonucleoprotein (RNP) complexes that contain large amounts of RNA	Synthesis is complex and energetically demanding
Highly conserved	Ribosomes are produced in abundance to make necessary proteins
Have a large and small subunit. Translation occurs at the interface, where the two subunits meet	Specialised proteins for ribosome synthesis are also produced in abundance
Codon anticodon binding occurs on small subunit (decoding centre), peptide bond formation occurs on large subunit (peptidyltransferase centre-PTC)	rRNA transcription and processing occur in nucleoli which are found in the nucleus
3 binding sites are found on the interface: A, P, E	Ribosomal subunits are generated and are only functional in the cytoplasm, they do not work in the nucleus
Charged tRNA initially binds to A site, then moves to P site and peptide bond forms, finally tRNA moves to E site, and then leaves the ribosome	

### Peptidyltransfer and Translation Steps

Peptidyltransfer	Initiation	Elongation	Termination
Charging enzymes attach amino acid to the 3' end of the tRNA via a carboxylic ester linkage to a carboxyl group	The start codon must be directed to the P site to start translation	Two tRNAs are bound to the ribosome at one time; A and P sites (pre-translocation state), or P and E sites (post-translocation state, ribosome has moved along the RNA)	Termination/-release factors recognise the stop codon

### Peptidyltransfer and Translation Steps (cont)

Amino acids are added to the carboxyl end of the polypeptide chain	Prokaryotes: a nucleotide sequence close to the start codon pairs with rRNA	Elongation factors are proteins that aid the elongation process. There are different types for specific functions.	Initial binding of RF1 or RF2 (prokaryotes), or eRF1 (eukaryotes) causes peptide hydrolysis
Peptidyltransfer reaction is the formation of a peptide bond between two amino acids	Allows initiation to occur on multiple sites along the sequence, useful for polycistronic mRNA	EF1A brings the charged tRNA to the ribosome	RF3 (prokaryote) or eRF1 (eukaryote) allows release of RF1/RF2 from ribosome
Aminoacyl tRNA-peptide bond is attached to the amino group	Eukaryotes: ribosome is targeted to the start of the transcript, the small subunit moves along the sequence until the start codon is recognised	EF2 aids the movement of the mRNA chain	RF3 is a GTPase
Peptidyl tRNA-peptide bond is attached to the carboxyl group	Small subunit moves along sequence until it recognises the start codon. Large subunit is recruited to start translation	Both are GTPases, and have the capacity to hydrolyse GTP to GDP. Each time an amino acid is added to the polypeptide chain GTP is hydrolysed into GDP	

