mRNA —tRNA—>Amino acid.
RNA code characteristics:
 4 nucleotides code for 64 codons (4³), 61 of which code for 20 amino acids.
Codon coding is degenerate: multiple codon codes for a single amino acid.
Code is universal (4 nucleotides), but meaning assigned to the codons are different (e.g. human and mitochondria)
tRNA characteristics:
Structure: 5' end D loop, 3' end T loop, 3' end CAA sequence binding to amino acid
More than 100 species, synthesised by RNA polymerase III.
• Each amino acid attached to the CAA site with a high energy bond catalysed by 1 of 20 amino acyl synthetase.
(ATP—>AMP)
Wobble phenomenon:
Due to loose structure of ribosome at mRNA 3' end and low specificity, extra pairing is allowed
Reading from 5' to 3' direction, 1st position of tRNA is the wobble position
O At wobble position, G and pair with U, while Inosine (deaminated A) from tRNA able to pair with all other nucleotide
except Guanine
Prokaryotic translation
 Shine Dalgarno sequence GGAGG around 10 base upstream of first mRNA codon
○ 16S rRNA + protein = 30S small subunit have E, P, A, sites
○ Initiation factor 3 (IF3) bind to E site, prevent large subunit binding.
○ IF1&2 duplex + GTP bind to A site
○ 30S subunit complex recognise Shine-Dalgano sequence, bind with AUG site
○ f-Met is recruited to P-site, IF3 detatch, allow 50S binding
○ 23S + 5S + protein = 50S large subunit binding, form 70S complex
 Binding of 50S, IF1&2&GTP induce GTP hydrolysis, release IF1&2 from A site, allow elongation to start
Prokaryotic translation elongation
 Elongation factor Tu (EF-Tu) responsible for selecting correct amino acyl tRNA to enter A site
∘ Elongation factor G (EF-G) responsible for translocation of ribosome down 1 unit in 5' —> 3', synthesising in 5' to 3'
direction (polypeptide not antiparallel). Protein synthesised in the N-terminus - C terminus direction.
o Amino acyl tRNA enter at A-site, form peptide bond with polypeptide chain at P site, move to P site, P site tRNA
exit via E site.
Prokaryotic termination
Three termination factors (RF1,2,3)
RF1&2 bind to A site at STOP codon, stop tRNA entry, hydrolyse polypeptide chain
RF3 proofreads the STOP codon, facilitate dissociation of ribosome subunit and RF 1&2
Eukaryotic translation preinitiation
 Eukaryotic initiation factor (eIF) 1 and 3 bind to E site, 1A bind to A site of the 40S small subunit (18S + protein).
o eIF2-GTP-Met bind to P site, eIF5 bind to E site, form 43S complex
o eIF4 complex containing many subunits bind to 5' end of mRNA, also bring poly-A tail to a loop
43S complex bind to eIF4 complex at 5' end
Eukaryotic translation initiation

sequence (5'A AUGG3')
○ eIF2-GTP hydrolyse, all initiation factor except 1A dissociates, 60S subunit (28S + 5.8S + 5S + protein = 60S)
binds form 80S, eIF 5B-GTP binds to eIF-1A at A site.
○ Hydrolysis of eIF5B-GTP, release of eIF5B and 1A, expose A site, elongation starts.
Eukaryotic elongation
o eEF1α-GTP bring tRNA to A site, hydrolysis cause ribosomal conformational change, catalyse peptide bond
formation
○ eEF2-GTP bind, hydrolysis cause translocation of ribosome towards 3' mRNA, release 1 tRNA.
Eukaryotic termination
○ At STOP codon, eRF1 and eRF3-GTP bind to A site, prevent tRNA entering.
○ eRF3-GTP hydrolyse, cleave polypeptide
 ABCE (ATP binding cassette) dissociates 60S subunit, exchange eRF1 with eIF1, 1A and 3, prevent 60S binding, resets the cycle.
• In eukaryotes, ribosome dissociate and assemble again around the mRNA loop created by eIF4 complex binding 5' end
and poly A tail
Antibiotics targeting translational mechanisms:
○ Tetracycline - prevent tRNA entry to A site
Streptomycin- prevent transition between initiation and elongation stages
○ Chloramphenicol - block peptidyl transferase
○ Erythromycin - Blocks E site
Prokaryotes couples transcription - translation
Eukaryotes couple transcription - processing in nucleus - export - translation

mRNA code combinations	
RNA structure, characteristic, synthesis	
Wobble phenomenon	
Prokaryotic initiation, elongation, termination	
Eukaryotic initiation, elongation, termination	
Antibiotic targets	
Central dogma in Pro/Eu	