the property of genetic codon: A triplet code which is degenerate. A striking feature is that more than one codon can specify an amino acid. This could decrease the effect of a point mutation. Makes the substitution of one gene for nonsense mutation. Code is universal but codon usage varies among different organisms. A specific first codon in the sequence establishes the reading frame in which a new codon begins every three nucleotide residues. In general, the reading frame without a termination codon among 50 or more codons is referred to as an open reading frame(ORF). Long ORFs usually correspond to genes that encode proteins.

Transfer RNA— tRNA are adaptor between codons and amino acids. tRNA is transcribed by RNA pol III and does not need a template. All mature tRNA has two arms that are critical for its adaptor function. The amino acid arm can carry specific amino acids esterified by its carboxyl group. The anticodon arm contains the anticodon. There are also rare bases such as D and phi on other arms which contribute to important interaction for the overall folding of tRNA molecules. There is a dedicated enzyme for adding each amino acid to the tRNA-amino acyl tRNA synthetase. This reaction occurs in two steps in the enzyme's active site. In step one, an enzyme-bound intermediate, aminoacyl-AMP is formed. In the second step, the aminoacyl group is transferred from enzyme-bound aminoacyl-AMP to its corresponding specific tRNA. The reaction of aminoacyl-tRNA formation is very accurate science aminoacyl-tRNA synthetases have a high ability of proofreading. The identity of the amino acid attached to a tRNA is not checked on the ribosome, so the attachment of the correct amino acid to the tRNA is essential to the fidelity of protein synthesis.

wobble hypothesis: the first two bases of an mRNA codon always form strong Watson-Crick base Paris with the corresponding bases of the tRNA anticodon. The wobble position which is nonstandard base pairing is on the first base of the anticodon, this pairs with the third base of the codon. The wobble (or third) base of the codon contributes to specificity, but, because it pairs only loosely with its corresponding base in the anticodon, it permits rapid dissociation of the tRNA from its codon during protein synthesis. It also decreases the necessary types of tRNA which increases the economic efficiency of translation.

The initiation in prokaryotic cells: Bacterial ribosomes have three sites that bind tRNAs, the aminoacyl (A) site, the peptidyl (P) site, and the exit (E) site. The A and P sites bind to aminoacyl-tRNAs, whereas the E site binds only to uncharged tRNAs that have completed their task on the ribosome. E site is largely confined to the 50S subunit. There is a specific amino acid needed to initiate protein synthesis. The AUG is the initiation codon which specifies an amino-terminal methionine residue. The unique type of $tRNA^{fmet}$ that binds the amino acid incorporated in response to the AUG initiation codon is N-formylmethionine(fMet). This makes the initiating fMet-$tRNA^{fmet}$ differ from the normal $tRNA^{met}$. The 30S ribosomal subunit binds two factors, IF-1 to A site in the ribosome and IF-3 to E site in the ribosome preventing the 30s and 50s. The mRNA then binds to the 30s subunit. The initiating AUG is guided to its correct position by the Shine Dolgarno sequence in the mRNA. this consensus sequence is an initiation signal. The 16s rRNA of the 30s ribosomal subunit binds to it. Then the initiating AUG is positioned at the P site, so the only site to which fMet-$tRNA^{fmet}$ can bind. The fMet-$tRNA^{fmet}$ is the only aminoacyl-tRNA that first binds to the P site to start a translation. The binding with the first fMet-$tRNA^{fmet}$ needs GTP-bound IF2. GTP-bound IF2 binds with the A site and recruits the fMet-$tRNA^{fmet.}$ Then the 50s subunit of ribosome binds to the complex, simultaneously, and the GTP bound to IF-2 is hydrolyzed to GDP and Pi, which are released from the complex. Then the 70s ribosome called the initiation complex from, containing mRNA and the first fMet-$tRNA^{met}$