Prokaryotic Translation
## Table T03: The Genetic Code

<table>
<thead>
<tr>
<th>First Position (5’-end)</th>
<th>Second Position</th>
<th>Third Position (3’-end)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>U</td>
<td>C</td>
</tr>
<tr>
<td>U</td>
<td>UUC Phe</td>
<td>UCU Ser</td>
</tr>
<tr>
<td>U</td>
<td>UCC Phe</td>
<td>UCC Ser</td>
</tr>
<tr>
<td>U</td>
<td>UUA Leu</td>
<td>UCA Ser</td>
</tr>
<tr>
<td>U</td>
<td>UUG Leu</td>
<td>UCG Ser</td>
</tr>
<tr>
<td>C</td>
<td>CUU Leu</td>
<td>CCU Pro</td>
</tr>
<tr>
<td>C</td>
<td>CUC Leu</td>
<td>CCC Pro</td>
</tr>
<tr>
<td>C</td>
<td>CUA Leu</td>
<td>CCA Pro</td>
</tr>
<tr>
<td>C</td>
<td>CUG Leu</td>
<td>CCG Pro</td>
</tr>
<tr>
<td>A</td>
<td>AUU Ile</td>
<td>ACU Thr</td>
</tr>
<tr>
<td>A</td>
<td>AUC Ile</td>
<td>ACC Thr</td>
</tr>
<tr>
<td>A</td>
<td>AUA Ile</td>
<td>ACA Thr</td>
</tr>
<tr>
<td>A</td>
<td>AUG Met Start</td>
<td>ACG Thr</td>
</tr>
<tr>
<td>G</td>
<td>GUU Val</td>
<td>GCU Ala</td>
</tr>
<tr>
<td>G</td>
<td>GUC Val</td>
<td>GCC Ala</td>
</tr>
<tr>
<td>G</td>
<td>GUA Val</td>
<td>GCA Ala</td>
</tr>
<tr>
<td>G</td>
<td>GUG Val</td>
<td>GCG Ala</td>
</tr>
</tbody>
</table>

**Start Codon**

**Stop Codon**

- **Nonpolar Side Chain**
- **Uncharged Polar Side Chain**
- **Charged Polar Side Chain**
Figure 39: Difference between an overlapping and a non-overlapping code.
**Wobble rules for codon-anticodon base pairing**

<table>
<thead>
<tr>
<th>5’ end of anticodon</th>
<th>3’ end of codon</th>
</tr>
</thead>
<tbody>
<tr>
<td>G</td>
<td>U or C</td>
</tr>
<tr>
<td>C</td>
<td>G only</td>
</tr>
<tr>
<td>A</td>
<td>U only</td>
</tr>
<tr>
<td>U</td>
<td>A or G</td>
</tr>
<tr>
<td>I</td>
<td>U, C, and A</td>
</tr>
</tbody>
</table>

Figure 41B: The table shows all possible wobble pairing.
Figure 09: The cloverleaf secondary structure.

Adapted from D. Voet and J. G. Voet. *Biochemistry, Third edition.*
Figure 11: Interaction between the anticodon on tRNA and the codon on mRNA.

Figure 6.31

Key bases in codon: anticodon pairing

Wobble position; base pairing more flexible here

mRNA

Codon

Alanine tRNA

Anticodon

C G G

G C U
Figure 13: Three-dimensional structure of tRNA.

Figure 18: Mirror symmetrical interactions of aminoacyl-tRNA synthetases.

Figure 6.34

Uncharged tRNA-specific for valine (tRNA\textsuperscript{Val})

Anticodon region

Amino acid (valine)

AMP

Aminoacyl-tRNA synthetase for valine

Anticodon loop

Charged valyl tRNA, ready for protein synthesis

Linkage of valine to tRNA\textsuperscript{Val}

Dino Moras
Figure 01: Cryo-electron microscopy reconstruction of the *Salmonella typhimurium* (close relative to *E. coli*) ribosome.

Photo courtesy of Danny Nam Ho and Joachim Frank, HHMI, Columbia University.
Figure 12: Translation initiation pathway in bacteria.

Figure 14A: Shine-Dalgarno sequences (ribosome-binding sites), which are located toward the 5’ end of mRNA, are shown for several *E. coli* mRNAs.

FIGURE 6.35

TRANSLATION: Initiation

- Initiator tRNA
- mRNA
- Ribosome binding site (RBS)
- Small 30S subunit
- Large 50S subunit
- GTP
- Add large subunit
- mRNA
- Incoming tRNA
- A site
- P site
- E site
- Peptide bond formation
- Translocation
- Cycle continues three times

TRANSLATION: Elongation

- Growing polypeptide
- mRNA
- E site
- P site
- A site
- Codon recognition
- GTP
- Peptide bond formation
- Cycle continues three times
Figure 23: Polypeptide chain elongation pathway in bacteria.

Figure 41: Bacterial polypeptide termination pathway.