Biochem I.

DNA Polymerase I

Hydrolysis site
3' → 5' exonuclease activity

DNA strand

E + ATP (or NAD⁺) → E-AMP + PP, (or NMN)

E-AMP + P—5'-DNA → E + AMP—P—5'-DNA

DNA-3'-OH + AMP—P—5'-DNA → DNA-3'-O—P—5'-DNA + AMP

DNA-3'-OH + P—5'-DNA + ATP (or NAD⁺) → DNA-3'-O—P—5'-DNA + AMP + PP, (or NMN)
Transcription

Initiation

Transcription starts here ↓

3'

5' -10

(A) CGTATGGTTGTTGGA
(B) GCTATGGTTATTTCA
(C) GTTAAGTACGACA
(D) GTGATACTGAGCACA
(E) GTTTCATGCCTCCA

TATAAT

Rifampicin (Rifamycin)

Figure 33-4
Prokaryotic promoter sequences showing homology in the -10 region. The sequences are from the (A) lac, (B) gal, and (C) trp operons of E. coli; (D) from λ phage, and (E) from φX174 phage. Homologies are shown in green and the -10 consensus sequence (deduced from a large number of promoter sequences) in red. The +1 nucleotides are shown in blue.

Elongation

RNA polymerase

Rewinding

Template strand

Coding strand

Unwinding

RNA-DNA hybrid helix

Elongation site

5' ppG ppp RNA

8' ppG Nascent RNA

Movement of polymerase

Termination

Rho protein

ATP

H₂O

ADP

Pi

Figure 33-11
DNA sequence corresponding to the 5' end of trp mRNA from E. coli. A twofold axis of symmetry (marked by the green symbol) relaxes the base pairs that are shaded yellow.

Figure 33-13
A stable hairpin structure can be formed by the base sequence of the 3' end of the mRNA transcript of the np gene of E. coli. The four U residues are also part of the termination signal.

Biochem I

C-Methylvaline

L-Methylvaline

Sarcosine

C-O

L-Proline

C-O

L-Valine

C-O

S-Valine

C-O

C-Threonine

C-O

C-Threonine

Phenoxazine ring

Figure 33-18
Structure of actinomycin D.
The Genetic Code

Wild-type citron
CAT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C

Base added
CAT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C

Base removed
CAT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C

Wild-type citron
CAT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C

Three bases added
CAT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C AT C

Insertion of three nucleotides at a closely situated site distorts the genetic message over a short stretch of the genetic segment but leaves the remainder of the message unaffected. Deletion of three neighboring nucleotides produces the same result. (After "The Genetic Code," by F. H. C. Crick, Scientific American, October 1962. Copyright © 1962 by Scientific American, Inc. All rights reserved.)

<table>
<thead>
<tr>
<th>Coding properties of polynucleotides</th>
<th>Expected product</th>
</tr>
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<tbody>
<tr>
<td>UCU UCC UCU UCC</td>
<td>Single sequence irrespective of phase</td>
</tr>
<tr>
<td>AAG AAG AAG AAG</td>
<td>Different sequences in different phases</td>
</tr>
<tr>
<td>A GA A GA A GA A GA A</td>
<td>Arg - Arg - Arg - Arg</td>
</tr>
<tr>
<td>AA GAA GAA GAA GAA AA</td>
<td>Glu - Glu - Glu</td>
</tr>
<tr>
<td>UAUC UAUC UAUC UAUC</td>
<td>Single sequence irrespective of phase</td>
</tr>
<tr>
<td>GAUA GAU AUA GAU GAU AUA GAU AUA GAU AUA</td>
<td>Single response irrespective of phase but no long peptide, owing to periodic termination</td>
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</table>

Use of repeat polynucleotides for determining the genetic code. The polynucleotides were used as messenger RNA in vitro in conjunction with a protein-synthesizing system from E. coli. The polypeptide chains produced were isolated and analyzed, and their composition defined the coding properties of the corresponding triplets. (Adapted from Khorana G: Harvey Lect 62:79, 1966)

<table>
<thead>
<tr>
<th>First position (5' end)</th>
<th>Second position</th>
<th>Third position (3' end)</th>
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<tbody>
<tr>
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<td>C</td>
<td>A</td>
</tr>
<tr>
<td>UUU</td>
<td>UCU</td>
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<td>UCC</td>
<td>UAC</td>
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<tr>
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<td>UCA</td>
<td>UAG</td>
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<tr>
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<td>UCG</td>
<td>UAG Stop</td>
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<tr>
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<tr>
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<td>C</td>
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<td>C</td>
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<tr>
<td>GUG</td>
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</table>

Radioactive amino acid
Trinucleotide
Ribosome
Filter