TRANSLATION
MIC 226

TRANSLATION

INTRODUCTION

Protein (amino acid polymer, N terminus, C terminus) Ribosomes 30 S subunit plus 50 S subunit for functional 70 S ribosome mRNA is read 5' to 3' Polysomes; Initiation codons Stop Codons Shine Dargamo

INITIATION

Initiator tRNA (N-formyl methioninyl tRNA Initiation complex

ELONGATION

Peptidyl transferase A, P, E sites on ribosome

TERMINATION

Stop codons
AMINO ACID ACTIVATION

OVERALL:

\[
\text{AMINO ACID} + \text{ATP} + \text{tRNA} \rightarrow \text{AMINO ACYL-tRNA} + \text{AMP} + \text{PP}_i
\]

STEP 1:

\[
\text{H}_2\text{N}-\text{C} \rightarrow \text{C}-\text{O}-\text{H} + \text{H}_2\text{O} \rightarrow \text{H}_2\text{N}-\text{C} \rightarrow \text{C}-\text{O}-\text{P} \rightarrow \text{O} \rightarrow \text{H}
\]

NUCLEOTIDYL TRANSFER

\[
\text{PP}_i \rightarrow \text{H}_2\text{N}-\text{C} \rightarrow \text{C}-\text{O}-\text{P} \rightarrow \text{O} \rightarrow \text{CH}_2
\]

- ANHYDRIDE

AMINO ACID + ATP \rightarrow AMINO ACYL-AMP + PP_i

[AMINO ACID ACTIVATING ENZYME = AMINO ACYL-tRNA SYNTHETASE]
**Gene:**
```
5' G\GAT GGA\G TGC A\ACG ATG GCG ATT
3' C/\CTA C/\TC ACC TTGC TAC CGC TAA
```

**Transcription**
```
5' P\P\P\P\G\AU GGA\G UGG A"ACG
```

**Translation**
```
PROTEIN CODING REGION
```

**Stop Codons:** UAA/UAG/UGA

**Promoter:**
```
5' +1
```

**Untranslated Region:**

**Code Nobels:**
- Holley
- Nirenberg
- Khorana
Ribosomes

Prokaryotic

70S ⇌ 50S' + 30S' subunits

Composition

<table>
<thead>
<tr>
<th>50S'</th>
<th>30S'</th>
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<tbody>
<tr>
<td>34</td>
<td>21</td>
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Number of different proteins:

Number of different tRNA molecules:
- One - 5S'
- One - 23S'
- One - 16S'

Polysomes
TRANSFER RNA (tRNA) ~60 each specific for 1 AMINO ACID + 1 CODON

tRNA

PHENYL-ALANINE

SPECIFIC FOR

PHE

tRNA

TRANSLATION

ANTICODON

3' AAG 5'

MRNA

5'...UUC...3'

CODON FOR PHENYL ALANINE

tRNA - IS AN ADAPTER - ADAPTS

AMINO ACID + CODON
- Genetic code is degenerate—different triplets encode the same amino acid
  
  ACA
  ACG
  ACC
  ACU  all code threonine

- "Wobble" means that some specific tRNA can read more than one codon
  
  A threonine tRNA with an anti-codon of 3' UGG 5'
  
  pairs with 5' ACC 3' OR ACU
  
  "Wobble" makes it possible
For an organism to translate all 61 codons with fewer than 61 tRNAs.

- Prokaryotes often have 60-85 tRNAs. Some different tRNAs carry the same amino acid.
- Some highly specialized prokaryotes have ~40 tRNA genes.
AMIDES

\[ \text{R-C-OH} + \text{NH}_3 \rightleftharpoons \text{R-C-N}^+ - \text{H} + \text{H}_2\text{O} \]

AMINE

\[ \text{R-C-N}^+ - \text{H} \]

AMIDE

\[ \text{R-C-N}^+ - \text{H} \]

MONO SUBSTITUTED

\[ \text{R-C-N}^+ - \text{H} \]

DISUBSTITUTED

\[ \text{H}_2\text{N-C-C-OH} + \text{H-N-C-C-OH} \]

PEPTIDE-BOND

\[ \text{H}_2\text{N-C-C-N-C-C-OH} + \text{H}_2\text{O} \]

PEPTIDE-AMIDE FORMED BETWEEN TWO AMINO ACIDS - ALANYL-GLYCINE
STEP 2: \[ \text{AMINO ACYL AMP} + \text{tRNA} \rightarrow \text{AMINO ACYL~tRNA} + \text{AMP} \]
INITIATING TRANSLATION:

1. FORMYL METHIONINE - tRNA
   [SPECIFIC FOR STARTING TRANSLATION]

METHIONINE (fM) + tRNA

+ ATP

+ ACTIVATING ENZYMES

FMET

NH₂ - C - C - O - tRNA

CH₂

CH₂

SI

CH₃

METHIONYL - tRNA

FORMYL GROUP

[FOLIC ACID]

HC - NH - C - C - O - tRNA

CH₂

CH₂

SI

CH₃

N-FORMYL METHIONYL - tRNA
INITIATION COMPLEXES

mRNA + 30S' + F.MET-TRNA
+ GTP + INITIATION PROTEINS

F.MET

30S' 30S INITIATION COMPLEX

mrna

S' UAC AUG...

PPP G

50 S' SUBUNIT 70S RIBOSOME

F.MET, UAC AUG

EEPAPA

EXIT PEPTIDYL ACCEPTOR
ELONGATION - POLYMERIZATION

F-MET

UAC AUG AGU

5' G P A 3'

F-MET → SER

UAC UCA AUG AGU UAU

5' G P A ...

PEPTIDYL TRANSFERASE → [CHLORAMPHENICOL]
TRANSLOCATION

F-MET-SER, TYR

[ERYTHROMYCIN]
Tetracycline, streptomycin, spectinomycin inhibit the function of 30S ribosome.
How do ribosomes know where to start translating?

A. How to distinguish initial AUG from internal AUG?

B. How to recognize several initiating AUG's in one mRNA

Poly cistronic mRNA
Ribosomes translate all three independently. How?
Protein coding regions are preceded by Shine-Dalgarno sequences [prokaryotes].

Shine-Dalgarno sequences:

mRNA

\[ 5' \text{GAU GGAG UGG AAC G AUG GCG AUU} \]

\( +1 \)

Shine-Dalgarno

\( \text{FMET ALA ILE} \ldots \)
Binding between Shine-Dalgarno + rRNA (16S) positions mRNA so that AUG occupies P site.
Ribosomes are ribozymes - the active site for catalyzing peptide bond formation is entirely RNA. 23S rRNA is peptidyl transferase.

Adenine [2451] participates in forming peptide bonds.

Growing peptide - CO -

Trna peptide site

Adenine N3 takes proton, nitrogen attacks C=O.

Acceptor site

H - N - H

H

< H bond

H - C - C - O

H R

tRNA

N - C - C - O

H

tRNA
H bond stabilizes intermediate

Proton transfers to tRNA oxygen

Electrons of oxyanion form C=O
PEPTIDE BOND FORMS

GROWING PEPTIDE - C - N - C - C - O -
     |       |     |
     H     R     O

TRNA

GROWING PEPTIDE HAS BEEN ADDED TO ONE MORE AMINO ACID

YOU CAN ALSO SAY: ONE MORE AMINO ACID HAS BEEN ADDED TO GROWING PEPTIDE

TRNA (3' END)