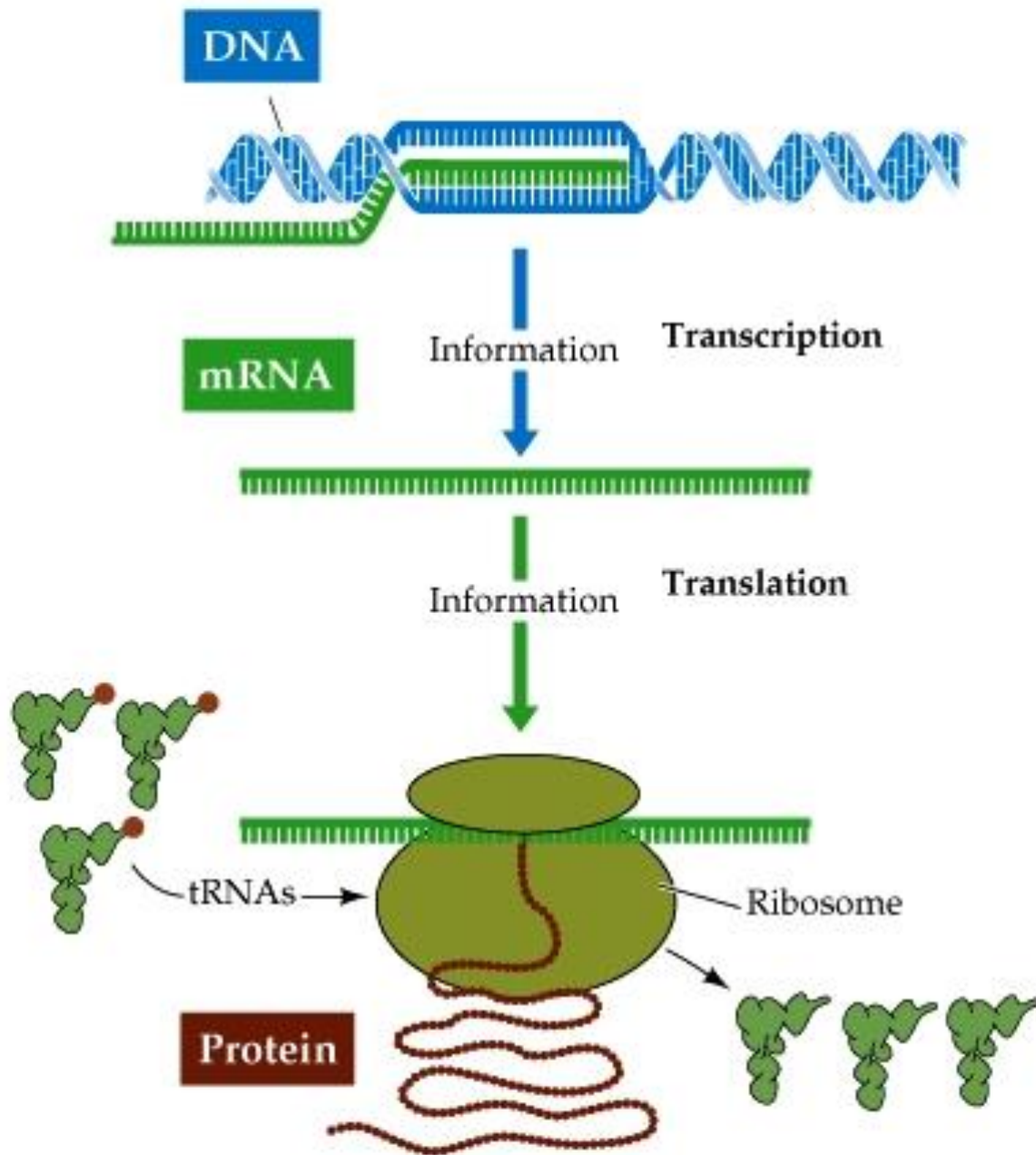


# An Introduction to electron cryo-microscopy, and how I cold nuked my sample into insights about ribosome function

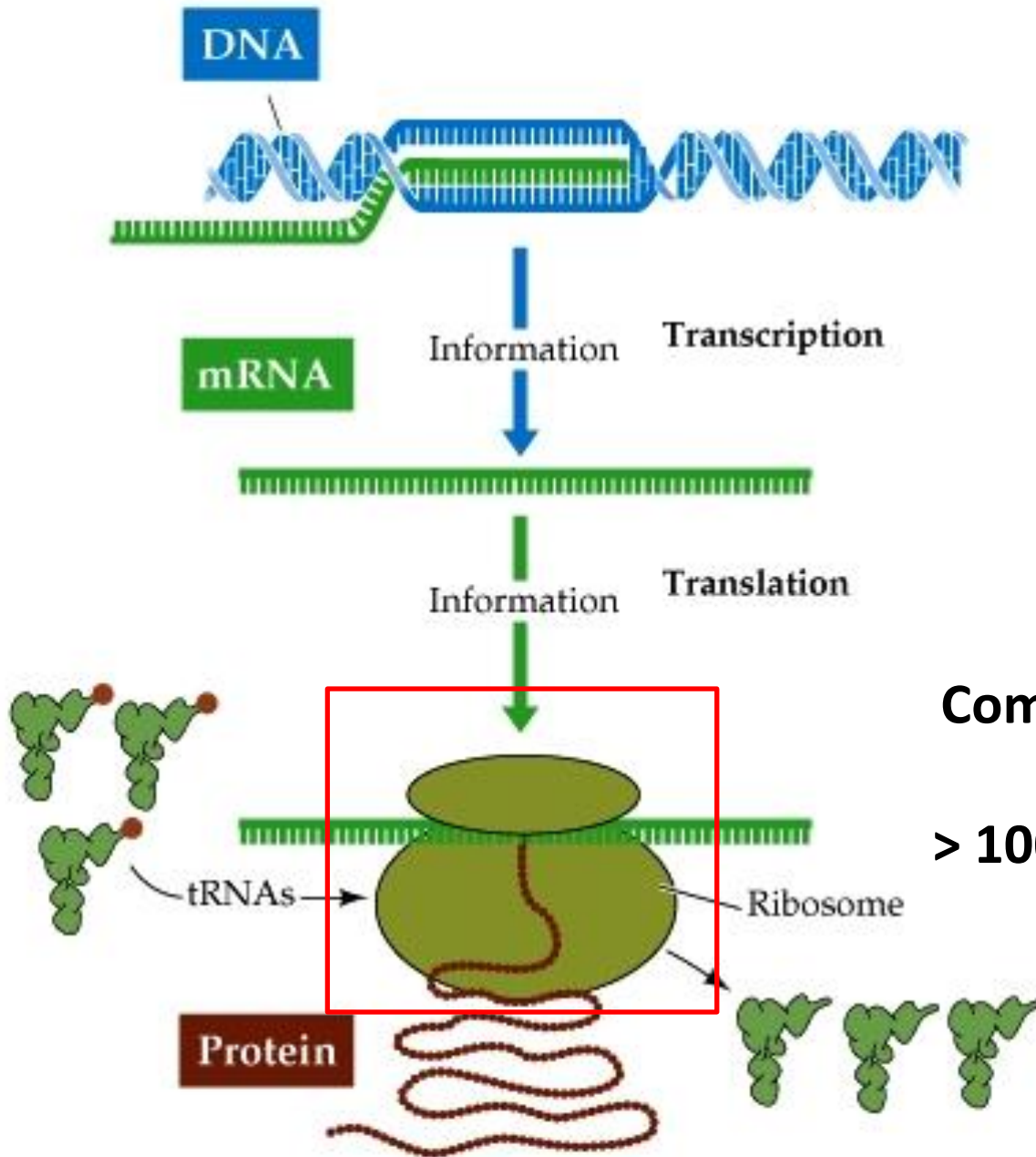
Axel Brilot

January 9th, 2014

# The Central Dogma

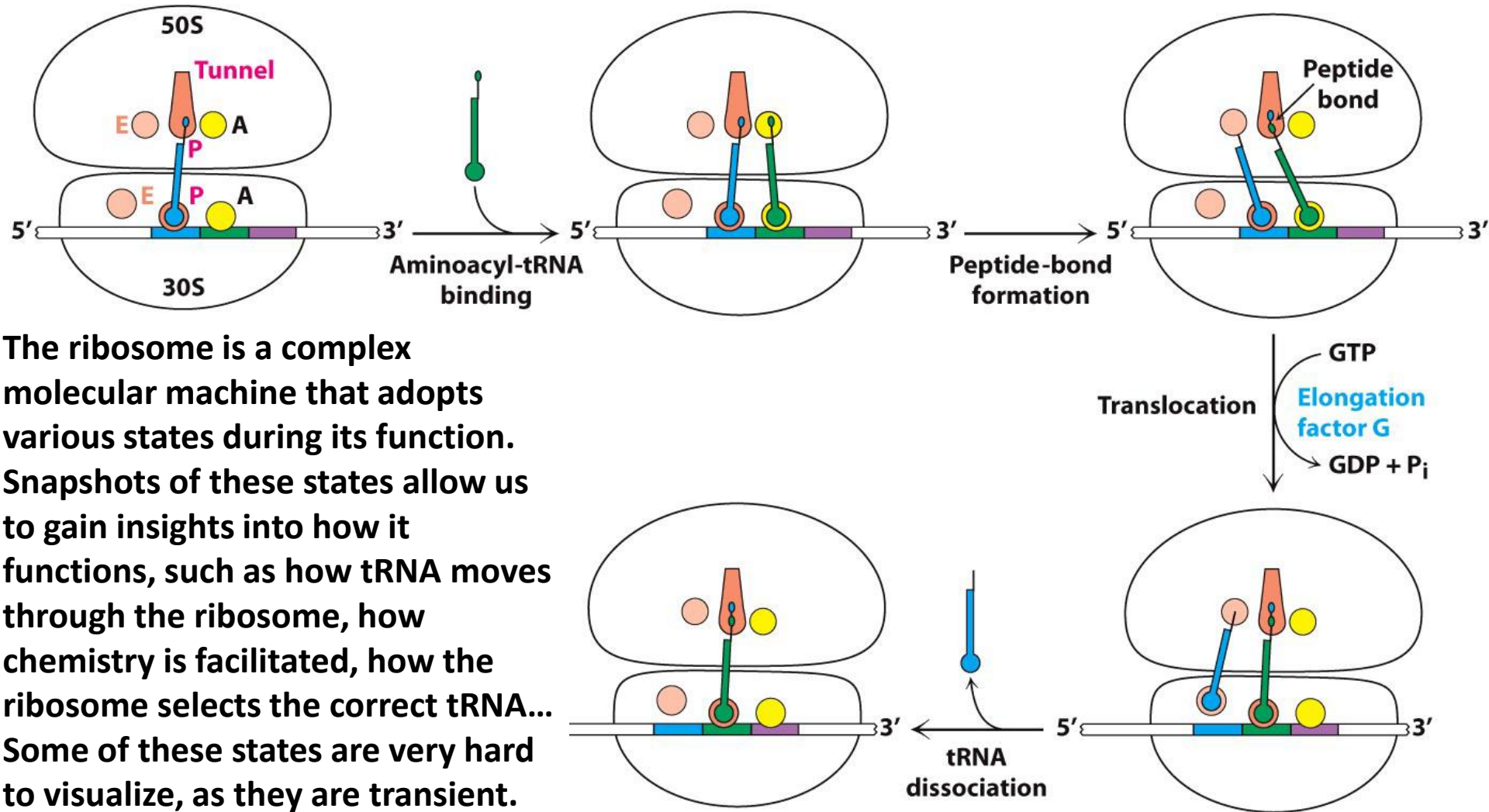


# The Central Dogma



**Complex Molecular Machine**  
**~55 polymers**  
**> 100'000 atoms per complex**

# Why Structure?



The ribosome is a complex molecular machine that adopts various states during its function. Snapshots of these states allow us to gain insights into how it functions, such as how tRNA moves through the ribosome, how chemistry is facilitated, how the ribosome selects the correct tRNA... Some of these states are very hard to visualize, as they are transient.

**Figure 40.7**  
*Biochemistry: A Short Course, Second Edition*  
© 2013 W. H. Freeman and Company



# Electron Microscopes

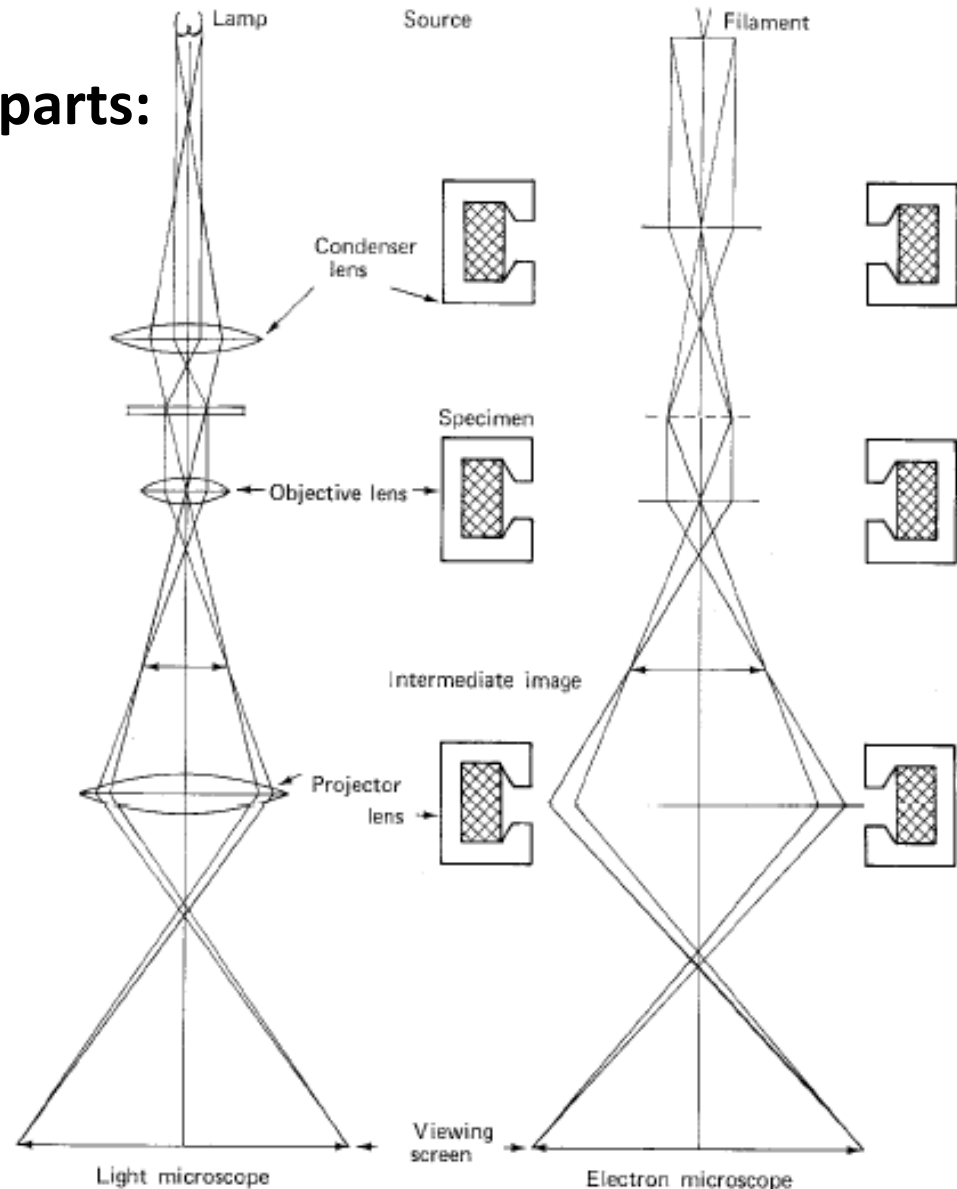


## Similarities with Light Microscopy

**Composed of the same basic parts:**

- “Light” Source
- Condenser lenses
- Sample holder
- Objective lens
- Projector lenses
- Camera

**Designed to record an image of a sample**



From: Principles and Practice of Electron Microscope Operation. Agar, Alderson & Chescoe

# Dissimilarities with Light Microscopy

## Lenses

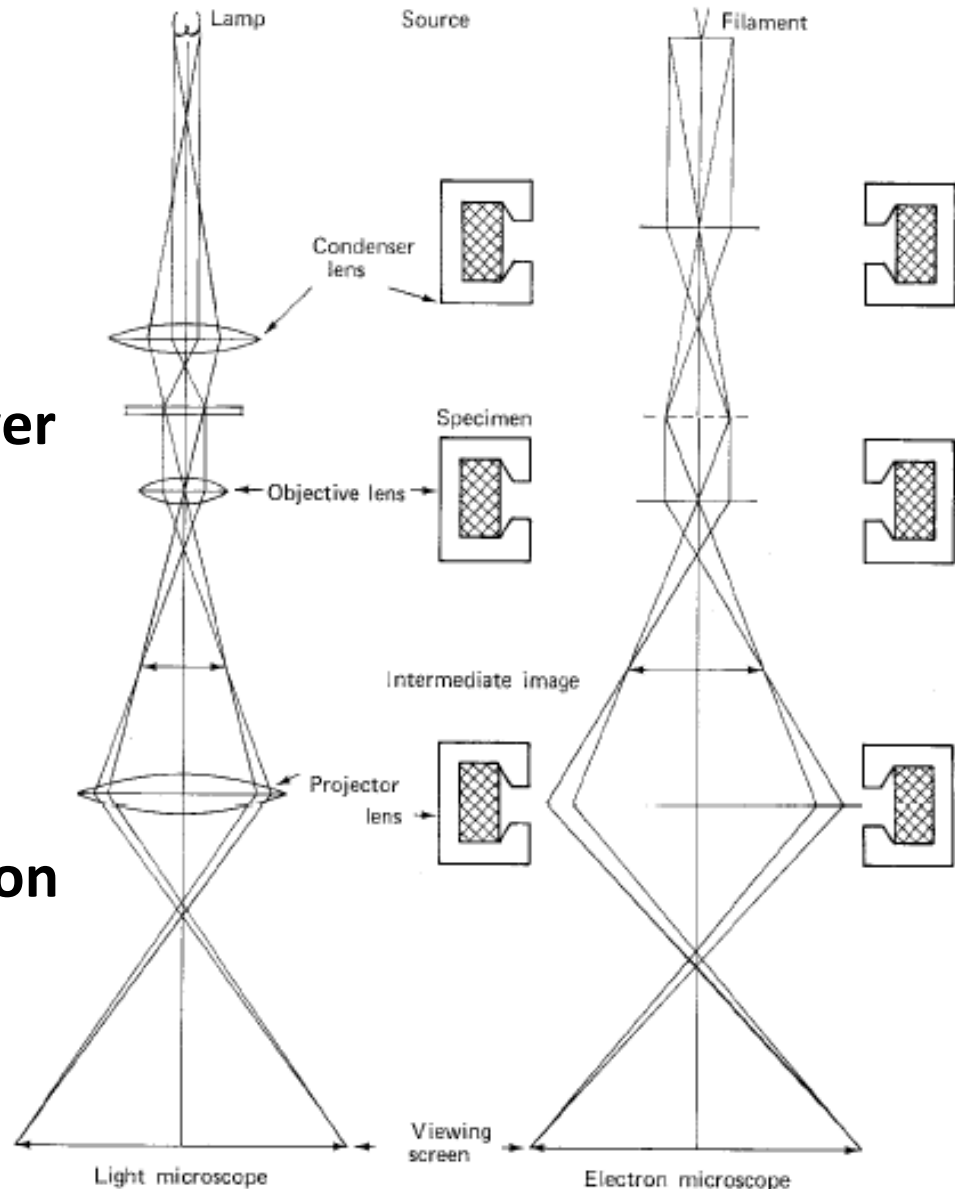
Magnetic lenses vs. glass lenses  
Different aberrations

## Magnification/Resolving Power

Related to the wavelength of light  
~ 100 nm for a light microscope  
Better than 0.1 nm for a TEM

## Mechanism of Image formation

Phase contrast, amplitude contrast



From: Principles and Practice of Electron  
Microscope Operation. Agar, Alderson & Chescoe

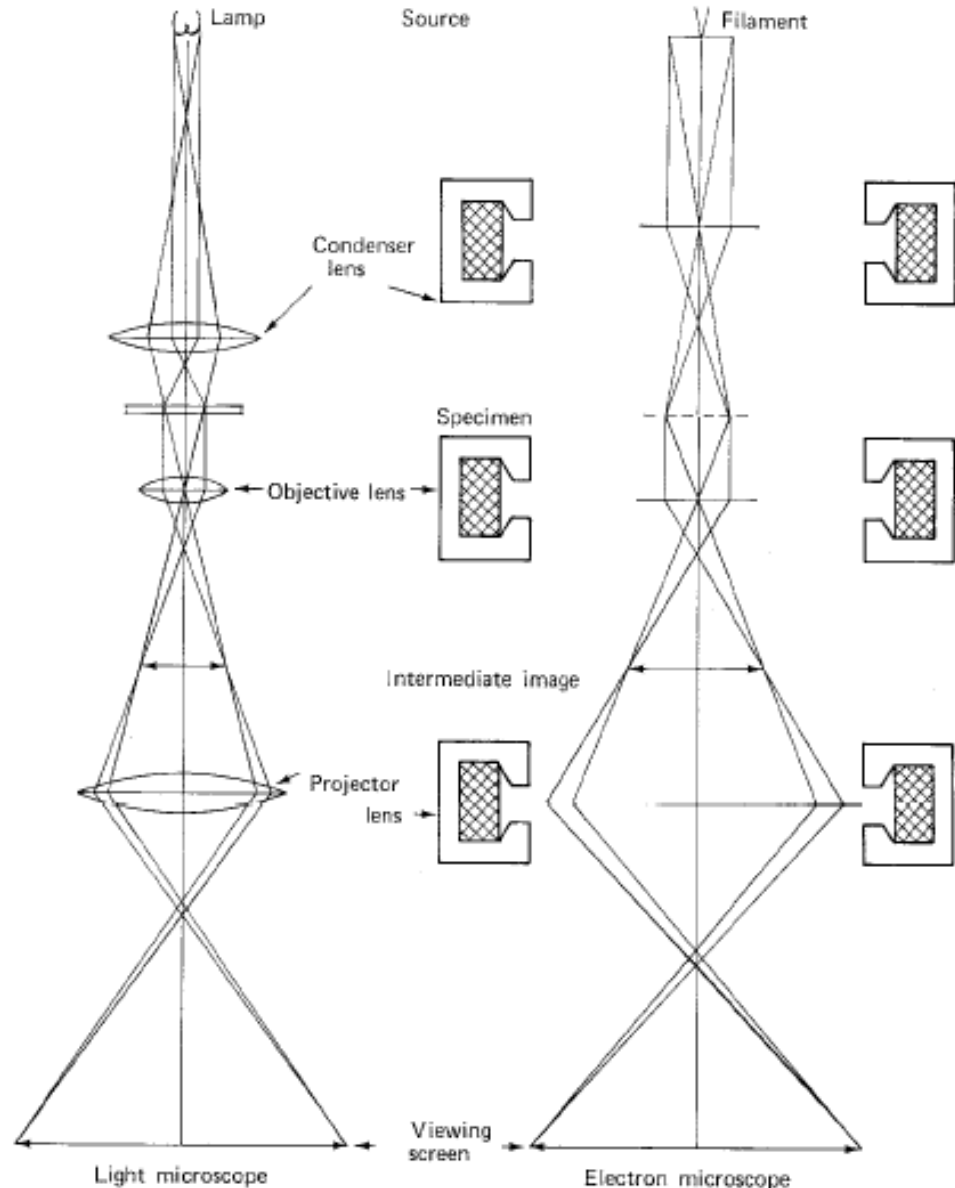
# Dissimilarities with light microscopy you might actually care about

## Vacuum

Samples in EM must be “dry”  
Dry samples are usually dead

## Radiation Damage

Electrons are ionizing radiation  
Severely limits the dose allowed



From: Principles and Practice of Electron  
Microscope Operation. Agar, Alderson & Chescoe

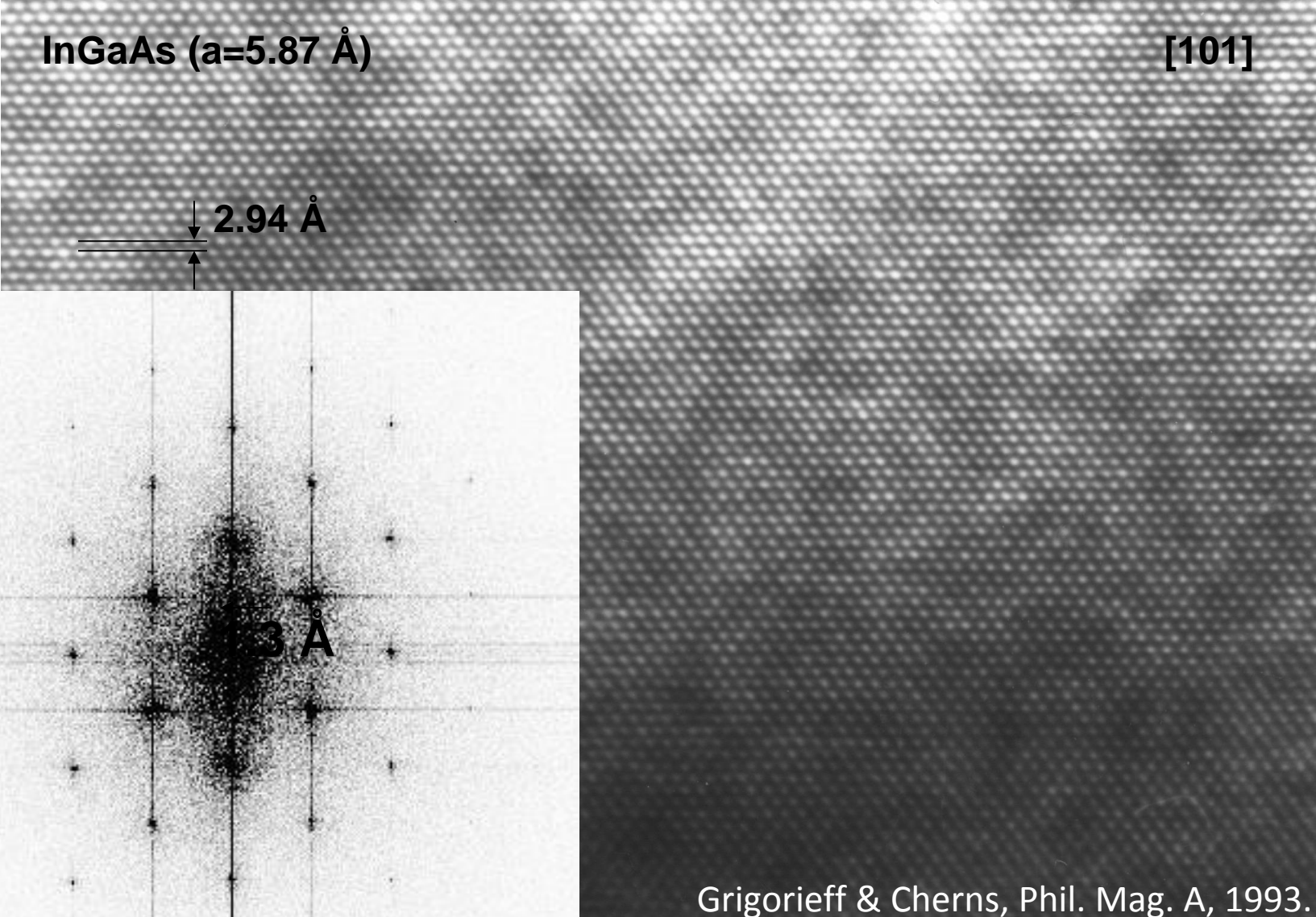


# Dissimilarities with light microscopy you might actually care about

InGaAs ( $a=5.87 \text{ \AA}$ )

[101]

2.94  $\text{\AA}$

A high-resolution transmission electron microscopy (HRTEM) image showing the atomic lattice of InGaAs. The lattice is oriented along the [101] direction. A scale bar indicates a distance of 2.94 Å between two adjacent atomic planes.

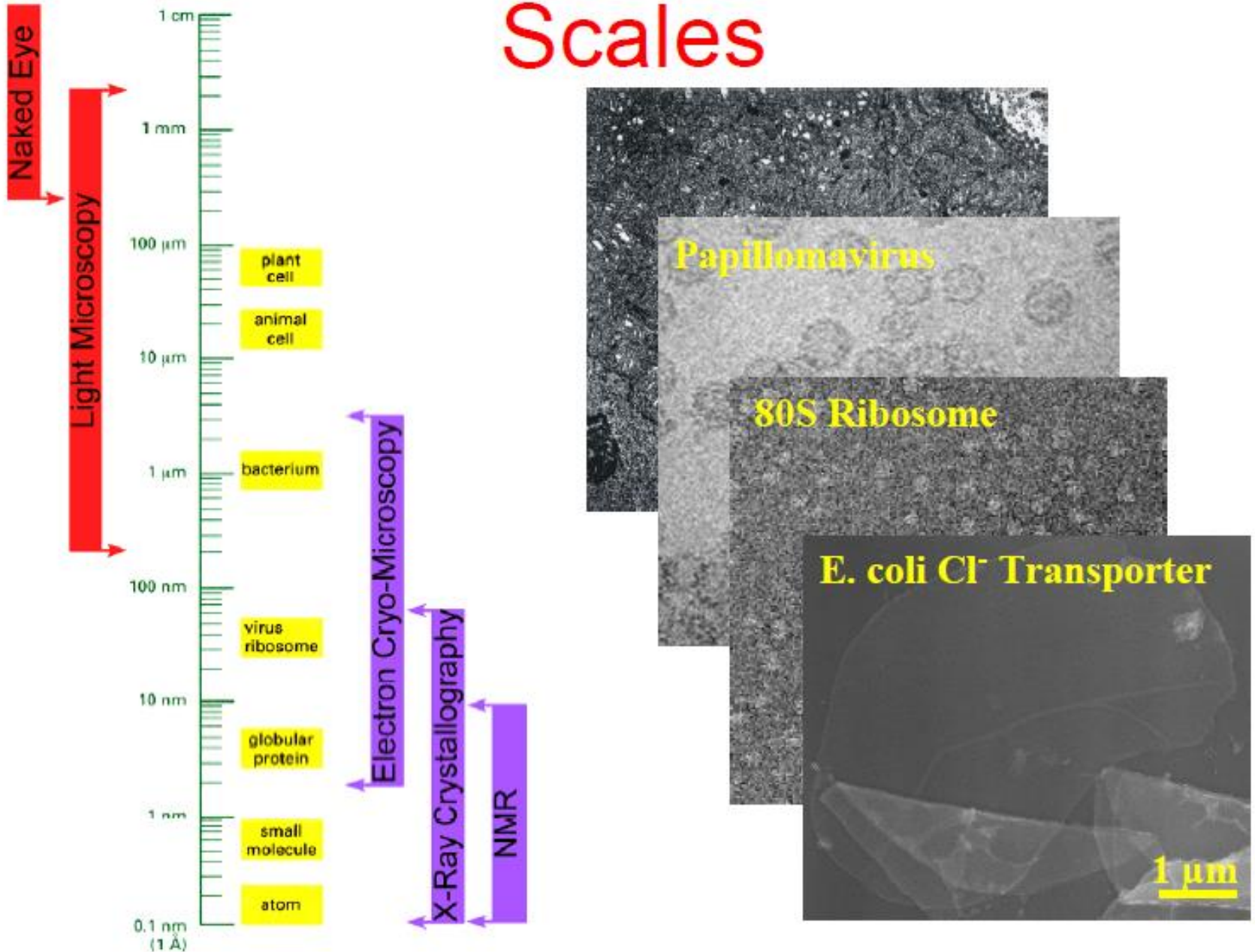
3  $\text{\AA}$

A selected area electron diffraction (SAED) pattern of InGaAs. The pattern shows a central spot surrounded by a grid of diffraction spots. A scale bar indicates a distance of 3 Å between two adjacent spots.

Grigorieff & Cherns, Phil. Mag. A, 1993.

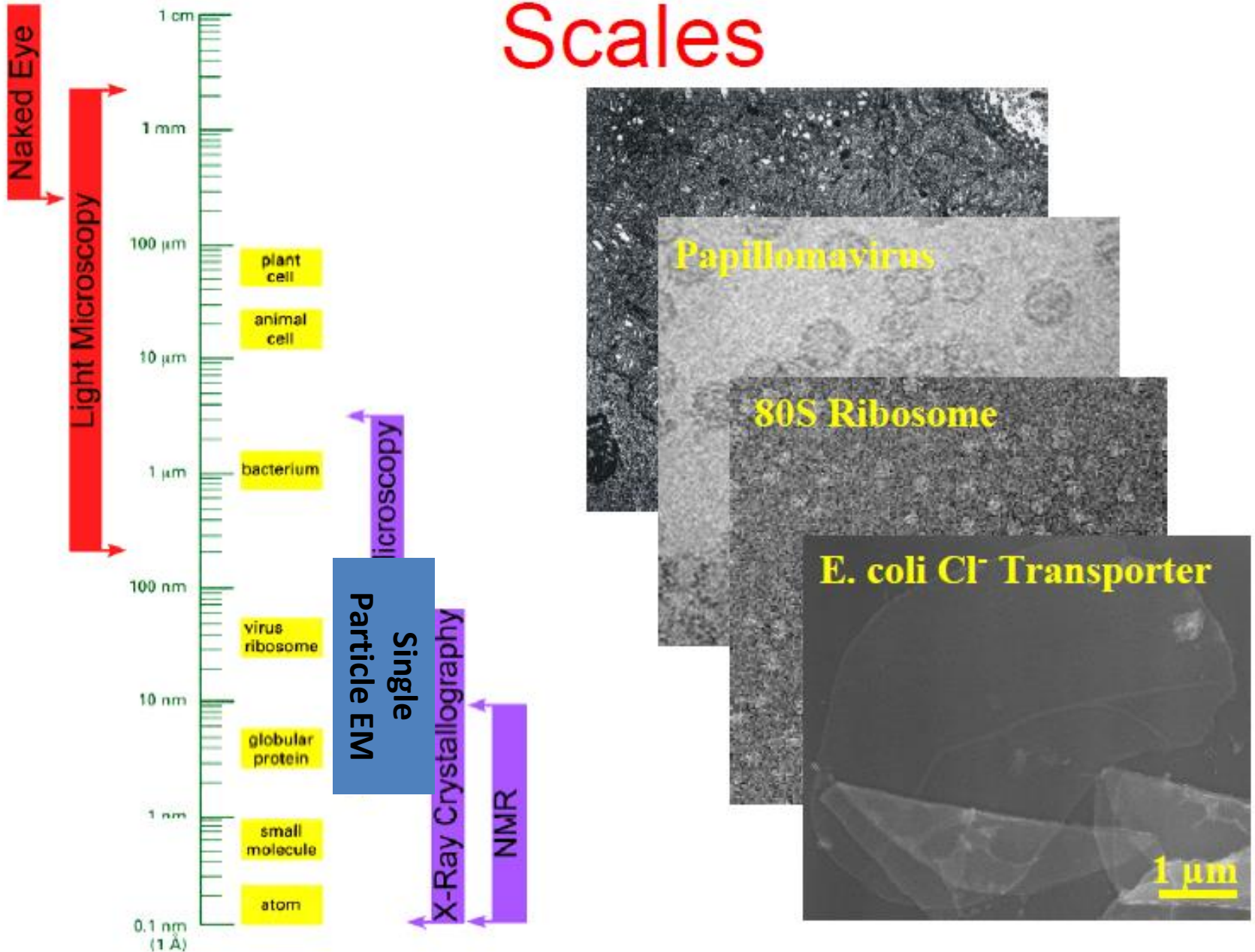
# Length scales studied by EM and other imaging methods

## Scales



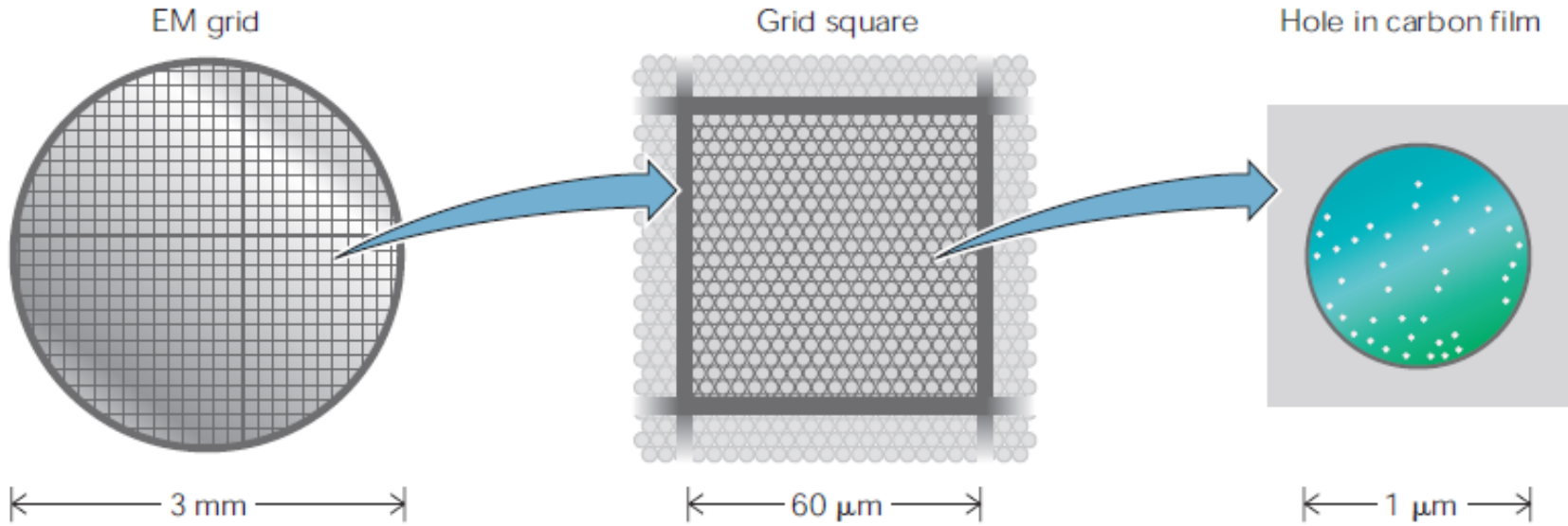
# Length scales studied by EM and other imaging methods

## Scales

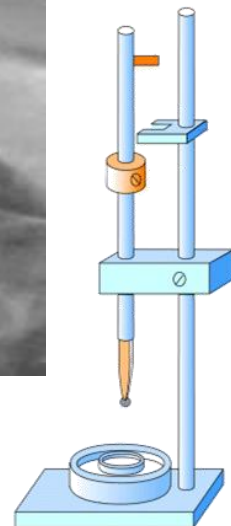
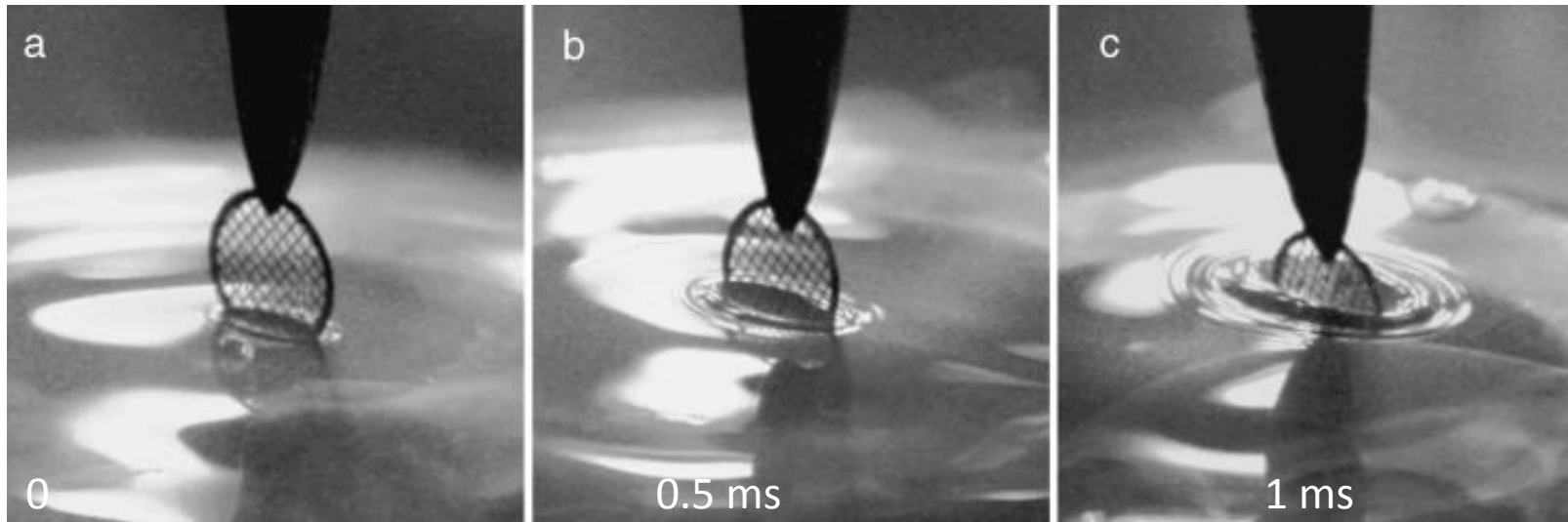




# Sample Preparation: Holey Grids and Plunge Freezing

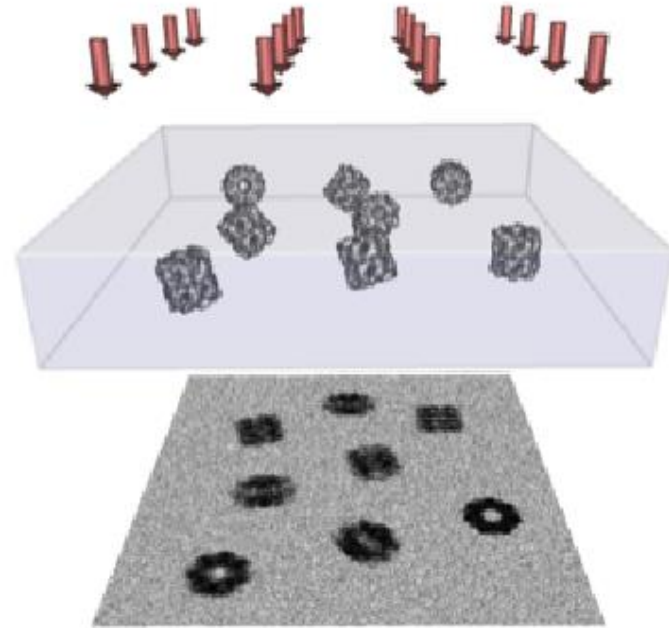


Wang & Sigworth, Physiology, 2009

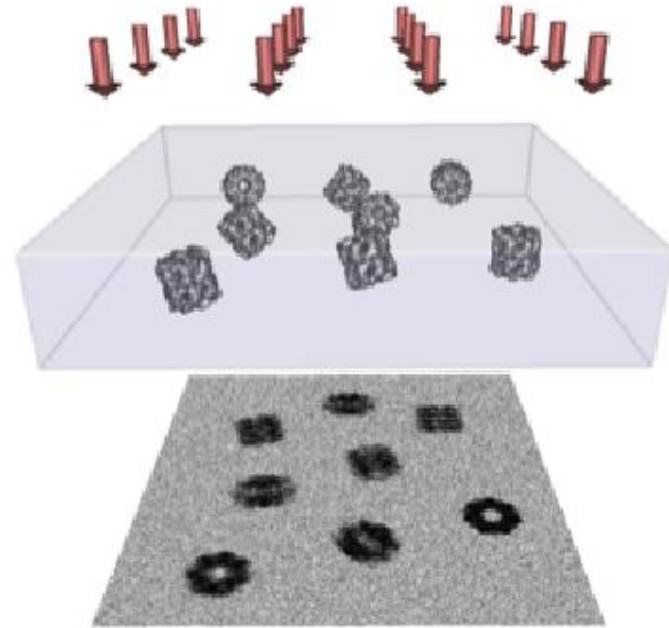
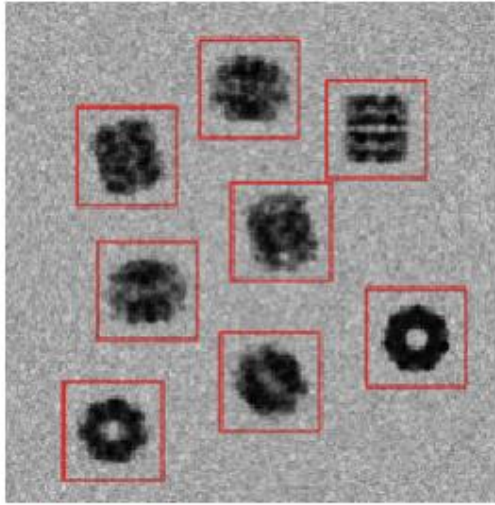


Kasas *et al.*, J. Microsc. 211(1):48 (Stolen from Alexis Rohou)

# Imaging & Reconstruction

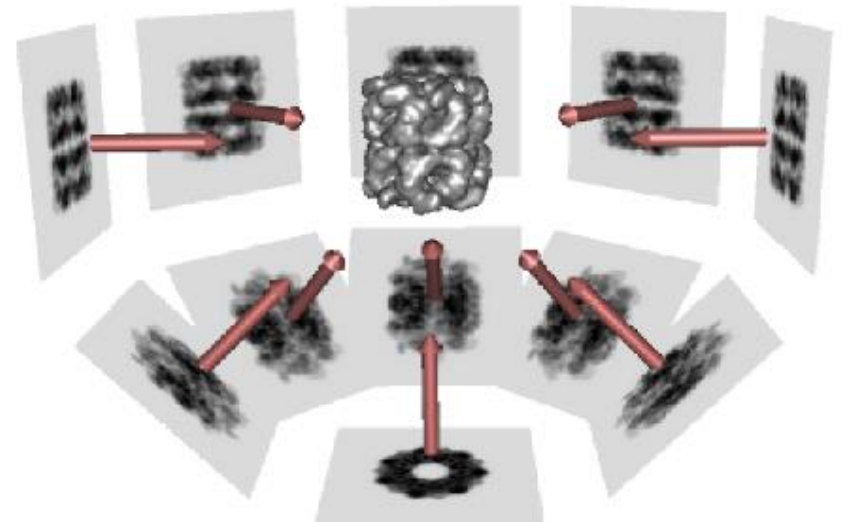
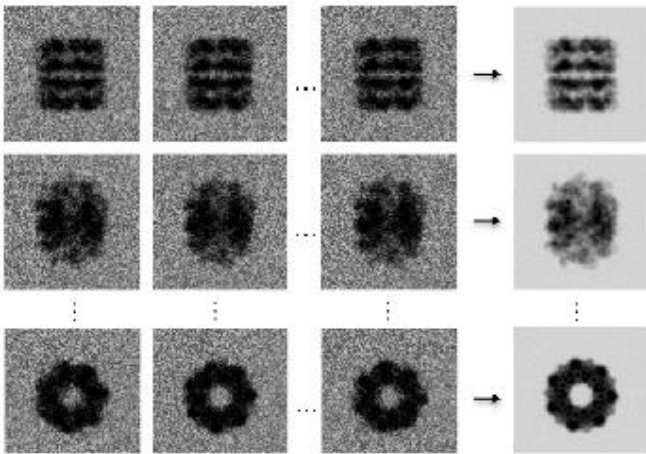
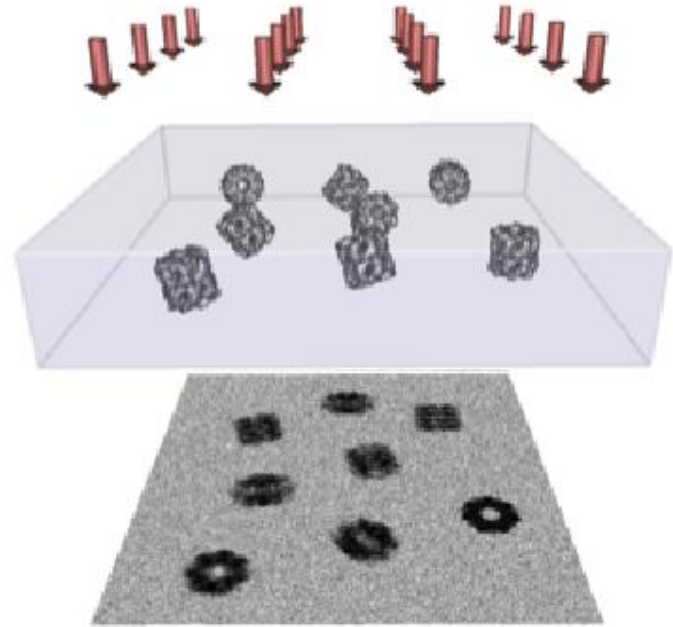
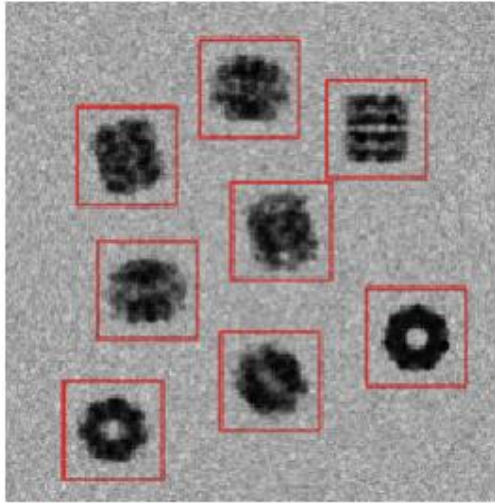


# Imaging & Reconstruction





# Imaging & Reconstruction



(Figures from Greg Pintilie, MIT,  
<http://people.csail.mit.edu/gdp/index.html>)

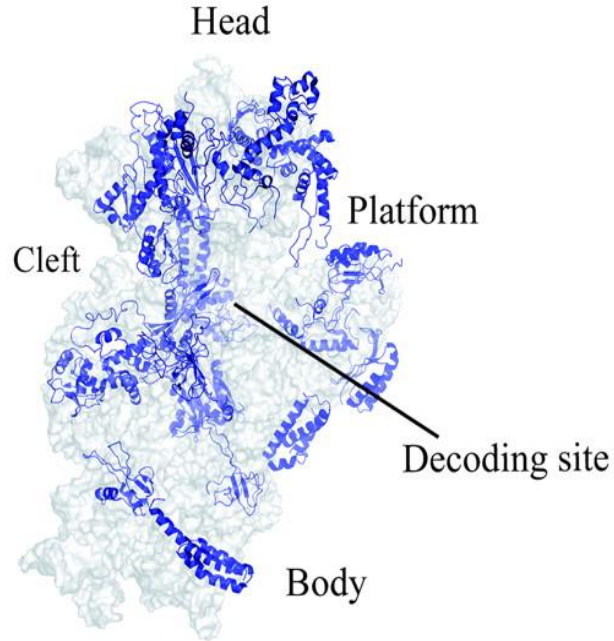
## Why Single-Particle EM?

Technique	Advantage	Problem
<b>Diffraction</b> <b>(X-ray, electrons)</b>	<b>Fast data collection</b> <b>Atomic resolution</b> <b>No weight limit</b>	<b>Crystals needed</b> <b>Large amounts of protein needed</b>
<b>NMR</b>	<b>No crystals needed</b> <b>Fast data collection</b> <b>Atomic resolution</b> <b>Protein dynamics</b>	<b>Weight limit <math>\approx 50</math> kD</b> <b>Large amounts of protein needed</b>
<b>Single particle electron microscopy</b>	<b>No crystals needed</b> <i>Can get data from heterogeneous samples</i> <b>No upper weight limit</b> <b>Little protein needed</b>	<b>Hard to get atomic resolution</b> <b>Slow data collection</b> <b>Lower weight limit <math>\approx 200</math> kD</b>

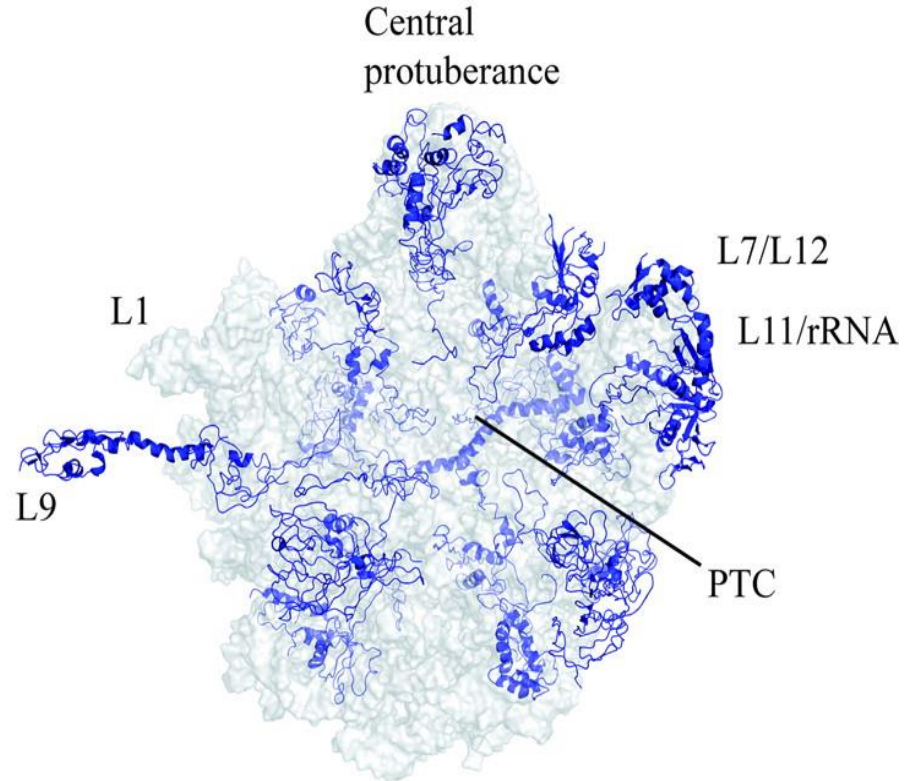
Structure of the ribosome with  
elongation factor G trapped in a pre-  
translocation state

# The 70S Ribosome

Tertiary structures of the 30S (A) and 50S (B) subunits, seen from the interface side

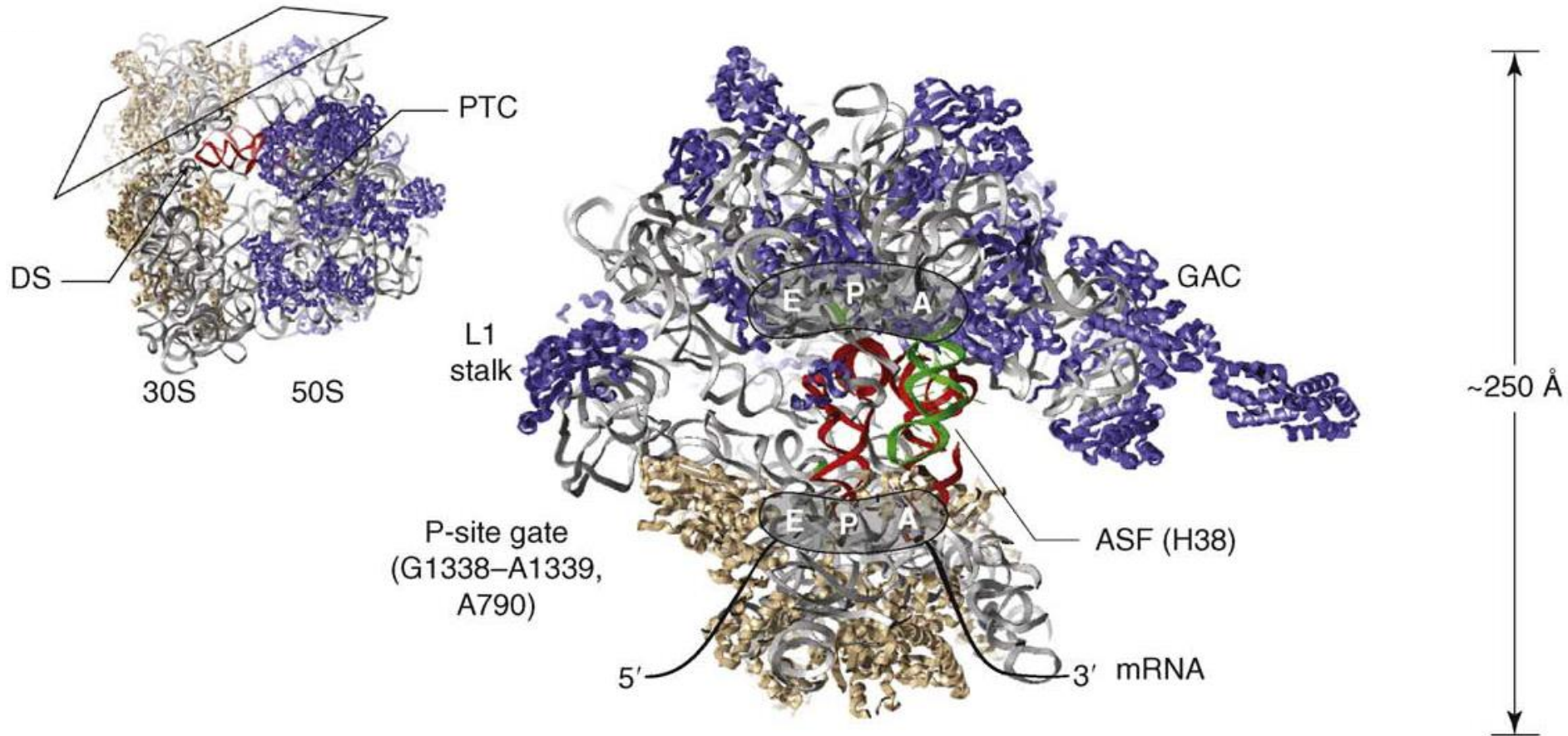


**30S: 1 RNA, 1522 nt  
20 proteins**



**50S: 2 RNA, 2893 nt, 120 nt  
33 proteins**

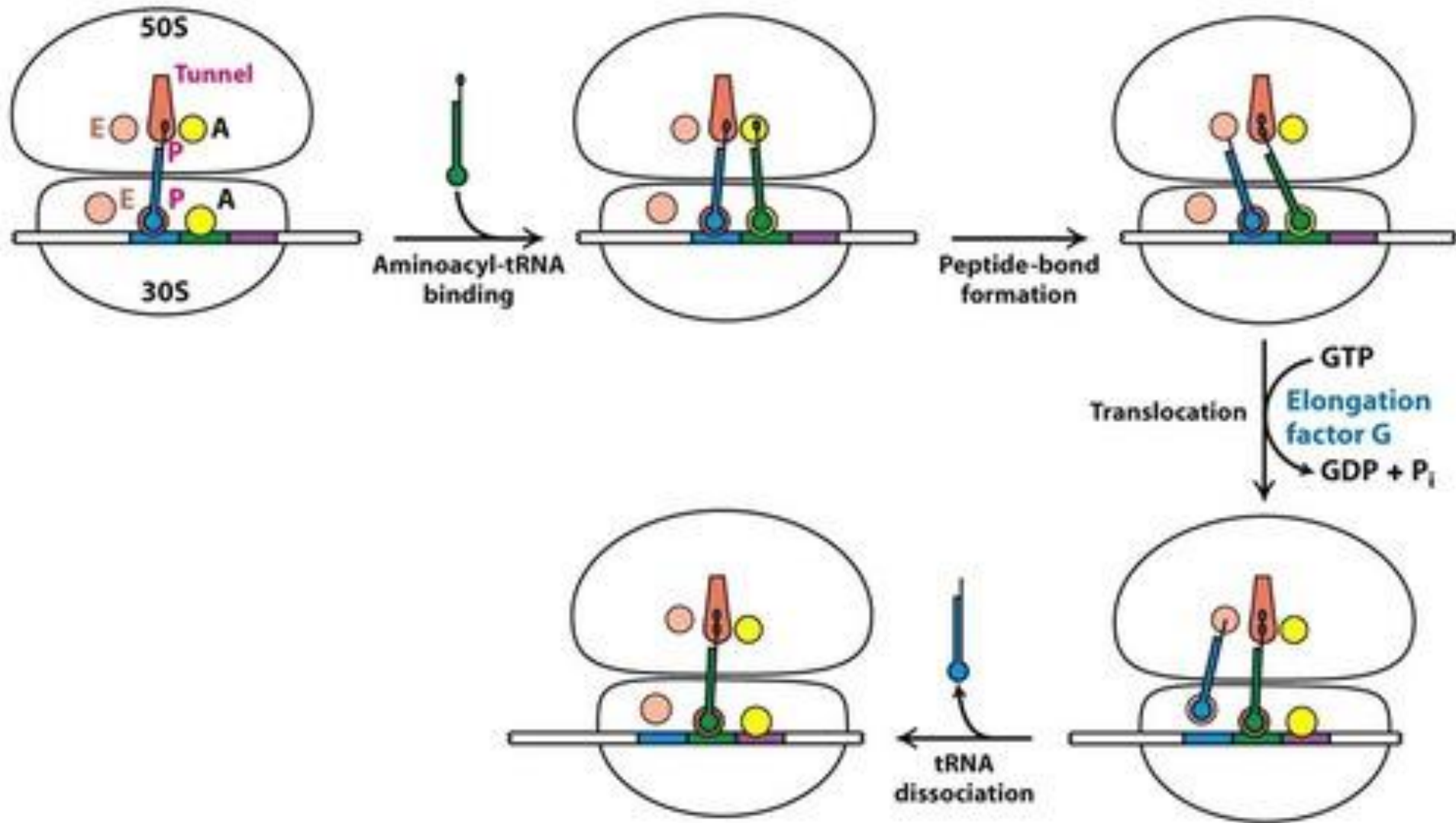
# The 70S Ribosome



**3 tRNA binding sites at the interface: A (Acceptor), P (Peptidyl), E (Exit)**  
**1 mRNA binding site on the 30S subunit**



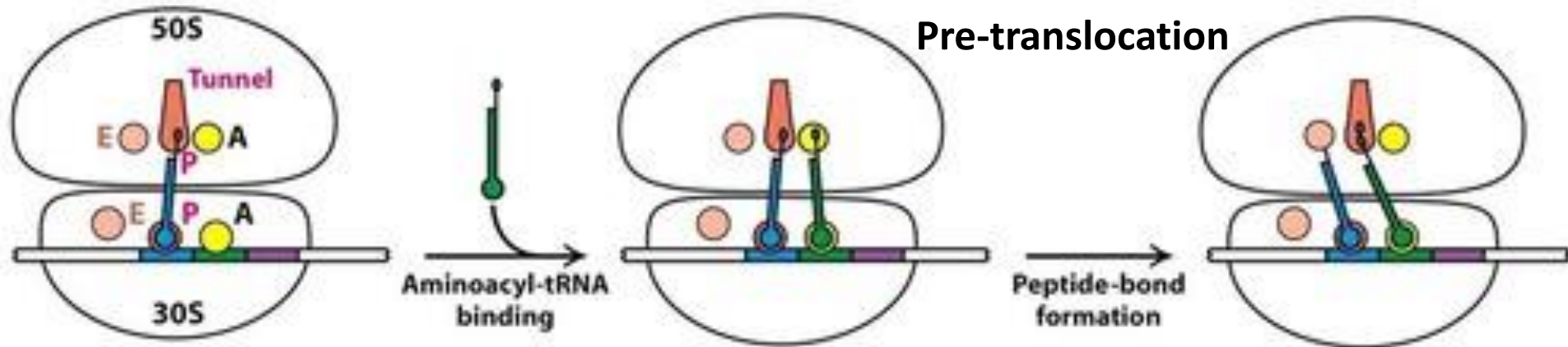
# Translation





# Translation

## Pre-translocation



**Critical step during elongation**

**Move peptidyl tRNA from A to P site**

**Move deacylated tRNA from P to E site**

**Spontaneous function of the ribosome**

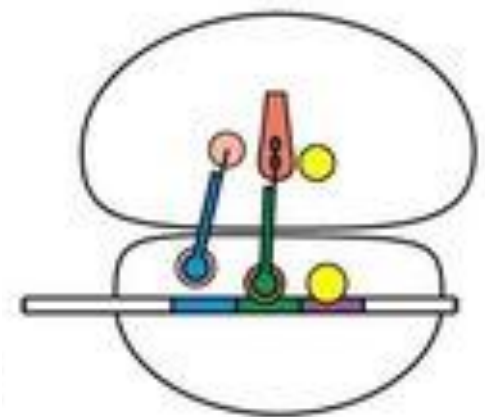
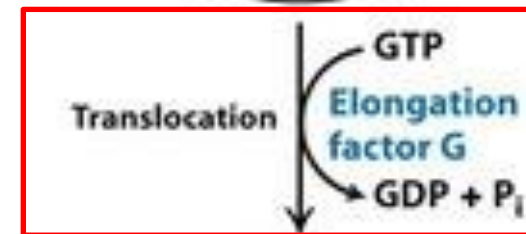
**Accelerated 4-5 order of magnitude by EF-G**

**Move 2 tRNA 20-30 Angstroms**

**Maintain the reading frame**

**Allow for in vivo elongation rate of 15-20**

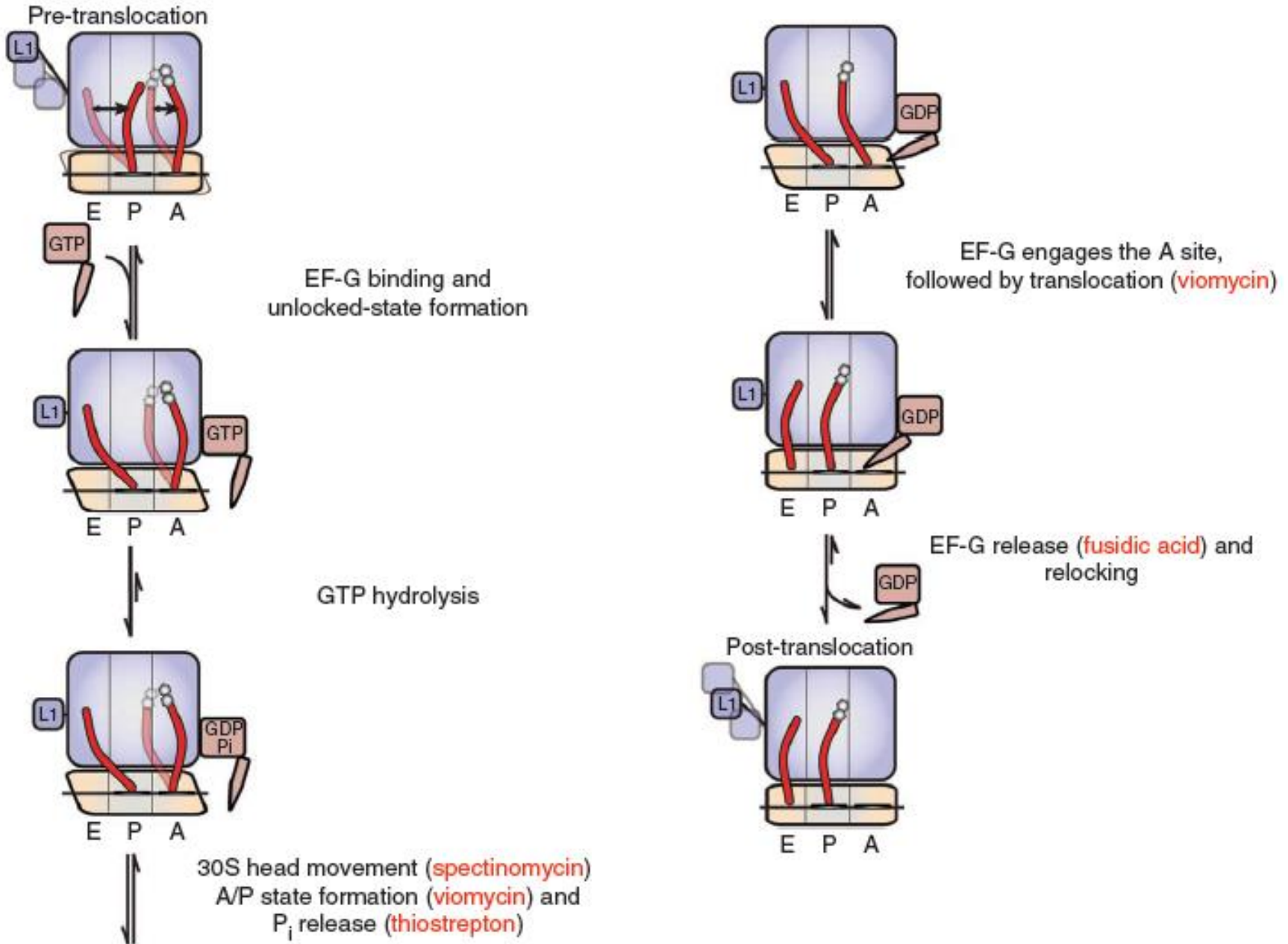
**a.a./s**



## Post-translocation

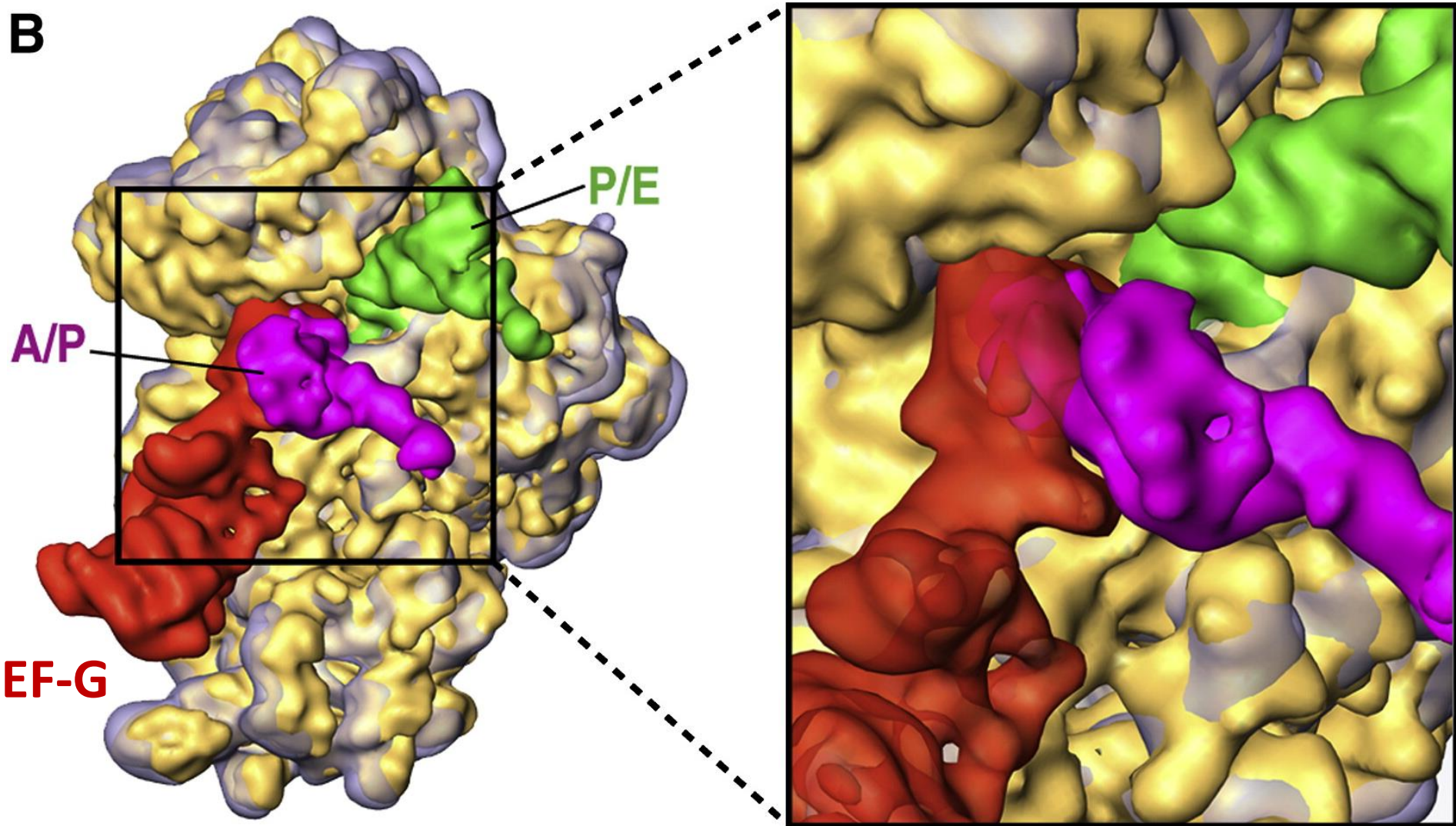
**What is the role of EF-G?**

# Antibiotics in Translocation



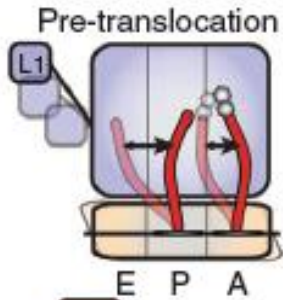
Steric clash of EF-G with A site in Post-translocation state.

**B**

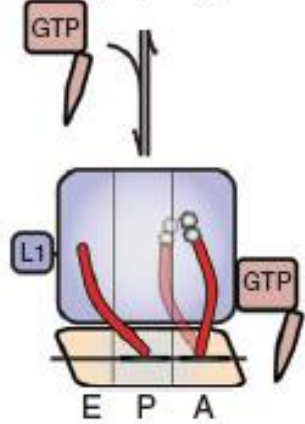




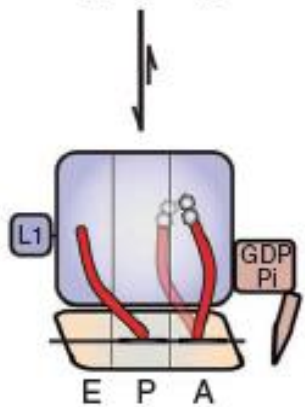
# Antibiotics in Translocation



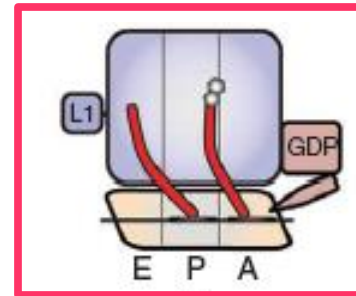
EF-G binding and  
unlocked-state formation



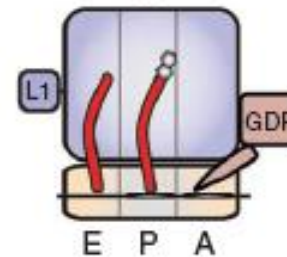
GTP hydrolysis



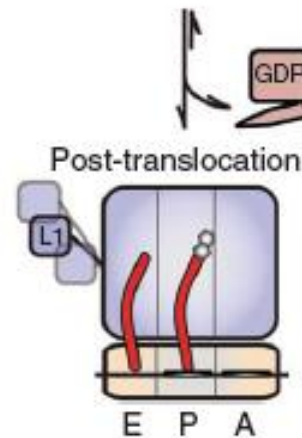
30S head movement (**spectinomycin**)  
A/P state formation (**viomycin**) and  
P<sub>i</sub> release (**thiostrepton**)



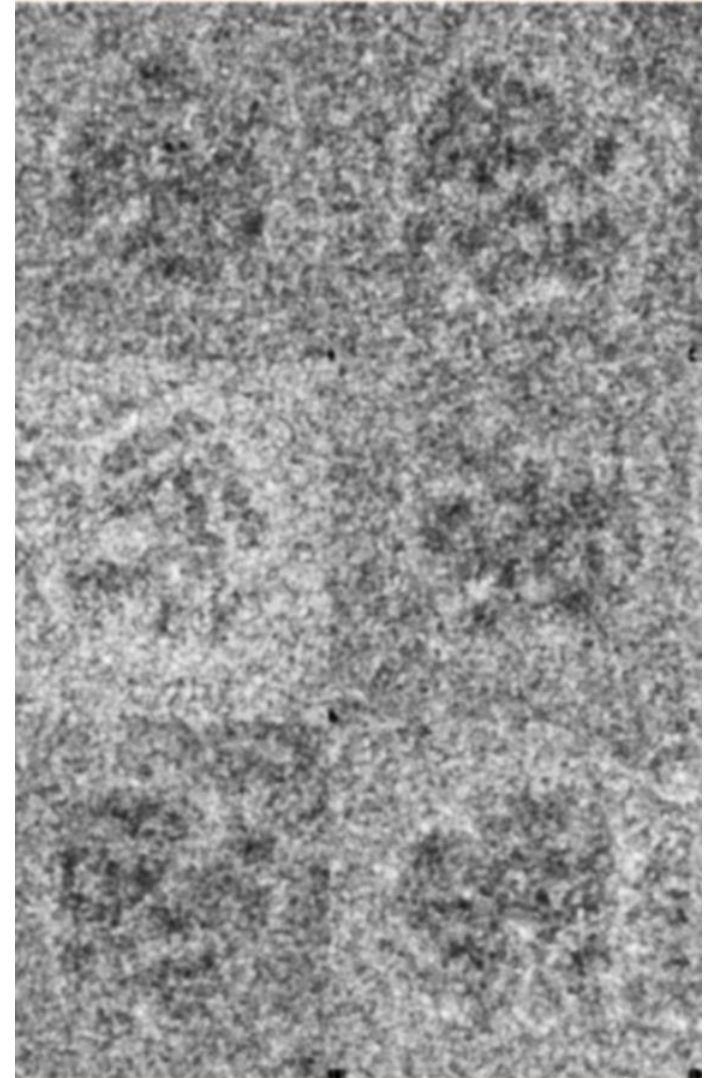
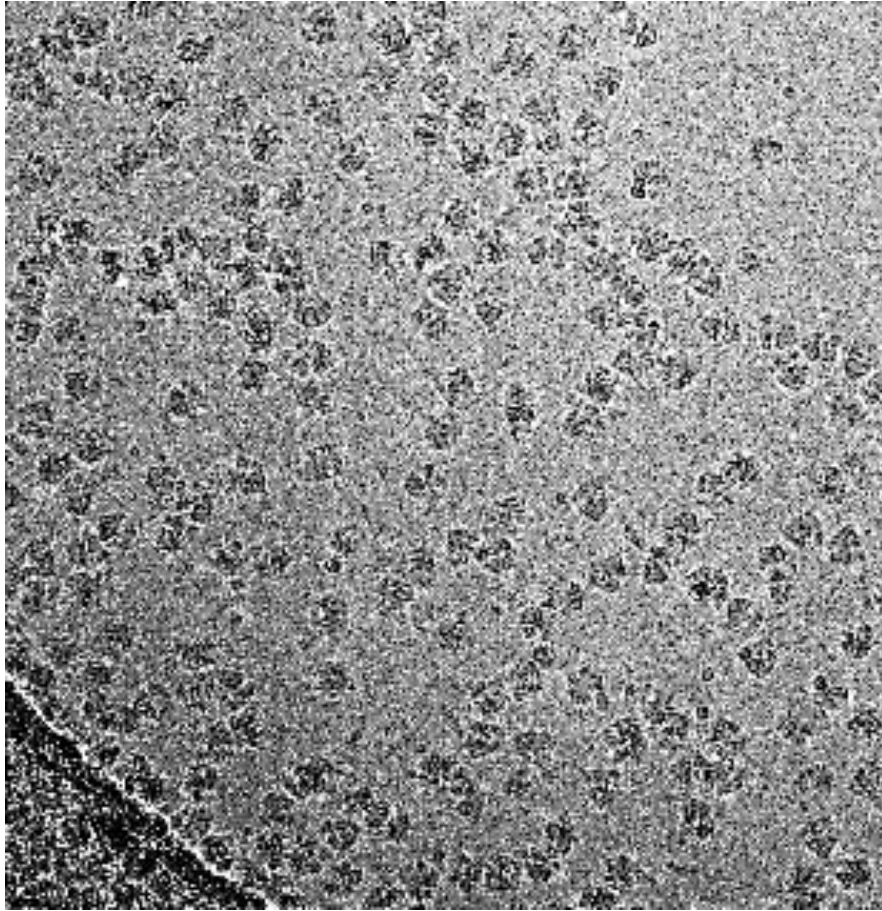
EF-G engages the A site,  
followed by translocation (**viomycin**)



EF-G release (**fusidic acid**) and  
relocking



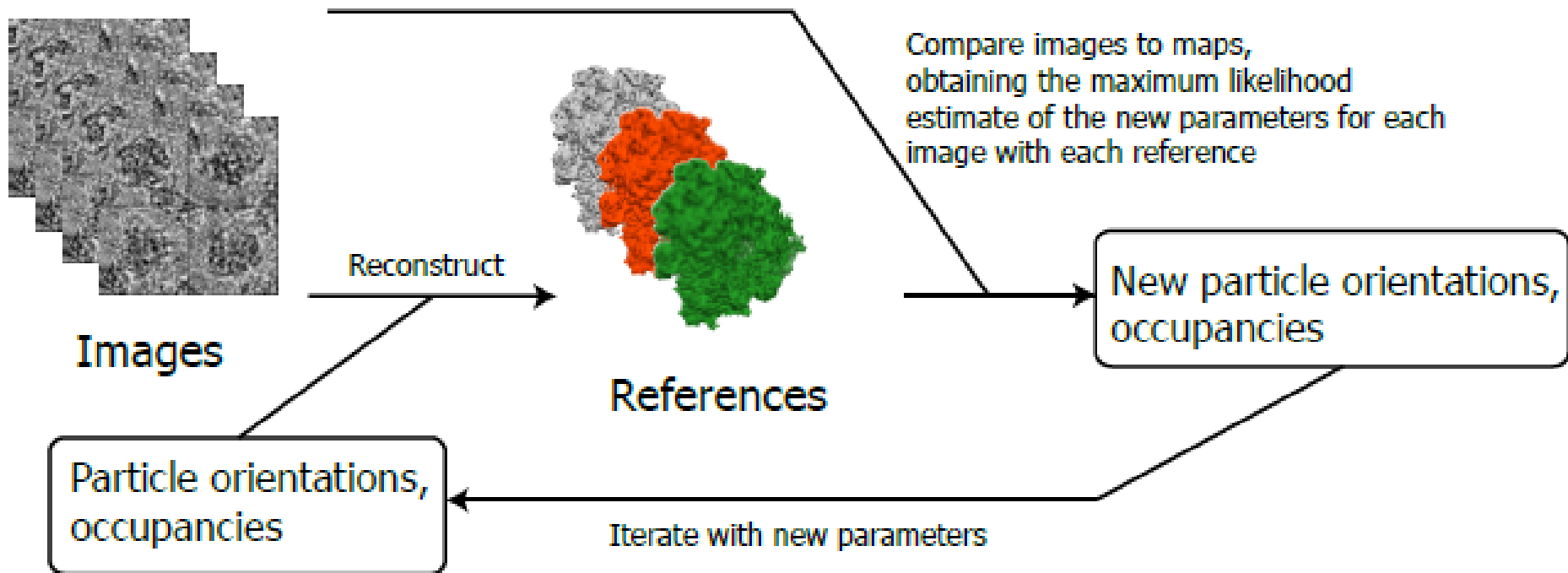
## The Raw Data



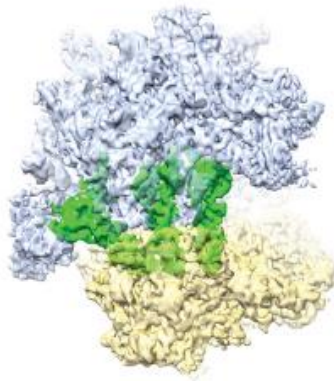
1.35 Million particles, collected on a Titan Krios Microscope at 300 kV.



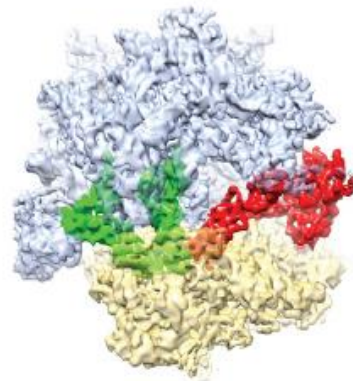
# The Expectation-Maximization algorithm



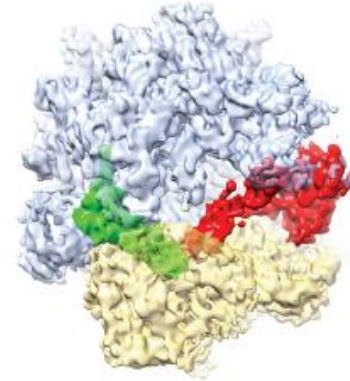
# The Results



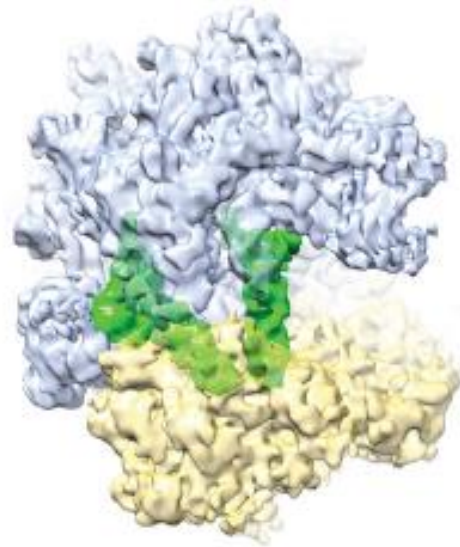
I. 3 tRNA  
(26.7%)



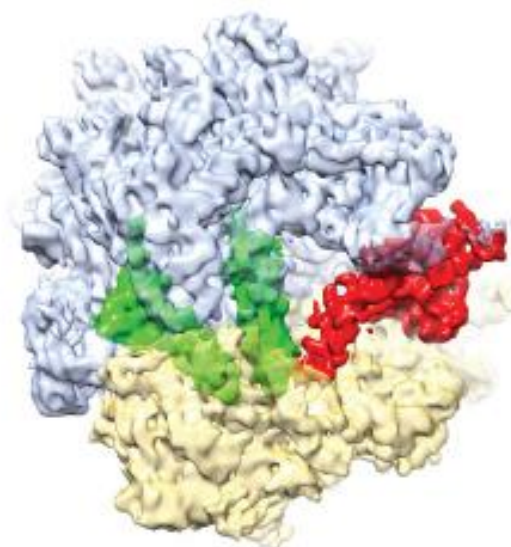
II. EF-G, P & E tRNA  
(13.4%)



III. EF-G, P site tRNA  
(6.8%)

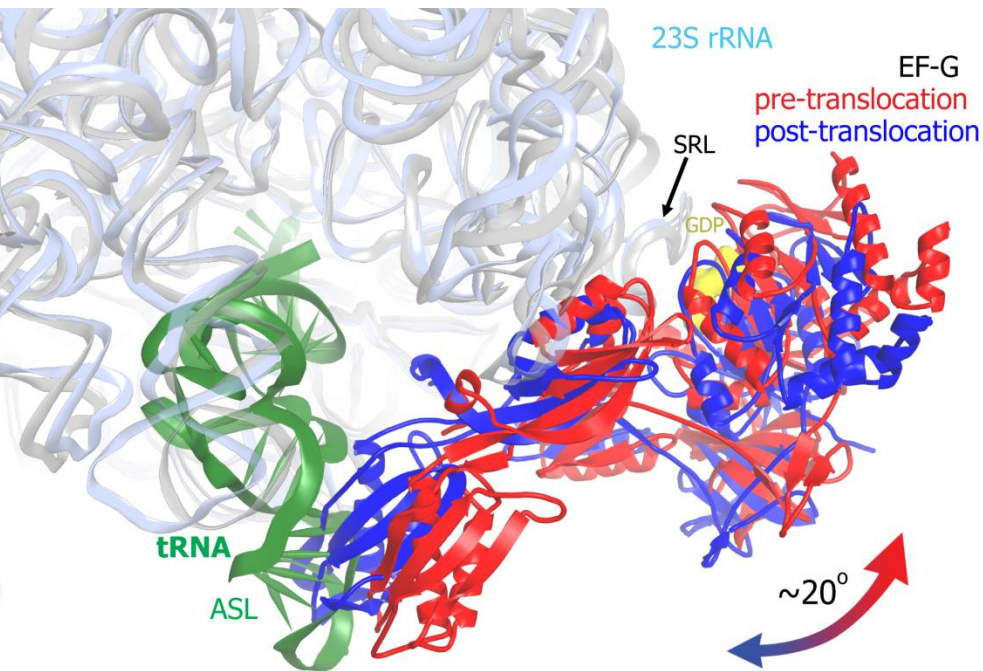


IV. A/P & P/E tRNA  
(3.5%)

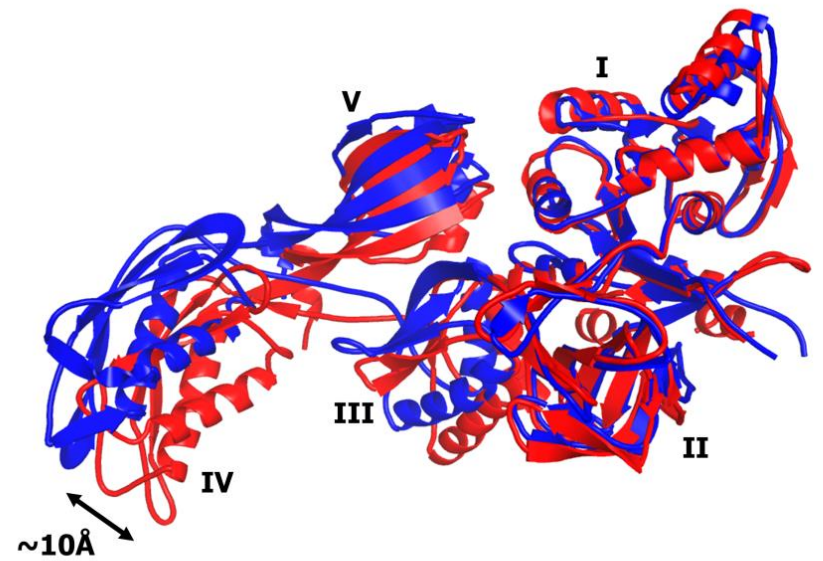


V. EF-G, A/P & P/E tRNA  
(2.4%)

# Conformational Changes of EF-G

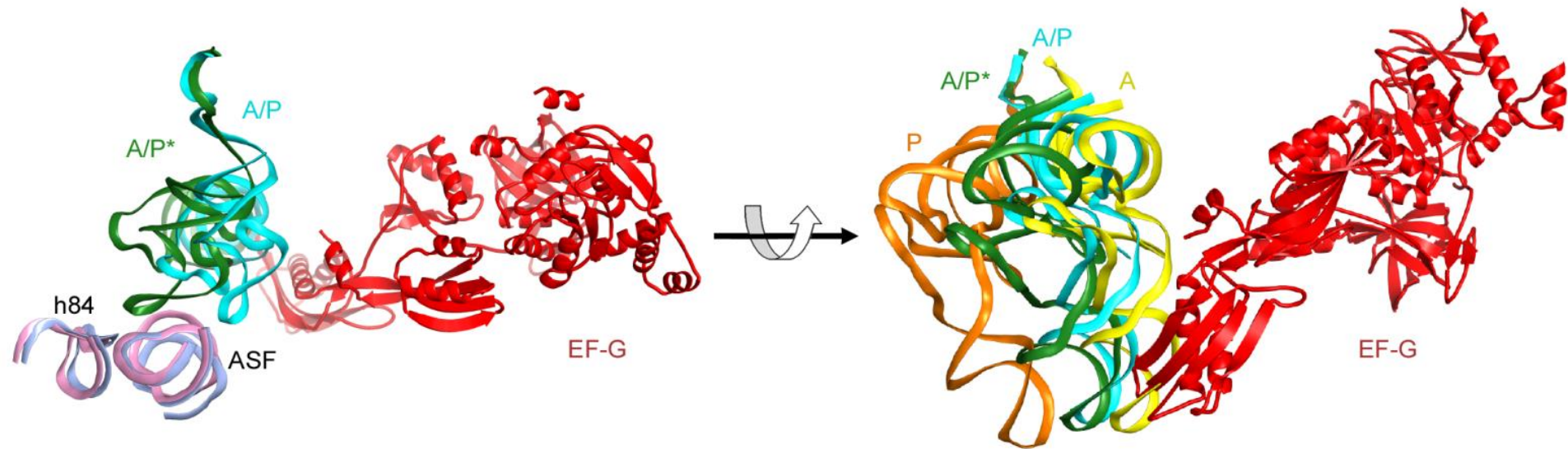


View of EF-G with pre and post-translocation 50S subunits aligned shows a rotation around the immobile SRL



View of EF-G with domains I-II aligned shows movement of domains III-IV-V relative to domains I-II

# EF-G binding induces a new tRNA hybrid state



## EF-G: Pre-translocation

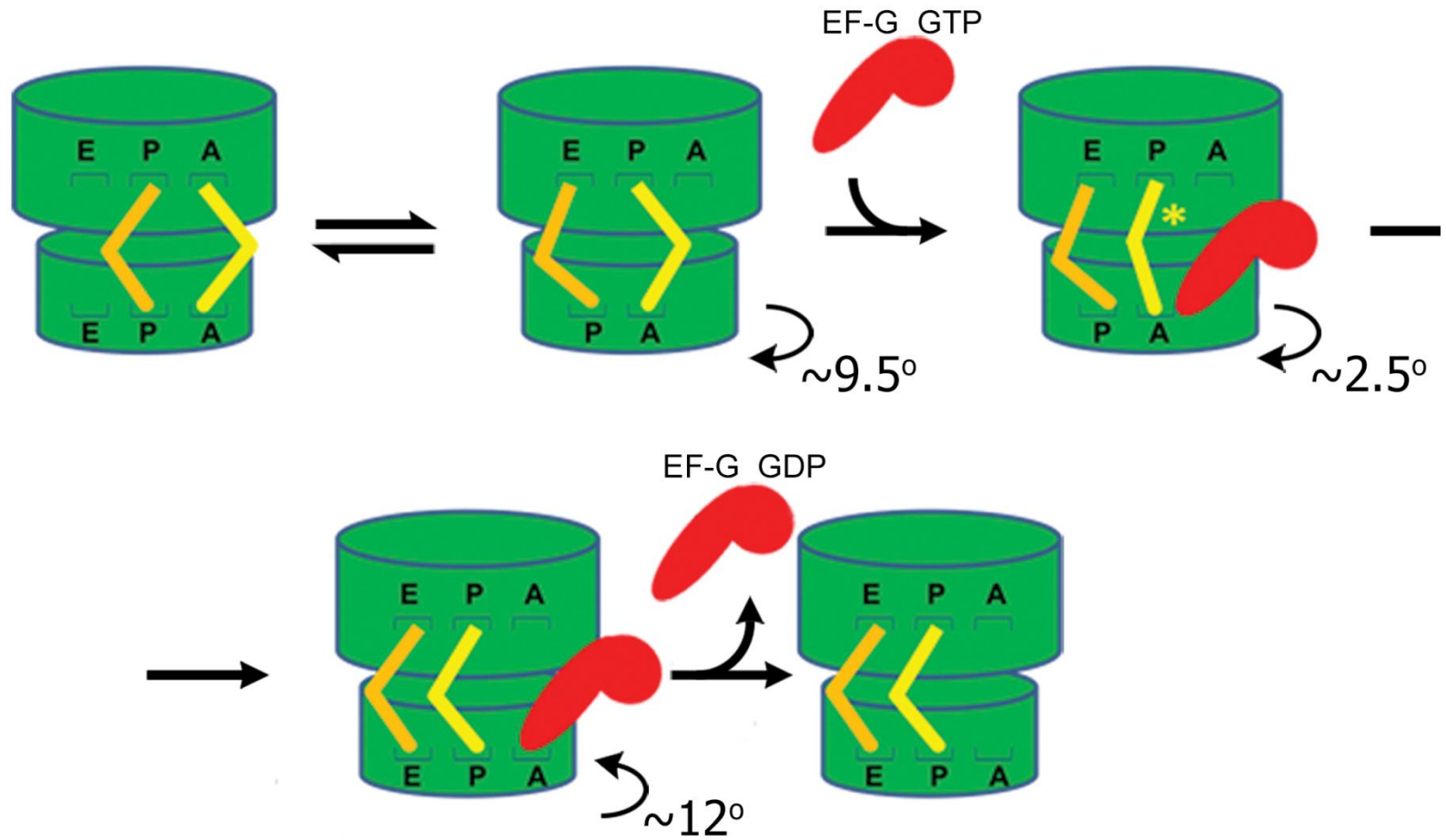
A/A: Classical pre-translocation state

A/P\*: EF-G Bound, pre-translocation state

A/P\*: No EF-G bound, pre-translocation state

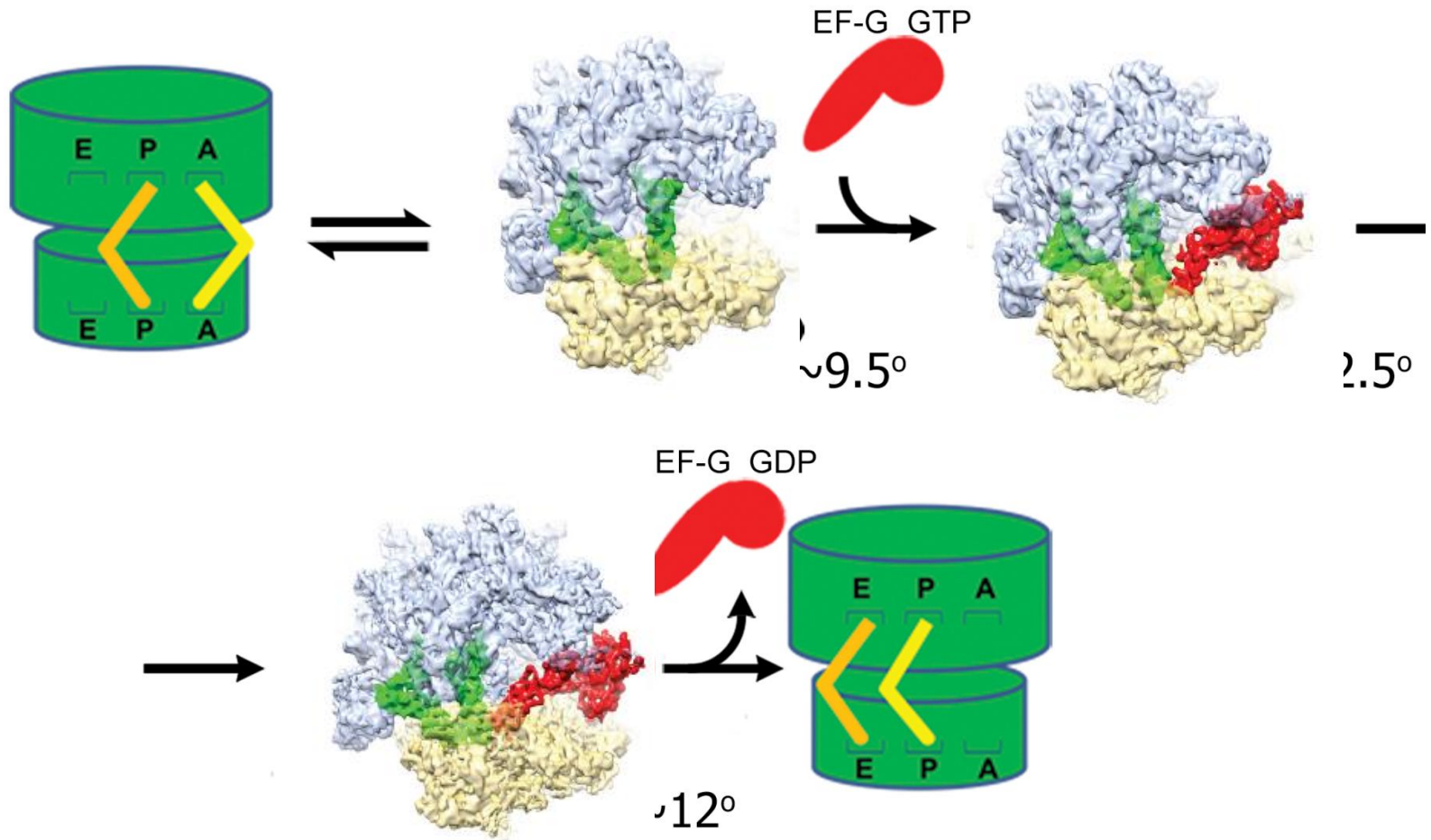
P/P: Classical Post-translocation State

# Schematic of EF-G catalyzed translocation





# Schematic of EF-G catalyzed translocation





# Our Collaborators



**Andrei Korostelev**  
**U. Mass. Med.**  
**TSV IRES**

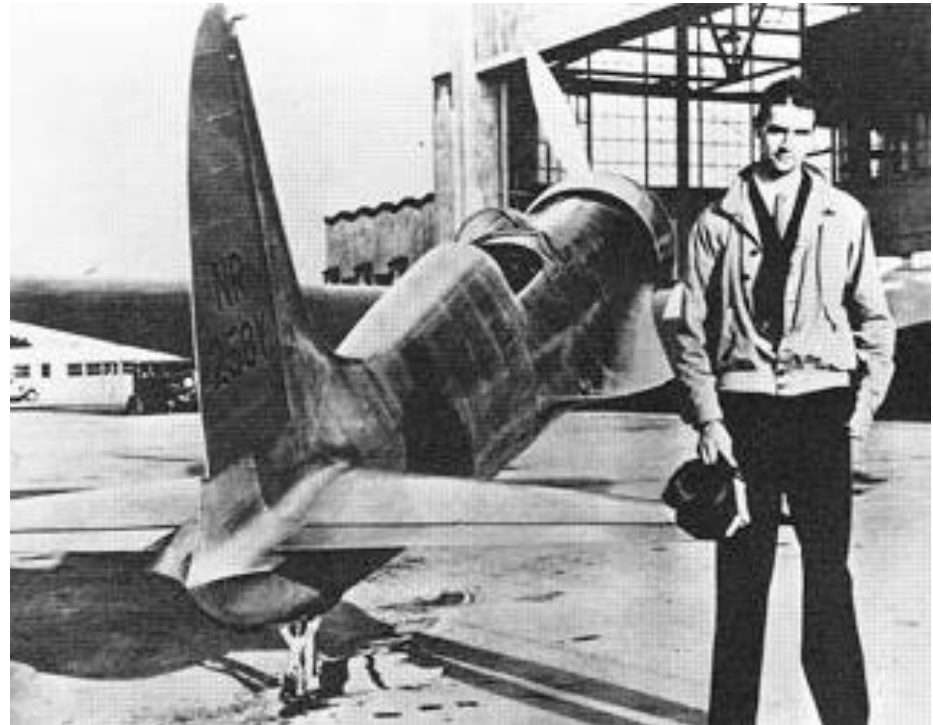


**Dmitri Ermolenko**  
**U. Rochester Med. Center**  
**EF-G complexes**

# Acknowledgments

**Brandeis University**  
**Grigorieff Group**  
Chen Xu  
Alexis Rohou  
Mike Rigney

## Funding



## Janelia Farm

Zhiheng Yu  
Jason De La Cruz

HHMI



**NSERC**  
**CRSNG**

