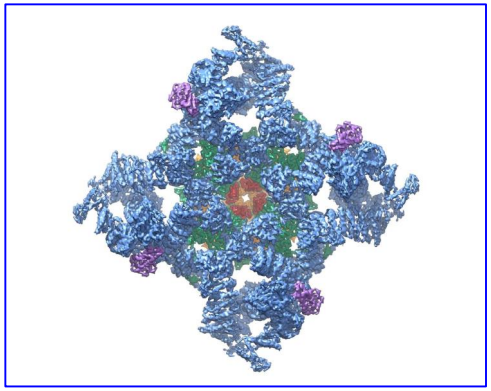
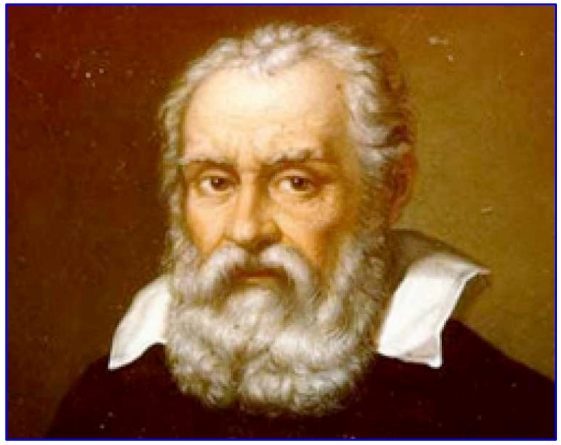
Single-Particle Cryo-Electron Microscopy



Joachim Frank
Department of Biochemistry and Molecular Biophysics
Department of Biological Sciences
Columbia University

Funding : NIH



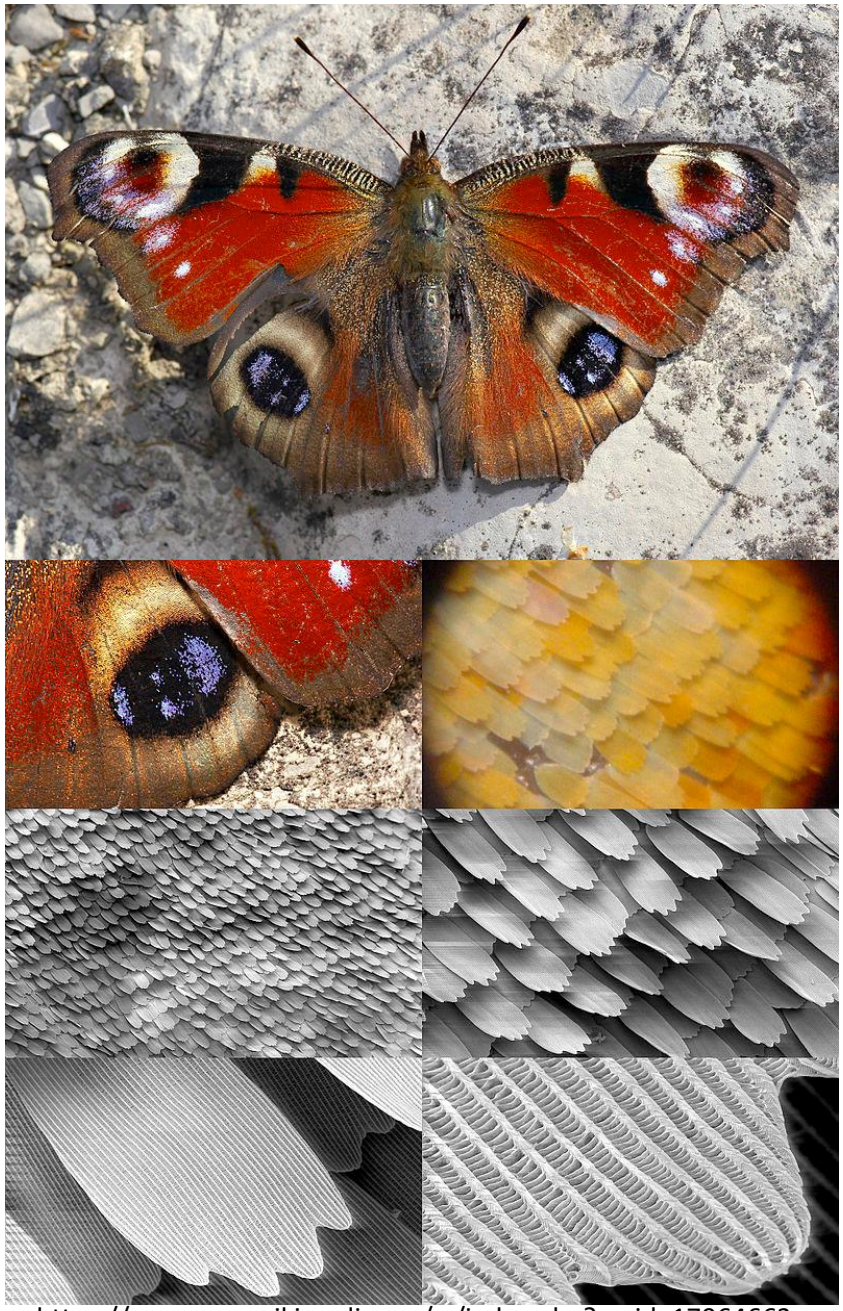
“The sun, with all those planets revolving around it and dependent on it, can still ripen a bunch of grapes as if it had nothing else in the universe to do”

– Galileo Galilei

In commemoration of Dr. Ernst Kinder, my first mentor at the University of Munich,who discovered with the electron microscope how butterfly wings get their colors

All by interference of light on colorless gratings!

magnification



https://commons.wikimedia.org/w/index.php?curid=17964663

Butterfly wings at different magnifications

This example suggests how we can make discoveries as we zoom in on the parts of an organism with increasing magnification:

- Organism

- Organ

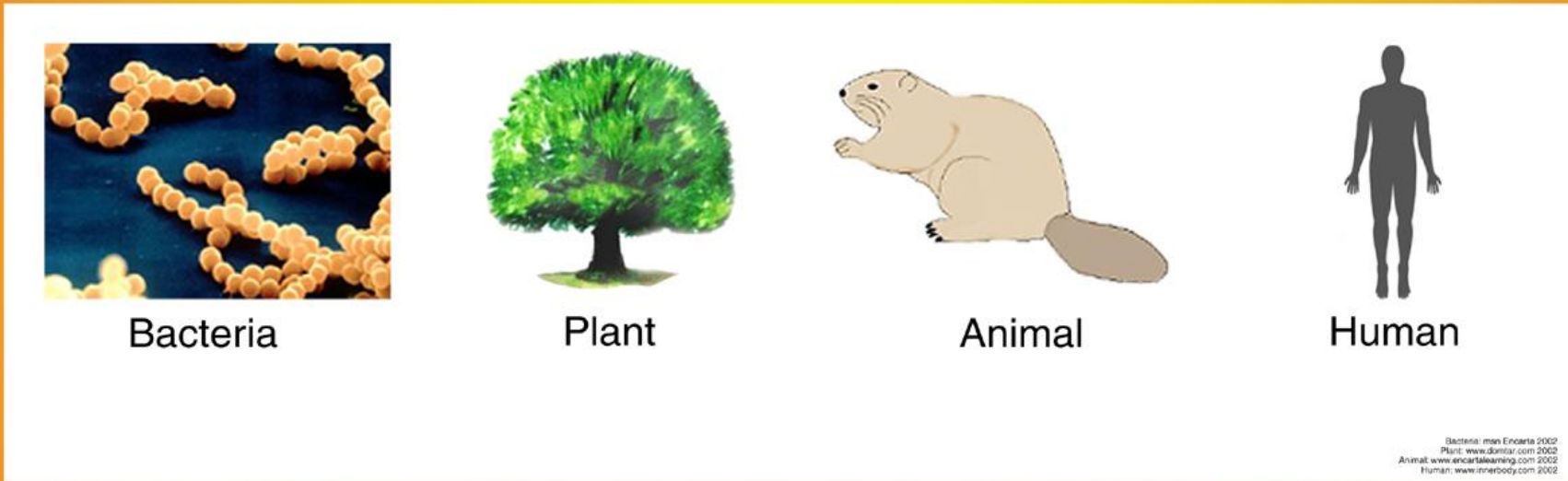
- Tissue

- Cell

- Organelle

- Molecule

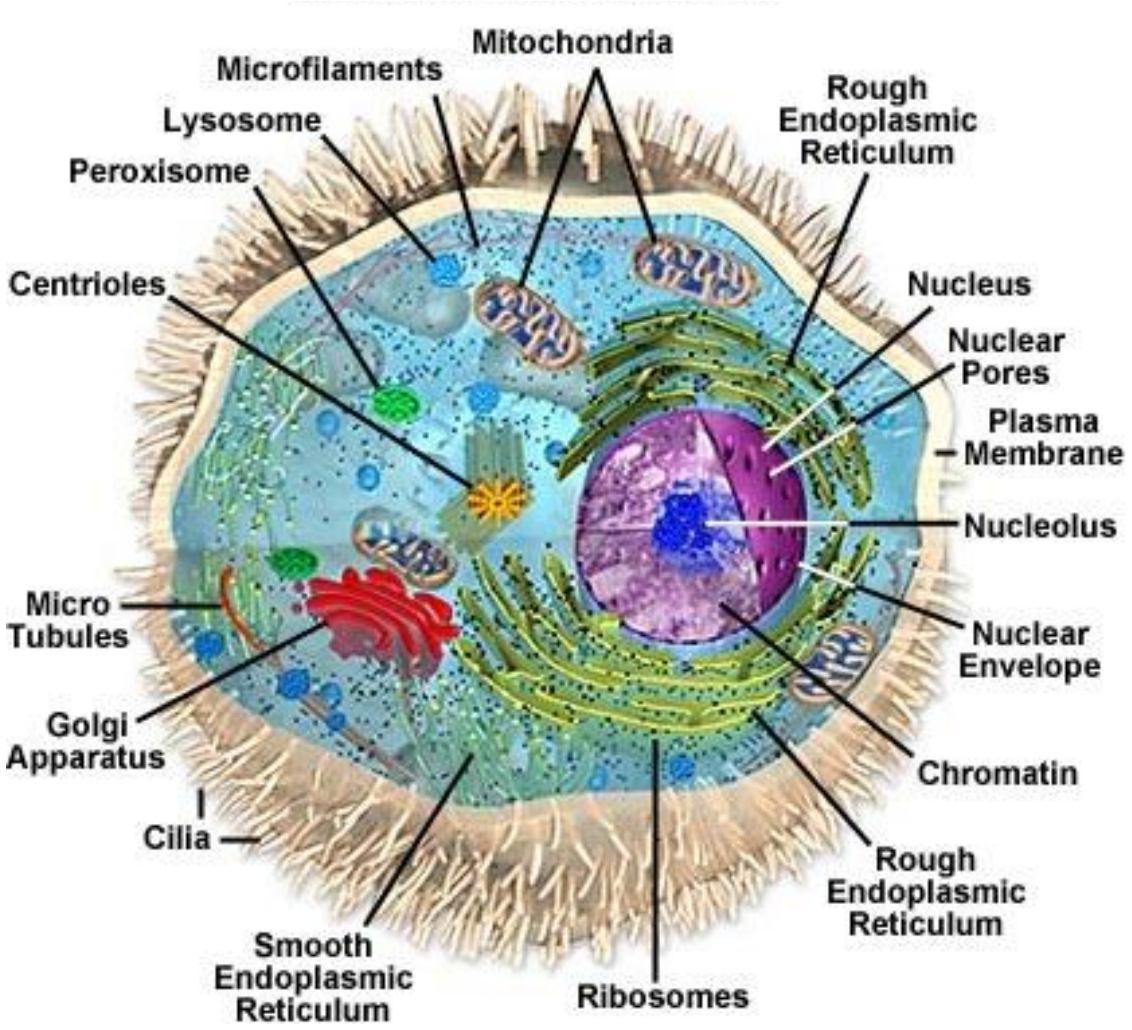
Universality of Life Processes on Earth



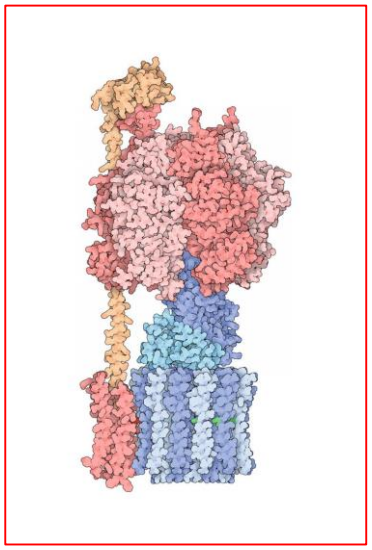
-- Plants, bacteria, animals, and humans may look quite different, but they are made up from very similar building blocks, the ***cells***.

-- A closer look at the cells of the different kingdoms of Life shows that the molecular structures and processes are in fact very similar: e.g., the way cells divide, make proteins, store energy, move needed products around.

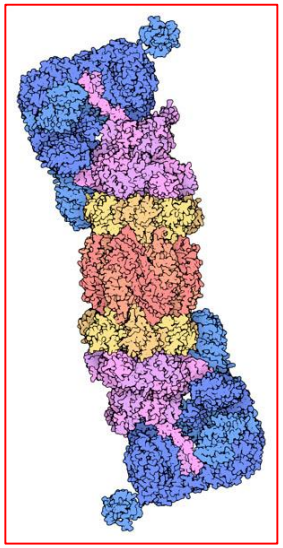
Animal Cell



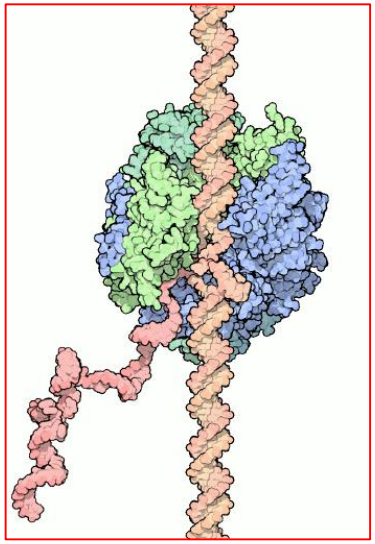
M.W. Davidson



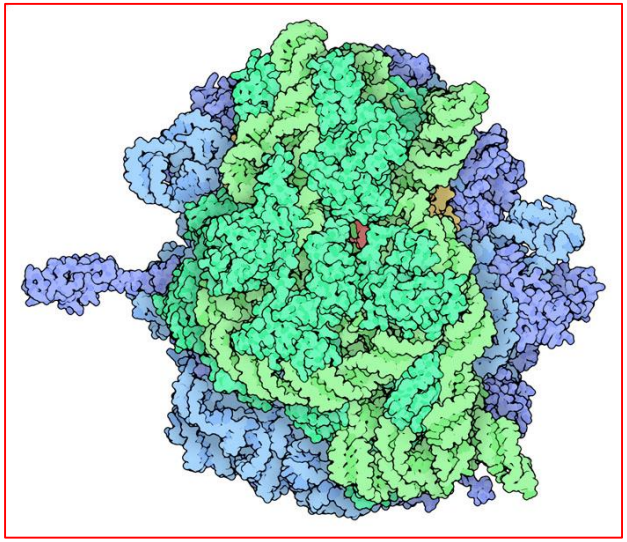
ATP Synthase:
makes ATP



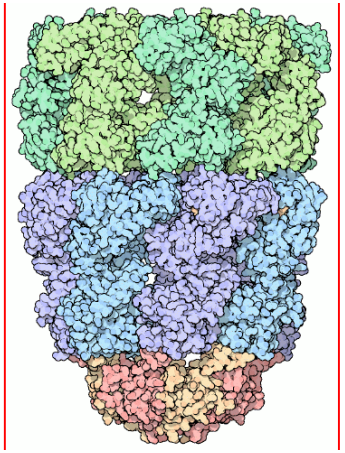
Proteasome:
recycles proteins



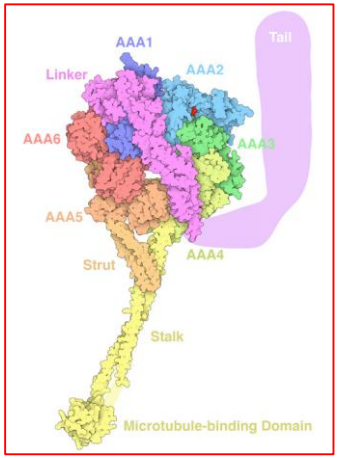
RNA Polymerase:
copies DNA → mRNA



Ribosome:
makes proteins

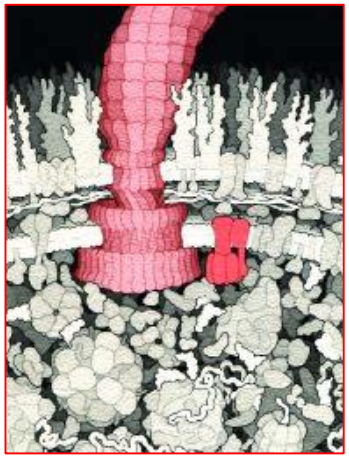


Chaperone:
folds proteins



Dynein:
transports molecules

Spliceosome:
edits mRNA

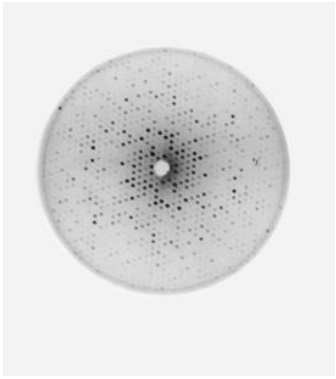


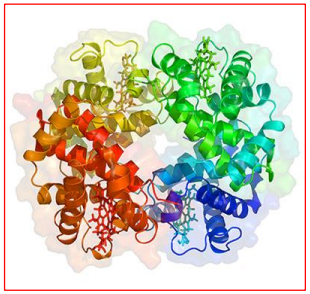
Flagella motor:
rotates flagella

David Goodsell

X-ray Crystallography

- Crystal: many copies of the molecule arranged in regular order.
- *Exposure to X-ray beam → diffraction pattern → structure determination.*
- X-ray beam must be high-intensity, crystal must be almost perfect.
- *To date ~ 100,000 structures solved by X-ray crystallography, available in public databanks.*
- Crystal packing → molecules not visualized in all conformations/binding states that important for function.
- *Many molecules do not form highly ordered crystals.*
- Sample quantity can be a big issue, as well.
-



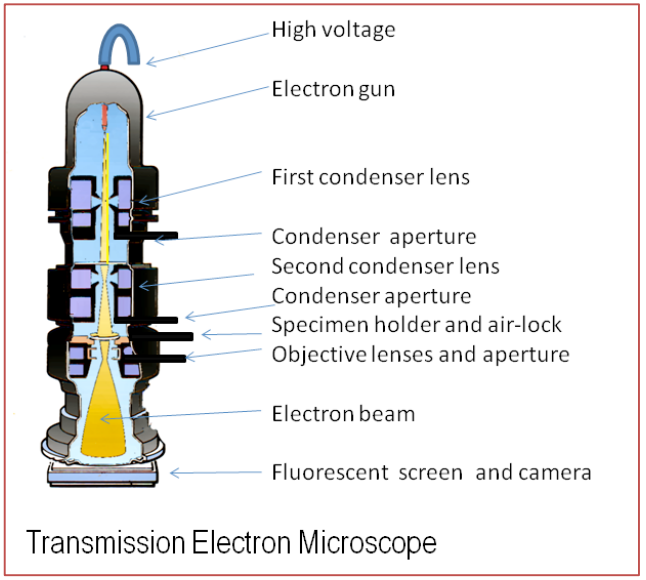


Max Perutz and John Kendrew with a model of hemoglobin, 1982

http://www.mfpl.ac.at/vips/max-f-perutz/

Electron Microscopy

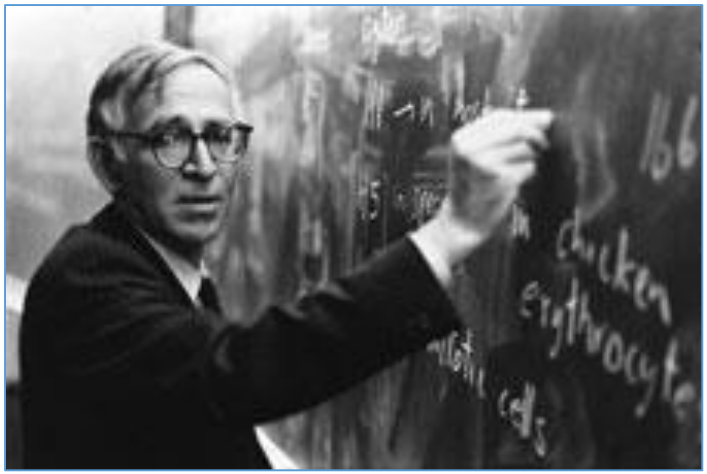
- Electron microscopy can be used to solve molecular structures, as well.
- *Projection images formed at very high magnification, e.g. 30,000 x.*
- To reconstruct an object, many different views must be collected.
- *Sample must be very thin, electrons are readily absorbed by matter.*
- Electrons strongly damage the molecules -- need for low dose! 10-20 electrons/square Angstrom.
- *BUT low dose → images are very noisy (shot noise)*
-



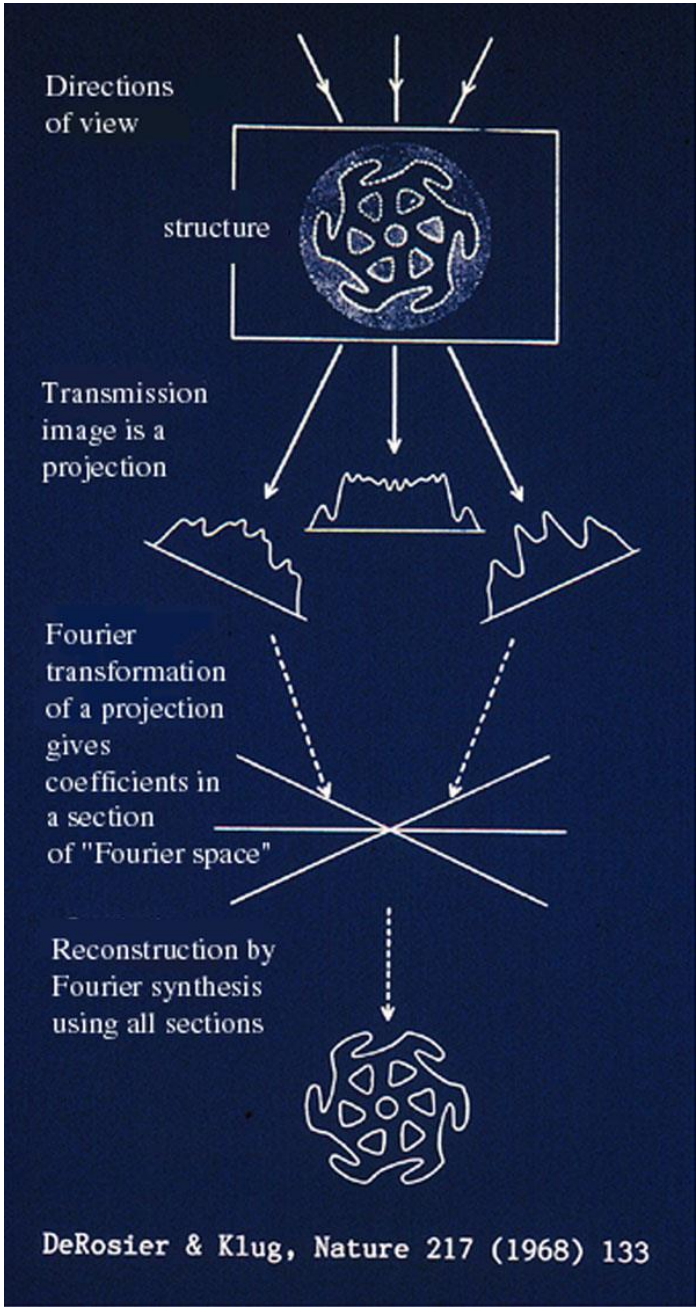
http://www.newworldencyclopedia.org/entry/File:Electron Microscope.png

Multiple EM views are needed

Pioneering work: 3D reconstruction of a bacteriophage tail using the Fourier-Bessel approach, 1968
(Negative staining used)



Aaron Klug and David DeRosier, LMB/MRC Cambridge



THREE-DIMENSIONAL RECONSTRUCTION: VIRUSES WITH ICOSAHEDRAL SYMMETRY (negative staining used)

Tony Crowther

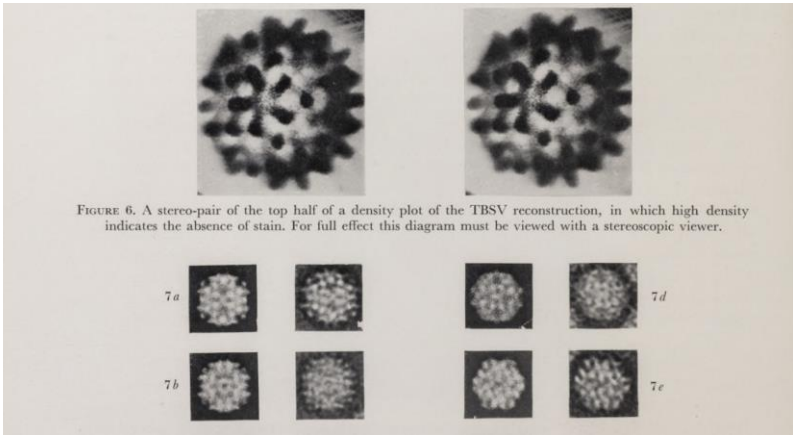


FIGURE 6. A stereo-pair of the top half of a density plot of the TBSV reconstruction, in which high density indicates the absence of stain. For full effect this diagram must be viewed with a stereoscopic viewer.

7a 7d

7b 7e

R. A. Crowther, Phil. Trans. Roy. Soc. 1971

Low-dose Electron microscopy -- Reconstruction from a 2D Crystal 1975 (Glucose embedding used)

Richard Henderson and Nigel Unwin

(Reprinted from Nature, Vol. 257, No. 5521, pp. 28–32, September 4, 1975)

Three-dimensional model of purple membrane obtained by electron microscopy

R. Henderson & P. N. T. Unwin

MRC Laboratory of Molecular Biology, Hills Road, Cambridge CB2 2QH, UK

A 7-Å resolution map of the purple membrane has been obtained by electron microscopy of tilted, unstained specimens. The protein in the membrane contains seven, closely packed, α-helical segments which extend roughly perpendicular to the plane of the membrane for most of its width. Lipid bilayer regions fill the spaces between the protein molecules.

The purple membrane is a specialised part of the cell membrane of *Halobacterium halobium*[3]. Oesterhelt and Stoeckenius[2] have shown that it functions *in vivo* as a light-driven hydrogen ion pump involved in photosynthesis. It contains identical protein molecules of molecular weight 26,000, which make up 75% of the total mass, and lipid which makes up the remaining 25% (ref. 3). Retinal, covalently linked to each protein molecule in a 1:1 ratio is responsible for the characteristic purple colour[3]. These components together form an extremely regular two-dimensional array[4].

We have studied the purple membrane by electron microscopy using a method for determining the projected structures of unstained crystalline specimens[5]. By applying the method to tilted specimens, and using the principles put forward by De Rosier and Klug[6] for the combination of such two-dimensional views, we have obtained a three-dimensional map of the membrane at 7 Å resolution. The map reveals the location of the protein and lipid components, the arrangement of the polypeptide chains within each protein molecule, and the relationship of the protein molecules in the lattice.

Electron microscopy and diffraction

The purple membrane was prepared under normal conditions from cultures of *H. halobium*[3] and applied to the microscope grid in the presence of 0.5% glucose. The purified membranes are mostly oval sheets up to 1.0 μm in diameter and about 45 Å thick[4,7]. The array of molecules making up these sheets is accurately described[7] as an almost perfect crystal of space group P3 ($a = 62$ Å) with a thickness of one unit cell only in the direction of the c axis. A single membrane thus contains up to 40,000 unit cells; that is 120,000 protein molecules (three per unit cell).

These large periodic arrays from which electron diffraction patterns and defocused bright field micrographs are recorded[5] enable us to overcome the principal problem normally associated with high resolution electron microscopy of unstained biological materials; that is, sensitivity to electron damage[8]. Only a small number of electrons can pass through each unit cell before it is destroyed, but because of the large number of unit cells, the information in the diffraction patterns and micrographs is sufficient to provide a picture of the average unit cell. The micrographs recorded with such low doses of electrons appear featureless, since the statistical fluctuation in the number of electrons striking the plate is large compared with the weak phase contrast (< 1%) produced by defocusing.

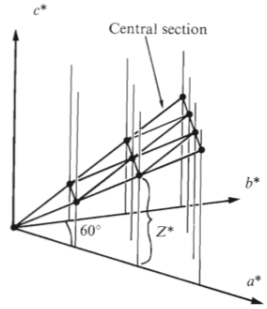


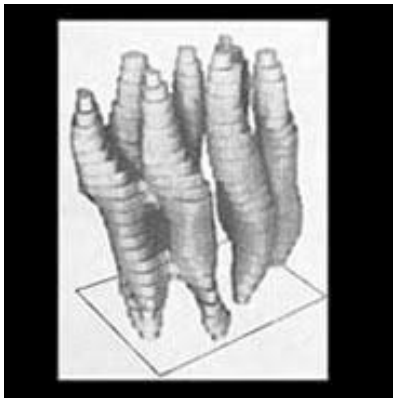
Fig. 1 Part of the three-dimensional reciprocal lattice showing the geometry of the lattice lines in the hexagonal space group P3. a^*, b^* and c^* are the reciprocal lattice vectors. a^* and b^* lie in, and c^* is perpendicular to the plane of the membrane. A central section which is perpendicular to the incident electron beam has been drawn through the lattice. The intersection of this central section with the reciprocal lattice is determined by the angle of tilt and the axis about which the membrane is tilted. Individual diffraction patterns and micrographs provide the amplitudes and phases in this section at the points shown. z^* represents the coordinate along the c^* direction of one of the points. The angle of tilt was measured to within 2° for each of the specially modified, tilted specimen holders, and the direction of the tilt axis on the photographic plate was established during operation of the microscope. However, estimates based on the geometry of the spacings of the lattice points (for high tilt angles), the variation of the degree of underfocus across the plate (for low tilt angles), and least squares refinement against data obtained at high tilt angles (for diffraction patterns) provided more accurate figures which were used in the calculation. The accuracy of measurement of both the amplitudes and phases depended on having sharp lattice lines. We therefore took care to ensure that, on the microscope grid, the membranes remained coherently ordered and flat to within 1/5°.

As a result, analysis of each micrograph by densitometry and computer processing[5] is required to combine the information from individual unit cells.

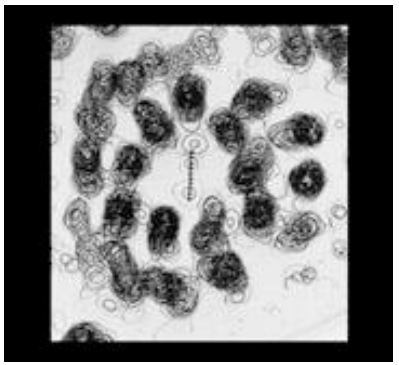
Solution of the three-dimensional structure of the purple membrane requires the determination of the amplitudes and phases in three dimensions of the Fourier terms into which it can be analysed. The diffraction pattern or Fourier transform of the membrane is not a three-dimensional lattice of points as is the case with a normal crystal, but since it is only one unit cell thick, a two-dimensional lattice of lines which are continuous in the direction of c^* (that is perpendicular to the membrane). A single electron diffraction experiment therefore

Purple membrane
Protein

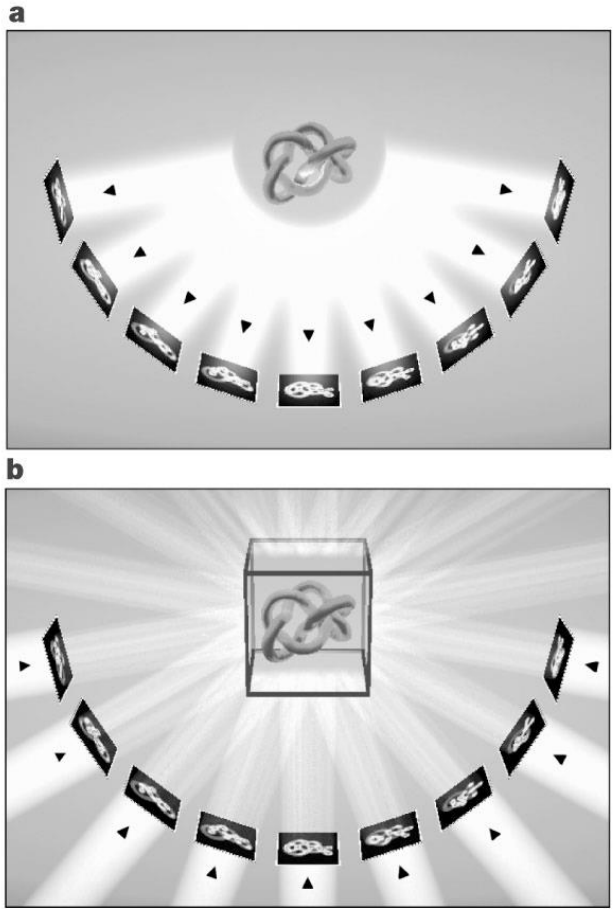
Bacteriorhodopsin



<u>Electron dose is spread over many repeats of the molecule in the crystal</u>



3D Reconstruction of Molecules by Electron Tomography

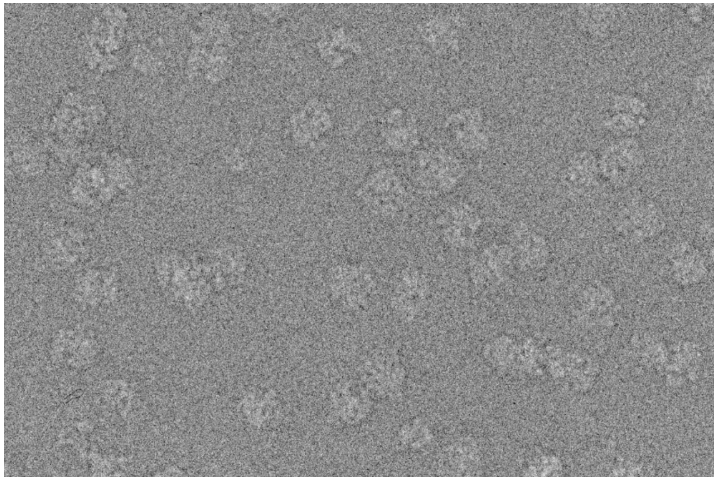


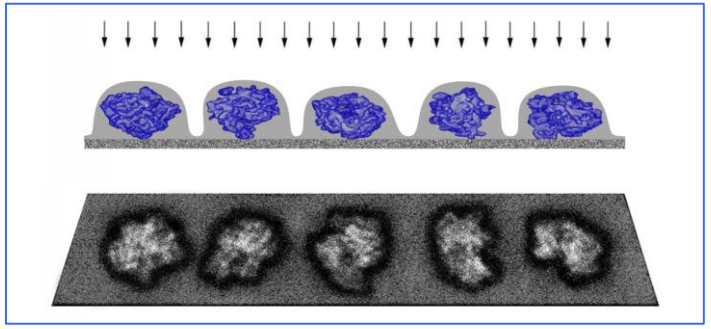
- Electron Tomography of single molecules
- Examples: fatty acid synthetase and ribosome
- BUT: Accumulated electron exposure exceeded 1000 e^-/A^2

Walter Hoppe MPG Archive

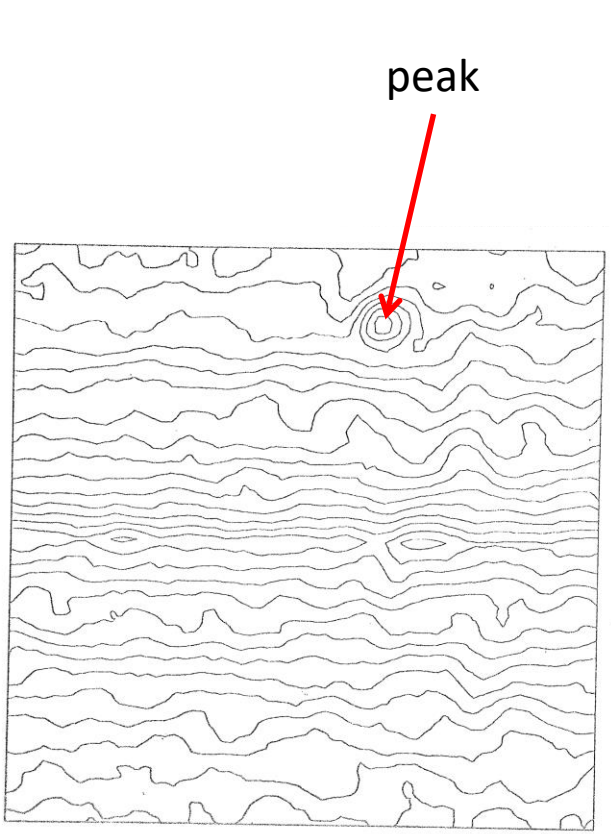
3D Reconstruction of Molecules by Single-Particle Techniques – the Concept

- Single-particle techniques: structural information from images of single (i.e., unattached) molecules in many copies.
- *Molecules are free to assume all naturally occurring conformations.*
- Molecules are randomly oriented.
- *A single snapshot may already give us hundreds of particle views.*
- As we collect more snapshots, more orientations will be covered, until we have enough for reconstructing the molecule in three dimensions.
-





EM images can be aligned to within better than 3 Angstrom!



. 11a,b Graphitfolie; Korrelationsfunktionen
(ber Teilbereich). Höhenschichtlinien:
Abstand 0.006, von 0.0 bis 0.03
Abstand 0.001, von 0.147 bis 0.166

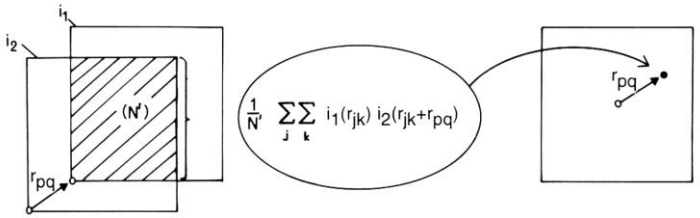


Fig. 3.8. Definition of the cross-correlation function. Image 1 is shifted with respect to image 2 by vector $\mathbf{r}_{pq}$. In this shifted position, the scalar product of the two images arrays is formed and put into the CCF matrix at position (p, q). The vector $\mathbf{r}_{pq}$ is now allowed to assume all positions on the sampling grid. In the end, the CCF matrix has an entry in each position. From Frank (1980). Reproduced with permission of Springer-Verlag, New York.

Cross-correlation function of
2 successive micrographs
of the same carbon film

J. Frank, Ph.D. thesis 1970

Ultramicroscopy 1 (1975) 159–162

SHORT NOTE

AVERAGING OF LOW EXPOSURE ELECTRON MICROGRAPHS OF NON-PERIODIC OBJECTS

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The Cavendish Laboratory, Free School Lane, Cambridge CB2 3RQ, UK

Received 20 October 1975

The investigation concerns the possibility of extending to non-periodic objects the low exposure averaging techniques recently proposed for non-destructive electron microscopy of periodic biological objects. Two methods are discussed which are based on cross-correlation and are in principle suited for solving this problem.

1. Introduction

Recent work on low exposure techniques combined with averaging [1–3] (called 'SNAP shot techniques' in [3]) shows that information can be retrieved from periodic biological objects at higher than conventionally available resolutions [4]. Unwin and Henderson [2] were able to achieve 7 Å image resolution, by re-6]. In these applications, the contrast of the individual marker atom image to be superposed is sufficient for straightforward alignment. However, the requirement of subminimum exposure poses a new problem: the alignment of features that are only faintly visible on a noisy background.

"If such methods (i.e., for averaging data from arrays of identical objects that are not periodic) were to be perfected, then, in the words of one scientist, "the sky would be the limit."

Arthur L. Robinson, Science 192 (1976) 360-363

Work Agenda

(At that point, the hard work had just begun!)

- Projection images of the molecule need to be aligned with one another
- *Concept and measurement of resolution, in the absence of a diffraction pattern*
- To do a reconstruction one needs to know the angle of each projection (in this technique, angles have to be determined without knowing the structure!)
- *Molecules normally have no symmetries*
- How to deal with heterogeneity ? (i.e., molecules are actually different from each other, and should be separated into “classes”)
- *How to develop programs as new ideas come along, without getting lost?*
- How to avoid re-writing a program each time you change your mind?
-

SPIDER -- Modular image processing program

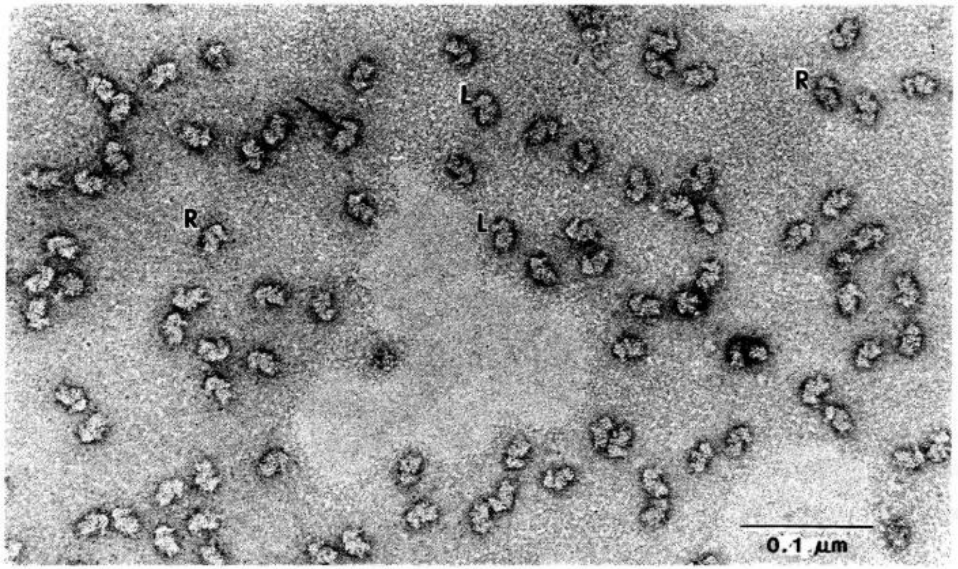
Toronto EM conference abstract 1978
Ultramicroscopy 1981

Some of the operations
(out of hundreds):

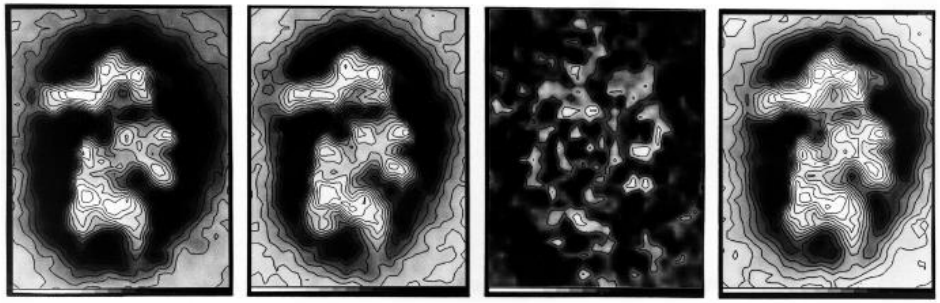
AC -- autocorrelation
CC – cross-correlate 2 images
FT -- Fourier transform
RT -- rotate
SH -- shift
WI -- window

“WORKBENCH” FOR PROCESSING IMAGES

Alignment and averaging



A



B C D E

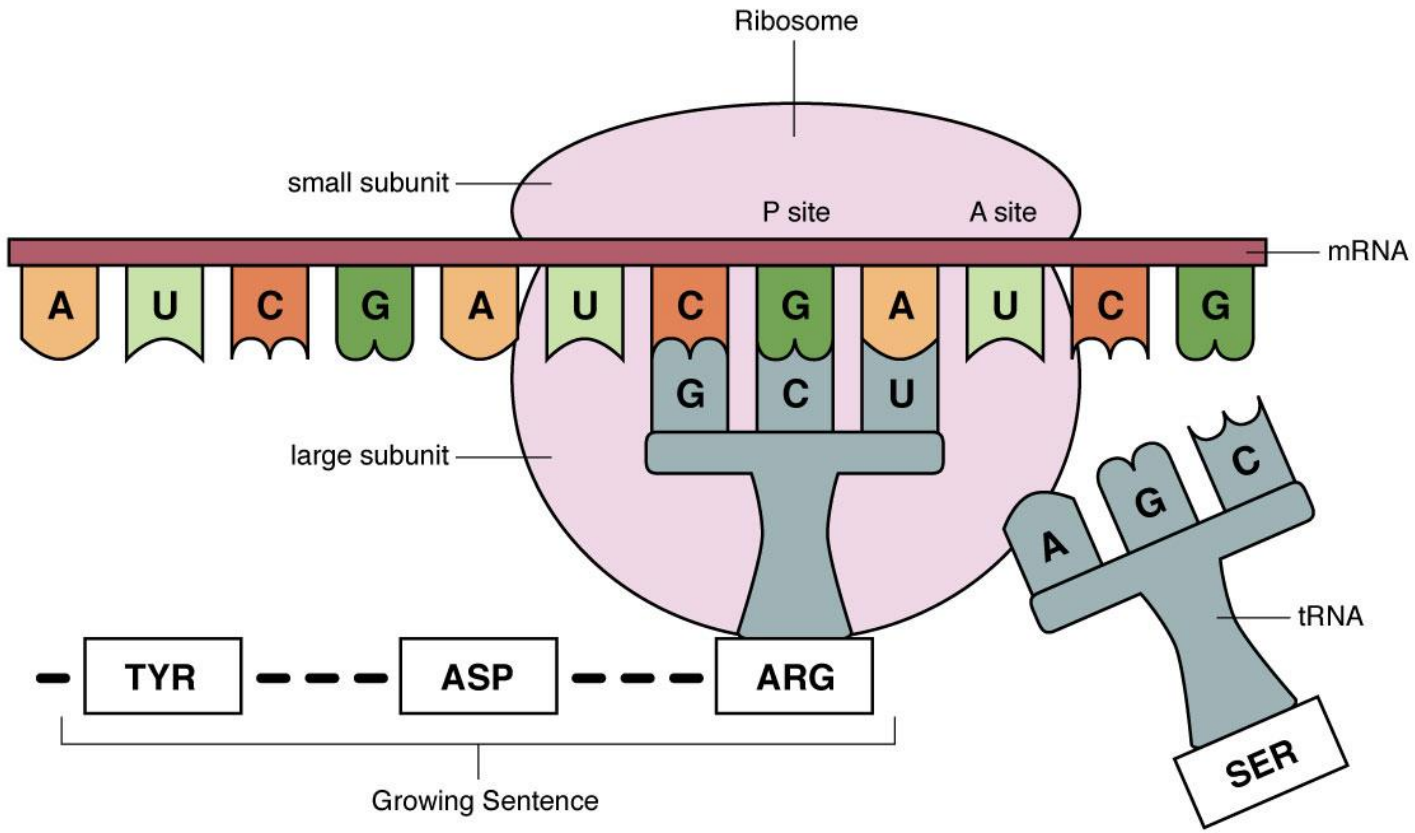
Proof of concept

40S subunits of HeLa (human) Ribosomes

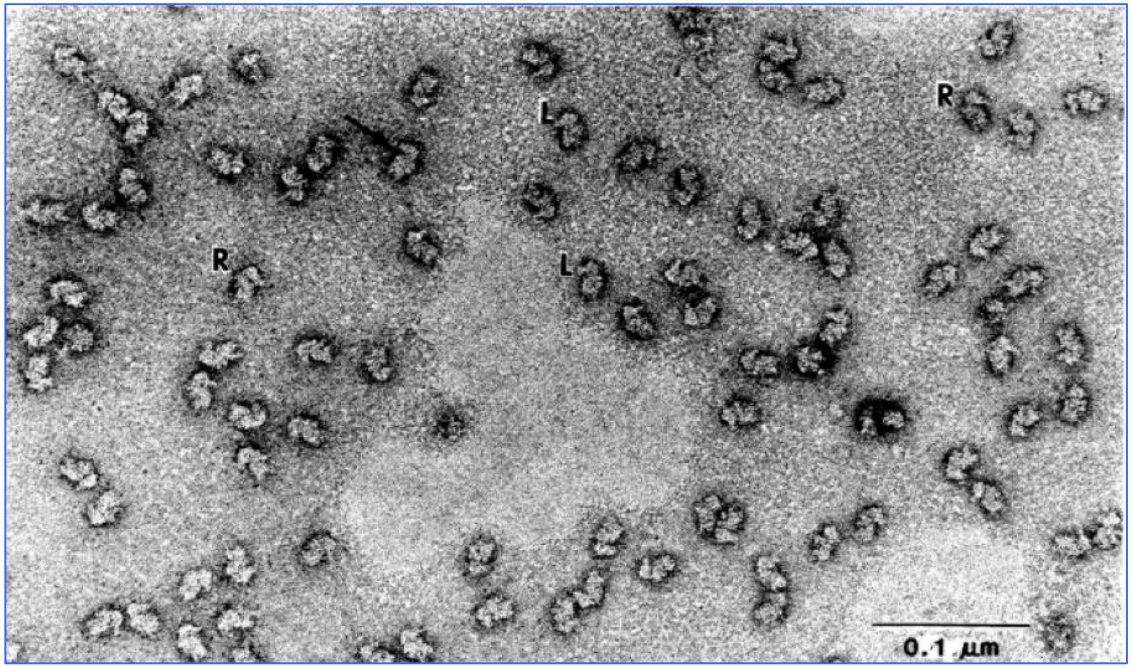
Average

Frank et al., Science 1981

How the ribosome translates from the language of the genetic code into the language of amino acids

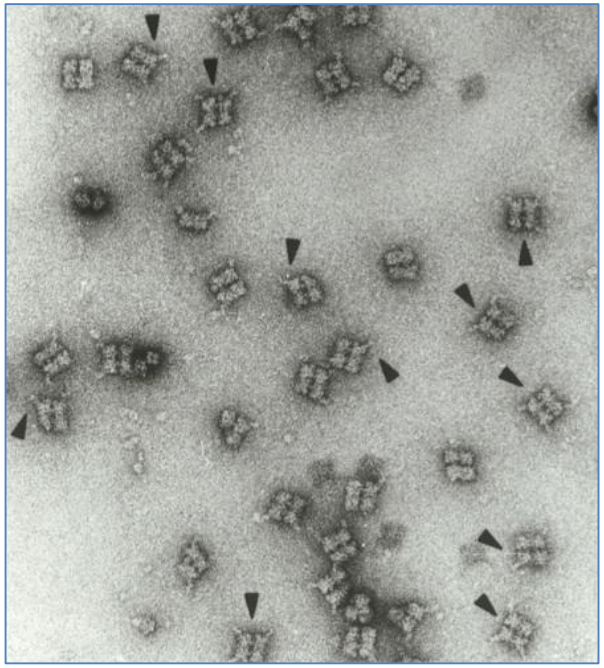


Problem of heterogeneity: molecules are in different orientations and conformations



Frank et al., Science 1981

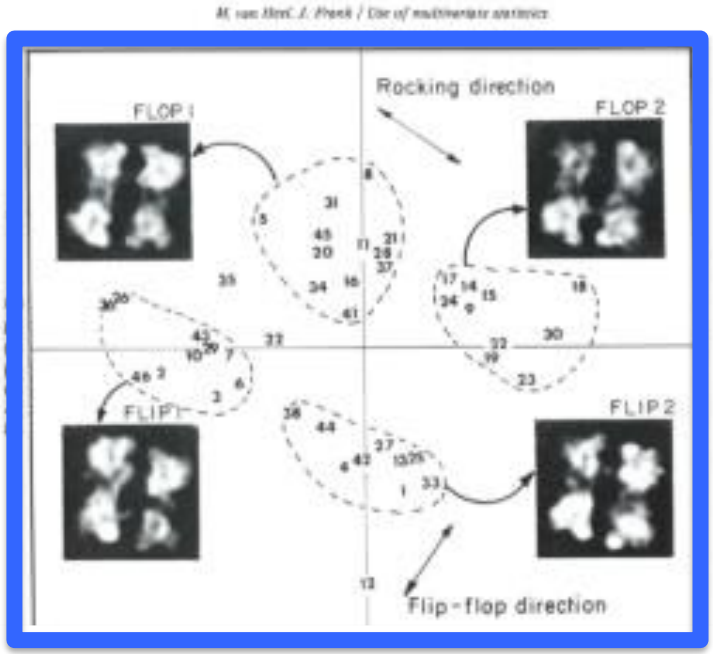
L and R views (flip and flop) of HeLa ribosomes



N. Boisset, thesis 1987

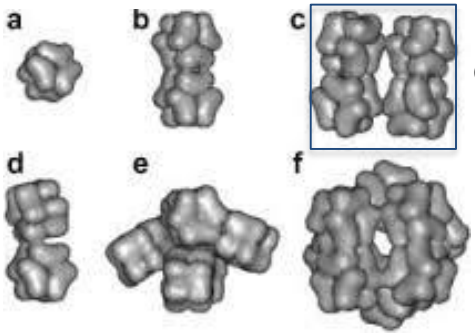
flip and flop views of hemocyanin

Multivariate analysis of aligned molecule images



Van Heel and Frank, Ultramicroscopy 1981

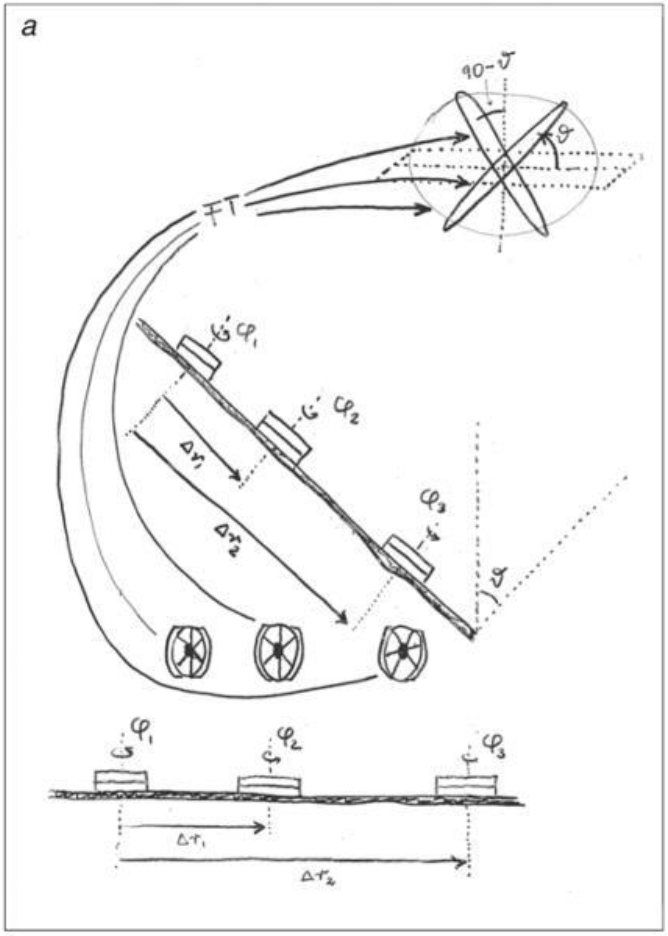
FLIP/FLOP and Rocking positions



dodecamer

Hemocyanins of Arthropods are oligomers of a basic unit

RANDOM-CONICAL RECONSTRUCTION – PRINCIPLE



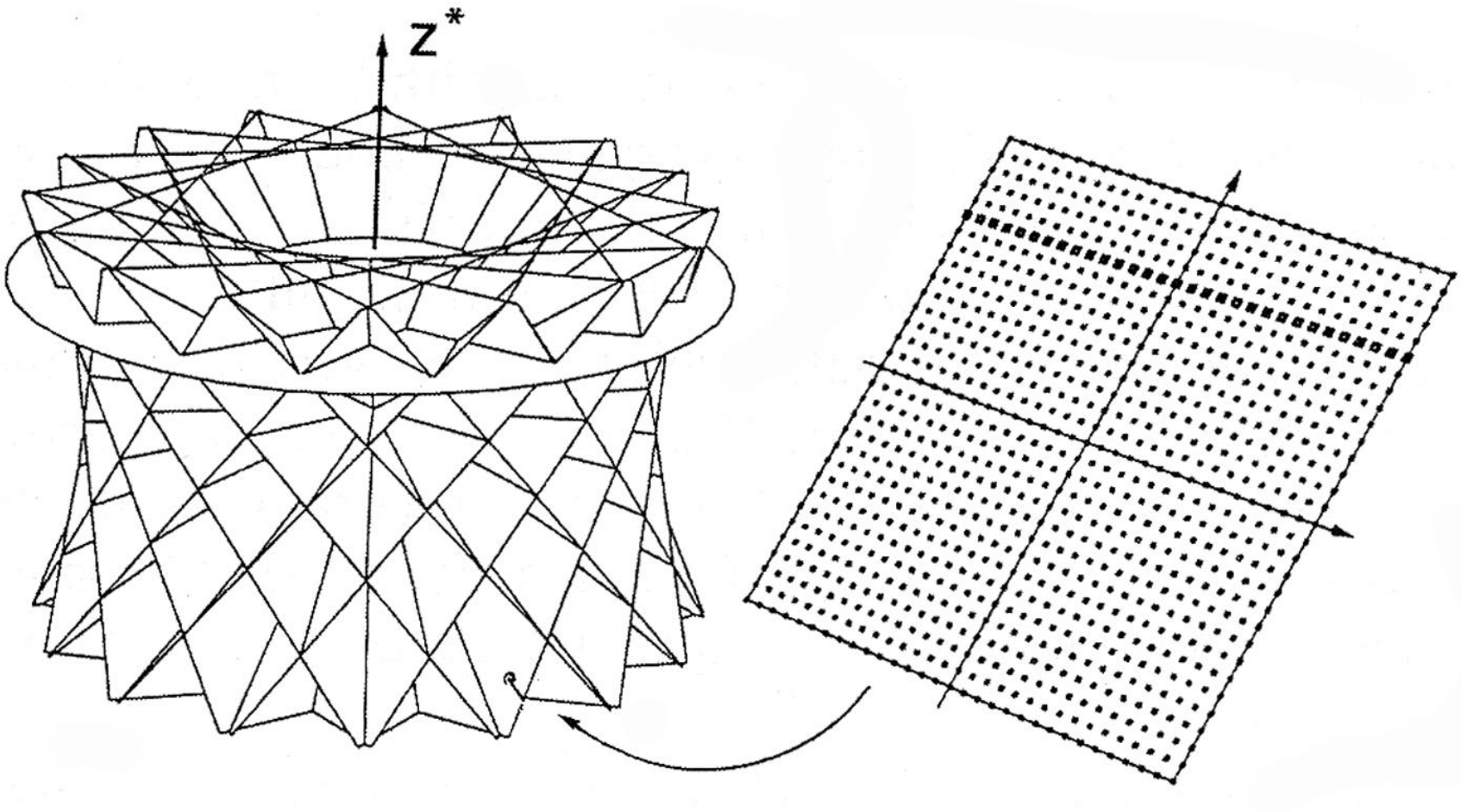
J. Frank, overhead 1979

RANDOM-CONICAL RECONSTRUCTION – PRINCIPLE

(FANCY VERSION)

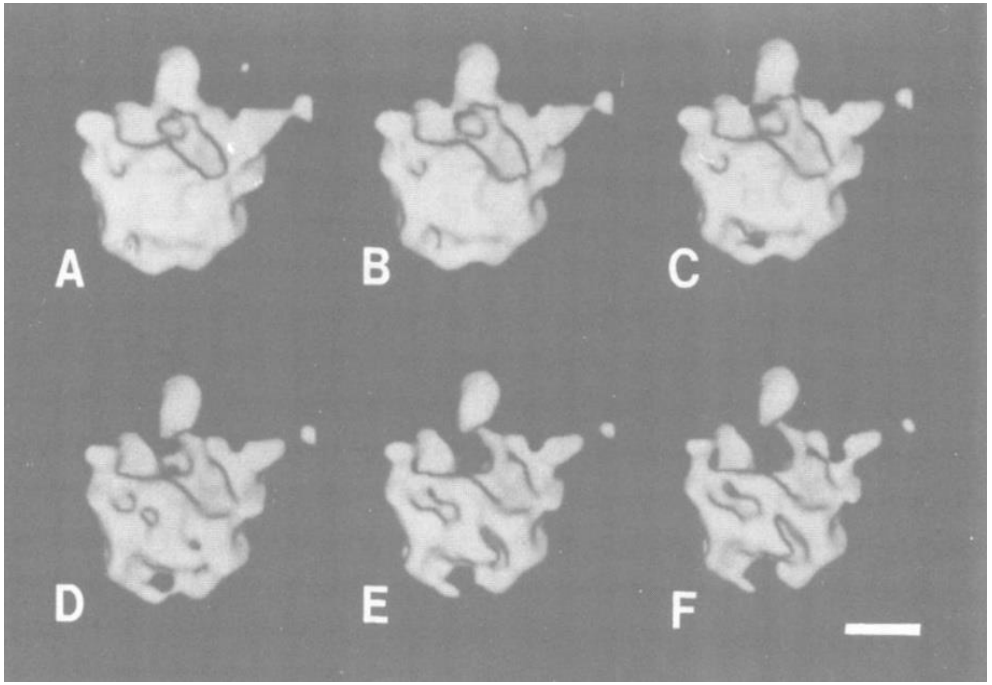
J. Frank, American Scientist 1998

Conical Data Collection Geometry in Fourier Space



Lanzavecchia et al., J. Struct Biol.

RECONSTRUCTION OF 50S RIBOSOMAL SUBUNIT FROM *E. COLI* RIBOSOME

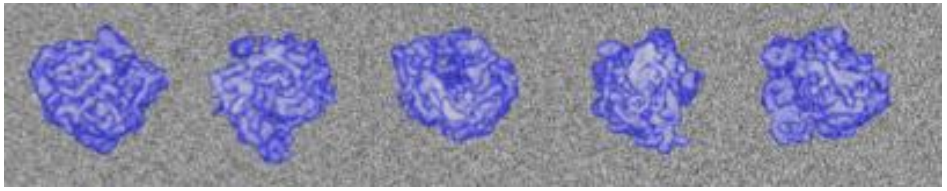


Radermacher et al., EMBO J. 1987


Nicholas Boisset
Raj Agrawal
Pawel Penczek
Rasmus Schroeder
Bob Grassucci
Martin Kessel
Michael Radermacher
ART STUDIO
Carmen Mannella
Manjuli Sharma
Jose-Maria Carazo
Montserrat Samso

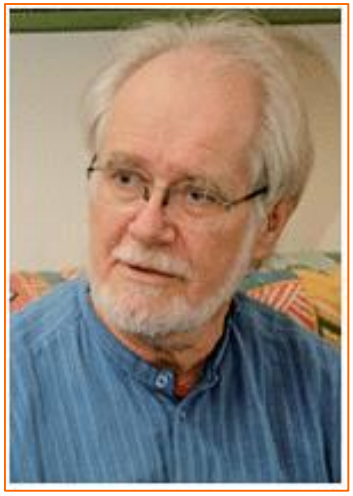
First 3D Reconstruction from Single Particles
Nobel Museum, Stockholm

Frozen-hydrated specimen / freeze-plunging / vitreous ice / cryo-EM

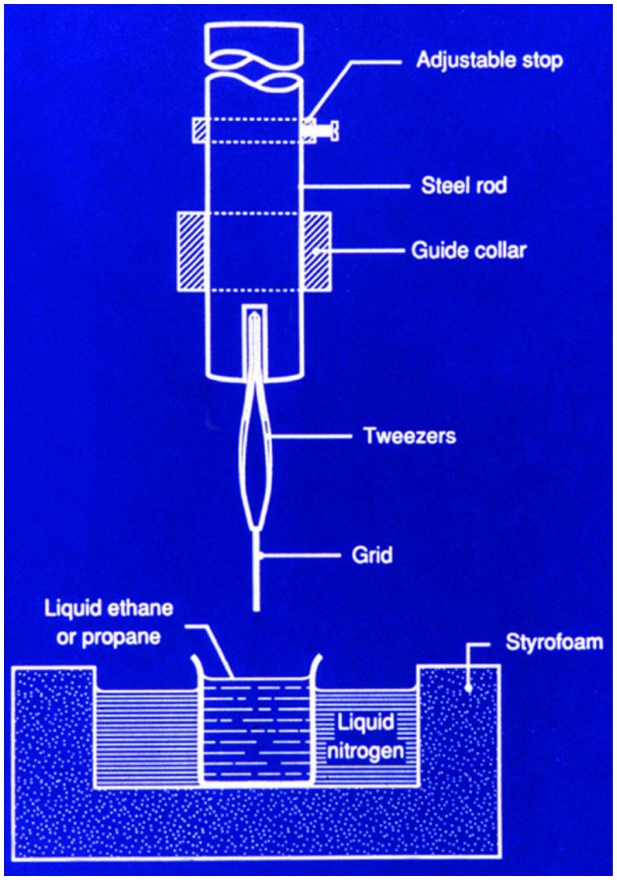


Molecules embedded in vitreous ice

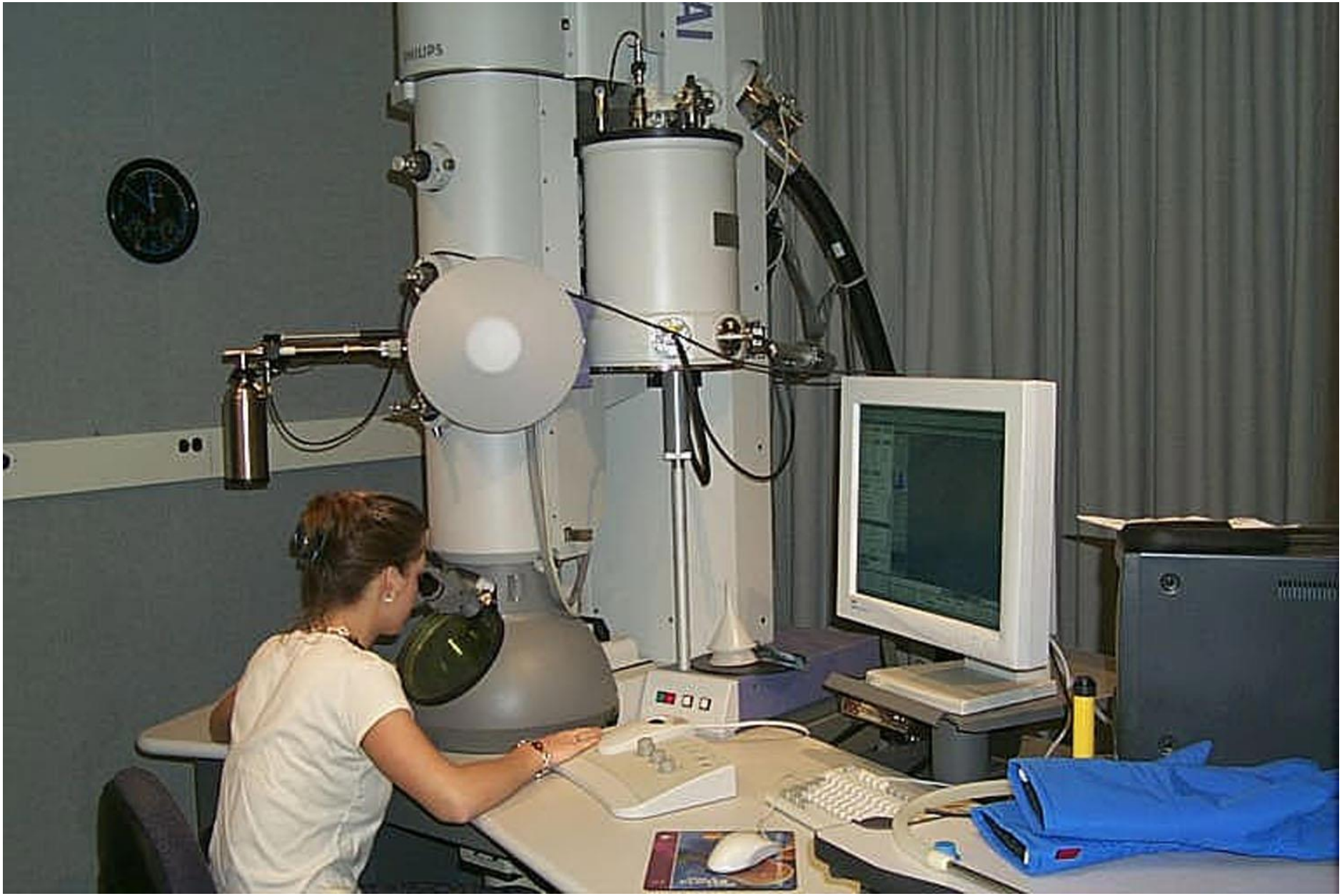
Robert Glaeser
1976



Jacques Dubochet
1981



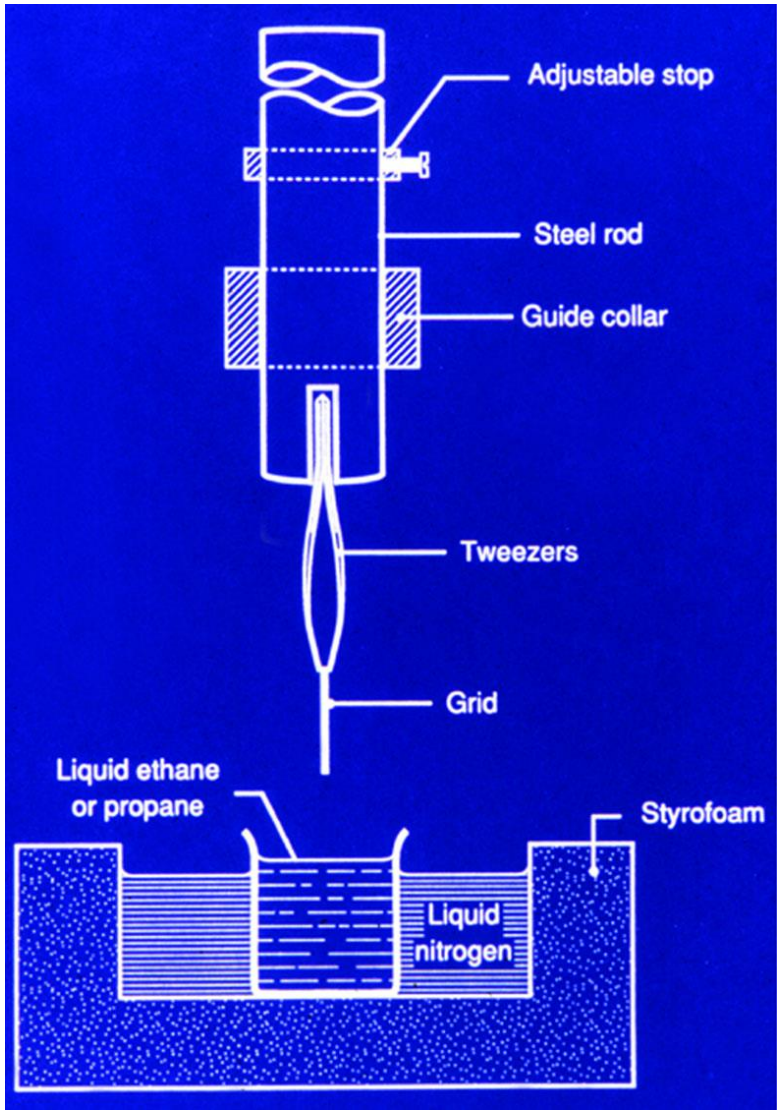
Plunge-freezer

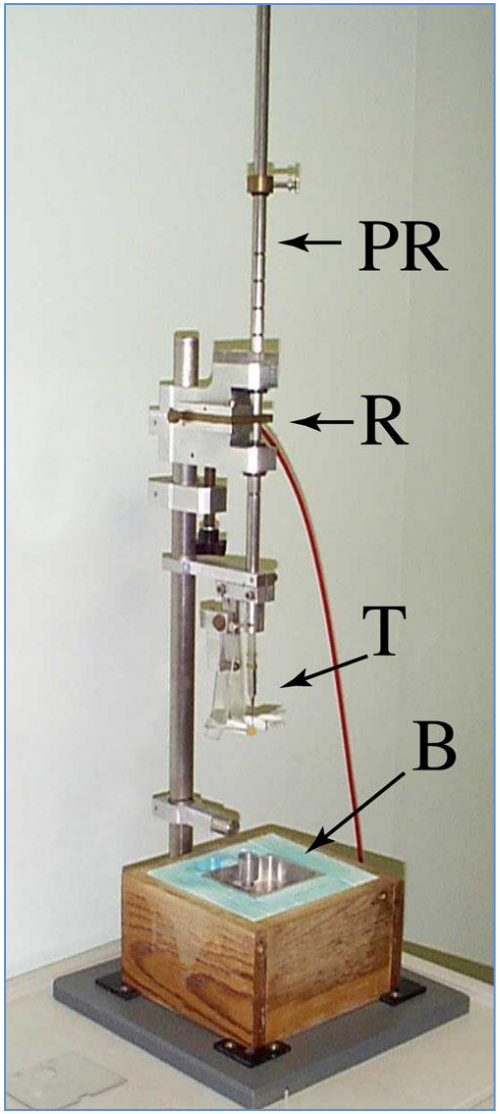

PHILIPS

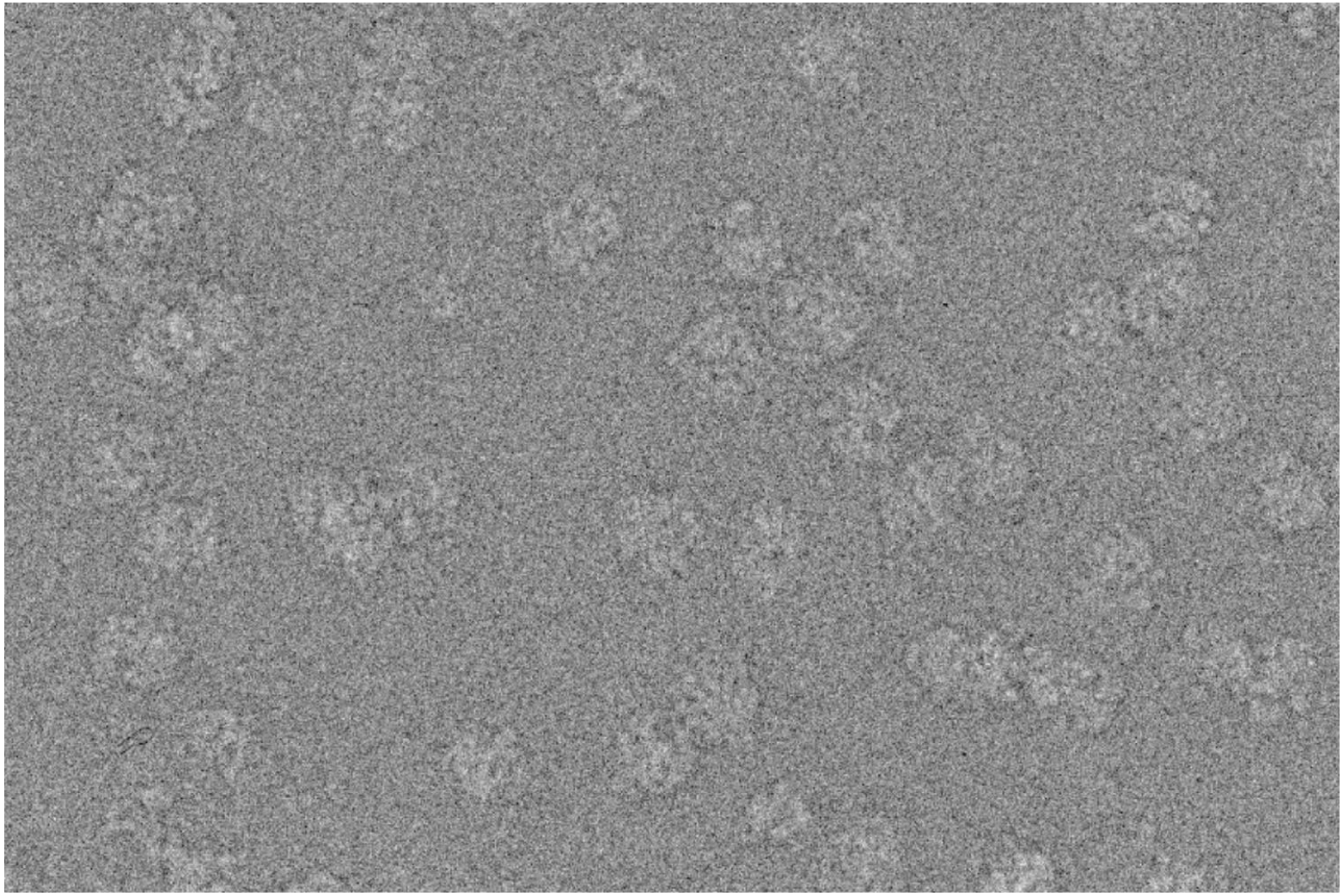
Plunge-Freezer

Manual

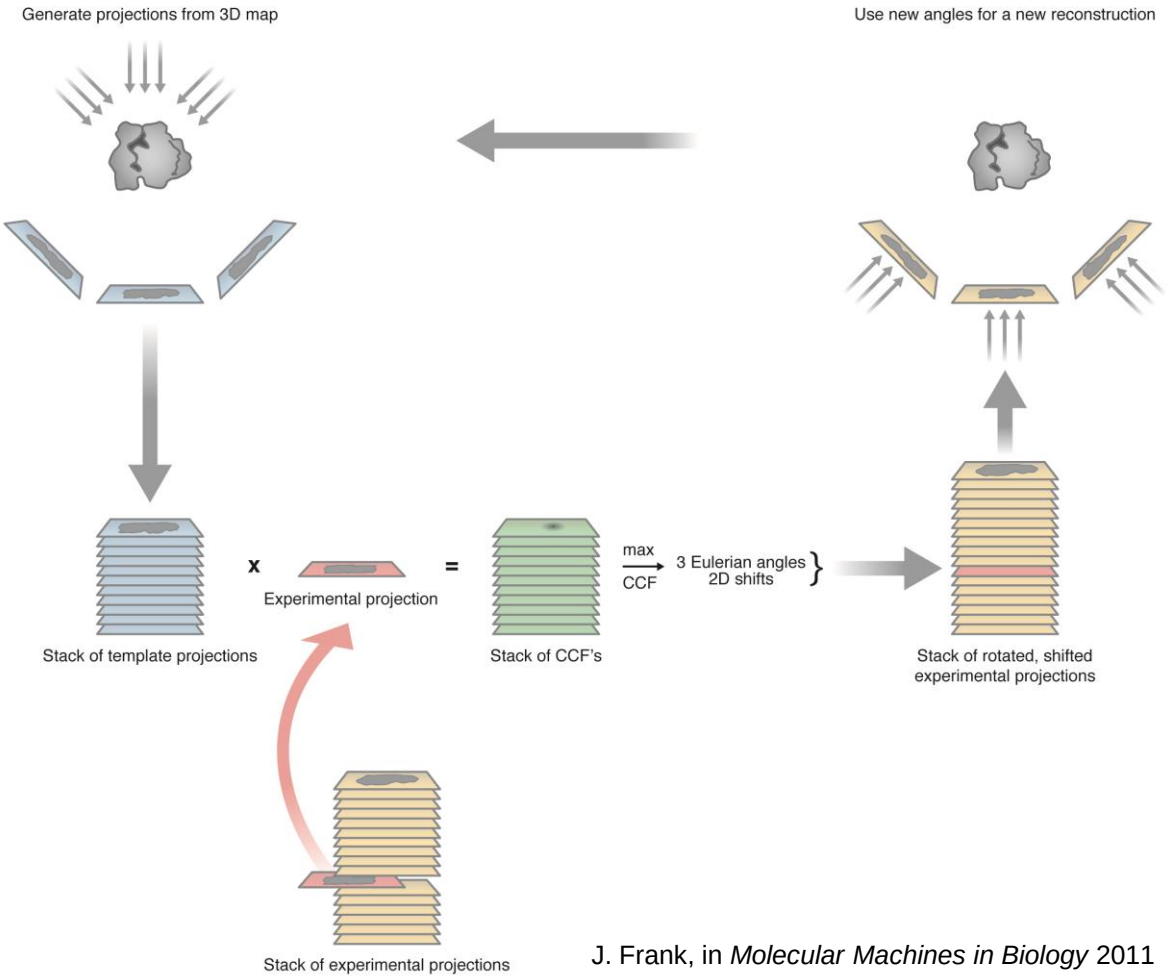
automated, climatized



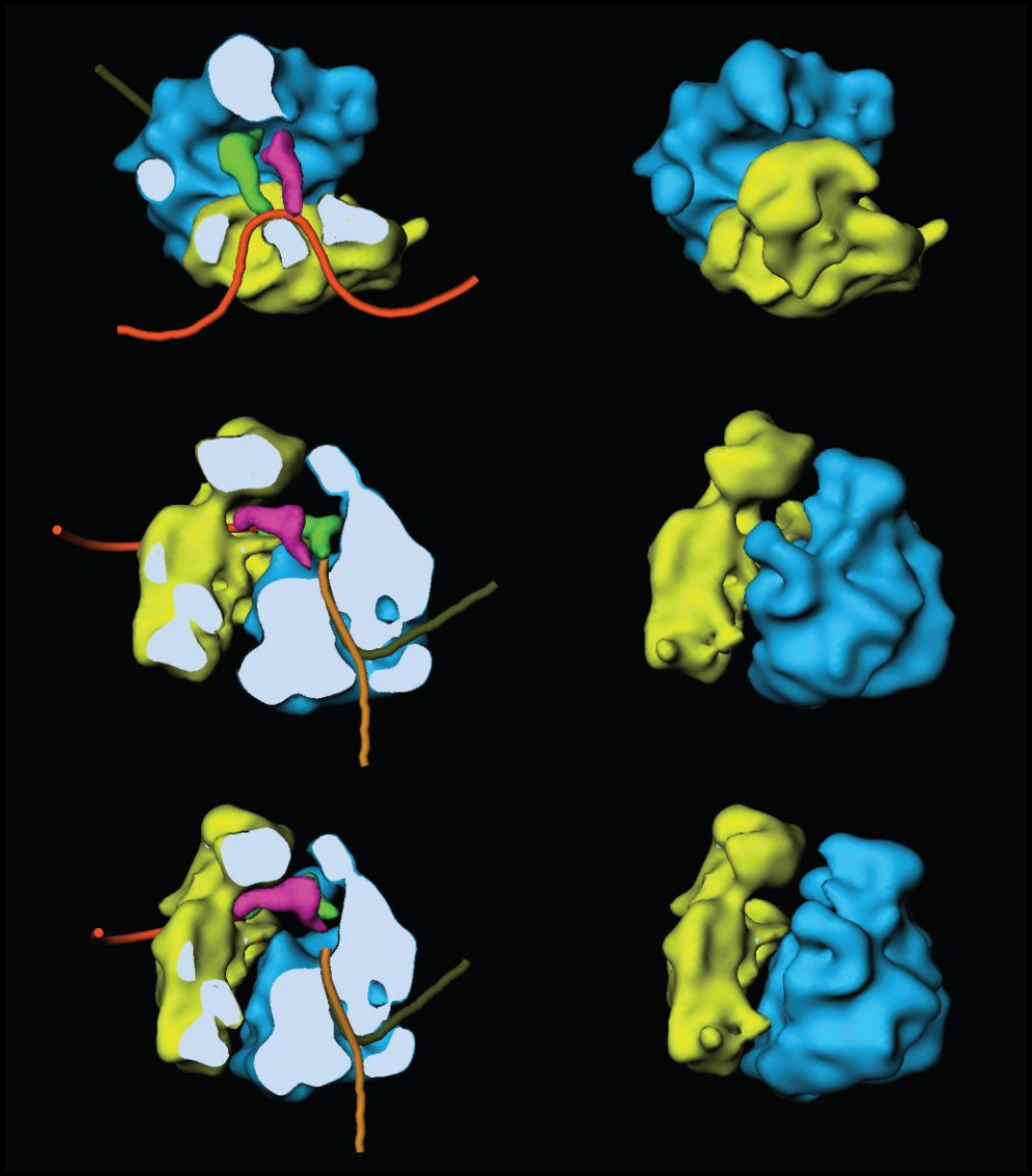




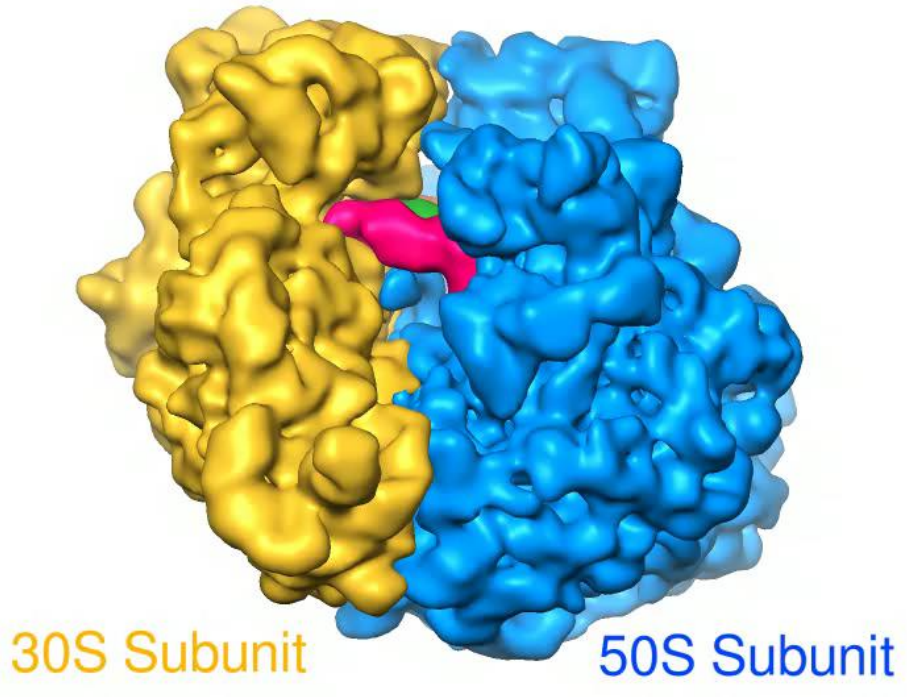
Iterative angular refinement



J. Frank, in *Molecular Machines in Biology* 2011

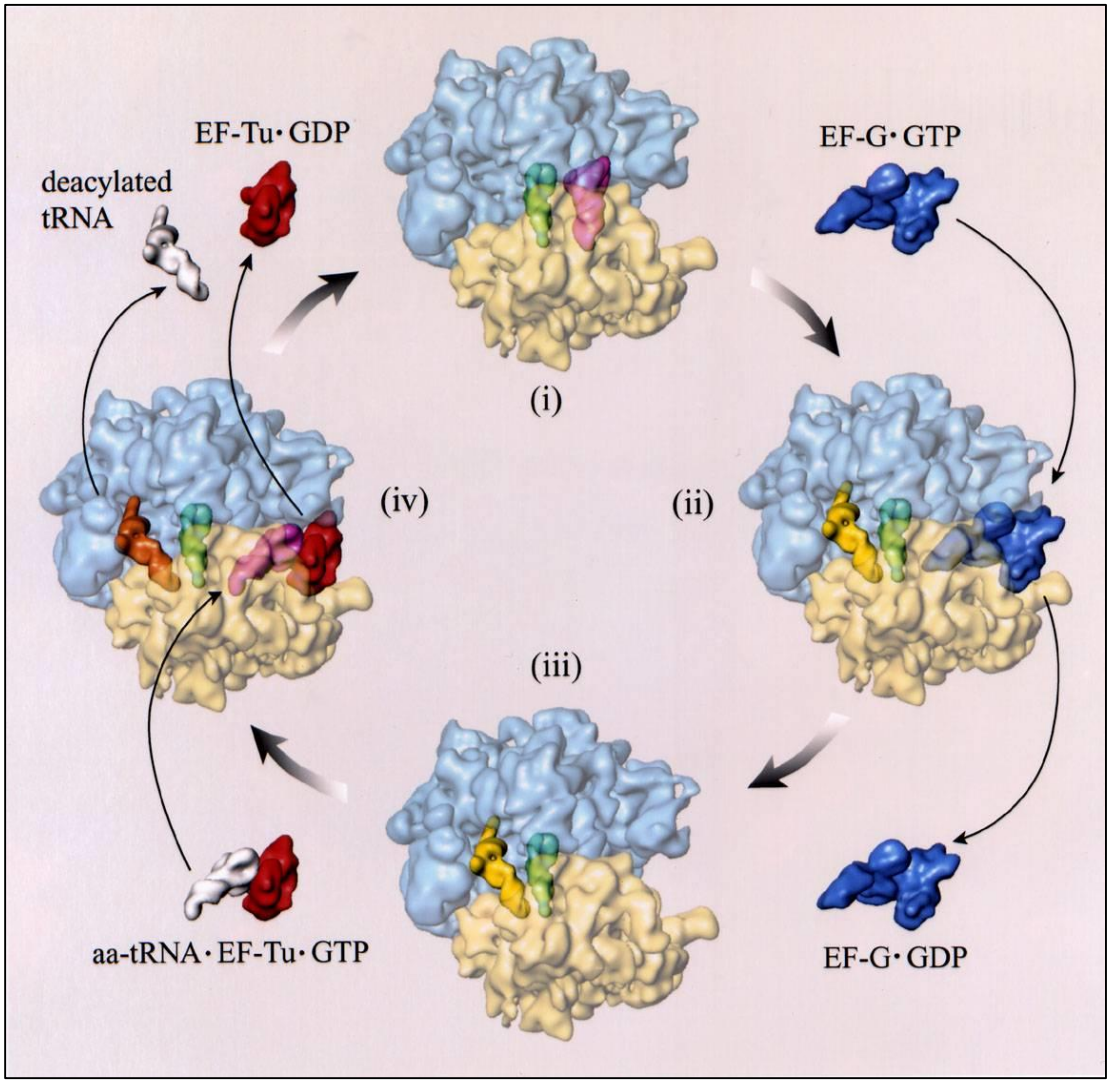


E. coli ribosome 1995


30S Subunit
50S Subunit

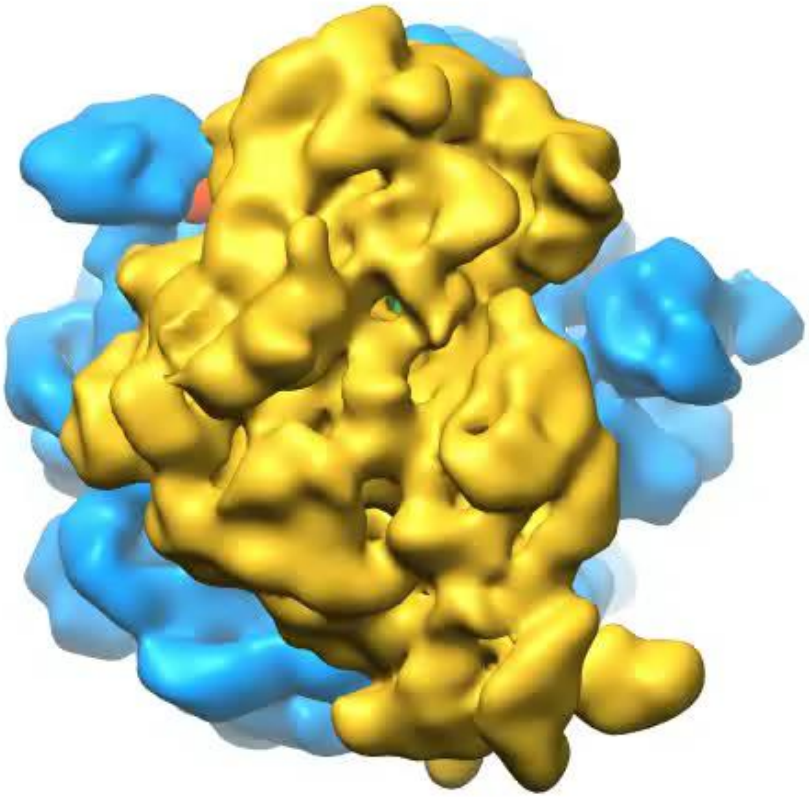
Elongation Cycle (for adding each amino acid)

Decoding



Translocation

DISCOVERY OF RATCHET-LIKE MOVEMENT DURING TRANSLOCATION

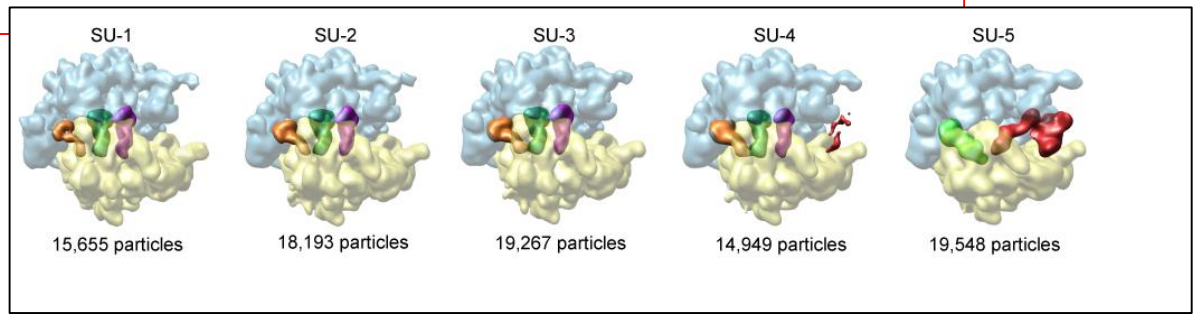


Frank and Agrawal, Nature 2000; Valle et al., Cell 2003

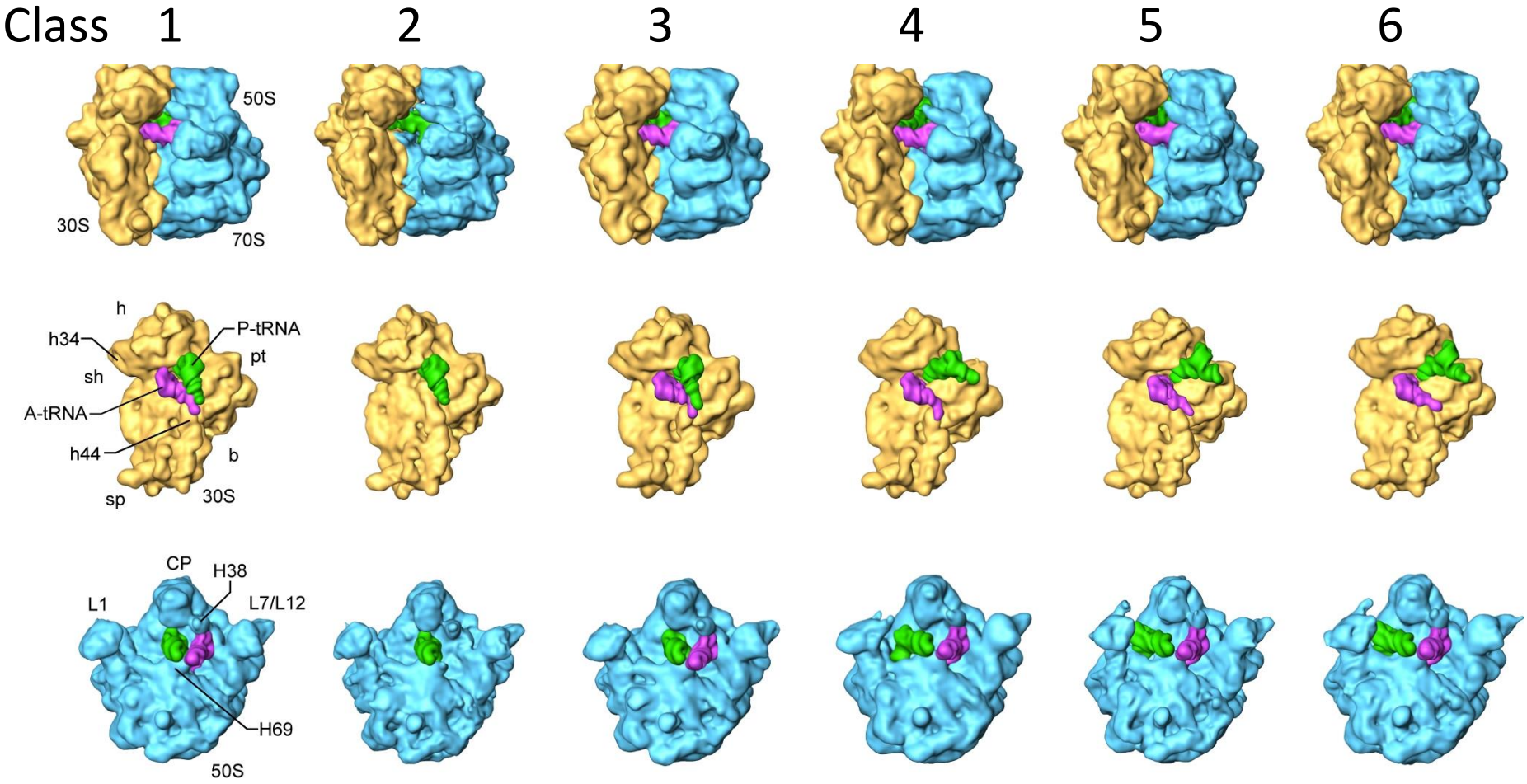
MAXIMUM LIKELIHOOD METHODS OF CLASSIFICATION

S.H.W. Scheres, H. Gao, M. Valle, G.T. Herman, P.P.B. Eggermont, J. Frank & J.M. Carazo (2007). "Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization." *Nat. Methods*, 4, 27-29.

S.H.W. Scheres (2012). "A Bayesian View on Cryo-EM Structure." J. Mol. Biol. 415, 406-418.



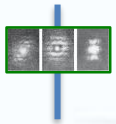
"**STORY IN A SAMPLE**" -- intermediate states in the ratchet-like motion and hybrid tRNA positions in the absence of EF-G

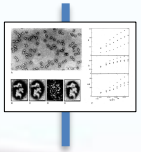


Agirrezabala et al., PNAS 2012

MILESTONES IN SINGLE-PARTICLE RECONSTRUCTION

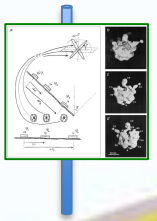
Alignment via CCF
Resolution estimation

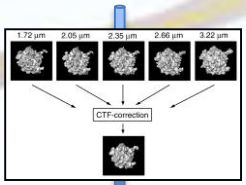




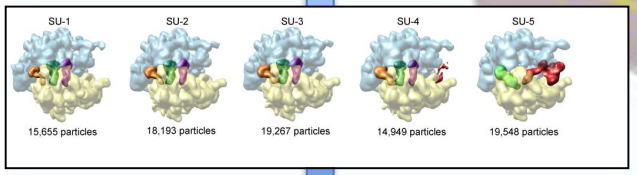
Multivariate statistical analysis
2D classification

Determine orientation
3D reconstruction

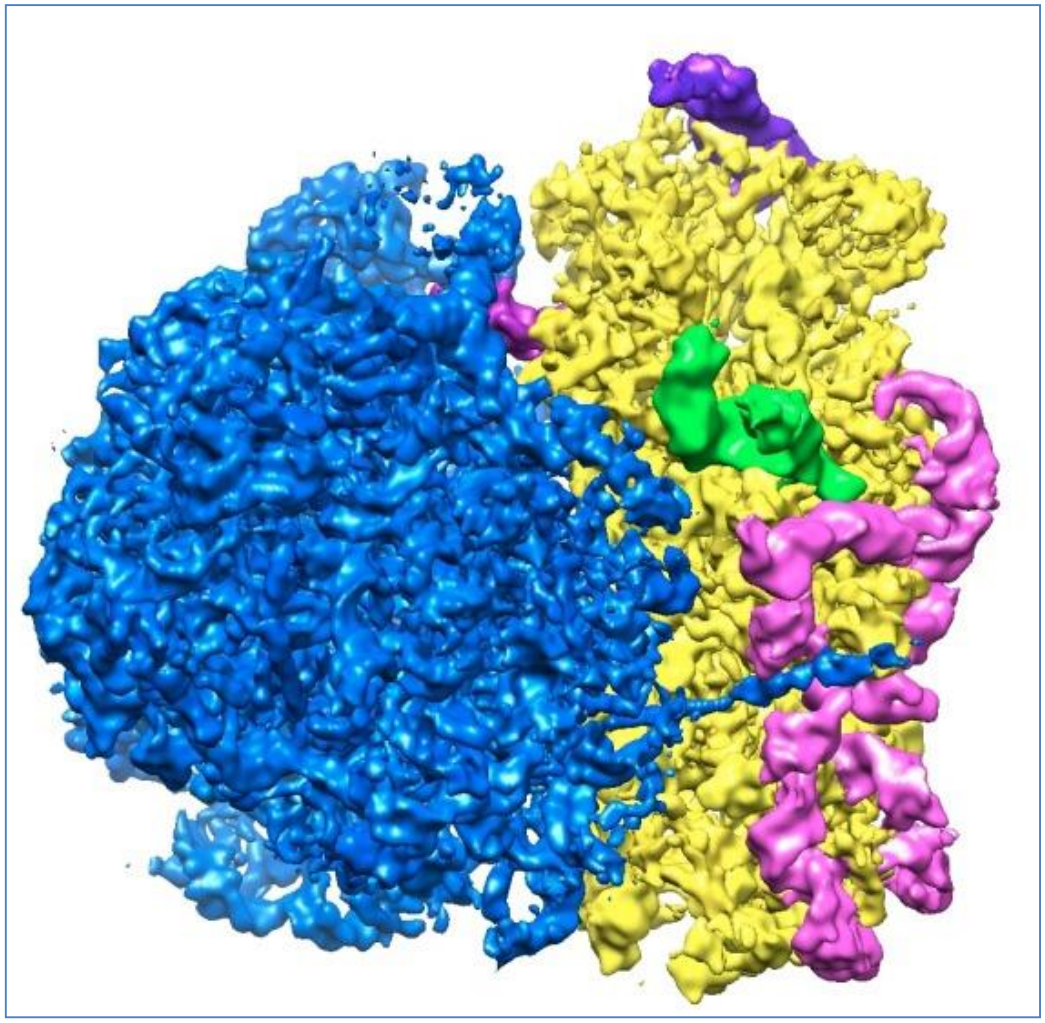




CTF correction via Wiener filter



Max likelihood 3D classification



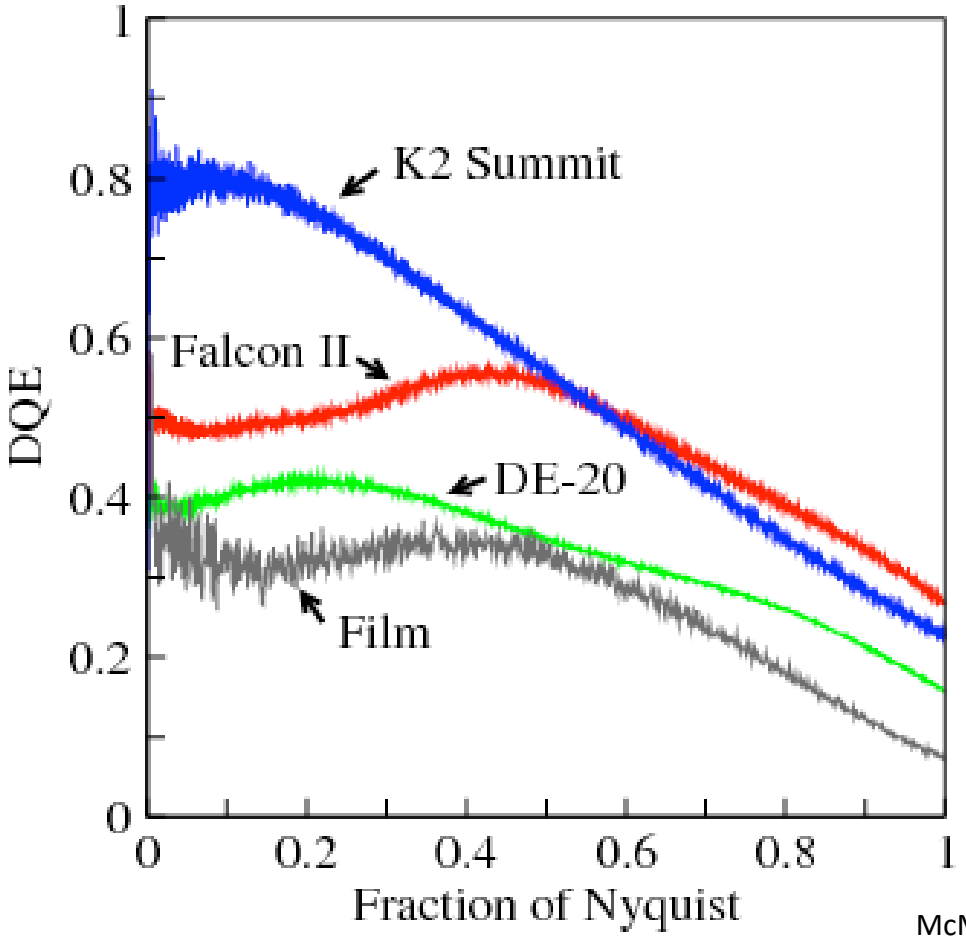
Hashem et al., Nature 2013

Best resolution from recording on film: 5.5Å

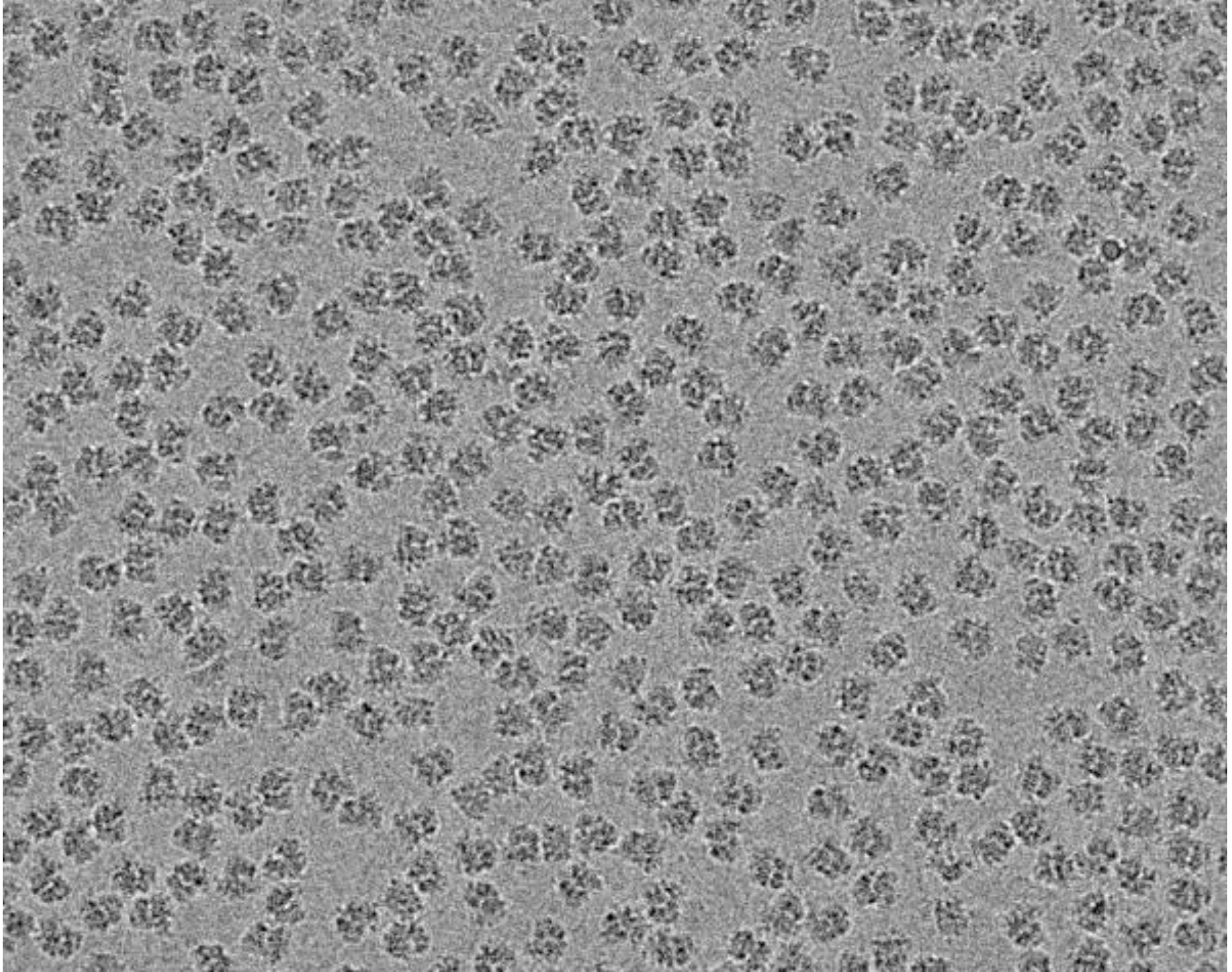
New era (since 2012): *New single-electron detecting cameras*

Detection Quantum Efficiency (DQE):

(how good is the recording device in capturing every single electron?)

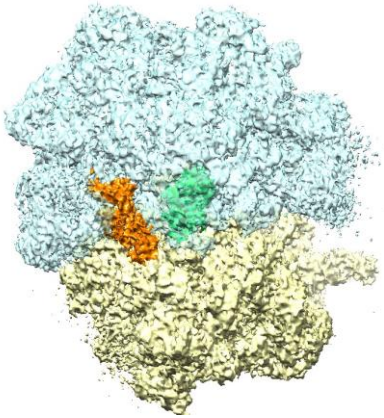


McMullan, G. et al. arXiv:1406.1389



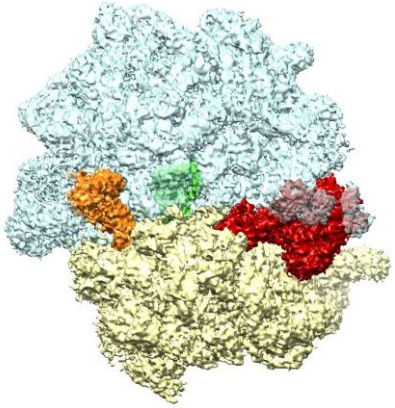
Elongation Factor G mutant H94A bound to the ribosome

nr 70S--P-E



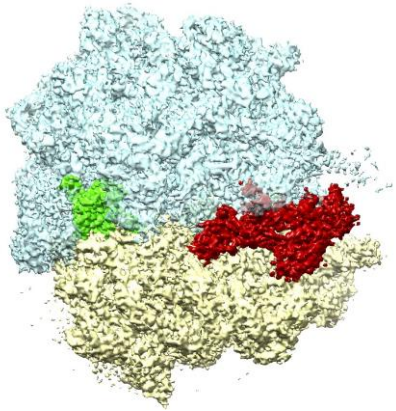
50,000

nr 70S--EF-G—P-E



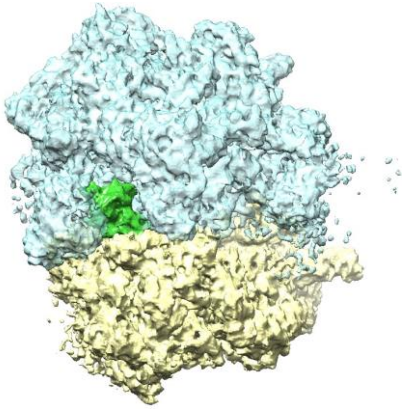
90,000

r 70S—EF-G—P/E



35,000

r 70S—P/E



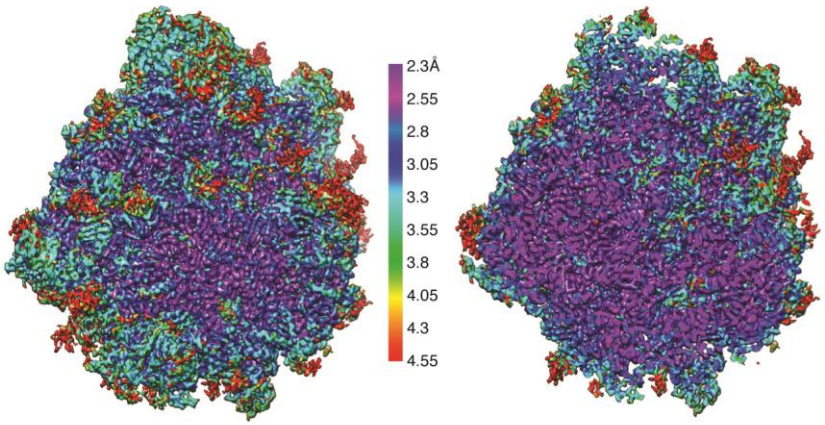
15,000

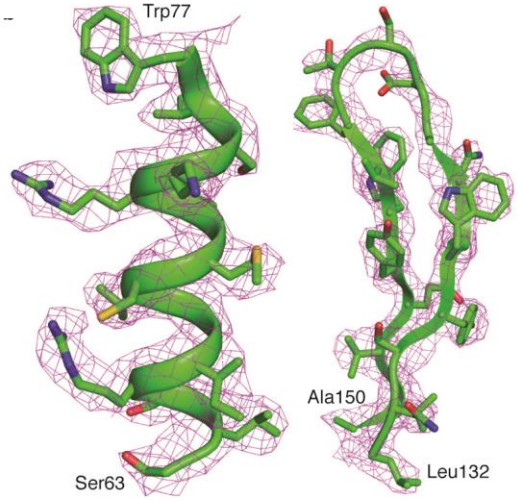
Example for maximum likelihood 3D classification
Multiple states in the same sample

Li et al., Science Advances 2015

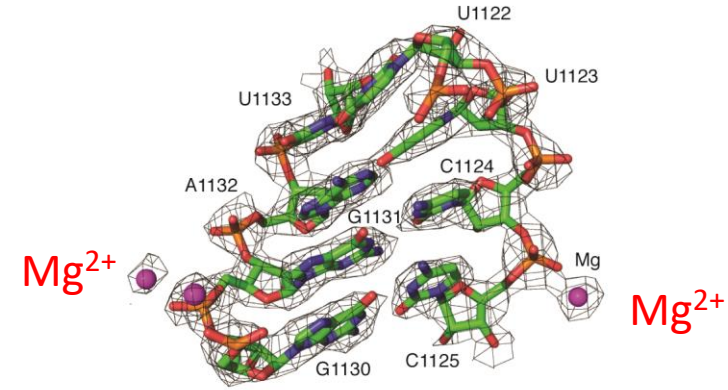
T. cruzi ribosome large subunit at 2.5 Å

Liu et al., PNAS 2016

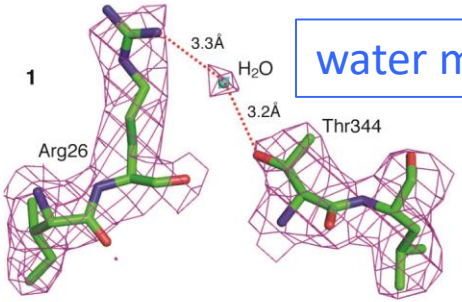




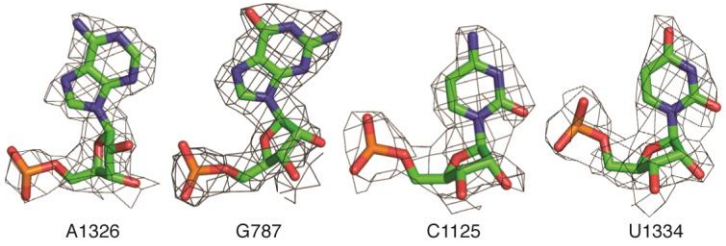
α-helix 2 strands of β-sheet

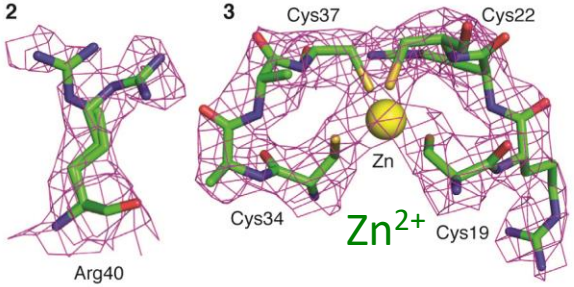


Mg^{2+} Mg^{2+}

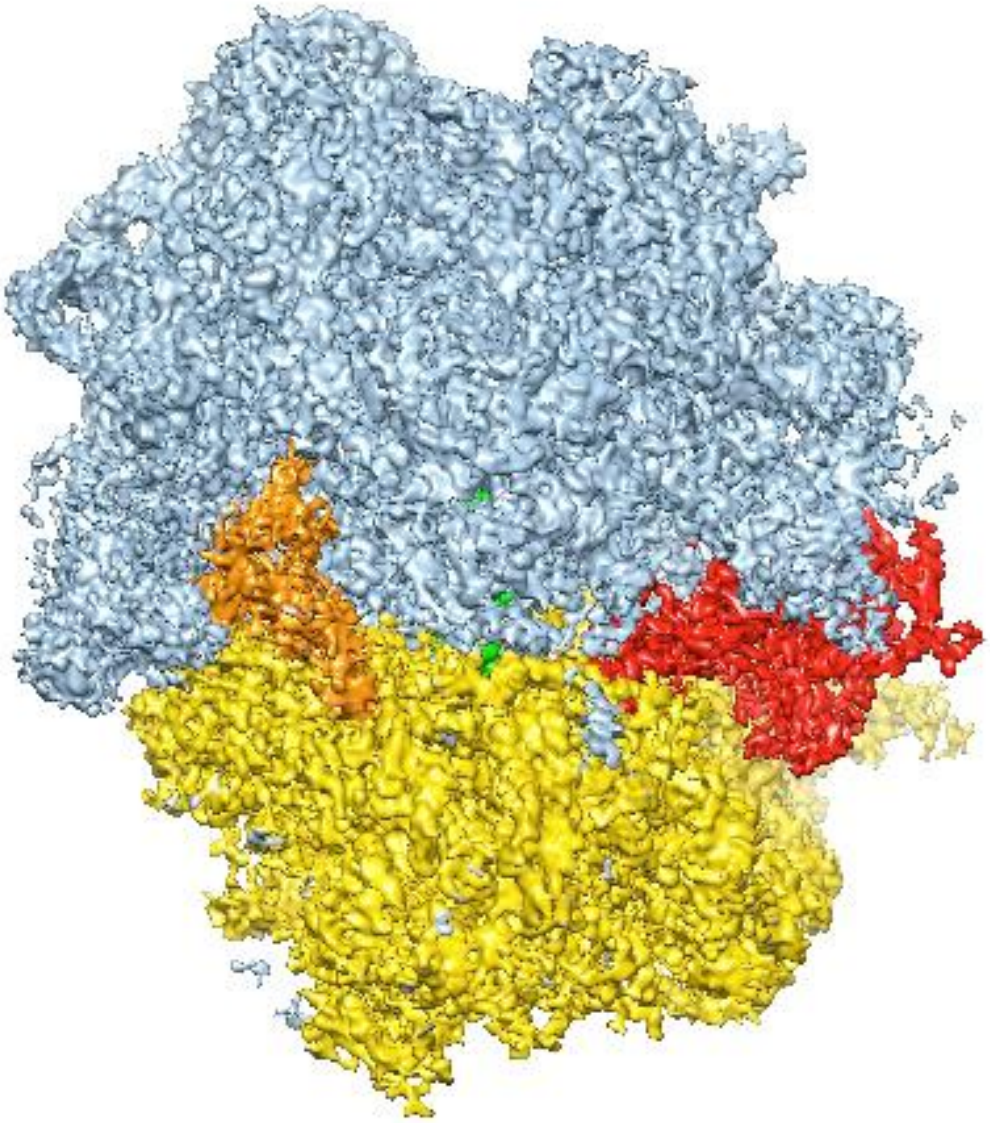


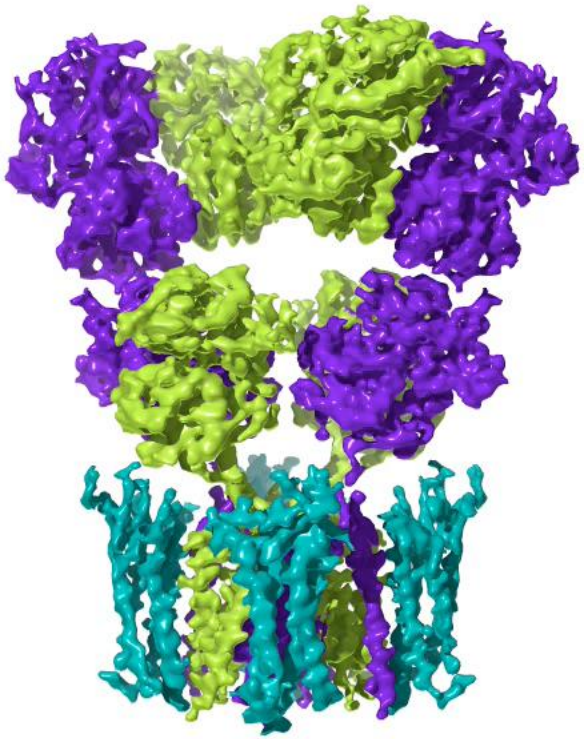
water molecule!





Zn^{2+}



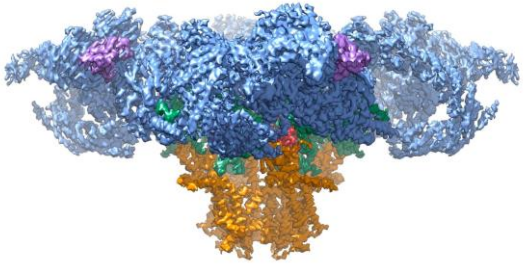


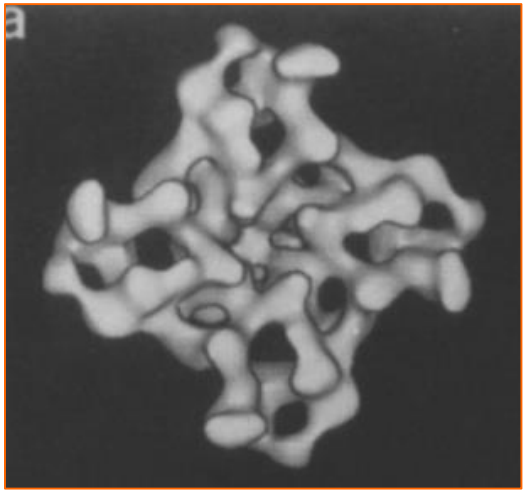
AMPA Receptor
Twomey et al., Nature 2017

Ryanodine Receptor

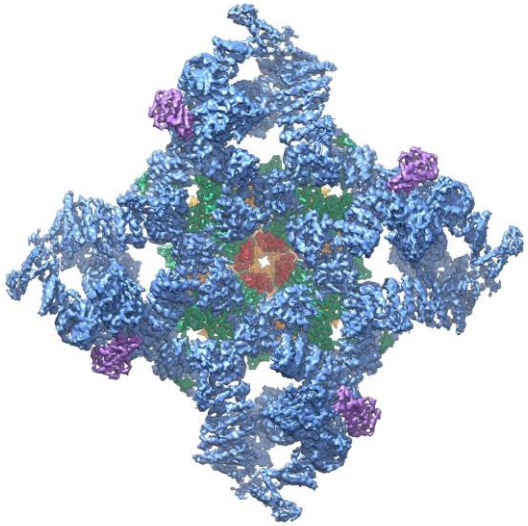
Zalk et al., Nature 2015

Des Georges et al., Cell 2016





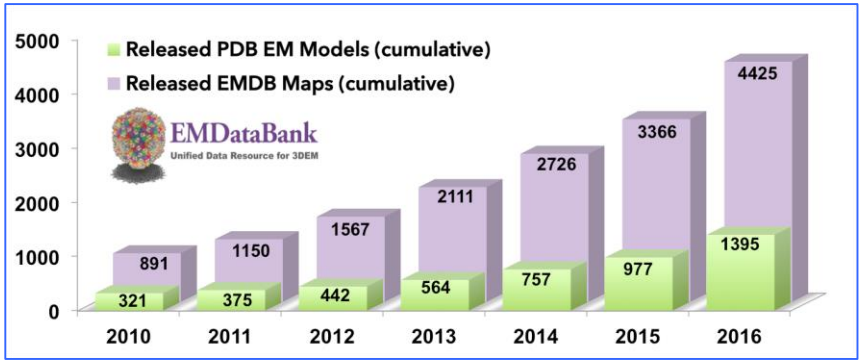
Radermacher et al., J. Cell Biol.
~30Å



Des Georges et al., Cell 2016
3.6Å

Conclusion -- Single-particle cryo-EM: A new era in structural biology A bright future!

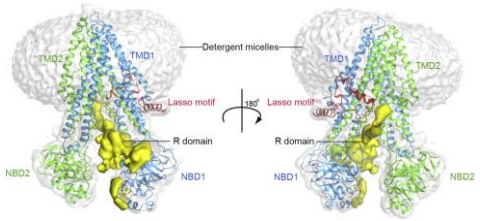
- No need for crystals!
- *Very small sample quantity needed*
- Resolution in the 3-4 Å range now routinely achievable
- *Multiple structures retrieved from the same sample → clues on function*
- Molecules in close-to-native conditions
- *Solving structures of membrane proteins much easier than with X-ray crystallography*
- Huge expansion of structural data base relevant for Molecular Medicine



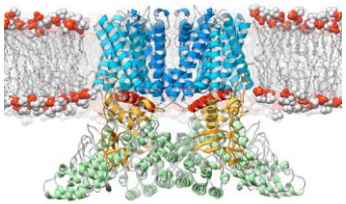
Impact in Biology and Molecular Medicine

The number of molecules with relevance to human health that can now be investigated is enormous. Among these:

1) Transmembrane proteins with particular biomedical significance, such as ion channels and receptors

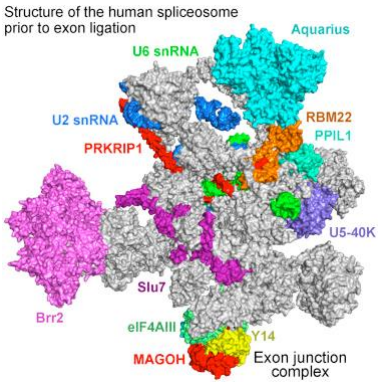


CFTCR
Zhang & Chen
Cell 2016



Pain receptor
Zubcevic et al.
NSMB 2016

1) Large molecular assemblies such as the spliceosome, which edits the genetic transcript



Spliceosome
Zheng et al.
Cell 2017

If we turn Galileo's telescope around and focus on the tiniest structures, we see another universe: the universe of life!

Ed Twomey - Jingji Zhang - Harry Kao - Francisco Acosta - Hstau Liao - Marcus Fislage - Suvrajit Maji - Sandip Kaledhonkar – Luke Goldstein - Jack Fu - Masgan Saidi
Wen Li – Lingwei Zhu - Andrey Malyutin – Bob Grassucci – Amy Jobe – Joachim Frank – Cristina Gutierrez-Vargas - Hengameh Fallah – Blanche Fields- Manasi Soman - Zheng Liu

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