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# **Realising the potential of Electron Cryomicroscopy**

•	Two-dimensional crystals	2D
•	Helical arrays (one-dimensional crystals)	1D
•	Single particles (with or without symmetry)	0D

• Tomography

# **3D structure by electron cryo-microscopy**

	present	theoretical
2D electron crystallography	(3 Å)	none
Helical arrays	(4 Å)	none
Single particle with symmetry no symmetry	(6-10 Å) (size, n (identit	none umber &) ty of particles)



(40 Å) 20 Å

resolution



### The multidrug transporter EmrE is an asymmetric homodimer Tate & Ubarretxena-Belandia, EMBO J. (2003) 22, 6175





Top view

### Side view

# **3D structures from 2D crystals**

Bacteriorhodopsin	3.5 Å	*
Bacteriorhodopsin	<b>3.0</b> Å	*
DOC bacteriorhodopsin	6.0 Å	
Bacteriorhodopsin p22121	6.5 Å	
Porin PhoE	6.0 Å	
Plant LHC-II	3.4 Å	*
Rhodopsin frog p2	6.5 Å	
Tubulin dimer	3.7 Å	*
Aquaporin-1	<b>3.</b> 8 Å	*
Aquaporin	4.0 Å	*
Halorhodopsin	5.0 Å	
Glutathione transferase	6.0 Å	
SecYEG complex	8.0 Å	
Plant photosystem II RC	8.0 Å	
Neurospora H+-ATPase	8.0 Å	
Gap junction channel	7.5 Å	
NhaA Na/H antiporter	7.0 Å	
Glycerol channel GlpF	6.9 Å	
Oxalic acid transporter OxlT	6.0 Å	
EmrE multidrug transporter	7.0 Å	





## <u>3D structures from helical or tubular arrays</u>

Acetylcholine receptor Bacterial flagellum

Microtubules

Calcium ATPase

TMV

4 Å Miyazawa, Fujiyoshi & Unwin (2003)
4 Å Yonekura, Maki-Yonekura, & Namba (2003)
8 Å Li, DeRosier, Nicholson, Nogales, & Downing (2002)
8 Å Zhang, Toyoshima, Yonekura, Green, & Stokes (1998)
10 Å Jeng, Crowther, Stubbs & Chiu (1989)

# 3D structures from single particles

icosahedral	
Hepatitis B cores	7.4 Å
Rice dwarf virus	6.8 Å
Herpes virus capsid	8.5 Å
Dengue virus	9.5 Å
Cytoplasmic polyhedrosis virus	8.0 Å
Semliki Forest virus	8.7 Å
Sindbis virus	9.5 Å
PM2 virus	8.5 Å
Reovirus virions	7.6 Å
Pyruvate dehydrogenase E2CD	8.7 Å
lower symmetry	
E. coli 70S ribosome	11.5 Å
Keyhole limpet hemocyanin	15.0 Å
Bacteriophage SPP1 connector	10.0 Å
GroEL	87Å

## Single particle approaches (Peter Rosenthal)

- Use of tilted pairs (absolute hand, parameter optimisation)
- Sharpening and signal-to-noise weighting













## Intact F1-Fo ATP synthase (John Rubinstein)

- 4500 particles of bovine mitochondrial complex imaged in ice
- image processing using Imagic and Frealign

### John Rubinstein

Abrahams, Leslie, Walker, Stock



Mitochondrial ATP synthase















**Chris Tate & Iban Ubarretxena-Belandia** - Structure of multi-drug transporter EmrE (6.5 Å) (Shuldiner, Baldwin)

### <u>1D</u>

Nigel Unwin - Acetylcholine receptor (4.0 Å) (Fujiyoshi, Miyazawa)

### <u>0D</u>

**Peter Rosenthal -** Improvement of methods for single particle electron microscopy developed on pyruvate d-ehydrogenase E2CD (8.7 Å) (Perham)

John Rubinstein - Intact F1-Fo ATP synthase (32 Å) (Walker)

Tomography Sam Li - Yeast spindles (Kilmartin)