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Towards automated serial electron diffraction for beam-sensitive materials

Stef Smeets Kavli Institute of Nanoscience Delft





Fourier Transform







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7

duck



myoglobin



	• • •	11/h
	•	• 170
	1/a	





Electron microscope



objective

aperture



Electron 'diffractometer'



Electrons as a radiation source



- Wavelength: ~0.025 Å @ 200 keV
- Probe electrostatic potential
- High vacuum (<10⁻³ mbar)
- Strong interaction (10⁶ stronger than X-rays)
- Require small samples (< 1 μm)



Cichocka et al., J. Appl. Cryst. (2018), 51:1652 Detector readout time Tilt range: up to 150° Oscillation angle: 0.1-0.5° Detector Rotation speed: 0.5-2.0°/s <5 minutes

3D Electron diffraction

Continuous rotation method

Nederlof *et al., Acta Cryst. D* (2013), 69:1223 Nannenga *et al., Nat. Methods* (2014), 11:927 Gemmi *et al., J. Appl. Cryst.* (2015), 48:718 Cichocka *et al., J. Appl. Cryst.* (2018), 51:1652

Zeolite mordenite

Rotate: -43.90° to 58.65° @ 0.45°/s (102.55°) Exposure: 0.5 s, oscillation angle: 0.23° JEOL 2100-LaB₆ @ 200 kV (Timepix camera)



250 nm



Cichocka et al., J. Appl. Crystallogr. 51 (2018), 1652



Radiation damage sensitivity

Material	Characteristic dose D _{ec} (e ⁻ /Å ²)
Bacteriorhodopsin	0.5
Amino acid (glycine)	1.6
Polyethylene	6.0
Coronene	70.0
Phthalocyanine	120.0
Zeolite (ZSM-5)	300.0
Calcite (200 kV)	39000.0

Egerton, Micron 119 (2019)



Amino acid



Coronene



Phthalocyanine



Bacteriorhodopsin



ZSM-5 zeolite

Radiation damage





1.60 e⁻/Ų *D* =

4.31 e⁻/Ų

6.10 e⁻/Å²

8.98 e⁻/Ų

S'ari et al., J. Phys. Conf. Ser. 644 (2015)

No standard for data collection

- No software many labs use ad hoc data collection protocols
- Manual data collection: tedious and not reproducible
- Lack of automation
 - Unnecessary dose accumulation
 - Low redundancy
 - Biased crystal selection





Protocol for serial electron crystallography

- Screen sample stage and generate global map
- Select and image regions of interest
- For each region:
 - Identify and **localize** crystals of interest
 - For each crystal:
 - Move crystal to the electron probe
 - Collect diffraction data



Sample preparation



Protein crystals (Mother licquor)



Crystalline powder (Disperse in EtOH)









Plunge freezing (liquid ethane)



158 crystals rotated 20° @ 1.70°/s | Total exposure: 12 s/crystal | 14 indexed (XDS)





#	a (Å)	b (Å)	<i>c</i> (Å)	в (°)
1	13.10	23.84	5.09	92.8
2	13.98	18.12	5.53	102.4
3	13.37	19.03	4.87	92.9
4	13.07	78.54	4.88	90.7
5	13.18	61.85	4.86	90.1
6	12.58	22.76	4.96	90.7
7	12.82	21.34	4.90	91.2
8	12.76	20.35	4.94	91.7
9	11.62	27.18	5.12	93.7
10	12.97	95.24	4.86	90.7
11	12.73	20.40	4.97	88.9
12	13.11	18.59	4.94	90.3
13	12.97	78.12	4.91	91.5
14	12.99	20.51	5.27	93.5
X-ray ref.	13.111	21.380	5.113	90.624

Indexing & cluster analysis



Summary

- Automatically collect ED data on very beam-sensitive crystals
- Protocol for minimal dose deposition before acquisition
- Automation is key enabling high-throughput acquition and data analysis
- Methods are equally suitable for biological as materials science problems







