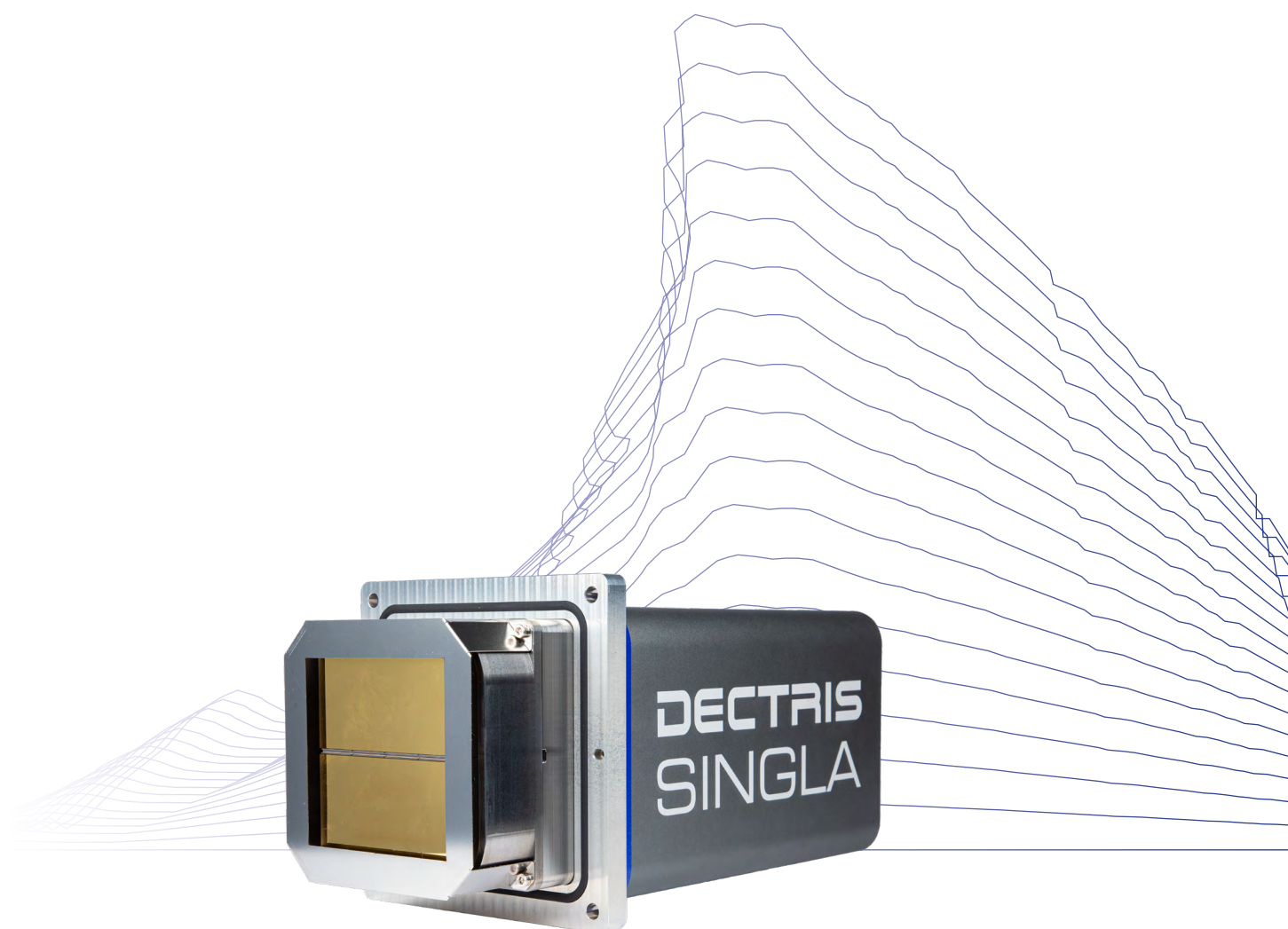


**DECTRIS**



# SINGLA

A fast and most sensitive hybrid-pixel camera for Life Science applications



# SINGLA

## DECTRIS SINGLA for cryoEM and 3DED

Your precious biological samples deserve the most sensitive electron camera! DECTRIS SINGLA® excels with a DQE of 98% and 53% at 0 and Nyquist frequencies, respectively. With its 1k x 1k field of view, this hybrid-pixel, electron-counting camera is best suited for single-particle electron cryomicroscopy at 100 keV (cryo-EM) and 3D Electron Diffraction (3DED) applications<sup>1,2</sup>.

SINGLA offers a fast and dead-time-free readout speed of up to 4,500 frames per second. The combination of high speed with a superior dynamic range and full radiation hardness makes it the ideal camera for continuous rotation electron diffraction of small-molecule and protein microcrystals. The camera is bottom-mounted and compatible with JEOL and Thermo Fisher Scientific Transmission Electron Microscopes. Integration into serialEM enables protocols for automated tilt series and single-particle acquisition.

### Technical Specifications

#### SINGLA

Frame rate (max.) [Hz]	2,250 at 16 bit 4,500 at 8 bit
Count rate capability (max.) [e <sup>-</sup> /s/pixel]	10 <sup>7</sup>
Number of pixels	1028 x 1062
Pixel size (W x H) [μm <sup>2</sup> ]	75 x 75
Sensor material	Silicon (450 μm)
Energy range [keV]	30 – 200
DQE(0) <sup>3</sup>	0.98 at 100 keV 0.90 at 200 keV

All specifications are subject to change without notice.

1 McMullan *et al.*, 2023, PNAS, 120 (49) e2312905120, <https://doi.org/10.1073/pnas.2312905120>

2 Waterman *et al.*, 2023, Structure 31, 1–8, <https://doi.org/10.1016/j.str.2023.07.004>

3 The values are based on reference 1 and S. Fernandez-Perez *et al.* 2021 JINST 16 P10034

# Enabling fast and accurate structure determination of biological molecules by cryo-EM at 100 keV

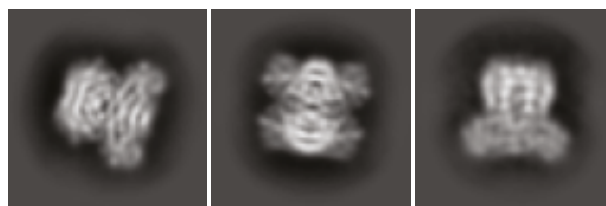
Cryo-EM at 100 keV was pioneered by the groups of Chris Russo and Richard Henderson from the LMB Structural Biology Division in Cambridge, UK. Their 2023 publication in PNAS<sup>1</sup> demonstrates that high-resolution structures can be obtained quickly from a small number of particles.



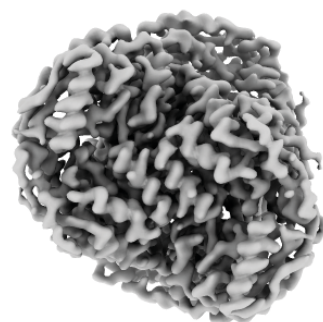
Micrograph of human aldehyde dehydrogenase (ALDH1A1), collected at 100 keV with a purpose-built electron cryo-microscope consisting of a York Probe Sources 100 keV FEG, a JEOL JEM1400 electron microscope, and a DECTRIS SINGLA camera. See Reference 1 for details.

Number of 1k x 1k micrographs	416
Nominal magnification	250,000x
Pixel size (phys. & super-resolution)	1.683 Å, 0.841 Å
Defocus (average, range)	0.7 µm, 0.1 – 1.4 µm
Number of raw frames	16,384
Frames after grouping	64
Total electron dose	40.6 e/Å <sup>2</sup>
Resolution (FSC = 0.143)	2.9 Å
Rosenthal B-factor	130 Å <sup>2</sup>
PDB code	8PVH
EMDB code	17966

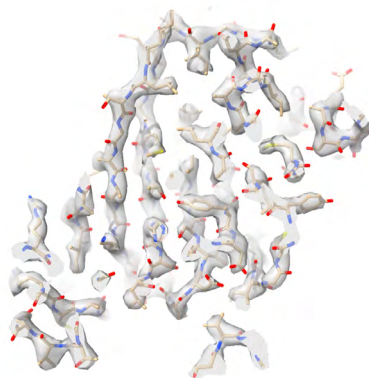
Data collection and analysis statistics.



Three selected reference free 2D class averages.



Final 3D map at 2.9 Å calculated from 64 frames (32,968 particles).



Map detail showing ALDH1A β-sheet at 2.9 Å resolution.

All data, images, and supporting information are from McMullan *et al.*, 2023, PNAS, 120 (49) e2312905120, <https://doi.org/10.1073/pnas.2312905120>

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