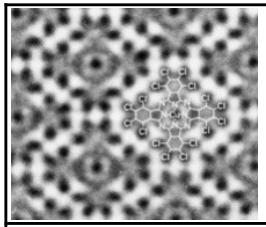
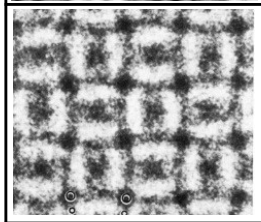


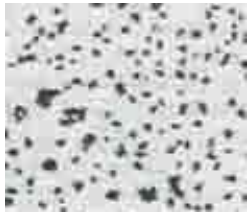
Chemica Scripta., 14, 47-61, 1979

It was demonstrated that the molecular structure of chlorinated copper phthalocyanine can be observed by electron microscopy.



Nature, 285, 95-97, 1980

Minimum Dose System was developed and demonstrated to enable molecular imaging of organic molecules (charge-transfer complexes).

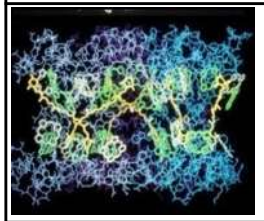


Nature, 327, 319-321, 1987

Dark-field electron microscopy showed that the surface films, which were thought to be homogeneous, were heterogeneous with holes.

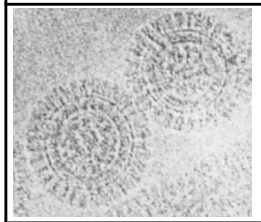
Ultramicroscopy, 38, 241-251, 1991
Proc. Jpn Acad., Ser. B, 91, 447-468, 2015

Development and improvement of original cryo-electron microscopes cooled to the temperature (4.2K) of liquid helium.



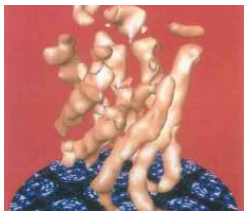
Nature, 367, 614-621, 1994

Using cryo-electron microscopy, an atomic model of Plant Light-Harvesting Complex was analysed by electron crystallography.



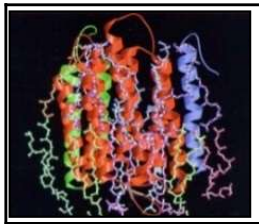
EMBO J., 13, 318-326, 1994

By observing influenza viruses embedded in ice, it was shown that the envelope was formed by an outer leaflet of lipid membrane and a lined structure.



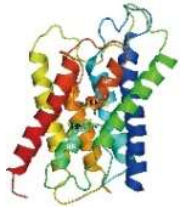
Nature, 387, 624-627, 1997

The helical structure of the human water channel AQP1 was analysed by electron crystallography at 6 Å resolution.



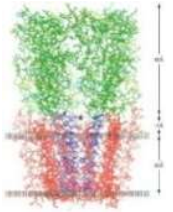
Nature, 389, 206-211, 1997

An efficient proton pumping mechanism was proposed based on the structure of bacteriorhodopsin containing lipid molecules at 3 Å resolution.



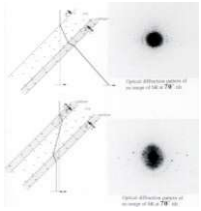
Nature, 407, 599-605, 2000

A model, H-bond isolation mechanism, was proposed to explain the mechanism of fast water permeation and high-water selectivity by analysing the structure of AQP1 using electron crystallography.



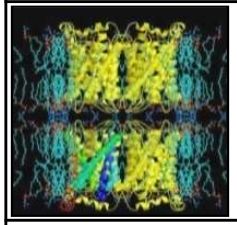
Nature, 423, 949-955, 2003

An atomic model of the acetylcholine receptor in its resting (closed) state was analysed in tubular crystals.



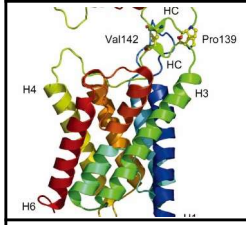
J. Struct. Biol., 146, 325-333, 2004

Development of the carbon sandwich method to reduce image degradation due to sample charge-up in cryo-EM imaging.



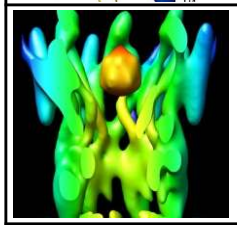
Nature, 438, 633-638, 2005

The structure of AQP0 was analysed by electron crystallography at 1.9 A resolution, distinguishing water molecules in the channel and lipid molecules in the 2D crystal.



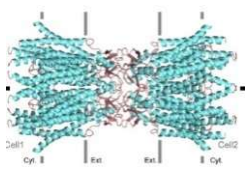
J. Mol. Biol., 355, 628-639, 2006

The structure of AQP4, which is the predominant water channel in the brain, was analysed by electron crystallography and found to be a channel with an adhesive function.



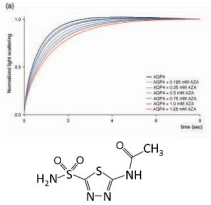
PNAS, 104, 10034-10039, 2007

The structure of the gap junction channel connexin26 was analysed by electron crystallography and a plug structure was discovered in the channel.



Nature, 458, 597-602, 2009

An atomic model of connexin 26 was proposed based on the structural analysis by X-ray crystallography for the putative open gap junction channel state.



J. Struct. Biol., 166, 16-21, 2009

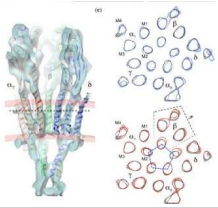
Acetazolamide was identified as a candidate drug for cerebral oedema as an inhibitor of AQP4 and its concentration-dependent reversible inhibition was confirmed.

Nat. Commun., 2, 155, 2011

The structure of a gastric drug-related H+,K+-ATPase inhibitor complexed with the proton pump was analysed by electron crystallography.

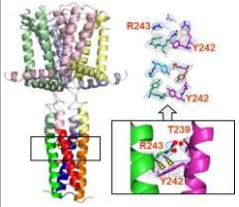
J. Struct. Biol., 175, 49-61, 2011

The structure of gap junctions in lateral giant fibres was analysed using electron tomography and vesicle connections were observed.



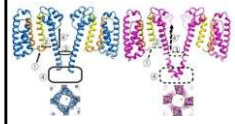
J. Mol. Biol., 422, 617-634, 2012

Using the spray-freeze trapping method, open and closed structures of the acetylcholine receptor were analysed and a model for the ligand gating mechanism was proposed.



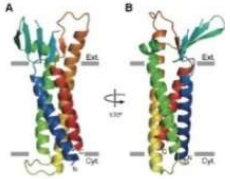
Nat. Commun., 3, 793, 2012

Structural and functional analyses show that the helical bundle formed by the C-terminus of voltage-gated Na+ channels controls the rate of inactivation.



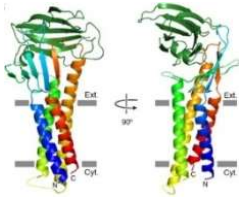
J. Mol. Biol., 425, 4074-4088, 2013

The structures of the two states of the voltage-gated Na+ channel in two-dimensional crystals were analysed by electron crystallography.



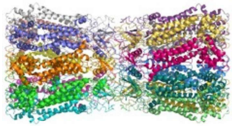
Science, 344, 304-307, 2014

Claudin is a key protein in tight junctions. It (claudin-15) was found to consist of four transmembrane helices and a β-sheet structure.



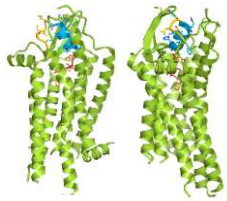
Science, 347, 775-778, 2015

The complex structure of claudin-19 and clostridium perfringens toxin was analysed by X-ray crystallography, and a model for the disassembly of tight junctions by the toxin was proposed.



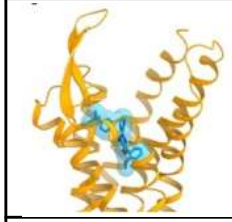
Nat. Commun., 7, 13681, 2016

High resolution structure of the invertebrate gap junction innexin was analysed using the single particle method.



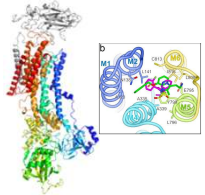
Nature, 537, 363-368, 2016

The structure of the endothelin receptor complex with the agonist endothelin-1 was analysed by X-ray crystallography.



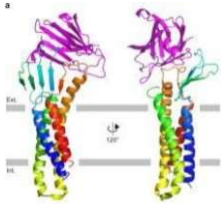
Nature Struct. Molec. Biol., 24, 758-764, 2017

X-ray crystallographic analyses of the structures of the complexes of the endothelin receptor with antagonists revealed details of ligand binding.



Nature, 556, 214-218, 2018

The structure of a gastric drug-related H+,K+-ATPase inhibitor complexed with the proton pump was analysed at high resolution by X-ray crystallography.

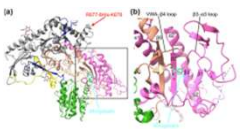


Nat. Commun., 10, 816, 2019

The bending of the third helix of claudins was shown to be an important determinant of tight junction properties.

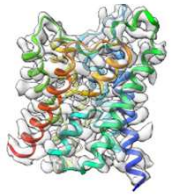
Ultramicroscopy, 237, 113512, 2022

Electron beam damage was measured on crystals of organic and biomolecules under liquid helium and liquid nitrogen cooling conditions, and the effect of reducing electron beam damage at liquid helium temperature was confirmed.



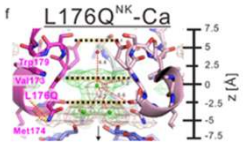
J. Mol. Biol., 435, 168049, 2023

The structure of the gabapentinoid drug mirogabalin bound to the α2δ1 subunit of the human voltage-gated calcium channel was analysed using single particle method, revealing the binding mode of the analgesic.



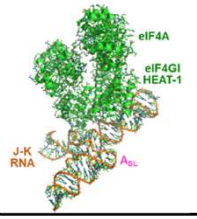
J. Struct. Biol., 215, 107984, 2023

Water channels are membrane proteins that are mostly embedded in lipid membranes, making them difficult to analyse, but the structure of the water channel AQP2 was successfully analysed using the single particle method.



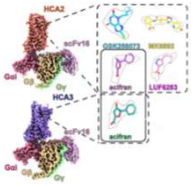
Nat. Commun., 14, 4236, 2023

Ion permeation of NMDA receptors and other receptors is inhibited by magnesium ions. The structure and mechanism by which ion permeation is inhibited by divalent cations using a tetrameric channel has been elucidated.



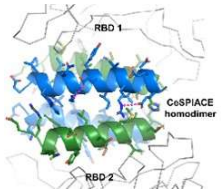
Nat. Commun., 14, 4977, 2023

Analysis of the structure of the complex formed by encephalomyocarditis virus RNA and the eukaryotic translation initiation factors 4G and 4A, and elucidation of the mechanism of this complex formation in collaboration with NMR methods.



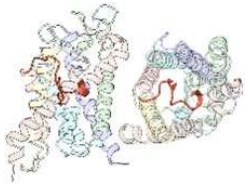
Nat. Commun., 14, 5899, 2023

The structures of the G protein-coupled receptors HCA2 and HCA3, which bind to agonists and form G protein complexes were analysed by single particle analyses of cryo-electron microscopy.



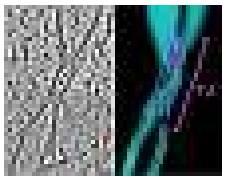
Proc. Natl. Acad. Sci. U. S. A., 122, e2413465122, 2025

A mutation-tolerant inhibitor peptide against variable SARS-CoV-2 spikes was developed by structure-guided engineering using cryo-EM and X-ray crystallography.



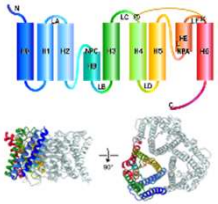
Nat. Commun., 16, 2653, 2025

AQP3 structures in different conditions were analysed by cryo-EM and suggested a possible gating mechanism by Y212, which forms an extracellular loop, inserted into the channel.



Sci. Adv., 11, eadx7431, 2025

Tight junctions (TJs) are paracellular barriers in epithelia, and their functional diversity is determined by the combination of 27 claudins (Cldns). We generated complete Cldn-null mouse epithelial cells to reconstitute the TJ barrier with individual Cldns classifying them into four main classes based on their measured functions. We also analysed the 3D structure of the apical region, including the TJ, by cryo-electron tomography.



Sci. Adv., 12, eaeb5769, 2026

We analysed the human AQP11 structure by cryo-electron microscopy at 2.3 Å resolution, revealing a unique trimeric architecture compared with other known tetrameric AQPs. The channel pore is broader and more hydrophobic than that of canonical AQP.