Contribution ID: **15** Type: **Flash Talk**

Using Deep Learning for interpreting macromolecular crystallography and electron cryomicroscopy data

Friday 8 December 2023 14:24 (12 minutes)

I will present applications of Deep Learning-based protein structure prediction tools, such as AlphaFold, for interpreting experimental data in macromolecular crystallography and electron cryomicroscopy. I will also show examples of my own Deep Learning tools trained to complement the use of predicted models for macromolecular structure determination.

(1) Chojnowski NAR 2023 51(15) 8255–8269 (10.1093/nar/gkad553)
(2) Chojnowski ActaD 2023 79(7) 559–568 (10.1107/S2059798323003765)
(3) Chojnowski ActaD 2022 78(7) 806-816 (10.1107/S2059798322005009)
(4) Chojnowski IUCrJ 2022 9(1) 86-97 (10.1107/S2052252521011088)
(5) Skalidis et al Structure 2022 30(4) 575-589 (10.1016/j.str.2022.01.001)

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Session Classification: Session III