# 5 years of Alphafoldology

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AlphaFold 2 was first presented at CASP 14 in December 2020. It was a major success in protein structure prediction, leading to a Nobel Prize in Chemistry last year. Especially since AlphaFoldDB and AlphaFold 2 source code opened in July 2021, the field of structural biology has moved towards the full structural description of all possible proteins with known and, to some extent, even unknown sequences. The speed and breadth of post-AlphaFold tools and services development, for which Marian Novotný and I coined the term „Alphafoldology“ in September 2021, has been breathtaking. In the lecture, I will review the current state-of-the-art of the Alphafoldology field and what usage it enables for biology and chemistry.