Event title	AlphaFold: what's in it for me?
Event type	Webinar
Date of event	18/04/2023
Time of event	1pm AEST
Topic description	AlphaFold has taken the scientific world by storm with the ability to accurately predict the structure of any protein in minutes using artificial intelligence (AI). From drug discovery to enzymes that degrade plastics, this promises to speed up and fundamentally change the way that protein structures are used in biological research. Beyond the hype, what does this mean for structural biology as a field (and as a career)? Dr Craig Morton, Drug Discovery Lead at the CSIRO, is an early adopter of AlphaFold and has decades of expertise in protein structure / function, protein modelling, protein – ligand interactions and computational small molecule drug discovery, with particular interest in anti-infective agents for the treatment of bacterial and viral diseases. Craig joins this webinar to share his perspective on the implications of AlphaFold for science and structural biology. He will give an overview of how AlphaFold works, ways to access AlphaFold, and some examples of how it can be used for protein structure/function analysis.
Format description	Webinar presentation followed by a brief question and answer session
Identifier(s)/URL	https://www.biocommons.org.au/events/alphafold
Licence	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials
Keywords	Bioinformatics http://edamontology.org/topic_0091 Machine learning http://edamontology.org/topic_3474 Structural biology http://edamontology.org/topic_1317 Proteins http://edamontology.org/topic_0078 Drug discovery http://edamontology.org/topic_3336 AlphaFold

	AI Artificial Intelligence Deep learning
Contact	training@biocommons.org.au
Audience	Researchers, computational biologists and bioinformaticians with an interest in structural biology or applications of deep learning and artificial intelligence to life science research.
Prerequisites	None
Technical requirements	None
Learning outcomes	By the end of this webinar you should be able to: ● Provide a high level description of how AlphaFold works ● Name ways to access AlphaFold ● Outline examples of how it can be used for protein structure/function analysis
Speakers	Dr Craig Morton, Principal Research Scientist and Drug Discovery Lead at the CSIRO
Related material	Highly accurate protein structure prediction with AlphaFold https://doi.org/10.1038/s41586-021-03819-2 ColabFold - Making protein folding accessible to all via Google Colab! https://youtu.be/Rfw7thgGTwI De novo design of transmembrane β barrels https://doi.org/10.1126/science.abc8182 Protein complex prediction with AlphaFold-Multimer https://doi.org/10.1101/2021.10.04.463034 Broadly applicable and accurate protein design by integrating structure prediction networks and diffusion generative models https://doi.org/10.1101/2022.12.09.519842 Evolutionary-scale prediction of atomic-level protein structure with a language model https://doi.org/10.1126/science.ade2574 Hallucinating symmetric protein assemblies https://doi.org/10.1126/science.add1964