Addendum: Accurate structure prediction of biomolecular interactions with AlphaFold 3

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In our original article, we provided an extensive description in the Supplementary Information of pseudocode underlying the functioning of our AlphaFold3 model, which allows prediction of the structure of complexes including proteins, nucleic acids, small molecules, ions and modified residues. Accompanying release of the paper we provided free non-commercial access to the AlphaFold3 server (https://alphafoldserver.com/welcome). Google DeepMind has now released the underlying inference code, which can be accessed here: https://github.com/google-deepmind/alphafold3.