Review of: "Systematic identification of conditionally folded intrinsically disordered regions by AlphaFold2"

Keiichi Homma

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The authors of the manuscript applied AlphaFold2 predictions of human protein structures to intrinsically disordered regions (IDRs). Their conclusion that AlphaFold2 identifies conditionally folded IDRs is very interesting. I also find it illuminating that 80% of IDRs in prokaryotic proteins conditionally fold, while less than 20% of IDRs in eukaryotic proteins do. Unfortunately the persuasive power of the manuscript suffers from their investigation of only a handful of examples of IDRs known to fold. If they analyze all available IDRs that have been reported to fold or at least a randomly selected subset, the conclusion will be far more convincing.