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Order in disorder revealed by evolutionary couplings

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Ágnes Tóth-Petróczy did her PhD, at the Weizmann Institute of Science, Rehovot, Israel. She studied the paths of evolving protein sequences under the supervision of Prof. Tawfik. In 2014, she moved to Harvard University in Boston to start a postdoctorat in the group of Prof Marks. As postdoctoral research fellow, she studied the structured states of disordered proteins from genomic sequences. From 2016 to 2018 Ágnes Tóth-Petróczy was a Bioinformatic Case Analyst at Brigham Genomic Medicine (Harvard Medical School and Brigham and Women's Hospital). Since April 2018 she is a Research Group Leader at MPI-CBG.

Career advice:

Cartoon caption: "Do you need to be a superwoman to do it all? NO. Just prioritise, compartmentalise your time, and outsource what is not fun."

Abstract:

Protein flexibility ranges from simple hinge movements to functional disorder. Around half of all human proteins contain apparently disordered regions with little 3D or functional information, and many of these proteins are associated with disease.
Building on the evolutionary couplings approach previously successful in predicting 3D states of ordered proteins and RNA, we developed a method to predict the potential for ordered states for disordered proteins with sufficiently rich evolutionary information.
The approach is highly accurate (79%) for residue interactions as tested in more than 60 known disordered regions captured in a bound or specific condition. Assessing the potential for structure of more than 1,000 apparently disordered regions of human proteins reveals a continuum of structural order with at least 50% with clear propensity for three- or two-dimensional states. Co-evolutionary constraints reveal hitherto unseen structures of functional importance in disordered proteins.

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