New research brings order to disordered proteins

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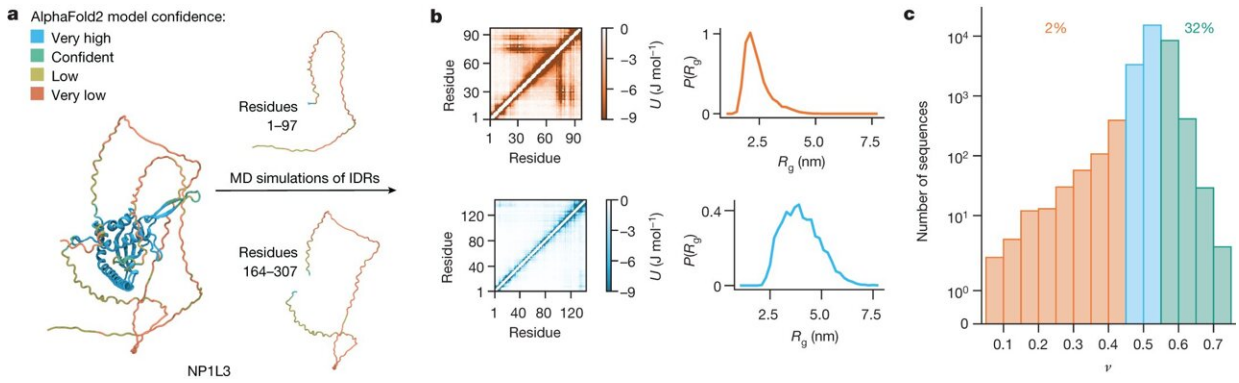

Schematic illustration of the approach used to obtain conformational properties for all of the IDRs in the human proteome. a, Selection of IDRs on the basis of the confidence of AlphaFold2 structural prediction, showing the selection of two IDRs from nucleosome assembly protein 1-like 3 (NP1L3; UniProt ID: Q99457) as an example. b, Molecular dynamics (MD) simulations of IDRs and calculation of conformational properties, showing interaction energy maps and distribution of the radius of gyration from the simulations of the two IDRs in NP1L3. Simulation data in b are averaged over five independent simulation replicates. c, Distribution of the Flory scaling exponent, ν, for 28,058 IDRs in the human proteome; note the logarithmic scale. A few IDRs have very small values of ν (0.3% have ν