John M Jumper

List of Publications by Year
in descending order

22 papers	30,105 citations	516710 16 h-index	677142 22 g-index
25 all docs	25 docs citations	25 times ranked	17073 citing authors

#	ARTICLE	IF	CITATIONS
1	Highly accurate protein structure prediction with AlphaFold. Nature, 2021, 596, 583-589.	27.8	17,754
2	AlphaFold Protein Structure Database: massively expanding the structural coverage of protein-sequence space with high-accuracy models. Nucleic Acids Research, 2022, 50, D439-D444.	14.5	3,692
3	Improved protein structure prediction using potentials from deep learning. Nature, 2020, 577, 706-710.	27.8	2,112
4	Highly accurate protein structure prediction for the human proteome. Nature, 2021, 596, 590-596.	27.8	1,773
5	Atomic-Level Characterization of the Structural Dynamics of Proteins. Science, 2010, 330, 341-346.	12.6	1,583
6	Effective gene expression prediction from sequence by integrating long-range interactions. Nature Methods, 2021, 18, 1196-1203.	19.0	385
7	Oncogenic Mutations Counteract Intrinsic Disorder in the EGFR Kinase and Promote Receptor Dimerization. Cell, 2012, 149, 860-870.	28.9	304
8	Protein structure prediction using multiple deep neural networks in the 13th Critical Assessment of Protein Structure Prediction (CASP13). Proteins: Structure, Function and Bioinformatics, 2019, 87, 1141-1148.	2.6	242
9	Applying and improving <scp>AlphaFold</scp> at <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1711-1721.	2.6	231
10	Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water. Science, 2017, 358, 238-241.	12.6	194
11	Protein structure predictions to atomic accuracy with AlphaFold. Nature Methods, 2022, 19, 11-12.	19.0	145
12	Loss of conformational entropy in protein folding calculated using realistic ensembles and its implications for NMR-based calculations. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15396-15401.	7.1	101
13	Free-Standing Kinked Silicon Nanowires for Probing Inter- and Intracellular Force Dynamics. Nano Letters, 2015, 15, 5492-5498.	9.1	43
14	Trajectory-based training enables protein simulations with accurate folding and Boltzmann ensembles in cpu-hours. PLoS Computational Biology, 2018, 14, e1006578.	3.2	33
15	Accurate calculation of side chain packing and free energy with applications to protein molecular dynamics. PLoS Computational Biology, 2018, 14, e1006342.	3.2	31
16	Response to Comment on â€œInnovative scattering analysis shows that hydrophobic disordered proteins are expanded in waterâ€• Science, 2018, 361, .	12.6	30
17	Structure of the decoy module of human glycoprotein 2 and uromodulin and its interaction with bacterial adhesin FimH. Nature Structural and Molecular Biology, 2022, 29, 190-193.	8.2	17
18	Discovery of archaeal fusexins homologous to eukaryotic HAP2/GCS1 gamete fusion proteins. Nature Communications, 2022, 13, .	12.8	17

#	Article	IF	Citations
19	Rotational Relaxation in <i>ortho</i>-Terphenyl: Using Atomistic Simulations to Bridge Theory and Experiment. Journal of Physical Chemistry B, 2013, 117, 12898-12907.	2.6	15
20	On the Interpretation of Force-Induced Unfolding Studies of Membrane Proteins Using Fast Simulations. Biophysical Journal, 2019, 117, 1429-1441.	0.5	12
21	A Membrane Burial Potential with H-Bonds and Applications to Curved Membranes and Fast Simulations. Biophysical Journal, 2018, 115, 1872-1884.	0.5	9
22	Structural basis of template strand deoxyuridine promoter recognition by a viral RNA polymerase. Nature Communications, 2022, 13, .	12.8	3