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	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
2	Protein structure predictions to atomic accuracy with AlphaFold. Nature Methods, 2022, 19, 11-12.	19.0	145
3	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
4	Structural basis of template strand deoxyuridine promoter recognition by a viral RNA polymerase. Nature Communications, 2022, 13, .	12.8	3
5	Discovery of archaeal fusexins homologous to eukaryotic HAP2/GCS1 gamete fusion proteins. Nature Communications, 2022, 13, .	12.8	17
6	Highly accurate protein structure prediction with AlphaFold. Nature, 2021, 596, 583-589.	27.8	17,754
7	Highly accurate protein structure prediction for the human proteome. Nature, 2021, 596, 590-596.	27.8	1,773
8	Applying and improving <scp>AlphaFold</scp> at <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1711-1721.	2.6	231
9	Effective gene expression prediction from sequence by integrating long-range interactions. Nature Methods, 2021, 18, 1196-1203.	19.0	385
10	Improved protein structure prediction using potentials from deep learning. Nature, 2020, 577, 706-710.	27.8	2,112
11	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
12	On the Interpretation of Force-Induced Unfolding Studies of Membrane Proteins Using Fast Simulations. Biophysical Journal, 2019, 117, 1429-1441.	0.5	12
13	A Membrane Burial Potential with H-Bonds and Applications to Curved Membranes and Fast Simulations. Biophysical Journal, 2018, 115, 1872-1884.	0.5	9
14	Accurate calculation of side chain packing and free energy with applications to protein molecular dynamics. PLoS Computational Biology, 2018, 14, e1006342.	3.2	31
15	Trajectory-based training enables protein simulations with accurate folding and Boltzmann ensembles in cpu-hours. PLoS Computational Biology, 2018, 14, e1006578.	3.2	33
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	Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water. Science, 2017, 358, 238-241.	12.6	194
18	Free-Standing Kinked Silicon Nanowires for Probing Inter- and Intracellular Force Dynamics. Nano Letters, 2015, 15, 5492-5498.	9.1	43

#	Article	IF	Citations
19	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
20	Rotational Relaxation in ortho-Terphenyl: Using Atomistic Simulations to Bridge Theory and Experiment. Journal of Physical Chemistry B, 2013, 117, 12898-12907.	2.6	15
21	Oncogenic Mutations Counteract Intrinsic Disorder in the EGFR Kinase and Promote Receptor Dimerization. Cell, 2012, 149, 860-870.	28.9	304
22	Atomic-Level Characterization of the Structural Dynamics of Proteins. Science, 2010, 330, 341-346.	12.6	1,583