Nicolas L Fawzi

List of Publications by Year
in descending order

64 papers	8,818 citations	101384 36 h-index	106150 65 g-index
76 all docs	76 docs citations	76 times ranked	7700 citing authors

#	Article	IF	Citations
1	Reversible Kinetic Trapping of FUS Biomolecular Condensates. Advanced Science, 2022, 9, e2104247.	5.6	28
2	An enhancer sequence in the intrinsically disordered region of <scp>FtsZ</scp> promotes polymerâ€guided substrate processing by <scp>ClpXP</scp> protease. Protein Science, 2022, 31, e4306.	3.1	4
3	Nâ€terminal acetylation modestly enhances phase separation and reduces aggregation of the lowâ€complexity domain of RNAâ€binding protein fused in sarcoma. Protein Science, 2021, 30, 1337-1349.	3.1	27
4	Membrane bending by protein phase separation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	125
5	A predictive coarse-grained model for position-specific effects of post-translational modifications. Biophysical Journal, 2021, 120, 1187-1197.	0.2	56
6	Interactions between ALS-linked FUS and nucleoporins are associated with defects in the nucleocytoplasmic transport pathway. Nature Neuroscience, 2021, 24, 1077-1088.	7.1	54
7	Phase separation of the LINE-1 ORF1 protein is mediated by the N-terminus and coiled-coil domain. Biophysical Journal, 2021, 120, 2181-2191.	0.2	32
8	CLAMP and Zelda function together to promote Drosophila zygotic genome activation. ELife, 2021, 10, .	2.8	40
9	The oncogenic transcription factor FUS-CHOP can undergo nuclear liquidâ€“liquid phase separation. Journal of Cell Science, 2021, 134, .	1.2	28
10	TDP-43 condensation properties specify its RNA-binding and regulatory repertoire. Cell, 2021, 184, 4680-4696.e22.	13.5	121
11	Biophysical studies of phase separation integrating experimental and computational methods. Current Opinion in Structural Biology, 2021, 70, 78-86.	2.6	35
12	Tyrosine phosphorylation regulates hnRNPA2 granule protein partitioning and reduces neurodegeneration. EMBO Journal, 2021, 40, e105001.	3.5	44
13	Molecular interactions contributing to FUS SYGQ LC-RGG phase separation and co-partitioning with RNA polymerase II heptads. Nature Structural and Molecular Biology, 2021, 28, 923-935.	3.6	75
14	The (un)structural biology of biomolecular liquid-liquid phase separation using NMR spectroscopy. Journal of Biological Chemistry, 2020, 295, 2375-2384.	1.6	87
15	Refining All-Atom Protein Force Fields for Polar-Rich, Prion-like, Low-Complexity Intrinsically Disordered Proteins. Journal of Physical Chemistry B, 2020, 124, 9505-9512.	1.2	40
16	Epigenetic cell fate in Candida albicans is controlled by transcription factor condensates acting at super-enhancer-like elements. Nature Microbiology, 2020, 5, 1374-1389.	5.9	34
17	Weak binding to the A2RE RNA rigidifies hnRNPA2 RRMs and reduces liquidâ€“liquid phase separation and aggregation. Nucleic Acids Research, 2020, 48, 10542-10554.	6.5	12
18	Molecular Details of Protein Condensates Probed by Microsecond Long Atomistic Simulations. Journal of Physical Chemistry B, 2020, 124, 11671-11679.	1.2	127

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19	TDP-43 Î±-helical structure tunes liquidâ€“liquid phase separation and function. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5883-5894.	3.3	258
20	SARSâ€CoVâ€2 nucleocapsid protein phaseâ€separates with RNA and with human hnRNPs. EMBO Journal, 2020, 39, e106478.	3.5	194
21	Molecular interactions underlying liquidâˆ'liquid phase separation of the FUS low-complexity domain. Nature Structural and Molecular Biology, 2019, 26, 637-648.	3.6	463
22	Physiological, Pathological, and Targetable Membraneless Organelles in Neurons. Trends in Neurosciences, 2019, 42, 693-708.	4.2	83
23	Phase separation in biology and diseaseâ€"a symposium report. Annals of the New York Academy of Sciences, 2019, 1452, 3-11.	1.8	14
24	EGFP insertional mutagenesis reveals multiple FXR2P fibrillar states with differing ribosome association in neurons. Biology Open, 2019, 8, .	0.6	1
25	Meta-analysis of Genetic Modifiers Reveals Candidate Dysregulated Pathways in Amyotrophic Lateral Sclerosis. Neuroscience, 2019, 396, A3-A20.	1.1	17
26	Nuclear Import Receptor Inhibits Phase Separation of FUS through Binding to Multiple Sites. Cell, 2018, 173, 693-705.e22.	13.5	253
27	A single Nâ€terminal phosphomimic disrupts TDPâ€43 polymerization, phase separation, and RNA splicing. EMBO Journal, 2018, 37, .	3.5	297
28	Mechanistic View of hnRNPA2 Low-Complexity Domain Structure, Interactions, and Phase Separation Altered by Mutation and Arginine Methylation. Molecular Cell, 2018, 69, 465-479.e7.	4.5	312
29	Synthesis and Characterization of a Magnetically Active ¹⁹F Molecular Beacon. Bioconjugate Chemistry, 2018, 29, 335-342.	1.8	9
30	Propyl-5-hydroxy-3-methyl-1-phenyl-1H-pyrazole-4-carbodithioate (HMPC): a new bacteriostatic agent against methicillinâ€"resistant Staphylococcus aureus. Scientific Reports, 2018, 8, 7062.	1.6	6
31	Protein Phase Separation: A New Phase in Cell Biology. Trends in Cell Biology, 2018, 28, 420-435.	3.6	1,439
32	Differential Occupancy of Two GA-Binding Proteins Promotes Targeting of the Drosophila Dosage Compensation Complex to the Male X Chromosome. Cell Reports, 2018, 22, 3227-3239.	2.9	39
33	Lysines in the RNA Polymerase II C-Terminal Domain Contribute to TAF15 Fibril Recruitment. Biochemistry, 2018, 57, 2549-2563.	1.2	31
34	The SH3 domain of Fyn kinase interacts with and induces liquidâ€“liquid phase separation of the low-complexity domain of hnRNPA2. Journal of Biological Chemistry, 2018, 293, 19522-19531.	1.6	38
35	Mice with endogenous <scp>TDP</scp> â€43 mutations exhibit gain of splicing function and characteristics of amyotrophic lateral sclerosis. EMBO Journal, 2018, 37, .	3.5	129
36	Protein quality and miRNA slicing get into phase. Nature Cell Biology, 2018, 20, 635-637.	4.6	7

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37	Probing the Atomic Structure of Transient Protein Contacts by Paramagnetic Relaxation Enhancement Solution NMR. Methods in Molecular Biology, 2018, 1688, 243-255.	0.4	10
38	Phase Separation of C9orf72 Dipeptide Repeats Perturbs Stress Granule Dynamics. Molecular Cell, 2017, 65, 1044-1055.e5.	4.5	437
39	Phosphorylation of the <scp>FUS</scp> lowâ€complexity domain disrupts phase separation, aggregation, and toxicity. EMBO Journal, 2017, 36, 2951-2967.	3.5	544
40	ALS Mutations Disrupt Phase Separation Mediated by Î±-Helical Structure in the TDP-43 Low-Complexity C-Terminal Domain. Structure, 2016, 24, 1537-1549.	1.6	617
41	Residue-by-Residue View of InÂVitro FUS Granules that Bind the C-Terminal Domain of RNA Polymerase II. Molecular Cell, 2015, 60, 231-241.	4.5	737
42	Characterizing Methylâ€Bearing Side Chain Contacts and Dynamics Mediating Amyloid Î² Protofibril Interactions Using ¹³C_{methyl}â€DEST and Lifetime Line Broadening. Angewandte Chemie - International Edition, 2014, 53, 10345-10349.	7.2	45
43	The C-Terminal Threonine of AÎ²43 Nucleates Toxic Aggregation via Structural and Dynamical Changes in Monomers and Protofibrils. Biochemistry, 2014, 53, 3095-3105.	1.2	36
44	Probing the transient dark state of substrate binding to GroEL by relaxation-based solution NMR. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11361-11366.	3.3	76
45	Coarse-Grained Simulations of Protein Aggregation. Methods in Molecular Biology, 2012, 899, 453-470.	0.4	3
46	Probing exchange kinetics and atomic resolution dynamics in high-molecular-weight complexes using dark-state exchange saturation transfer NMR spectroscopy. Nature Protocols, 2012, 7, 1523-1533.	5.5	98
47	An efficient protocol for incorporation of an unnatural amino acid in perdeuterated recombinant proteins using glucose-based media. Journal of Biomolecular NMR, 2012, 52, 191-195.	1.6	15
48	Homogeneous and Heterogeneous Tertiary Structure Ensembles of Amyloid-Î² Peptides. Biochemistry, 2011, 50, 7612-7628.	1.2	130
49	Atomic-resolution dynamics on the surface of amyloid-Î² protofibrils probed by solution NMR. Nature, 2011, 480, 268-272.	13.7	374
50	A rigid disulfide-linked nitroxide side chain simplifies the quantitative analysis of PRE data. Journal of Biomolecular NMR, 2011, 51, 105-114.	1.6	56
51	Automated sequence- and stereo-specific assignment of methyl-labeled proteins by paramagnetic relaxation and methylâ€“methyl nuclear overhauser enhancement spectroscopy. Journal of Biomolecular NMR, 2011, 51, 319-328.	1.6	51
52	How hot? Systematic convergence of the replica exchange method using multiple reservoirs. Journal of Computational Chemistry, 2010, 31, 620-627.	1.5	19
53	Mechanistic details of a proteinâ€“protein association pathway revealed by paramagnetic relaxation enhancement titration measurements. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1379-1384.	3.3	80
54	Kinetics of Amyloid Î² Monomer-to-Oligomer Exchange by NMR Relaxation. Journal of the American Chemical Society, 2010, 132, 9948-9951.	6.6	179

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55	A coarseâ€grained Î±â€carbon protein model with anisotropic hydrogenâ€bonding. Proteins: Structure, Function and Bioinformatics, 2008, 70, 626-638.	1.5	48
56	Protofibril Assemblies of the Arctic, Dutch, and Flemish Mutants of the Alzheimer's AÎ²1â€“40 Peptide. Biophysical Journal, 2008, 94, 2007-2016.	0.2	54
57	Structure and Dynamics of the AÎ²_{21â€“30} Peptide from the Interplay of NMR Experiments and Molecular Simulations. Journal of the American Chemical Society, 2008, 130, 6145-6158.	6.6	153
58	Contrasting Disease and Nondisease Protein Aggregation by Molecular Simulation. Accounts of Chemical Research, 2008, 41, 1037-1047.	7.6	34
59	Determining the Critical Nucleus and Mechanism of Fibril Elongation of the Alzheimerâ€™s AÎ²1â€“40 Peptide. Journal of Molecular Biology, 2007, 365, 535-550.	2.0	88
60	Hydrophobic Potential of Mean Force as a Solvation Function for Protein Structure Prediction. Structure, 2007, 15, 727-740.	1.6	52
61	Optimization of DsRed production inEscherichia coli: Effect of ribosome binding site sequestration on translation efficiency. Biotechnology and Bioengineering, 2005, 92, 553-558.	1.7	27
62	Protein folding by distributed computing and the denatured state ensemble. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16684-16689.	3.3	22
63	Influence of denatured and intermediate states of folding on protein aggregation. Protein Science, 2005, 14, 993-1003.	3.1	45
64	Coarse-grained sequences for protein folding and design. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10712-10717.	3.3	109