

Nicolas L Fawzi

List of Publications by Year in descending order

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64
papers

8,818
citations

101543

36
h-index

106344

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. <i>Advanced Science</i> , 2022, 9, e2104247.	11.2	28
2	An enhancer sequence in the intrinsically disordered region of <scp>FtsZ</scp> promotes polymerâ€guided substrate processing by <scp>ClpXP</scp> protease. <i>Protein Science</i> , 2022, 31, e4306.	7.6	4
3	Nâ€terminal acetylation modestly enhances phase separation and reduces aggregation of the lowâ€complexity domain of RNAâ€binding protein fused in sarcoma. <i>Protein Science</i> , 2021, 30, 1337-1349.	7.6	27
4	Membrane bending by protein phase separation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	125
5	A predictive coarse-grained model for position-specific effects of post-translational modifications. <i>Biophysical Journal</i> , 2021, 120, 1187-1197.	0.5	56
6	Interactions between ALS-linked FUS and nucleoporins are associated with defects in the nucleocytoplasmic transport pathway. <i>Nature Neuroscience</i> , 2021, 24, 1077-1088.	14.8	54
7	Phase separation of the LINE-1 ORF1 protein is mediated by the N-terminus and coiled-coil domain. <i>Biophysical Journal</i> , 2021, 120, 2181-2191.	0.5	32
8	CLAMP and Zelda function together to promote <i>Drosophila</i> zygotic genome activation. <i>ELife</i> , 2021, 10, .	6.0	40
9	The oncogenic transcription factor FUS-CHOP can undergo nuclear liquidâ€liquid phase separation. <i>Journal of Cell Science</i> , 2021, 134, .	2.0	28
10	TDP-43 condensation properties specify its RNA-binding and regulatory repertoire. <i>Cell</i> , 2021, 184, 4680-4696.e22.	28.9	121
11	Biophysical studies of phase separation integrating experimental and computational methods. <i>Current Opinion in Structural Biology</i> , 2021, 70, 78-86.	5.7	35
12	Tyrosine phosphorylation regulates hnRNPA2 granule protein partitioning and reduces neurodegeneration. <i>EMBO Journal</i> , 2021, 40, e105001.	7.8	44
13	Molecular interactions contributing to FUS SYGQ LC-RGG phase separation and co-partitioning with RNA polymerase II heptads. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 923-935.	8.2	75
14	The (un)structural biology of biomolecular liquid-liquid phase separation using NMR spectroscopy. <i>Journal of Biological Chemistry</i> , 2020, 295, 2375-2384.	3.4	87
15	Refining All-Atom Protein Force Fields for Polar-Rich, Prion-like, Low-Complexity Intrinsically Disordered Proteins. <i>Journal of Physical Chemistry B</i> , 2020, 124, 9505-9512.	2.6	40
16	Epigenetic cell fate in <i>Candida albicans</i> is controlled by transcription factor condensates acting at super-enhancer-like elements. <i>Nature Microbiology</i> , 2020, 5, 1374-1389.	13.3	34
17	Weak binding to the A2RE RNA rigidifies hnRNPA2 RRM and reduces liquidâ€liquid phase separation and aggregation. <i>Nucleic Acids Research</i> , 2020, 48, 10542-10554.	14.5	12
18	Molecular Details of Protein Condensates Probed by Microsecond Long Atomistic Simulations. <i>Journal of Physical Chemistry B</i> , 2020, 124, 11671-11679.	2.6	127

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19	TDP-43 α -helical structure tunes liquid-liquid phase separation and function. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5883-5894.	7.1	258
20	SARS-CoV-2 nucleocapsid protein phase-separates with RNA and with human hnRNPs. EMBO Journal, 2020, 39, e106478.	7.8	194
21	Molecular interactions underlying liquid-liquid phase separation of the FUS low-complexity domain. Nature Structural and Molecular Biology, 2019, 26, 637-648.	8.2	463
22	Physiological, Pathological, and Targetable Membraneless Organelles in Neurons. Trends in Neurosciences, 2019, 42, 693-708.	8.6	83
23	Phase separation in biology and disease—a symposium report. Annals of the New York Academy of Sciences, 2019, 1452, 3-11.	3.8	14
24	EGFP insertional mutagenesis reveals multiple FXR2P fibrillar states with differing ribosome association in neurons. Biology Open, 2019, 8, .	1.2	1
25	Meta-analysis of Genetic Modifiers Reveals Candidate Dysregulated Pathways in Amyotrophic Lateral Sclerosis. Neuroscience, 2019, 396, A3-A20.	2.3	17
26	Nuclear Import Receptor Inhibits Phase Separation of FUS through Binding to Multiple Sites. Cell, 2018, 173, 693-705.e22.	28.9	253
27	A single N-terminal phosphomimic disrupts TDP α 43 polymerization, phase separation, and RNA splicing. EMBO Journal, 2018, 37, .	7.8	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.	9.7	312
29	Synthesis and Characterization of a Magnetically Active ¹⁹ F Molecular Beacon. Bioconjugate Chemistry, 2018, 29, 335-342.	3.6	9
30	Propyl-5-hydroxy-3-methyl-1-phenyl-1H-pyrazole-4-carbodithioate (HMPC): a new bacteriostatic agent against methicillin-resistant Staphylococcus aureus. Scientific Reports, 2018, 8, 7062.	3.3	6
31	Protein Phase Separation: A New Phase in Cell Biology. Trends in Cell Biology, 2018, 28, 420-435.	7.9	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.	6.4	39
33	Lysines in the RNA Polymerase II C-Terminal Domain Contribute to TAF15 Fibril Recruitment. Biochemistry, 2018, 57, 2549-2563.	2.5	31
34	The SH3 domain of Fyn kinase interacts with and induces liquid-liquid phase separation of the low-complexity domain of hnRNPA2. Journal of Biological Chemistry, 2018, 293, 19522-19531.	3.4	38
35	Mice with endogenous α TDP α 43 mutations exhibit gain of splicing function and characteristics of amyotrophic lateral sclerosis. EMBO Journal, 2018, 37, .	7.8	129
36	Protein quality and miRNA slicing get into phase. Nature Cell Biology, 2018, 20, 635-637.	10.3	7

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37	Probing the Atomic Structure of Transient Protein Contacts by Paramagnetic Relaxation Enhancement Solution NMR. <i>Methods in Molecular Biology</i> , 2018, 1688, 243-255.	0.9	10
38	Phase Separation of C9orf72 Dipeptide Repeats Perturbs Stress Granule Dynamics. <i>Molecular Cell</i> , 2017, 65, 1044-1055.e5.	9.7	437
39	Phosphorylation of the <sc>FUS</sc> low-complexity domain disrupts phase separation, aggregation, and toxicity. <i>EMBO Journal</i> , 2017, 36, 2951-2967.	7.8	544
40	ALS Mutations Disrupt Phase Separation Mediated by α -Helical Structure in the TDP-43 Low-Complexity C-Terminal Domain. <i>Structure</i> , 2016, 24, 1537-1549.	3.3	617
41	Residue-by-Residue View of In Vitro FUS Granules that Bind the C-Terminal Domain of RNA Polymerase II. <i>Molecular Cell</i> , 2015, 60, 231-241.	9.7	737
42	Characterizing Methyl-Bearing Side Chain Contacts and Dynamics Mediating Amyloid β Protofibril Interactions Using ^{13}C -methyl-DEST and Lifetime Line Broadening. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 10345-10349.	13.8	45
43	The C-Terminal Threonine of $\text{A}\beta_{43}$ Nucleates Toxic Aggregation via Structural and Dynamical Changes in Monomers and Protofibrils. <i>Biochemistry</i> , 2014, 53, 3095-3105.	2.5	36
44	Probing the transient dark state of substrate binding to GroEL by relaxation-based solution NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11361-11366.	7.1	76
45	Coarse-Grained Simulations of Protein Aggregation. <i>Methods in Molecular Biology</i> , 2012, 899, 453-470.	0.9	3
46	Probing exchange kinetics and atomic resolution dynamics in high-molecular-weight complexes using dark-state exchange saturation transfer NMR spectroscopy. <i>Nature Protocols</i> , 2012, 7, 1523-1533.	12.0	98
47	An efficient protocol for incorporation of an unnatural amino acid in perdeuterated recombinant proteins using glucose-based media. <i>Journal of Biomolecular NMR</i> , 2012, 52, 191-195.	2.8	15
48	Homogeneous and Heterogeneous Tertiary Structure Ensembles of Amyloid- β Peptides. <i>Biochemistry</i> , 2011, 50, 7612-7628.	2.5	130
49	Atomic-resolution dynamics on the surface of amyloid- β protofibrils probed by solution NMR. <i>Nature</i> , 2011, 480, 268-272.	27.8	374
50	A rigid disulfide-linked nitroxide side chain simplifies the quantitative analysis of PRE data. <i>Journal of Biomolecular NMR</i> , 2011, 51, 105-114.	2.8	56
51	Automated sequence- and stereo-specific assignment of methyl-labeled proteins by paramagnetic relaxation and methyl-nuclear overhauser enhancement spectroscopy. <i>Journal of Biomolecular NMR</i> , 2011, 51, 319-328.	2.8	51
52	How hot? Systematic convergence of the replica exchange method using multiple reservoirs. <i>Journal of Computational Chemistry</i> , 2010, 31, 620-627.	3.3	19
53	Mechanistic details of a protein-protein association pathway revealed by paramagnetic relaxation enhancement titration measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1379-1384.	7.1	80
54	Kinetics of Amyloid β Monomer-to-Oligomer Exchange by NMR Relaxation. <i>Journal of the American Chemical Society</i> , 2010, 132, 9948-9951.	13.7	179

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55	A coarse-grained carbon protein model with anisotropic hydrogen bonding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 626-638.	2.6	48
56	Protofibril Assemblies of the Arctic, Dutch, and Flemish Mutants of the Alzheimer's A ²¹⁻⁴⁰ Peptide. <i>Biophysical Journal</i> , 2008, 94, 2007-2016.	0.5	54
57	Structure and Dynamics of the A ²¹⁻³⁰ Peptide from the Interplay of NMR Experiments and Molecular Simulations. <i>Journal of the American Chemical Society</i> , 2008, 130, 6145-6158.	13.7	153
58	Contrasting Disease and Nondisease Protein Aggregation by Molecular Simulation. <i>Accounts of Chemical Research</i> , 2008, 41, 1037-1047.	15.6	34
59	Determining the Critical Nucleus and Mechanism of Fibril Elongation of the Alzheimer's A ²¹⁻⁴⁰ Peptide. <i>Journal of Molecular Biology</i> , 2007, 365, 535-550.	4.2	88
60	Hydrophobic Potential of Mean Force as a Solvation Function for Protein Structure Prediction. <i>Structure</i> , 2007, 15, 727-740.	3.3	52
61	Optimization of DsRed production in <i>Escherichia coli</i> : Effect of ribosome binding site sequestration on translation efficiency. <i>Biotechnology and Bioengineering</i> , 2005, 92, 553-558.	3.3	27
62	Protein folding by distributed computing and the denatured state ensemble. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16684-16689.	7.1	22
63	Influence of denatured and intermediate states of folding on protein aggregation. <i>Protein Science</i> , 2005, 14, 993-1003.	7.6	45
64	Coarse-grained sequences for protein folding and design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10712-10717.	7.1	109