

# Alex S Holehouse

## List of Publications by Year in descending order

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Version: 2024-02-01

74  
papers

9,814  
citations

109264

35  
h-index

106281

65  
g-index

110  
all docs

110  
docs citations

110  
times ranked

7023  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Molecular Grammar Governing the Driving Forces for Phase Separation of Prion-like RNA Binding Proteins. <i>Cell</i> , 2018, 174, 688-699.e16.	13.5	1,372
2	Valence and patterning of aromatic residues determine the phase behavior of prion-like domains. <i>Science</i> , 2020, 367, 694-699.	6.0	675
3	Sequence Determinants of Intracellular Phase Separation by Complex Coacervation of a Disordered Protein. <i>Molecular Cell</i> , 2016, 63, 72-85.	4.5	622
4	RNA-Induced Conformational Switching and Clustering of G3BP Drive Stress Granule Assembly by Condensation. <i>Cell</i> , 2020, 181, 346-361.e17.	13.5	557
5	Physical Principles Underlying the Complex Biology of Intracellular Phase Transitions. <i>Annual Review of Biophysics</i> , 2020, 49, 107-133.	4.5	544
6	Phase separation of a yeast prion protein promotes cellular fitness. <i>Science</i> , 2018, 359, .	6.0	534
7	Intrinsically disordered linkers determine the interplay between phase separation and gelation in multivalent proteins. <i>ELife</i> , 2017, 6, .	2.8	514
8	Phase behaviour of disordered proteins underlying low density and high permeability of liquid organelles. <i>Nature Chemistry</i> , 2017, 9, 1118-1125.	6.6	447
9	Spontaneous driving forces give rise to protein <sup>+</sup> RNA condensates with coexisting phases and complex material properties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7889-7898.	3.3	365
10	CIDER: Resources to Analyze Sequence-Ensemble Relationships of Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2017, 112, 16-21.	0.2	356
11	The SARS-CoV-2 nucleocapsid protein is dynamic, disordered, and phase separates with RNA. <i>Nature Communications</i> , 2021, 12, 1936.	5.8	334
12	Sequence Determinants of the Conformational Properties of an Intrinsically Disordered Protein Prior to and upon Multisite Phosphorylation. <i>Journal of the American Chemical Society</i> , 2016, 138, 15323-15335.	6.6	217
13	Quantitative analysis of multilayer organization of proteins and RNA in nuclear speckles at super resolution. <i>Journal of Cell Science</i> , 2017, 130, 4180-4192.	1.2	206
14	Functional Implications of Intracellular Phase Transitions. <i>Biochemistry</i> , 2018, 57, 2415-2423.	1.2	189
15	Nucleo-cytoplasmic Partitioning of ARF Proteins Controls Auxin Responses in <i>Arabidopsis thaliana</i> . <i>Molecular Cell</i> , 2019, 76, 177-190.e5.	4.5	165
16	SARS-CoV-2 requires cholesterol for viral entry and pathological syncytia formation. <i>ELife</i> , 2021, 10, .	2.8	160
17	Intrinsically disordered protein regions and phase separation: sequence determinants of assembly or lack thereof. <i>Emerging Topics in Life Sciences</i> , 2020, 4, 307-329.	1.1	159
18	Phase Separation of Intrinsically Disordered Proteins. <i>Methods in Enzymology</i> , 2018, 611, 1-30.	0.4	141

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19	Arginine-Enriched Mixed-Charge Domains Provide Cohesion for Nuclear Speckle Condensation. <i>Molecular Cell</i> , 2020, 77, 1237-1250.e4.	4.5	137
20	A High-Throughput Mutational Scan of an Intrinsically Disordered Acidic Transcriptional Activation Domain. <i>Cell Systems</i> , 2018, 6, 444-455.e6.	2.9	135
21	Differential solvation of intrinsically disordered linkers drives the formation of spatially organized droplets in ternary systems of linear multivalent proteins. <i>New Journal of Physics</i> , 2018, 20, 045002.	1.2	115
22	Quantitative Assessments of the Distinct Contributions of Polypeptide Backbone Amides versus Side Chain Groups to Chain Expansion via Chemical Denaturation. <i>Journal of the American Chemical Society</i> , 2015, 137, 2984-2995.	6.6	104
23	Metapredict: a fast, accurate, and easy-to-use predictor of consensus disorder and structure. <i>Biophysical Journal</i> , 2021, 120, 4312-4319.	0.2	103
24	Transcription factor dimerization activates the p300 acetyltransferase. <i>Nature</i> , 2018, 562, 538-544.	13.7	100
25	A prion-like protein regulator of seed germination undergoes hydration-dependent phase separation. <i>Cell</i> , 2021, 184, 4284-4298.e27.	13.5	99
26	Collapse Transitions of Proteins and the Interplay Among Backbone, Sidechain, and Solvent Interactions. <i>Annual Review of Biophysics</i> , 2018, 47, 19-39.	4.5	98
27	Emerging Roles for Phase Separation in Plants. <i>Developmental Cell</i> , 2020, 55, 69-83.	3.1	84
28	Conformational preferences and phase behavior of intrinsically disordered low complexity sequences: insights from multiscale simulations. <i>Current Opinion in Structural Biology</i> , 2019, 56, 1-10.	2.6	82
29	Connecting Coil-to-Globule Transitions to Full Phase Diagrams for Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2020, 119, 402-418.	0.2	82
30	Sequence-to-Conformation Relationships of Disordered Regions Tethered to Folded Domains of Proteins. <i>Journal of Molecular Biology</i> , 2018, 430, 2403-2421.	2.0	60
31	Directed mutational scanning reveals a balance between acidic and hydrophobic residues in strong human activation domains. <i>Cell Systems</i> , 2022, 13, 334-345.e5.	2.9	58
32	Clustering of Aromatic Residues in Prion-like Domains Can Tune the Formation, State, and Organization of Biomolecular Condensates. <i>Biochemistry</i> , 2021, 60, 3566-3581.	1.2	56
33	Revealing the Hidden Sensitivity of Intrinsically Disordered Proteins to their Chemical Environment. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 10131-10136.	2.1	54
34	Biological Phase Separation and Biomolecular Condensates in Plants. <i>Annual Review of Plant Biology</i> , 2021, 72, 17-46.	8.6	53
35	Evolutionary fine-tuning of conformational ensembles in FimH during host-pathogen interactions. <i>Science Advances</i> , 2017, 3, e1601944.	4.7	50
36	Unfolded states under folding conditions accommodate sequence-specific conformational preferences with random coil-like dimensions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12301-12310.	3.3	50

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37	OSCAR Is a Receptor for Surfactant Protein D That Activates TNF- $\hat{\alpha}$ Release from Human CCR2+ Inflammatory Monocytes. <i>Journal of Immunology</i> , 2015, 194, 3317-3326.	0.4	47
38	ProteomeScout: a repository and analysis resource for post-translational modifications and proteins. <i>Nucleic Acids Research</i> , 2015, 43, D521-D530.	6.5	42
39	Controlling Structural Bias in Intrinsically Disordered Proteins Using Solution Space Scanning. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 1794-1805.	2.3	36
40	A survey-based analysis of the academic job market. <i>ELife</i> , 2020, 9, .	2.8	36
41	CIDER: Classification of Intrinsically Disordered Ensemble Regions. <i>Biophysical Journal</i> , 2015, 108, 228a.	0.2	32
42	Encoding phase transitions. <i>Nature Materials</i> , 2015, 14, 1083-1084.	13.3	28
43	Integrating single-molecule spectroscopy and simulations for the study of intrinsically disordered proteins. <i>Methods</i> , 2021, 193, 116-135.	1.9	25
44	Differing biophysical properties underpin the unique signaling potentials within the plant phytochrome photoreceptor families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	24
45	Folded domain charge properties influence the conformational behavior of disordered tails. <i>Current Research in Structural Biology</i> , 2021, 3, 216-228.	1.1	24
46	Adaptable P body physical states differentially regulate bicoid mRNA storage during early <i>Drosophila</i> development. <i>Developmental Cell</i> , 2021, 56, 2886-2901.e6.	3.1	24
47	Liquid Phase Partitioning in Virus Replication: Observations and Opportunities. <i>Annual Review of Virology</i> , 2022, 9, 285-306.	3.0	24
48	Design and characterization of mutant and wildtype huntingtin proteins produced from a toolkit of scalable eukaryotic expression systems. <i>Journal of Biological Chemistry</i> , 2019, 294, 6986-7001.	1.6	23
49	SWI/SNF senses carbon starvation with a pH-sensitive low-complexity sequence. <i>ELife</i> , 2022, 11, .	2.8	23
50	SAXS versus FRET: A Matter of Heterogeneity?. <i>Biophysical Journal</i> , 2017, 113, 971-973.	0.2	21
51	To Mix, or To Demix, That Is the Question. <i>Biophysical Journal</i> , 2017, 112, 565-567.	0.2	17
52	IDPs and IDRs in biomolecular condensates. , 2019, , 209-255.		13
53	Sequence determinants of in cell condensate morphology, dynamics, and oligomerization as measured by number and brightness analysis. <i>Cell Communication and Signaling</i> , 2021, 19, 65.	2.7	12
54	PARROT is a flexible recurrent neural network framework for analysis of large protein datasets. <i>ELife</i> , 2021, 10, .	2.8	12

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55	Analyzing the Sequences of Intrinsically Disordered Regions with CIDER and localCIDER. <i>Methods in Molecular Biology</i> , 2020, 2141, 103-126.	0.4	11
56	Investigating the ferric ion binding site of magnetite biomineralisation protein Mms6. <i>PLoS ONE</i> , 2020, 15, e0228708.	1.1	10
57	Reproducible Analysis of Post-Translational Modifications in Proteomes—Application to Human Mutations. <i>PLoS ONE</i> , 2015, 10, e0144692.	1.1	9
58	The Unfolded State of the C-Terminal Domain of L9 Expands at Low but Not at Elevated Temperatures. <i>Biophysical Journal</i> , 2018, 115, 655-663.	0.2	9
59	The Cold-Unfolded State Is Expanded but Contains Long- and Medium-Range Contacts and Is Poorly Described by Homopolymer Models. <i>Biochemistry</i> , 2020, 59, 3290-3299.	1.2	8
60	Protein products of nonstop mRNA disrupt nucleolar homeostasis. <i>Cell Stress and Chaperones</i> , 2021, 26, 549-561.	1.2	7
61	FUS Zigzags Its Way to Cross Beta. <i>Cell</i> , 2017, 171, 499-500.	13.5	4
62	Step on the cGAS! Viral inhibition of cGAS phase separation with cytosolic DNA. <i>Molecular Cell</i> , 2021, 81, 2688-2689.	4.5	3
63	Hydration-Dependent Phase Separation of a Prion-Like Protein Regulates Seed Germination During Water Stress. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3
64	Intrinsically disordered CO2 sensors. <i>Nature Cell Biology</i> , 2022, 24, 1013-1014.	4.6	2
65	Developing a novel integrated model of p38 MAPK and glucocorticoid signalling pathways. , 2012, , .		1
66	A General Framework for Predicting and Understanding Sequence-Encoded Phase Diagrams of Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2018, 114, 4a.	0.2	1
67	Large-Scale Analysis of the Evolution of Functions Mediated by Intrinsically Disordered Regions. <i>Biophysical Journal</i> , 2018, 114, 79a.	0.2	1
68	Hyperphosphorylation tunes TDP <sup>43</sup> solubility. <i>EMBO Journal</i> , 2022, 41, e111062.	3.5	1
69	Mapping from sequence to droplets. <i>Nature Reviews Molecular Cell Biology</i> , 2021, 22, 163-163.	16.1	0
70	A Phase-Separating Molecular Tether for Lariat Debranching Enzyme is Defective in Non-Photosensitive Trichothiodystrophy. <i>FASEB Journal</i> , 2021, 35, .	0.2	0
71	Investigating the ferric ion binding site of magnetite biomineralisation protein Mms6. , 2020, 15, e0228708.		0
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73	Investigating the ferric ion binding site of magnetite biomineralisation protein Mms6. , 2020, 15, e0228708.		0
74	Investigating the ferric ion binding site of magnetite biomineralisation protein Mms6. , 2020, 15, e0228708.		0