## Alex S Holehouse

List of Publications by Year in descending order

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109264 106281 9,814 74 35 65 citations h-index g-index papers 110 110 110 7023 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Directed mutational scanning reveals a balance between acidic and hydrophobic residues in strong human activation domains. Cell Systems, 2022, 13, 334-345.e5.	2.9	58
2	SWI/SNF senses carbon starvation with a pH-sensitive low-complexity sequence. ELife, 2022, 11, .	2.8	23
3	Hyperphosphorylation tunes TDPâ€43 solubility. EMBO Journal, 2022, 41, e111062.	3.5	1
4	Liquid Phase Partitioning in Virus Replication: Observations and Opportunities. Annual Review of Virology, 2022, 9, 285-306.	3.0	24
5	Intrinsically disordered CO2 sensors. Nature Cell Biology, 2022, 24, 1013-1014.	4.6	2
6	Mapping from sequence to droplets. Nature Reviews Molecular Cell Biology, 2021, 22, 163-163.	16.1	0
7	Protein products of nonstop mRNA disrupt nucleolar homeostasis. Cell Stress and Chaperones, 2021, 26, 549-561.	1.2	7
8	The SARS-CoV-2 nucleocapsid protein is dynamic, disordered, and phase separates with RNA. Nature Communications, 2021, 12, 1936.	5.8	334
9	SARS-CoV-2 requires cholesterol for viral entry and pathological syncytia formation. ELife, 2021, 10, .	2.8	160
10	A Phaseâ€Separating Molecular Tether for Lariat Debranching Enzyme is Defective in Nonâ€Photosensitive Trichothiodystrophy. FASEB Journal, 2021, 35, .	0.2	0
11	Differing biophysical properties underpin the unique signaling potentials within the plant phytochrome photoreceptor families. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	24
12	Biological Phase Separation and Biomolecular Condensates in Plants. Annual Review of Plant Biology, 2021, 72, 17-46.	8.6	53
13	Sequence determinants of in cell condensate morphology, dynamics, and oligomerization as measured by number and brightness analysis. Cell Communication and Signaling, 2021, 19, 65.	2.7	12
14	Step on the cGAS! Viral inhibition of cGAS phase separation with cytosolic DNA. Molecular Cell, 2021, 81, 2688-2689.	4.5	3
15	A prion-like protein regulator of seed germination undergoes hydration-dependent phase separation. Cell, 2021, 184, 4284-4298.e27.	13.5	99
16	PARROT is a flexible recurrent neural network framework for analysis of large protein datasets. ELife, 2021, 10, .	2.8	12
17	Metapredict: a fast, accurate, and easy-to-use predictor of consensus disorder and structure. Biophysical Journal, 2021, 120, 4312-4319.	0.2	103
18	Integrating single-molecule spectroscopy and simulations for the study of intrinsically disordered proteins. Methods, 2021, 193, 116-135.	1.9	25

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19	Folded domain charge properties influence the conformational behavior of disordered tails. Current Research in Structural Biology, 2021, 3, 216-228.	1.1	24
20	Adaptable P body physical states differentially regulate bicoid mRNA storage during early Drosophila development. Developmental Cell, 2021, 56, 2886-2901.e6.	3.1	24
21	Clustering of Aromatic Residues in Prion-like Domains Can Tune the Formation, State, and Organization of Biomolecular Condensates. Biochemistry, 2021, 60, 3566-3581.	1.2	56
22	Connecting Coil-to-Globule Transitions to Full Phase Diagrams for Intrinsically Disordered Proteins. Biophysical Journal, 2020, 119, 402-418.	0.2	82
23	Emerging Roles for Phase Separation in Plants. Developmental Cell, 2020, 55, 69-83.	3.1	84
24	Revealing the Hidden Sensitivity of Intrinsically Disordered Proteins to their Chemical Environment. Journal of Physical Chemistry Letters, 2020, 11, 10131-10136.	2.1	54
25	The Cold-Unfolded State Is Expanded but Contains Long- and Medium-Range Contacts and Is Poorly Described by Homopolymer Models. Biochemistry, 2020, 59, 3290-3299.	1.2	8
26	Investigating the ferric ion binding site of magnetite biomineralisation protein Mms6. PLoS ONE, 2020, 15, e0228708.	1.1	10
27	Valence and patterning of aromatic residues determine the phase behavior of prion-like domains. Science, 2020, 367, 694-699.	6.0	675
28	Arginine-Enriched Mixed-Charge Domains Provide Cohesion for Nuclear Speckle Condensation. Molecular Cell, 2020, 77, 1237-1250.e4.	4.5	137
29	Physical Principles Underlying the Complex Biology of Intracellular Phase Transitions. Annual Review of Biophysics, 2020, 49, 107-133.	4.5	544
30	Controlling Structural Bias in Intrinsically Disordered Proteins Using Solution Space Scanning. Journal of Chemical Theory and Computation, 2020, 16, 1794-1805.	2.3	36
31	RNA-Induced Conformational Switching and Clustering of G3BP Drive Stress Granule Assembly by Condensation. Cell, 2020, 181, 346-361.e17.	13.5	557
32	Analyzing the Sequences of Intrinsically Disordered Regions with CIDER and localCIDER. Methods in Molecular Biology, 2020, 2141, 103-126.	0.4	11
33	Intrinsically disordered protein regions and phase separation: sequence determinants of assembly or lack thereof. Emerging Topics in Life Sciences, 2020, 4, 307-329.	1.1	159
34	A survey-based analysis of the academic job market. ELife, 2020, 9, .	2.8	36
35	Investigating the ferric ion binding site of magnetite biomineralisation protein Mms6. , 2020, 15, e0228708.		0
36	Investigating the ferric ion binding site of magnetite biomineralisation protein Mms6. , 2020, 15, e0228708.		0

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37	Investigating the ferric ion binding site of magnetite biomineralisation protein Mms6., 2020, 15, e0228708.		О
38	Investigating the ferric ion binding site of magnetite biomineralisation protein Mms6. , 2020, 15, e0228708.		0
39	Nucleo-cytoplasmic Partitioning of ARF Proteins Controls Auxin Responses in Arabidopsis thaliana. Molecular Cell, 2019, 76, 177-190.e5.	4.5	165
40	Unfolded states under folding conditions accommodate sequence-specific conformational preferences with random coil-like dimensions. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12301-12310.	3.3	50
41	IDPs and IDRs in biomolecular condensates. , 2019, , 209-255.		13
42	Design and characterization of mutant and wildtype huntingtin proteins produced from a toolkit of scalable eukaryotic expression systems. Journal of Biological Chemistry, 2019, 294, 6986-7001.	1.6	23
43	Spontaneous driving forces give rise to proteinâ^'RNA condensates with coexisting phases and complex material properties. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7889-7898.	3.3	365
44	Conformational preferences and phase behavior of intrinsically disordered low complexity sequences: insights from multiscale simulations. Current Opinion in Structural Biology, 2019, 56, 1-10.	2.6	82
45	A General Framework for Predicting and Understanding Sequence-Encoded Phase Diagrams of Intrinsically Disordered Proteins. Biophysical Journal, 2018, 114, 4a.	0.2	1
46	Collapse Transitions of Proteins and the Interplay Among Backbone, Sidechain, and Solvent Interactions. Annual Review of Biophysics, 2018, 47, 19-39.	4.5	98
47	Functional Implications of Intracellular Phase Transitions. Biochemistry, 2018, 57, 2415-2423.	1.2	189
48	Phase separation of a yeast prion protein promotes cellular fitness. Science, 2018, 359, .	6.0	534
49	A High-Throughput Mutational Scan of an Intrinsically Disordered Acidic Transcriptional Activation Domain. Cell Systems, 2018, 6, 444-455.e6.	2.9	135
50	Differential solvation of intrinsically disordered linkers drives the formation of spatially organized droplets in ternary systems of linear multivalent proteins. New Journal of Physics, 2018, 20, 045002.	1.2	115
51	Phase Separation of Intrinsically Disordered Proteins. Methods in Enzymology, 2018, 611, 1-30.	0.4	141
52	Large-Scale Analysis of the Evolution of Functions Mediated by Intrinsically Disordered Regions. Biophysical Journal, 2018, 114, 79a.	0.2	1
53	Transcription factor dimerization activates the p300 acetyltransferase. Nature, 2018, 562, 538-544.	13.7	100
54	Sequence-to-Conformation Relationships of Disordered Regions Tethered to Folded Domains of Proteins. Journal of Molecular Biology, 2018, 430, 2403-2421.	2.0	60

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55	A Molecular Grammar Governing the Driving Forces for Phase Separation of Prion-like RNA Binding Proteins. Cell, 2018, 174, 688-699.e16.	13.5	1,372
56	The Unfolded State of the C-Terminal Domain of L9 Expands at Low but Not at Elevated Temperatures. Biophysical Journal, 2018, 115, 655-663.	0.2	9
57	CIDER: Resources to Analyze Sequence-Ensemble Relationships of Intrinsically Disordered Proteins. Biophysical Journal, 2017, 112, 16-21.	0.2	356
58	Evolutionary fine-tuning of conformational ensembles in FimH during host-pathogen interactions. Science Advances, 2017, 3, e1601944.	4.7	50
59	To Mix, or To Demix, That Is the Question. Biophysical Journal, 2017, 112, 565-567.	0.2	17
60	FUS Zigzags Its Way to Cross Beta. Cell, 2017, 171, 499-500.	13.5	4
61	SAXS versus FRET: A Matter of Heterogeneity?. Biophysical Journal, 2017, 113, 971-973.	0.2	21
62	Quantitative analysis of multilayer organization of proteins and RNA in nuclear speckles at super resolution. Journal of Cell Science, 2017, 130, 4180-4192.	1.2	206
63	Phase behaviour of disordered proteins underlying low density and high permeability of liquid organelles. Nature Chemistry, 2017, 9, 1118-1125.	6.6	447
64	Intrinsically disordered linkers determine the interplay between phase separation and gelation in multivalent proteins. ELife, $2017$ , $6$ , .	2.8	514
65	Sequence Determinants of Intracellular Phase Separation by Complex Coacervation of a Disordered Protein. Molecular Cell, 2016, 63, 72-85.	4.5	622
66	Sequence Determinants of the Conformational Properties of an Intrinsically Disordered Protein Prior to and upon Multisite Phosphorylation. Journal of the American Chemical Society, 2016, 138, 15323-15335.	6.6	217
67	CIDER: Classification of Intrinsically Disordered Ensemble Regions. Biophysical Journal, 2015, 108, 228a.	0.2	32
68	Reproducible Analysis of Post-Translational Modifications in Proteomesâ€"Application to Human Mutations. PLoS ONE, 2015, 10, e0144692.	1.1	9
69	OSCAR Is a Receptor for Surfactant Protein D That Activates TNF-α Release from Human CCR2+ Inflammatory Monocytes. Journal of Immunology, 2015, 194, 3317-3326.	0.4	47
70	Quantitative Assessments of the Distinct Contributions of Polypeptide Backbone Amides versus Side Chain Groups to Chain Expansion via Chemical Denaturation. Journal of the American Chemical Society, 2015, 137, 2984-2995.	6.6	104
71	ProteomeScout: a repository and analysis resource for post-translational modifications and proteins. Nucleic Acids Research, 2015, 43, D521-D530.	6.5	42
72	Encoding phase transitions. Nature Materials, 2015, 14, 1083-1084.	13.3	28

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73	Developing a novel integrated model of p38 MAPK and glucocorticoid signalling pathways. , 2012, , .		1
74	Hydration-Dependent Phase Separation of a Prion-Like Protein Regulates Seed Germination During Water Stress. SSRN Electronic Journal, 0, , .	0.4	3