

# Alan M Moses

## List of Publications by Year in descending order

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Version: 2024-02-01

70  
papers

8,299  
citations

101543

36  
h-index

95266

68  
g-index

84  
all docs

84  
docs citations

84  
times ranked

12340  
citing authors

#	ARTICLE	IF	CITATIONS
1	Stochastic models for single-cell data: Current challenges and the way forward. FEBS Journal, 2022, 289, 647-658.	4.7	6
2	Discovering molecular features of intrinsically disordered regions by using evolution for contrastive learning. PLoS Computational Biology, 2022, 18, e1010238.	3.2	16
3	Identifying molecular features that are associated with biological function of intrinsically disordered protein regions. ELife, 2021, 10, .	6.0	47
4	A flexible repertoire of transcription factor binding sites and a diversity threshold determines enhancer activity in embryonic stem cells. Genome Research, 2021, 31, 564-575.	5.5	36
5	A functionally divergent intrinsically disordered region underlying the conservation of stochastic signaling. PLoS Genetics, 2021, 17, e1009629.	3.5	6
6	A recurrent SHANK3 frameshift variant in Autism Spectrum Disorder. Npj Genomic Medicine, 2021, 6, 91.	3.8	9
7	Learning Biology Through Puzzle-solving: Unbiased Automatic Understanding of Microscopy Images with Self-supervised Learning. Microscopy and Microanalysis, 2020, 26, 690-692.	0.4	0
8	Phase Separation as a Missing Mechanism for Interpretation of Disease Mutations. Cell, 2020, 183, 1742-1756.	28.9	147
9	Exploring whole-genome duplicate gene retention with complex genetic interaction analysis. Science, 2020, 368, .	12.6	79
10	Condensation of Ded1p Promotes a Translational Switch from Housekeeping to Stress Protein Production. Cell, 2020, 181, 818-831.e19.	28.9	130
11	Cdk1 Controls Global Epigenetic Landscape in Embryonic Stem Cells. Molecular Cell, 2020, 78, 459-476.e13.	9.7	76
12	Whence Blobs? Phylogenetics of functional protein condensates. Biochemical Society Transactions, 2020, 48, 2151-2158.	3.4	7
13	Entropy and Information within Intrinsically Disordered Protein Regions. Entropy, 2019, 21, 662.	2.2	41
14	YeastSpotter: accurate and parameter-free web segmentation for microscopy images of yeast cells. Bioinformatics, 2019, 35, 4525-4527.	4.1	70
15	Learning unsupervised feature representations for single cell microscopy images with paired cell inpainting. PLoS Computational Biology, 2019, 15, e1007348.	3.2	69
16	A Noisy Analog-to-Digital Converter Connects Cytosolic Calcium Bursts to Transcription Factor Nuclear Localization Pulses in Yeast. G3: Genes, Genomes, Genetics, 2019, 9, 561-570.	1.8	4
17	Variational infinite heterogeneous mixture model for semi-supervised clustering of heart enhancers. Bioinformatics, 2019, 35, 3232-3239.	4.1	1
18	Proteome-wide signatures of function in highly diverged intrinsically disordered regions. ELife, 2019, 8, .	6.0	131

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19	NoLogo: a new statistical model highlights the diversity and suggests new classes of Crm1-dependent nuclear export signals. <i>BMC Bioinformatics</i> , 2018, 19, 65.	2.6	8
20	Short linear motifs in intrinsically disordered regions modulate HOG signaling capacity. <i>BMC Systems Biology</i> , 2018, 12, 75.	3.0	11
21	Integrating images from multiple microscopy screens reveals diverse patterns of change in the subcellular localization of proteins. <i>ELife</i> , 2018, 7, .	6.0	24
22	Extracting and Integrating Protein Localization Changes from Multiple Image Screens of Yeast Cells. <i>Bio-protocol</i> , 2018, 8, e3022.	0.4	1
23	Selection maintains signaling function of a highly diverged intrinsically disordered region. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1450-E1459.	7.1	65
24	Introduction of Premature Stop Codons as an Evolutionary Strategy To Rescue Signaling Network Function. <i>ACS Synthetic Biology</i> , 2017, 6, 446-454.	3.8	3
25	Functional Analysis of Kinases and Transcription Factors in <i>Saccharomyces cerevisiae</i> Using an Integrated Overexpression Library. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 911-921.	1.8	19
26	Parallel reorganization of protein function in the spindle checkpoint pathway through evolutionary paths in the fitness landscape that appear neutral in laboratory experiments. <i>PLoS Genetics</i> , 2017, 13, e1006735.	3.5	9
27	New <i>BAR</i> tools for mining expression data and exploring <i>Cis</i> elements in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2016, 88, 490-504.	5.7	75
28	Decreased Transcription Factor Binding Levels Nearby Primate Pseudogenes Suggest Regulatory Degeneration. <i>Molecular Biology and Evolution</i> , 2016, 33, 1478-1485.	8.9	1
29	An Unsupervised kNN Method to Systematically Detect Changes in Protein Localization in High-Throughput Microscopy Images. <i>PLoS ONE</i> , 2016, 11, e0158712.	2.5	11
30	Short linear motifs – ex nihilo evolution of protein regulation. <i>Cell Communication and Signaling</i> , 2015, 13, 43.	6.5	171
31	Yeast Proteome Dynamics from Single Cell Imaging and Automated Analysis. <i>Cell</i> , 2015, 161, 1413-1424.	28.9	254
32	Computational learning on specificity-determining residue-nucleotide interactions. <i>Nucleic Acids Research</i> , 2015, 43, gkv1134.	14.5	20
33	The Structure of an NDR/LATS Kinase–Mob Complex Reveals a Novel Kinase–Coactivator System and Substrate Docking Mechanism. <i>PLoS Biology</i> , 2015, 13, e1002146.	5.6	45
34	Polymorphism Analysis Reveals Reduced Negative Selection and Elevated Rate of Insertions and Deletions in Intrinsically Disordered Protein Regions. <i>Genome Biology and Evolution</i> , 2015, 7, 1815-1826.	2.5	27
35	CYCLoPs: A Comprehensive Database Constructed from Automated Analysis of Protein Abundance and Subcellular Localization Patterns in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1223-1232.	1.8	69
36	Local statistics allow quantification of cell-to-cell variability from high-throughput microscope images. <i>Bioinformatics</i> , 2015, 31, 940-947.	4.1	16

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37	Detecting Functional Divergence after Gene Duplication through Evolutionary Changes in Posttranslational Regulatory Sequences. <i>PLoS Computational Biology</i> , 2014, 10, e1003977.	3.2	39
38	Turnover of protein phosphorylation evolving under stabilizing selection. <i>Frontiers in Genetics</i> , 2014, 5, 245.	2.3	43
39	Insights into molecular evolution from yeast genomics. <i>Yeast</i> , 2014, 31, 233-241.	1.7	6
40	A High-Definition View of Functional Genetic Variation from Natural Yeast Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 872-888.	8.9	328
41	A Mesoscale Abscisic Acid Hormone Interactome Reveals a Dynamic Signaling Landscape in Arabidopsis. <i>Developmental Cell</i> , 2014, 29, 360-372.	7.0	109
42	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. <i>Nature Genetics</i> , 2013, 45, 891-898.	21.4	350
43	Unsupervised Clustering of Subcellular Protein Expression Patterns in High-Throughput Microscopy Images Reveals Protein Complexes and Functional Relationships between Proteins. <i>PLoS Computational Biology</i> , 2013, 9, e1003085.	3.2	33
44	Proteome-Wide Discovery of Evolutionary Conserved Sequences in Disordered Regions. <i>Science Signaling</i> , 2012, 5, rs1.	3.6	109
45	Predicting kinase substrates using conservation of local motif density. <i>Bioinformatics</i> , 2012, 28, 962-969.	4.1	15
46	A quantitative literature-curated gold standard for kinase-substrate pairs. <i>Genome Biology</i> , 2011, 12, R39.	9.6	56
47	Modeling the evolution of a classic genetic switch. <i>BMC Systems Biology</i> , 2011, 5, 24.	3.0	5
48	Whole-Genome Analysis Reveals That Active Heat Shock Factor Binding Sites Are Mostly Associated with Non-Heat Shock Genes in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2011, 6, e15934.	2.5	78
49	Revealing the genetic structure of a trait by sequencing a population under selection. <i>Genome Research</i> , 2011, 21, 1131-1138.	5.5	263
50	In vitro evolution goes deep. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 8071-8072.	7.1	2
51	Polymorphism, Divergence, and the Role of Recombination in <i>Saccharomyces cerevisiae</i> Genome Evolution. <i>Molecular Biology and Evolution</i> , 2011, 28, 1745-1754.	8.9	36
52	Trait Variation in Yeast Is Defined by Population History. <i>PLoS Genetics</i> , 2011, 7, e1002111.	3.5	311
53	Moving from transcriptional to phospho-evolution: generalizing regulatory evolution?. <i>Trends in Genetics</i> , 2010, 26, 462-467.	6.7	48
54	Evidence for widespread adaptive evolution of gene expression in budding yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2977-2982.	7.1	161

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55	Evolution of Characterized Phosphorylation Sites in Budding Yeast. <i>Molecular Biology and Evolution</i> , 2010, 27, 2027-2037.	8.9	62
56	NLStradamus: a simple Hidden Markov Model for nuclear localization signal prediction. <i>BMC Bioinformatics</i> , 2009, 10, 202.	2.6	526
57	Statistical tests for natural selection on regulatory regions based on the strength of transcription factor binding sites. <i>BMC Evolutionary Biology</i> , 2009, 9, 286.	3.2	26
58	Population genomics of domestic and wild yeasts. <i>Nature</i> , 2009, 458, 337-341.	27.8	1,391
59	Inferring Selection on Amino Acid Preference in Protein Domains. <i>Molecular Biology and Evolution</i> , 2008, 26, 527-536.	8.9	9
60	Regulatory evolution in proteins by turnover and lineage-specific changes of cyclin-dependent kinase consensus sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17713-17718.	7.1	62
61	TreeFam: 2008 Update. <i>Nucleic Acids Research</i> , 2007, 36, D735-D740.	14.5	294
62	Clustering of phosphorylation site recognition motifs can be exploited to predict the targets of cyclin-dependent kinase. <i>Genome Biology</i> , 2007, 8, R23.	9.6	74
63	Determining Physical Constraints in Transcriptional Initiation Complexes Using DNA Sequence Analysis. <i>PLoS ONE</i> , 2007, 2, e1199.	2.5	8
64	In vivo enhancer analysis of human conserved non-coding sequences. <i>Nature</i> , 2006, 444, 499-502.	27.8	1,072
65	Widespread Discordance of Gene Trees with Species Tree in <i>Drosophila</i> : Evidence for Incomplete Lineage Sorting. <i>PLoS Genetics</i> , 2006, 2, e173.	3.5	319
66	Large-Scale Turnover of Functional Transcription Factor Binding Sites in <i>Drosophila</i> . <i>PLoS Computational Biology</i> , 2006, 2, e130.	3.2	231
67	Conservation and Evolution of Cis-Regulatory Systems in Ascomycete Fungi. <i>PLoS Biology</i> , 2004, 2, e398.	5.6	207
68	MONKEY: identifying conserved transcription-factor binding sites in multiple alignments using a binding site-specific evolutionary model. <i>Genome Biology</i> , 2004, 5, R98.	9.6	134
69	Position specific variation in the rate of evolution in transcription factor binding sites. <i>BMC Evolutionary Biology</i> , 2003, 3, 19.	3.2	130
70	Statistical Modeling and Machine Learning for Molecular Biology. , 0, , .		10