

# Alexander J Hartemink

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

5,276  
citations

201674

27  
h-index

315739

38  
g-index

52  
all docs

52  
docs citations

52  
times ranked

10247  
citing authors

#	ARTICLE	IF	CITATIONS
1	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	5.5	1,708
2	Convergent transcriptional specializations in the brains of humans and song-learning birds. <i>Science</i> , 2014, 346, 1256846.	12.6	379
3	Computational and experimental identification of novel human imprinted genes. <i>Genome Research</i> , 2007, 17, 1723-1730.	5.5	344
4	Global control of cell-cycle transcription by coupled CDK and network oscillators. <i>Nature</i> , 2008, 453, 944-947.	27.8	269
5	<i>Drosophila</i> ORC localizes to open chromatin and marks sites of cohesin complex loading. <i>Genome Research</i> , 2010, 20, 201-211.	5.5	248
6	Genome-wide prediction of imprinted murine genes. <i>Genome Research</i> , 2005, 15, 875-884.	5.5	237
7	Synergistic and tunable human gene activation by combinations of synthetic transcription factors. <i>Nature Methods</i> , 2013, 10, 239-242.	19.0	222
8	SLICER: inferring branched, nonlinear cellular trajectories from single cell RNA-seq data. <i>Genome Biology</i> , 2016, 17, 106.	8.8	155
9	Reverse engineering gene regulatory networks. <i>Nature Biotechnology</i> , 2005, 23, 554-555.	17.5	141
10	MATCHER: manifold alignment reveals correspondence between single cell transcriptome and epigenome dynamics. <i>Genome Biology</i> , 2017, 18, 138.	8.8	131
11	Distinguishing direct versus indirect transcription factor-DNA interactions. <i>Genome Research</i> , 2009, 19, 2090-2100.	5.5	128
12	Computational Inference of Neural Information Flow Networks. <i>PLoS Computational Biology</i> , 2006, 2, e161.	3.2	124
13	Glucocorticoid receptor recruits to enhancers and drives activation by motif-directed binding. <i>Genome Research</i> , 2018, 28, 1272-1284.	5.5	102
14	Core and region-enriched networks of behaviorally regulated genes and the singing genome. <i>Science</i> , 2014, 346, 1256780.	12.6	97
15	An ensemble model of competitive multi-factor binding of the genome. <i>Genome Research</i> , 2009, 19, 2101-2112.	5.5	94
16	INFORMATIVE STRUCTURE PRIORS: JOINT LEARNING OF DYNAMIC REGULATORY NETWORKS FROM MULTIPLE TYPES OF DATA. , 2004, , .		87
17	A Nucleosome-Guided Map of Transcription Factor Binding Sites in Yeast. <i>PLoS Computational Biology</i> , 2007, 3, e215.	3.2	85
18	Verification of systems biology research in the age of collaborative competition. <i>Nature Biotechnology</i> , 2011, 29, 811-815.	17.5	83

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19	Genome-wide chromatin footprinting reveals changes in replication origin architecture induced by pre-RC assembly. <i>Genes and Development</i> , 2015, 29, 212-224.	5.9	82
20	Combining location and expression data for principled discovery of genetic regulatory network models. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2002, , 437-49.	0.7	63
21	Automated constraint-based nucleotide sequence selection for DNA computation. <i>BioSystems</i> , 1999, 52, 227-235.	2.0	56
22	Establishment of Expression in the SHORTROOT-SCARECROW Transcriptional Cascade through Opposing Activities of Both Activators and Repressors. <i>Developmental Cell</i> , 2016, 39, 585-596.	7.0	54
23	Informative priors based on transcription factor structural class improve de novo motif discovery. <i>Bioinformatics</i> , 2006, 22, e384-e392.	4.1	48
24	Mapping nucleosome positions using DNase-seq. <i>Genome Research</i> , 2016, 26, 351-364.	5.5	46
25	Finding regulatory DNA motifs using alignment-free evolutionary conservation information. <i>Nucleic Acids Research</i> , 2010, 38, e90-e90.	14.5	38
26	Sequence features of DNA binding sites reveal structural class of associated transcription factor. <i>Bioinformatics</i> , 2006, 22, 157-163.	4.1	33
27	Joint Classifier and Feature Optimization for Comprehensive Cancer Diagnosis Using Gene Expression Data. <i>Journal of Computational Biology</i> , 2004, 11, 227-242.	1.6	32
28	A Probabilistic Model for Cell Cycle Distributions in Synchrony Experiments. <i>Cell Cycle</i> , 2007, 6, 478-488.	2.6	29
29	Nucleosome Occupancy Information Improves de novo Motif Discovery. , 2007, , 107-121.		23
30	Identification of Tat-SF1 cellular targets by exon array analysis reveals dual roles in transcription and splicing. <i>Rna</i> , 2011, 17, 665-674.	3.5	16
31	INFLUENCE OF NETWORK TOPOLOGY AND DATA COLLECTION ON NETWORK INFERENCE. , 2002, , .		15
32	Characterization of dependencies between growth and division in budding yeast. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20160993.	3.4	13
33	INTRINSIC DISORDER WITHIN AND FLANKING THE DNA-BINDING DOMAINS OF HUMAN TRANSCRIPTION FACTORS. , 2011, , .		12
34	Learning proteinâ€“DNA interaction landscapes by integrating experimental data through computational models. <i>Bioinformatics</i> , 2014, 30, 2868-2874.	4.1	12
35	Local nucleosome dynamics and eviction following a double-strand break are reversible by NHEJ-mediated repair in the absence of DNA replication. <i>Genome Research</i> , 2021, 31, 775-788.	5.5	10
36	A Fast, Alignment-Free, Conservation-Based Method for Transcription Factor Binding Site Discovery. , 2008, , 98-111.		10

#	ARTICLE	IF	CITATIONS
37	A branching process model for flow cytometry and budding index measurements in cell synchrony experiments. <i>Annals of Applied Statistics</i> , 2009, 3, 1521-1541.	1.1	9
38	USING DNA DUPLEX STABILITY INFORMATION FOR TRANSCRIPTION FACTOR BINDING SITE DISCOVERY. , 2007, , .		9
39	Branching process deconvolution algorithm reveals a detailed cell-cycle transcription program. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E968-77.	7.1	8
40	Linking the dynamics of chromatin occupancy and transcription with predictive models. <i>Genome Research</i> , 2021, 31, 1035-1046.	5.5	7
41	FINDING DIAGNOSTIC BIOMARKERS IN PROTEOMIC SPECTRA. , 2005, , .		6
42	RoboCOP: jointly computing chromatin occupancy profiles for numerous factors from chromatin accessibility data. <i>Nucleic Acids Research</i> , 2021, 49, 7925-7938.	14.5	3
43	Cell-Cycle-Dependent Chromatin Dynamics at Replication Origins. <i>Genes</i> , 2021, 12, 1998.	2.4	3
44	Session Introduction. , 2004, , .		1
45	Joint learning from multiple types of genomic data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005, , 445-6.	0.7	1
46	Profiling the quantitative occupancy of myriad transcription factors across conditions by modeling chromatin accessibility data. <i>Genome Research</i> , 2022, 32, 1183-1198.	5.5	1
47	Cell-cycle phenotyping with conditional random fields: A case study in <i>Saccharomyces cerevisiae</i> . , 2013, , .		0
48	Session Introduction. , 2002, , .		0
49	A nucleosome-guided map of transcription factor binding sites in yeast. <i>PLoS Computational Biology</i> , 2005, preprint, e215.	3.2	0
50	RoboCOP: Multivariate State Space Model Integrating Epigenomic Accessibility Data to Elucidate Genome-Wide Chromatin Occupancy. <i>Lecture Notes in Computer Science</i> , 2020, 12074, 136-151.	1.3	0