

Alexander J Hartemink

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3013979/publications.pdf>

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	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
2	Linking the dynamics of chromatin occupancy and transcription with predictive models. <i>Genome Research</i> , 2021, 31, 1035-1046.	5.5	7
3	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
4	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
5	Cell-Cycle-Dependent Chromatin Dynamics at Replication Origins. <i>Genes</i> , 2021, 12, 1998.	2.4	3
6	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
7	Glucocorticoid receptor recruits to enhancers and drives activation by motif-directed binding. <i>Genome Research</i> , 2018, 28, 1272-1284.	5.5	102
8	Characterization of dependencies between growth and division in budding yeast. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20160993.	3.4	13
9	MATCHER: manifold alignment reveals correspondence between single cell transcriptome and epigenome dynamics. <i>Genome Biology</i> , 2017, 18, 138.	8.8	131
10	SLICER: inferring branched, nonlinear cellular trajectories from single cell RNA-seq data. <i>Genome Biology</i> , 2016, 17, 106.	8.8	155
11	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
12	Mapping nucleosome positions using DNase-seq. <i>Genome Research</i> , 2016, 26, 351-364.	5.5	46
13	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
14	Learning protein-DNA interaction landscapes by integrating experimental data through computational models. <i>Bioinformatics</i> , 2014, 30, 2868-2874.	4.1	12
15	Convergent transcriptional specializations in the brains of humans and song-learning birds. <i>Science</i> , 2014, 346, 1256846.	12.6	379
16	Core and region-enriched networks of behaviorally regulated genes and the singing genome. <i>Science</i> , 2014, 346, 1256780.	12.6	97
17	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
18	Cell-cycle phenotyping with conditional random fields: A case study in <i>Saccharomyces cerevisiae</i> . , 2013, , .		0

#	ARTICLE	IF	CITATIONS
19	Synergistic and tunable human gene activation by combinations of synthetic transcription factors. <i>Nature Methods</i> , 2013, 10, 239-242.	19.0	222
20	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	5.5	1,708
21	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
22	INTRINSIC DISORDER WITHIN AND FLANKING THE DNA-BINDING DOMAINS OF HUMAN TRANSCRIPTION FACTORS. , 2011, , .		12
23	Verification of systems biology research in the age of collaborative competition. <i>Nature Biotechnology</i> , 2011, 29, 811-815.	17.5	83
24	Finding regulatory DNA motifs using alignment-free evolutionary conservation information. <i>Nucleic Acids Research</i> , 2010, 38, e90-e90.	14.5	38
25	<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
26	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
27	Distinguishing direct versus indirect transcription factorâ€“DNA interactions. <i>Genome Research</i> , 2009, 19, 2090-2100.	5.5	128
28	An ensemble model of competitive multi-factor binding of the genome. <i>Genome Research</i> , 2009, 19, 2101-2112.	5.5	94
29	Global control of cell-cycle transcription by coupled CDK and network oscillators. <i>Nature</i> , 2008, 453, 944-947.	27.8	269
30	A Fast, Alignment-Free, Conservation-Based Method for Transcription Factor Binding Site Discovery. , 2008, , 98-111.		10
31	Computational and experimental identification of novel human imprinted genes. <i>Genome Research</i> , 2007, 17, 1723-1730.	5.5	344
32	A Nucleosome-Guided Map of Transcription Factor Binding Sites in Yeast. <i>PLoS Computational Biology</i> , 2007, 3, e215.	3.2	85
33	A Probabilistic Model for Cell Cycle Distributions in Synchrony Experiments. <i>Cell Cycle</i> , 2007, 6, 478-488.	2.6	29
34	Nucleosome Occupancy Information Improves de novo Motif Discovery. , 2007, , 107-121.		23
35	USING DNA DUPLEX STABILITY INFORMATION FOR TRANSCRIPTION FACTOR BINDING SITE DISCOVERY. , 2007, , .		9
36	Informative priors based on transcription factor structural class improve de novo motif discovery. <i>Bioinformatics</i> , 2006, 22, e384-e392.	4.1	48

#	ARTICLE	IF	CITATIONS
37	Computational Inference of Neural Information Flow Networks. PLoS Computational Biology, 2006, 2, e161.	3.2	124
38	Sequence features of DNA binding sites reveal structural class of associated transcription factor. Bioinformatics, 2006, 22, 157-163.	4.1	33
39	FINDING DIAGNOSTIC BIOMARKERS IN PROTEOMIC SPECTRA. , 2005, , .		6
40	Reverse engineering gene regulatory networks. Nature Biotechnology, 2005, 23, 554-555.	17.5	141
41	Genome-wide prediction of imprinted murine genes. Genome Research, 2005, 15, 875-884.	5.5	237
42	A nucleosome-guided map of transcription factor binding sites in yeast. PLoS Computational Biology, 2005, preprint, e215.	3.2	0
43	Joint learning from multiple types of genomic data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 445-6.	0.7	1
44	Joint Classifier and Feature Optimization for Comprehensive Cancer Diagnosis Using Gene Expression Data. Journal of Computational Biology, 2004, 11, 227-242.	1.6	32
45	Session Introduction. , 2004, , .		1
46	INFORMATIVE STRUCTURE PRIORS: JOINT LEARNING OF DYNAMIC REGULATORY NETWORKS FROM MULTIPLE TYPES OF DATA. , 2004, , .		87
47	INFLUENCE OF NETWORK TOPOLOGY AND DATA COLLECTION ON NETWORK INFERENCE. , 2002, , .		15
48	Session Introduction. , 2002, , .		0
49	Combining location and expression data for principled discovery of genetic regulatory network models. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2002, , 437-49.	0.7	63
50	Automated constraint-based nucleotide sequence selection for DNA computation. BioSystems, 1999, 52, 227-235.	2.0	56