

Liqun Xi

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

1,136
citations

759233

12
h-index

794594

19
g-index

19
all docs

19
docs citations

19
times ranked

1391
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide Mapping of the Nucleosome Landscape by Micrococcal Nuclease and Chemical Mapping. <i>Trends in Genetics</i> , 2017, 33, 495-507.	6.7	34
2	Insights into Nucleosome Organization in Mouse Embryonic Stem Cells through Chemical Mapping. <i>Cell</i> , 2016, 167, 1555-1570.e15.	28.9	164
3	Differential Nucleosome Occupancies across Oct4-Sox2 Binding Sites in Murine Embryonic Stem Cells. <i>PLoS ONE</i> , 2015, 10, e0127214.	2.5	6
4	Single-cell nucleosome mapping reveals the molecular basis of gene expression heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2462-71.	7.1	96
5	A Locally Convuluted Cluster Model for Nucleosome Positioning Signals in Chemical Maps. <i>Journal of the American Statistical Association</i> , 2014, 109, 48-62.	3.1	8
6	Archaeal nucleosome positioning in vivo and in vitro is directed by primary sequence motifs. <i>BMC Genomics</i> , 2013, 14, 391.	2.8	52
7	Chemical map of <i>Schizosaccharomyces pombe</i> reveals species-specific features in nucleosome positioning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20158-20163.	7.1	89
8	High-resolution nucleosome mapping of targeted regions using BAC-based enrichment. <i>Nucleic Acids Research</i> , 2013, 41, e87-e87.	14.5	18
9	A Chemical Approach to Mapping Nucleosomes at Base Pair Resolution in Yeast. <i>Methods in Enzymology</i> , 2012, 513, 315-334.	1.0	20
10	A map of nucleosome positions in yeast at base-pair resolution. <i>Nature</i> , 2012, 486, 496-501.	27.8	405
11	Predicting nucleosome positioning using a duration Hidden Markov Model. <i>BMC Bioinformatics</i> , 2010, 11, 346.	2.6	120
12	ESTIMATION OF THE NUMBER OF PEOPLE IN A DEMONSTRATION. <i>Australian and New Zealand Journal of Statistics</i> , 2010, 52, 17-26.	0.9	13
13	Estimation in capture-recapture models when covariates are subject to measurement errors and missing data. <i>Canadian Journal of Statistics</i> , 2009, 37, 645-658.	0.9	13
14	The Minimum Capture Proportion for Reliable Estimation in Capture-Recapture Models. <i>Biometrics</i> , 2008, 64, 242-249.	1.4	7
15	Preferentially Quantized Linker DNA Lengths in <i>Saccharomyces cerevisiae</i> . <i>PLoS Computational Biology</i> , 2008, 4, e1000175.	3.2	65
16	A Unified Likelihood-Based Approach for Estimating Population Size in Continuous-Time Capture-Recapture Experiments with Frailty. <i>Biometrics</i> , 2007, 63, 228-236.	1.4	14
17	Estimating Population Size in a Continuous-time Removal Experiment with a Known Sub-population Size Ratio. <i>Environmental and Ecological Statistics</i> , 2006, 13, 109-124.	3.5	1
18	A BETA-BINOMIAL MODEL FOR ESTIMATING THE SIZE OF A HETEROGENEOUS POPULATION. <i>Australian and New Zealand Journal of Statistics</i> , 2005, 47, 299-308.	0.9	1

#	ARTICLE	IF	CITATIONS
19	A Semiparametric Method for Estimating Population Size for Capture-Recapture Experiments with Random Covariates in Continuous Time. <i>Biometrics</i> , 2005, 61, 1085-1092.	1.4	10