

Roger P Alexander

List of Publications by Year in Descending Order

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Version: 2024-04-23

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

21
papers

15,074
citations

18
h-index

36
g-index

36
ext. papers

18,462
ext. citations

20.4
avg, IF

8.06
L-index

#	Paper	IF	Citations
21	Open Problems in Extracellular RNA Data Analysis: Insights From an ERCC Online Workshop.. <i>Frontiers in Genetics</i> , 2021 , 12, 778416	4.5	0
20	exRNA Atlas Analysis Reveals Distinct Extracellular RNA Cargo Types and Their Carriers Present across Human Biofluids. <i>Cell</i> , 2019 , 177, 463-477.e15	56.2	144
19	Small RNA Sequencing across Diverse Biofluids Identifies Optimal Methods for exRNA Isolation. <i>Cell</i> , 2019 , 177, 446-462.e16	56.2	142
18	Overview of Protocols for Studying Extracellular RNA and Extracellular Vesicles. <i>Methods in Molecular Biology</i> , 2018 , 1740, 17-21	1.4	8
17	Extending gene ontology in the context of extracellular RNA and vesicle communication. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 19	2.2	23
16	Integration of extracellular RNA profiling data using metadata, biomedical ontologies and Linked Data technologies. <i>Journal of Extracellular Vesicles</i> , 2015 , 4, 27497	16.4	34
15	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014 , 512, 445-8	50.4	207
14	Identification of genes critical for resistance to infection by West Nile virus using RNA-Seq analysis. <i>Viruses</i> , 2013 , 5, 1664-81	6.2	18
13	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
12	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012 , 489, 91-100	50.4	1104
11	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012 , 22, 1658-67	9.7	133
10	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. <i>Genome Biology</i> , 2011 , 12, R15	18.3	96
9	Annotating non-coding regions of the genome. <i>Nature Reviews Genetics</i> , 2010 , 11, 559-71	30.1	303
8	Improved reconstruction of in silico gene regulatory networks by integrating knockout and perturbation data. <i>PLoS ONE</i> , 2010 , 5, e8121	3.7	73
7	Comparing genomes to computer operating systems in terms of the topology and evolution of their regulatory control networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 9186-91	11.5	60
6	Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , 2010 , 330, 1775-87	33.3	744
5	CheV: CheW-like coupling proteins at the core of the chemotaxis signaling network. <i>Trends in Microbiology</i> , 2010 , 18, 494-503	12.4	50

4	RodZ, a component of the bacterial core morphogenic apparatus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 1239-44	11.5	124
3	Understanding modularity in molecular networks requires dynamics. <i>Science Signaling</i> , 2009 , 2, pe44	8.8	72
2	Evolutionary genomics reveals conserved structural determinants of signaling and adaptation in microbial chemoreceptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 2885-90	11.5	191
1	Comparative genomic and protein sequence analyses of a complex system controlling bacterial chemotaxis. <i>Methods in Enzymology</i> , 2007 , 422, 1-31	1.7	96