

# Roger P Alexander

## List of Publications by Year in descending order

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Version: 2024-02-01

36  
papers

20,169  
citations

393982

19  
h-index

713013

21  
g-index

36  
all docs

36  
docs citations

36  
times ranked

40266  
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
2	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012, 489, 91-100.	13.7	1,384
3	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
4	Annotating non-coding regions of the genome. <i>Nature Reviews Genetics</i> , 2010, 11, 559-571.	7.7	398
5	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448.	13.7	289
6	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, 2885-2890.	3.3	235
7	exRNA Atlas Analysis Reveals Distinct Extracellular RNA Cargo Types and Their Carriers Present across Human Biofluids. <i>Cell</i> , 2019, 177, 463-477.e15.	13.5	228
8	Small RNA Sequencing across Diverse Biofluids Identifies Optimal Methods for exRNA Isolation. <i>Cell</i> , 2019, 177, 446-462.e16.	13.5	214
9	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	2.4	166
10	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, 1239-1244.	3.3	156
11	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. <i>Genome Biology</i> , 2011, 12, R15.	13.9	118
12	Comparative Genomic and Protein Sequence Analyses of a Complex System Controlling Bacterial Chemotaxis. <i>Methods in Enzymology</i> , 2007, 422, 3-31.	0.4	110
13	Improved Reconstruction of In Silico Gene Regulatory Networks by Integrating Knockout and Perturbation Data. <i>PLoS ONE</i> , 2010, 5, e8121.	1.1	97
14	Understanding Modularity in Molecular Networks Requires Dynamics. <i>Science Signaling</i> , 2009, 2, pe44.	1.6	82
15	CheV: CheW-like coupling proteins at the core of the chemotaxis signaling network. <i>Trends in Microbiology</i> , 2010, 18, 494-503.	3.5	77
16	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, 9186-9191.	3.3	75
17	Integration of extracellular RNA profiling data using metadata, biomedical ontologies and Linked Data technologies. <i>Journal of Extracellular Vesicles</i> , 2015, 4, 27497.	5.5	48
18	Identification of Genes Critical for Resistance to Infection by West Nile Virus Using RNA-Seq Analysis. <i>Viruses</i> , 2013, 5, 1664-1681.	1.5	25

#	ARTICLE	IF	CITATIONS
19	Extending gene ontology in the context of extracellular RNA and vesicle communication. Journal of Biomedical Semantics, 2016, 7, 19.	0.9	24
20	Overview of Protocols for Studying Extracellular RNA and Extracellular Vesicles. Methods in Molecular Biology, 2018, 1740, 17-21.	0.4	10
21	Open Problems in Extracellular RNA Data Analysis: Insights From an ERCC Online Workshop. Frontiers in Genetics, 2021, 12, 778416.	1.1	2
22	Serum Collection Procedure (Small Scale) for the analysis of extracellular RNA. Protocol Exchange, 0, , .	0.3	1
23	RNA isolation from human serum and plasma samples using the Norgen exosomal RNA purification mini kit. Protocol Exchange, 0, , .	0.3	1
24	Cell Culture Supernatant Collection. Protocol Exchange, 0, , .	0.3	1
25	Enrichment of extracellular vesicles from serum or plasma via ultracentrifugation. Protocol Exchange, 0, , .	0.3	0
26	Enrichment of extracellular vesicles using Millipore membrane filters. Protocol Exchange, 0, , .	0.3	0
27	Isolation of extracellular vesicles and RNA using the miRcury Biofluids Kit. Protocol Exchange, 0, , .	0.3	0
28	Extracellular RNA isolation using the SeraMir Kit. Protocol Exchange, 0, , .	0.3	0
29	Urine Collection Procedure for the analysis of extracellular RNA. Protocol Exchange, 0, , .	0.3	0
30	qPCR of Genomic DNA to assess DNA contamination of extracellular RNA samples. Protocol Exchange, 0, , .	0.3	0
31	Isolation of extracellular vesicles and RNA from serum or plasma using the ExoRNeasy Mini Kit.. Protocol Exchange, 0, , .	0.3	0
32	Isolation of extracellular vesicles from serum or plasma using the ME Kit. Protocol Exchange, 0, , .	0.3	0
33	Bile Sample Collection for the analysis of extracellular RNA. Protocol Exchange, 0, , .	0.3	0
34	RiboGreen Quantification using a qPCR machine. Protocol Exchange, 0, , .	0.3	0
35	RNA isolation using the miRNeasy Micro Kit. Protocol Exchange, 0, , .	0.3	0
36	Exosome isolation from serum using ExoQuick reagent. Protocol Exchange, 0, , .	0.3	0