

Rory Johnson

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

39,152
citations

53794

45
h-index

95266

68
g-index

84
all docs

84
docs citations

84
times ranked

58555
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
2	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	27.8	4,484
3	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012, 22, 1775-1789.	5.5	4,428
4	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	14.5	2,350
5	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	27.8	1,966
6	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
7	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	12.6	1,127
8	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923.	14.5	633
9	Human long non-coding RNAs promote pluripotency and neuronal differentiation by association with chromatin modifiers and transcription factors. <i>EMBO Journal</i> , 2012, 31, 522-533.	7.8	461
10	Towards a complete map of the human long non-coding RNA transcriptome. <i>Nature Reviews Genetics</i> , 2018, 19, 535-548.	16.3	451
11	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	27.8	424
12	Deep sequencing of subcellular RNA fractions shows splicing to be predominantly co-transcriptional in the human genome but inefficient for lncRNAs. <i>Genome Research</i> , 2012, 22, 1616-1625.	5.5	401
13	Long non-coding RNAs in Huntington's disease neurodegeneration. <i>Neurobiology of Disease</i> , 2012, 46, 245-254.	4.4	356
14	Genome-wide computational identification and manual annotation of human long noncoding RNA genes. <i>Rna</i> , 2010, 16, 1478-1487.	3.5	354
15	A microRNA-based gene dysregulation pathway in Huntington's disease. <i>Neurobiology of Disease</i> , 2008, 29, 438-445.	4.4	338
16	The RIDL hypothesis: transposable elements as functional domains of long noncoding RNAs. <i>Rna</i> , 2014, 20, 959-976.	3.5	246
17	Genome-wide profiling of the cardiac transcriptome after myocardial infarction identifies novel heart-specific long non-coding RNAs. <i>European Heart Journal</i> , 2015, 36, 353-368.	2.2	244
18	LncAtlas database for subcellular localization of long noncoding RNAs. <i>Rna</i> , 2017, 23, 1080-1087.	3.5	230

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19	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. <i>Nature Genetics</i> , 2017, 49, 1731-1740.	21.4	227
20	CARMEN, a human super enhancer-associated long noncoding RNA controlling cardiac specification, differentiation and homeostasis. <i>Journal of Molecular and Cellular Cardiology</i> , 2015, 89, 98-112.	1.9	223
21	Global Positioning System: Understanding Long Noncoding RNAs through Subcellular Localization. <i>Molecular Cell</i> , 2019, 73, 869-883.	9.7	214
22	MacroRNA underdogs in a microRNA world: Evolutionary, regulatory, and biomedical significance of mammalian long non-protein-coding RNA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010, 1799, 597-615.	1.9	200
23	Cytoplasmic long noncoding RNAs are frequently bound to and degraded at ribosomes in human cells. <i>Rna</i> , 2016, 22, 867-882.	3.5	194
24	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	5.5	175
25	REST Regulates Distinct Transcriptional Networks in Embryonic and Neural Stem Cells. <i>PLoS Biology</i> , 2008, 6, e256.	5.6	172
26	Hacking the Cancer Genome: Profiling Therapeutically Actionable Long Non-coding RNAs Using CRISPR-Cas9 Screening. <i>Cancer Cell</i> , 2019, 35, 545-557.	16.8	163
27	Distinct Profiles of REST Interactions with Its Target Genes at Different Stages of Neuronal Development. <i>Molecular Biology of the Cell</i> , 2005, 16, 5630-5638.	2.1	157
28	Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. <i>Genome Research</i> , 2012, 22, 1231-1242.	5.5	143
29	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. <i>Communications Biology</i> , 2020, 3, 56.	4.4	140
30	The role of REST in transcriptional and epigenetic dysregulation in Huntington's disease. <i>Neurobiology of Disease</i> , 2010, 39, 28-39.	4.4	134
31	Functional importance of cardiac enhancer-associated noncoding RNAs in heart development and disease. <i>Journal of Molecular and Cellular Cardiology</i> , 2014, 76, 55-70.	1.9	124
32	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
33	Identification of the REST regulon reveals extensive transposable element-mediated binding site duplication. <i>Nucleic Acids Research</i> , 2006, 34, 3862-3877.	14.5	121
34	The Long Non-Coding RNAs: A New (P)layer in the "Dark Matter". <i>Frontiers in Genetics</i> , 2011, 2, 107.	2.3	113
35	Gene Dysregulation in Huntington's Disease: REST, MicroRNAs and Beyond. <i>NeuroMolecular Medicine</i> , 2009, 11, 183-199.	3.4	104
36	DECKO: Single-oligo, dual-CRISPR deletion of genomic elements including long non-coding RNAs. <i>BMC Genomics</i> , 2015, 16, 846.	2.8	100

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37	Discovery of Cancer Driver Long Noncoding RNAs across 1112 Tumour Genomes: New Candidates and Distinguishing Features. <i>Scientific Reports</i> , 2017, 7, 41544.	3.3	98
38	Human accelerated region 1 noncoding RNA is repressed by REST in Huntington's disease. <i>Physiological Genomics</i> , 2010, 41, 269-274.	2.3	97
39	Regulation of neural macroRNAs by the transcriptional repressor REST. <i>Rna</i> , 2009, 15, 85-96.	3.5	90
40	Scalable Design of Paired CRISPR Guide RNAs for Genomic Deletion. <i>PLoS Computational Biology</i> , 2017, 13, e1005341.	3.2	64
41	Ancient exapted transposable elements promote nuclear enrichment of human long noncoding RNAs. <i>Genome Research</i> , 2019, 29, 208-222.	5.5	64
42	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, 4330.	12.8	60
43	Transcriptional dysregulation of coding and non-coding genes in cellular models of Huntington's disease. <i>Biochemical Society Transactions</i> , 2009, 37, 1270-1275.	3.4	59
44	Neurodegeneration as an RNA disorder. <i>Progress in Neurobiology</i> , 2012, 99, 293-315.	5.7	52
45	Is REST a regulator of pluripotency?. <i>Nature</i> , 2009, 457, E5-E6.	27.8	51
46	Coassembly of REST and its cofactors at sites of gene repression in embryonic stem cells. <i>Genome Research</i> , 2011, 21, 1284-1293.	5.5	46
47	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. <i>Genome Research</i> , 2015, 25, 1256-1267.	5.5	46
48	Evolution of the Vertebrate Gene Regulatory Network Controlled by the Transcriptional Repressor REST. <i>Molecular Biology and Evolution</i> , 2009, 26, 1491-1507.	8.9	36
49	A Point Mutation in a lincRNA Upstream of GDNF Is Associated to a Canine Insensitivity to Pain: A Spontaneous Model for Human Sensory Neuropathies. <i>PLoS Genetics</i> , 2016, 12, e1006482.	3.5	31
50	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748.	12.8	27
51	Human vtRNA1-1 Levels Modulate Signaling Pathways and Regulate Apoptosis in Human Cancer Cells. <i>Biomolecules</i> , 2020, 10, 614.	4.0	24
52	Cancer LncRNA Census 2 (CLC2): an enhanced resource reveals clinical features of cancer lncRNAs. <i>NAR Cancer</i> , 2021, 3, zcab013.	3.1	21
53	LnCompare: gene set feature analysis for human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2019, 47, W523-W529.	14.5	20
54	MapToCleave: High-throughput profiling of microRNA biogenesis in living cells. <i>Cell Reports</i> , 2021, 37, 110015.	6.4	18

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55	A Genome-Wide Screen for Genetic Variants That Modify the Recruitment of REST to Its Target Genes. PLoS Genetics, 2012, 8, e1002624.	3.5	17
56	The Origins and the Biological Consequences of the Pur/Pyr DNA-RNA Asymmetry. Chem, 2019, 5, 1619-1631.	11.7	13
57	Noncoding RNAs: biology and applications a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 118-141.	3.8	13
58	CASPR, an analysis pipeline for single and paired guide RNA CRISPR screens, reveals optimal target selection for long non-coding RNAs. Bioinformatics, 2020, 36, 1673-1680.	4.1	12
59	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
60	Enhancing CRISPR deletion via pharmacological delay of DNA-PKcs. Genome Research, 2021, 31, 461-471.	5.5	9
61	New insights into non-coding RNA networks in Huntington's disease. Experimental Neurology, 2011, 231, 191-194.	4.1	7
62	Paired guide RNA CRISPR-Cas9 screening for protein-coding genes and lncRNAs involved in transdifferentiation of human B-cells to macrophages. BMC Genomics, 2022, 23, .	2.8	7
63	Annotation of Full-Length Long Noncoding RNAs with Capture Long-Read Sequencing (CLS). Methods in Molecular Biology, 2021, 2254, 133-159.	0.9	3
64	Capturing a Long Look at Our Genetic Library. Cell Systems, 2018, 6, 153-155.	6.2	2
65	Designing libraries for pooled CRISPR functional screens of long noncoding RNAs. Mammalian Genome, 2022, 33, 312-327.	2.2	2
66	Lessons from the functional characterization of lncRNAs: introduction to mammalian genome special issue. Mammalian Genome, 2022, , .	2.2	1