

Rory Johnson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9387105/publications.pdf>

Version: 2024-02-01

66
papers

39,152
citations

53751

45
h-index

95218

68
g-index

84
all docs

84
docs citations

84
times ranked

58555
citing authors

#	ARTICLE	IF	CITATIONS
1	Designing libraries for pooled CRISPR functional screens of long noncoding RNAs. <i>Mammalian Genome</i> , 2022, 33, 312-327.	1.0	2
2	Lessons from the functional characterization of lncRNAs: introduction to mammalian genome special issue. <i>Mammalian Genome</i> , 2022, , .	1.0	1
3	Paired guide RNA CRISPR-Cas9 screening for protein-coding genes and lncRNAs involved in transdifferentiation of human B-cells to macrophages. <i>BMC Genomics</i> , 2022, 23, .	1.2	7
4	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923.	6.5	633
5	Enhancing CRISPR deletion via pharmacological delay of DNA-PKcs. <i>Genome Research</i> , 2021, 31, 461-471.	2.4	9
6	Cancer lncRNA Census 2 (CLC2): an enhanced resource reveals clinical features of cancer lncRNAs. <i>NAR Cancer</i> , 2021, 3, zcab013.	1.6	21
7	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	5.8	11
8	Annotation of Full-Length Long Noncoding RNAs with Capture Long-Read Sequencing (CLS). <i>Methods in Molecular Biology</i> , 2021, 2254, 133-159.	0.4	3
9	Noncoding RNAs: biology and applications – a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 118-141.	1.8	13
10	MapToCleave: High-throughput profiling of microRNA biogenesis in living cells. <i>Cell Reports</i> , 2021, 37, 110015.	2.9	18
11	CASPR, an analysis pipeline for single and paired guide RNA CRISPR screens, reveals optimal target selection for long non-coding RNAs. <i>Bioinformatics</i> , 2020, 36, 1673-1680.	1.8	12
12	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
13	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
14	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748.	5.8	27
15	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, 4330.	5.8	60
16	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	13.7	424
17	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
18	Cancer lncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. <i>Communications Biology</i> , 2020, 3, 56.	2.0	140

#	ARTICLE	IF	CITATIONS
19	Human vtRNA1-1 Levels Modulate Signaling Pathways and Regulate Apoptosis in Human Cancer Cells. <i>Biomolecules</i> , 2020, 10, 614.	1.8	24
20	LnCompare: gene set feature analysis for human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2019, 47, W523-W529.	6.5	20
21	The Origins and the Biological Consequences of the Pur/Pyr DNA-RNA Asymmetry. <i>CheM</i> , 2019, 5, 1619-1631.	5.8	13
22	Global Positioning System: Understanding Long Noncoding RNAs through Subcellular Localization. <i>Molecular Cell</i> , 2019, 73, 869-883.	4.5	214
23	Hacking the Cancer Genome: Profiling Therapeutically Actionable Long Non-coding RNAs Using CRISPR-Cas9 Screening. <i>Cancer Cell</i> , 2019, 35, 545-557.	7.7	163
24	Ancient exapted transposable elements promote nuclear enrichment of human long noncoding RNAs. <i>Genome Research</i> , 2019, 29, 208-222.	2.4	64
25	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	6.5	2,350
26	Capturing a Long Look at Our Genetic Library. <i>Cell Systems</i> , 2018, 6, 153-155.	2.9	2
27	Towards a complete map of the human long non-coding RNA transcriptome. <i>Nature Reviews Genetics</i> , 2018, 19, 535-548.	7.7	451
28	Discovery of Cancer Driver Long Noncoding RNAs across 1112 Tumour Genomes: New Candidates and Distinguishing Features. <i>Scientific Reports</i> , 2017, 7, 41544.	1.6	98
29	LncAtlas database for subcellular localization of long noncoding RNAs. <i>Rna</i> , 2017, 23, 1080-1087.	1.6	230
30	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. <i>Nature Genetics</i> , 2017, 49, 1731-1740.	9.4	227
31	Scalable Design of Paired CRISPR Guide RNAs for Genomic Deletion. <i>PLoS Computational Biology</i> , 2017, 13, e1005341.	1.5	64
32	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.	1.5	31
33	Cytoplasmic long noncoding RNAs are frequently bound to and degraded at ribosomes in human cells. <i>Rna</i> , 2016, 22, 867-882.	1.6	194
34	DECKO: Single-oligo, dual-CRISPR deletion of genomic elements including long non-coding RNAs. <i>BMC Genomics</i> , 2015, 16, 846.	1.2	100
35	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	6.0	1,127
36	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.	0.9	223

#	ARTICLE	IF	CITATIONS
37	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. <i>Genome Research</i> , 2015, 25, 1256-1267.	2.4	46
38	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.	1.0	244
39	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	2.4	175
40	The RIDL hypothesis: transposable elements as functional domains of long noncoding RNAs. <i>Rna</i> , 2014, 20, 959-976.	1.6	246
41	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.	0.9	124
42	A Genome-Wide Screen for Genetic Variants That Modify the Recruitment of REST to Its Target Genes. <i>PLoS Genetics</i> , 2012, 8, e1002624.	1.5	17
43	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
44	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.	2.4	401
45	Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. <i>Genome Research</i> , 2012, 22, 1231-1242.	2.4	143
46	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.	2.4	4,428
47	Neurodegeneration as an RNA disorder. <i>Progress in Neurobiology</i> , 2012, 99, 293-315.	2.8	52
48	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.	3.5	461
49	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	13.7	4,484
50	Long non-coding RNAs in Huntington's disease neurodegeneration. <i>Neurobiology of Disease</i> , 2012, 46, 245-254.	2.1	356
51	New insights into non-coding RNA networks in Huntington's disease. <i>Experimental Neurology</i> , 2011, 231, 191-194.	2.0	7
52	Coassembly of REST and its cofactors at sites of gene repression in embryonic stem cells. <i>Genome Research</i> , 2011, 21, 1284-1293.	2.4	46
53	The Long Non-Coding RNAs: A New (P)layer in the "Dark Matter". <i>Frontiers in Genetics</i> , 2011, 2, 107.	1.1	113
54	Human accelerated region 1 noncoding RNA is repressed by REST in Huntington's disease. <i>Physiological Genomics</i> , 2010, 41, 269-274.	1.0	97

#	ARTICLE	IF	CITATIONS
55	The role of REST in transcriptional and epigenetic dysregulation in Huntington's disease. <i>Neurobiology of Disease</i> , 2010, 39, 28-39.	2.1	134
56	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.	0.9	200
57	Genome-wide computational identification and manual annotation of human long noncoding RNA genes. <i>Rna</i> , 2010, 16, 1478-1487.	1.6	354
58	Regulation of neural macroRNAs by the transcriptional repressor REST. <i>Rna</i> , 2009, 15, 85-96.	1.6	90
59	Evolution of the Vertebrate Gene Regulatory Network Controlled by the Transcriptional Repressor REST. <i>Molecular Biology and Evolution</i> , 2009, 26, 1491-1507.	3.5	36
60	Gene Dysregulation in Huntington's Disease: REST, MicroRNAs and Beyond. <i>NeuroMolecular Medicine</i> , 2009, 11, 183-199.	1.8	104
61	Is REST a regulator of pluripotency?. <i>Nature</i> , 2009, 457, E5-E6.	13.7	51
62	Transcriptional dysregulation of coding and non-coding genes in cellular models of Huntington's disease. <i>Biochemical Society Transactions</i> , 2009, 37, 1270-1275.	1.6	59
63	A microRNA-based gene dysregulation pathway in Huntington's disease. <i>Neurobiology of Disease</i> , 2008, 29, 438-445.	2.1	338
64	REST Regulates Distinct Transcriptional Networks in Embryonic and Neural Stem Cells. <i>PLoS Biology</i> , 2008, 6, e256.	2.6	172
65	Identification of the REST regulon reveals extensive transposable element-mediated binding site duplication. <i>Nucleic Acids Research</i> , 2006, 34, 3862-3877.	6.5	121
66	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.	0.9	157