

Philipp Kapranov

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

25,490
citations

66343

42
h-index

98798

67
g-index

67
all docs

67
docs citations

67
times ranked

32079
citing authors

#	ARTICLE	IF	CITATIONS
1	Methods to Analyze the Non-Coding RNA Interactome—Recent Advances and Challenges. <i>Frontiers in Genetics</i> , 2022, 13, 857759.	2.3	6
2	Hovlinc is a recently evolved class of ribozyme found in human lincRNA. <i>Nature Chemical Biology</i> , 2021, 17, 601-607.	8.0	26
3	Very long intergenic non-coding (vlinc) RNAs directly regulate multiple genes in cis and trans. <i>BMC Biology</i> , 2021, 19, 108.	3.8	14
4	Chromatin lincRNA Platr10 controls stem cell pluripotency by coordinating an intrachromosomal regulatory network. <i>Genome Biology</i> , 2021, 22, 233.	8.8	12
5	Complex Age- and Cancer-Related Changes in Human Blood Transcriptome—Implications for Pan-Cancer Diagnostics. <i>Frontiers in Genetics</i> , 2021, 12, 746879.	2.3	7
6	Editorial: Recent Progresses of Non-coding RNAs in Biological and Medical Research. <i>Frontiers in Genetics</i> , 2020, 11, 187.	2.3	1
7	A CRISPR/Cas13-based approach demonstrates biological relevance of vlinc class of long non-coding RNAs in anticancer drug response. <i>Scientific Reports</i> , 2020, 10, 1794.	3.3	49
8	Reverse-genetics studies of lincRNAs—what we have learnt and paths forward. <i>Genome Biology</i> , 2020, 21, 93.	8.8	55
9	Emerging Technologies for Genome-Wide Profiling of DNA Breakage. <i>Frontiers in Genetics</i> , 2020, 11, 610386.	2.3	6
10	Diversification of Retinoblastoma Protein Function Associated with Cis and Trans Adaptations. <i>Molecular Biology and Evolution</i> , 2019, 36, 2790-2804.	8.9	7
11	Novel approach reveals genomic landscapes of single-strand DNA breaks with nucleotide resolution in human cells. <i>Nature Communications</i> , 2019, 10, 5799.	12.8	38
12	Strategies to Annotate and Characterize Long Noncoding RNAs: Advantages and Pitfalls. <i>Trends in Genetics</i> , 2018, 34, 704-721.	6.7	86
13	Identification of novel GLI1 target genes and regulatory circuits in human cancer cells. <i>Molecular Oncology</i> , 2018, 12, 1718-1734.	4.6	30
14	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , 2016, 44, 3233-3252.	14.5	31
15	A vlincRNA participates in senescence maintenance by relieving H2AZ-mediated repression at the INK4 locus. <i>Nature Communications</i> , 2015, 6, 5971.	12.8	56
16	The Bromodomain protein BRD4 controls HOTAIR, a long noncoding RNA essential for glioblastoma proliferation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8326-8331.	7.1	186
17	The Landscape of long noncoding RNA classification. <i>Trends in Genetics</i> , 2015, 31, 239-251.	6.7	942
18	Identification of novel non-coding RNA-based negative feedback regulating the expression of the oncogenic transcription factor GLI1. <i>Molecular Oncology</i> , 2014, 8, 912-926.	4.6	33

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19	Efficient Production of Dual Recombinant Adeno-Associated Viral Vectors for Factor VIII Delivery. <i>Human Gene Therapy Methods</i> , 2014, 25, 261-268.	2.1	33
20	Dark matter RNA illuminates the puzzle of genome-wide association studies. <i>BMC Medicine</i> , 2014, 12, 97.	5.5	34
21	Proteomics Analysis of Co-Purifying Cellular Proteins Associated with rAAV Vectors. <i>PLoS ONE</i> , 2014, 9, e86453.	2.5	22
22	Genome-wide analysis of A-to-I RNA editing by single-molecule sequencing in <i>Drosophila</i> . <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1333-1339.	8.2	132
23	On the importance of small changes in RNA expression. <i>Methods</i> , 2013, 63, 18-24.	3.8	49
24	A concept of eliminating nonhomologous recombination for scalable and safe AAV vector generation for human gene therapy. <i>Nucleic Acids Research</i> , 2013, 41, 6609-6617.	14.5	22
25	VlincRNAs controlled by retroviral elements are a hallmark of pluripotency and cancer. <i>Genome Biology</i> , 2013, 14, R73.	9.6	78
26	Single-step capture and sequencing of natural DNA for detection of <i>BRCA1</i> mutations. <i>Genome Research</i> , 2012, 22, 340-345.	5.5	30
27	Native Molecular State of Adeno-Associated Viral Vectors Revealed by Single-Molecule Sequencing. <i>Human Gene Therapy</i> , 2012, 23, 46-55.	2.7	51
28	5-hmC in the brain is abundant in synaptic genes and shows differences at the exon-intron boundary. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1037-1043.	8.2	221
29	Intronic RNAs constitute the major fraction of the non-coding RNA in mammalian cells. <i>BMC Genomics</i> , 2012, 13, 504.	2.8	106
30	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	27.8	4,484
31	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. <i>PLoS ONE</i> , 2012, 7, e28213.	2.5	61
32	Dark Matter RNA: Existence, Function, and Controversy. <i>Frontiers in Genetics</i> , 2012, 3, 60.	2.3	75
33	Genomic "Dark Matter" Implications for Understanding Human Disease Mechanisms, Diagnostics, and Cures. <i>Frontiers in Genetics</i> , 2012, 3, 95.	2.3	8
34	Dark matter RNA: an intelligent scaffold for the dynamic regulation of the nuclear information landscape. <i>Frontiers in Genetics</i> , 2012, 3, 57.	2.3	23
35	Protocol Dependence of Sequencing-Based Gene Expression Measurements. <i>PLoS ONE</i> , 2011, 6, e19287.	2.5	97
36	Genome-wide mapping of 5-hydroxymethylcytosine in embryonic stem cells. <i>Nature</i> , 2011, 473, 394-397.	27.8	738

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37	True single-molecule DNA sequencing of a pleistocene horse bone. <i>Genome Research</i> , 2011, 21, 1705-1719.	5.5	114
38	The transcriptional diversity of 25 <i>Drosophila</i> cell lines. <i>Genome Research</i> , 2011, 21, 301-314.	5.5	235
39	The majority of total nuclear-encoded non-ribosomal RNA in a human cell is 'dark matter' un-annotated RNA. <i>BMC Biology</i> , 2010, 8, 149.	3.8	266
40	New class of gene-termini-associated human RNAs suggests a novel RNA copying mechanism. <i>Nature</i> , 2010, 466, 642-646.	27.8	98
41	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010, 7, 528-534.	19.0	152
42	Genome-Wide Mapping Indicates That p73 and p63 Co-Occupy Target Sites and Have Similar DNA-Binding Profiles In Vivo. <i>PLoS ONE</i> , 2010, 5, e11572.	2.5	42
43	Error Tolerant Indexing and Alignment of Short Reads with Covering Template Families. <i>Journal of Computational Biology</i> , 2010, 17, 1397-1411.	1.6	23
44	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
45	Comprehensive Polyadenylation Site Maps in Yeast and Human Reveal Pervasive Alternative Polyadenylation. <i>Cell</i> , 2010, 143, 1018-1029.	28.9	370
46	Variation in novel exons (RACEfrags) of the MECP2 gene in Rett syndrome patients and controls. <i>Human Mutation</i> , 2009, 30, E866-E879.	2.5	1
47	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. <i>Blood</i> , 2009, 113, 2526-2534.	1.4	330
48	Efficient targeted transcript discovery via array-based normalization of RACE libraries. <i>Nature Methods</i> , 2008, 5, 629-635.	19.0	41
49	Whole-genome maps of USF1 and USF2 binding and histone H3 acetylation reveal new aspects of promoter structure and candidate genes for common human disorders. <i>Genome Research</i> , 2008, 18, 380-392.	5.5	85
50	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008, 18, 393-403.	5.5	117
51	Prominent use of distal 5' transcription start sites and discovery of a large number of additional exons in ENCODE regions. <i>Genome Research</i> , 2007, 17, 746-759.	5.5	173
52	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007, 17, 852-864.	5.5	150
53	Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution. <i>Genome Research</i> , 2007, 17, 839-851.	5.5	191
54	RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. <i>Science</i> , 2007, 316, 1484-1488.	12.6	2,250

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55	Genome-wide transcription and the implications for genomic organization. <i>Nature Reviews Genetics</i> , 2007, 8, 413-423.	16.3	652
56	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
57	CD127 expression inversely correlates with FoxP3 and suppressive function of human CD4+ T reg cells. <i>Journal of Experimental Medicine</i> , 2006, 203, 1701-1711.	8.5	2,292
58	Biological function of unannotated transcription during the early development of <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , 2006, 38, 1151-1158.	21.4	168
59	Microarray-based DNA methylation profiling: technology and applications. <i>Nucleic Acids Research</i> , 2006, 34, 528-542.	14.5	271
60	Examples of the complex architecture of the human transcriptome revealed by RACE and high-density tiling arrays. <i>Genome Research</i> , 2005, 15, 987-997.	5.5	263
61	Temporal profile of replication of human chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6419-6424.	7.1	105
62	Transcriptional Maps of 10 Human Chromosomes at 5-Nucleotide Resolution. <i>Science</i> , 2005, 308, 1149-1154.	12.6	1,073
63	Novel RNAs Identified From an In-Depth Analysis of the Transcriptome of Human Chromosomes 21 and 22. <i>Genome Research</i> , 2004, 14, 331-342.	5.5	460
64	Unbiased Mapping of Transcription Factor Binding Sites along Human Chromosomes 21 and 22 Points to Widespread Regulation of Noncoding RNAs. <i>Cell</i> , 2004, 116, 499-509.	28.9	1,047
65	Large-Scale Transcriptional Activity in Chromosomes 21 and 22. <i>Science</i> , 2002, 296, 916-919.	12.6	793
66	Nodule-Specific Regulation of Phosphatidylinositol Transfer Protein Expression in <i>Lotus japonicus</i> . <i>Plant Cell</i> , 2001, 13, 1369-1382.	6.6	16
67	The <i>Lotus japonicus</i> LjNOD70 nodulin gene encodes a protein with similarities to transporters. <i>Plant Molecular Biology</i> , 1998, 37, 651-661.	3.9	30