Philipp Kapranov

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8448548/publications.pdf

Version: 2024-02-01

67	25,490	66343	98798
papers	citations	42	67
		h-index	g-index

67	67	67	32079
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
2	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	27.8	4,484
3	CD127 expression inversely correlates with FoxP3 and suppressive function of human CD4+ T reg cells. Journal of Experimental Medicine, 2006, 203, 1701-1711.	8.5	2,292
4	RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. Science, 2007, 316, 1484-1488.	12.6	2,250
5	Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE. Science, 2010, 330, 1787-1797.	12.6	1,124
6	Transcriptional Maps of 10 Human Chromosomes at 5-Nucleotide Resolution. Science, 2005, 308, 1149-1154.	12.6	1,073
7	Unbiased Mapping of Transcription Factor Binding Sites along Human Chromosomes 21 and 22 Points to Widespread Regulation of Noncoding RNAs. Cell, 2004, 116, 499-509.	28.9	1,047
8	The Landscape of long noncoding RNA classification. Trends in Genetics, 2015, 31, 239-251.	6.7	942
9	Large-Scale Transcriptional Activity in Chromosomes 21 and 22. Science, 2002, 296, 916-919.	12.6	793
10	Genome-wide mapping of 5-hydroxymethylcytosine in embryonic stem cells. Nature, 2011, 473, 394-397.	27.8	738
11	Genome-wide transcription and the implications for genomic organization. Nature Reviews Genetics, 2007, 8, 413-423.	16.3	652
12	Novel RNAs Identified From an In-Depth Analysis of the Transcriptome of Human Chromosomes 21 and 22. Genome Research, 2004, 14, 331-342.	5.5	460
13	Comprehensive Polyadenylation Site Maps in Yeast and Human Reveal Pervasive Alternative Polyadenylation. Cell, 2010, 143, 1018-1029.	28.9	370
14	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. Blood, 2009, 113, 2526-2534.	1.4	330
15	Microarray-based DNA methylation profiling: technology and applications. Nucleic Acids Research, 2006, 34, 528-542.	14.5	271
16	The majority of total nuclear-encoded non-ribosomal RNA in a human cell is 'dark matter' un-annotated RNA. BMC Biology, 2010, 8, 149.	3.8	266
17	Examples of the complex architecture of the human transcriptome revealed by RACE and high-density tiling arrays. Genome Research, 2005, 15, 987-997.	5.5	263
18	The transcriptional diversity of 25 Drosophila cell lines. Genome Research, 2011, 21, 301-314.	5.5	235

#	Article	IF	Citations
19	5-hmC in the brain is abundant in synaptic genes and shows differences at the exon-intron boundary. Nature Structural and Molecular Biology, 2012, 19, 1037-1043.	8.2	221
20	Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution. Genome Research, 2007, 17, 839-851.	5.5	191
21	The Bromodomain protein BRD4 controls HOTAIR, a long noncoding RNA essential for glioblastoma proliferation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8326-8331.	7.1	186
22	Prominent use of distal 5' transcription start sites and discovery of a large number of additional exons in ENCODE regions. Genome Research, 2007, 17, 746-759.	5.5	173
23	Biological function of unannotated transcription during the early development of Drosophila melanogaster. Nature Genetics, 2006, 38, 1151-1158.	21.4	168
24	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. Nature Methods, 2010, 7, 528-534.	19.0	152
25	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	5.5	150
26	Genome-wide analysis of A-to-I RNA editing by single-molecule sequencing in Drosophila. Nature Structural and Molecular Biology, 2013, 20, 1333-1339.	8.2	132
27	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. Genome Research, 2008, 18, 393-403.	5.5	117
28	True single-molecule DNA sequencing of a pleistocene horse bone. Genome Research, 2011, 21, 1705-1719.	5.5	114
29	Intronic RNAs constitute the major fraction of the non-coding RNA in mammalian cells. BMC Genomics, 2012, 13, 504.	2.8	106
30	Temporal profile of replication of human chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 6419-6424.	7.1	105
31	New class of gene-termini-associated human RNAs suggests a novel RNA copying mechanism. Nature, 2010, 466, 642-646.	27.8	98
32	Protocol Dependence of Sequencing-Based Gene Expression Measurements. PLoS ONE, 2011, 6, e19287.	2.5	97
33	Strategies to Annotate and Characterize Long Noncoding RNAs: Advantages and Pitfalls. Trends in Genetics, 2018, 34, 704-721.	6.7	86
34	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. Genome Research, 2008, 18, 380-392.	5.5	85
35	VlincRNAs controlled by retroviral elements are a hallmark of pluripotency and cancer. Genome Biology, 2013, 14, R73.	9.6	78
36	Dark Matter RNA: Existence, Function, and Controversy. Frontiers in Genetics, 2012, 3, 60.	2.3	75

#	Article	IF	Citations
37	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. PLoS ONE, 2012, 7, e28213.	2.5	61
38	A vlincRNA participates in senescence maintenance by relieving H2AZ-mediated repression at the INK4 locus. Nature Communications, 2015, 6, 5971.	12.8	56
39	Reverse-genetics studies of lncRNAsâ€"what we have learnt and paths forward. Genome Biology, 2020, 21, 93.	8.8	55
40	Native Molecular State of Adeno-Associated Viral Vectors Revealed by Single-Molecule Sequencing. Human Gene Therapy, 2012, 23, 46-55.	2.7	51
41	On the importance of small changes in RNA expression. Methods, 2013, 63, 18-24.	3.8	49
42	A CRISPR/Cas13-based approach demonstrates biological relevance of vlinc class of long non-coding RNAs in anticancer drug response. Scientific Reports, 2020, 10, 1794.	3.3	49
43	Genome-Wide Mapping Indicates That p73 and p63 Co-Occupy Target Sites and Have Similar DNA-Binding Profiles In Vivo. PLoS ONE, 2010, 5, e11572.	2.5	42
44	Efficient targeted transcript discovery via array-based normalization of RACE libraries. Nature Methods, 2008, 5, 629-635.	19.0	41
45	Novel approach reveals genomic landscapes of single-strand DNA breaks with nucleotide resolution in human cells. Nature Communications, 2019, 10, 5799.	12.8	38
46	Dark matter RNA illuminates the puzzle of genome-wide association studies. BMC Medicine, 2014, 12, 97.	5.5	34
47	Identification of novel nonâ€coding RNAâ€based negative feedback regulating the expression of the oncogenic transcription factor GLI1. Molecular Oncology, 2014, 8, 912-926.	4.6	33
48	Efficient Production of Dual Recombinant Adeno-Associated Viral Vectors for Factor VIII Delivery. Human Gene Therapy Methods, 2014, 25, 261-268.	2.1	33
49	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. Nucleic Acids Research, 2016, 44, 3233-3252.	14.5	31
50	The Lotus japonicus LjNOD70 nodulin gene encodes a protein with similarities to transporters. Plant Molecular Biology, 1998, 37, 651-661.	3.9	30
51	Single-step capture and sequencing of natural DNA for detection of BRCA1 mutations. Genome Research, 2012, 22, 340-345.	5.5	30
52	Identification of novel GLI1 target genes and regulatory circuits in human cancer cells. Molecular Oncology, 2018, 12, 1718-1734.	4.6	30
53	Hovlinc is a recently evolved class of ribozyme found in human lncRNA. Nature Chemical Biology, 2021, 17, 601-607.	8.0	26
54	Error Tolerant Indexing and Alignment of Short Reads with Covering Template Families. Journal of Computational Biology, 2010, 17, 1397-1411.	1.6	23

#	Article	IF	Citations
55	Dark matter RNA: an intelligent scaffold for the dynamic regulation of the nuclear information landscape. Frontiers in Genetics, 2012, 3, 57.	2.3	23
56	A concept of eliminating nonhomologous recombination for scalable and safe AAV vector generation for human gene therapy. Nucleic Acids Research, 2013, 41, 6609-6617.	14.5	22
57	Proteomics Analysis of Co-Purifying Cellular Proteins Associated with rAAV Vectors. PLoS ONE, 2014, 9, e86453.	2.5	22
58	Nodule-Specific Regulation of Phosphatidylinositol Transfer Protein Expression in Lotus japonicus. Plant Cell, 2001, 13, 1369-1382.	6.6	16
59	Very long intergenic non-coding (vlinc) RNAs directly regulate multiple genes in cis and trans. BMC Biology, 2021, 19, 108.	3.8	14
60	Chromatin lncRNA Platr10 controls stem cell pluripotency by coordinating an intrachromosomal regulatory network. Genome Biology, 2021, 22, 233.	8.8	12
61	Genomic â€œDark Matterâ€: Implications for Understanding Human Disease Mechanisms, Diagnostics, and Cures. Frontiers in Genetics, 2012, 3, 95.	2.3	8
62	Diversification of Retinoblastoma Protein Function Associated with Cis and Trans Adaptations. Molecular Biology and Evolution, 2019, 36, 2790-2804.	8.9	7
63	Complex Age- and Cancer-Related Changes in Human Blood Transcriptomeâ€”Implications for Pan-Cancer Diagnostics. Frontiers in Genetics, 2021, 12, 746879.	2.3	7
64	Emerging Technologies for Genome-Wide Profiling of DNA Breakage. Frontiers in Genetics, 2020, 11, 610386.	2.3	6
65	Methods to Analyze the Non-Coding RNA Interactomeâ€”Recent Advances and Challenges. Frontiers in Genetics, 2022, 13, 857759.	2.3	6
66	Variation in novel exons (RACEfrags) of theMECP2gene in Rett syndrome patients and controls. Human Mutation, 2009, 30, E866-E879.	2.5	1
67	Editorial: Recent Progresses of Non-coding RNAs in Biological and Medical Research. Frontiers in Genetics, 2020, 11, 187.	2.3	1