

Nicolas Robine

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

7,660
citations

201674

27
h-index

276875

41
g-index

53
all docs

53
docs citations

53
times ranked

14706
citing authors

#	ARTICLE	IF	CITATIONS
1	Altering the Intestinal Microbiota during a Critical Developmental Window Has Lasting Metabolic Consequences. <i>Cell</i> , 2014, 158, 705-721.	28.9	1,493
2	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
3	Organoid Profiling Identifies Common Responders to Chemotherapy in Pancreatic Cancer. <i>Cancer Discovery</i> , 2018, 8, 1112-1129.	9.4	676
4	Conserved vertebrate <i>mir-451</i> provides a platform for Dicer-independent, Ago2-mediated microRNA biogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15163-15168.	7.1	389
5	Detection of a Recurrent <i>DNAJB1-PRKACA</i> Chimeric Transcript in Fibrolamellar Hepatocellular Carcinoma. <i>Science</i> , 2014, 343, 1010-1014.	12.6	388
6	Maternal mRNA deadenylation and decay by the piRNA pathway in the early <i>Drosophila</i> embryo. <i>Nature</i> , 2010, 467, 1128-1132.	27.8	386
7	Histone H3 lysine 4 trimethylation marks meiotic recombination initiation sites. <i>EMBO Journal</i> , 2009, 28, 99-111.	7.8	329
8	A Broadly Conserved Pathway Generates 3'UTR-Directed Primary piRNAs. <i>Current Biology</i> , 2009, 19, 2066-2076.	3.9	304
9	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. <i>Cell</i> , 2020, 183, 818-834.e13.	28.9	287
10	Immunogenic neoantigens derived from gene fusions stimulate T cell responses. <i>Nature Medicine</i> , 2019, 25, 767-775.	30.7	282
11	Genome-wide cell-free DNA mutational integration enables ultra-sensitive cancer monitoring. <i>Nature Medicine</i> , 2020, 26, 1114-1124.	30.7	216
12	Deep annotation of <i>Drosophila melanogaster</i> microRNAs yields insights into their processing, modification, and emergence. <i>Genome Research</i> , 2011, 21, 203-215.	5.5	207
13	Human papillomavirus and the landscape of secondary genetic alterations in oral cancers. <i>Genome Research</i> , 2019, 29, 1-17.	5.5	166
14	Abundant primary piRNAs, endo-siRNAs, and microRNAs in a <i>Drosophila</i> ovary cell line. <i>Genome Research</i> , 2009, 19, 1776-1785.	5.5	164
15	Identification of Three Rheumatoid Arthritis Disease Subtypes by Machine Learning Integration of Synovial Histologic Features and <i>scRNA</i> Sequencing Data. <i>Arthritis and Rheumatology</i> , 2018, 70, 690-701.	5.6	157
16	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020, 183, 197-210.e32.	28.9	141
17	Genome-Wide Redistribution of Meiotic Double-Strand Breaks in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2007, 27, 1868-1880.	2.3	90
18	Genome-wide somatic variant calling using localized colored de Bruijn graphs. <i>Communications Biology</i> , 2018, 1, 20.	4.4	85

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19	Structural insights into mis-regulation of protein kinase A in human tumors. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1374-1379.	7.1	78
20	Computational and experimental identification of mirtrons in <i>Drosophila melanogaster</i> and <i>Caenorhabditis elegans</i> . Genome Research, 2011, 21, 286-300.	5.5	71
21	Genetic mechanisms of primary chemotherapy resistance in pediatric acute myeloid leukemia. Leukemia, 2019, 33, 1934-1943.	7.2	69
22	Diversity of miRNAs, siRNAs, and piRNAs across 25 <i>Drosophila</i> cell lines. Genome Research, 2014, 24, 1236-1250.	5.5	66
23	Common and distinct patterns of terminal modifications to mirtrons and canonical microRNAs. Rna, 2012, 18, 177-192.	3.5	64
24	R2D2 Organizes Small Regulatory RNA Pathways in <i>Drosophila</i> . Molecular and Cellular Biology, 2011, 31, 884-896.	2.3	57
25	<i>YES1</i> amplification is a mechanism of acquired resistance to EGFR inhibitors identified by transposon mutagenesis and clinical genomics. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6030-E6038.	7.1	44
26	Deep whole-genome sequencing of 3 cancer cell lines on 2 sequencing platforms. Scientific Reports, 2019, 9, 19123.	3.3	39
27	Comparing sequencing assays and human-machine analyses in actionable genomics for glioblastoma. Neurology: Genetics, 2017, 3, e164.	1.9	32
28	Genome-wide Expression Profiling, In Vivo DNA Binding Analysis, and Probabilistic Motif Prediction Reveal Novel Abf1 Target Genes during Fermentation, Respiration, and Sporulation in Yeast. Molecular Biology of the Cell, 2008, 19, 2193-2207.	2.1	29
29	A <i>Drosophila</i> genetic screen yields allelic series of core microRNA biogenesis factors and reveals post-developmental roles for microRNAs. Rna, 2011, 17, 1997-2010.	3.5	28
30	taxMaps: comprehensive and highly accurate taxonomic classification of short-read data in reasonable time. Genome Research, 2018, 28, 751-758.	5.5	25
31	Prognostic value of miR-375 and miR-214-3p in early stage oral squamous cell carcinoma. American Journal of Translational Research (discontinued), 2014, 6, 580-92.	0.0	24
32	Analytical Validation of Clinical Whole-Genome and Transcriptome Sequencing of Patient-Derived Tumors for Reporting Targetable Variants in Cancer. Journal of Molecular Diagnostics, 2018, 20, 822-835.	2.8	23
33	Diverse tumorigenic consequences of human papillomavirus integration in primary oropharyngeal cancers. Genome Research, 2022, 32, 55-70.	5.5	18
34	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	6.4	16
35	Somatic whole genome dynamics of precancer in Barrett's esophagus reveals features associated with disease progression. Nature Communications, 2022, 13, 2300.	12.8	13
36	Occult polyclonality of preclinical pancreatic cancer models drives in vitro evolution. Nature Communications, 2022, 13, .	12.8	13

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37	Gene expression signatures of individual ductal carcinoma in situ lesions identify processes and biomarkers associated with progression towards invasive ductal carcinoma. <i>Nature Communications</i> , 2022, 13, .	12.8	12
38	Sequencing and curation strategies for identifying candidate glioblastoma treatments. <i>BMC Medical Genomics</i> , 2019, 12, 56.	1.5	7
39	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419.	5.6	6
40	Retromer dysfunction in amyotrophic lateral sclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	5
41	New York's Polyethnic-1000: a regional initiative to understand how diverse ancestries influence the risk, progression, and treatment of cancers. <i>Trends in Cancer</i> , 2022, 8, 269-272.	7.4	3
42	P23: CAP: a Web-based platform for CGH-array management and analysis. <i>European Journal of Medical Genetics</i> , 2005, 48, 471-472.	1.3	0
43	SCANVIS: a tool for SCoring, ANnotating and VISualizing splice junctions. <i>Bioinformatics</i> , 2019, 35, 4843-4845.	4.1	0
44	Immune-Mediated Reprogramming of Intestinal Stem Cells Drives STAT1-Dependent Myc Expression and Epithelial Regeneration in GI-Gvhd. <i>Blood</i> , 2021, 138, 86-86.	1.4	0