

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	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
2	Diverse tumorigenic consequences of human papillomavirus integration in primary oropharyngeal cancers. <i>Genome Research</i> , 2022, 32, 55-70.	5.5	18
3	Somatic whole genome dynamics of precancer in Barrett's esophagus reveals features associated with disease progression. <i>Nature Communications</i> , 2022, 13, 2300.	12.8	13
4	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
5	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
6	Occult polyclonality of preclinical pancreatic cancer models drives in vitro evolution. <i>Nature Communications</i> , 2022, 13, .	12.8	13
7	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021, 34, 108707.	6.4	16
8	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419.	5.6	6
9	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
10	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020, 183, 197-210.e32.	28.9	141
11	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
12	Genome-wide cell-free DNA mutational integration enables ultra-sensitive cancer monitoring. <i>Nature Medicine</i> , 2020, 26, 1114-1124.	30.7	216
13	SCANVIS: a tool for SCoring, ANnotating and VISualizing splice junctions. <i>Bioinformatics</i> , 2019, 35, 4843-4845.	4.1	0
14	Immunogenic neoantigens derived from gene fusions stimulate T cell responses. <i>Nature Medicine</i> , 2019, 25, 767-775.	30.7	282
15	Sequencing and curation strategies for identifying candidate glioblastoma treatments. <i>BMC Medical Genomics</i> , 2019, 12, 56.	1.5	7
16	Genetic mechanisms of primary chemotherapy resistance in pediatric acute myeloid leukemia. <i>Leukemia</i> , 2019, 33, 1934-1943.	7.2	69
17	Deep whole-genome sequencing of 3 cancer cell lines on 2 sequencing platforms. <i>Scientific Reports</i> , 2019, 9, 19123.	3.3	39
18	Human papillomavirus and the landscape of secondary genetic alterations in oral cancers. <i>Genome Research</i> , 2019, 29, 1-17.	5.5	166

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19	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
20	taxMaps: comprehensive and highly accurate taxonomic classification of short-read data in reasonable time. <i>Genome Research</i> , 2018, 28, 751-758.	5.5	25
21	Genome-wide somatic variant calling using localized colored de Bruijn graphs. <i>Communications Biology</i> , 2018, 1, 20.	4.4	85
22	Organoid Profiling Identifies Common Responders to Chemotherapy in Pancreatic Cancer. <i>Cancer Discovery</i> , 2018, 8, 1112-1129.	9.4	676
23	Analytical Validation of Clinical Whole-Genome and Transcriptome Sequencing of Patient-Derived Tumors for Reporting Targetable Variants in Cancer. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 822-835.	2.8	23
24	<i>YES1</i> amplification is a mechanism of acquired resistance to EGFR inhibitors identified by transposon mutagenesis and clinical genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6030-E6038.	7.1	44
25	Comparing sequencing assays and human-machine analyses in actionable genomics for glioblastoma. <i>Neurology: Genetics</i> , 2017, 3, e164.	1.9	32
26	Structural insights into mis-regulation of protein kinase A in human tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1374-1379.	7.1	78
27	Diversity of miRNAs, siRNAs, and piRNAs across 25 <i>Drosophila</i> cell lines. <i>Genome Research</i> , 2014, 24, 1236-1250.	5.5	66
28	Detection of a Recurrent <i>DNAJB1-PRKACA</i> Chimeric Transcript in Fibrolamellar Hepatocellular Carcinoma. <i>Science</i> , 2014, 343, 1010-1014.	12.6	388
29	Altering the Intestinal Microbiota during a Critical Developmental Window Has Lasting Metabolic Consequences. <i>Cell</i> , 2014, 158, 705-721.	28.9	1,493
30	Prognostic value of miR-375 and miR-214-3p in early stage oral squamous cell carcinoma. <i>American Journal of Translational Research (discontinued)</i> , 2014, 6, 580-92.	0.0	24
31	Common and distinct patterns of terminal modifications to mirtrons and canonical microRNAs. <i>Rna</i> , 2012, 18, 177-192.	3.5	64
32	Computational and experimental identification of mirtrons in <i>Drosophila melanogaster</i> and <i>Caenorhabditis elegans</i> . <i>Genome Research</i> , 2011, 21, 286-300.	5.5	71
33	R2D2 Organizes Small Regulatory RNA Pathways in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 884-896.	2.3	57
34	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
35	A <i>Drosophila</i> genetic screen yields allelic series of core microRNA biogenesis factors and reveals post-developmental roles for microRNAs. <i>Rna</i> , 2011, 17, 1997-2010.	3.5	28
36	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

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37	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
38	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
39	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
40	A Broadly Conserved Pathway Generates 5'UTR-Directed Primary piRNAs. <i>Current Biology</i> , 2009, 19, 2066-2076.	3.9	304
41	Histone H3 lysine 4 trimethylation marks meiotic recombination initiation sites. <i>EMBO Journal</i> , 2009, 28, 99-111.	7.8	329
42	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. <i>Molecular Biology of the Cell</i> , 2008, 19, 2193-2207.	2.1	29
43	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
44	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