

Nicolas Rapin

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

5,674
citations

186209

28
h-index

233338

45
g-index

53
all docs

53
docs citations

53
times ranked

13629
citing authors

#	ARTICLE	IF	CITATIONS
1	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	13.7	2,269
2	Computational Immunology Meets Bioinformatics: The Use of Prediction Tools for Molecular Binding in the Simulation of the Immune System. <i>PLoS ONE</i> , 2010, 5, e9862.	1.1	535
3	EZH2 is a potential therapeutic target for H3K27M-mutant pediatric gliomas. <i>Nature Medicine</i> , 2017, 23, 483-492.	15.2	392
4	BloodSpot: a database of gene expression profiles and transcriptional programs for healthy and malignant haematopoiesis. <i>Nucleic Acids Research</i> , 2016, 44, D917-D924.	6.5	242
5	Loss of <i>TET2</i> in hematopoietic cells leads to DNA hypermethylation of active enhancers and induction of leukemogenesis. <i>Genes and Development</i> , 2015, 29, 910-922.	2.7	213
6	Quantitative single-cell proteomics as a tool to characterize cellular hierarchies. <i>Nature Communications</i> , 2021, 12, 3341.	5.8	197
7	BloodSpot: a database of healthy and malignant haematopoiesis updated with purified and single cell mRNA sequencing profiles. <i>Nucleic Acids Research</i> , 2019, 47, D881-D885.	6.5	172
8	SNHG5 promotes colorectal cancer cell survival by counteracting STAU1-mediated mRNA destabilization. <i>Nature Communications</i> , 2016, 7, 13875.	5.8	170
9	Comparing cancer vs normal gene expression profiles identifies new disease entities and common transcriptional programs in AML patients. <i>Blood</i> , 2014, 123, 894-904.	0.6	133
10	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , 2017, 18, 18.	3.8	97
11	Leukemogenic nucleophosmin mutation disrupts the transcription factor hub that regulates granulomonocytic fates. <i>Journal of Clinical Investigation</i> , 2018, 128, 4260-4279.	3.9	97
12	<i>C/EBPβ</i> Is Required for Long-Term Self-Renewal and Lineage Priming of Hematopoietic Stem Cells and for the Maintenance of Epigenetic Configurations in Multipotent Progenitors. <i>PLoS Genetics</i> , 2014, 10, e1004079.	1.5	85
13	Immune system simulation online. <i>Bioinformatics</i> , 2011, 27, 2013-2014.	1.8	82
14	Characterization of the enhancer and promoter landscape of inflammatory bowel disease from human colon biopsies. <i>Nature Communications</i> , 2018, 9, 1661.	5.8	78
15	Temporal mapping of CEBPA and CEBPB binding during liver regeneration reveals dynamic occupancy and specific regulatory codes for homeostatic and cell cycle gene batteries. <i>Genome Research</i> , 2013, 23, 592-603.	2.4	73
16	ERG promotes the maintenance of hematopoietic stem cells by restricting their differentiation. <i>Genes and Development</i> , 2015, 29, 1915-1929.	2.7	71
17	HemaExplorer: a database of mRNA expression profiles in normal and malignant haematopoiesis. <i>Nucleic Acids Research</i> , 2013, 41, D1034-D1039.	6.5	65
18	Initiation of MLL-rearranged AML is dependent on <i>C/EBPβ</i> . <i>Journal of Experimental Medicine</i> , 2014, 211, 5-13.	4.2	62

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19	MHC motif viewer. Immunogenetics, 2008, 60, 759-765.	1.2	60
20	Oral vitamin C supplementation to patients with myeloid cancer on azacitidine treatment: Normalization of plasma vitamin C induces epigenetic changes. Clinical Epigenetics, 2019, 11, 143.	1.8	55
21	Enhancer and Transcription Factor Dynamics during Myeloid Differentiation Reveal an Early Differentiation Block in Cebpa null Progenitors. Cell Reports, 2018, 23, 2744-2757.	2.9	45
22	The splicing factor RBM25 controls MYC activity in acute myeloid leukemia. Nature Communications, 2019, 10, 172.	5.8	42
23	Differences in Cell Cycle Status Underlie Transcriptional Heterogeneity in the HSC Compartment. Cell Reports, 2018, 24, 766-780.	2.9	40
24	ImmunoGrid: towards agent-based simulations of the human immune system at a natural scale <sup />. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2010, 368, 2799-2815.	1.6	39
25	SinaPlot: An Enhanced Chart for Simple and Truthful Representation of Single Observations Over Multiple Classes. Journal of Computational and Graphical Statistics, 2018, 27, 673-676.	0.9	37
26	ImmunoGrid, an integrative environment for large-scale simulation of the immune system for vaccine discovery, design and optimization. Briefings in Bioinformatics, 2008, 10, 330-340.	3.2	36
27	The MHC Motif Viewer: A Visualization Tool for MHC Binding Motifs. Current Protocols in Immunology, 2010, 88, Unit 18.17.	3.6	32
28	HemaExplorer: a Web server for easy and fast visualization of gene expression in normal and malignant hematopoiesis. Blood, 2012, 119, 6394-6395.	0.6	32
29	Intestinal transporters for endogenic and pharmaceutical organic anions: the challenges of deriving in-vitro kinetic parameters for the prediction of clinically relevant drug-drug interactions. Journal of Pharmacy and Pharmacology, 2012, 64, 1523-1548.	1.2	30
30	Mutant CEBPA directly drives the expression of the targetable tumor-promoting factor CD73 in AML. Science Advances, 2019, 5, eaaw4304.	4.7	28
31	Peak-valley-peak pattern of histone modifications delineates active regulatory elements and their directionality. Nucleic Acids Research, 2016, 44, 4037-4051.	6.5	26
32	Modelling the Human Immune System by Combining Bioinformatics and Systems Biology Approaches. Journal of Biological Physics, 2006, 32, 335-353.	0.7	19
33	TGIF1 is a negative regulator of MLL-rearranged acute myeloid leukemia. Leukemia, 2015, 29, 1018-1031.	3.3	17
34	Bistability in autoimmune diseases. Autoimmunity, 2011, 44, 256-260.	1.2	12
35	CTLs' repertoire shaping in the thymus: A Monte Carlo simulation. Autoimmunity, 2011, 44, 261-270.	1.2	10
36	Human adult HSCs can be discriminated from lineage-committed HPCs by the expression of endomucin. Blood Advances, 2018, 2, 1628-1632.	2.5	10

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37	Lack of the p42 form of C/EBP β leads to spontaneous immortalization and lineage infidelity of committed myeloid progenitors. <i>Experimental Hematology</i> , 2013, 41, 882-893.e16.	0.2	8
38	Cellular origin of prognostic chromosomal aberrations in AML patients. <i>Leukemia</i> , 2015, 29, 1785-1789.	3.3	8
39	Gaboxadol has affinity for the proton-coupled amino acid transporter 1, SLC36A1 (hPAT1)â€”A modelling approach to determine IC50 values of the three ionic species of gaboxadol. <i>European Journal of Pharmaceutical Sciences</i> , 2011, 42, 192-198.	1.9	7
40	Simulating kinetic parameters in transporter mediated permeability across Caco-2 cells. A case study of estrone-3-sulfate. <i>European Journal of Pharmaceutical Sciences</i> , 2011, 44, 218-226.	1.9	7
41	MicroRNA-941 Expression in Polymorphonuclear Granulocytes Is Not Related to Granulomatosis with Polyangiitis. <i>PLoS ONE</i> , 2016, 11, e0164985.	1.1	7
42	ERG Controls B Cell Development by Promoting Igh V-to-DJ Recombination. <i>Cell Reports</i> , 2019, 29, 2756-2769.e6.	2.9	7
43	Oncogenic fusion proteins expressed in immature hematopoietic cells fail to recapitulate the transcriptional changes observed in human AML. <i>Oncogenesis</i> , 2014, 3, e106-e106.	2.1	6
44	PTBP1 promotes hematopoietic stem cell maintenance and red blood cell development by ensuring sufficient availability of ribosomal constituents. <i>Cell Reports</i> , 2022, 39, 110793.	2.9	3
45	Bloodspot: A Web Resource Facilitating the Analysis of Transcriptional Programs in Normal and Malignant Hematopoiesis. <i>Blood</i> , 2015, 126, 2358-2358.	0.6	1
46	The splice factor PTBP1 regulates hematopoietic stem cell function and red blood cell development. <i>Experimental Hematology</i> , 2016, 44, S95-S96.	0.2	0
47	The PRC2 component JARID2 is dispensable for hematopoietic stem cells, but critical for maintenance of leukemic stem cells. <i>Experimental Hematology</i> , 2016, 44, S47.	0.2	0
48	Arrested Differentiation in Acute Myeloid Leukemia (AML) with Silenced Ankyrin Repeat and SOCS Box Protein 3 (ASB3) Expression. <i>Blood</i> , 2012, 120, 1232-1232.	0.6	0
49	Hemaexplorer 2.0: A Free Access Internet Platform For Visualization Of Gene Expression In AML Patients and The Normal Hematopoietic Hierarchy. <i>Blood</i> , 2013, 122, 2590-2590.	0.6	0
50	Improving The Analysis Of Gene Expression Profiles By Comparing AML Blasts With Their Nearest Normal Counterparts. <i>Blood</i> , 2013, 122, 2568-2568.	0.6	0
51	The Mechanisms By Which Mutant-NPM1 Uncouples Differentiation from Proliferation Are Reversed By Several Drugs, Enabling Rational Multi-Component Non-Cytotoxic Differentiation Therapy. <i>Blood</i> , 2017, 130, 878-878.	0.6	0