

# 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	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
2	Quantitative single-cell proteomics as a tool to characterize cellular hierarchies. <i>Nature Communications</i> , 2021, 12, 3341.	5.8	197
3	Mutant CEBPA directly drives the expression of the targetable tumor-promoting factor CD73 in AML. <i>Science Advances</i> , 2019, 5, eaaw4304.	4.7	28
4	The splicing factor RBM25 controls MYC activity in acute myeloid leukemia. <i>Nature Communications</i> , 2019, 10, 172.	5.8	42
5	Oral vitamin C supplementation to patients with myeloid cancer on azacitidine treatment: Normalization of plasma vitamin C induces epigenetic changes. <i>Clinical Epigenetics</i> , 2019, 11, 143.	1.8	55
6	ERG Controls B Cell Development by Promoting Igh V-to-DJ Recombination. <i>Cell Reports</i> , 2019, 29, 2756-2769.e6.	2.9	7
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	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
9	SinaPlot: An Enhanced Chart for Simple and Truthful Representation of Single Observations Over Multiple Classes. <i>Journal of Computational and Graphical Statistics</i> , 2018, 27, 673-676.	0.9	37
10	Human adult HSCs can be discriminated from lineage-committed HPCs by the expression of endomucin. <i>Blood Advances</i> , 2018, 2, 1628-1632.	2.5	10
11	Enhancer and Transcription Factor Dynamics during Myeloid Differentiation Reveal an Early Differentiation Block in Cebpa null Progenitors. <i>Cell Reports</i> , 2018, 23, 2744-2757.	2.9	45
12	Differences in Cell Cycle Status Underlie Transcriptional Heterogeneity in the HSC Compartment. <i>Cell Reports</i> , 2018, 24, 766-780.	2.9	40
13	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
14	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , 2017, 18, 18.	3.8	97
15	EZH2 is a potential therapeutic target for H3K27M-mutant pediatric gliomas. <i>Nature Medicine</i> , 2017, 23, 483-492.	15.2	392
16	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
17	MicroRNA-941 Expression in Polymorphonuclear Granulocytes Is Not Related to Granulomatosis with Polyangiitis. <i>PLoS ONE</i> , 2016, 11, e0164985.	1.1	7
18	SNHG5 promotes colorectal cancer cell survival by counteracting STAU1-mediated mRNA destabilization. <i>Nature Communications</i> , 2016, 7, 13875.	5.8	170

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19	Peak-valley-peak pattern of histone modifications delineates active regulatory elements and their directionality. <i>Nucleic Acids Research</i> , 2016, 44, 4037-4051.	6.5	26
20	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
21	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
22	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
23	TGIF1 is a negative regulator of MLL-rearranged acute myeloid leukemia. <i>Leukemia</i> , 2015, 29, 1018-1031.	3.3	17
24	Cellular origin of prognostic chromosomal aberrations in AML patients. <i>Leukemia</i> , 2015, 29, 1785-1789.	3.3	8
25	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
26	ERG promotes the maintenance of hematopoietic stem cells by restricting their differentiation. <i>Genes and Development</i> , 2015, 29, 1915-1929.	2.7	71
27	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
28	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
29	<i>C/EBP<math>\beta</math></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
30	Initiation of MLL-rearranged AML is dependent on <i>C/EBP<math>\beta</math></i> . <i>Journal of Experimental Medicine</i> , 2014, 211, 5-13.	4.2	62
31	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	13.7	2,269
32	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
33	Lack of the p42 form of <i>C/EBP<math>\beta</math></i> leads to spontaneous immortalization and lineage infidelity of committed myeloid progenitors. <i>Experimental Hematology</i> , 2013, 41, 882-893.e16.	0.2	8
34	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
35	HemaExplorer: a database of mRNA expression profiles in normal and malignant haematopoiesis. <i>Nucleic Acids Research</i> , 2013, 41, D1034-D1039.	6.5	65
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	HemaExplorer: a Web server for easy and fast visualization of gene expression in normal and malignant hematopoiesis. <i>Blood</i> , 2012, 119, 6394-6395.	0.6	32
39	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. <i>Journal of Pharmacy and Pharmacology</i> , 2012, 64, 1523-1548.	1.2	30
40	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
41	Bistability in autoimmune diseases. <i>Autoimmunity</i> , 2011, 44, 256-260.	1.2	12
42	CTLs' repertoire shaping in the thymus: A Monte Carlo simulation. <i>Autoimmunity</i> , 2011, 44, 261-270.	1.2	10
43	Gaboxadol has affinity for the proton-coupled amino acid transporter 1, SLC36A1 (hPAT1) – 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
44	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
45	Immune system simulation online. <i>Bioinformatics</i> , 2011, 27, 2013-2014.	1.8	82
46	ImmunoGrid: towards agent-based simulations of the human immune system at a natural scale <sup />. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2010, 368, 2799-2815.	1.6	39
47	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
48	The MHC Motif Viewer: A Visualization Tool for MHC Binding Motifs. <i>Current Protocols in Immunology</i> , 2010, 88, Unit 18.17.	3.6	32
49	MHC motif viewer. <i>Immunogenetics</i> , 2008, 60, 759-765.	1.2	60
50	ImmunoGrid, an integrative environment for large-scale simulation of the immune system for vaccine discovery, design and optimization. <i>Briefings in Bioinformatics</i> , 2008, 10, 330-340.	3.2	36
51	Modelling the Human Immune System by Combining Bioinformatics and Systems Biology Approaches. <i>Journal of Biological Physics</i> , 2006, 32, 335-353.	0.7	19