

# Catrina C Fronick

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

5,594  
citations

279798

23  
h-index

276875

41  
g-index

50  
all docs

50  
docs citations

50  
times ranked

12056  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic and Transcriptional Contributions to Relapse in Normal Karyotype Acute Myeloid Leukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 32-49.	5.0	14
2	Recurrent switch 2 domain <i>RAC2</i> mutations in intravascular large B-cell lymphoma. <i>Blood Advances</i> , 2022, 6, 6051-6055.	5.2	3
3	Convergent Clonal Evolution of Signaling Gene Mutations Is a Hallmark of Myelodysplastic Syndrome Progression. <i>Blood Cancer Discovery</i> , 2022, 3, 330-345.	5.0	10
4	Rapid and Extraction-Free Detection of SARS-CoV-2 from Saliva by Colorimetric Reverse-Transcription Loop-Mediated Isothermal Amplification. <i>Clinical Chemistry</i> , 2021, 67, 415-424.	3.2	192
5	A domestic cat whole exome sequencing resource for trait discovery. <i>Scientific Reports</i> , 2021, 11, 7159.	3.3	13
6	Heterogeneity of meningeal B cells reveals a lymphopoietic niche at the CNS borders. <i>Science</i> , 2021, 373, .	12.6	218
7	Immunosuppression and outcomes in adult patients with de novo acute myeloid leukemia with normal karyotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	24
8	Harnessing Expressed Single Nucleotide Variation and Single Cell RNA Sequencing To Define Immune Cell Chimerism in the Rejecting Kidney Transplant. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 1977-1986.	6.1	71
9	TREM2 Modulation Remodels the Tumor Myeloid Landscape Enhancing Anti-PD-1 Immunotherapy. <i>Cell</i> , 2020, 182, 886-900.e17.	28.9	309
10	Sequence analysis in <i>Bos taurus</i> reveals pervasiveness of X <sup>Y</sup> arms races in mammalian lineages. <i>Genome Research</i> , 2020, 30, 1716-1726.	5.5	29
11	Remethylation of <i>Dnmt3a</i> hematopoietic cells is associated with partial correction of gene dysregulation and reduced myeloid skewing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3123-3134.	7.1	27
12	The clonal evolution of metastatic colorectal cancer. <i>Science Advances</i> , 2020, 6, eaay9691.	10.3	41
13	Draft Genome Sequences of Two Polycyclic Tetramate Macrolactam Producers, <i>Streptomyces</i> sp. Strains JV180 and SP18CM02. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
14	Identification of predicted neoantigen vaccine candidates in follicular lymphoma patients.. <i>Journal of Clinical Oncology</i> , 2020, 38, 8054-8054.	1.6	0
15	Signaling Gene Mutations Are Characterized By Diverse Patterns of Expansion and Contraction during Progression from MDS to Secondary AML. <i>Blood</i> , 2020, 136, 2-3.	1.4	0
16	A general approach for detecting expressed mutations in AML cells using single cell RNA-sequencing. <i>Nature Communications</i> , 2019, 10, 3660.	12.8	147
17	Subsets of ILC3-like cells generate a diversity spectrum of innate lymphoid cells in human mucosal tissues. <i>Nature Immunology</i> , 2019, 20, 980-991.	14.5	141
18	Single-Cell Transcriptomic and Proteomic Diversity in Multiple Myeloma. <i>Blood</i> , 2019, 134, 5531-5531.	1.4	1

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19	The Molecular Basis of Long First Remissions in Normal Karyotype AML Patients. <i>Blood</i> , 2019, 134, 3827-3827.	1.4	0
20	Whole Genome Bisulfite Sequencing of 63 Primary AML Samples Identifies a Unique DNA Hypermethylation Signature for Mutant IDH1/2 Cases That Is Different from That of TET2 Mutant AML. <i>Blood</i> , 2019, 134, 3755-3755.	1.4	0
21	An "off-the-shelf" fratricide-resistant CAR-T for the treatment of T cell hematologic malignancies. <i>Leukemia</i> , 2018, 32, 1970-1983.	7.2	282
22	High-Dimensional Analysis Delineates Myeloid and Lymphoid Compartment Remodeling during Successful Immune-Checkpoint Cancer Therapy. <i>Cell</i> , 2018, 175, 1014-1030.e19.	28.9	292
23	The prognostic effects of somatic mutations in ER-positive breast cancer. <i>Nature Communications</i> , 2018, 9, 3476.	12.8	89
24	A multiple myeloma-specific capture sequencing platform discovers novel translocations and frequent, risk-associated point mutations in IGLL5. <i>Blood Cancer Journal</i> , 2018, 8, 35.	6.2	41
25	Subclones dominate at MDS progression following allogeneic hematopoietic cell transplant. <i>JCI Insight</i> , 2018, 3, .	5.0	48
26	Evidence for Complete Mutation Clearance in Normal Karyotype AML Patients with Very Long (> 5) Tj ETQqO O O rgBT /Overlock 10 Tf 50	1.4	0
27	Improving Risk Assessment of AML with a Precision Genomic Strategy to Assess Mutation Clearance. <i>Blood</i> , 2018, 132, 5277-5277.	1.4	0
28	Direct Detection of Expressed Mutations in AML Cells Using Single Cell RNA-Sequencing, and Its Impact on Defining Sources of Expression Heterogeneity. <i>Blood</i> , 2018, 132, 1314-1314.	1.4	0
29	Recurrent somatic mutations affecting B-cell receptor signaling pathway genes in follicular lymphoma. <i>Blood</i> , 2017, 129, 473-483.	1.4	147
30	Brief Report: The Role of Rare Protein-Coding Variants in Anti-Tumor Necrosis Factor Treatment Response in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2017, 69, 735-741.	5.6	8
31	Haploinsufficiency for DNA methyltransferase 3A predisposes hematopoietic cells to myeloid malignancies. <i>Journal of Clinical Investigation</i> , 2017, 127, 3657-3674.	8.2	80
32	An Off-the-Shelf, Fratricide-Resistant CAR-T for the Treatment of T Cell Hematologic Malignancies. <i>Blood</i> , 2017, 130, 844-844.	1.4	2
33	TP53 and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes. <i>New England Journal of Medicine</i> , 2016, 375, 2023-2036.	27.0	663
34	The <i>Physarum polycephalum</i> Genome Reveals Extensive Use of Prokaryotic Two-Component and Metazoan-Type Tyrosine Kinase Signaling. <i>Genome Biology and Evolution</i> , 2016, 8, 109-125.	2.5	87
35	Rare Pre-Existing MDS Subclones Contribute to Secondary AML Progression. <i>Blood</i> , 2016, 128, 959-959.	1.4	12
36	Dynamic Changes in MDS Clonal Architecture Following Allogeneic Stem Cell Transplant. <i>Blood</i> , 2016, 128, 5506-5506.	1.4	0

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37	Optimizing Cancer Genome Sequencing and Analysis. <i>Cell Systems</i> , 2015, 1, 210-223.	6.2	174
38	Genetic Heterogeneity of Induced Pluripotent Stem Cells: Results from 24 Clones Derived from a Single C57BL/6 Mouse. <i>PLoS ONE</i> , 2015, 10, e0120585.	2.5	12
39	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14936-14941.	7.1	329
40	Recurrent Somatic Genomic Alterations in Follicular NHL (FL) Revealed By Exome and Custom-Capture Next Generation Sequencing. <i>Blood</i> , 2015, 126, 574-574.	1.4	2
41	Dynamic Changes in the Clonal Structure of MDS and AML in Response to Epigenetic Therapy. <i>Blood</i> , 2015, 126, 610-610.	1.4	3
42	TYK2 Protein-Coding Variants Protect against Rheumatoid Arthritis and Autoimmunity, with No Evidence of Major Pleiotropic Effects on Non-Autoimmune Complex Traits. <i>PLoS ONE</i> , 2015, 10, e0122271.	2.5	120
43	Specific Patterns of DNA Remethylation in the Bone Marrow Cells of Dnmt3a Deficient Mice after Induced Expression of Wild Type Human DNMT3A. <i>Blood</i> , 2015, 126, 433-433.	1.4	0
44	Subtelomeric CTCF and cohesin binding site organization using improved subtelomere assemblies and a novel annotation pipeline. <i>Genome Research</i> , 2014, 24, 1039-1050.	5.5	64
45	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	27.8	320
46	Whole-Genome Bisulfite Sequencing of Primary AML Cells with the DNMT3A R882H Mutation Identifies Regions of Focal Hypomethylation That Are Associated with Open Chromatin. <i>Blood</i> , 2014, 124, 608-608.	1.4	3
47	Genome remodelling in a basal-like breast cancer metastasis and xenograft. <i>Nature</i> , 2010, 464, 999-1005.	27.8	1,077
48	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. <i>Science</i> , 2010, 330, 1549-1551.	12.6	492