

# Catrina C Fronick

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3720395/publications.pdf>

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  | Genome remodelling in a basal-like breast cancer metastasis and xenograft. <i>Nature</i> , 2010, 464, 999-1005.   | 27.8 | 1,077     |
| 2  | <i>TP53</i> and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes. <i>New England Journal of Medicine</i> , 2016, 375, 2023-2036.  | 27.0 | 663       |
| 3  | Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. <i>Science</i> , 2010, 330, 1549-1551.  | 12.6 | 492       |
| 4  | 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       |
| 5  | Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.   | 27.8 | 320       |
| 6  | TREM2 Modulation Remodels the Tumor Myeloid Landscape Enhancing Anti-PD-1 Immunotherapy. <i>Cell</i> , 2020, 182, 886-900.e17.  | 28.9 | 309       |
| 7  | 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       |
| 8  | An "off-the-shelf" fratricide-resistant CART for the treatment of T cell hematologic malignancies. <i>Leukemia</i> , 2018, 32, 1970-1983.   | 7.2  | 282       |
| 9  | Heterogeneity of meningeal B cells reveals a lymphopoietic niche at the CNS borders. <i>Science</i> , 2021, 373, .  | 12.6 | 218       |
| 10 | 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       |
| 11 | Optimizing Cancer Genome Sequencing and Analysis. <i>Cell Systems</i> , 2015, 1, 210-223.   | 6.2  | 174       |
| 12 | Recurrent somatic mutations affecting B-cell receptor signaling pathway genes in follicular lymphoma. <i>Blood</i> , 2017, 129, 473-483.  | 1.4  | 147       |
| 13 | 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       |
| 14 | Subsets of ILC3~ILC1-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       |
| 15 | 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       |
| 16 | The prognostic effects of somatic mutations in ER-positive breast cancer. <i>Nature Communications</i> , 2018, 9, 3476.   | 12.8 | 89        |
| 17 | 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        |
| 18 | Haploinsufficiency for DNA methyltransferase 3A predisposes hematopoietic cells to myeloid malignancies. <i>Journal of Clinical Investigation</i> , 2017, 127, 3657-3674.   | 8.2  | 80        |

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|----|--|------|-----------|
| 19 | 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        |
| 20 | 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        |
| 21 | Subclones dominate at MDS progression following allogeneic hematopoietic cell transplant. <i>JCI Insight</i> , 2018, 3, .  | 5.0  | 48        |
| 22 | 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        |
| 23 | The clonal evolution of metastatic colorectal cancer. <i>Science Advances</i> , 2020, 6, eaay9691.   | 10.3 | 41        |
| 24 | 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        |
| 25 | 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        |
| 26 | 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        |
| 27 | Genetic and Transcriptional Contributions to Relapse in Normal Karyotype Acute Myeloid Leukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 32-49.   | 5.0  | 14        |
| 28 | A domestic cat whole exome sequencing resource for trait discovery. <i>Scientific Reports</i> , 2021, 11, 7159.  | 3.3  | 13        |
| 29 | 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        |
| 30 | Rare Pre-Existing MDS Subclones Contribute to Secondary AML Progression. <i>Blood</i> , 2016, 128, 959-959.  | 1.4  | 12        |
| 31 | 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        |
| 32 | 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         |
| 33 | 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         |
| 34 | 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         |
| 35 | 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         |
| 36 | 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         |

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|----|---|-----|-----------|
| 37 | An Off-the-Shelf, Fratricide-Resistant CAR-T for the Treatment of T Cell Hematologic Malignancies. Blood, 2017, 130, 844-844.   | 1.4 | 2         |
| 38 | Draft Genome Sequences of Two Polycyclic Tetramate Macrolactam Producers, Streptomyces sp. Strains JV180 and SP18CM02. Microbiology Resource Announcements, 2020, 9, .  | 0.6 | 1         |
| 39 | Single-Cell Transcriptomic and Proteomic Diversity in Multiple Myeloma. Blood, 2019, 134, 5531-5531.  | 1.4 | 1         |
| 40 | Specific Patterns of DNA Remethylation in the Bone Marrow Cells of Dnmt3a Deficient Mice after Induced Expression of Wild Type Human DNMT3A. Blood, 2015, 126, 433-433.   | 1.4 | 0         |
| 41 | Dynamic Changes in MDS Clonal Architecture Following Allogeneic Stem Cell Transplant. Blood, 2016, 128, 5506-5506.  | 1.4 | 0         |
| 42 | 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         |
| 43 | Improving Risk Assessment of AML with a Precision Genomic Strategy to Assess Mutation Clearance. Blood, 2018, 132, 5277-5277.   | 1.4 | 0         |
| 44 | Direct Detection of Expressed Mutations in AML Cells Using Single Cell RNA-Sequencing, and Its Impact on Defining Sources of Expression Heterogeneity. Blood, 2018, 132, 1314-1314.                                 | 1.4 | 0         |
| 45 | The Molecular Basis of Long First Remissions in Normal Karyotype AML Patients. Blood, 2019, 134, 3827-3827.   | 1.4 | 0         |
| 46 | 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. Blood, 2019, 134, 3755-3755. | 1.4 | 0         |
| 47 | Identification of predicted neoantigen vaccine candidates in follicular lymphoma patients.. Journal of Clinical Oncology, 2020, 38, 8054-8054.  | 1.6 | 0         |
| 48 | Signaling Gene Mutations Are Characterized By Diverse Patterns of Expansion and Contraction during Progression from MDS to Secondary AML. Blood, 2020, 136, 2-3.  | 1.4 | 0         |