# Raul Rabadan

List of Publications by Year
in descending order

| | | | |
|---|---|---|---|
| 236 papers | 25,742 citations | 11651<br>70 h-index | 7518<br>151 g-index |
| 270 all docs | 270 docs citations | 270 times ranked | 36265 citing authors |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 1 | Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563. | 28.9 | 1,695 |
| 2 | Promotion of Hepatocellular Carcinoma by the Intestinal Microbiota and TLR4. Cancer Cell, 2012, 21, 504-516. | 16.8 | 1,051 |
| 3 | *BRAF* Mutations in Hairy-Cell Leukemia. New England Journal of Medicine, 2011, 364, 2305-2315. | 27.0 | 949 |
| 4 | Analysis of the coding genome of diffuse large B-cell lymphoma. Nature Genetics, 2011, 43, 830-837. | 21.4 | 871 |
| 5 | Inactivating mutations of acetyltransferase genes in B-cell lymphoma. Nature, 2011, 471, 189-195. | 27.8 | 822 |
| 6 | Transforming Fusions of *FGFR* and *TACC* Genes in Human Glioblastoma. Science, 2012, 337, 1231-1235. | 12.6 | 716 |
| 7 | Clonal evolution of glioblastoma under therapy. Nature Genetics, 2016, 48, 768-776. | 21.4 | 591 |
| 8 | Immune and genomic correlates of response to anti-PD-1 immunotherapy in glioblastoma. Nature Medicine, 2019, 25, 462-469. | 30.7 | 569 |
| 9 | Analysis of the chronic lymphocytic leukemia coding genome: role of *NOTCH1* mutational activation. Journal of Experimental Medicine, 2011, 208, 1389-1401. | 8.5 | 565 |
| 10 | Recurrent mutations in epigenetic regulators, RHOA and FYN kinase in peripheral T cell lymphomas. Nature Genetics, 2014, 46, 166-170. | 21.4 | 534 |
| 11 | The integrated landscape of driver genomic alterations in glioblastoma. Nature Genetics, 2013, 45, 1141-1149. | 21.4 | 524 |
| 12 | Genetics of Follicular Lymphoma Transformation. Cell Reports, 2014, 6, 130-140. | 6.4 | 471 |
| 13 | Leukaemogenesis induced by an activating β-catenin mutation in osteoblasts. Nature, 2014, 506, 240-244. | 27.8 | 455 |
| 14 | Genetic inactivation of the polycomb repressive complex 2 in T cell acute lymphoblastic leukemia. Nature Medicine, 2012, 18, 298-302. | 30.7 | 453 |
| 15 | Integrated mutational and cytogenetic analysis identifies new prognostic subgroups in chronic lymphocytic leukemia. Blood, 2013, 121, 1403-1412. | 1.4 | 420 |
| 16 | Mutations of NOTCH1 are an independent predictor of survival in chronic lymphocytic leukemia. Blood, 2012, 119, 521-529. | 1.4 | 394 |
| 17 | Convergent Mutations and Kinase Fusions Lead to Oncogenic STAT3 Activation in Anaplastic Large Cell Lymphoma. Cancer Cell, 2015, 27, 516-532. | 16.8 | 378 |
| 18 | RNA Exosome-Regulated Long Non-Coding RNA Transcription Controls Super-Enhancer Activity. Cell, 2015, 161, 774-789. | 28.9 | 370 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 19 | The coding genome of splenic marginal zone lymphoma: activation of *NOTCH2* and other pathways regulating marginal zone development. Journal of Experimental Medicine, 2012, 209, 1537-1551. | 8.5 | 363 |
| 20 | Mutations of the SF3B1 splicing factor in chronic lymphocytic leukemia: association with progression and fludarabine-refractoriness. Blood, 2011, 118, 6904-6908. | 1.4 | 342 |
| 21 | The mutational landscape of cutaneous T cell lymphoma and Sézary syndrome. Nature Genetics, 2015, 47, 1465-1470. | 21.4 | 322 |
| 22 | Longitudinal molecular trajectories of diffuse glioma in adults. Nature, 2019, 576, 112-120. | 27.8 | 320 |
| 23 | Activating mutations in the NT5C2 nucleotidase gene drive chemotherapy resistance in relapsed ALL. Nature Medicine, 2013, 19, 368-371. | 30.7 | 304 |
| 24 | D=4 chiral string compactifications from intersecting branes. Journal of Mathematical Physics, 2001, 42, 3103-3126. | 1.1 | 302 |
| 25 | Clinical impact of small TP53 mutated subclones in chronic lymphocytic leukemia. Blood, 2014, 123, 2139-2147. | 1.4 | 302 |
| 26 | Codon usage bias and the evolution of influenza A viruses. Codon Usage Biases of Influenza Virus. BMC Evolutionary Biology, 2010, 10, 253. | 3.2 | 295 |
| 27 | Restoration of Replication Fork Stability in BRCA1- and BRCA2-Deficient Cells by Inactivation of SNF2-Family Fork Remodelers. Molecular Cell, 2017, 68, 414-430.e8. | 9.7 | 295 |
| 28 | PHF6 mutations in T-cell acute lymphoblastic leukemia. Nature Genetics, 2010, 42, 338-342. | 21.4 | 282 |
| 29 | Genetic lesions associated with chronic lymphocytic leukemia transformation to Richter syndrome. Journal of Experimental Medicine, 2013, 210, 2273-2288. | 8.5 | 255 |
| 30 | Geographic Dependence, Surveillance, and Origins of the 2009 Influenza A (H1N1) Virus. New England Journal of Medicine, 2009, 361, 115-119. | 27.0 | 252 |
| 31 | Patterns of Evolution and Host Gene Mimicry in Influenza and Other RNA Viruses. PLoS Pathogens, 2008, 4, e1000079. | 4.7 | 236 |
| 32 | Whole-exome sequencing identifies somatic mutations of BCOR in acute myeloid leukemia with normal karyotype. Blood, 2011, 118, 6153-6163. | 1.4 | 227 |
| 33 | Spatiotemporal genomic architecture informs precision oncology in glioblastoma. Nature Genetics, 2017, 49, 594-599. | 21.4 | 223 |
| 34 | The Egyptian Rousette Genome Reveals Unexpected Features of Bat Antiviral Immunity. Cell, 2018, 173, 1098-1110.e18. | 28.9 | 220 |
| 35 | Single-cell topological RNA-seq analysis reveals insights into cellular differentiation and development. Nature Biotechnology, 2017, 35, 551-560. | 17.5 | 215 |
| 36 | A Nondegenerate Code of Deleterious Variants in Mendelian Loci Contributes to Complex Disease Risk. Cell, 2013, 155, 70-80. | 28.9 | 209 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------| 
| 37 | Somatic mutations and cell identity linked by Genotyping of Transcriptomes. Nature, 2019, 571, 355-360. | 27.8 | 206 |
| 38 | Topology of viral evolution. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18566-18571. | 7.1 | 204 |
| 39 | Heart and Skeletal Muscle Inflammation of Farmed Salmon Is Associated with Infection with a Novel Reovirus. PLoS ONE, 2010, 5, e11487. | 2.5 | 198 |
| 40 | Drugâ€"drug interaction through molecular structure similarity analysis. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 1066-1074. | 4.4 | 185 |
| 41 | Double <i>PIK3CA</i> mutations in cis increase oncogenicity and sensitivity to PI3KÎ± inhibitors. Science, 2019, 366, 714-723. | 12.6 | 185 |
| 42 | Disease-associated mutation in <i>SRSF2</i> misregulates splicing by altering RNA-binding affinities. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4726-34. | 7.1 | 175 |
| 43 | Pervasive mutations of JAK-STAT pathway genes in classical Hodgkin lymphoma. Blood, 2018, 131, 2454-2465. | 1.4 | 167 |
| 44 | Glioma progression is shaped by genetic evolution and microenvironment interactions. Cell, 2022, 185, 2184-2199.e16. | 28.9 | 163 |
| 45 | Emergence of Fatal Avian Influenza in New England Harbor Seals. MBio, 2012, 3, e00166-12. | 4.1 | 161 |
| 46 | An NF-Î°B Transcription-Factor-Dependent Lineage-Specific Transcriptional Program Promotes Regulatory T Cell Identity and Function. Immunity, 2017, 47, 450-465.e5. | 14.3 | 161 |
| 47 | Noncoding RNA transcription targets AID to divergently transcribed loci in B cells. Nature, 2014, 514, 389-393. | 27.8 | 159 |
| 48 | Promotion of cholangiocarcinoma growth by diverse cancer-associated fibroblast subpopulations. Cancer Cell, 2021, 39, 866-882.e11. | 16.8 | 159 |
| 49 | iPLA2Î²-mediated lipid detoxification controls p53-driven ferroptosis independent of GPX4. Nature Communications, 2021, 12, 3644. | 12.8 | 153 |
| 50 | Mutational landscape, clonal evolution patterns, and role of RAS mutations in relapsed acute lymphoblastic leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11306-11311. | 7.1 | 151 |
| 51 | The genetics of nodal marginal zone lymphoma. Blood, 2016, 128, 1362-1373. | 1.4 | 147 |
| 52 | The 2019 mathematical oncology roadmap. Physical Biology, 2019, 16, 041005. | 1.8 | 147 |
| 53 | Pharmacogenomic landscape of patient-derived tumor cells informs precision oncology therapy. Nature Genetics, 2018, 50, 1399-1411. | 21.4 | 145 |
| 54 | Functional interrogation of DNA damage response variants with base editing screens. Cell, 2021, 184, 1081-1097.e19. | 28.9 | 145 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 55 | Highly Conserved Regions of Influenza A Virus Polymerase Gene Segments Are Critical for Efficient Viral RNA Packaging. Journal of Virology, 2008, 82, 2295-2304. | 3.4 | 144 |
| 56 | A Targetable GATA2-IGF2 Axis Confers Aggressiveness in Lethal Prostate Cancer. Cancer Cell, 2015, 27, 223-239. | 16.8 | 128 |
| 57 | Saa3 is a key mediator of the protumorigenic properties of cancer-associated fibroblasts in pancreatic tumors. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1147-E1156. | 7.1 | 128 |
| 58 | Distinct Viral and Mutational Spectrum of Endemic Burkitt Lymphoma. PLoS Pathogens, 2015, 11, e1005158. | 4.7 | 127 |
| 59 | Comparison of Avian and Human Influenza A Viruses Reveals a Mutational Bias on the Viral Genomes. Journal of Virology, 2006, 80, 11887-11891. | 3.4 | 114 |
| 60 | arcasHLA: high-resolution HLA typing from RNAseq. Bioinformatics, 2020, 36, 33-40. | 4.1 | 113 |
| 61 | MGMT genomic rearrangements contribute to chemotherapy resistance in gliomas. Nature Communications, 2020, 11, 3883. | 12.8 | 110 |
| 62 | Comprehensive characterization of protein–protein interactions perturbed by disease mutations. Nature Genetics, 2021, 53, 342-353. | 21.4 | 109 |
| 63 | A Structure-Informed Atlas of Human-Virus Interactions. Cell, 2019, 178, 1526-1541.e16. | 28.9 | 108 |
| 64 | Activating mutations and translocations in the guanine exchange factor VAV1 in peripheral T-cell lymphomas. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 764-769. | 7.1 | 100 |
| 65 | Identification of a new subclass of ALK-negative ALCL expressing aberrant levels of ERBB4 transcripts. Blood, 2016, 127, 221-232. | 1.4 | 97 |
| 66 | Transcriptomics Identify CD9 as a Marker of Murine IL-10-Competent Regulatory B Cells. Cell Reports, 2015, 13, 1110-1117. | 6.4 | 95 |
| 67 | Quantitative Analysis of Immune Infiltrates in Primary Melanoma. Cancer Immunology Research, 2018, 6, 481-493. | 3.4 | 92 |
| 68 | Clonal evolution mechanisms in NT5C2 mutant-relapsed acute lymphoblastic leukaemia. Nature, 2018, 553, 511-514. | 27.8 | 90 |
| 69 | Mitochondrial DNA Haplogroup D4a Is a Marker for Extreme Longevity in Japan. PLoS ONE, 2008, 3, e2421. | 2.5 | 88 |
| 70 | FBXW7 Mutations in Melanoma and a New Therapeutic Paradigm. Journal of the National Cancer Institute, 2014, 106, dju107. | 6.3 | 87 |
| 71 | Disease-Causing Mutations in SF3B1 Alter Splicing by Disrupting Interaction with SUGP1. Molecular Cell, 2019, 76, 82-95.e7. | 9.7 | 84 |
| 72 | Genetic lesions associated with chronic lymphocytic leukemia chemo-refractoriness. Blood, 2014, 123, 2378-2388. | 1.4 | 78 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 73 | Complete Regression of Advanced Pancreatic Ductal Adenocarcinomas upon Combined Inhibition of EGFR and C-RAF. Cancer Cell, 2019, 35, 573-587.e6. | 16.8 | 75 |
| 74 | Mutations in the RNA Splicing Factor SF3B1 Promote Tumorigenesis through MYC Stabilization. Cancer Discovery, 2020, 10, 806-821. | 9.4 | 73 |
| 75 | Patterns of Oligonucleotide Sequences in Viral and Host Cell RNA Identify Mediators of the Host Innate Immune System. PLoS ONE, 2009, 4, e5969. | 2.5 | 73 |
| 76 | Tissue-Resident Memory T Cells Mediate Immune Homeostasis in the Human Pancreas through the PD-1/PD-L1 Pathway. Cell Reports, 2019, 29, 3916-3932.e5. | 6.4 | 69 |
| 77 | A single-cell atlas of the mouse and human prostate reveals heterogeneity and conservation of epithelial progenitors. ELife, 2020, 9, . | 6.0 | 69 |
| 78 | Biclustering of Adverse Drug Events in the FDA's Spontaneous Reporting System. Clinical Pharmacology and Therapeutics, 2011, 89, 243-250. | 4.7 | 67 |
| 79 | <i>Phf6</i> Loss Enhances HSC Self-Renewal Driving Tumor Initiation and Leukemia Stem Cell Activity in T-ALL. Cancer Discovery, 2019, 9, 436-451. | 9.4 | 67 |
| 80 | The <i>miR-424(322)/503</i> cluster orchestrates remodeling of the epithelium in the involuting mammary gland. Genes and Development, 2014, 28, 765-782. | 5.9 | 66 |
| 81 | The B-cell receptor controls fitness of MYC-driven lymphoma cells via GSK3$\beta$ inhibition. Nature, 2017, 546, 302-306. | 27.8 | 64 |
| 82 | Midkine rewires the melanoma microenvironment toward a tolerogenic and immune-resistant state. Nature Medicine, 2020, 26, 1865-1877. | 30.7 | 62 |
| 83 | Viral reassortment as an information exchange between viral segments. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3341-3346. | 7.1 | 61 |
| 84 | Differential levels of transcription of p53â€‐regulated genes by the arginine/proline polymorphism: p53 with arginine at codon 72 favors apoptosis. FASEB Journal, 2010, 24, 1347-1353. | 0.5 | 60 |
| 85 | Pegasus: a comprehensive annotation and prediction tool for detection of driver gene fusions in cancer. BMC Systems Biology, 2014, 8, 97. | 3.0 | 60 |
| 86 | Predicting Clinical Outcomes in Glioblastoma: An Application of Topological and Functional Data Analysis. Journal of the American Statistical Association, 2020, 115, 1139-1150. | 3.1 | 60 |
| 87 | Blastic plasmacytoid dendritic cell neoplasm: genomics mark epigenetic dysregulation as a primary therapeutic target. Haematologica, 2019, 104, 729-737. | 3.5 | 58 |
| 88 | Nonâ€‐random reassortment in human influenza A viruses. Influenza and Other Respiratory Viruses, 2008, 2, 9-22. | 3.4 | 57 |
| 89 | Single-cell characterization of macrophages in glioblastoma reveals MARCO as a mesenchymal pro-tumor marker. Genome Medicine, 2021, 13, 88. | 8.2 | 57 |
| 90 | Oligonucleotide Motifs That Disappear during the Evolution of Influenza Virus in Humans Increase Alpha Interferon Secretion by Plasmacytoid Dendritic Cells. Journal of Virology, 2011, 85, 3893-3904. | 3.4 | 56 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 91 | Facilitating adverse drug event detection in pharmacovigilance databases using molecular structure similarity: application to rhabdomyolysis. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, i73-i80. | 4.4 | 56 |
| 92 | Evolutionary Dynamics of Pandemic Methicillin-Sensitive *Staphylococcus aureus* ST398 and Its International Spread via Routes of Human Migration. MBio, 2017, 8, . | 4.1 | 56 |
| 93 | Nuclear Proximity of Mtr4 to RNA Exosome Restricts DNA Mutational Asymmetry. Cell, 2017, 169, 523-537.e15. | 28.9 | 56 |
| 94 | Novel insights into the genetics and epigenetics of MALT lymphoma unveiled by next generation sequencing analyses. Haematologica, 2019, 104, e558-e561. | 3.5 | 55 |
| 95 | Germ-Cell-Specific Inflammasome Component NLRP14 Negatively Regulates Cytosolic Nucleic Acid Sensing to Promote Fertilization. Immunity, 2017, 46, 621-634. | 14.3 | 54 |
| 96 | p53 Maintains Baseline Expression of Multiple Tumor Suppressor Genes. Molecular Cancer Research, 2017, 15, 1051-1062. | 3.4 | 51 |
| 97 | Photon Regeneration from Pseudoscalars at X-Ray Laser Facilities. Physical Review Letters, 2006, 96, 110407. | 7.8 | 49 |
| 98 | A MYC and RAS co-activation signature in localized prostate cancer drives bone metastasis and castration resistance. Nature Cancer, 2020, 1, 1082-1096. | 13.2 | 49 |
| 99 | Reassortment Patterns in Swine Influenza Viruses. PLoS ONE, 2009, 4, e7366. | 2.5 | 46 |
| 100 | Longitudinal active sampling for respiratory viral infections across age groups. Influenza and Other Respiratory Viruses, 2019, 13, 226-232. | 3.4 | 46 |
| 101 | Topological Data Analysis Generates High-Resolution, Genome-wide Maps of Human Recombination. Cell Systems, 2016, 3, 83-94. | 6.2 | 45 |
| 102 | Genomic Characterization of Dysplastic Nevi Unveils Implications for Diagnosis ofÂMelanoma. Journal of Investigative Dermatology, 2017, 137, 905-909. | 0.7 | 45 |
| 103 | The Long Noncoding RNA Paupar Modulates PAX6 Regulatory Activities to Promote Alpha Cell Development and Function. Cell Metabolism, 2019, 30, 1091-1106.e8. | 16.2 | 45 |
| 104 | Global Patterns of Recombination across Human Viruses. Molecular Biology and Evolution, 2021, 38, 2520-2531. | 8.9 | 44 |
| 105 | Differences in Patient Age Distribution between Influenza A Subtypes. PLoS ONE, 2009, 4, e6832. | 2.5 | 43 |
| 106 | Tumor evolutionary directed graphs and the history of chronic lymphocytic leukemia. ELife, 2014, 3, . | 6.0 | 43 |
| 107 | Stability in asymptotically AdS spaces. Journal of High Energy Physics, 2005, 2005, 016-016. | 4.7 | 42 |
| 108 | De novo transcriptome reconstruction and annotation of the Egyptian rousette bat. BMC Genomics, 2015, 16, 1033. | 2.8 | 42 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 109 | A novel patient-derived tumorgraft model with TRAF1-ALK anaplastic large-cell lymphoma translocation. Leukemia, 2015, 29, 1390-1401. | 7.2 | 42 |
| 110 | Discovering Disease Associations by Integrating Electronic Clinical Data and Medical Literature. PLoS ONE, 2011, 6, e21132. | 2.5 | 41 |
| 111 | Increased *HOXA5* expression provides a selective advantage for gain of whole chromosome 7 in IDH wild-type glioblastoma. Genes and Development, 2018, 32, 512-523. | 5.9 | 40 |
| 112 | Genomic Characterization of HIV-Associated Plasmablastic Lymphoma Identifies Pervasive Mutations in the JAK–STAT Pathway. Blood Cancer Discovery, 2020, 1, 112-125. | 5.0 | 40 |
| 113 | SPECTRAL SIGNATURES OF PHOTON-PARTICLE OSCILLATIONS FROM CELESTIAL OBJECTS. Astrophysical Journal, Supplement Series, 2009, 180, 1-29. | 7.7 | 39 |
| 114 | Network Analysis of Global Influenza Spread. PLoS Computational Biology, 2010, 6, e1001005. | 3.2 | 39 |
| 115 | Comprehensive characterisation of compartment-specific long non-coding RNAs associated with pancreatic ductal adenocarcinoma. Gut, 2019, 68, 499-511. | 12.1 | 39 |
| 116 | ERK1/2 phosphorylation predicts survival following anti-PD-1 immunotherapy in recurrent glioblastoma. Nature Cancer, 2021, 2, 1372-1386. | 13.2 | 39 |
| 117 | Generation of Live Attenuated Influenza Virus by Using Codon Usage Bias. Journal of Virology, 2015, 89, 10762-10773. | 3.4 | 38 |
| 118 | Inference of Ancestral Recombination Graphs through Topological Data Analysis. PLoS Computational Biology, 2016, 12, e1005071. | 3.2 | 38 |
| 119 | Kinase-dead ATM protein is highly oncogenic and can be preferentially targeted by Topo-isomerase I inhibitors. ELife, 2016, 5, . | 6.0 | 38 |
| 120 | Identification of relevant genetic alterations in cancer using topological data analysis. Nature Communications, 2020, 11, 3808. | 12.8 | 38 |
| 121 | Genetic mechanisms of HLA-I loss and immune escape in diffuse large B cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 7.1 | 38 |
| 122 | CD8+ T-cell–Mediated Immunoediting Influences Genomic Evolution and Immune Evasion in Murine Gliomas. Clinical Cancer Research, 2020, 26, 4390-4401. | 7.0 | 36 |
| 123 | SAVI: a statistical algorithm for variant frequency identification. BMC Systems Biology, 2013, 7, S2. | 3.0 | 35 |
| 124 | The possibility of cancer immune editing in gliomas. A critical review. OncoImmunology, 2018, 7, e1445458. | 4.6 | 35 |
| 125 | Anomalies in the Influenza Virus Genome Database: New Biology or Laboratory Errors?. Journal of Virology, 2008, 82, 8947-8950. | 3.4 | 34 |
| 126 | Clinical impact of small subclones harboring *NOTCH1* , *SF3B1* or *BIRC3* mutations in chronic lymphocytic leukemia. Haematologica, 2016, 101, e135-e138. | 3.5 | 34 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 127 | E3-ubiquitin ligase Nedd4 determines the fate of AID-associated RNA polymerase II in B cells. Genes and Development, 2013, 27, 1821-1833. | 5.9 | 32 |
| 128 | Genetic similarity between cancers and comorbid Mendelian diseases identifies candidate driver genes. Nature Communications, 2015, 6, 7033. | 12.8 | 32 |
| 129 | Mutational and functional genetics mapping of chemotherapy resistance mechanisms in relapsed acute lymphoblastic leukemia. Nature Cancer, 2020, 1, 1113-1127. | 13.2 | 32 |
| 130 | A Phase I Study of the Combination of Pexidartinib and Sirolimus to Target Tumor-Associated Macrophages in Unresectable Sarcoma and Malignant Peripheral Nerve Sheath Tumors. Clinical Cancer Research, 2021, 27, 5519-5527. | 7.0 | 31 |
| 131 | A Random Matrix Theory Approach to Denoise Single-Cell Data. Patterns, 2020, 1, 100035. | 5.9 | 30 |
| 132 | Pan-cancer analysis identifies mutations in *SUGP1* that recapitulate mutant SF3B1 splicing dysregulation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10305-10312. | 7.1 | 30 |
| 133 | Reprogramming eukaryotic translation with ligand-responsive synthetic RNA switches. Nature Methods, 2016, 13, 453-458. | 19.0 | 28 |
| 134 | Precision Medicine for Acute Kidney Injury (AKI): Redefining AKI by Agnostic Kidney Tissue Interrogation and Genetics. Seminars in Nephrology, 2018, 38, 40-51. | 1.6 | 28 |
| 135 | Copy number profiling across glioblastoma populations has implications for clinical trial design. Neuro-Oncology, 2018, 20, 1368-1373. | 1.2 | 28 |
| 136 | Distinct genomic profile and specific targeted drug responses in adult cerebellar glioblastoma. Neuro-Oncology, 2019, 21, 47-58. | 1.2 | 28 |
| 137 | Secretome analysis of patient-derived GBM tumor spheres identifies midkine as a potent therapeutic target. Experimental and Molecular Medicine, 2019, 51, 1-11. | 7.7 | 28 |
| 138 | The Contribution of the PB1-F2 Protein to the Fitness of Influenza A Viruses and its Recent Evolution in the 2009 Influenza A (H1N1) Pandemic Virus. PLOS Currents, 2009, 1, RRN1006. | 1.4 | 28 |
| 139 | Data-driven discovery of seasonally linked diseases from an Electronic Health Records system. BMC Bioinformatics, 2014, 15, S3. | 2.6 | 27 |
| 140 | Assessment of T-cell receptor repertoire and clonal expansion in peripheral T-cell lymphoma using RNA-seq data. Scientific Reports, 2017, 7, 11301. | 3.3 | 27 |
| 141 | Interrogation of Eukaryotic Stop Codon Readthrough Signals by *in Vitro* RNA Selection. Biochemistry, 2019, 58, 1167-1178. | 2.5 | 27 |
| 142 | GATA3-Controlled Nucleosome Eviction Drives *MYC* Enhancer Activity in T-cell Development and Leukemia. Cancer Discovery, 2019, 9, 1774-1791. | 9.4 | 27 |
| 143 | SF3B1 mutant-induced missplicing of MAP3K7 causes anemia in myelodysplastic syndromes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 7.1 | 26 |
| 144 | GAB2 induces tumor angiogenesis in NRAS-driven melanoma. Oncogene, 2013, 32, 3627-3637. | 5.9 | 25 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 145 | High-resolution Genomic Surveillance of 2014 Ebolavirus Using Shared Subclonal Variants. PLOS Currents, 2015, 7, . | 1.4 | 23 |
| 146 | Mutant SF3B1 promotes AKT- and NF-κB–driven mammary tumorigenesis. Journal of Clinical Investigation, 2021, 131, . | 8.2 | 22 |
| 147 | A pan-cancer analysis of driver gene mutations, DNA methylation and gene expressions reveals that chromatin remodeling is a major mechanism inducing global changes in cancer epigenomes. BMC Medical Genomics, 2018, 11, 98. | 1.5 | 21 |
| 148 | Repurposing dasatinib for diffuse large B cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16981-16986. | 7.1 | 21 |
| 149 | Frequency Analysis Techniques for Identification of Viral Genetic Data. MBio, 2010, 1, . | 4.1 | 20 |
| 150 | Prognostic and therapeutic role of targetable lesions in B-lineage acute lymphoblastic leukemia without recurrent fusion genes. Oncotarget, 2016, 7, 13886-13901. | 1.8 | 20 |
| 151 | Inter‐and intra‐patient clonal and subclonal heterogeneity of chronic lymphocytic leukaemia: evidences from circulating and lymph nodal compartments. British Journal of Haematology, 2016, 172, 371-383. | 2.5 | 20 |
| 152 | High tumor mutational burden and T-cell activation are associated with long-term response to anti-PD1 therapy in Lynch syndrome recurrent glioblastoma patient. Cancer Immunology, Immunotherapy, 2021, 70, 831-842. | 4.2 | 20 |
| 153 | Genetic landscape of ultra-stable chronic lymphocytic leukemia patients. Annals of Oncology, 2018, 29, 966-972. | 1.2 | 19 |
| 154 | FYN–TRAF3IP2 induces NF-κB signaling-driven peripheral T-cell lymphoma. Nature Cancer, 2021, 2, 98-113. | 13.2 | 19 |
| 155 | Computing the Role of Alternative Splicing in Cancer. Trends in Cancer, 2021, 7, 347-358. | 7.4 | 19 |
| 156 | An Information-Theoretic Analysis of Genetics, Gender and Age in Cancer Patients. PLoS ONE, 2008, 3, e1951. | 2.5 | 18 |
| 157 | MutComFocal: an integrative approach to identifying recurrent and focal genomic alterations in tumor samples. BMC Systems Biology, 2013, 7, 25. | 3.0 | 18 |
| 158 | Linking Transcriptomic and Imaging Data Defines Features of a Favorable Tumor Immune Microenvironment and Identifies a Combination Biomarker for Primary Melanoma. Cancer Research, 2020, 80, 1078-1087. | 0.9 | 18 |
| 159 | Beyond NPM-anaplastic lymphoma kinase driven lymphomagenesis. Current Opinion in Hematology, 2013, 20, 374-381. | 2.5 | 17 |
| 160 | Genomic Characterization of HIV-Associated Plasmablastic Lymphoma Identifies Pervasive Mutations in the JAK–STAT Pathway. Blood Cancer Discovery, 2020, 1, 112-125. | 5.0 | 17 |
| 161 | Fractal-like Distributions over the Rational Numbers in High-throughput Biological and Clinical Data. Scientific Reports, 2011, 1, 191. | 3.3 | 16 |
| 162 | Pharmacogenomic analysis of patient-derived tumor cells in gynecologic cancers. Genome Biology, 2019, 20, 253. | 8.8 | 16 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 163 | Hypermutagenesis in untreated adult gliomas due to inherited mismatch mutations. International Journal of Cancer, 2019, 144, 3023-3030. | 5.1 | 16 |
| 164 | Recombination and lineage-specific mutations linked to the emergence of SARS-CoV-2. Genome Medicine, 2021, 13, 124. | 8.2 | 16 |
| 165 | Darwin or Lamarck? Future Challenges in Evolutionary Algorithms for Knowledge Discovery and Data Mining. Lecture Notes in Computer Science, 2014, , 35-56. | 1.3 | 15 |
| 166 | An information theoretic method to identify combinations of genomic alterations that promote glioblastoma. Journal of Molecular Cell Biology, 2015, 7, 203-213. | 3.3 | 14 |
| 167 | Identification of potentially oncogenic alterations from tumor-only samples reveals Fanconi anemia pathway mutations in bladder carcinomas. Npj Genomic Medicine, 2017, 2, 29. | 3.8 | 14 |
| 168 | CtIP-mediated DNA resection is dispensable for IgH class switch recombination by alternative end-joining. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25700-25711. | 7.1 | 13 |
| 169 | Host Dependent Evolutionary Patterns and the Origin of 2009 H1N1 Pandemic Influenza. PLOS Currents, 2010, 2, RRN1147. | 1.4 | 13 |
| 170 | Multiscale Topology of Chromatin Folding. , 2016, , . | | 13 |
| 171 | Oncogenic Vav1-Myo1f induces therapeutically targetable macrophage-rich tumor microenvironment in peripheral TÂcell lymphoma. Cell Reports, 2022, 39, 110695. | 6.4 | 13 |
| 172 | Signs of the 2009 Influenza Pandemic in the New York-Presbyterian Hospital Electronic Health Records. PLoS ONE, 2010, 5, e12658. | 2.5 | 12 |
| 173 | Subversion of Serotonin Receptor Signaling in Osteoblasts by Kynurenine Drives Acute Myeloid Leukemia. Cancer Discovery, 2022, 12, 1106-1127. | 9.4 | 12 |
| 174 | Non-perturbative orientifold transitions at the conifold. Journal of High Energy Physics, 2005, 2005, 026-026. | 4.7 | 11 |
| 175 | Quantifying Pathogen Surveillance Using Temporal Genomic Data. MBio, 2013, 4, e00524-12. | 4.1 | 11 |
| 176 | A Novel JAK1 Mutant Breast Implant-Associated Anaplastic Large Cell Lymphoma Patient-Derived Xenograft Fostering Pre-Clinical Discoveries. Cancers, 2020, 12, 1603. | 3.7 | 11 |
| 177 | Reassortment Patterns in Swine Influenza Viruses. PLOS Currents, 2009, 1, RRN1008. | 1.4 | 11 |
| 178 | Transcriptome reconstruction and annotation of cynomolgus and African green monkey. BMC Genomics, 2014, 15, 846. | 2.8 | 10 |
| 179 | A Case of Tâ€cell Acute Lymphoblastic Leukemia Relapsed As Myeloid Acute Leukemia. Pediatric Blood and Cancer, 2016, 63, 1660-1663. | 1.5 | 10 |
| 180 | Evolutionary scalpels for dissecting tumor ecosystems. Biochimica Et Biophysica Acta: Reviews on Cancer, 2017, 1867, 69-83. | 7.4 | 10 |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 181 | The Holdout Randomization Test for Feature Selection in Black Box Models. Journal of Computational and Graphical Statistics, 2022, 31, 151-162. | 1.7 | 10 |
| 182 | Transcriptional control of CBX5 by the RNA-binding proteins RBMX and RBMXL1 maintains chromatin state in myeloid leukemia. Nature Cancer, 2021, 2, 741-757. | 13.2 | 10 |
| 183 | Can patient selection and neoadjuvant administration resuscitate PD-1 inhibitors for glioblastoma?. Journal of Neurosurgery, 2020, 132, 1667-1672. | 1.6 | 10 |
| 184 | Viral diversity and clonal evolution from unphased genomic data. BMC Genomics, 2014, 15, S17. | 2.8 | 9 |
| 185 | Topological Data Analysis of Single-Cell Hi-C Contact Maps. Abel Symposia, 2020, , 147-162. | 0.3 | 9 |
| 186 | Neoadjuvant chemoradiation alters the immune microenvironment in pancreatic ductal adenocarcinoma. OncoImmunology, 2022, 11, 2066767. | 4.6 | 9 |
| 187 | Darwin, Lamarck, or Baldwin: Applying Evolutionary Algorithms to Machine Learning Techniques. , 2014, , . | | 8 |
| 188 | On Statistical Modeling of Sequencing Noise in High Depth Data to Assess Tumor Evolution. Journal of Statistical Physics, 2018, 172, 143-155. | 1.2 | 8 |
| 189 | Quantifying Genetic Innovation: Mathematical Foundations for the Topological Study of Reticulate Evolution. SIAM Journal on Applied Algebra and Geometry, 2020, 4, 141-184. | 1.4 | 8 |
| 190 | Dose–response modeling in high-throughput cancer drug screenings: an end-to-end approach. Biostatistics, 2022, 23, 643-665. | 1.5 | 8 |
| 191 | Moduli Spaces of Phylogenetic Trees Describing Tumor Evolutionary Patterns. Lecture Notes in Computer Science, 2014, , 528-539. | 1.3 | 8 |
| 192 | A Recoding Method to Improve the Humoral Immune Response to an HIV DNA Vaccine. PLoS ONE, 2008, 3, e3214. | 2.5 | 8 |
| 193 | PDK1 Is Required for Maintenance of CD4+ Foxp3+ Regulatory T Cell Function. Journal of Immunology, 2021, 206, 1776-1783. | 0.8 | 7 |
| 194 | Loss of PBRM1 Alters Promoter Histone Modifications and Activates ALDH1A1 to Drive Renal Cell Carcinoma. Molecular Cancer Research, 2022, 20, 1193-1207. | 3.4 | 7 |
| 195 | The UVSSA complex alleviates MYC-driven transcription stress. Journal of Cell Biology, 2021, 220, . | 5.2 | 6 |
| 196 | HLA Typing from RNA Sequencing and Applications to Cancer. Methods in Molecular Biology, 2020, 2120, 71-92. | 0.9 | 6 |
| 197 | Evolution of the Influenza A Virus: Some New Advances. Evolutionary Bioinformatics, 2007, 3, 117693430700300. | 1.2 | 5 |
| 198 | How many neutrophils are enough (redux, redux)?. Journal of Clinical Investigation, 2012, 122, 2776-2779. | 8.2 | 5 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 199 | Refined karyotype-based prognostic stratification of chronic lymphocytic leukemia with a low- and very-low-risk genetic profile. Leukemia, 2018, 32, 543-546. | 7.2 | 4 |
| 200 | Active surveillance documents rates of clinical care seeking due to respiratory illness. Influenza and Other Respiratory Viruses, 2020, 14, 499-506. | 3.4 | 4 |
| 201 | TOP2B Enzymatic Activity on Promoters and Introns Modulates Multiple Oncogenes in Human Gliomas. Clinical Cancer Research, 2021, 27, 5669-5680. | 7.0 | 4 |
| 202 | Evolution of the influenza a virus: some new advances. Evolutionary Bioinformatics, 2008, 3, 299-307. | 1.2 | 4 |
| 203 | Identifying Hosts of Families of Viruses: A Machine Learning Approach. PLoS ONE, 2011, 6, e27631. | 2.5 | 3 |
| 204 | Next Generation Syndromic SurveillanceMolecular Epidemiology, Electronic Health Records and the Pandemic Influenza A (H1N1) Virus. PLOS Currents, 2009, 1, RRN1012. | 1.4 | 3 |
| 205 | Convergent Mutations and Kinase Fusions Lead to Oncogenic STAT3 Activation in Anaplastic Large Cell Lymphoma. Cancer Cell, 2015, 27, 744. | 16.8 | 2 |
| 206 | A Fast Semi-Automatic Segmentation Tool for Processing Brain Tumor Images. Lecture Notes in Computer Science, 2017, , 170-181. | 1.3 | 2 |
| 207 | Double Empirical Bayes Testing. International Statistical Review, 2020, 88, S91-S113. | 1.9 | 2 |
| 208 | RNA Sequencing of Hodgkin Lymphoma Reed-Sternberg Cells Uncovers a Plasma Cell Signature and Escape from NK Cell Recognition. Blood, 2019, 134, 549-549. | 1.4 | 2 |
| 209 | Molecular Genetic Analysis of Myelodysplastic Syndromes (MDS) Patients with Ring Sideroblasts (RS); Independent Confirmation of Association of SF3B1 Mutations with Better Prognosis. Blood, 2014, 124, 3237-3237. | 1.4 | 2 |
| 210 | ParMap, an algorithm for the identification of small genomic insertions and deletions in nextgen sequencing data. BMC Research Notes, 2010, 3, 147. | 1.4 | 1 |
| 211 | A Random Categorization Model for Hierarchical Taxonomies. Scientific Reports, 2017, 7, 17051. | 3.3 | 1 |
| 212 | Recurrent Rhoa Mutations In Peripheral T-Cell Lymphoma. Blood, 2013, 122, 846-846. | 1.4 | 1 |
| 213 | Whole-Exome Sequencing Identifies Recurrent Mutations of BCOR in Acute Myeloid Leukemia with Normal Karyotype. Blood, 2011, 118, 71-71. | 1.4 | 1 |
| 214 | Small Subclones Harboring NOTCH1, SF3B1 or BIRC3 Mutations Are Clinically Irrelevant in Chronic Lymphocytic Leukemia. Blood, 2014, 124, 295-295. | 1.4 | 1 |
| 215 | JAK-STAT in lymphoproliferative disorders. Oncoscience, 2015, 2, 737-738. | 2.2 | 1 |
| 216 | Quantifying Reticulation in Phylogenetic Complexes Using Homology. , 2016, , . | | 1 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 217 | High Throughput Droplet Single-Cell Genotyping of Transcriptomes (GoT) Reveals the Cell Identity Dependency of the Transcriptional Output of Somatic Mutations. Blood, 2018, 132, 541-541. | 1.4 | 1 |
| 218 | 91â€¦Impact of ultra-fast â€˜FLASHâ€™ radiotherapy on single cell immunogenomics in diffuse intrinsic pontine glioma (DIPG). , 2021, 9, A100-A100. | | 1 |
| 219 | GENO-06A PAN-GLIOMA CHARACTERIZATION OF GENOMIC, EPIGENOMIC AND TRANSCRIPTOMIC ACTIVITIES REVEALS NOVEL RELATIONSHIPS BETWEEN HISTOLOGICAL SUBTYPES AND MOLECULAR SIGNATURES. Neuro-Oncology, 2015, 17, v92.2-v92. | 1.2 | 0 |
| 220 | GENE-17. TOP2B REGULATES CDK4 SPLICE VARIANTS IN GLIOMAS. Neuro-Oncology, 2018, 20, vi106-vi106. | 1.2 | 0 |
| 221 | DDIS-13. UNDERSTANDING GLIOBLASTOMA SUSCEPTIBILITY TO TOP2-TARGETING DRUGS FOR PERSONALIZED THERAPY. Neuro-Oncology, 2018, 20, vi71-vi72. | 1.2 | 0 |
| 222 | How Can We Treat the Virus and Prevent Infections?. , 2021, , 100-113. | | 0 |
| 223 | What Is a Coronavirus?. , 2021, , 22-33. | | 0 |
| 224 | How Is the Coronavirus Spreading?. , 2021, , 7-21. | | 0 |
| 225 | How Did the COVID-19 Outbreak Start and Evolve?. , 2021, , 45-77. | | 0 |
| 226 | How Is the Coronavirus Changing?. , 2021, , 34-44. | | 0 |
| 227 | How Does the COVID-19 Outbreak Compare to Seasonal and Pandemic Influenza?. , 2021, , 88-99. | | 0 |
| 228 | How Does the COVID-19 Outbreak Compare to the SARS Outbreak in 2003?. , 2021, , 78-87. | | 0 |
| 229 | The Emergence of 2009 H1N1 Pandemic Influenza. , 2011, , 95-111. | | 0 |
| 230 | The Genome of Chronic Lymphocytic Leukemia. Blood, 2010, 116, 51-51. | 1.4 | 0 |
| 231 | Mutations in the RNA Splicing Factor SF3B1 Promote Transformation through MYC Stabilization. Blood, 2018, 132, 882-882. | 1.4 | 0 |
| 232 | HHV-6 in the Lymphoma Microenvironment: Both Chicken and Egg?. Blood, 2021, 138, 1377-1377. | 1.4 | 0 |
| 233 | Expression of Vav1-Myo1F Fusion Affects T-Cell Differentiation and Induces T-Cell Lymphoma. Blood, 2020, 136, 4-4. | 1.4 | 0 |
| 234 | Transcriptional Control of HP1a By the RNA Binding Proteins Rbmx/L1 Maintain Chromatin State in Myeloid Leukemia. Blood, 2020, 136, 15-15. | 1.4 | 0 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 235 | Mechanisms of Therapeutic Response to Tipifarnib in a Mouse Model of Angioimmunoblastic T-Cell Lymphoma. Blood, 2020, 136, 9-9. | 1.4 | 0 |
| 236 | DIPG-45. Radiation induces a robust interferon response in Diffuse Midline Glioma (DMG), improving the potential for combination immunotherapy. Neuro-Oncology, 2022, 24, i28-i29. | 1.2 | 0 |