# Raul Rabadan

## List of Publications by Citations

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|---|---|---|---|
| 241 papers | 18,378 citations | 64 h-index | 133 g-index |
| 270 ext. papers | 22,907 ext. citations | 13.6 avg, IF | 6.28 L-index |

| # | Paper | IF | Citations |
|---|-------|----|-----------|
| 241 | Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. *Cell*, **2016**, 164, 550-63 | 56.2 | 1140 |
| 240 | BRAF mutations in hairy-cell leukemia. *New England Journal of Medicine*, **2011**, 364, 2305-15 | 59.2 | 791 |
| 239 | Promotion of hepatocellular carcinoma by the intestinal microbiota and TLR4. *Cancer Cell*, **2012**, 21, 504-16 | 21.3 | 790 |
| 238 | Analysis of the coding genome of diffuse large B-cell lymphoma. *Nature Genetics*, **2011**, 43, 830-7 | 36.3 | 760 |
| 237 | Inactivating mutations of acetyltransferase genes in B-cell lymphoma. *Nature*, **2011**, 471, 189-95 | 50.4 | 684 |
| 236 | Transforming fusions of FGFR and TACC genes in human glioblastoma. *Science*, **2012**, 337, 1231-5 | 33.3 | 567 |
| 235 | Analysis of the chronic lymphocytic leukemia coding genome: role of NOTCH1 mutational activation. *Journal of Experimental Medicine*, **2011**, 208, 1389-401 | 16.6 | 483 |
| 234 | Recurrent mutations in epigenetic regulators, RHOA and FYN kinase in peripheral T cell lymphomas. *Nature Genetics*, **2014**, 46, 166-70 | 36.3 | 413 |
| 233 | The integrated landscape of driver genomic alterations in glioblastoma. *Nature Genetics*, **2013**, 45, 1141-9 | 36.3 | 400 |
| 232 | Clonal evolution of glioblastoma under therapy. *Nature Genetics*, **2016**, 48, 768-76 | 36.3 | 390 |
| 231 | Genetic inactivation of the polycomb repressive complex 2 in T cell acute lymphoblastic leukemia. *Nature Medicine*, **2012**, 18, 298-301 | 50.5 | 374 |
| 230 | Genetics of follicular lymphoma transformation. *Cell Reports*, **2014**, 6, 130-40 | 10.6 | 371 |
| 229 | Leukaemogenesis induced by an activating β-catenin mutation in osteoblasts. *Nature*, **2014**, 506, 240-4 | 50.4 | 360 |
| 228 | Integrated mutational and cytogenetic analysis identifies new prognostic subgroups in chronic lymphocytic leukemia. *Blood*, **2013**, 121, 1403-12 | 2.2 | 357 |
| 227 | Mutations of NOTCH1 are an independent predictor of survival in chronic lymphocytic leukemia. *Blood*, **2012**, 119, 521-9 | 2.2 | 337 |
| 226 | Immune and genomic correlates of response to anti-PD-1 immunotherapy in glioblastoma. *Nature Medicine*, **2019**, 25, 462-469 | 50.5 | 314 |
| 225 | Mutations of the SF3B1 splicing factor in chronic lymphocytic leukemia: association with progression and fludarabine-refractoriness. *Blood*, **2011**, 118, 6904-8 | 2.2 | 298 |

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|---|---|---|---|
| 224 | The coding genome of splenic marginal zone lymphoma: activation of NOTCH2 and other pathways regulating marginal zone development. *Journal of Experimental Medicine*, **2012**, 209, 1537-51 | 16.6 | 289 |
| 223 | Convergent mutations and kinase fusions lead to oncogenic STAT3 activation in anaplastic large cell lymphoma. *Cancer Cell*, **2015**, 27, 516-32 | 24.3 | 283 |
| 222 | RNA exosome-regulated long non-coding RNA transcription controls super-enhancer activity. *Cell*, **2015**, 161, 774-89 | 56.2 | 280 |
| 221 | D=4 chiral string compactifications from intersecting branes. *Journal of Mathematical Physics*, **2001**, 42, 3103-3126 | 1.2 | 276 |
| 220 | Clinical impact of small TP53 mutated subclones in chronic lymphocytic leukemia. *Blood*, **2014**, 123, 2139-47 | 2.2 | 247 |
| 219 | Activating mutations in the NT5C2 nucleotidase gene drive chemotherapy resistance in relapsed ALL. *Nature Medicine*, **2013**, 19, 368-71 | 50.5 | 244 |
| 218 | The mutational landscape of cutaneous T cell lymphoma and Sézary syndrome. *Nature Genetics*, **2015**, 47, 1465-70 | 36.3 | 234 |
| 217 | PHF6 mutations in T-cell acute lymphoblastic leukemia. *Nature Genetics*, **2010**, 42, 338-42 | 36.3 | 231 |
| 216 | Geographic dependence, surveillance, and origins of the 2009 influenza A (H1N1) virus. *New England Journal of Medicine*, **2009**, 361, 115-9 | 59.2 | 220 |
| 215 | Genetic lesions associated with chronic lymphocytic leukemia transformation to Richter syndrome. *Journal of Experimental Medicine*, **2013**, 210, 2273-88 | 16.6 | 195 |
| 214 | Whole-exome sequencing identifies somatic mutations of BCOR in acute myeloid leukemia with normal karyotype. *Blood*, **2011**, 118, 6153-63 | 2.2 | 191 |
| 213 | Patterns of evolution and host gene mimicry in influenza and other RNA viruses. *PLoS Pathogens*, **2008**, 4, e1000079 | 7.6 | 190 |
| 212 | Codon usage bias and the evolution of influenza A viruses. Codon Usage Biases of Influenza Virus. *BMC Evolutionary Biology*, **2010**, 10, 253 | 3 | 187 |
| 211 | 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 | 17.6 | 181 |
| 210 | Heart and skeletal muscle inflammation of farmed salmon is associated with infection with a novel reovirus. *PLoS ONE*, **2010**, 5, e11487 | 3.7 | 173 |
| 209 | A nondegenerate code of deleterious variants in Mendelian loci contributes to complex disease risk. *Cell*, **2013**, 155, 70-80 | 56.2 | 160 |
| 208 | Longitudinal molecular trajectories of diffuse glioma in adults. *Nature*, **2019**, 576, 112-120 | 50.4 | 151 |
| 207 | Spatiotemporal genomic architecture informs precision oncology in glioblastoma. *Nature Genetics*, **2017**, 49, 594-599 | 36.3 | 141 |

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| 206 | Single-cell topological RNA-seq analysis reveals insights into cellular differentiation and development. *Nature Biotechnology*, **2017**, 35, 551-560 | 44.5 | 138 |
| 205 | Disease-associated mutation in SRSF2 misregulates splicing by altering RNA-binding affinities. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E4726-34 | 11.5 | 136 |
| 204 | Topology of viral evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 18566-71 | 11.5 | 135 |
| 203 | Highly conserved regions of influenza a virus polymerase gene segments are critical for efficient viral RNA packaging. *Journal of Virology*, **2008**, 82, 2295-304 | 6.6 | 129 |
| 202 | The Egyptian Rousette Genome Reveals Unexpected Features of Bat Antiviral Immunity. *Cell*, **2018**, 173, 1098-1110.e18 | 56.2 | 121 |
| 201 | Drug-drug interaction through molecular structure similarity analysis. *Journal of the American Medical Informatics Association: JAMIA*, **2012**, 19, 1066-74 | 8.6 | 121 |
| 200 | Emergence of fatal avian influenza in New England harbor seals. *MBio*, **2012**, 3, e00166-12 | 7.8 | 119 |
| 199 | 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 | 11.5 | 117 |
| 198 | Noncoding RNA transcription targets AID to divergently transcribed loci in B cells. *Nature*, **2014**, 514, 389-93 | 50.4 | 117 |
| 197 | An NF-ᴋB Transcription-Factor-Dependent Lineage-Specific Transcriptional Program Promotes Regulatory T Cell Identity and Function. *Immunity*, **2017**, 47, 450-465.e5 | 32.3 | 115 |
| 196 | Double mutations in cis increase oncogenicity and sensitivity to PI3Kᴂ inhibitors. *Science*, **2019**, 366, 714-723 | 33.3 | 102 |
| 195 | Comparison of avian and human influenza A viruses reveals a mutational bias on the viral genomes. *Journal of Virology*, **2006**, 80, 11887-91 | 6.6 | 101 |
| 194 | Somatic mutations and cell identity linked by Genotyping of Transcriptomes. *Nature*, **2019**, 571, 355-360 | 50.4 | 95 |
| 193 | A targetable GATA2-IGF2 axis confers aggressiveness in lethal prostate cancer. *Cancer Cell*, **2015**, 27, 223-39 | 24.3 | 94 |
| 192 | Pharmacogenomic landscape of patient-derived tumor cells informs precision oncology therapy. *Nature Genetics*, **2018**, 50, 1399-1411 | 36.3 | 94 |
| 191 | Pervasive mutations of JAK-STAT pathway genes in classical Hodgkin lymphoma. *Blood*, **2018**, 131, 2454-2465 | 22.1 | 89 |
| 190 | The genetics of nodal marginal zone lymphoma. *Blood*, **2016**, 128, 1362-73 | 2.2 | 88 |
| 189 | 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 | 11.5 | 84 |

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|---|---|---|---|
| 188 | The 2019 mathematical oncology roadmap. *Physical Biology*, **2019**, 16, 041005 | 3 | 78 |
| 187 | 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 | 78 |
| 186 | GENE-17. TOP2B REGULATES CDK4 SPLICE VARIANTS IN GLIOMAS. *Neuro-Oncology*, **2018**, 20, vi106-vi106 | | 78 |
| 185 | DDIS-13. UNDERSTANDING GLIOBLASTOMA SUSCEPTIBILITY TO TOP2-TARGETING DRUGS FOR PERSONALIZED THERAPY. *Neuro-Oncology*, **2018**, 20, vi71-vi72 | 1 | 78 |
| 184 | Mitochondrial DNA haplogroup D4a is a marker for extreme longevity in Japan. *PLoS ONE*, **2008**, 3, e2421 | 3.7 | 77 |
| 183 | Distinct Viral and Mutational Spectrum of Endemic Burkitt Lymphoma. *PLoS Pathogens*, **2015**, 11, e1005158 | 7.3 | 74 |
| 182 | Transcriptomics Identify CD9 as a Marker of Murine IL-10-Competent Regulatory B Cells. *Cell Reports*, **2015**, 13, 1110-1117 | 10.6 | 69 |
| 181 | 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 | 11.5 | 67 |
| 180 | Clonal evolution mechanisms in NT5C2 mutant-relapsed acute lymphoblastic leukaemia. *Nature*, **2018**, 553, 511-514 | 50.4 | 67 |
| 179 | A Structure-Informed Atlas of Human-Virus Interactions. *Cell*, **2019**, 178, 1526-1541.e16 | 56.2 | 65 |
| 178 | Identification of a new subclass of ALK-negative ALCL expressing aberrant levels of ERBB4 transcripts. *Blood*, **2016**, 127, 221-32 | 2.2 | 65 |
| 177 | Genetic lesions associated with chronic lymphocytic leukemia chemo-refractoriness. *Blood*, **2014**, 123, 2378-88 | 2.2 | 64 |
| 176 | FBXW7 mutations in melanoma and a new therapeutic paradigm. *Journal of the National Cancer Institute*, **2014**, 106, dju107 | 9.7 | 63 |
| 175 | Patterns of oligonucleotide sequences in viral and host cell RNA identify mediators of the host innate immune system. *PLoS ONE*, **2009**, 4, e5969 | 3.7 | 61 |
| 174 | Biclustering of adverse drug events in the FDA's spontaneous reporting system. *Clinical Pharmacology and Therapeutics*, **2011**, 89, 243-50 | 6.1 | 58 |
| 173 | The miR-424(322)/503 cluster orchestrates remodeling of the epithelium in the involuting mammary gland. *Genes and Development*, **2014**, 28, 765-82 | 12.6 | 52 |
| 172 | Quantitative Analysis of Immune Infiltrates in Primary Melanoma. *Cancer Immunology Research*, **2018**, 6, 481-493 | 12.5 | 51 |
| 171 | Differential levels of transcription of p53-regulated genes by the arginine/proline polymorphism: p53 with arginine at codon 72 favors apoptosis. *FASEB Journal*, **2010**, 24, 1347-53 | 0.9 | 51 |

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| 170 | 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, 3893-904 | 6.6 | 50 |
| 169 | Pegasus: a comprehensive annotation and prediction tool for detection of driver gene fusions in cancer. *BMC Systems Biology*, **2014**, 8, 97 | 3.5 | 47 |
| 168 | Viral reassortment as an information exchange between viral segments. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 3341-6 | 11.5 | 47 |
| 167 | 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 Suppl 1, i73-80 | 8.6 | 47 |
| 166 | MGMT genomic rearrangements contribute to chemotherapy resistance in gliomas. *Nature Communications*, **2020**, 11, 3883 | 17.4 | 47 |
| 165 | Photon regeneration from pseudoscalars at X-ray laser facilities. *Physical Review Letters*, **2006**, 96, 110407 | 7.4 | 45 |
| 164 | The B-cell receptor controls fitness of MYC-driven lymphoma cells via GSK3 inhibition. *Nature*, **2017**, 546, 302-306 | 50.4 | 43 |
| 163 | Non-random reassortment in human influenza A viruses. *Influenza and Other Respiratory Viruses*, **2008**, 2, 9-22 | 5.6 | 43 |
| 162 | Disease-Causing Mutations in SF3B1 Alter Splicing by Disrupting Interaction with SUGP1. *Molecular Cell*, **2019**, 76, 82-95.e7 | 17.6 | 42 |
| 161 | Reassortment patterns in Swine influenza viruses. *PLoS ONE*, **2009**, 4, e7366 | 3.7 | 41 |
| 160 | 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 | 10.6 | 40 |
| 159 | p53 Maintains Baseline Expression of Multiple Tumor Suppressor Genes. *Molecular Cancer Research*, **2017**, 15, 1051-1062 | 6.6 | 39 |
| 158 | Complete Regression of Advanced Pancreatic Ductal Adenocarcinomas upon Combined Inhibition of EGFR and C-RAF. *Cancer Cell*, **2019**, 35, 573-587.e6 | 24.3 | 37 |
| 157 | Discovering disease associations by integrating electronic clinical data and medical literature. *PLoS ONE*, **2011**, 6, e21132 | 3.7 | 37 |
| 156 | Stability in asymptotically AdS spaces. *Journal of High Energy Physics*, **2005**, 2005, 016-016 | 5.4 | 37 |
| 155 | Tumor evolutionary directed graphs and the history of chronic lymphocytic leukemia. *ELife*, **2014**, 3, | 8.9 | 37 |
| 154 | Functional interrogation of DNA damage response variants with base editing screens. *Cell*, **2021**, 184, 1081-1097.e19 | 56.2 | 37 |
| 153 | Differences in patient age distribution between influenza A subtypes. *PLoS ONE*, **2009**, 4, e6832 | 3.7 | 35 |

152 Blastic plasmacytoid dendritic cell neoplasm: genomics mark epigenetic dysregulation as a primary therapeutic target. *Haematologica*, **2019**, 104, 729-737 — 6.6 — 33

151 A novel patient-derived tumorgraft model with TRAF1-ALK anaplastic large-cell lymphoma translocation. *Leukemia*, **2015**, 29, 1390-401 — 10.7 — 32

150 Network analysis of global influenza spread. *PLoS Computational Biology*, **2010**, 6, e1001005 — 5 — 32

149 Comprehensive characterisation of compartment-specific long non-coding RNAs associated with pancreatic ductal adenocarcinoma. *Gut*, **2019**, 68, 499-511 — 19.2 — 32

148 Nuclear Proximity of Mtr4 to RNA Exosome Restricts DNA Mutational Asymmetry. *Cell*, **2017**, 169, 523-537.e15 — 36.2 — 31

147 Novel insights into the genetics and epigenetics of MALT lymphoma unveiled by next generation sequencing analyses. *Haematologica*, **2019**, 104, e558-e561 — 6.6 — 31

146 SPECTRAL SIGNATURES OF PHOTON-PARTICLE OSCILLATIONS FROM CELESTIAL OBJECTS. *Astrophysical Journal, Supplement Series*, **2009**, 180, 1-29 — 8 — 31

145 Anomalies in the influenza virus genome database: new biology or laboratory errors?. *Journal of Virology*, **2008**, 82, 8947-50 — 6.6 — 31

144 Loss Enhances HSC Self-Renewal Driving Tumor Initiation and Leukemia Stem Cell Activity in T-ALL. *Cancer Discovery*, **2019**, 9, 436-451 — 24.4 — 31

143 Evolutionary Dynamics of Pandemic Methicillin-Sensitive Staphylococcus aureus ST398 and Its International Spread via Routes of Human Migration. *MBio*, **2017**, 8, — 7.8 — 30

142 Germ-Cell-Specific Inflammasome Component NLRP14 Negatively Regulates Cytosolic Nucleic Acid Sensing to Promote Fertilization. *Immunity*, **2017**, 46, 621-634 — 32.3 — 30

141 The Long Noncoding RNA Paupar Modulates PAX6 Regulatory Activities to Promote Alpha Cell Development and Function. *Cell Metabolism*, **2019**, 30, 1091-1106.e8 — 24.6 — 30

140 Clinical impact of small subclones harboring NOTCH1, SF3B1 or BIRC3 mutations in chronic lymphocytic leukemia. *Haematologica*, **2016**, 101, e135-8 — 6.6 — 30

139 arcasHLA: high-resolution HLA typing from RNAseq. *Bioinformatics*, **2020**, 36, 33-40 — 7.2 — 30

138 Mutations in the RNA Splicing Factor SF3B1 Promote Tumorigenesis through MYC Stabilization. *Cancer Discovery*, **2020**, 10, 806-821 — 24.4 — 30

137 Genomic Characterization of Dysplastic Nevi Unveils Implications for Diagnosis of ´Melanoma. *Journal of Investigative Dermatology*, **2017**, 137, 905-909 — 4.3 — 29

136 SAVI: a statistical algorithm for variant frequency identification. *BMC Systems Biology*, **2013**, 7 Suppl 2, S2 — 3.5 — 29

135 Topological Data Analysis Generates High-Resolution, Genome-wide Maps of Human Recombination. *Cell Systems*, **2016**, 3, 83-94 — 10.6 — 27

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| 134 | De novo transcriptome reconstruction and annotation of the Egyptian rousette bat. *BMC Genomics*, **2015**, 16, 1033 | 4.5 | 27 |
| 133 | Kinase-dead ATM protein is highly oncogenic and can be preferentially targeted by Topo-isomerase I inhibitors. *ELife*, **2016**, 5, | 8.9 | 27 |
| 132 | Comprehensive characterization of protein-protein interactions perturbed by disease mutations. *Nature Genetics*, **2021**, 53, 342-353 | 36.3 | 27 |
| 131 | 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 | | 26 |
| 130 | Longitudinal active sampling for respiratory viral infections across age groups. *Influenza and Other Respiratory Viruses*, **2019**, 13, 226-232 | 5.6 | 26 |
| 129 | Generation of Live Attenuated Influenza Virus by Using Codon Usage Bias. *Journal of Virology*, **2015**, 89, 10762-73 | 6.6 | 25 |
| 128 | The possibility of cancer immune editing in gliomas. A critical review. *OncoImmunology*, **2018**, 7, e1445452 | 7.2 | 25 |
| 127 | E3-ubiquitin ligase Nedd4 determines the fate of AID-associated RNA polymerase II in B cells. *Genes and Development*, **2013**, 27, 1821-33 | 12.6 | 25 |
| 126 | Predicting Clinical Outcomes in Glioblastoma: An Application of Topological and Functional Data Analysis. *Journal of the American Statistical Association*, **2020**, 115, 1139-1150 | 2.8 | 25 |
| 125 | iPLA2 mediated lipid detoxification controls p53-driven ferroptosis independent of GPX4. *Nature Communications*, **2021**, 12, 3644 | 17.4 | 24 |
| 124 | Inference of Ancestral Recombination Graphs through Topological Data Analysis. *PLoS Computational Biology*, **2016**, 12, e1005071 | 5 | 24 |
| 123 | Promotion of cholangiocarcinoma growth by diverse cancer-associated fibroblast subpopulations. *Cancer Cell*, **2021**, 39, 866-882.e11 | 24.3 | 23 |
| 122 | Genetic similarity between cancers and comorbid Mendelian diseases identifies candidate driver genes. *Nature Communications*, **2015**, 6, 7033 | 17.4 | 22 |
| 121 | Increased expression provides a selective advantage for gain of whole chromosome 7 in IDH wild-type glioblastoma. *Genes and Development*, **2018**, 32, 512-523 | 12.6 | 21 |
| 120 | Reprogramming eukaryotic translation with ligand-responsive synthetic RNA switches. *Nature Methods*, **2016**, 13, 453-8 | 21.6 | 21 |
| 119 | Data-driven discovery of seasonally linked diseases from an Electronic Health Records system. *BMC Bioinformatics*, **2014**, 15 Suppl 6, S3 | 3.6 | 20 |
| 118 | Frequency analysis techniques for identification of viral genetic data. *MBio*, **2010**, 1, | 7.8 | 20 |
| 117 | Distinct genomic profile and specific targeted drug responses in adult cerebellar glioblastoma. *Neuro-Oncology*, **2019**, 21, 47-58 | 1 | 19 |

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| 116 | GAB2 induces tumor angiogenesis in NRAS-driven melanoma. *Oncogene*, **2013**, 32, 3627-37 | 9.2 | 19 |
| 115 | High-resolution Genomic Surveillance of 2014 Ebolavirus Using Shared Subclonal Variants. *PLOS Currents*, **2015**, 7, | | 19 |
| 114 | A single-cell atlas of the mouse and human prostate reveals heterogeneity and conservation of epithelial progenitors. *ELife*, **2020**, 9, | 8.9 | 19 |
| 113 | Secretome analysis of patient-derived GBM tumor spheres identifies midkine as a potent therapeutic target. *Experimental and Molecular Medicine*, **2019**, 51, 1-11 | 12.8 | 19 |
| 112 | Precision Medicine for Acute Kidney Injury (AKI): Redefining AKI by Agnostic Kidney Tissue Interrogation and Genetics. *Seminars in Nephrology*, **2018**, 38, 40-51 | 4.8 | 18 |
| 111 | Copy number profiling across glioblastoma populations has implications for clinical trial design. *Neuro-Oncology*, **2018**, 20, 1368-1373 | 1 | 18 |
| 110 | MutComFocal: an integrative approach to identifying recurrent and focal genomic alterations in tumor samples. *BMC Systems Biology*, **2013**, 7, 25 | 3.5 | 18 |
| 109 | Assessment of T-cell receptor repertoire and clonal expansion in peripheral T-cell lymphoma using RNA-seq data. *Scientific Reports*, **2017**, 7, 11301 | 4.9 | 18 |
| 108 | A MYC and RAS co-activation signature in localized prostate cancer drives bone metastasis and castration resistance. *Nature Cancer*, **2020**, 1, 1082-1096 | 15.4 | 18 |
| 107 | GATA3-Controlled Nucleosome Eviction Drives Enhancer Activity in T-cell Development and Leukemia. *Cancer Discovery*, **2019**, 9, 1774-1791 | 24.4 | 17 |
| 106 | An information-theoretic analysis of genetics, gender and age in cancer patients. *PLoS ONE*, **2008**, 3, e1951 | 3.7 | 16 |
| 105 | Beyond NPM-anaplastic lymphoma kinase driven lymphomagenesis: alternative drivers in anaplastic large cell lymphoma. *Current Opinion in Hematology*, **2013**, 20, 374-81 | 3.3 | 15 |
| 104 | Recombination and lineage-specific mutations linked to the emergence of SARS-CoV-2 **2021**, | | 15 |
| 103 | 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 | 4.5 | 15 |
| 102 | Prognostic and therapeutic role of targetable lesions in B-lineage acute lymphoblastic leukemia without recurrent fusion genes. *Oncotarget*, **2016**, 7, 13886-901 | 3.3 | 14 |
| 101 | Interrogation of Eukaryotic Stop Codon Readthrough Signals by in Vitro RNA Selection. *Biochemistry*, **2019**, 58, 1167-1178 | 3.2 | 13 |
| 100 | Genetic landscape of ultra-stable chronic lymphocytic leukemia patients. *Annals of Oncology*, **2018**, 29, 966-972 | 10.3 | 13 |
| 99 | Genomic Characterization of HIV-Associated Plasmablastic Lymphoma Identifies Pervasive Mutations in the JAK-STAT Pathway. *Blood Cancer Discovery*, **2020**, 1, 112-125 | 7 | 13 |

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| 98 | A Random Matrix Theory Approach to Denoise Single-Cell Data. *Patterns*, **2020**, 1, 100035 | 5.1 | 13 |
| 97 | Identification of relevant genetic alterations in cancer using topological data analysis. *Nature Communications*, **2020**, 11, 3808 | 17.4 | 13 |
| 96 | Global Patterns of Recombination across Human Viruses. *Molecular Biology and Evolution*, **2021**, 38, 2520-2531 | 13 | 13 |
| 95 | Identification of potentially oncogenic alterations from tumor-only samples reveals Fanconi anemia pathway mutations in bladder carcinomas. *Npj Genomic Medicine*, **2017**, 2, 29 | 6.2 | 12 |
| 94 | An information theoretic method to identify combinations of genomic alterations that promote glioblastoma. *Journal of Molecular Cell Biology*, **2015**, 7, 203-13 | 6.3 | 12 |
| 93 | Darwin or Lamarck? Future Challenges in Evolutionary Algorithms for Knowledge Discovery and Data Mining. *Lecture Notes in Computer Science*, **2014**, 35-56 | 0.9 | 12 |
| 92 | Midkine rewires the melanoma microenvironment toward a tolerogenic and immune-resistant state. *Nature Medicine*, **2020**, 26, 1865-1877 | 50.5 | 12 |
| 91 | Hypermutagenesis in untreated adult gliomas due to inherited mismatch mutations. *International Journal of Cancer*, **2019**, 144, 3023-3030 | 7.5 | 12 |
| 90 | Pan-cancer analysis identifies mutations in that recapitulate mutant SF3B1 splicing dysregulation. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 10305-10312 | 11.5 | 11 |
| 89 | Non-perturbative orientifold transitions at the conifold. *Journal of High Energy Physics*, **2005**, 2005, 026-026 | 9.6 | 11 |
| 88 | Fractal-like distributions over the rational numbers in high-throughput biological and clinical data. *Scientific Reports*, **2011**, 1, 191 | 4.9 | 10 |
| 87 | Signs of the 2009 influenza pandemic in the New York-Presbyterian Hospital electronic health records. *PLoS ONE*, **2010**, 5, e12658 | 3.7 | 10 |
| 86 | Host Dependent Evolutionary Patterns and the Origin of 2009 H1N1 Pandemic Influenza: Alexander Solovyov*, Benjamin Greenbaum*, Gustavo Palacios, W. Ian Lipkin and Raul Rabadan (* Joint First Authors). *PLOS Currents*, **2010**, 2, RRN1147 | | 10 |
| 85 | Single-cell characterization of macrophages in glioblastoma reveals MARCO as a mesenchymal pro-tumor marker. *Genome Medicine*, **2021**, 13, 88 | 14.4 | 10 |
| 84 | Evolutionary scalpels for dissecting tumor ecosystems. *Biochimica Et Biophysica Acta: Reviews on Cancer*, **2017**, 1867, 69-83 | 11.2 | 9 |
| 83 | CD8 T-cell-Mediated Immunoediting Influences Genomic Evolution and Immune Evasion in Murine Gliomas. *Clinical Cancer Research*, **2020**, 26, 4390-4401 | 12.9 | 9 |
| 82 | Transcriptome reconstruction and annotation of cynomolgus and African green monkey. *BMC Genomics*, **2014**, 15, 846 | 4.5 | 9 |
| 81 | Reassortment patterns in Swine influenza viruses. *PLOS Currents*, **2009**, 1, RRN1008 | | 9 |

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| 80 | Multiscale Topology of Chromatin Folding **2016**, | | 9 |
| 79 | Pharmacogenomic analysis of patient-derived tumor cells in gynecologic cancers. *Genome Biology*, **2019**, 20, 253 | 18.3 | 9 |
| 78 | 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 | 11.5 | 8 |
| 77 | Viral diversity and clonal evolution from unphased genomic data. *BMC Genomics*, **2014**, 15 Suppl 6, S17 | 4.5 | 8 |
| 76 | Quantifying pathogen surveillance using temporal genomic data. *MBio*, **2013**, 4, e00524-12 | 7.8 | 8 |
| 75 | A recoding method to improve the humoral immune response to an HIV DNA vaccine. *PLoS ONE*, **2008**, 3, e3214 | 3.7 | 8 |
| 74 | Moduli Spaces of Phylogenetic Trees Describing Tumor Evolutionary Patterns. *Lecture Notes in Computer Science*, **2014**, 528-539 | 0.9 | 8 |
| 73 | Genomic characterization of HIV-associated plasmablastic lymphoma identifies pervasive mutations in the JAK-STAT pathway. *Blood Cancer Discovery*, **2020**, 1, 112-125 | 7 | 8 |
| 72 | 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 | 7.4 | 8 |
| 71 | 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 | 3.7 | 8 |
| 70 | Recombination and lineage-specific mutations linked to the emergence of SARS-CoV-2. *Genome Medicine*, **2021**, 13, 124 | 14.4 | 8 |
| 69 | Mutational and functional genetics mapping of chemotherapy resistance mechanisms in relapsed acute lymphoblastic leukemia. *Nature Cancer*, **2020**, 1, 1113-1127 | 15.4 | 7 |
| 68 | A Case of T-cell Acute Lymphoblastic Leukemia Relapsed As Myeloid Acute Leukemia. *Pediatric Blood and Cancer*, **2016**, 63, 1660-3 | 3 | 7 |
| 67 | 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 | 10.1 | 6 |
| 66 | Topological Data Analysis of Single-Cell Hi-C Contact Maps. *Abel Symposia*, **2020**, 147-162 | 0.9 | 6 |
| 65 | Computing the Role of Alternative Splicing in Cancer. *Trends in Cancer*, **2021**, 7, 347-358 | 12.5 | 6 |
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| 28 | SF3B1 mutant-induced missplicing of MAP3K7 causes anemia in myelodysplastic syndromes | | 1 |
| 27 | Identification of Relevant Genetic Alterations in Cancer using Topological Data Analysis | | 1 |

# List of Publications