Raul Rabadan

List of Publications by Year
in descending order

236 papers	25,742 citations	11646 70 h-index	7517 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	BRAFMutations 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 Î²-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

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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 SÃ©zary 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

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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 PIK3CA mutations in cis increase oncogenicity and sensitivity to PI3KÎ± inhibitors. Science, 2019, 366, 714-723.	12.6	185
42	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.	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-ÎºB 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

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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 proteinâ€“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

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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	Phf6 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 miR-424(322)/503 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 GSK3Î² 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

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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

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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 JAKâ€“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-cellâ€“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

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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

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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-Î²Bâ€“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	Interâ€•and intraâ€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	FYNâ€“TRAF3IP2 induces NF-Î²B 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 JAKâ€“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

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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

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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
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