Raul Rabadan

List of Publications by Year
in descending order

236 papers	25,742 citations	13332 70 h-index	8627 151 g-index
270 all docs	270 docs citations	270 times ranked	39392 citing authors

#	Article	IF	Citations
1	Dose–response modeling in high-throughput cancer drug screenings: an end-to-end approach. Biostatistics, 2022, 23, 643-665.	0.9	8
2	The Holdout Randomization Test for Feature Selection in Black Box Models. Journal of Computational and Graphical Statistics, 2022, 31, 151-162.	0.9	10
3	Subversion of Serotonin Receptor Signaling in Osteoblasts by Kynurenine Drives Acute Myeloid Leukemia. Cancer Discovery, 2022, 12, 1106-1127.	7.7	12
4	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, .	3.3	26
5	Loss of PBRM1 Alters Promoter Histone Modifications and Activates ALDH1A1 to Drive Renal Cell Carcinoma. Molecular Cancer Research, 2022, 20, 1193-1207.	1.5	7
6	Oncogenic Vav1-Myo1f induces therapeutically targetable macrophage-rich tumor microenvironment in peripheral TÂcell lymphoma. Cell Reports, 2022, 39, 110695.	2.9	13
7	Neoadjuvant chemoradiation alters the immune microenvironment in pancreatic ductal adenocarcinoma. OncoImmunology, 2022, 11, 2066767.	2.1	9
8	Glioma progression is shaped by genetic evolution and microenvironment interactions. Cell, 2022, 185, 2184-2199.e16.	13.5	163
9	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.	0.6	0
10	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.	2.0	20
11	FYN–TRAF3IP2 induces NF-ÎºB signaling-driven peripheral T-cell lymphoma. Nature Cancer, 2021, 2, 98-113.	5.7	19
12	The UVSSA complex alleviates MYC-driven transcription stress. Journal of Cell Biology, 2021, 220, .	2.3	6
13	Comprehensive characterization of protein–protein interactions perturbed by disease mutations. Nature Genetics, 2021, 53, 342-353.	9.4	109
14	Global Patterns of Recombination across Human Viruses. Molecular Biology and Evolution, 2021, 38, 2520-2531.	3.5	44
15	Functional interrogation of DNA damage response variants with base editing screens. Cell, 2021, 184, 1081-1097.e19.	13.5	145
16	PDK1 Is Required for Maintenance of CD4+ Foxp3+ Regulatory T Cell Function. Journal of Immunology, 2021, 206, 1776-1783.	0.4	7
17	Computing the Role of Alternative Splicing in Cancer. Trends in Cancer, 2021, 7, 347-358.	3.8	19
18	Single-cell characterization of macrophages in glioblastoma reveals MARCO as a mesenchymal pro-tumor marker. Genome Medicine, 2021, 13, 88.	3.6	57

#	Article	IF	Citations
19	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, .	3.3	38
20	Promotion of cholangiocarcinoma growth by diverse cancer-associated fibroblast subpopulations. Cancer Cell, 2021, 39, 866-882.e11.	7.7	159
21	iPLA2Î²-mediated lipid detoxification controls p53-driven ferroptosis independent of GPX4. Nature Communications, 2021, 12, 3644.	5.8	153
22	Transcriptional control of CBX5 by the RNA-binding proteins RBMX and RBMXL1 maintains chromatin state in myeloid leukemia. Nature Cancer, 2021, 2, 741-757.	5.7	10
23	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.	3.2	31
24	TOP2B Enzymatic Activity on Promoters and Introns Modulates Multiple Oncogenes in Human Gliomas. Clinical Cancer Research, 2021, 27, 5669-5680.	3.2	4
25	Recombination and lineage-specific mutations linked to the emergence of SARS-CoV-2. Genome Medicine, 2021, 13, 124.	3.6	16
26	How Can We Treat the Virus and Prevent Infections?. , 2021, , 100-113.		0
27	What Is a Coronavirus?. , 2021, , 22-33.		0
28	How Is the Coronavirus Spreading?. , 2021, , 7-21.		0
29	How Did the COVID-19 Outbreak Start and Evolve?. , 2021, , 45-77.		0
30	How Is the Coronavirus Changing?. , 2021, , 34-44.		0
31	How Does the COVID-19 Outbreak Compare to Seasonal and Pandemic Influenza?. , 2021, , 88-99.		0
32	How Does the COVID-19 Outbreak Compare to the SARS Outbreak in 2003?. , 2021, , 78-87.		0
33	Mutant SF3B1 promotes AKT- and NF-Î°Bâ€"driven mammary tumorigenesis. Journal of Clinical Investigation, 2021, 131, .	3.9	22
34	ERK1/2 phosphorylation predicts survival following anti-PD-1 immunotherapy in recurrent glioblastoma. Nature Cancer, 2021, 2, 1372-1386.	5.7	39
35	91â€¦Impact of ultra-fast â€˜FLASHâ€™ radiotherapy on single cell immunogenomics in diffuse intrinsic pontine glioma (DIPG). , 2021, 9, A100-A100.		1
36	HHV-6 in the Lymphoma Microenvironment: Both Chicken and Egg?. Blood, 2021, 138, 1377-1377.	0.6	0

#	Article	IF	Citations
37	arcasHLA: high-resolution HLA typing from RNAseq. Bioinformatics, 2020, 36, 33-40.	1.8	113
38	Predicting Clinical Outcomes in Glioblastoma: An Application of Topological and Functional Data Analysis. Journal of the American Statistical Association, 2020, 115, 1139-1150.	1.8	60
39	Midkine rewires the melanoma microenvironment toward a tolerogenic and immune-resistant state. Nature Medicine, 2020, 26, 1865-1877.	15.2	62
40	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.	3.3	13
41	A MYC and RAS co-activation signature in localized prostate cancer drives bone metastasis and castration resistance. Nature Cancer, 2020, 1, 1082-1096.	5.7	49
42	A Random Matrix Theory Approach to Denoise Single-Cell Data. Patterns, 2020, 1, 100035.	3.1	30
43	Double Empirical Bayes Testing. International Statistical Review, 2020, 88, S91-S113.	1.1	2
44	Identification of relevant genetic alterations in cancer using topological data analysis. Nature Communications, 2020, 11, 3808.	5.8	38
45	MGMT genomic rearrangements contribute to chemotherapy resistance in gliomas. Nature Communications, 2020, 11, 3883.	5.8	110
46	Genomic Characterization of HIV-Associated Plasmablastic Lymphoma Identifies Pervasive Mutations in the JAK–STAT Pathway. Blood Cancer Discovery, 2020, 1, 112-125.	2.6	17
47	Mutational and functional genetics mapping of chemotherapy resistance mechanisms in relapsed acute lymphoblastic leukemia. Nature Cancer, 2020, 1, 1113-1127.	5.7	32
48	Active surveillance documents rates of clinical care seeking due to respiratory illness. Influenza and Other Respiratory Viruses, 2020, 14, 499-506.	1.5	4
49	CD8+ T-cell–Mediated Immunoediting Influences Genomic Evolution and Immune Evasion in Murine Gliomas. Clinical Cancer Research, 2020, 26, 4390-4401.	3.2	36
50	A Novel JAK1 Mutant Breast Implant-Associated Anaplastic Large Cell Lymphoma Patient-Derived Xenograft Fostering Pre-Clinical Discoveries. Cancers, 2020, 12, 1603.	1.7	11
51	Quantifying Genetic Innovation: Mathematical Foundations for the Topological Study of Reticulate Evolution. SIAM Journal on Applied Algebra and Geometry, 2020, 4, 141-184.	0.9	8
52	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.	0.4	18
53	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.	3.3	30
54	Mutations in the RNA Splicing Factor SF3B1 Promote Tumorigenesis through MYC Stabilization. Cancer Discovery, 2020, 10, 806-821.	7.7	73

#	ARTICLE	IF	CITATIONS
55	Topological Data Analysis of Single-Cell Hi-C Contact Maps. Abel Symposia, 2020, , 147-162.	0.3	9
56	Genomic Characterization of HIV-Associated Plasmablastic Lymphoma Identifies Pervasive Mutations in the JAK–STAT Pathway. Blood Cancer Discovery, 2020, 1, 112-125.	2.6	40
57	Can patient selection and neoadjuvant administration resuscitate PD-1 inhibitors for glioblastoma?. Journal of Neurosurgery, 2020, 132, 1667-1672.	0.9	10
58	A single-cell atlas of the mouse and human prostate reveals heterogeneity and conservation of epithelial progenitors. ELife, 2020, 9, .	2.8	69
59	HLA Typing from RNA Sequencing and Applications to Cancer. Methods in Molecular Biology, 2020, 2120, 71-92.	0.4	6
60	Expression of Vav1-Myo1F Fusion Affects T-Cell Differentiation and Induces T-Cell Lymphoma. Blood, 2020, 136, 4-4.	0.6	0
61	Transcriptional Control of HP1a By the RNA Binding Proteins Rbmx/L1 Maintain Chromatin State in Myeloid Leukemia. Blood, 2020, 136, 15-15.	0.6	0
62	Mechanisms of Therapeutic Response to Tipifarnib in a Mouse Model of Angioimmunoblastic T-Cell Lymphoma. Blood, 2020, 136, 9-9.	0.6	0
63	Distinct genomic profile and specific targeted drug responses in adult cerebellar glioblastoma. Neuro-Oncology, 2019, 21, 47-58.	0.6	28
64	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.	3.3	21
65	Somatic mutations and cell identity linked by Genotyping of Transcriptomes. Nature, 2019, 571, 355-360.	13.7	206
66	The Long Noncoding RNA Paupar Modulates PAX6 Regulatory Activities to Promote Alpha Cell Development and Function. Cell Metabolism, 2019, 30, 1091-1106.e8.	7.2	45
67	Double *PIK3CA* mutations in cis increase oncogenicity and sensitivity to PI3Kα inhibitors. Science, 2019, 366, 714-723.	6.0	185
68	Disease-Causing Mutations in SF3B1 Alter Splicing by Disrupting Interaction with SUGP1. Molecular Cell, 2019, 76, 82-95.e7.	4.5	84
69	A Structure-Informed Atlas of Human-Virus Interactions. Cell, 2019, 178, 1526-1541.e16.	13.5	108
70	Interrogation of Eukaryotic Stop Codon Readthrough Signals by *in Vitro* RNA Selection. Biochemistry, 2019, 58, 1167-1178.	1.2	27
71	The 2019 mathematical oncology roadmap. Physical Biology, 2019, 16, 041005.	0.8	147
72	Novel insights into the genetics and epigenetics of MALT lymphoma unveiled by next generation sequencing analyses. Haematologica, 2019, 104, e558-e561.	1.7	55

#	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.	7.7	75
74	Immune and genomic correlates of response to anti-PD-1 immunotherapy in glioblastoma. Nature Medicine, 2019, 25, 462-469.	15.2	569
75	Longitudinal active sampling for respiratory viral infections across age groups. Influenza and Other Respiratory Viruses, 2019, 13, 226-232.	1.5	46
76	GATA3-Controlled Nucleosome Eviction Drives *MYC* Enhancer Activity in T-cell Development and Leukemia. Cancer Discovery, 2019, 9, 1774-1791.	7.7	27
77	Pharmacogenomic analysis of patient-derived tumor cells in gynecologic cancers. Genome Biology, 2019, 20, 253.	3.8	16
78	Longitudinal molecular trajectories of diffuse glioma in adults. Nature, 2019, 576, 112-120.	13.7	320
79	Secretome analysis of patient-derived GBM tumor spheres identifies midkine as a potent therapeutic target. Experimental and Molecular Medicine, 2019, 51, 1-11.	3.2	28
80	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.	2.9	69
81	*Phf6* Loss Enhances HSC Self-Renewal Driving Tumor Initiation and Leukemia Stem Cell Activity in T-ALL. Cancer Discovery, 2019, 9, 436-451.	7.7	67
82	Blastic plasmacytoid dendritic cell neoplasm: genomics mark epigenetic dysregulation as a primary therapeutic target. Haematologica, 2019, 104, 729-737.	1.7	58
83	Hypermutagenesis in untreated adult gliomas due to inherited mismatch mutations. International Journal of Cancer, 2019, 144, 3023-3030.	2.3	16
84	Comprehensive characterisation of compartment-specific long non-coding RNAs associated with pancreatic ductal adenocarcinoma. Gut, 2019, 68, 499-511.	6.1	39
85	RNA Sequencing of Hodgkin Lymphoma Reed-Sternberg Cells Uncovers a Plasma Cell Signature and Escape from NK Cell Recognition. Blood, 2019, 134, 549-549.	0.6	2
86	Quantitative Analysis of Immune Infiltrates in Primary Melanoma. Cancer Immunology Research, 2018, 6, 481-493.	1.6	92
87	The possibility of cancer immune editing in gliomas. A critical review. OncoImmunology, 2018, 7, e1445458.	2.1	35
88	The Egyptian Rousette Genome Reveals Unexpected Features of Bat Antiviral Immunity. Cell, 2018, 173, 1098-1110.e18.	13.5	220
89	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.	2.7	40
90	Pervasive mutations of JAK-STAT pathway genes in classical Hodgkin lymphoma. Blood, 2018, 131, 2454-2465.	0.6	167

#	Article	IF	Citations
91	Clonal evolution mechanisms in NT5C2 mutant-relapsed acute lymphoblastic leukaemia. Nature, 2018, 553, 511-514.	13.7	90
92	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.	3.3	128
93	Genetic landscape of ultra-stable chronic lymphocytic leukemia patients. Annals of Oncology, 2018, 29, 966-972.	0.6	19
94	On Statistical Modeling of Sequencing Noise in High Depth Data to Assess Tumor Evolution. Journal of Statistical Physics, 2018, 172, 143-155.	0.5	8
95	Precision Medicine for Acute Kidney Injury (AKI): Redefining AKI by Agnostic Kidney Tissue Interrogation and Genetics. Seminars in Nephrology, 2018, 38, 40-51.	0.6	28
96	Refined karyotype-based prognostic stratification of chronic lymphocytic leukemia with a low- and very-low-risk genetic profile. Leukemia, 2018, 32, 543-546.	3.3	4
97	GENE-17. TOP2B REGULATES CDK4 SPLICE VARIANTS IN GLIOMAS. Neuro-Oncology, 2018, 20, vi106-vi106.	0.6	0
98	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.	0.7	21
99	DDIS-13. UNDERSTANDING GLIOBLASTOMA SUSCEPTIBILITY TO TOP2-TARGETING DRUGS FOR PERSONALIZED THERAPY. Neuro-Oncology, 2018, 20, vi71-vi72.	0.6	0
100	Pharmacogenomic landscape of patient-derived tumor cells informs precision oncology therapy. Nature Genetics, 2018, 50, 1399-1411.	9.4	145
101	Copy number profiling across glioblastoma populations has implications for clinical trial design. Neuro-Oncology, 2018, 20, 1368-1373.	0.6	28
102	Mutations in the RNA Splicing Factor SF3B1 Promote Transformation through MYC Stabilization. Blood, 2018, 132, 882-882.	0.6	0
103	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.	0.6	1
104	Evolutionary Dynamics of Pandemic Methicillin-Sensitive *Staphylococcus aureus* ST398 and Its International Spread via Routes of Human Migration. MBio, 2017, 8, .	1.8	56
105	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.	3.3	100
106	Spatiotemporal genomic architecture informs precision oncology in glioblastoma. Nature Genetics, 2017, 49, 594-599.	9.4	223
107	Nuclear Proximity of Mtr4 to RNA Exosome Restricts DNA Mutational Asymmetry. Cell, 2017, 169, 523-537.e15.	13.5	56
108	Germ-Cell-Specific Inflammasome Component NLRP14 Negatively Regulates Cytosolic Nucleic Acid Sensing to Promote Fertilization. Immunity, 2017, 46, 621-634.	6.6	54

#	Article	IF	Citations
109	p53 Maintains Baseline Expression of Multiple Tumor Suppressor Genes. Molecular Cancer Research, 2017, 15, 1051-1062.	1.5	51
110	Single-cell topological RNA-seq analysis reveals insights into cellular differentiation and development. Nature Biotechnology, 2017, 35, 551-560.	9.4	215
111	Genomic Characterization of Dysplastic Nevi Unveils Implications for Diagnosis ofÂMelanoma. Journal of Investigative Dermatology, 2017, 137, 905-909.	0.3	45
112	The B-cell receptor controls fitness of MYC-driven lymphoma cells via GSK3Î² inhibition. Nature, 2017, 546, 302-306.	13.7	64
113	Evolutionary scalpels for dissecting tumor ecosystems. Biochimica Et Biophysica Acta: Reviews on Cancer, 2017, 1867, 69-83.	3.3	10
114	A Fast Semi-Automatic Segmentation Tool for Processing Brain Tumor Images. Lecture Notes in Computer Science, 2017, , 170-181.	1.0	2
115	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.	4.5	295
116	Assessment of T-cell receptor repertoire and clonal expansion in peripheral T-cell lymphoma using RNA-seq data. Scientific Reports, 2017, 7, 11301.	1.6	27
117	An NF-κB Transcription-Factor-Dependent Lineage-Specific Transcriptional Program Promotes Regulatory T Cell Identity and Function. Immunity, 2017, 47, 450-465.e5.	6.6	161
118	Identification of potentially oncogenic alterations from tumor-only samples reveals Fanconi anemia pathway mutations in bladder carcinomas. Npj Genomic Medicine, 2017, 2, 29.	1.7	14
119	A Random Categorization Model for Hierarchical Taxonomies. Scientific Reports, 2017, 7, 17051.	1.6	1
120	Prognostic and therapeutic role of targetable lesions in B-lineage acute lymphoblastic leukemia without recurrent fusion genes. Oncotarget, 2016, 7, 13886-13901.	0.8	20
121	Inference of Ancestral Recombination Graphs through Topological Data Analysis. PLoS Computational Biology, 2016, 12, e1005071.	1.5	38
122	Kinase-dead ATM protein is highly oncogenic and can be preferentially targeted by Topo-isomerase I inhibitors. ELife, 2016, 5, .	2.8	38
123	A Case of Tâ€cell Acute Lymphoblastic Leukemia Relapsed As Myeloid Acute Leukemia. Pediatric Blood and Cancer, 2016, 63, 1660-1663.	0.8	10
124	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.	1.2	20
125	Clinical impact of small subclones harboring <i>NOTCH1</i> , <i>SF3B1</i> or <i>BIRC3</i> mutations in chronic lymphocytic leukemia. Haematologica, 2016, 101, e135-e138.	1.7	34
126	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.	3.3	151

#	Article	IF	Citations
127	Topological Data Analysis Generates High-Resolution, Genome-wide Maps of Human Recombination. Cell Systems, 2016, 3, 83-94.	2.9	45
128	The genetics of nodal marginal zone lymphoma. Blood, 2016, 128, 1362-1373.	0.6	147
129	Identification of a new subclass of ALK-negative ALCL expressing aberrant levels of ERBB4 transcripts. Blood, 2016, 127, 221-232.	0.6	97
130	Clonal evolution of glioblastoma under therapy. Nature Genetics, 2016, 48, 768-776.	9.4	591
131	Reprogramming eukaryotic translation with ligand-responsive synthetic RNA switches. Nature Methods, 2016, 13, 453-458.	9.0	28
132	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	13.5	1,695
133	Multiscale Topology of Chromatin Folding. , 2016, , .		13
134	Quantifying Reticulation in Phylogenetic Complexes Using Homology. , 2016, , .		1
135	Transcriptomics Identify CD9 as a Marker of Murine IL-10-Competent Regulatory B Cells. Cell Reports, 2015, 13, 1110-1117.	2.9	95
136	De novo transcriptome reconstruction and annotation of the Egyptian rousette bat. BMC Genomics, 2015, 16, 1033.	1.2	42
137	Distinct Viral and Mutational Spectrum of Endemic Burkitt Lymphoma. PLoS Pathogens, 2015, 11, e1005158.	2.1	127
138	An information theoretic method to identify combinations of genomic alterations that promote glioblastoma. Journal of Molecular Cell Biology, 2015, 7, 203-213.	1.5	14
139	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.	0.6	0
140	A Targetable GATA2-IGF2 Axis Confers Aggressiveness in Lethal Prostate Cancer. Cancer Cell, 2015, 27, 223-239.	7.7	128
141	Convergent Mutations and Kinase Fusions Lead to Oncogenic STAT3 Activation in Anaplastic Large Cell Lymphoma. Cancer Cell, 2015, 27, 744.	7.7	2
142	A novel patient-derived tumorgraft model with TRAF1-ALK anaplastic large-cell lymphoma translocation. Leukemia, 2015, 29, 1390-1401.	3.3	42
143	Convergent Mutations and Kinase Fusions Lead to Oncogenic STAT3 Activation in Anaplastic Large Cell Lymphoma. Cancer Cell, 2015, 27, 516-532.	7.7	378
144	Genetic similarity between cancers and comorbid Mendelian diseases identifies candidate driver genes. Nature Communications, 2015, 6, 7033.	5.8	32

#	ARTICLE	IF	CITATIONS
145	RNA Exosome-Regulated Long Non-Coding RNA Transcription Controls Super-Enhancer Activity. Cell, 2015, 161, 774-789.	13.5	370
146	Generation of Live Attenuated Influenza Virus by Using Codon Usage Bias. Journal of Virology, 2015, 89, 10762-10773.	1.5	38
147	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.	3.3	175
148	The mutational landscape of cutaneous T cell lymphoma and SÃ©zary syndrome. Nature Genetics, 2015, 47, 1465-1470.	9.4	322
149	High-resolution Genomic Surveillance of 2014 Ebolavirus Using Shared Subclonal Variants. PLOS Currents, 2015, 7, .	1.4	23
150	JAK-STAT in lymphoproliferative disorders. Oncoscience, 2015, 2, 737-738.	0.9	1
151	Darwin, Lamarck, or Baldwin: Applying Evolutionary Algorithms to Machine Learning Techniques. , 2014, , .		8
152	Darwin or Lamarck? Future Challenges in Evolutionary Algorithms for Knowledge Discovery and Data Mining. Lecture Notes in Computer Science, 2014, , 35-56.	1.0	15
153	FBXW7 Mutations in Melanoma and a New Therapeutic Paradigm. Journal of the National Cancer Institute, 2014, 106, dju107.	3.0	87
154	Transcriptome reconstruction and annotation of cynomolgus and African green monkey. BMC Genomics, 2014, 15, 846.	1.2	10
155	Pegasus: a comprehensive annotation and prediction tool for detection of driver gene fusions in cancer. BMC Systems Biology, 2014, 8, 97.	3.0	60
156	Clinical impact of small TP53 mutated subclones in chronic lymphocytic leukemia. Blood, 2014, 123, 2139-2147.	0.6	302
157	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.	2.7	66
158	Recurrent mutations in epigenetic regulators, RHOA and FYN kinase in peripheral T cell lymphomas. Nature Genetics, 2014, 46, 166-170.	9.4	534
159	Leukaemogenesis induced by an activating Î²-catenin mutation in osteoblasts. Nature, 2014, 506, 240-244.	13.7	455
160	Noncoding RNA transcription targets AID to divergently transcribed loci in B cells. Nature, 2014, 514, 389-393.	13.7	159
161	Genetic lesions associated with chronic lymphocytic leukemia chemo-refractoriness. Blood, 2014, 123, 2378-2388.	0.6	78
162	Data-driven discovery of seasonally linked diseases from an Electronic Health Records system. BMC Bioinformatics, 2014, 15, S3.	1.2	27

#	Article	IF	Citations
163	Genetics of Follicular Lymphoma Transformation. Cell Reports, 2014, 6, 130-140.	2.9	471
164	Viral diversity and clonal evolution from unphased genomic data. BMC Genomics, 2014, 15, S17.	1.2	9
165	Moduli Spaces of Phylogenetic Trees Describing Tumor Evolutionary Patterns. Lecture Notes in Computer Science, 2014, , 528-539.	1.0	8
166	Tumor evolutionary directed graphs and the history of chronic lymphocytic leukemia. ELife, 2014, 3, .	2.8	43
167	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.	0.6	2
168	Small Subclones Harboring NOTCH1, SF3B1 or BIRC3 Mutations Are Clinically Irrelevant in Chronic Lymphocytic Leukemia. Blood, 2014, 124, 295-295.	0.6	1
169	The integrated landscape of driver genomic alterations in glioblastoma. Nature Genetics, 2013, 45, 1141-1149.	9.4	524
170	MutComFocal: an integrative approach to identifying recurrent and focal genomic alterations in tumor samples. BMC Systems Biology, 2013, 7, 25.	3.0	18
171	A Nondegenerate Code of Deleterious Variants in Mendelian Loci Contributes to Complex Disease Risk. Cell, 2013, 155, 70-80.	13.5	209
172	Genetic lesions associated with chronic lymphocytic leukemia transformation to Richter syndrome. Journal of Experimental Medicine, 2013, 210, 2273-2288.	4.2	255
173	SAVI: a statistical algorithm for variant frequency identification. BMC Systems Biology, 2013, 7, S2.	3.0	35
174	Integrated mutational and cytogenetic analysis identifies new prognostic subgroups in chronic lymphocytic leukemia. Blood, 2013, 121, 1403-1412.	0.6	420
175	Activating mutations in the NT5C2 nucleotidase gene drive chemotherapy resistance in relapsed ALL. Nature Medicine, 2013, 19, 368-371.	15.2	304
176	Quantifying Pathogen Surveillance Using Temporal Genomic Data. MBio, 2013, 4, e00524-12.	1.8	11
177	Topology of viral evolution. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18566-18571.	3.3	204
178	GAB2 induces tumor angiogenesis in NRAS-driven melanoma. Oncogene, 2013, 32, 3627-3637.	2.6	25
179	Beyond NPM-anaplastic lymphoma kinase driven lymphomagenesis. Current Opinion in Hematology, 2013, 20, 374-381.	1.2	17
180	E3-ubiquitin ligase Nedd4 determines the fate of AID-associated RNA polymerase II in B cells. Genes and Development, 2013, 27, 1821-1833.	2.7	32

#	Article	IF	Citations
181	Recurrent Rhoa Mutations In Peripheral T-Cell Lymphoma. Blood, 2013, 122, 846-846.	0.6	1
182	Drugâ€"drug interaction through molecular structure similarity analysis. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 1066-1074.	2.2	185
183	Emergence of Fatal Avian Influenza in New England Harbor Seals. MBio, 2012, 3, e00166-12.	1.8	161
184	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.	3.3	61
185	The coding genome of splenic marginal zone lymphoma: activation of <i>NOTCH2</i> and other pathways regulating marginal zone development. Journal of Experimental Medicine, 2012, 209, 1537-1551.	4.2	363
186	Mutations of NOTCH1 are an independent predictor of survival in chronic lymphocytic leukemia. Blood, 2012, 119, 521-529.	0.6	394
187	Transforming Fusions of <i>FGFR</i> and <i>TACC</i> Genes in Human Glioblastoma. Science, 2012, 337, 1231-1235.	6.0	716
188	Genetic inactivation of the polycomb repressive complex 2 in T cell acute lymphoblastic leukemia. Nature Medicine, 2012, 18, 298-302.	15.2	453
189	Promotion of Hepatocellular Carcinoma by the Intestinal Microbiota and TLR4. Cancer Cell, 2012, 21, 504-516.	7.7	1,051
190	How many neutrophils are enough (redux, redux)?. Journal of Clinical Investigation, 2012, 122, 2776-2779.	3.9	5
191	<i>BRAF</i> Mutations in Hairy-Cell Leukemia. New England Journal of Medicine, 2011, 364, 2305-2315.	13.9	949
192	Analysis of the coding genome of diffuse large B-cell lymphoma. Nature Genetics, 2011, 43, 830-837.	9.4	871
193	Analysis of the chronic lymphocytic leukemia coding genome: role of <i>NOTCH1</i> mutational activation. Journal of Experimental Medicine, 2011, 208, 1389-1401.	4.2	565
194	Mutations of the SF3B1 splicing factor in chronic lymphocytic leukemia: association with progression and fludarabine-refractoriness. Blood, 2011, 118, 6904-6908.	0.6	342
195	Inactivating mutations of acetyltransferase genes in B-cell lymphoma. Nature, 2011, 471, 189-195.	13.7	822
196	Discovering Disease Associations by Integrating Electronic Clinical Data and Medical Literature. PLoS ONE, 2011, 6, e21132.	1.1	41
197	Identifying Hosts of Families of Viruses: A Machine Learning Approach. PLoS ONE, 2011, 6, e27631.	1.1	3
198	Fractal-like Distributions over the Rational Numbers in High-throughput Biological and Clinical Data. Scientific Reports, 2011, 1, 191.	1.6	16

#	Article	IF	Citations
199	Biclustering of Adverse Drug Events in the FDA's Spontaneous Reporting System. Clinical Pharmacology and Therapeutics, 2011, 89, 243-250.	2.3	67
200	Whole-exome sequencing identifies somatic mutations of BCOR in acute myeloid leukemia with normal karyotype. Blood, 2011, 118, 6153-6163.	0.6	227
201	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.	1.5	56
202	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.	2.2	56
203	The Emergence of 2009 H1N1 Pandemic Influenza. , 2011, , 95-111.		0
204	Whole-Exome Sequencing Identifies Recurrent Mutations of BCOR in Acute Myeloid Leukemia with Normal Karyotype. Blood, 2011, 118, 71-71.	0.6	1
205	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
206	ParMap, an algorithm for the identification of small genomic insertions and deletions in nextgen sequencing data. BMC Research Notes, 2010, 3, 147.	0.6	1
207	PHF6 mutations in T-cell acute lymphoblastic leukemia. Nature Genetics, 2010, 42, 338-342.	9.4	282
208	Signs of the 2009 Influenza Pandemic in the New York-Presbyterian Hospital Electronic Health Records. PLoS ONE, 2010, 5, e12658.	1.1	12
209	Network Analysis of Global Influenza Spread. PLoS Computational Biology, 2010, 6, e1001005.	1.5	39
210	Frequency Analysis Techniques for Identification of Viral Genetic Data. MBio, 2010, 1, .	1.8	20
211	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.	0.2	60
212	Host Dependent Evolutionary Patterns and the Origin of 2009 H1N1 Pandemic Influenza. PLOS Currents, 2010, 2, RRN1147.	1.4	13
213	Heart and Skeletal Muscle Inflammation of Farmed Salmon Is Associated with Infection with a Novel Reovirus. PLoS ONE, 2010, 5, e11487.	1.1	198
214	The Genome of Chronic Lymphocytic Leukemia. Blood, 2010, 116, 51-51.	0.6	0
215	Reassortment Patterns in Swine Influenza Viruses. PLoS ONE, 2009, 4, e7366.	1.1	46
216	Geographic Dependence, Surveillance, and Origins of the 2009 Influenza A (H1N1) Virus. New England Journal of Medicine, 2009, 361, 115-119.	13.9	252

#	Article	IF	Citations
217	SPECTRAL SIGNATURES OF PHOTON-PARTICLE OSCILLATIONS FROM CELESTIAL OBJECTS. Astrophysical Journal, Supplement Series, 2009, 180, 1-29.	3.0	39
218	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
219	Reassortment Patterns in Swine Influenza Viruses. PLOS Currents, 2009, 1, RRN1008.	1.4	11
220	Next Generation Syndromic SurveillanceMolecular Epidemiology, Electronic Health Records and the Pandemic Influenza A (H1N1) Virus. PLOS Currents, 2009, 1, RRN1012.	1.4	3
221	Patterns of Oligonucleotide Sequences in Viral and Host Cell RNA Identify Mediators of the Host Innate Immune System. PLoS ONE, 2009, 4, e5969.	1.1	73
222	Differences in Patient Age Distribution between Influenza A Subtypes. PLoS ONE, 2009, 4, e6832.	1.1	43
223	Nonâ€random reassortment in human influenza A viruses. Influenza and Other Respiratory Viruses, 2008, 2, 9-22.	1.5	57
224	Highly Conserved Regions of Influenza A Virus Polymerase Gene Segments Are Critical for Efficient Viral RNA Packaging. Journal of Virology, 2008, 82, 2295-2304.	1.5	144
225	Patterns of Evolution and Host Gene Mimicry in Influenza and Other RNA Viruses. PLoS Pathogens, 2008, 4, e1000079.	2.1	236
226	Anomalies in the Influenza Virus Genome Database: New Biology or Laboratory Errors?. Journal of Virology, 2008, 82, 8947-8950.	1.5	34
227	An Information-Theoretic Analysis of Genetics, Gender and Age in Cancer Patients. PLoS ONE, 2008, 3, e1951.	1.1	18
228	Mitochondrial DNA Haplogroup D4a Is a Marker for Extreme Longevity in Japan. PLoS ONE, 2008, 3, e2421.	1.1	88
229	A Recoding Method to Improve the Humoral Immune Response to an HIV DNA Vaccine. PLoS ONE, 2008, 3, e3214.	1.1	8
230	Evolution of the influenza a virus: some new advances. Evolutionary Bioinformatics, 2008, 3, 299-307.	0.6	4
231	Evolution of the Influenza A Virus: Some New Advances. Evolutionary Bioinformatics, 2007, 3, 117693430700300.	0.6	5
232	Comparison of Avian and Human Influenza A Viruses Reveals a Mutational Bias on the Viral Genomes. Journal of Virology, 2006, 80, 11887-11891.	1.5	114
233	Photon Regeneration from Pseudoscalars at X-Ray Laser Facilities. Physical Review Letters, 2006, 96, 110407.	2.9	49
234	Stability in asymptotically AdS spaces. Journal of High Energy Physics, 2005, 2005, 016-016.	1.6	42

#	Article	IF	Citations
235	Non-perturbative orientifold transitions at the conifold. Journal of High Energy Physics, 2005, 2005, 026-026.	1.6	11
236	D=4 chiral string compactifications from intersecting branes. Journal of Mathematical Physics, 2001, 42, 3103-3126.	0.5	302