

Raul Rabadan

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	SF3B1 mutant-induced missplicing of MAP3K7 causes anemia in myelodysplastic syndromes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	4
240	Oncogenic Vav1-Myo1f induces therapeutically targetable macrophage-rich tumor microenvironment in peripheral T'cell lymphoma.. <i>Cell Reports</i> , 2022 , 39, 110695	10.6	1
239	Neoadjuvant chemoradiation alters the immune microenvironment in pancreatic ductal adenocarcinoma.. <i>Onc Immunology</i> , 2022 , 11, 2066767	7.2	3
238	DIPG-45. Radiation induces a robust interferon response in Diffuse Midline Glioma (DMG), improving the potential for combination immunotherapy. <i>Neuro-Oncology</i> , 2022 , 24, i28-i29	1	
237	ERK1/2 phosphorylation predicts survival following anti-PD-1 immunotherapy in recurrent glioblastoma.. <i>Nature Cancer</i> , 2021 , 2, 1372-1386	15.4	3
236	91 Impact of ultra-fast FLASH radiotherapy on single cell immunogenomics in diffuse intrinsic pontine glioma (DIPG) 2021 , 9, A100-A100		0
235	HHV-6 in the Lymphoma Microenvironment: Both Chicken and Egg?. <i>Blood</i> , 2021 , 138, 1377-1377	2.2	
234	Recombination and lineage-specific mutations linked to the emergence of SARS-CoV-2 2021 ,		15
233	PDK1 Is Required for Maintenance of CD4 Foxp3 Regulatory T Cell Function. <i>Journal of Immunology</i> , 2021 , 206, 1776-1783	5.3	2
232	Computing the Role of Alternative Splicing in Cancer. <i>Trends in Cancer</i> , 2021 , 7, 347-358	12.5	6
231	Single-cell characterization of macrophages in glioblastoma reveals MARCO as a mesenchymal pro-tumor marker. <i>Genome Medicine</i> , 2021 , 13, 88	14.4	10
230	Genetic mechanisms of HLA-I loss and immune escape in diffuse large B cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	5
229	Promotion of cholangiocarcinoma growth by diverse cancer-associated fibroblast subpopulations. <i>Cancer Cell</i> , 2021 , 39, 866-882.e11	24.3	23
228	iPLA2-mediated lipid detoxification controls p53-driven ferroptosis independent of GPX4. <i>Nature Communications</i> , 2021 , 12, 3644	17.4	24
227	High tumor mutational burden and T-cell activation are associated with long-term response to anti-PD1 therapy in Lynch syndrome recurrent glioblastoma patient. <i>Cancer Immunology, Immunotherapy</i> , 2021 , 70, 831-842	7.4	8
226	induces NF- κ B signaling-driven peripheral T cell lymphoma. <i>Nature Cancer</i> , 2021 , 2, 98-113	15.4	5
225	Dose-response modeling in high-throughput cancer drug screenings: an end-to-end approach. <i>Biostatistics</i> , 2021 ,	3.7	4

224	The UVSSA complex alleviates MYC-driven transcription stress. <i>Journal of Cell Biology</i> , 2021 , 220,	7.3	3
223	Comprehensive characterization of protein-protein interactions perturbed by disease mutations. <i>Nature Genetics</i> , 2021 , 53, 342-353	36.3	27
222	Global Patterns of Recombination across Human Viruses. <i>Molecular Biology and Evolution</i> , 2021 , 38, 2520-2531	8.5	13
221	Functional interrogation of DNA damage response variants with base editing screens. <i>Cell</i> , 2021 , 184, 1081-1097.e19	56.2	37
220	Transcriptional control of CBX5 by the RNA binding proteins RBMX and RBMXL1 maintains chromatin state in myeloid leukemia. <i>Nature Cancer</i> , 2021 , 2, 741-757	15.4	4
219	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. <i>Clinical Cancer Research</i> , 2021 , 27, 5519-5527	12.9	4
218	TOP2B Enzymatic Activity on Promoters and Introns Modulates Multiple Oncogenes in Human Gliomas. <i>Clinical Cancer Research</i> , 2021 , 27, 5669-5680	12.9	1
217	Recombination and lineage-specific mutations linked to the emergence of SARS-CoV-2. <i>Genome Medicine</i> , 2021 , 13, 124	14.4	8
216	How Can We Treat the Virus and Prevent Infections? 2021 , 100-113		
215	What Is a Coronavirus? 2021 , 22-33		
214	How Is the Coronavirus Spreading? 2021 , 7-21		
213	Figure and Quotation Credits 2021 , 131-135		
212	Summary of Common Misunderstandings 2021 , 118-120		
211	How Did the COVID-19 Outbreak Start and Evolve? 2021 , 45-77		
210	How Is the Coronavirus Changing? 2021 , 34-44		
209	How Does the COVID-19 Outbreak Compare to Seasonal and Pandemic Influenza? 2021 , 88-99		
208	How Does the COVID-19 Outbreak Compare to the SARS Outbreak in 2003? 2021 , 78-87		
207	Mutant SF3B1 promotes AKT- and NF- κ B-driven mammary tumorigenesis. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	6

206	Active surveillance documents rates of clinical care seeking due to respiratory illness. <i>Influenza and Other Respiratory Viruses</i> , 2020 , 14, 499-506	5.6	2
205	CD8 T-cell-Mediated Immunoediting Influences Genomic Evolution and Immune Evasion in Murine Gliomas. <i>Clinical Cancer Research</i> , 2020 , 26, 4390-4401	12.9	9
204	A Novel JAK1 Mutant Breast Implant-Associated Anaplastic Large Cell Lymphoma Patient-Derived Xenograft Fostering Pre-Clinical Discoveries. <i>Cancers</i> , 2020 , 12,	6.6	3
203	Quantifying Genetic Innovation: Mathematical Foundations for the Topological Study of Reticulate Evolution. <i>SIAM Journal on Applied Algebra and Geometry</i> , 2020 , 4, 141-184	1.5	4
202	Linking Transcriptomic and Imaging Data Defines Features of a Favorable Tumor Immune Microenvironment and Identifies a Combination Biomarker for Primary Melanoma. <i>Cancer Research</i> , 2020 , 80, 1078-1087	10.1	6
201	Pan-cancer analysis identifies mutations in that recapitulate mutant SF3B1 splicing dysregulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 10305-10312	11.5	11
200	Expression of Vav1-Myo1F Fusion Affects T-Cell Differentiation and Induces T-Cell Lymphoma. <i>Blood</i> , 2020 , 136, 4-4	2.2	
199	Transcriptional Control of HP1a By the RNA Binding Proteins RbmX/L1 Maintain Chromatin State in Myeloid Leukemia. <i>Blood</i> , 2020 , 136, 15-15	2.2	
198	Mechanisms of Therapeutic Response to Tipifarnib in a Mouse Model of Angioimmunoblastic T-Cell Lymphoma. <i>Blood</i> , 2020 , 136, 9-9	2.2	
197	Genomic Characterization of HIV-Associated Plasmablastic Lymphoma Identifies Pervasive Mutations in the JAK/STAT Pathway. <i>Blood Cancer Discovery</i> , 2020 , 1, 112-125	7	13
196	HLA Typing from RNA Sequencing and Applications to Cancer. <i>Methods in Molecular Biology</i> , 2020 , 2120, 71-92	1.4	0
195	A single-cell atlas of the mouse and human prostate reveals heterogeneity and conservation of epithelial progenitors. <i>ELife</i> , 2020 , 9,	8.9	19
194	Topological Data Analysis of Single-Cell Hi-C Contact Maps. <i>Abel Symposia</i> , 2020 , 147-162	0.9	6
193	Midkine rewires the melanoma microenvironment toward a tolerogenic and immune-resistant state. <i>Nature Medicine</i> , 2020 , 26, 1865-1877	50.5	12
192	CtIP-mediated DNA resection is dispensable for IgH class switch recombination by alternative end-joining. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 25700-25711	11.5	5
191	A MYC and RAS co-activation signature in localized prostate cancer drives bone metastasis and castration resistance. <i>Nature Cancer</i> , 2020 , 1, 1082-1096	15.4	18
190	A Random Matrix Theory Approach to Denoise Single-Cell Data. <i>Patterns</i> , 2020 , 1, 100035	5.1	13
189	Double Empirical Bayes Testing.. <i>International Statistical Review</i> , 2020 , 88, S91-S113	1.4	2

188	Identification of relevant genetic alterations in cancer using topological data analysis. <i>Nature Communications</i> , 2020 , 11, 3808	17.4	13
187	MGMT genomic rearrangements contribute to chemotherapy resistance in gliomas. <i>Nature Communications</i> , 2020 , 11, 3883	17.4	47
186	Genomic characterization of HIV-associated plasmablastic lymphoma identifies pervasive mutations in the JAK-STAT pathway. <i>Blood Cancer Discovery</i> , 2020 , 1, 112-125	7	8
185	Mutational and functional genetics mapping of chemotherapy resistance mechanisms in relapsed acute lymphoblastic leukemia. <i>Nature Cancer</i> , 2020 , 1, 1113-1127	15.4	7
184	arcasHLA: high-resolution HLA typing from RNAseq. <i>Bioinformatics</i> , 2020 , 36, 33-40	7.2	30
183	Predicting Clinical Outcomes in Glioblastoma: An Application of Topological and Functional Data Analysis. <i>Journal of the American Statistical Association</i> , 2020 , 115, 1139-1150	2.8	25
182	Mutations in the RNA Splicing Factor SF3B1 Promote Tumorigenesis through MYC Stabilization. <i>Cancer Discovery</i> , 2020 , 10, 806-821	24.4	30
181	Disease-Causing Mutations in SF3B1 Alter Splicing by Disrupting Interaction with SUGP1. <i>Molecular Cell</i> , 2019 , 76, 82-95.e7	17.6	42
180	A Structure-Informed Atlas of Human-Virus Interactions. <i>Cell</i> , 2019 , 178, 1526-1541.e16	56.2	65
179	Interrogation of Eukaryotic Stop Codon Readthrough Signals by in Vitro RNA Selection. <i>Biochemistry</i> , 2019 , 58, 1167-1178	3.2	13
178	The 2019 mathematical oncology roadmap. <i>Physical Biology</i> , 2019 , 16, 041005	3	78
177	Novel insights into the genetics and epigenetics of MALT lymphoma unveiled by next generation sequencing analyses. <i>Haematologica</i> , 2019 , 104, e558-e561	6.6	31
176	Complete Regression of Advanced Pancreatic Ductal Adenocarcinomas upon Combined Inhibition of EGFR and C-RAF. <i>Cancer Cell</i> , 2019 , 35, 573-587.e6	24.3	37
175	Immune and genomic correlates of response to anti-PD-1 immunotherapy in glioblastoma. <i>Nature Medicine</i> , 2019 , 25, 462-469	50.5	314
174	Distinct genomic profile and specific targeted drug responses in adult cerebellar glioblastoma. <i>Neuro-Oncology</i> , 2019 , 21, 47-58	1	19
173	Repurposing dasatinib for diffuse large B cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 16981-16986	11.5	8
172	Somatic mutations and cell identity linked by Genotyping of Transcriptomes. <i>Nature</i> , 2019 , 571, 355-360	50.4	95
171	The Long Noncoding RNA Paupar Modulates PAX6 Regulatory Activities to Promote Alpha Cell Development and Function. <i>Cell Metabolism</i> , 2019 , 30, 1091-1106.e8	24.6	30

170	Double mutations in cis increase oncogenicity and sensitivity to PI3K inhibitors. <i>Science</i> , 2019 , 366, 714-723	3.3	102
169	RNA Sequencing of Hodgkin Lymphoma Reed-Sternberg Cells Uncovers a Plasma Cell Signature and Escape from NK Cell Recognition. <i>Blood</i> , 2019 , 134, 549-549	2.2	1
168	Can patient selection and neoadjuvant administration resuscitate PD-1 inhibitors for glioblastoma?. <i>Journal of Neurosurgery</i> , 2019 , 132, 1667-1672	3.2	5
167	Longitudinal active sampling for respiratory viral infections across age groups. <i>Influenza and Other Respiratory Viruses</i> , 2019 , 13, 226-232	5.6	26
166	GATA3-Controlled Nucleosome Eviction Drives Enhancer Activity in T-cell Development and Leukemia. <i>Cancer Discovery</i> , 2019 , 9, 1774-1791	24.4	17
165	Pharmacogenomic analysis of patient-derived tumor cells in gynecologic cancers. <i>Genome Biology</i> , 2019 , 20, 253	18.3	9
164	Longitudinal molecular trajectories of diffuse glioma in adults. <i>Nature</i> , 2019 , 576, 112-120	50.4	151
163	Secretome analysis of patient-derived GBM tumor spheres identifies midkine as a potent therapeutic target. <i>Experimental and Molecular Medicine</i> , 2019 , 51, 1-11	12.8	19
162	Tissue-Resident Memory T Cells Mediate Immune Homeostasis in the Human Pancreas through the PD-1/PD-L1 Pathway. <i>Cell Reports</i> , 2019 , 29, 3916-3932.e5	10.6	40
161	Loss Enhances HSC Self-Renewal Driving Tumor Initiation and Leukemia Stem Cell Activity in T-ALL. <i>Cancer Discovery</i> , 2019 , 9, 436-451	24.4	31
160	Blastic plasmacytoid dendritic cell neoplasm: genomics mark epigenetic dysregulation as a primary therapeutic target. <i>Haematologica</i> , 2019 , 104, 729-737	6.6	33
159	Hypermutagenesis in untreated adult gliomas due to inherited mismatch mutations. <i>International Journal of Cancer</i> , 2019 , 144, 3023-3030	7.5	12
158	Comprehensive characterisation of compartment-specific long non-coding RNAs associated with pancreatic ductal adenocarcinoma. <i>Gut</i> , 2019 , 68, 499-511	19.2	32
157	Quantitative Analysis of Immune Infiltrates in Primary Melanoma. <i>Cancer Immunology Research</i> , 2018 , 6, 481-493	12.5	51
156	The possibility of cancer immune editing in gliomas. A critical review. <i>Oncotarget</i> , 2018 , 9, 14454-14458	5.82	25
155	The Egyptian Roussette Genome Reveals Unexpected Features of Bat Antiviral Immunity. <i>Cell</i> , 2018 , 173, 1098-1110.e18	56.2	121
154	Increased expression provides a selective advantage for gain of whole chromosome 7 in IDH wild-type glioblastoma. <i>Genes and Development</i> , 2018 , 32, 512-523	12.6	21
153	Pervasive mutations of JAK-STAT pathway genes in classical Hodgkin lymphoma. <i>Blood</i> , 2018 , 131, 2454-2465	24.65	89

152	Clonal evolution mechanisms in NT5C2 mutant-relapsed acute lymphoblastic leukaemia. <i>Nature</i> , 2018 , 553, 511-514	50.4	67
151	Saa3 is a key mediator of the protumorigenic properties of cancer-associated fibroblasts in pancreatic tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E1147-E1156	11.5	84
150	Genetic landscape of ultra-stable chronic lymphocytic leukemia patients. <i>Annals of Oncology</i> , 2018 , 29, 966-972	10.3	13
149	On statistical modeling of sequencing noise in high depth data to assess tumor evolution. <i>Journal of Statistical Physics</i> , 2018 , 172, 143-155	1.5	4
148	Precision Medicine for Acute Kidney Injury (AKI): Redefining AKI by Agnostic Kidney Tissue Interrogation and Genetics. <i>Seminars in Nephrology</i> , 2018 , 38, 40-51	4.8	18
147	Refined karyotype-based prognostic stratification of chronic lymphocytic leukemia with a low- and very-low-risk genetic profile. <i>Leukemia</i> , 2018 , 32, 543-546	10.7	2
146	Copy number profiling across glioblastoma populations has implications for clinical trial design. <i>Neuro-Oncology</i> , 2018 , 20, 1368-1373	1	18
145	Mutations in the RNA Splicing Factor SF3B1 Promote Transformation through MYC Stabilization. <i>Blood</i> , 2018 , 132, 882-882	2.2	
144	High Throughput Droplet Single-Cell Genotyping of Transcriptomes (GoT) Reveals the Cell Identity Dependency of the Transcriptional Output of Somatic Mutations. <i>Blood</i> , 2018 , 132, 541-541	2.2	1
143	GENE-17. TOP2B REGULATES CDK4 SPLICE VARIANTS IN GLIOMAS. <i>Neuro-Oncology</i> , 2018 , 20, vi106-vi106		78
142	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. <i>BMC Medical Genomics</i> , 2018 , 11, 98	3.7	8
141	DDIS-13. UNDERSTANDING GLIOBLASTOMA SUSCEPTIBILITY TO TOP2-TARGETING DRUGS FOR PERSONALIZED THERAPY. <i>Neuro-Oncology</i> , 2018 , 20, vi71-vi72	1	78
140	Pharmacogenomic landscape of patient-derived tumor cells informs precision oncology therapy. <i>Nature Genetics</i> , 2018 , 50, 1399-1411	36.3	94
139	Evolutionary Dynamics of Pandemic Methicillin-Sensitive Staphylococcus aureus ST398 and Its International Spread via Routes of Human Migration. <i>MBio</i> , 2017 , 8,	7.8	30
138	Activating mutations and translocations in the guanine exchange factor VAV1 in peripheral T-cell lymphomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 764-769	11.5	67
137	Spatiotemporal genomic architecture informs precision oncology in glioblastoma. <i>Nature Genetics</i> , 2017 , 49, 594-599	36.3	141
136	Nuclear Proximity of Mtr4 to RNA Exosome Restricts DNA Mutational Asymmetry. <i>Cell</i> , 2017 , 169, 523-537	37.1	153
135	Germ-Cell-Specific Inflammasome Component NLRP14 Negatively Regulates Cytosolic Nucleic Acid Sensing to Promote Fertilization. <i>Immunity</i> , 2017 , 46, 621-634	32.3	30

134	p53 Maintains Baseline Expression of Multiple Tumor Suppressor Genes. <i>Molecular Cancer Research</i> , 2017 , 15, 1051-1062	6.6	39
133	Single-cell topological RNA-seq analysis reveals insights into cellular differentiation and development. <i>Nature Biotechnology</i> , 2017 , 35, 551-560	44.5	138
132	Genomic Characterization of Dysplastic Nevi Unveils Implications for Diagnosis of Melanoma. <i>Journal of Investigative Dermatology</i> , 2017 , 137, 905-909	4.3	29
131	The B-cell receptor controls fitness of MYC-driven lymphoma cells via GSK3 β inhibition. <i>Nature</i> , 2017 , 546, 302-306	50.4	43
130	Evolutionary scalpels for dissecting tumor ecosystems. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2017 , 1867, 69-83	11.2	9
129	A Fast Semi-Automatic Segmentation Tool for Processing Brain Tumor Images. <i>Lecture Notes in Computer Science</i> , 2017 , 170-181	0.9	1
128	Restoration of Replication Fork Stability in BRCA1- and BRCA2-Deficient Cells by Inactivation of SNF2-Family Fork Remodelers. <i>Molecular Cell</i> , 2017 , 68, 414-430.e8	17.6	181
127	Assessment of T-cell receptor repertoire and clonal expansion in peripheral T-cell lymphoma using RNA-seq data. <i>Scientific Reports</i> , 2017 , 7, 11301	4.9	18
126	An NF- κ B Transcription-Factor-Dependent Lineage-Specific Transcriptional Program Promotes Regulatory T Cell Identity and Function. <i>Immunity</i> , 2017 , 47, 450-465.e5	32.3	115
125	Identification of potentially oncogenic alterations from tumor-only samples reveals Fanconi anemia pathway mutations in bladder carcinomas. <i>Npj Genomic Medicine</i> , 2017 , 2, 29	6.2	12
124	A Random Categorization Model for Hierarchical Taxonomies. <i>Scientific Reports</i> , 2017 , 7, 17051	4.9	
123	Mutational landscape, clonal evolution patterns, and role of RAS mutations in relapsed acute lymphoblastic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 11306-11311	11.5	117
122	Topological Data Analysis Generates High-Resolution, Genome-wide Maps of Human Recombination. <i>Cell Systems</i> , 2016 , 3, 83-94	10.6	27
121	The genetics of nodal marginal zone lymphoma. <i>Blood</i> , 2016 , 128, 1362-73	2.2	88
120	Identification of a new subclass of ALK-negative ALCL expressing aberrant levels of ERBB4 transcripts. <i>Blood</i> , 2016 , 127, 221-32	2.2	65
119	Clonal evolution of glioblastoma under therapy. <i>Nature Genetics</i> , 2016 , 48, 768-76	36.3	390
118	Reprogramming eukaryotic translation with ligand-responsive synthetic RNA switches. <i>Nature Methods</i> , 2016 , 13, 453-8	21.6	21
117	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140

116	Multiscale Topology of Chromatin Folding 2016 ,		9
115	Prognostic and therapeutic role of targetable lesions in B-lineage acute lymphoblastic leukemia without recurrent fusion genes. <i>Oncotarget</i> , 2016 , 7, 13886-901	3.3	14
114	Inference of Ancestral Recombination Graphs through Topological Data Analysis. <i>PLoS Computational Biology</i> , 2016 , 12, e1005071	5	24
113	Kinase-dead ATM protein is highly oncogenic and can be preferentially targeted by Topo-isomerase I inhibitors. <i>ELife</i> , 2016 , 5,	8.9	27
112	A Case of T-cell Acute Lymphoblastic Leukemia Relapsed As Myeloid Acute Leukemia. <i>Pediatric Blood and Cancer</i> , 2016 , 63, 1660-3	3	7
111	Inter- and intra-patient clonal and subclonal heterogeneity of chronic lymphocytic leukaemia: evidences from circulating and lymph nodal compartments. <i>British Journal of Haematology</i> , 2016 , 172, 371-383	4.5	15
110	Clinical impact of small subclones harboring NOTCH1, SF3B1 or BIRC3 mutations in chronic lymphocytic leukemia. <i>Haematologica</i> , 2016 , 101, e135-8	6.6	30
109	Convergent Mutations and Kinase Fusions Lead to Oncogenic STAT3 Activation in Anaplastic Large Cell Lymphoma. <i>Cancer Cell</i> , 2015 , 27, 744	24.3	2
108	A novel patient-derived tumorgraft model with TRAF1-ALK anaplastic large-cell lymphoma translocation. <i>Leukemia</i> , 2015 , 29, 1390-401	10.7	32
107	Convergent mutations and kinase fusions lead to oncogenic STAT3 activation in anaplastic large cell lymphoma. <i>Cancer Cell</i> , 2015 , 27, 516-32	24.3	283
106	Genetic similarity between cancers and comorbid Mendelian diseases identifies candidate driver genes. <i>Nature Communications</i> , 2015 , 6, 7033	17.4	22
105	RNA exosome-regulated long non-coding RNA transcription controls super-enhancer activity. <i>Cell</i> , 2015 , 161, 774-89	56.2	280
104	Generation of Live Attenuated Influenza Virus by Using Codon Usage Bias. <i>Journal of Virology</i> , 2015 , 89, 10762-73	6.6	25
103	Disease-associated mutation in SRSF2 misregulates splicing by altering RNA-binding affinities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E4726-34	11.5	136
102	The mutational landscape of cutaneous T cell lymphoma and S _z ary syndrome. <i>Nature Genetics</i> , 2015 , 47, 1465-70	36.3	234
101	Transcriptomics Identify CD9 as a Marker of Murine IL-10-Competent Regulatory B Cells. <i>Cell Reports</i> , 2015 , 13, 1110-1117	10.6	69
100	De novo transcriptome reconstruction and annotation of the Egyptian rousette bat. <i>BMC Genomics</i> , 2015 , 16, 1033	4.5	27
99	Distinct Viral and Mutational Spectrum of Endemic Burkitt Lymphoma. <i>PLoS Pathogens</i> , 2015 , 11, e1005158	15.8	74

98	An information theoretic method to identify combinations of genomic alterations that promote glioblastoma. <i>Journal of Molecular Cell Biology</i> , 2015 , 7, 203-13	6.3	12
97	GENO-06A PAN-GLIOMA CHARACTERIZATION OF GENOMIC, EPIGENOMIC AND TRANSCRIPTOMIC ACTIVITIES REVEALS NOVEL RELATIONSHIPS BETWEEN HISTOLOGICAL SUBTYPES AND MOLECULAR SIGNATURES. <i>Neuro-Oncology</i> , 2015 , 17, v92.2-v92	1	78
96	A targetable GATA2-IGF2 axis confers aggressiveness in lethal prostate cancer. <i>Cancer Cell</i> , 2015 , 27, 223-39	24.3	94
95	High-resolution Genomic Surveillance of 2014 Ebolavirus Using Shared Subclonal Variants. <i>PLOS Currents</i> , 2015 , 7,		19
94	JAK-STAT in lymphoproliferative disorders. <i>Oncoscience</i> , 2015 , 2, 737-8	0.8	1
93	The miR-424(322)/503 cluster orchestrates remodeling of the epithelium in the involuting mammary gland. <i>Genes and Development</i> , 2014 , 28, 765-82	12.6	52
92	Recurrent mutations in epigenetic regulators, RHOA and FYN kinase in peripheral T cell lymphomas. <i>Nature Genetics</i> , 2014 , 46, 166-70	36.3	413
91	Leukaemogenesis induced by an activating Ectenin mutation in osteoblasts. <i>Nature</i> , 2014 , 506, 240-4	50.4	360
90	Noncoding RNA transcription targets AID to divergently transcribed loci in B cells. <i>Nature</i> , 2014 , 514, 389-93	50.4	117
89	Genetic lesions associated with chronic lymphocytic leukemia chemo-refractoriness. <i>Blood</i> , 2014 , 123, 2378-88	2.2	64
88	Data-driven discovery of seasonally linked diseases from an Electronic Health Records system. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 6, S3	3.6	20
87	Genetics of follicular lymphoma transformation. <i>Cell Reports</i> , 2014 , 6, 130-40	10.6	371
86	Viral diversity and clonal evolution from unphased genomic data. <i>BMC Genomics</i> , 2014 , 15 Suppl 6, S17	4.5	8
85	Darwin, Lamarck, or Baldwin: Applying Evolutionary Algorithms to Machine Learning Techniques 2014 ,		5
84	Darwin or Lamarck? Future Challenges in Evolutionary Algorithms for Knowledge Discovery and Data Mining. <i>Lecture Notes in Computer Science</i> , 2014 , 35-56	0.9	12
83	FBXW7 mutations in melanoma and a new therapeutic paradigm. <i>Journal of the National Cancer Institute</i> , 2014 , 106, dju107	9.7	63
82	Transcriptome reconstruction and annotation of cynomolgus and African green monkey. <i>BMC Genomics</i> , 2014 , 15, 846	4.5	9
81	Pegasus: a comprehensive annotation and prediction tool for detection of driver gene fusions in cancer. <i>BMC Systems Biology</i> , 2014 , 8, 97	3.5	47

80	High-resolution genomic surveillance of 2014 ebolavirus using shared subclonal variants 2014 ,		2
79	Clinical impact of small TP53 mutated subclones in chronic lymphocytic leukemia. <i>Blood</i> , 2014 , 123, 2139-2147	2.47	247
78	Tumor evolutionary directed graphs and the history of chronic lymphocytic leukemia. <i>ELife</i> , 2014 , 3,	8.9	37
77	Moduli Spaces of Phylogenetic Trees Describing Tumor Evolutionary Patterns. <i>Lecture Notes in Computer Science</i> , 2014 , 528-539	0.9	8
76	Characterizing Scales of Genetic Recombination and Antibiotic Resistance in Pathogenic Bacteria Using Topological Data Analysis. <i>Lecture Notes in Computer Science</i> , 2014 , 540-551	0.9	4
75	Molecular Genetic Analysis of Myelodysplastic Syndromes (MDS) Patients with Ring Sideroblasts (RS); Independent Confirmation of Association of SF3B1 Mutations with Better Prognosis. <i>Blood</i> , 2014 , 124, 3237-3237	2.2	
74	Small Subclones Harboring NOTCH1, SF3B1 or BIRC3 Mutations Are Clinically Irrelevant in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2014 , 124, 295-295	2.2	1
73	The integrated landscape of driver genomic alterations in glioblastoma. <i>Nature Genetics</i> , 2013 , 45, 1141-1146	36.3	400
72	MutComFocal: an integrative approach to identifying recurrent and focal genomic alterations in tumor samples. <i>BMC Systems Biology</i> , 2013 , 7, 25	3.5	18
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