

Roland Eils

List of Publications by Citations

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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.

436
papers

40,264
citations

88
h-index

195
g-index

475
ext. papers

51,861
ext. citations

11.3
avg, IF

7.1
L-index

#	Paper	IF	Citations
436	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013 , 500, 415-21	50.4	5895
435	Complex heatmaps reveal patterns and correlations in multidimensional genomic data. <i>Bioinformatics</i> , 2016 , 32, 2847-9	7.2	2316
434	International network of cancer genome projects. <i>Nature</i> , 2010 , 464, 993-8	50.4	1613
433	circlize Implements and enhances circular visualization in R. <i>Bioinformatics</i> , 2014 , 30, 2811-2	7.2	1242
432	The Human Cell Atlas. <i>ELife</i> , 2017 , 6,	8.9	937
431	Systemic spread is an early step in breast cancer. <i>Cancer Cell</i> , 2008 , 13, 58-68	24.3	892
430	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. <i>Nature</i> , 2010 , 464, 721-7	50.4	668
429	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010 , 28, 827-38	44.5	644
428	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012 , 488, 100-5	50.4	623
427	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , 2018 , 555, 321-327	50.4	603
426	Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. <i>Cell</i> , 2012 , 148, 59-71	56.2	600
425	Three-dimensional maps of all chromosomes in human male fibroblast nuclei and prometaphase rosettes. <i>PLoS Biology</i> , 2005 , 3, e157	9.7	577
424	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. <i>Nature Genetics</i> , 2013 , 45, 927-32	36.3	550
423	SARS-CoV-2 receptor ACE2 and TMPRSS2 are primarily expressed in bronchial transient secretory cells. <i>EMBO Journal</i> , 2020 , 39, e105114	13	538
422	From latent disseminated cells to overt metastasis: genetic analysis of systemic breast cancer progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 7737-42	11.5	517
421	COVID-19 severity correlates with airway epithelium-immune cell interactions identified by single-cell analysis. <i>Nature Biotechnology</i> , 2020 , 38, 970-979	44.5	487
420	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. <i>Cell</i> , 2016 , 164, 1060-1073	36.2	483

419	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017 , 547, 311-317	50.4	472
418	Genome sequencing of SHH medulloblastoma predicts genotype-related response to smoothed inhibition. <i>Cancer Cell</i> , 2014 , 25, 393-405	24.3	469
417	Olfactory transmucosal SARS-CoV-2 invasion as a port of central nervous system entry in individuals with COVID-19. <i>Nature Neuroscience</i> , 2021 , 24, 168-175	25.5	459
416	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. <i>Nature</i> , 2014 , 506, 445-50	50.4	434
415	Omic data from evolved E. coli are consistent with computed optimal growth from genome-scale models. <i>Molecular Systems Biology</i> , 2010 , 6, 390	12.2	419
414	Recruitment and activation of a lipid kinase by hepatitis C virus NS5A is essential for integrity of the membranous replication compartment. <i>Cell Host and Microbe</i> , 2011 , 9, 32-45	23.4	385
413	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. <i>Nature</i> , 2014 , 511, 428-34	50.4	377
412	Nuclear envelope breakdown proceeds by microtubule-induced tearing of the lamina. <i>Cell</i> , 2002 , 108, 83-96	56.2	371
411	Identification of regulatory networks in HSCs and their immediate progeny via integrated proteome, transcriptome, and DNA methylome analysis. <i>Cell Stem Cell</i> , 2014 , 15, 507-522	18	320
410	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. <i>Cancer Cell</i> , 2016 , 29, 379-393	24.3	319
409	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. <i>Nature Genetics</i> , 2012 , 44, 1316-20	36.3	317
408	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. <i>Nature</i> , 2014 , 510, 537-41	50.4	296
407	Transient colocalization of X-inactivation centres accompanies the initiation of X inactivation. <i>Nature Cell Biology</i> , 2006 , 8, 293-9	23.4	276
406	Modulation of serines 17 and 24 in the LC3-interacting region of Bnip3 determines pro-survival mitophagy versus apoptosis. <i>Journal of Biological Chemistry</i> , 2013 , 288, 1099-113	5.4	275
405	Integrative genomic analyses reveal an androgen-driven somatic alteration landscape in early-onset prostate cancer. <i>Cancer Cell</i> , 2013 , 23, 159-70	24.3	259
404	SARS-CoV-2 receptor ACE2 and TMPRSS2 are primarily expressed in bronchial transient secretory cells. <i>EMBO Journal</i> , e105114	13	255
403	Mathematical modeling reveals threshold mechanism in CD95-induced apoptosis. <i>Journal of Cell Biology</i> , 2004 , 166, 839-51	7.3	254
402	Global chromosome positions are transmitted through mitosis in mammalian cells. <i>Cell</i> , 2003 , 112, 751-6	56.2	237

401	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. <i>Nature</i> , 2016 , 530, 57-62	50.4	234
400	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
399	Acute myeloid leukemias with reciprocal rearrangements can be distinguished by specific gene expression profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 10008-13	11.5	215
398	Customized oligonucleotide microarray gene expression-based classification of neuroblastoma patients outperforms current clinical risk stratification. <i>Journal of Clinical Oncology</i> , 2006 , 24, 5070-8	2.2	212
397	Large-scale in silico modeling of metabolic interactions between cell types in the human brain. <i>Nature Biotechnology</i> , 2010 , 28, 1279-85	44.5	206
396	Genomic analysis of single cytokeratin-positive cells from bone marrow reveals early mutational events in breast cancer. <i>Cancer Cell</i> , 2005 , 8, 227-39	24.3	204
395	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015 , 6, 10001	17.4	199
394	A contractile nuclear actin network drives chromosome congression in oocytes. <i>Nature</i> , 2005 , 436, 812-850.4	50.4	186
393	Three-dimensional reconstruction of painted human interphase chromosomes: active and inactive X chromosome territories have similar volumes but differ in shape and surface structure. <i>Journal of Cell Biology</i> , 1996 , 135, 1427-40	7.3	185
392	Mutations in the SIX1/2 pathway and the DROSHA/DGCR8 miRNA microprocessor complex underlie high-risk blastemal type Wilms tumors. <i>Cancer Cell</i> , 2015 , 27, 298-311	24.3	183
391	Compartmentalization of interphase chromosomes observed in simulation and experiment. <i>Journal of Molecular Biology</i> , 1999 , 285, 1053-65	6.5	177
390	Artesunate activates mitochondrial apoptosis in breast cancer cells via iron-catalyzed lysosomal reactive oxygen species production. <i>Journal of Biological Chemistry</i> , 2011 , 286, 6587-601	5.4	174
389	Automatic identification of subcellular phenotypes on human cell arrays. <i>Genome Research</i> , 2004 , 14, 1130-6	9.7	166
388	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. <i>Lancet Oncology</i> , 2018 , 19, 785-798	21.7	159
387	Secretory meningiomas are defined by combined KLF4 K409Q and TRAF7 mutations. <i>Acta Neuropathologica</i> , 2013 , 125, 351-8	14.3	158
386	Engineering light-inducible nuclear localization signals for precise spatiotemporal control of protein dynamics in living cells. <i>Nature Communications</i> , 2014 , 5, 4404	17.4	157
385	Dynamics of HIV-1 assembly and release. <i>PLoS Pathogens</i> , 2009 , 5, e1000652	7.6	150
384	CYP3A5 mediates basal and acquired therapy resistance in different subtypes of pancreatic ductal adenocarcinoma. <i>Nature Medicine</i> , 2016 , 22, 278-87	50.5	148

383	Visualizing telomere dynamics in living mammalian cells using PNA probes. <i>EMBO Journal</i> , 2003 , 22, 6631-41	1.4	148
382	Cross-platform analysis of cancer microarray data improves gene expression based classification of phenotypes. <i>BMC Bioinformatics</i> , 2005 , 6, 265	3.6	146
381	Metabolic-energy-dependent movement of PML bodies within the mammalian cell nucleus. <i>Nature Cell Biology</i> , 2002 , 4, 106-10	23.4	145
380	Etiology-dependent molecular mechanisms in human hepatocarcinogenesis. <i>Hepatology</i> , 2008 , 47, 511-20	1.2	140
379	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. <i>Nature Medicine</i> , 2016 , 22, 1314-1320	50.5	137
378	Genome-wide transcriptional analysis of the human cell cycle identifies genes differentially regulated in normal and cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 955-60	11.5	134
377	Optogenetic control of nuclear protein export. <i>Nature Communications</i> , 2016 , 7, 10624	17.4	132
376	Gene expression signature predicting pathologic complete response with gemcitabine, epirubicin, and docetaxel in primary breast cancer. <i>Journal of Clinical Oncology</i> , 2006 , 24, 1839-45	2.2	129
375	Group testing for pathway analysis improves comparability of different microarray datasets. <i>Bioinformatics</i> , 2006 , 22, 2500-6	7.2	119
374	Model-based dissection of CD95 signaling dynamics reveals both a pro- and antiapoptotic role of c-FLIPL. <i>Journal of Cell Biology</i> , 2010 , 190, 377-89	7.3	118
373	Dynamics within the CD95 death-inducing signaling complex decide life and death of cells. <i>Molecular Systems Biology</i> , 2010 , 6, 352	12.2	117
372	Integrative genomic and transcriptomic analysis of leiomyosarcoma. <i>Nature Communications</i> , 2018 , 9, 144	17.4	115
371	The landscape of viral associations in human cancers. <i>Nature Genetics</i> , 2020 , 52, 320-330	36.3	113
370	Screening drug effects in patient-derived cancer cells links organoid responses to genome alterations. <i>Molecular Systems Biology</i> , 2017 , 13, 955	12.2	113
369	High-precision distance measurements and volume-conserving segmentation of objects near and below the resolution limit in three-dimensional confocal fluorescence microscopy. <i>Journal of Microscopy</i> , 1998 , 189, 118-136	1.9	110
368	Engineered anti-CRISPR proteins for optogenetic control of CRISPR-Cas9. <i>Nature Methods</i> , 2018 , 15, 924-927	21.6	109
367	Tagmentation-based whole-genome bisulfite sequencing. <i>Nature Protocols</i> , 2013 , 8, 2022-32	18.8	108
366	The 3D positioning of ANT2 and ANT3 genes within female X chromosome territories correlates with gene activity. <i>Experimental Cell Research</i> , 1999 , 252, 363-75	4.2	107

365	Prognostic impact of gene expression-based classification for neuroblastoma. <i>Journal of Clinical Oncology</i> , 2010 , 28, 3506-15	2.2	106
364	One, two or three? Probing the stoichiometry of membrane proteins by single-molecule localization microscopy. <i>Scientific Reports</i> , 2015 , 5, 14072	4.9	105
363	The mutational pattern of primary lymphoma of the central nervous system determined by whole-exome sequencing. <i>Leukemia</i> , 2015 , 29, 677-85	10.7	104
362	Synergy between medical informatics and bioinformatics: facilitating genomic medicine for future health care. <i>Journal of Biomedical Informatics</i> , 2004 , 37, 30-42	10.2	103
361	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. <i>Nature Genetics</i> , 2015 , 47, 1316-1325	36.3	101
360	Prediction of clinical outcome and biological characterization of neuroblastoma by expression profiling. <i>Oncogene</i> , 2005 , 24, 7902-12	9.2	100
359	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. <i>Nature Genetics</i> , 2015 , 47, 22-30	36.3	99
358	Microarray-based copy number and expression profiling in dedifferentiated and pleomorphic liposarcoma. <i>Cancer Research</i> , 2002 , 62, 2993-8	10.1	97
357	Autoantibodies against the exocrine pancreas in autoimmune pancreatitis: gene and protein expression profiling and immunoassays identify pancreatic enzymes as a major target of the inflammatory process. <i>American Journal of Gastroenterology</i> , 2010 , 105, 2060-71	0.7	96
356	Concurrent detection of autolysosome formation and lysosomal degradation by flow cytometry in a high-content screen for inducers of autophagy. <i>BMC Biology</i> , 2011 , 9, 38	7.3	95
355	Optimal experimental design for parameter estimation of a cell signaling model. <i>PLoS Computational Biology</i> , 2009 , 5, e1000558	5	95
354	Computational imaging in cell biology. <i>Journal of Cell Biology</i> , 2003 , 161, 477-81	7.3	95
353	NK cells switch from granzyme B to death receptor-mediated cytotoxicity during serial killing. <i>Journal of Experimental Medicine</i> , 2019 , 216, 2113-2127	16.6	94
352	Time-resolved analysis and visualization of dynamic processes in living cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 7950-5	11.5	94
351	Enhancer hijacking activates oncogenic transcription factor NR4A3 in acinic cell carcinomas of the salivary glands. <i>Nature Communications</i> , 2019 , 10, 368	17.4	89
350	Four-dimensional imaging and quantitative reconstruction to analyse complex spatiotemporal processes in live cells. <i>Nature Cell Biology</i> , 2001 , 3, 852-5	23.4	89
349	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , 2018 , 34, 996-1011.e8	24.3	89
348	Deterministic and probabilistic approaches for tracking virus particles in time-lapse fluorescence microscopy image sequences. <i>Medical Image Analysis</i> , 2009 , 13, 325-42	15.4	86

347	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , 2019 , 10, 470	17.4	84
346	Nuclear architecture and the induction of chromosomal aberrations. <i>Mutation Research - Reviews in Genetic Toxicology</i> , 1996 , 366, 97-116		84
345	Precision oncology based on omics data: The NCT Heidelberg experience. <i>International Journal of Cancer</i> , 2017 , 141, 877-886	7.5	82
344	An optimized, fully automated system for fast and accurate identification of chromosomal rearrangements by multiplex-FISH (M-FISH). <i>Cytogenetic and Genome Research</i> , 1998 , 82, 160-71	1.9	82
343	Identifying essential genes in bacterial metabolic networks with machine learning methods. <i>BMC Systems Biology</i> , 2010 , 4, 56	3.5	81
342	Analysis of CD95 threshold signaling: triggering of CD95 (FAS/APO-1) at low concentrations primarily results in survival signaling. <i>Journal of Biological Chemistry</i> , 2007 , 282, 13664-71	5.4	81
341	Decision making in NK cells. <i>Cell Communication and Signaling</i> , 2009 , 7,	7.5	78
340	Topology of genes and nontranscribed sequences in human interphase nuclei. <i>Experimental Cell Research</i> , 2004 , 301, 266-79	4.2	77
339	High-resolution genomic profiling reveals association of chromosomal aberrations on 1q and 16p with histologic and genetic subgroups of invasive breast cancer. <i>Clinical Cancer Research</i> , 2006 , 12, 345-52	12.9	76
338	Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. <i>Molecular Systems Biology</i> , 2016 , 12, 861	12.2	71
337	Separate and variably shaped chromosome arm domains are disclosed by chromosome arm painting in human cell nuclei. <i>Chromosome Research</i> , 1998 , 6, 25-33	4.4	70
336	Web-based design and analysis tools for CRISPR base editing. <i>BMC Bioinformatics</i> , 2018 , 19, 542	3.6	70
335	Herpesviral replication compartments move and coalesce at nuclear speckles to enhance export of viral late mRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E136-44	11.5	69
334	Breast cancer: a candidate gene approach across the estrogen metabolic pathway. <i>Breast Cancer Research and Treatment</i> , 2008 , 108, 137-49	4.4	68
333	EnrichedHeatmap: an R/Bioconductor package for comprehensive visualization of genomic signal associations. <i>BMC Genomics</i> , 2018 , 19, 234	4.5	67
332	Microarray analysis reveals differential gene expression patterns and regulation of single target genes contributing to the opposing phenotype of TrkA- and TrkB-expressing neuroblastomas. <i>Oncogene</i> , 2005 , 24, 165-77	9.2	67
331	MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. <i>Nature Communications</i> , 2016 , 7, 11807	17.4	65
330	Hypertension delays viral clearance and exacerbates airway hyperinflammation in patients with COVID-19. <i>Nature Biotechnology</i> , 2021 , 39, 705-716	44.5	65

329	Genetic polymorphisms in phase I and phase II enzymes and breast cancer risk associated with menopausal hormone therapy in postmenopausal women. <i>Breast Cancer Research and Treatment</i> , 2010 , 119, 463-74	4.4	64
328	Argonaute—a database for gene regulation by mammalian microRNAs. <i>Nucleic Acids Research</i> , 2006 , 34, D115-8	20.1	64
327	Genome-wide expression screens indicate a global role for protein kinase CK2 in chromatin remodeling. <i>Journal of Cell Science</i> , 2003 , 116, 1563-77	5.3	63
326	Subtelomeric chromosome rearrangements are detected using an innovative 12-color FISH assay (M-TEL). <i>Nature Medicine</i> , 2001 , 7, 497-501	50.5	63
325	Pre-activated antiviral innate immunity in the upper airways controls early SARS-CoV-2 infection in children. <i>Nature Biotechnology</i> , 2021 ,	44.5	63
324	BRCA1-associated breast and ovarian cancer risks in Poland: no association with commonly studied polymorphisms. <i>Breast Cancer Research and Treatment</i> , 2010 , 119, 201-11	4.4	62
323	A cryptic t(5;11)(q35;p15.5) in 2 children with acute myeloid leukemia with apparently normal karyotypes, identified by a multiplex fluorescence in situ hybridization telomere assay. <i>Blood</i> , 2002 , 99, 2526-31	2.2	62
322	A comprehensive comparison of tools for differential ChIP-seq analysis. <i>Briefings in Bioinformatics</i> , 2016 , 17, 953-966	13.4	62
321	Estimating novel potential drug targets of Plasmodium falciparum by analysing the metabolic network of knock-out strains in silico. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 351-8	4.5	61
320	Comparison of normalization methods for Illumina BeadChip HumanHT-12 v3. <i>BMC Genomics</i> , 2010 , 11, 349	4.5	60
319	Spatial distributions of early and late replicating chromatin in interphase chromosome territories. <i>Experimental Cell Research</i> , 1998 , 243, 398-407	4.2	60
318	Pancreatic Ductal Adenocarcinoma Subtyping Using the Biomarkers Hepatocyte Nuclear Factor-1A and Cytokeratin-81 Correlates with Outcome and Treatment Response. <i>Clinical Cancer Research</i> , 2018 , 24, 351-359	12.9	60
317	A highly standardized, robust, and cost-effective method for genome-wide transcriptome analysis of peripheral blood applicable to large-scale clinical trials. <i>Genomics</i> , 2006 , 87, 653-64	4.3	59
316	Integrative DNA methylation and gene expression analysis in high-grade soft tissue sarcomas. <i>Genome Biology</i> , 2013 , 14, r137	18.3	58
315	Coverage bias and sensitivity of variant calling for four whole-genome sequencing technologies. <i>PLoS ONE</i> , 2013 , 8, e66621	3.7	58
314	Mechismo: predicting the mechanistic impact of mutations and modifications on molecular interactions. <i>Nucleic Acids Research</i> , 2015 , 43, e10	20.1	57
313	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021 , 184, 2239-2254.e39	56.2	57
312	Maternal phthalate exposure promotes allergic airway inflammation over 2 generations through epigenetic modifications. <i>Journal of Allergy and Clinical Immunology</i> , 2018 , 141, 741-753	11.5	56

311	Negative feedback in the bone morphogenetic protein 4 (BMP4) synexpression group governs its dynamic signaling range and canalizes development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 10202-7	11.5	56
310	Comparison of performance of one-color and two-color gene-expression analyses in predicting clinical endpoints of neuroblastoma patients. <i>Pharmacogenomics Journal</i> , 2010 , 10, 258-66	3.5	56
309	4-D single particle tracking of synthetic and proteinaceous microspheres reveals preferential movement of nuclear particles along chromatin - poor tracks. <i>BMC Cell Biology</i> , 2004 , 5, 45		56
308	Polymorphisms in the BRCA1 and ABCB1 genes modulate menopausal hormone therapy associated breast cancer risk in postmenopausal women. <i>Breast Cancer Research and Treatment</i> , 2010 , 120, 727-36	4.4	55
307	Applying Support Vector Machines for Gene Ontology based gene function prediction. <i>BMC Bioinformatics</i> , 2004 , 5, 116	3.6	55
306	BioModels: expanding horizons to include more modelling approaches and formats. <i>Nucleic Acids Research</i> , 2018 , 46, D1248-D1253	20.1	54
305	Local gene density predicts the spatial position of genetic loci in the interphase nucleus. <i>Experimental Cell Research</i> , 2005 , 311, 14-26	4.2	54
304	Predicting protein subcellular locations using hierarchical ensemble of Bayesian classifiers based on Markov chains. <i>BMC Bioinformatics</i> , 2006 , 7, 298	3.6	54
303	Distinct gene expression patterns associated with FLT3- and NRAS-activating mutations in acute myeloid leukemia with normal karyotype. <i>Oncogene</i> , 2005 , 24, 1580-8	9.2	54
302	Revised risk estimation and treatment stratification of low- and intermediate-risk neuroblastoma patients by integrating clinical and molecular prognostic markers. <i>Clinical Cancer Research</i> , 2015 , 21, 1904-15	12.9	53
301	CCM2 mediates death signaling by the TrkA receptor tyrosine kinase. <i>Neuron</i> , 2009 , 63, 585-91	13.9	53
300	SARS-CoV-2-mediated dysregulation of metabolism and autophagy uncovers host-targeting antivirals. <i>Nature Communications</i> , 2021 , 12, 3818	17.4	53
299	Global gene expression profiling and cluster analysis in <i>Xenopus laevis</i> . <i>Mechanisms of Development</i> , 2005 , 122, 441-75	1.7	51
298	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. <i>Nature Communications</i> , 2018 , 9, 4782	17.4	51
297	Hypermutation of the inactive X chromosome is a frequent event in cancer. <i>Cell</i> , 2013 , 155, 567-81	56.2	50
296	Cell-specific CRISPR-Cas9 activation by microRNA-dependent expression of anti-CRISPR proteins. <i>Nucleic Acids Research</i> , 2019 , 47, e75	20.1	49
295	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019 , 10, 1459	17.4	49
294	An integrated genome research network for studying the genetics of alcohol addiction. <i>Addiction Biology</i> , 2010 , 15, 369-79	4.6	49

293	Automatic analysis of dividing cells in live cell movies to detect mitotic delays and correlate phenotypes in time. <i>Genome Research</i> , 2009 , 19, 2113-24	9.7	49
292	SplicingCompass: differential splicing detection using RNA-seq data. <i>Bioinformatics</i> , 2013 , 29, 1141-8	7.2	48
291	Intra- and interdimeric caspase-8 self-cleavage controls strength and timing of CD95-induced apoptosis. <i>Science Signaling</i> , 2014 , 7, ra23	8.8	48
290	Quantitative motion analysis and visualization of cellular structures. <i>Methods</i> , 2003 , 29, 3-13	4.6	47
289	Nuclear NR4A3 Immunostaining Is a Specific and Sensitive Novel Marker for Acinic Cell Carcinoma of the Salivary Glands. <i>American Journal of Surgical Pathology</i> , 2019 , 43, 1264-1272	6.7	47
288	Integration of activating and inhibitory receptor signaling by regulated phosphorylation of Vav1 in immune cells. <i>Science Signaling</i> , 2011 , 4, ra36	8.8	45
287	Prenatal maternal stress and wheeze in children: novel insights into epigenetic regulation. <i>Scientific Reports</i> , 2016 , 6, 28616	4.9	44
286	Recurrent RHOA mutations in pediatric Burkitt lymphoma treated according to the NHL-BFM protocols. <i>Genes Chromosomes and Cancer</i> , 2014 , 53, 911-6	5	44
285	Gene network dynamics controlling keratinocyte migration. <i>Molecular Systems Biology</i> , 2008 , 4, 199	12.2	44
284	Inflammation-mediated skin tumorigenesis induced by epidermal c-Fos. <i>Genes and Development</i> , 2013 , 27, 1959-73	12.6	43
283	Distinct molecular phenotype of malignant CD34(+) hematopoietic stem and progenitor cells in chronic myelogenous leukemia. <i>Oncogene</i> , 2005 , 24, 5313-24	9.2	43
282	Inferring genetic regulatory logic from expression data. <i>Bioinformatics</i> , 2005 , 21, 2706-13	7.2	42
281	The Human Cell Atlas 2017 ,		41
280	Live cell dynamics of promyelocytic leukemia nuclear bodies upon entry into and exit from mitosis. <i>Molecular Biology of the Cell</i> , 2008 , 19, 3147-62	3.5	41
279	Classification accuracy in multiple color fluorescence imaging microscopy. <i>Cytometry</i> , 2000 , 41, 139-147		41
278	Single-Nucleus and In Situ RNA-Sequencing Reveal Cell Topographies in the Human Pancreas. <i>Gastroenterology</i> , 2021 , 160, 1330-1344.e11	13.3	41
277	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , 2020 , 11, 733	17.4	40
276	mediates the impact of prenatal bisphenol A exposure on long-term body weight development. <i>Clinical Epigenetics</i> , 2018 , 10, 58	7.7	40

275	RNAiAther, an automated pipeline for the statistical analysis of high-throughput RNAi screens. <i>Bioinformatics</i> , 2009 , 25, 678-9	7.2	40
274	GOPET: a tool for automated predictions of Gene Ontology terms. <i>BMC Bioinformatics</i> , 2006 , 7, 161	3.6	40
273	Comprehensive Analysis of Chromatin States in Atypical Teratoid/Rhabdoid Tumor Identifies Diverging Roles for SWI/SNF and Polycomb in Gene Regulation. <i>Cancer Cell</i> , 2019 , 35, 95-110.e8	24.3	40
272	A framework for modelling gene regulation which accommodates non-equilibrium mechanisms. <i>BMC Biology</i> , 2014 , 12, 102	7.3	39
271	Multi-parametric analysis and modeling of relationships between mitochondrial morphology and apoptosis. <i>PLoS ONE</i> , 2012 , 7, e28694	3.7	39
270	Understanding apoptosis by systems biology approaches. <i>Molecular BioSystems</i> , 2009 , 5, 1105-11		39
269	Quantitative imaging of pre-mRNA splicing factors in living cells. <i>Molecular Biology of the Cell</i> , 2000 , 11, 413-8	3.5	39
268	Genome sequencing: a systematic review of health economic evidence. <i>Health Economics Review</i> , 2013 , 3, 29	2	38
267	Caspase-8 cleaves its substrates from the plasma membrane upon CD95-induced apoptosis. <i>Cell Death and Differentiation</i> , 2013 , 20, 599-610	12.7	38
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