Roland Eils

List of Publications by Year
in descending order

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429 papers	59,531 citations	2427 97 h-index	1385 222 g-index
475 all docs	475 docs citations	475 times ranked	88227 citing authors

#	Article	IF	Citations
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
2	Complex heatmaps reveal patterns and correlations in multidimensional genomic data. Bioinformatics, 2016, 32, 2847-2849.	4.1	5,891
3	circlizeimplements and enhances circular visualization in R. Bioinformatics, 2014, 30, 2811-2812.	4.1	2,736
4	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
5	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
6	Systemic Spread Is an Early Step in Breast Cancer. Cancer Cell, 2008, 13, 58-68.	16.8	1,076
7	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
8	Olfactory transmucosal SARS-CoV-2 invasion as a port of central nervous system entry in individuals with COVID-19. Nature Neuroscience, 2021, 24, 168-175.	14.8	991
9	COVID-19 severity correlates with airway epitheliumâ€“immune cell interactions identified by single-cell analysis. Nature Biotechnology, 2020, 38, 970-979.	17.5	887
10	<scp>SARS</scp> â€CoVâ€2 receptor <scp>ACE</scp> 2 and <scp>TMPRSS</scp> 2 are primarily expressed in bronchial transient secretory cells. EMBO Journal, 2020, 39, e105114.	7.8	812
11	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
12	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
13	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. Nature, 2010, 464, 721-727.	27.8	768
14	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	27.8	765
15	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. Cell, 2012, 148, 59-71.	28.9	743
16	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. Cell, 2016, 164, 1060-1072.	28.9	702
17	Three-Dimensional Maps of All Chromosomes in Human Male Fibroblast Nuclei and Prometaphase Rosettes. PLoS Biology, 2005, 3, e157.	5.6	683
18	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	21.4	674

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19	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. Cancer Cell, 2014, 25, 393-405.	16.8	627
20	Omic data from evolved E. coli are consistent with computed optimal growth from genomeâ€scale models. Molecular Systems Biology, 2010, 6, 390.	7.2	615
21	From latent disseminated cells to overt metastasis: Genetic analysis of systemic breast cancer progression. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7737-7742.	7.1	588
22	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. Nature, 2014, 506, 445-450.	27.8	521
23	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
24	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methylome Analysis. Cell Stem Cell, 2014, 15, 507-522.	11.1	439
25	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. Cancer Cell, 2016, 29, 379-393.	16.8	438
26	Recruitment and Activation of a Lipid Kinase by Hepatitis C Virus NS5A Is Essential for Integrity of the Membranous Replication Compartment. Cell Host and Microbe, 2011, 9, 32-45.	11.0	435
27	Nuclear Envelope Breakdown Proceeds by Microtubule-Induced Tearing of the Lamina. Cell, 2002, 108, 83-96.	28.9	422
28	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
29	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. Nature Genetics, 2012, 44, 1316-1320.	21.4	389
30	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. Nature, 2014, 510, 537-541.	27.8	378
31	Modulation of Serines 17 and 24 in the LC3-interacting Region of Bnip3 Determines Pro-survival Mitophagy versus Apoptosis. Journal of Biological Chemistry, 2013, 288, 1099-1113.	3.4	374
32	SARS-CoV-2 receptor ACE2 and TMPRSS2 are primarily expressed in bronchial transient secretory cells. EMBO Journal, 0, , e105114.	7.8	340
33	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. Nature, 2016, 530, 57-62.	27.8	318
34	Transient colocalization of X-inactivation centres accompanies the initiation of X inactivation. Nature Cell Biology, 2006, 8, 293-299.	10.3	304
35	Mathematical modeling reveals threshold mechanism in CD95-induced apoptosis. Journal of Cell Biology, 2004, 166, 839-851.	5.2	301
36	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. Cancer Cell, 2013, 23, 159-170.	16.8	292

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37	SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis. Cell, 2021, 184, 6243-6261.e27.	28.9	277
38	Global Chromosome Positions Are Transmitted through Mitosis in Mammalian Cells. Cell, 2003, 112, 751-764.	28.9	268
39	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. Lancet Oncology, The, 2018, 19, 785-798.	10.7	268
40	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
41	The landscape of viral associations in human cancers. Nature Genetics, 2020, 52, 320-330.	21.4	261
42	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	28.9	260
43	Mutations in the SIX1/2 Pathway and the DROSHA/DGCR8 miRNA Microprocessor Complex Underlie High-Risk Blastemal Type Wilms Tumors. Cancer Cell, 2015, 27, 298-311.	16.8	248
44	Acute myeloid leukemias with reciprocal rearrangements can be distinguished by specific gene expression profiles. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10008-10013.	7.1	246
45	Large-scale in silico modeling of metabolic interactions between cell types in the human brain. Nature Biotechnology, 2010, 28, 1279-1285.	17.5	246
46	Customized Oligonucleotide Microarray Gene Expressionâ€“Based Classification of Neuroblastoma Patients Outperforms Current Clinical Risk Stratification. Journal of Clinical Oncology, 2006, 24, 5070-5078.	1.6	243
47	Genomic analysis of single cytokeratin-positive cells from bone marrow reveals early mutational events in breast cancer. Cancer Cell, 2005, 8, 227-239.	16.8	239
48	Pre-activated antiviral innate immunity in the upper airways controls early SARS-CoV-2 infection in children. Nature Biotechnology, 2022, 40, 319-324.	17.5	229
49	A contractile nuclear actin network drives chromosome congression in oocytes. Nature, 2005, 436, 812-818.	27.8	220
50	Three-dimensional reconstruction of painted human interphase chromosomes: active and inactive X chromosome territories have similar volumes but differ in shape and surface structure.. Journal of Cell Biology, 1996, 135, 1427-1440.	5.2	215
51	NK cells switch from granzyme B to death receptorâ€“mediated cytotoxicity during serial killing. Journal of Experimental Medicine, 2019, 216, 2113-2127.	8.5	210
52	Secretory meningiomas are defined by combined KLF4 K409Q and TRAF7 mutations. Acta Neuropathologica, 2013, 125, 351-358.	7.7	208
53	Engineering light-inducible nuclear localization signals for precise spatiotemporal control of protein dynamics in living cells. Nature Communications, 2014, 5, 4404.	12.8	203
54	Artesunate Activates Mitochondrial Apoptosis in Breast Cancer Cells via Iron-catalyzed Lysosomal Reactive Oxygen Species Production. Journal of Biological Chemistry, 2011, 286, 6587-6601.	3.4	201

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55	Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144.	12.8	197
56	Virus-induced senescence is a driver and therapeutic target in COVID-19. Nature, 2021, 599, 283-289.	27.8	195
57	Compartmentalization of Interphase Chromosomes Observed in Simulation and Experiment. Journal of Molecular Biology, 1999, 285, 1053-1065.	4.2	190
58	Automatic Identification of Subcellular Phenotypes on Human Cell Arrays. Genome Research, 2004, 14, 1130-1136.	5.5	190
59	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	16.8	190
60	CYP3A5 mediates basal and acquired therapy resistance in different subtypes of pancreatic ductal adenocarcinoma. Nature Medicine, 2016, 22, 278-287.	30.7	184
61	Cross-platform analysis of cancer microarray data improves gene expression based classification of phenotypes. BMC Bioinformatics, 2005, 6, 265.	2.6	183
62	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. Nature Medicine, 2016, 22, 1314-1320.	30.7	183
63	Optogenetic control of nuclear protein export. Nature Communications, 2016, 7, 10624.	12.8	183
64	Dynamics of HIV-1 Assembly and Release. PLoS Pathogens, 2009, 5, e1000652.	4.7	178
65	Visualizing telomere dynamics in living mammalian cells using PNA probes. EMBO Journal, 2003, 22, 6631-6641.	7.8	176
66	Etiology-dependent molecular mechanisms in human hepatocarcinogenesis. Hepatology, 2008, 47, 511-520.	7.3	173
67	SARS-CoV-2-mediated dysregulation of metabolism and autophagy uncovers host-targeting antivirals. Nature Communications, 2021, 12, 3818.	12.8	172
68	Screening drug effects in patientâ€derived cancer cells links organoid responses to genome alterations. Molecular Systems Biology, 2017, 13, 955.	7.2	163
69	Tagmentation-based whole-genome bisulfite sequencing. Nature Protocols, 2013, 8, 2022-2032.	12.0	161
70	Engineered anti-CRISPR proteins for optogenetic control of CRISPRâ€“Cas9. Nature Methods, 2018, 15, 924-927.	19.0	161
71	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. Nature Communications, 2019, 10, 470.	12.8	156
72	Metabolic-energy-dependent movement of PML bodies within the mammalian cell nucleus. Nature Cell Biology, 2002, 4, 106-110.	10.3	153

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73	Enhancer hijacking activates oncogenic transcription factor NR4A3 in acinic cell carcinomas of the salivary glands. Nature Communications, 2019, 10, 368.	12.8	153
74	EnrichedHeatmap: an R/Bioconductor package for comprehensive visualization of genomic signal associations. BMC Genomics, 2018, 19, 234.	2.8	152
75	One, two or three? Probing the stoichiometry of membrane proteins by single-molecule localization microscopy. Scientific Reports, 2015, 5, 14072.	3.3	148
76	Gene Expression Signature Predicting Pathologic Complete Response With Gemcitabine, Epirubicin, and Docetaxel in Primary Breast Cancer. Journal of Clinical Oncology, 2006, 24, 1839-1845.	1.6	146
77	Genome-wide transcriptional analysis of the human cell cycle identifies genes differentially regulated in normal and cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 955-960.	7.1	145
78	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. Nature Genetics, 2015, 47, 22-30.	21.4	141
79	The mutational pattern of primary lymphoma of the central nervous system determined by whole-exome sequencing. Leukemia, 2015, 29, 677-685.	7.2	139
80	Model-based dissection of CD95 signaling dynamics reveals both a pro- and antiapoptotic role of c-FLIPL. Journal of Cell Biology, 2010, 190, 377-389.	5.2	135
81	Precision oncology based on omics data: The NCT Heidelberg experience. International Journal of Cancer, 2017, 141, 877-886.	5.1	133
82	Dynamics within the CD95 deathâ€inducing signaling complex decide life and death of cells. Molecular Systems Biology, 2010, 6, 352.	7.2	130
83	Computational imaging in cell biology. Journal of Cell Biology, 2003, 161, 477-481.	5.2	129
84	Synergy between medical informatics and bioinformatics: facilitating genomic medicine for future health care. Journal of Biomedical Informatics, 2004, 37, 30-42.	4.3	129
85	Group testing for pathway analysis improves comparability of different microarray datasets. Bioinformatics, 2006, 22, 2500-2506.	4.1	129
86	Prognostic Impact of Gene Expressionâ€“Based Classification for Neuroblastoma. Journal of Clinical Oncology, 2010, 28, 3506-3515.	1.6	129
87	Hypertension delays viral clearance and exacerbates airway hyperinflammation in patients with COVID-19. Nature Biotechnology, 2021, 39, 705-716.	17.5	129
88	Web-based design and analysis tools for CRISPR base editing. BMC Bioinformatics, 2018, 19, 542.	2.6	127
89	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. American Journal of Gastroenterology, 2010, 105, 2060-2071.	0.4	126
90	Complement activation induces excessive T cell cytotoxicity in severe COVID-19. Cell, 2022, 185, 493-512.e25.	28.9	122

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91	Highâ€precision distance measurements and volumeâ€conserving segmentation of objects near and below the resolution limit in threeâ€dimensional confocal fluorescence microscopy. Journal of Microscopy, 1998, 189, 118-136.	1.8	121
92	Concurrent detection of autolysosome formation and lysosomal degradation by flow cytometry in a high-content screen for inducers of autophagy. BMC Biology, 2011, 9, 38.	3.8	119
93	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. Nature Genetics, 2015, 47, 1316-1325.	21.4	119
94	Nuclear architecture and the induction of chromosomal aberrations. Mutation Research - Reviews in Genetic Toxicology, 1996, 366, 97-116.	2.9	115
95	Optimal Experimental Design for Parameter Estimation of a Cell Signaling Model. PLoS Computational Biology, 2009, 5, e1000558.	3.2	114
96	The 3D Positioning of ANT2 and ANT3 Genes within Female X Chromosome Territories Correlates with Gene Activity. Experimental Cell Research, 1999, 252, 363-375.	2.6	113
97	Prediction of clinical outcome and biological characterization of neuroblastoma by expression profiling. Oncogene, 2005, 24, 7902-7912.	5.9	113
98	Single-Nucleus and In Situ RNAâ€“Sequencing Reveal Cell Topographies in the Human Pancreas. Gastroenterology, 2021, 160, 1330-1344.e11.	1.3	112
99	Microarray-based copy number and expression profiling in dedifferentiated and pleomorphic liposarcoma. Cancer Research, 2002, 62, 2993-8.	0.9	111
100	Identifying essential genes in bacterial metabolic networks with machine learning methods. BMC Systems Biology, 2010, 4, 56.	3.0	108
101	An optimized, fully automated system for fast and accurate identification of chromosomal rearrangements by multiplex-FISH (M-FISH). Cytogenetic and Genome Research, 1998, 82, 160-171.	1.1	104
102	MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. Nature Communications, 2016, 7, 11807.	12.8	103
103	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. Nature Communications, 2018, 9, 4782.	12.8	103
104	Time-resolved analysis and visualization of dynamic processes in living cells. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 7950-7955.	7.1	101
105	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	12.8	99
106	Four-dimensional imaging and quantitative reconstruction to analyse complex spatiotemporal processes in live cells. Nature Cell Biology, 2001, 3, 852-855.	10.3	98
107	Deterministic and probabilistic approaches for tracking virus particles in time-lapse fluorescence microscopy image sequences. Medical Image Analysis, 2009, 13, 325-342.	11.6	98
108	Analysis of CD95 Threshold Signaling. Journal of Biological Chemistry, 2007, 282, 13664-13671.	3.4	97

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109	Environmentâ€induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. Molecular Systems Biology, 2016, 12, 861.	7.2	97
110	Mechismo: predicting the mechanistic impact of mutations and modifications on molecular interactions. Nucleic Acids Research, 2015, 43, e10-e10.	14.5	95
111	Memory-like HCV-specific CD8+ T cells retain a molecular scar after cure of chronic HCV infection. Nature Immunology, 2021, 22, 229-239.	14.5	95
112	Nuclear NR4A3 Immunostaining Is a Specific and Sensitive Novel Marker for Acinic Cell Carcinoma of the Salivary Glands. American Journal of Surgical Pathology, 2019, 43, 1264-1272.	3.7	94
113	Maternal phthalate exposure promotes allergic airway inflammation over 2 generations through epigenetic modifications. Journal of Allergy and Clinical Immunology, 2018, 141, 741-753.	2.9	92
114	Herpesviral replication compartments move and coalesce at nuclear speckles to enhance export of viral late mRNA. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E136-44.	7.1	89
115	A comprehensive comparison of tools for differential ChIP-seq analysis. Briefings in Bioinformatics, 2016, 17, bbv110.	6.5	89
116	Topology of genes and nontranscribed sequences in human interphase nuclei. Experimental Cell Research, 2004, 301, 266-279.	2.6	88
117	Separate and variably shaped chromosome arm domains are disclosed by chromosome arm painting in human cell nuclei. Chromosome Research, 1998, 6, 25-33.	2.2	87
118	Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications, 2020, 11, 733.	12.8	87
119	High-Resolution Genomic Profiling Reveals Association of Chromosomal Aberrations on 1q and 16p with Histologic and Genetic Subgroups of Invasive Breast Cancer. Clinical Cancer Research, 2006, 12, 345-352.	7.0	85
120	Pancreatic Ductal Adenocarcinoma Subtyping Using the Biomarkers Hepatocyte Nuclear Factor-1A and Cytokeratin-81 Correlates with Outcome and Treatment Response. Clinical Cancer Research, 2018, 24, 351-359.	7.0	81
121	Estimating novel potential drug targets of Plasmodium falciparum by analysing the metabolic network of knock-out strains in silico. Infection, Genetics and Evolution, 2009, 9, 351-358.	2.3	80
122	Revised Risk Estimation and Treatment Stratification of Low- and Intermediate-Risk Neuroblastoma Patients by Integrating Clinical and Molecular Prognostic Markers. Clinical Cancer Research, 2015, 21, 1904-1915.	7.0	80
123	BioModels: expanding horizons to include more modelling approaches and formats. Nucleic Acids Research, 2018, 46, D1248-D1253.	14.5	80
124	Cell-specific CRISPRâ€“Cas9 activation by microRNA-dependent expression of anti-CRISPR proteins. Nucleic Acids Research, 2019, 47, e75-e75.	14.5	79
125	Integrative DNA methylation and gene expression analysis in high-grade soft tissue sarcomas. Genome Biology, 2013, 14, r137.	9.6	78
126	Microarray analysis reveals differential gene expression patterns and regulation of single target genes contributing to the opposing phenotype of TrkA- and TrkB-expressing neuroblastomas. Oncogene, 2005, 24, 165-177.	5.9	76

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127	Breast cancer: a candidate gene approach across the estrogen metabolic pathway. Breast Cancer Research and Treatment, 2008, 108, 137-149.	2.5	74
128	Coverage Bias and Sensitivity of Variant Calling for Four Whole-genome Sequencing Technologies. PLoS ONE, 2013, 8, e66621.	2.5	74
129	Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. Acta Neuropathologica, 2019, 138, 295-308.	7.7	74
130	Subtelomeric chromosome rearrangements are detected using an innovative 12-color FISH assay (M-TEL). Nature Medicine, 2001, 7, 497-501.	30.7	72
131	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. Blood, 2002, 99, 2526-2531.	1.4	72
132	Predicting protein subcellular locations using hierarchical ensemble of Bayesian classifiers based on Markov chains. BMC Bioinformatics, 2006, 7, 298.	2.6	72
133	Argonaute--a database for gene regulation by mammalian microRNAs. Nucleic Acids Research, 2006, 34, D115-D118.	14.5	72
134	MEST mediates the impact of prenatal bisphenol A exposure on long-term body weight development. Clinical Epigenetics, 2018, 10, 58.	4.1	72
135	Classification accuracy in multiple color fluorescence imaging microscopy. Cytometry, 2000, 41, 139-147.	1.8	71
136	BRCA1-associated breast and ovarian cancer risks in Poland: no association with commonly studied polymorphisms. Breast Cancer Research and Treatment, 2010, 119, 201-211.	2.5	70
137	Spatial Distributions of Early and Late Replicating Chromatin in Interphase Chromosome Territories. Experimental Cell Research, 1998, 243, 398-407.	2.6	69
138	Genome-wide expression screens indicate a global role for protein kinase CK2 in chromatin remodeling. Journal of Cell Science, 2003, 116, 1563-1577.	2.0	69
139	Genetic polymorphisms in phase I and phase II enzymes and breast cancer risk associated with menopausal hormone therapy in postmenopausal women. Breast Cancer Research and Treatment, 2010, 119, 463-474.	2.5	69
140	A highly standardized, robust, and cost-effective method for genome-wide transcriptome analysis of peripheral blood applicable to large-scale clinical trials. Genomics, 2006, 87, 653-664.	2.9	68
141	Comparison of normalization methods for Illumina BeadChip HumanHT-12 v3. BMC Genomics, 2010, 11, 349.	2.8	68
142	4-D single particle tracking of synthetic and proteinaceous microspheres reveals preferential movement of nuclear particles along chromatin - poor tracks. BMC Cell Biology, 2004, 5, 45.	3.0	67
143	Negative feedback in the bone morphogenetic protein 4 (BMP4) synexpression group governs its dynamic signaling range and canalizes development. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10202-10207.	7.1	67
144	Hypermutation of the Inactive X Chromosome Is a Frequent Event in Cancer. Cell, 2013, 155, 567-581.	28.9	67

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145	Estimating the activity of transcription factors by the effect on their target genes. Bioinformatics, 2014, 30, i401-i407.	4.1	66
146	Distinct gene expression patterns associated with FLT3- and NRAS-activating mutations in acute myeloid leukemia with normal karyotype. Oncogene, 2005, 24, 1580-1588.	5.9	65
147	Comprehensive Analysis of Chromatin States in Atypical Teratoid/Rhabdoid Tumor Identifies Diverging Roles for SWI/SNF and Polycomb in Gene Regulation. Cancer Cell, 2019, 35, 95-110.e8.	16.8	65
148	HiGHmed â€“ An Open Platform Approach to Enhance Care and Research across Institutional Boundaries. Methods of Information in Medicine, 2018, 57, e66-e81.	1.2	64
149	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. Nature Communications, 2019, 10, 1635.	12.8	64
150	Intra- and Interdimeric Caspase-8 Self-Cleavage Controls Strength and Timing of CD95-Induced Apoptosis. Science Signaling, 2014, 7, ra23.	3.6	63
151	Comparison of performance of one-color and two-color gene-expression analyses in predicting clinical endpoints of neuroblastoma patients. Pharmacogenomics Journal, 2010, 10, 258-266.	2.0	62
152	SplicingCompass: differential splicing detection using RNA-Seq data. Bioinformatics, 2013, 29, 1141-1148.	4.1	61
153	Applying Support Vector Machines for Gene Ontology based gene function prediction. BMC Bioinformatics, 2004, 5, 116.	2.6	60
154	Global gene expression profiling and cluster analysis in Xenopus laevis. Mechanisms of Development, 2005, 122, 441-475.	1.7	59
155	Single-cell analysis of patient-derived PDAC organoids reveals cell state heterogeneity and a conserved developmental hierarchy. Nature Communications, 2021, 12, 5826.	12.8	59
156	Automatic analysis of dividing cells in live cell movies to detect mitotic delays and correlate phenotypes in time. Genome Research, 2009, 19, 2113-2124.	5.5	58
157	CCM2 Mediates Death Signaling by the TrkA Receptor Tyrosine Kinase. Neuron, 2009, 63, 585-591.	8.1	58
158	Polymorphisms in the BRCA1 and ABCB1 genes modulate menopausal hormone therapy associated breast cancer risk in postmenopausal women. Breast Cancer Research and Treatment, 2010, 120, 727-736.	2.5	58
159	An integrated genome research network for studying the genetics of alcohol addiction. Addiction Biology, 2010, 15, 369-379.	2.6	57
160	Integration of Activating and Inhibitory Receptor Signaling by Regulated Phosphorylation of Vav1 in Immune Cells. Science Signaling, 2011, 4, ra36.	3.6	56
161	Local gene density predicts the spatial position of genetic loci in the interphase nucleus. Experimental Cell Research, 2005, 311, 14-26.	2.6	55
162	Prenatal maternal stress and wheeze in children: novel insights into epigenetic regulation. Scientific Reports, 2016, 6, 28616.	3.3	55

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163	The role of Vimentin in Regulating Cell Invasive Migration in Dense Cultures of Breast Carcinoma Cells. Nano Letters, 2017, 17, 6941-6948.	9.1	55
164	Inferring genetic regulatory logic from expression data. Bioinformatics, 2005, 21, 2706-2713.	4.1	53
165	Inflammation-mediated skin tumorigenesis induced by epidermal c-Fos. Genes and Development, 2013, 27, 1959-1973.	5.9	53
166	A framework for modelling gene regulation which accommodates non-equilibrium mechanisms. BMC Biology, 2014, 12, 102.	3.8	53
167	Gene network dynamics controlling keratinocyte migration. Molecular Systems Biology, 2008, 4, 199.	7.2	52
168	Caspase-8 cleaves its substrates from the plasma membrane upon CD95-induced apoptosis. Cell Death and Differentiation, 2013, 20, 599-610.	11.2	52
169	Cell segmentation-free inference of cell types from in situ transcriptomics data. Nature Communications, 2021, 12, 3545.	12.8	52
170	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	12.8	52
171	Quantitative motion analysis and visualization of cellular structures. Methods, 2003, 29, 3-13.	3.8	51
172	Recurrent RHOA mutations in pediatric <scp>B</scp>urkitt lymphoma treated according to the NHLâ€BFM protocols. Genes Chromosomes and Cancer, 2014, 53, 911-916.	2.8	51
173	Live Cell Dynamics of Promyelocytic Leukemia Nuclear Bodies upon Entry into and Exit from Mitosis. Molecular Biology of the Cell, 2008, 19, 3147-3162.	2.1	50
174	Genome sequencing: a systematic review of health economic evidence. Health Economics Review, 2013, 3, 29.	2.0	50
175	OTP: An automatized system for managing and processing NGS data. Journal of Biotechnology, 2017, 261, 53-62.	3.8	50
176	Impact of clinical exomes in neurodevelopmental and neurometabolic disorders. Molecular Genetics and Metabolism, 2017, 121, 297-307.	1.1	50
177	RNAither, an automated pipeline for the statistical analysis of high-throughput RNAi screens. Bioinformatics, 2009, 25, 678-679.	4.1	48
178	Glioblastoma epigenome profiling identifies SOX10 as a master regulator of molecular tumour subtype. Nature Communications, 2020, 11, 6434.	12.8	48
179	Aspects of three-dimensional chromosome reorganization during the onset of human male meiotic prophase. Journal of Cell Science, 1998, 111, 2337-2351.	2.0	47
180	Distinct molecular phenotype of malignant CD34+ hematopoietic stem and progenitor cells in chronic myelogenous leukemia. Oncogene, 2005, 24, 5313-5324.	5.9	46

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181	Understanding apoptosis by systems biology approaches. Molecular BioSystems, 2009, 5, 1105.	2.9	45
182	Suppression of Early Hematogenous Dissemination of Human Breast Cancer Cells to Bone Marrow by Retinoic Acidâ€“Induced 2. Cancer Discovery, 2015, 5, 506-519.	9.4	45
183	Coupling Cas9 to artificial inhibitory domains enhances CRISPR-Cas9 target specificity. Science Advances, 2020, 6, eaay0187.	10.3	45
184	Quantitative Imaging of Pre-mRNA Splicing Factors in Living Cells. Molecular Biology of the Cell, 2000, 11, 413-418.	2.1	44
185	GOPET: a tool for automated predictions of Gene Ontology terms. BMC Bioinformatics, 2006, 7, 161.	2.6	44
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