

# Roland Eils

## 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.

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	Neural network-based integration of polygenic and clinical information: development and validation of a prediction model for 10-year risk of major adverse cardiac events in the UK Biobank cohort.. <i>The Lancet Digital Health</i> , <b>2022</b> , 4, e84-e94	14.4	2
435	Age-Related Differences in Structure and Function of Nasal Epithelial Cultures From Healthy Children and Elderly People.. <i>Frontiers in Immunology</i> , <b>2022</b> , 13, 822437	8.4	0
434	SSAM-lite: A Light-Weight Web App for Rapid Analysis of Spatially Resolved Transcriptomics Data.. <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 785877	4.5	0
433	Temporal control of the integrated stress response by a stochastic molecular switch.. <i>Science Advances</i> , <b>2022</b> , 8, eabk2022	14.3	0
432	A targetable Plaque Macrophage subset, [CD11b+DEspR+] immunotype, is associated with severity and mortality in acute respiratory distress syndrome (ARDS) and COVID-19-ARDS.. <i>Scientific Reports</i> , <b>2022</b> , 12, 5583	4.9	0
431	The genomic and transcriptional landscape of primary central nervous system lymphoma.. <i>Nature Communications</i> , <b>2022</b> , 13, 2558	17.4	4
430	Complement activation induces excessive T cell cytotoxicity in severe COVID-19.. <i>Cell</i> , <b>2021</b> ,	56.2	9
429	SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis.. <i>Cell</i> , <b>2021</b> , 184, 6243-6261.e27	56.2	9
428	Single-cell analysis of patient-derived PDAC organoids reveals cell state heterogeneity and a conserved developmental hierarchy. <i>Nature Communications</i> , <b>2021</b> , 12, 5826	17.4	8
427	Single-Nucleus and In Situ RNA-Sequencing Reveal Cell Topographies in the Human Pancreas. <i>Gastroenterology</i> , <b>2021</b> , 160, 1330-1344.e11	13.3	41
426	Functional States in Tumor-Initiating Cell Differentiation in Human Colorectal Cancer. <i>Cancers</i> , <b>2021</b> , 13,	6.6	2
425	Hyperinflammation as underlying mechanism predisposing patients with cardiovascular diseases for severe COVID-19. <i>European Heart Journal</i> , <b>2021</b> , 42, 1720-1721	9.5	3
424	Gene Expression in Solitary Fibrous Tumors (SFTs) Correlates with Anatomic Localization and NAB2-STAT6 Gene Fusion Variants. <i>American Journal of Pathology</i> , <b>2021</b> , 191, 602-617	5.8	9
423	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , <b>2021</b> , 184, 2239-2254.e39	56.2	57
422	Integrative Ranking of Enhancer Networks Facilitates the Discovery of Epigenetic Markers in Cancer. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 664654	4.5	
421	A method for the rational selection of drug repurposing candidates from multimodal knowledge harmonization. <i>Scientific Reports</i> , <b>2021</b> , 11, 11049	4.9	3
420	Knowledge bases and software support for variant interpretation in precision oncology. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	4

419	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , <b>2021</b> , 35, 2002-2016	10.7	3
418	Cell segmentation-free inference of cell types from in situ transcriptomics data. <i>Nature Communications</i> , <b>2021</b> , 12, 3545	17.4	14
417	SARS-CoV-2-mediated dysregulation of metabolism and autophagy uncovers host-targeting antivirals. <i>Nature Communications</i> , <b>2021</b> , 12, 3818	17.4	53
416	Analysis of mutational signatures with yet another package for signature analysis. <i>Genes Chromosomes and Cancer</i> , <b>2021</b> , 60, 314-331	5	12
415	Olfactory transmucosal SARS-CoV-2 invasion as a port of central nervous system entry in individuals with COVID-19. <i>Nature Neuroscience</i> , <b>2021</b> , 24, 168-175	25.5	459
414	Optogenetic control of <i>Neisseria meningitidis</i> Cas9 genome editing using an engineered, light-switchable anti-CRISPR protein. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e29	20.1	8
413	Hypertension delays viral clearance and exacerbates airway hyperinflammation in patients with COVID-19. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 705-716	44.5	65
412	Putative second hit rare genetic variants in families with seemingly GBA-associated ParkinsonB disease. <i>Npj Genomic Medicine</i> , <b>2021</b> , 6, 2	6.2	1
411	Memory-like HCV-specific CD8 T cells retain a molecular scar after cure of chronic HCV infection. <i>Nature Immunology</i> , <b>2021</b> , 22, 229-239	19.1	27
410	Differentially methylated regions within lung cancer risk loci are enriched in deregulated enhancers. <i>Epigenetics</i> , <b>2021</b> , 1-16	5.7	1
409	Lipomatous Solitary Fibrous Tumors Harbor Rare NAB2-STAT6 Fusion Variants and Show Up-Regulation of the Gene PPARG, Encoding for a Regulator of Adipocyte Differentiation. <i>American Journal of Pathology</i> , <b>2021</b> , 191, 1314-1324	5.8	3
408	The DNA methylation landscape of multiple myeloma shows extensive inter- and inpatient heterogeneity that fuels transcriptomic variability. <i>Genome Medicine</i> , <b>2021</b> , 13, 127	14.4	1
407	Pre-activated antiviral innate immunity in the upper airways controls early SARS-CoV-2 infection in children. <i>Nature Biotechnology</i> , <b>2021</b> ,	44.5	63
406	Virus-induced senescence is a driver and therapeutic target in COVID-19. <i>Nature</i> , <b>2021</b> , 599, 283-289	50.4	38
405	An Engineering Approach Towards Multi-site Virtual Molecular Tumor Board Software. <i>Communications in Computer and Information Science</i> , <b>2021</b> , 156-170	0.3	
404	Gene set inference from single-cell sequencing data using a hybrid of matrix factorization and variational autoencoders. <i>Nature Machine Intelligence</i> , <b>2020</b> , 2, 800-809	22.5	1
403	Automated 3D light-sheet screening with high spatiotemporal resolution reveals mitotic phenotypes. <i>Journal of Cell Science</i> , <b>2020</b> , 133,	5.3	14
402	Integrative Analysis of Multi-omics Data Identified EGFR and PTGS2 as Key Nodes in a Gene Regulatory Network Related to Immune Phenotypes in Head and Neck Cancer. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 3616-3628	12.9	21

401	COVID-19 severity correlates with airway epithelium-immune cell interactions identified by single-cell analysis. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 970-979	44.5	487
400	NOTCH target gene HES5 mediates oncogenic and tumor suppressive functions in hepatocarcinogenesis. <i>Oncogene</i> , <b>2020</b> , 39, 3128-3144	9.2	13
399	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , <b>2020</b> , 11, 733	17.4	40
398	The landscape of viral associations in human cancers. <i>Nature Genetics</i> , <b>2020</b> , 52, 320-330	36.3	113
397	Coupling Cas9 to artificial inhibitory domains enhances CRISPR-Cas9 target specificity. <i>Science Advances</i> , <b>2020</b> , 6, eaay0187	14.3	21
396	Computational design of anti-CRISPR proteins with improved inhibition potency. <i>Nature Chemical Biology</i> , <b>2020</b> , 16, 725-730	11.7	7
395	Whole-genome fingerprint of the DNA methylome during chemically induced differentiation of the human AML cell line HL-60/S4. <i>Biology Open</i> , <b>2020</b> , 9,	2.2	1
394	Follicular T helper cells shape the HCV-specific CD4+ T cell repertoire after virus elimination. <i>Journal of Clinical Investigation</i> , <b>2020</b> , 130, 998-1009	15.9	26
393	ShinyButchR: Interactive NMF-based decomposition workflow of genome-scale datasets. <i>Biology Methods and Protocols</i> , <b>2020</b> , 5, bpaa022	2.4	2
392	Membership Inference Against DNA Methylation Databases <b>2020</b> ,		1
391	Transcriptome profiling reveals Silibinin dose-dependent response network in non-small lung cancer cells. <i>PeerJ</i> , <b>2020</b> , 8, e10373	3.1	3
390	Genetic Interactions and Tissue Specificity Modulate the Association of Mutations with Drug Response. <i>Molecular Cancer Therapeutics</i> , <b>2020</b> , 19, 927-936	6.1	0
389	Framework for quality assessment of whole genome cancer sequences. <i>Nature Communications</i> , <b>2020</b> , 11, 5040	17.4	1
388	Nuclear NR4A2 (Nurr1) Immunostaining is a Novel Marker for Acinic Cell Carcinoma of the Salivary Glands Lacking the Classic NR4A3 (NOR-1) Upregulation. <i>American Journal of Surgical Pathology</i> , <b>2020</b> , 44, 1290-1292	6.7	7
387	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , <b>2020</b> , 11, 4748	17.4	10
386	Glioblastoma epigenome profiling identifies SOX10 as a master regulator of molecular tumour subtype. <i>Nature Communications</i> , <b>2020</b> , 11, 6434	17.4	7
385	SARS-CoV-2 receptor ACE2 and TMPRSS2 are primarily expressed in bronchial transient secretory cells. <i>EMBO Journal</i> , <b>2020</b> , 39, e105114	13	538
384	Pheno-seq - linking visual features and gene expression in 3D cell culture systems. <i>Scientific Reports</i> , <b>2019</b> , 9, 12367	4.9	10

383	Segregation and potential functional impact of a rare stop-gain PABPC4L variant in familial atypical Parkinsonism. <i>Scientific Reports</i> , <b>2019</b> , 9, 13576	4.9	1
382	Enhancer hijacking activates oncogenic transcription factor NR4A3 in acinic cell carcinomas of the salivary glands. <i>Nature Communications</i> , <b>2019</b> , 10, 368	17.4	89
381	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , <b>2019</b> , 10, 470	17.4	84
380	TGFβ-induced cytoskeletal remodeling mediates elevation of cell stiffness and invasiveness in NSCLC. <i>Scientific Reports</i> , <b>2019</b> , 9, 7667	4.9	17
379	Impact of cancer mutational signatures on transcription factor motifs in the human genome. <i>BMC Medical Genomics</i> , <b>2019</b> , 12, 64	3.7	9
378	Somatic mutations and promotor methylation of the ryanodine receptor 2 is a common event in the pathogenesis of head and neck cancer. <i>International Journal of Cancer</i> , <b>2019</b> , 145, 3299-3310	7.5	19
377	Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. <i>Acta Neuropathologica</i> , <b>2019</b> , 138, 295-308	14.3	27
376	Leveraging implicit knowledge in neural networks for functional dissection and engineering of proteins. <i>Nature Machine Intelligence</i> , <b>2019</b> , 1, 225-235	22.5	10
375	Longitudinal trends of serum IgE and IL5RA expression throughout childhood are associated with asthma but not with persistent wheeze. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , <b>2019</b> , 74, 2002-2006	9.3	2
374	Cell-specific CRISPR-Cas9 activation by microRNA-dependent expression of anti-CRISPR proteins. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, e75	20.1	49
373	Response to olaparib in a germline mutated prostate cancer and genetic events associated with resistance. <i>Journal of Physical Education and Sports Management</i> , <b>2019</b> , 5,	2.8	21
372	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. <i>Nature Communications</i> , <b>2019</b> , 10, 1635	17.4	33
371	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , <b>2019</b> , 10, 1459	17.4	49
370	NK cells switch from granzyme B to death receptor-mediated cytotoxicity during serial killing. <i>Journal of Experimental Medicine</i> , <b>2019</b> , 216, 2113-2127	16.6	94
369	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> , <b>2019</b> , 43, 1264-1272	6.7	47
368	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> , <b>2019</b> , 35, 95-110.e8	24.3	40
367	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , <b>2018</b> , 555, 321-327	50.4	603
366	BioModels: expanding horizons to include more modelling approaches and formats. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D1248-D1253	20.1	54

365	Cutis laxa, exocrine pancreatic insufficiency and altered cellular metabolomics as additional symptoms in a new patient with ATP6AP1-CDG. <i>Molecular Genetics and Metabolism</i> , <b>2018</b> , 123, 364-374	3.7	15
364	Integrative genomic and transcriptomic analysis of leiomyosarcoma. <i>Nature Communications</i> , <b>2018</b> , 9, 144	17.4	115
363	mediates the impact of prenatal bisphenol A exposure on long-term body weight development. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 58	7.7	40
362	Maternal phthalate exposure promotes allergic airway inflammation over 2 generations through epigenetic modifications. <i>Journal of Allergy and Clinical Immunology</i> , <b>2018</b> , 141, 741-753	11.5	56
361	HiGHmed - An Open Platform Approach to Enhance Care and Research across Institutional Boundaries. <i>Methods of Information in Medicine</i> , <b>2018</b> , 57, e66-e81	1.5	37
360	Dissecting Privacy Risks in Biomedical Data <b>2018</b> ,		6
359	EnrichedHeatmap: an R/Bioconductor package for comprehensive visualization of genomic signal associations. <i>BMC Genomics</i> , <b>2018</b> , 19, 234	4.5	67
358	Genomic features of renal cell carcinoma with venous tumor thrombus. <i>Scientific Reports</i> , <b>2018</b> , 8, 7477	4.9	9
357	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. <i>Lancet Oncology, The</i> , <b>2018</b> , 19, 785-798	21.7	159
356	Unraveling mitotic protein networks by 3D multiplexed epitope drug screening. <i>Molecular Systems Biology</i> , <b>2018</b> , 14, e8238	12.2	0
355	Rigid and non-rigid registration of polarized light imaging data for 3D reconstruction of the temporal lobe of the human brain at micrometer resolution. <i>NeuroImage</i> , <b>2018</b> , 181, 235-251	7.9	12
354	Familial Cancer Variant Prioritization Pipeline version 2 (FCVPPv2) applied to a papillary thyroid cancer family. <i>Scientific Reports</i> , <b>2018</b> , 8, 11635	4.9	15
353	Tagmentation-Based Library Preparation for Low DNA Input Whole Genome Bisulfite Sequencing. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1708, 105-122	1.4	7
352	Early-onset childhood atopic dermatitis is related to NLRP2 repression. <i>Journal of Allergy and Clinical Immunology</i> , <b>2018</b> , 141, 1482-1485.e16	11.5	12
351	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> , <b>2018</b> , 24, 351-359	12.9	60
350	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. <i>Nature Communications</i> , <b>2018</b> , 9, 4782	17.4	51
349	Web-based design and analysis tools for CRISPR base editing. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 542	3.6	70
348	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , <b>2018</b> , 34, 996-1011.e8	24.3	89

347	Single-Fluorescent Protein Reporters Allow Parallel Quantification of Natural Killer Cell-Mediated Granzyme and Caspase Activities in Single Target Cells. <i>Frontiers in Immunology</i> , <b>2018</b> , 9, 1840	8.4	9
346	Engineered anti-CRISPR proteins for optogenetic control of CRISPR-Cas9. <i>Nature Methods</i> , <b>2018</b> , 15, 924-927	21.6	109
345	Controlling Cells with Light and LOV. <i>Advanced Biology</i> , <b>2018</b> , 2, 1800098	3.5	9
344	The transcriptomic and epigenetic map of vascular quiescence in the continuous lung endothelium. <i>ELife</i> , <b>2018</b> , 7,	8.9	25
343	Nucleosome repositioning during differentiation of a human myeloid leukemia cell line. <i>Nucleus</i> , <b>2017</b> , 8, 188-204	3.9	12
342	The benzene metabolite 1,4-benzoquinone reduces regulatory T-cell function: A potential mechanism for tobacco smoke-associated atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , <b>2017</b> , 140, 603-605	11.5	2
341	Diagnosis of CoPAN by whole exome sequencing: Waking up a sleeping tiger's eye. <i>American Journal of Medical Genetics, Part A</i> , <b>2017</b> , 173, 1878-1886	2.5	21
340	Meningiomas induced by low-dose radiation carry structural variants of NF2 and a distinct mutational signature. <i>Acta Neuropathologica</i> , <b>2017</b> , 134, 155-158	14.3	19
339	Quantitative diagnosis of breast tumors by morphometric classification of microenvironmental myoepithelial cells using a machine learning approach. <i>Scientific Reports</i> , <b>2017</b> , 7, 46732	4.9	19
338	Precision oncology based on omics data: The NCT Heidelberg experience. <i>International Journal of Cancer</i> , <b>2017</b> , 141, 877-886	7.5	82
337	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. <i>Journal of Experimental Medicine</i> , <b>2017</b> , 214, 2073-2088	16.6	23
336	DDX3X mutations in two girls with a phenotype overlapping Toriello-Carey syndrome. <i>American Journal of Medical Genetics, Part A</i> , <b>2017</b> , 173, 1369-1373	2.5	23
335	Quantification of substrate and cellular strains in stretchable 3D cell cultures: an experimental and computational framework. <i>Journal of Microscopy</i> , <b>2017</b> , 266, 115-125	1.9	2
334	The Human Cell Atlas <b>2017</b> ,		41
333	The role of Vimentin in Regulating Cell Invasive Migration in Dense Cultures of Breast Carcinoma Cells. <i>Nano Letters</i> , <b>2017</b> , 17, 6941-6948	11.5	37
332	Transcription factors, coregulators, and epigenetic marks are linearly correlated and highly redundant. <i>PLoS ONE</i> , <b>2017</b> , 12, e0186324	3.7	10
331	Correlated receptor transport processes buffer single-cell heterogeneity. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005779	5	5
330	Quantitative Single-Molecule Localization Microscopy (qSMLM) of Membrane Proteins Based on Kinetic Analysis of Fluorophore Blinking Cycles. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1663, 115-126	1.4	5



329	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , <b>2017</b> , 547, 311-317	50.4	472
328	Workflows for microscopy image analysis and cellular phenotyping. <i>Journal of Biotechnology</i> , <b>2017</b> , 261, 70-75	3.7	14
327	OTP: An automatized system for managing and processing NGS data. <i>Journal of Biotechnology</i> , <b>2017</b> , 261, 53-62	3.7	21
326	Screening drug effects in patient-derived cancer cells links organoid responses to genome alterations. <i>Molecular Systems Biology</i> , <b>2017</b> , 13, 955	12.2	113
325	Identifying Personal DNA Methylation Profiles by Genotype Inference <b>2017</b> ,		14
324	Impact of clinical exomes in neurodevelopmental and neurometabolic disorders. <i>Molecular Genetics and Metabolism</i> , <b>2017</b> , 121, 297-307	3.7	30
323	Mutant KIT as imatinib-sensitive target in metastatic sinonasal carcinoma. <i>Annals of Oncology</i> , <b>2017</b> , 28, 142-148	10.3	16
322	TALEN/CRISPR-mediated engineering of a promoterless anti-viral RNAi hairpin into an endogenous miRNA locus. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e3	20.1	6
321	The Human Cell Atlas. <i>ELife</i> , <b>2017</b> , 6,	8.9	937
320	Identification of immunotherapeutic targets by genomic profiling of rectal NET metastases. <i>Oncotarget</i> , <b>2016</b> , 5, e1213931	7.2	8
319	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. <i>Nature Medicine</i> , <b>2016</b> , 22, 1314-1320	50.5	137
318	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , <b>2016</b> , 167, 1145-1149	56.2	232
317	MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. <i>Nature Communications</i> , <b>2016</b> , 7, 11807	17.4	65
316	Pedigree based DNA sequencing pipeline for germline genomes of cancer families. <i>Hereditary Cancer in Clinical Practice</i> , <b>2016</b> , 14, 16	2.3	5
315	Spatial niche formation but not malignant progression is a driving force for intratumoural heterogeneity. <i>Nature Communications</i> , <b>2016</b> , 7, ncomms11845	17.4	29
314	Prenatal maternal stress and wheeze in children: novel insights into epigenetic regulation. <i>Scientific Reports</i> , <b>2016</b> , 6, 28616	4.9	44
313	Death receptor-based enrichment of Cas9-expressing cells. <i>BMC Biotechnology</i> , <b>2016</b> , 16, 17	3.5	9
312	gtrellis: an R/Bioconductor package for making genome-level Trellis graphics. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 169	3.6	10



311	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. <i>Nature</i> , <b>2016</b> , 530, 57-62	50.4	234
310	HilbertCurve: an R/Bioconductor package for high-resolution visualization of genomic data. <i>Bioinformatics</i> , <b>2016</b> , 32, 2372-4	7.2	16
309	Optogenetic control of nuclear protein export. <i>Nature Communications</i> , <b>2016</b> , 7, 10624	17.4	132
308	CYP3A5 mediates basal and acquired therapy resistance in different subtypes of pancreatic ductal adenocarcinoma. <i>Nature Medicine</i> , <b>2016</b> , 22, 278-87	50.5	148
307	Increased vitamin D levels at birth and in early infancy increase offspring allergy risk-evidence for involvement of epigenetic mechanisms. <i>Journal of Allergy and Clinical Immunology</i> , <b>2016</b> , 137, 610-3	11.5	32
306	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. <i>Cancer Cell</i> , <b>2016</b> , 29, 379-393	24.3	319
305	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. <i>Cell</i> , <b>2016</b> , 164, 1060-1073	36.2	483
304	Mixed Integer Linear Programming based machine learning approach identifies regulators of telomerase in yeast. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e93	20.1	8
303	Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. <i>Molecular Systems Biology</i> , <b>2016</b> , 12, 861	12.2	71
302	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. <i>Haematologica</i> , <b>2016</b> , 101, 1380-1389	6.6	31
301	Role of the ESCRT Complexes in Telomere Biology. <i>MBio</i> , <b>2016</b> , 7,	7.8	8
300	Copy Number Alterations in Enzyme-Coding and Cancer-Causing Genes Reprogram Tumor Metabolism. <i>Cancer Research</i> , <b>2016</b> , 76, 4058-67	10.1	16
299	Complex heatmaps reveal patterns and correlations in multidimensional genomic data. <i>Bioinformatics</i> , <b>2016</b> , 32, 2847-9	7.2	2316
298	A comprehensive comparison of tools for differential ChIP-seq analysis. <i>Briefings in Bioinformatics</i> , <b>2016</b> , 17, 953-966	13.4	62
297	Optogenetic Control of Nuclear Protein Import in Living Cells Using Light-Inducible Nuclear Localization Signals (LINuS). <i>Current Protocols in Chemical Biology</i> , <b>2016</b> , 8, 131-145	1.8	10
296	Biologische Anwendungen aus dem Baukasten. <i>BioSpektrum</i> , <b>2015</b> , 21, 30-31	0.1	
295	Suppression of early hematogenous dissemination of human breast cancer cells to bone marrow by retinoic Acid-induced 2. <i>Cancer Discovery</i> , <b>2015</b> , 5, 506-19	24.4	27
294	Loss of function of PGAP1 as a cause of severe encephalopathy identified by Whole Exome Sequencing: Lessons of the bioinformatics pipeline. <i>Molecular and Cellular Probes</i> , <b>2015</b> , 29, 323-9	3.3	21

293	MapMyFlu: visualizing spatio-temporal relationships between related influenza sequences. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W547-51	20.1	5
292	Hypermutation takes the driver's seat. <i>Genome Medicine</i> , <b>2015</b> , 7, 31	14.4	14
291	SIPA1L3 identified by linkage analysis and whole-exome sequencing as a novel gene for autosomal recessive congenital cataract. <i>European Journal of Human Genetics</i> , <b>2015</b> , 23, 1627-33	5.3	15
290	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. <i>Nature Genetics</i> , <b>2015</b> , 47, 1316-1325	36.3	101
289	Tracking Virus Particles in Fluorescence Microscopy Images Using Multi-Scale Detection and Multi-Frame Association. <i>IEEE Transactions on Image Processing</i> , <b>2015</b> , 24, 4122-36	8.7	16
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23	Automated recognition of mitotic patterns in fluorescence microscopy images of human cells		4
22	Systems biology of apoptosis <sup>349-372</sup>		2
21	Feature Selection for Evaluating Fluorescence Microscopy Images in Genome-Wide Cell Screens		1
20	Assessing the similarity of spatial configurations using distance differences and bending energy: application to chromosomal interphase arrangements in HeLa cell clones		1
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18	CD95 receptor activation by ligand-induced trimerization is independent of its partial pre-ligand assembly		1
17	Cell-specific CRISPR/Cas9 activation by microRNA-dependent expression of anti-CRISPR proteins		3
16	Computational design of anti-CRISPR proteins with improved inhibition potency and expanded specificity		2
15	Framework for quality assessment of whole genome, cancer sequences		6
14	Large-Scale Uniform Analysis of Cancer Whole Genomes in Multiple Computing Environments		14
13	Deciphering programs of transcriptional regulation by combined deconvolution of multiple omics layers		6
12	Single-cell analysis of patient-derived PDAC organoids reveals cell state heterogeneity and a conserved developmental hierarchy		2
11	The COVID-19 PHARMACOME: A method for the rational selection of drug repurposing candidates from multimodal knowledge harmonization		2
10	Integrative Ranking Of Enhancer Networks Facilitates The Discovery Of Epigenetic Markers In Cancer		1
9	Identification and prioritisation of causal variants in human genetic disorders from exome or whole genome sequencing data		1
8	ACEseq Allele specific copy number estimation from whole genome sequencing		17
7	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity		5
6	Modeling glioblastoma invasion using human brain organoids and single-cell transcriptomics		1

5	Single nucleus and in situ RNA sequencing reveals cell topographies in the human pancreas	6
4	Cell segmentation-free inference of cell types from in situ transcriptomics data	9
3	Optogenetic control of <i>Neisseria meningitidis</i> Cas9 genome editing using an engineered, light-switchable anti-CRISPR protein	1
2	Pre-activated anti-viral innate immunity in the upper airways controls early SARS-CoV-2 infection in children	2
1	Dynamics of SARS-CoV-2 host cell interactions inferred from transcriptome analyses	1