Matthias Schlesner

List of Publications by Year
in descending order

114 papers	26,586 citations	61945 43 h-index	22808 112 g-index
133 all docs	133 docs citations	133 times ranked	49295 citing authors

#	Article	IF	Citations
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	13.7	8,060
2	Complex heatmaps reveal patterns and correlations in multidimensional genomic data. Bioinformatics, 2016, 32, 2847-2849.	1.8	5,891
3	circlizeimplements and enhances circular visualization in R. Bioinformatics, 2014, 30, 2811-2812.	1.8	2,736
4	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	13.7	1,068
5	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	13.7	787
6	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. Cell, 2016, 164, 1060-1072.	13.5	702
7	The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128.	13.7	690
8	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	9.4	674
9	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. Nature Genetics, 2012, 44, 1316-1320.	9.4	389
10	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	5.8	266
11	Next-generation personalised medicine for high-risk paediatric cancer patients â€“ The INFORM pilot study. European Journal of Cancer, 2016, 65, 91-101.	1.3	262
12	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	13.5	260
13	Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144.	5.8	197
14	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	7.7	190
15	NRG1 Fusions in KRAS Wild-Type Pancreatic Cancer. Cancer Discovery, 2018, 8, 1087-1095.	7.7	189
16	A recurrent 11q aberration pattern characterizes a subset of MYC-negative high-grade B-cell lymphomas resembling Burkitt lymphoma. Blood, 2014, 123, 1187-1198.	0.6	185
17	CYP3A5 mediates basal and acquired therapy resistance in different subtypes of pancreatic ductal adenocarcinoma. Nature Medicine, 2016, 22, 278-287.	15.2	184
18	Evolutionary Trajectories of IDHWT Glioblastomas Reveal a Common Path of Early Tumorigenesis Instigated Years ahead of Initial Diagnosis. Cancer Cell, 2019, 35, 692-704.e12.	7.7	172

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19	Screening drug effects in patientâ€derived cancer cells links organoid responses to genome alterations. Molecular Systems Biology, 2017, 13, 955.	3.2	163
20	Precision oncology based on omics data: The NCT Heidelberg experience. International Journal of Cancer, 2017, 141, 877-886.	2.3	133
21	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.	9.4	119
22	MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. Nature Communications, 2016, 7, 11807.	5.8	103
23	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. Nature Communications, 2018, 9, 4782.	5.8	103
24	B-cellâ€“specific conditional expression of Myd88p.L252P leads to the development of diffuse large B-cell lymphoma in mice. Blood, 2016, 127, 2732-2741.	0.6	99
25	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	5.8	99
26	Environmentâ€induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. Molecular Systems Biology, 2016, 12, 861.	3.2	97
27	Mechismo: predicting the mechanistic impact of mutations and modifications on molecular interactions. Nucleic Acids Research, 2015, 43, e10-e10.	6.5	95
28	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. Nature Cell Biology, 2020, 22, 896-906.	4.6	93
29	RAS-pathway mutation patterns define epigenetic subclasses in juvenile myelomonocytic leukemia. Nature Communications, 2017, 8, 2126.	5.8	91
30	Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications, 2020, 11, 733.	5.8	87
31	What do we learn from high-throughput protein interaction data?. Expert Review of Proteomics, 2004, 1, 111-121.	1.3	86
32	Genetic lesions of the <scp>TRAF</scp>3 and <scp>MAP</scp>3K14 genes in classical <scp>H</scp>odgkin lymphoma. British Journal of Haematology, 2012, 157, 702-708.	1.2	84
33	Harmonization and Standardization of Panel-Based Tumor Mutational Burden Measurement: Real-World Results and Recommendations ofÂtheÂQuality in Pathology Study. Journal of Thoracic Oncology, 2020, 15, 1177-1189.	0.5	81
34	Identification of Archaea-specific chemotaxis proteins which interact with the flagellar apparatus. BMC Microbiology, 2009, 9, 56.	1.3	76
35	Recurrent Somatic PDGFRB Mutations in Sporadic Infantile/Solitary Adult Myofibromas But Not in Angioleiomyomas and Myopericytomas. American Journal of Surgical Pathology, 2017, 41, 195-203.	2.1	76
36	Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. Acta Neuropathologica, 2019, 138, 295-308.	3.9	74

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37	The mutational landscape of Burkitt-like lymphoma with 11q aberration is distinct from that of Burkitt lymphoma. Blood, 2019, 133, 962-966.	0.6	69
38	Hypermutation of the Inactive X Chromosome Is a Frequent Event in Cancer. Cell, 2013, 155, 567-581.	13.5	67
39	Aggressive PDACs Show Hypomethylation of Repetitive Elements and the Execution of an Intrinsic IFN Program Linked to a Ductal Cell of Origin. Cancer Discovery, 2021, 11, 638-659.	7.7	65
40	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. Nature Communications, 2019, 10, 1635.	5.8	64
41	Cell segmentation-free inference of cell types from in situ transcriptomics data. Nature Communications, 2021, 12, 3545.	5.8	52
42	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	5.8	52
43	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.	1.5	51
44	Impact of clinical exomes in neurodevelopmental and neurometabolic disorders. Molecular Genetics and Metabolism, 2017, 121, 297-307.	0.5	50
45	IG-MYC+ neoplasms with precursor B-cell phenotype are molecularly distinct from Burkitt lymphomas. Blood, 2018, 132, 2280-2285.	0.6	50
46	YAP1-fusions in pediatric NF2-wildtype meningioma. Acta Neuropathologica, 2020, 139, 215-218.	3.9	45
47	Spatial niche formation but not malignant progression is a driving force for intratumoural heterogeneity. Nature Communications, 2016, 7, ncomms11845.	5.8	44
48	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. Haematologica, 2016, 101, 1380-1389.	1.7	43
49	The transcriptomic and epigenetic map of vascular quiescence in the continuous lung endothelium. ELife, 2018, 7, .	2.8	43
50	DDX3X mutations in two girls with a phenotype overlapping Toriælloâ€“Carey syndrome. American Journal of Medical Genetics, Part A, 2017, 173, 1369-1373.	0.7	41
51	Analysis of mutational signatures with yet another package for signature analysis. Genes Chromosomes and Cancer, 2021, 60, 314-331.	1.5	40
52	The protein interaction network of a taxis signal transduction system in a Halophilic Archaeon. BMC Microbiology, 2012, 12, 272.	1.3	37
53	Hotspot DNMT3A mutations in clonal hematopoiesis and acute myeloid leukemia sensitize cells to azacytidine via viral mimicry response. Nature Cancer, 2021, 2, 527-544.	5.7	37
54	Response to olaparib in a PALB2 germline mutated prostate cancer and genetic events associated with resistance. Journal of Physical Education and Sports Management, 2019, 5, a003657.	0.5	36

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55	Temporal multi-omics identifies LRG1 as a vascular niche instructor of metastasis. Science Translational Medicine, 2021, 13, eabe6805.	5.8	36
56	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	3.3	34
57	Longitudinal therapy monitoring of ALK-positive lung cancer by combined copy number and targeted mutation profiling of cell-free DNA. EBioMedicine, 2020, 62, 103103.	2.7	32
58	cola: an R/Bioconductor package for consensus partitioning through a general framework. Nucleic Acids Research, 2021, 49, e15-e15.	6.5	32
59	Globally altered epigenetic landscape and delayed osteogenic differentiation in H3.3-G34W-mutant giant cell tumor of bone. Nature Communications, 2020, 11, 5414.	5.8	31
60	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. Journal of Experimental Medicine, 2017, 214, 2073-2088.	4.2	30
61	Familial Cancer Variant Prioritization Pipeline version 2 (FCVPPv2) applied to a papillary thyroid cancer family. Scientific Reports, 2018, 8, 11635.	1.6	30
62	The PCBP1 gene encoding poly(rc) binding protein i is recurrently mutated in <scp>B</scp>urkitt lymphoma. Genes Chromosomes and Cancer, 2015, 54, 555-564.	1.5	29
63	NOTCH target gene HES5 mediates oncogenic and tumor suppressive functions in hepatocarcinogenesis. Oncogene, 2020, 39, 3128-3144.	2.6	28
64	Analysis of mutational signatures in exomes from B-cell lymphoma cell lines suggest APOBEC3 family members to be involved in the pathogenesis of primary effusion lymphoma. Leukemia, 2015, 29, 1612-1615.	3.3	26
65	Meningiomas induced by low-dose radiation carry structural variants of NF2 and a distinct mutational signature. Acta Neuropathologica, 2017, 134, 155-158.	3.9	26
66	Tumor cell network integration in glioma represents a stemness feature. Neuro-Oncology, 2021, 23, 757-769.	0.6	25
67	Cryptic insertion of MYC exons 2 and 3 into the immunoglobulin heavy chain locus detected by whole genome sequencing in a case of â€œMYC-negativeâ€•Burkitt lymphoma. Haematologica, 2020, 105, e202-e205.	1.7	24
68	Cutis laxa, exocrine pancreatic insufficiency and altered cellular metabolomics as additional symptoms in a new patient with ATP6AP1-CDG. Molecular Genetics and Metabolism, 2018, 123, 364-374.	0.5	23
69	Response to â€œUnexpected mutations after CRISPRâ€“Cas9 editing in vivoâ€• Nature Methods, 2018, 15, 239-240.	9.0	22
70	Clonal Evolution In Patients With Chronic Lymphocytic Leukemia (CLL) Developing Resistance To BTK Inhibition. Blood, 2013, 122, 866-866.	0.6	22
71	gtrellis: an R/Bioconductor package for making genome-level Trellis graphics. BMC Bioinformatics, 2016, 17, 169.	1.2	21
72	Early identification of disease progression in ALK-rearranged lung cancer using circulating tumor DNA analysis. Npj Precision Oncology, 2021, 5, 100.	2.3	21

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73	Genomic features of renal cell carcinoma with venous tumor thrombus. Scientific Reports, 2018, 8, 7477.	1.6	19
74	Distributed Ledger Technology in genomics: a call for Europe. European Journal of Human Genetics, 2020, 28, 139-140.	1.4	19
75	Identification of SLC20A1 and SLC15A4 among other genes as potential risk factors for combined pituitary hormone deficiency. Genetics in Medicine, 2018, 20, 728-736.	1.1	18
76	Timed Ang2-Targeted Therapy Identifies the Angiopoietinâ€“Tie Pathway as Key Regulator of Fatal Lymphogenous Metastasis. Cancer Discovery, 2021, 11, 424-445.	7.7	18
77	Homozygous missense mutation in theLMAN2Lgene segregates with intellectual disability in a large consanguineous Pakistani family. Journal of Medical Genetics, 2016, 53, 138-144.	1.5	16
78	Pheno-seq â€“ linking visual features and gene expression in 3D cell culture systems. Scientific Reports, 2019, 9, 12367.	1.6	16
79	Hypermutation takes the driverâ€™s seat. Genome Medicine, 2015, 7, 31.	3.6	15
80	SIPA1L3 identified by linkage analysis and whole-exome sequencing as a novel gene for autosomal recessive congenital cataract. European Journal of Human Genetics, 2015, 23, 1627-1633.	1.4	15
81	Identification of immunotherapeutic targets by genomic profiling of rectal NET metastases. OncoImmunology, 2016, 5, e1213931.	2.1	14
82	Patient-specific molecular alterations are associated with metastatic clear cell renal cell cancer progressing under tyrosine kinase inhibitor therapy. Oncotarget, 2017, 8, 74049-74057.	0.8	14
83	Protease activation mutants elicit protective immunity against highly pathogenic avian influenza viruses of subtype H7 in chickens and mice. Emerging Microbes and Infections, 2013, 2, 1-9.	3.0	13
84	Exome sequencing reveals a novel CWF19L1 mutation associated with intellectual disability and cerebellar atrophy. American Journal of Medical Genetics, Part A, 2016, 170, 1502-1509.	0.7	13
85	Serial liquid biopsies for detection of treatment failure and profiling of resistance mechanisms in KLC1â€“ALK-rearranged lung cancer. Journal of Physical Education and Sports Management, 2019, 5, a004630.	0.5	13
86	Molecular profiling of pediatric meningiomas shows tumor characteristics distinct from adult meningiomas. Acta Neuropathologica, 2021, 142, 873-886.	3.9	12
87	Putative second hit rare genetic variants in families with seemingly GBA-associated Parkinsonâ€™s disease. Npj Genomic Medicine, 2021, 6, 2.	1.7	11
88	ShinyButchR: Interactive NMF-based decomposition workflow of genome-scale datasets. Biology Methods and Protocols, 2020, 5, bpaa022.	1.0	11
89	iTReX: Interactive exploration of mono- and combination therapy dose response profiling data. Pharmacological Research, 2022, 175, 105996.	3.1	11
90	Germline Variants of CYBA and TRPM4 Predispose to Familial Colorectal Cancer. Cancers, 2022, 14, 670.	1.7	11

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91	Structure of the archaeal chemotaxis protein CheY in a domain-swapped dimeric conformation. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 576-585.	0.4	10
92	A novel homozygous ARL13B variant in patients with Joubert syndrome impairs its guanine nucleotide-exchange factor activity. European Journal of Human Genetics, 2017, 25, 1324-1334.	1.4	9
93	IFNÎ²1 secreted by breast cancer cells undergoing chemotherapy reprograms stromal fibroblasts to support tumour growth after treatment. Molecular Oncology, 2021, 15, 1308-1329.	2.1	9
94	Combinations of Low-Frequency Genetic Variants Might Predispose to Familial Pancreatic Cancer. Journal of Personalized Medicine, 2021, 11, 631.	1.1	9
95	TALEN/CRISPR-mediated engineering of a promoterless anti-viral RNAi hairpin into an endogenous miRNA locus. Nucleic Acids Research, 2017, 45, e3-e3.	6.5	8
96	Genome-Wide DNA Methylation Profiling in Early Stage I Lung Adenocarcinoma Reveals Predictive Aberrant Methylation in the Promoter Region of the Long Noncoding RNA PLUT: An Exploratory Study. Journal of Thoracic Oncology, 2020, 15, 1338-1350.	0.5	8
97	Pedigree based DNA sequencing pipeline for germline genomes of cancer families. Hereditary Cancer in Clinical Practice, 2016, 14, 16.	0.6	7
98	Identification of <i>Transient Receptor Potential Channel 4-Associated Protein</i> as a Novel Candidate Gene Causing Congenital Primary Hypothyroidism. Hormone Research in Paediatrics, 2020, 93, 16-29.	0.8	7
99	Characterization of rare germline variants in familial multiple myeloma. Blood Cancer Journal, 2021, 11, 33.	2.8	7
100	Evaluation of Whole Genome Sequencing Data. Methods in Molecular Biology, 2019, 1956, 321-336.	0.4	6
101	Whole Exome Sequencing Identifies APCDD1 and HDAC5 Genes as Potentially Cancer Predisposing in Familial Colorectal Cancer. International Journal of Molecular Sciences, 2021, 22, 1837.	1.8	6
102	A scoping review of distributed ledger technology in genomics: thematic analysis and directions for future research. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1433-1444.	2.2	6
103	Genetic Interactions and Tissue Specificity Modulate the Association of Mutations with Drug Response. Molecular Cancer Therapeutics, 2020, 19, 927-936.	1.9	5
104	Framework for quality assessment of whole genome cancer sequences. Nature Communications, 2020, 11, 5040.	5.8	5
105	DNMT1 Deficiency Impacts on Plasmacytoid Dendritic Cells in Homeostasis and Autoimmune Disease. Journal of Immunology, 2022, 208, 358-370.	0.4	5
106	Segregation and potential functional impact of a rare stop-gain PABPC4L variant in familial atypical Parkinsonism. Scientific Reports, 2019, 9, 13576.	1.6	3
107	Immunohistochemical detection of inhibitor of DNA binding 3 mutational variants in mature aggressive B-cell lymphoma. Haematologica, 2016, 101, e259-e261.	1.7	2
108	Cancer Predisposition Genes in Cancer-Free Families. Cancers, 2020, 12, 2770.	1.7	2

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109	Differentially methylated regions within lung cancer risk loci are enriched in deregulated enhancers. Epigenetics, 2022, 17, 117-132.	1.3	2
110	Whole-Exome Sequencing Identifies a Novel Germline Variant in PTK7 Gene in Familial Colorectal Cancer. International Journal of Molecular Sciences, 2022, 23, 1295.	1.8	2
111	Whole exome sequencing identifies novel germline variants of SLC15A4 gene as potentially cancer predisposing in familial colorectal cancer. Molecular Genetics and Genomics, 2022, , 1.	1.0	1
112	A Novel Low-Risk Germline Variant in the SH2 Domain of the SRC Gene Affects Multiple Pathways in Familial Colorectal Cancer. Journal of Personalized Medicine, 2021, 11, 262.	1.1	0
113	TMOD-04. IMAGE-BASED DRUG RESPONSE PROFILING FROM PEDIATRIC TUMOR CELL SPHEROIDS USING PATIENT-BY-PATIENT DEEP TRANSFER LEARNING. Neuro-Oncology, 2021, 23, i36-i36.	0.6	0
114	Multiomics analysis of pediatric solid tumors within the INFORM precision oncology study: From functional drug profiling to biomarker identification.. Journal of Clinical Oncology, 2022, 40, 10036-10036.	0.8	0