Matthias Schlesner

List of Publications by Citations

116 papers	15,421 citations	36 h-index	124 g-index
133 ext. papers	22,116 ext. citations	12.7 avg, IF	6.32 L-index

#	Paper	IF	Citations
116	Signatures of mutational processes in human cancer. *Nature*, **2013**, 500, 415-21	50.4	5895
115	Complex heatmaps reveal patterns and correlations in multidimensional genomic data. *Bioinformatics*, **2016**, 32, 2847-9	7.2	2316
114	circlize Implements and enhances circular visualization in R. *Bioinformatics*, **2014**, 30, 2811-2	7.2	1242
113	The landscape of genomic alterations across childhood cancers. *Nature*, **2018**, 555, 321-327	50.4	603
112	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. *Nature Genetics*, **2013**, 45, 927-32	36.3	550
111	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. *Cell*, **2016**, 164, 1060-1072	36.2	483
110	The whole-genome landscape of medulloblastoma subtypes. *Nature*, **2017**, 547, 311-317	50.4	472
109	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. *Nature Genetics*, **2012**, 44, 1316-20	36.3	317
108	The evolutionary history of 2,658 cancers. *Nature*, **2020**, 578, 122-128	50.4	307
107	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. *Nature Communications*, **2015**, 6, 10001	17.4	199
106	Next-generation personalised medicine for high-risk paediatric cancer patients - The INFORM pilot study. *European Journal of Cancer*, **2016**, 65, 91-101	7.5	186
105	CYP3A5 mediates basal and acquired therapy resistance in different subtypes of pancreatic ductal adenocarcinoma. *Nature Medicine*, **2016**, 22, 278-87	50.5	148
104	A recurrent 11q aberration pattern characterizes a subset of MYC-negative high-grade B-cell lymphomas resembling Burkitt lymphoma. *Blood*, **2014**, 123, 1187-98	2.2	131
103	Integrative genomic and transcriptomic analysis of leiomyosarcoma. *Nature Communications*, **2018**, 9, 144	17.4	115
102	Screening drug effects in patient-derived cancer cells links organoid responses to genome alterations. *Molecular Systems Biology*, **2017**, 13, 955	12.2	113
101	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	36.3	101
100	Fusions in Wild-Type Pancreatic Cancer. *Cancer Discovery*, **2018**, 8, 1087-1095	24.4	99

99	Evolutionary Trajectories of IDH Glioblastomas Reveal a Common Path of Early Tumorigenesis Instigated Years ahead of Initial Diagnosis. *Cancer Cell*, **2019**, 35, 692-704.e12	24.3	92
98	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. *Cancer Cell*, **2018**, 34, 996-1011.e8	24.3	89
97	Precision oncology based on omics data: The NCT Heidelberg experience. *International Journal of Cancer*, **2017**, 141, 877-886	7.5	82
96	B-cell-specific conditional expression of Myd88p.L252P leads to the development of diffuse large B-cell lymphoma in mice. *Blood*, **2016**, 127, 2732-41	2.2	78
95	Genetic lesions of the TRAF3 and MAP3K14 genes in classical Hodgkin lymphoma. *British Journal of Haematology*, **2012**, 157, 702-8	4.5	71
94	Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. *Molecular Systems Biology*, **2016**, 12, 861	12.2	71
93	What do we learn from high-throughput protein interaction data?. *Expert Review of Proteomics*, **2004**, 1, 111-21	4.2	69
92	Identification of Archaea-specific chemotaxis proteins which interact with the flagellar apparatus. *BMC Microbiology*, **2009**, 9, 56	4.5	67
91	MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. *Nature Communications*, **2016**, 7, 11807	17.4	65
90	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	6.7	60
89	Mechismo: predicting the mechanistic impact of mutations and modifications on molecular interactions. *Nucleic Acids Research*, **2015**, 43, e10	20.1	57
88	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. *Cell*, **2021**, 184, 2239-2254.e39	56.2	57
87	RAS-pathway mutation patterns define epigenetic subclasses in juvenile myelomonocytic leukemia. *Nature Communications*, **2017**, 8, 2126	17.4	52
86	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. *Nature Communications*, **2018**, 9, 4782	17.4	51
85	Hypermutation of the inactive X chromosome is a frequent event in cancer. *Cell*, **2013**, 155, 567-81	56.2	50
84	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. *Nature Communications*, **2019**, 10, 1459	17.4	49
83	Harmonization and Standardization of Panel-Based Tumor Mutational Burden Measurement: Real-World Results and Recommendations of the Quality in Pathology Study. *Journal of Thoracic Oncology*, **2020**, 15, 1177-1189	8.9	45
82	Recurrent RHOA mutations in pediatric Burkitt lymphoma treated according to the NHL-BFM protocols. *Genes Chromosomes and Cancer*, **2014**, 53, 911-6	5	44

81	Genomic footprints of activated telomere maintenance mechanisms in cancer. *Nature Communications*, **2020**, 11, 733	17.4	40
80	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. *Nature Communications*, **2019**, 10, 1635	17.4	33
79	The protein interaction network of a taxis signal transduction system in a halophilic archaeon. *BMC Microbiology*, **2012**, 12, 272	4.5	32
78	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	6.6	31
77	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. *Nature Cell Biology*, **2020**, 22, 896-906	23.4	30
76	Impact of clinical exomes in neurodevelopmental and neurometabolic disorders. *Molecular Genetics and Metabolism*, **2017**, 121, 297-307	3.7	30
75	Spatial niche formation but not malignant progression is a driving force for intratumoural heterogeneity. *Nature Communications*, **2016**, 7, ncomms11845	17.4	29
74	The mutational landscape of Burkitt-like lymphoma with 11q aberration is distinct from that of Burkitt lymphoma. *Blood*, **2019**, 133, 962-966	2.2	29
73	The evolutionary history of 2,658 cancers		28
72	Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. *Acta Neuropathologica*, **2019**, 138, 295-308	14.3	27
71	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes		25
70	The transcriptomic and epigenetic map of vascular quiescence in the continuous lung endothelium. *ELife*, **2018**, 7,	8.9	25
69	YAP1-fusions in pediatric NF2-wildtype meningioma. *Acta Neuropathologica*, **2020**, 139, 215-218	14.3	24
68	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	24.4	24
67	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. *Journal of Experimental Medicine*, **2017**, 214, 2073-2088	16.6	23
66	DDX3X mutations in two girls with a phenotype overlapping Toriello-Carey syndrome. *American Journal of Medical Genetics, Part A*, **2017**, 173, 1369-1373	2.5	23
65	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". *Nature Methods*, **2018**, 15, 239-2406	24.6	22
64	Response to olaparib in a germline mutated prostate cancer and genetic events associated with resistance. *Journal of Physical Education and Sports Management*, **2019**, 5,	2.8	21

63	The PCBP1 gene encoding poly(rC) binding protein I is recurrently mutated in Burkitt lymphoma. *Genes Chromosomes and Cancer*, **2015**, 54, 555-64	5	21
62	Clonal Evolution In Patients With Chronic Lymphocytic Leukemia (CLL) Developing Resistance To BTK Inhibition. *Blood*, **2013**, 122, 866-866	2.2	20
61	Meningiomas induced by low-dose radiation carry structural variants of NF2 and a distinct mutational signature. *Acta Neuropathologica*, **2017**, 134, 155-158	14.3	19
60	IG- neoplasms with precursor B-cell phenotype are molecularly distinct from Burkitt lymphomas. *Blood*, **2018**, 132, 2280-2285	2.2	19
59	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, 1612-5	10.7	17
58	ACEseq allele specific copy number estimation from whole genome sequencing		17
57	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, 1627-33	5.3	15
56	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	3.7	15
55	Familial Cancer Variant Prioritization Pipeline version 2 (FCVPPv2) applied to a papillary thyroid cancer family. *Scientific Reports*, **2018**, 8, 11635	4.9	15
54	Cryptic insertion of exons 2 and 3 into the immunoglobulin heavy chain locus detected by whole genome sequencing in a case of "-negative" Burkitt lymphoma. *Haematologica*, **2020**, 105, e202-e205	6.6	15
53	Hypermutation takes the driver's seat. *Genome Medicine*, **2015**, 7, 31	14.4	14
52	Longitudinal therapy monitoring of ALK-positive lung cancer by combined copy number and targeted mutation profiling of cell-free DNA. *EBioMedicine*, **2020**, 62, 103103	8.8	14
51	Cell segmentation-free inference of cell types from in situ transcriptomics data. *Nature Communications*, **2021**, 12, 3545	17.4	14
50	NOTCH target gene HES5 mediates oncogenic and tumor suppressive functions in hepatocarcinogenesis. *Oncogene*, **2020**, 39, 3128-3144	9.2	13
49	Germline determinants of the somatic mutation landscape in 2,642 cancer genomes		13
48	Globally altered epigenetic landscape and delayed osteogenic differentiation in H3.3-G34W-mutant giant cell tumor of bone. *Nature Communications*, **2020**, 11, 5414	17.4	13
47	Timed Ang2-Targeted Therapy Identifies the Angiopoietin-Tie Pathway as Key Regulator of Fatal Lymphogenous Metastasis. *Cancer Discovery*, **2021**, 11, 424-445	24.4	12
46	Analysis of mutational signatures with yet another package for signature analysis. *Genes Chromosomes and Cancer*, **2021**, 60, 314-331	5	12

45	Temporal multi-omics identifies LRG1 as a vascular niche instructor of metastasis. *Science Translational Medicine*, **2021**, 13, eabe6805	17.5	11
44	Pheno-seq - linking visual features and gene expression in 3D cell culture systems. *Scientific Reports*, **2019**, 9, 12367	4.9	10
43	gtrellis: an R/Bioconductor package for making genome-level Trellis graphics. *BMC Bioinformatics*, **2016**, 17, 169	3.6	10
42	Homozygous missense mutation in the LMAN2L gene segregates with intellectual disability in a large consanguineous Pakistani family. *Journal of Medical Genetics*, **2016**, 53, 138-44	5.8	10
41	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, e7	18.9	10
40	Hotspot DNMT3A mutations in clonal hematopoiesis and acute myeloid leukemia sensitize cells to azacytidine via viral mimicry response.. *Nature Cancer*, **2021**, 2, 527-544	15.4	10
39	Distributed Ledger Technology in genomics: a call for Europe. *European Journal of Human Genetics*, **2020**, 28, 139-140	5.3	10
38	Identification of SLC20A1 and SLC15A4 among other genes as potential risk factors for combined pituitary hormone deficiency. *Genetics in Medicine*, **2018**, 20, 728-736	8.1	10
37	Genomic features of renal cell carcinoma with venous tumor thrombus. *Scientific Reports*, **2018**, 8, 7477	4.9	9
36	Cell segmentation-free inference of cell types from in situ transcriptomics data		9
35	Identification of immunotherapeutic targets by genomic profiling of rectal NET metastases. *OncoImmunology*, **2016**, 5, e1213931	7.2	8
34	Exome sequencing reveals a novel CWF19L1 mutation associated with intellectual disability and cerebellar atrophy. *American Journal of Medical Genetics, Part A*, **2016**, 170, 1502-9	2.5	8
33	cola: an R/Bioconductor package for consensus partitioning through a general framework. *Nucleic Acids Research*, **2021**, 49, e15	20.1	8
32	Patient-specific molecular alterations are associated with metastatic clear cell renal cell cancer progressing under tyrosine kinase inhibitor therapy. *Oncotarget*, **2017**, 8, 74049-74057	3.3	7
31	Structure of the archaeal chemotaxis protein CheY in a domain-swapped dimeric conformation. *Acta Crystallographica Section F, Structural Biology Communications*, **2019**, 75, 576-585	1.1	7
30	Tumor cell network integration in glioma represents a stemness feature. *Neuro-Oncology*, **2021**, 23, 757-769		7
29	TALEN/CRISPR-mediated engineering of a promoterless anti-viral RNAi hairpin into an endogenous miRNA locus. *Nucleic Acids Research*, **2017**, 45, e3	20.1	6
28	Deciphering programs of transcriptional regulation by combined deconvolution of multiple omics layers		6

27	Serial liquid biopsies for detection of treatment failure and profiling of resistance mechanisms in -rearranged lung cancer. *Journal of Physical Education and Sports Management*, **2019**, 5,	2.8	6
26	Pedigree based DNA sequencing pipeline for germline genomes of cancer families. *Hereditary Cancer in Clinical Practice*, **2016**, 14, 16	2.3	5
25	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	5.3	4
24	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	8.9	4
23	IFN secreted by breast cancer cells undergoing chemotherapy reprograms stromal fibroblasts to support tumour growth after treatment. *Molecular Oncology*, **2021**, 15, 1308-1329	7.9	4
22	The genomic and transcriptional landscape of primary central nervous system lymphoma.. *Nature Communications*, **2022**, 13, 2558	17.4	4
21	Germline Variants of and Predispose to Familial Colorectal Cancer.. *Cancers*, **2022**, 14,	6.6	3
20	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. *Leukemia*, **2021**, 35, 2002-2016	10.7	3
19	Identification of Transient Receptor Potential Channel 4-Associated Protein as a Novel Candidate Gene Causing Congenital Primary Hypothyroidism. *Hormone Research in Paediatrics*, **2020**, 93, 16-29	3.3	2
18	Early identification of disease progression in ALK-rearranged lung cancer using circulating tumor DNA analysis. *Npj Precision Oncology*, **2021**, 5, 100	9.8	2
17	ShinyButchR: Interactive NMF-based decomposition workflow of genome-scale datasets. *Biology Methods and Protocols*, **2020**, 5, bpaa022	2.4	2
16	iTReX: Interactive exploration of mono- and combination therapy dose response profiling data. *Pharmacological Research*, **2021**, 175, 105996	10.2	2
15	Integrated phospho-proteogenomic and single-cell transcriptomic analysis of meningiomas establishes robust subtyping and reveals subtype-specific immune invasion		2
14	Combinations of Low-Frequency Genetic Variants Might Predispose to Familial Pancreatic Cancer. *Journal of Personalized Medicine*, **2021**, 11,	3.6	2
13	Evaluation of Whole Genome Sequencing Data. *Methods in Molecular Biology*, **2019**, 1956, 321-336	1.4	2
12	Whole Exome Sequencing Identifies and Genes as Potentially Cancer Predisposing in Familial Colorectal Cancer. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	2
11	Segregation and potential functional impact of a rare stop-gain PABPC4L variant in familial atypical Parkinsonism. *Scientific Reports*, **2019**, 9, 13576	4.9	1
10	Identification and prioritisation of causal variants in human genetic disorders from exome or whole genome sequencing data		1

9	Framework for quality assessment of whole genome cancer sequences. *Nature Communications*, **2020**, 11, 5040	17.4	1
8	Immunohistochemical detection of inhibitor of DNA binding 3 mutational variants in mature aggressive B-cell lymphoma. *Haematologica*, **2016**, 101, e259-61	6.6	1
7	Putative second hit rare genetic variants in families with seemingly GBA-associated Parkinson's disease. *Npj Genomic Medicine*, **2021**, 6, 2	6.2	1
6	Characterization of rare germline variants in familial multiple myeloma. *Blood Cancer Journal*, **2021**, 11, 33	7	1
5	Differentially methylated regions within lung cancer risk loci are enriched in deregulated enhancers. *Epigenetics*, **2021**, 1-16	5.7	1
4	Molecular profiling of pediatric meningiomas shows tumor characteristics distinct from adult meningiomas. *Acta Neuropathologica*, **2021**, 142, 873-886	14.3	1
3	Genetic Interactions and Tissue Specificity Modulate the Association of Mutations with Drug Response. *Molecular Cancer Therapeutics*, **2020**, 19, 927-936	6.1	0
2	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	1	
1	Whole exome sequencing identifies novel germline variants of SLC15A4 gene as potentially cancer predisposing in familial colorectal cancer.. *Molecular Genetics and Genomics*, **2022**, 1	3.1	