Tobias Rausch

List of Publications by Citations

82 papers	25,830 citations	34 h-index	94 g-index
94 ext. papers	33,414 ext. citations	13.8 avg, IF	7.29 L-index

#	Paper	IF	Citations
82	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
81	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
80	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. *Nature*, **2012**, 482, 226-31	50.4	1655
79	An integrated map of structural variation in 2,504 human genomes. *Nature*, **2015**, 526, 75-81	50.4	1368
78	DELLY: structural variant discovery by integrated paired-end and split-read analysis. *Bioinformatics*, **2012**, 28, i333-i339	7.2	1069
77	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
76	Mapping copy number variation by population-scale genome sequencing. *Nature*, **2011**, 470, 59-65	50.4	833
75	Dissecting the genomic complexity underlying medulloblastoma. *Nature*, **2012**, 488, 100-5	50.4	623
74	Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. *Cell*, **2012**, 148, 59-71	56.2	600
73	Genome sequencing of SHH medulloblastoma predicts genotype-related response to smoothened inhibition. *Cancer Cell*, **2014**, 25, 393-405	24.3	469
72	Assembly and diploid architecture of an individual human genome via single-molecule technologies. *Nature Methods*, **2015**, 12, 780-6	21.6	383
71	Multi-platform discovery of haplotype-resolved structural variation in human genomes. *Nature Communications*, **2019**, 10, 1784	17.4	346
70	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
69	The genomic and transcriptomic landscape of a HeLa cell line. *G3: Genes, Genomes, Genetics*, **2013**, 3, 1213-24	3.2	269
68	Integrative genomic analyses reveal an androgen-driven somatic alteration landscape in early-onset prostate cancer. *Cancer Cell*, **2013**, 23, 159-70	24.3	259
67	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. *Nature Communications*, **2014**, 5, 3934	17.4	253
66	SeqAn an efficient, generic C++ library for sequence analysis. *BMC Bioinformatics*, **2008**, 9, 11	3.6	210

65	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	21.7	159
64	RazerS--fast read mapping with sensitivity control. *Genome Research*, **2009**, 19, 1646-54	9.7	104
63	Whole-exome sequencing links caspase recruitment domain 11 (CARD11) inactivation to severe combined immunodeficiency. *Journal of Allergy and Clinical Immunology*, **2013**, 131, 1376-83.e3	11.5	103
62	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. *Science* , **2021**, 372,	33.3	100
61	The activating STAT5B N642H mutation is a common abnormality in pediatric T-cell acute lymphoblastic leukemia and confers a higher risk of relapse. *Haematologica*, **2014**, 99, e188-92	6.6	82
60	EMBR-10. GENOMIC COMPLEXITY AND EVOLUTION OF EMBRYONAL TUMORS WITH MULTILAYERED ROSETTES (ETMR). *Neuro-Oncology*, **2018**, 20, i70-i70	1	78
59	MEDU-11. MOLECULAR CHARACTERIZATION OF ETMRs REVEALS A ROLE FOR R-LOOP MEDIATED CHROMOSOMAL INSTABILITY. *Neuro-Oncology*, **2019**, 21, ii105-ii105	1	78
58	MBCL-21. GERMLINE ELONGATOR MUTATIONS IN SONIC HEDGEHOG MEDULLOBLASTOMA. *Neuro-Oncology*, **2020**, 22, iii392-iii393	1	78
57	Identification of a genetically defined ultra-high-risk group in relapsed pediatric T-lymphoblastic leukemia. *Blood Cancer Journal*, **2017**, 7, e523	7	54
56	Impact of genomic structural variation in Drosophila melanogaster based on population-scale sequencing. *Genome Research*, **2013**, 23, 568-79	9.7	53
55	Pediatric T-cell lymphoblastic leukemia evolves into relapse by clonal selection, acquisition of mutations and promoter hypomethylation. *Haematologica*, **2015**, 100, 1442-50	6.6	50
54	Highly recurrent mutations of SGK1, DUSP2 and JUNB in nodular lymphocyte predominant Hodgkin lymphoma. *Leukemia*, **2016**, 30, 844-53	10.7	48
53	Germline Elongator mutations in Sonic Hedgehog medulloblastoma. *Nature*, **2020**, 580, 396-401	50.4	47
52	The molecular landscape of ETMR at diagnosis and relapse. *Nature*, **2019**, 576, 274-280	50.4	46
51	Identification of cytokine-induced modulation of microRNA expression and secretion as measured by a novel microRNA specific qPCR assay. *Scientific Reports*, **2015**, 5, 11590	4.9	42
50	Segment-based multiple sequence alignment. *Bioinformatics*, **2008**, 24, i187-92	7.2	39
49	A highly soluble Sleeping Beauty transposase improves control of gene insertion. *Nature Biotechnology*, **2019**, 37, 1502-1512	44.5	36
48	The NSL complex maintains nuclear architecture stability via lamin A/C acetylation. *Nature Cell Biology*, **2019**, 21, 1248-1260	23.4	34

47	Alfred: interactive multi-sample BAM alignment statistics, feature counting and feature annotation for long- and short-read sequencing. *Bioinformatics*, **2019**, 35, 2489-2491	7.2	29
46	Genomic structural variations lead to dysregulation of important coding and non-coding RNA species in dilated cardiomyopathy. *EMBO Molecular Medicine*, **2018**, 10, 107-120	12	29
45	Identification of novel follicular dendritic cell sarcoma markers, FDCSP and SRGN, by whole transcriptome sequencing. *Oncotarget*, **2017**, 8, 16463-16472	3.3	28
44	Multi-platform discovery of haplotype-resolved structural variation in human genomes		26
43	A consistency-based consensus algorithm for de novo and reference-guided sequence assembly of short reads. *Bioinformatics*, **2009**, 25, 1118-24	7.2	24
42	, , , and are frequently mutated in T-cell/histiocyte-rich large B-cell lymphoma. *Haematologica*, **2019**, 104, 330-337	6.6	23
41	PDX models recapitulate the genetic and epigenetic landscape of pediatric T-cell leukemia. *EMBO Molecular Medicine*, **2018**, 10,	12	20
40	Tracy: basecalling, alignment, assembly and deconvolution of sanger chromatogram trace files. *BMC Genomics*, **2020**, 21, 230	4.5	19
39	Personality similarity between teachers and their students influences teacher judgement of student achievement. *Educational Psychology*, **2016**, 36, 863-878	2.2	18
38	Characterization of Two Historic Smallpox Specimens from a Czech Museum. *Viruses*, **2017**, 9,	6.2	18
37	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. *Nature Biotechnology*, **2020**, 38, 343-354	44.5	17
36	Identification of novel sequence variations in microRNAs in chronic lymphocytic leukemia. *Carcinogenesis*, **2014**, 35, 992-1002	4.6	15
35	Accuracy of Teacher Judgments **2014**, 27-43		14
34	Germline determinants of the somatic mutation landscape in 2,642 cancer genomes		13
33	MCM3AP and POMP Mutations Cause a DNA-Repair and DNA-Damage-Signaling Defect in an Immunodeficient Child. *Human Mutation*, **2016**, 37, 257-68	4.7	12
32	Identification of a Ninein (NIN) mutation in a family with spondyloepimetaphyseal dysplasia with joint laxity (leptodactylic type)-like phenotype. *Matrix Biology*, **2013**, 32, 387-92	11.4	12
31	Missense variants in NOX1 and p22phox in a case of very-early-onset inflammatory bowel disease are functionally linked to NOD2. *Journal of Physical Education and Sports Management*, **2019**, 5,	2.8	11
30	Fast and Adaptive Variable Order Markov Chain Construction. *Lecture Notes in Computer Science*, **2008**, 306-317	0.9	11

29	Pangenome-based genome inference		11
28	A novel autosomal recessive TERT T1129P mutation in a dyskeratosis congenita family leads to cellular senescence and loss of CD34+ hematopoietic stem cells not reversible by mTOR-inhibition. *Aging*, **2015**, 7, 911-27	5.6	10
27	The effects of common structural variants on 3D chromatin structure. *BMC Genomics*, **2020**, 21, 95	4.5	9
26	VISOR: a versatile haplotype-aware structural variant simulator for short- and long-read sequencing. *Bioinformatics*, **2020**, 36, 1267-1269	7.2	8
25	TRiCoLOR: tandem repeat profiling using whole-genome long-read sequencing data. *GigaScience*, **2020**, 9,	7.6	7
24	Potential protective role of Grainyhead-like genes in the development of clear cell renal cell carcinoma. *Molecular Carcinogenesis*, **2017**, 56, 2414-2423	5	6
23	Coordinated expression and genetic polymorphisms in Grainyhead-like genes in human non-melanoma skin cancers. *BMC Cancer*, **2018**, 18, 23	4.8	6
22	A parallel genetic algorithm to discover patterns in genetic markers that indicate predisposition to multifactorial disease. *Computers in Biology and Medicine*, **2008**, 38, 826-36	7	6
21	Local emergence and decline of a SARS-CoV-2 variant with mutations L452R and N501Y in the spike protein		6
20	Genomic insights into the pathogenesis of Epstein-Barr virus-associated diffuse large B-cell lymphoma by whole-genome and targeted amplicon sequencing. *Blood Cancer Journal*, **2021**, 11, 102	7	6
19	Mit Wissen zu akkurateren Urteilen?. *Zeitschrift Fur Entwicklungspsychologie Und Padagogische Psychologie*, **2015**, 47, 147-158	0.8	4
18	Metagenomic analysis of primary colorectal carcinomas and their metastases identifies potential microbial risk factors. *Molecular Oncology*, **2021**, 15, 3363-3384	7.9	4
17	De novo assembly of 64 haplotype-resolved human genomes of diverse ancestry and integrated analysis of structural variation		3
16	Chromatin accessibility landscape of pediatric T-lymphoblastic leukemia and human T-cell precursors. *EMBO Molecular Medicine*, **2020**, 12, e12104	12	3
15	Robust consensus computation. *BMC Bioinformatics*, **2008**, 9,	3.6	2
14	ToTem: a tool for variant calling pipeline optimization. *BMC Bioinformatics*, **2018**, 19, 243	3.6	1
13	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. *BMC Proceedings*, **2012**, 6,	2.3	1
12	Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes.. *Nature Genetics*, **2022**,	36.3	1

11	Longitudinal Multilevel Omic Analysis of Pediatric T-ALL Reveals Distinct Mechanisms for Disease Progression in Type 1 and in Type 2 Relapses. *Blood*, **2018**, 132, 2826-2826	2.2
10	Pediatric T-ALLs Developing into a Type 2 Relapse Originate from Cells That Carry the Potential of Variable Maturation into Subclones with Distinct Chromatin Landscapes. *Blood*, **2018**, 132, 1545-1545	2.2
9	Targeted Deep Sequencing of Genetic Alterations Identified By Whole Exome Sequencing Reveals Clonal Evolution in Pediatric T-Lymphoblastic Leukemia. *Blood*, **2014**, 124, 491-491	2.2
8	Gene Panel Sequencing of Primary and Relapsed Pediatric T-ALL Shows That Relapse-Specific Mutations Are Diverse and Mostly Non-Recurrent. *Blood*, **2015**, 126, 1428-1428	2.2
7	Identification of an Ultra High-Risk and Targetable Molecular Signature in Relapsed Pediatric T-ALL. *Blood*, **2016**, 128, 1084-1084	2.2
6	Practical Multiple Sequence Alignment **2010**, 21-43	
5	Mutational Analysis of Mir-29 Family Members in Chronic Lymphocytic Leukemia. *Blood*, **2011**, 118, 1770-1770	2.2
4	Sequence Variations in miRNA Genes Are Common and May Affect Their Expression in Patients with Chronic Lymphocytic Leukemia. *Blood*, **2012**, 120, 3895-3895	2.2
3	Whole-Exome Sequencing Links CARD11 Inactivation with SCID. *Blood*, **2012**, 120, 258-258	2.2
2	Whole Exome Sequencing Identifies Novel Lyst-Missense Mutations In Incomplete Childhood Chediak-Higashi-Syndrome Presenting As Hemphagocytic Lymphohistiocytosis (HLH). *Blood*, **2013**, 122, 3479-3479	2.2
1	Whole Exome Sequencing In Relapsed Pediatric T-ALL: Progression Into Relapse Is Characterized By An Increased Number Of Somatic Mutations and a Conservation Of Mutations In Leukemogenic Driver Genes. *Blood*, **2013**, 122, 228-228	2.2