Tobias Rausch

List of Publications by Year
in descending order

83 papers	37,647 citations	87723 38 h-index	91712 69 g-index
94 all docs	94 docs citations	94 times ranked	64556 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
3	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. Nature, 2012, 482, 226-231.	13.7	2,129
4	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
5	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
6	DELLY: structural variant discovery by integrated paired-end and split-read analysis. Bioinformatics, 2012, 28, i333-i339.	1.8	1,785
7	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991
8	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	13.7	765
9	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. Cell, 2012, 148, 59-71.	13.5	743
10	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
11	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. Cancer Cell, 2014, 25, 393-405.	7.7	627
12	Assembly and diploid architecture of an individual human genome via single-molecule technologies. Nature Methods, 2015, 12, 780-786.	9.0	465
13	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
14	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. Nature Communications, 2014, 5, 3934.	5.8	364
15	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
16	The Genomic and Transcriptomic Landscape of a HeLa Cell Line. G3: Genes, Genomes, Genetics, 2013, 3, 1213-1224.	0.8	355
17	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. Cancer Cell, 2013, 23, 159-170.	7.7	292
18	SeqAn An efficient, generic C++ library for sequence analysis. BMC Bioinformatics, 2008, 9, 11.	1.2	287

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19	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.	5.1	268
20	Whole-exome sequencing links caspase recruitment domainÂ11 (CARD11) inactivation to severe combined immunodeficiency. Journal of Allergy and Clinical Immunology, 2013, 131, 1376-1383.e3.	1.5	127
21	RazerSâ€"fast read mapping with sensitivity control. Genome Research, 2009, 19, 1646-1654.	2.4	125
22	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-e192.	1.7	114
23	The molecular landscape of ETMR at diagnosis and relapse. Nature, 2019, 576, 274-280.	13.7	94
24	Germline Elongator mutations in Sonic Hedgehog medulloblastoma. Nature, 2020, 580, 396-401.	13.7	94
25	Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. Nature Genetics, 2022, 54, 518-525.	9.4	92
26	Highly recurrent mutations of SGK1, DUSP2 and JUNB in nodular lymphocyte predominant Hodgkin lymphoma. Leukemia, 2016, 30, 844-853.	3.3	80
27	Impact of genomic structural variation in Drosophila melanogaster based on population-scale sequencing. Genome Research, 2013, 23, 568-579.	2.4	72
28	Identification of a genetically defined ultra-high-risk group in relapsed pediatric T-lymphoblastic leukemia. Blood Cancer Journal, 2017, 7, e523-e523.	2.8	69
29	Pediatric T-cell lymphoblastic leukemia evolves into relapse by clonal selection, acquisition of mutations and promoter hypomethylation. Haematologica, 2015, 100, 1442-1450.	1.7	65
30	A highly soluble Sleeping Beauty transposase improves control of gene insertion. Nature Biotechnology, 2019, 37, 1502-1512.	9.4	63
31	Tracy: basecalling, alignment, assembly and deconvolution of sanger chromatogram trace files. BMC Genomics, 2020, 21, 230.	1.2	63
32	The NSL complex maintains nuclear architecture stability via lamin A/C acetylation. Nature Cell Biology, 2019, 21, 1248-1260.	4.6	61
33	Alfred: interactive multi-sample BAM alignment statistics, feature counting and feature annotation for long- and short-read sequencing. Bioinformatics, 2019, 35, 2489-2491.	1.8	61
34	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. Nature Biotechnology, 2020, 38, 343-354.	9.4	59
35	Identification of cytokine-induced modulation of microRNA expression and secretion as measured by a novel microRNA specific qPCR assay. Scientific Reports, 2015, 5, 11590.	1.6	55
36	JUNB, DUSP2, SGK1, SOCS1 and CREBBP are frequently mutated in T-cell/histiocyte-rich large B-cell lymphoma. Haematologica, 2019, 104, 330-337.	1.7	45

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37	Segment-based multiple sequence alignment. Bioinformatics, 2008, 24, i187-i192.	1.8	44
38	Genomic structural variations lead to dysregulation of important coding and nonâ€coding RNA species in dilated cardiomyopathy. EMBO Molecular Medicine, 2018, 10, 107-120.	3.3	43
39	Identification of novel follicular dendritic cell sarcoma markers, FDCSP and SRGN, by whole transcriptome sequencing. Oncotarget, 2017, 8, 16463-16472.	0.8	43
40	<scp>PDX</scp> models recapitulate the genetic and epigenetic landscape of pediatric Tâ€cell leukemia. EMBO Molecular Medicine, 2018, 10, .	3.3	38
41	Neutralizing antibody response against the B.1.617.2 (delta) and the B.1.1.529 (omicron) variants after a third mRNA SARS-CoV-2 vaccine dose in kidney transplant recipients. American Journal of Transplantation, 2022, 22, 1873-1883.	2.6	37
42	A consistency-based consensus algorithm for de novo and reference-guided sequence assembly of short reads. Bioinformatics, 2009, 25, 1118-1124.	1.8	30
43	VISOR: a versatile haplotype-aware structural variant simulator for short- and long-read sequencing. Bioinformatics, 2020, 36, 1267-1269.	1.8	29
44	Genomic insights into the pathogenesis of Epsteinâ€“Barr virus-associated diffuse large B-cell lymphoma by whole-genome and targeted amplicon sequencing. Blood Cancer Journal, 2021, 11, 102.	2.8	28
45	Characterization of Two Historic Smallpox Specimens from a Czech Museum. Viruses, 2017, 9, 200.	1.5	27
46	The effects of common structural variants on 3D chromatin structure. BMC Genomics, 2020, 21, 95.	1.2	23
47	Personality similarity between teachers and their students influences teacher judgement of student achievement. Educational Psychology, 2016, 36, 863-878.	1.2	22
48	Identification of novel sequence variations in microRNAs in chronic lymphocytic leukemia. Carcinogenesis, 2014, 35, 992-1002.	1.3	18
49	MCM3APandPOMPMutations Cause a DNA-Repair and DNA-Damage-Signaling Defect in an Immunodeficient Child. Human Mutation, 2016, 37, 257-268.	1.1	18
50	Metagenomic analysis of primary colorectal carcinomas and their metastases identifies potential microbial risk factors. Molecular Oncology, 2021, 15, 3363-3384.	2.1	17
51	Accuracy of Teacher Judgments. , 2014, , 27-43.		17
52	Identification of a Ninein (NIN) mutation in a family with spondyloepimetaphyseal dysplasia with joint laxity (leptodactylic type)-like phenotype. Matrix Biology, 2013, 32, 387-392.	1.5	15
53	TRiCoLOR: tandem repeat profiling using whole-genome long-read sequencing data. GigaScience, 2020, 9, .	3.3	15
54	Fast and Adaptive Variable Order Markov Chain Construction. Lecture Notes in Computer Science, 2008, , 306-317.	1.0	15

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55	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, a002428.	0.5	13
56	Chromatin accessibility landscape of pediatric Tâ€lymphoblastic leukemia and human Tâ€cell precursors. EMBO Molecular Medicine, 2020, 12, e12104.	3.3	13
57	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, 911-927.	1.4	13
58	Potential protective role of Grainyheadâ€like genes in the development of clear cell renal cell carcinoma. Molecular Carcinogenesis, 2017, 56, 2414-2423.	1.3	11
59	Coordinated expression and genetic polymorphisms in Grainyhead-like genes in human non-melanoma skin cancers. BMC Cancer, 2018, 18, 23.	1.1	10
60	A parallel genetic algorithm to discover patterns in genetic markers that indicate predisposition to multifactorial disease. Computers in Biology and Medicine, 2008, 38, 826-836.	3.9	9
61	Constitutional PIGA mutations cause a novel subtype of hemochromatosis in patients with neurologic dysfunction. Blood, 2022, 139, 1418-1422.	0.6	8
62	Mit Wissen zu akkurateren Urteilen?. Zeitschrift Fur Entwicklungspsychologie Und Padagogische Psychologie, 2015, 47, 147-158.	0.3	4
63	Pediatric T-ALL type-1 and type-2 relapses develop along distinct pathways of clonal evolution. Leukemia, 2022, 36, 1759-1768.	3.3	4
64	Robust consensus computation. BMC Bioinformatics, 2008, 9, .	1.2	3
65	ToTem: a tool for variant calling pipeline optimization. BMC Bioinformatics, 2018, 19, 243.	1.2	2
66	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. BMC Proceedings, 2012, 6, .	1.8	1
67	Abstract 4872: ICGC PedBrain Tumor - Next-generation sequencing identifies novel subgroup-specific mutations and copy number aberrations in medulloblastoma. Cancer Research, 2012, 72, 4872-4872.	0.4	1
68	Evidence for the Association between the Intronic Haplotypes of Ionotropic Glutamate Receptors and First-Episode Schizophrenia. Journal of Personalized Medicine, 2021, 11, 1250.	1.1	1
69	EMBR-10. GENOMIC COMPLEXITY AND EVOLUTION OF EMBRYONAL TUMORS WITH MULTILAYERED ROSETTES (ETMR). Neuro-Oncology, 2018, 20, i70-i70.	0.6	0
70	MEDU-11. MOLECULAR CHARACTERIZATION OF ETMRs REVEALS A ROLE FOR R-LOOP MEDIATED CHROMOSOMAL INSTABILITY. Neuro-Oncology, 2019, 21, ii105-ii105.	0.6	0
71	Practical Multiple Sequence Alignment. , 2010, , 21-43.		0
72	Mutational Analysis of Mir-29 Family Members in Chronic Lymphocytic Leukemia. Blood, 2011, 118, 1770-1770.	0.6	0

#	Article	IF	Citations
73	Sequence Variations in miRNA Genes Are Common and May Affect Their Expression in Patients with Chronic Lymphocytic Leukemia. Blood, 2012, 120, 3895-3895.	0.6	0
74	Whole-Exome Sequencing Links CARD11 Inactivation with SCID. Blood, 2012, 120, 258-258.	0.6	0
75	Whole Exome Sequencing Identifies Novel Lyst-Missense Mutations In Incomplete Childhood Chediak-Higashi-Syndrome Presenting As Hemphagocytic Lymphohistiocytosis (HLH). Blood, 2013, 122, 3479-3479.	0.6	0
76	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.	0.6	0
77	Targeted Deep Sequencing of Genetic Alterations Identified By Whole Exome Sequencing Reveals Clonal Evolution in Pediatric T-Lymphoblastic Leukemia. Blood, 2014, 124, 491-491.	0.6	0
78	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.	0.6	0
79	Identification of an Ultra High-Risk and Targetable Molecular Signature in Relapsed Pediatric T-ALL. Blood, 2016, 128, 1084-1084.	0.6	0
80	Abstract 3172: Targeting genomic instability in embryonal tumors with multilayered rosettes (ETMR). , 2018, , .		0
81	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.	0.6	0
82	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.	0.6	0
83	MBCL-21. GERMLINE ELONGATOR MUTATIONS IN SONIC HEDGEHOG MEDULLOBLASTOMA. Neuro-Oncology, 2020, 22, iii392-iii393.	0.6	0