

Tobias Rausch

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

37,647
citations

87888

38
h-index

91884

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.	27.8	13,998
2	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
3	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. Nature, 2012, 482, 226-231.	27.8	2,129
4	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
5	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
6	DELLY: structural variant discovery by integrated paired-end and split-read analysis. Bioinformatics, 2012, 28, i333-i339.	4.1	1,785
7	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
8	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	27.8	765
9	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. Cell, 2012, 148, 59-71.	28.9	743
10	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
11	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothed Inhibition. Cancer Cell, 2014, 25, 393-405.	16.8	627
12	Assembly and diploid architecture of an individual human genome via single-molecule technologies. Nature Methods, 2015, 12, 780-786.	19.0	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.	21.4	389
14	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. Nature Communications, 2014, 5, 3934.	12.8	364
15	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
16	The Genomic and Transcriptomic Landscape of a HeLa Cell Line. G3: Genes, Genomes, Genetics, 2013, 3, 1213-1224.	1.8	355
17	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. Cancer Cell, 2013, 23, 159-170.	16.8	292
18	SeqAn An efficient, generic C++ library for sequence analysis. BMC Bioinformatics, 2008, 9, 11.	2.6	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. <i>Lancet Oncology</i> , The, 2018, 19, 785-798.	10.7	268
20	Whole-exome sequencing links caspase recruitment domain 11 (CARD11) inactivation to severe combined immunodeficiency. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, 1376-1383.e3.	2.9	127
21	Razer-Satraplatin fast read mapping with sensitivity control. <i>Genome Research</i> , 2009, 19, 1646-1654.	5.5	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. <i>Haematologica</i> , 2014, 99, e188-e192.	3.5	114
23	The molecular landscape of ETMR at diagnosis and relapse. <i>Nature</i> , 2019, 576, 274-280.	27.8	94
24	Germline Elongator mutations in Sonic Hedgehog medulloblastoma. <i>Nature</i> , 2020, 580, 396-401.	27.8	94
25	Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. <i>Nature Genetics</i> , 2022, 54, 518-525.	21.4	92
26	Highly recurrent mutations of SGK1, DUSP2 and JUNB in nodular lymphocyte predominant Hodgkin lymphoma. <i>Leukemia</i> , 2016, 30, 844-853.	7.2	80
27	Impact of genomic structural variation in <i>Drosophila melanogaster</i> based on population-scale sequencing. <i>Genome Research</i> , 2013, 23, 568-579.	5.5	72
28	Identification of a genetically defined ultra-high-risk group in relapsed pediatric T-lymphoblastic leukemia. <i>Blood Cancer Journal</i> , 2017, 7, e523-e523.	6.2	69
29	Pediatric T-cell lymphoblastic leukemia evolves into relapse by clonal selection, acquisition of mutations and promoter hypomethylation. <i>Haematologica</i> , 2015, 100, 1442-1450.	3.5	65
30	A highly soluble Sleeping Beauty transposase improves control of gene insertion. <i>Nature Biotechnology</i> , 2019, 37, 1502-1512.	17.5	63
31	Tracy: basecalling, alignment, assembly and deconvolution of sanger chromatogram trace files. <i>BMC Genomics</i> , 2020, 21, 230.	2.8	63
32	The NSL complex maintains nuclear architecture stability via lamin A/C acetylation. <i>Nature Cell Biology</i> , 2019, 21, 1248-1260.	10.3	61
33	Alfred: interactive multi-sample BAM alignment statistics, feature counting and feature annotation for long- and short-read sequencing. <i>Bioinformatics</i> , 2019, 35, 2489-2491.	4.1	61
34	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. <i>Nature Biotechnology</i> , 2020, 38, 343-354.	17.5	59
35	Identification of cytokine-induced modulation of microRNA expression and secretion as measured by a novel microRNA specific qPCR assay. <i>Scientific Reports</i> , 2015, 5, 11590.	3.3	55
36	JUNB, DUSP2, SGK1, SOCS1 and CREBBP are frequently mutated in T-cell/histiocyte-rich large B-cell lymphoma. <i>Haematologica</i> , 2019, 104, 330-337.	3.5	45

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37	Segment-based multiple sequence alignment. <i>Bioinformatics</i> , 2008, 24, i187-i192.	4.1	44
38	Genomic structural variations lead to dysregulation of important coding and non-coding RNA species in dilated cardiomyopathy. <i>EMBO Molecular Medicine</i> , 2018, 10, 107-120.	6.9	43
39	Identification of novel follicular dendritic cell sarcoma markers, FDCSP and SRGN, by whole transcriptome sequencing. <i>Oncotarget</i> , 2017, 8, 16463-16472.	1.8	43
40	<sc>PDX</sc> models recapitulate the genetic and epigenetic landscape of pediatric T-cell leukemia. <i>EMBO Molecular Medicine</i> , 2018, 10, .	6.9	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. <i>American Journal of Transplantation</i> , 2022, 22, 1873-1883.	4.7	37
42	A consistency-based consensus algorithm for <i>de novo</i> and reference-guided sequence assembly of short reads. <i>Bioinformatics</i> , 2009, 25, 1118-1124.	4.1	30
43	VISOR: a versatile haplotype-aware structural variant simulator for short- and long-read sequencing. <i>Bioinformatics</i> , 2020, 36, 1267-1269.	4.1	29
44	Genomic insights into the pathogenesis of Epstein-Barr virus-associated diffuse large B-cell lymphoma by whole-genome and targeted amplicon sequencing. <i>Blood Cancer Journal</i> , 2021, 11, 102.	6.2	28
45	Characterization of Two Historic Smallpox Specimens from a Czech Museum. <i>Viruses</i> , 2017, 9, 200.	3.3	27
46	The effects of common structural variants on 3D chromatin structure. <i>BMC Genomics</i> , 2020, 21, 95.	2.8	23
47	Personality similarity between teachers and their students influences teacher judgement of student achievement. <i>Educational Psychology</i> , 2016, 36, 863-878.	2.7	22
48	Identification of novel sequence variations in microRNAs in chronic lymphocytic leukemia. <i>Carcinogenesis</i> , 2014, 35, 992-1002.	2.8	18
49	<i>MCM3AP</i> and <i>POMP</i> Mutations Cause a DNA-Repair and DNA-Damage-Signaling Defect in an Immunodeficient Child. <i>Human Mutation</i> , 2016, 37, 257-268.	2.5	18
50	Metagenomic analysis of primary colorectal carcinomas and their metastases identifies potential microbial risk factors. <i>Molecular Oncology</i> , 2021, 15, 3363-3384.	4.6	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. <i>Matrix Biology</i> , 2013, 32, 387-392.	3.6	15
53	TRiCoLoR: tandem repeat profiling using whole-genome long-read sequencing data. <i>GigaScience</i> , 2020, 9, .	6.4	15
54	Fast and Adaptive Variable Order Markov Chain Construction. <i>Lecture Notes in Computer Science</i> , 2008, , 306-317.	1.3	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. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a002428.	1.2	13
56	Chromatin accessibility landscape of pediatric T-lymphoblastic leukemia and human T-cell precursors. <i>EMBO Molecular Medicine</i> , 2020, 12, e12104.	6.9	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. <i>Aging</i> , 2015, 7, 911-927.	3.1	13
58	Potential protective role of Grainyhead-like genes in the development of clear cell renal cell carcinoma. <i>Molecular Carcinogenesis</i> , 2017, 56, 2414-2423.	2.7	11
59	Coordinated expression and genetic polymorphisms in Grainyhead-like genes in human non-melanoma skin cancers. <i>BMC Cancer</i> , 2018, 18, 23.	2.6	10
60	A parallel genetic algorithm to discover patterns in genetic markers that indicate predisposition to multifactorial disease. <i>Computers in Biology and Medicine</i> , 2008, 38, 826-836.	7.0	9
61	Constitutional PIGA mutations cause a novel subtype of hemochromatosis in patients with neurologic dysfunction. <i>Blood</i> , 2022, 139, 1418-1422.	1.4	8
62	Mit Wissen zu akkurateren Urteilen?. <i>Zeitschrift Fur Entwicklungspsychologie Und Padagogische Psychologie</i> , 2015, 47, 147-158.	1.1	4
63	Pediatric T-ALL type-1 and type-2 relapses develop along distinct pathways of clonal evolution. <i>Leukemia</i> , 2022, 36, 1759-1768.	7.2	4
64	Robust consensus computation. <i>BMC Bioinformatics</i> , 2008, 9, .	2.6	3
65	ToTem: a tool for variant calling pipeline optimization. <i>BMC Bioinformatics</i> , 2018, 19, 243.	2.6	2
66	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. <i>BMC Proceedings</i> , 2012, 6, .	1.6	1
67	Abstract 4872: ICGC PedBrain Tumor - Next-generation sequencing identifies novel subgroup-specific mutations and copy number aberrations in medulloblastoma. <i>Cancer Research</i> , 2012, 72, 4872-4872.	0.9	1
68	Evidence for the Association between the Intronic Haplotypes of Ionotropic Glutamate Receptors and First-Episode Schizophrenia. <i>Journal of Personalized Medicine</i> , 2021, 11, 1250.	2.5	1
69	EMBR-10. GENOMIC COMPLEXITY AND EVOLUTION OF EMBRYONAL TUMORS WITH MULTILAYERED ROSETTES (ETMR). <i>Neuro-Oncology</i> , 2018, 20, i70-i70.	1.2	0
70	MEDU-11. MOLECULAR CHARACTERIZATION OF ETMRs REVEALS A ROLE FOR R-LOOP MEDIATED CHROMOSOMAL INSTABILITY. <i>Neuro-Oncology</i> , 2019, 21, ii105-ii105.	1.2	0
71	Practical Multiple Sequence Alignment. , 2010, , 21-43.		0
72	Mutational Analysis of Mir-29 Family Members in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2011, 118, 1770-1770.	1.4	0

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73	Sequence Variations in miRNA Genes Are Common and May Affect Their Expression in Patients with Chronic Lymphocytic Leukemia. <i>Blood</i> , 2012, 120, 3895-3895.	1.4	0
74	Whole-Exome Sequencing Links CARD11 Inactivation with SCID. <i>Blood</i> , 2012, 120, 258-258.	1.4	0
75	Whole Exome Sequencing Identifies Novel Lyst-Missense Mutations In Incomplete Childhood Chediak-Higashi-Syndrome Presenting As Hemphagocytic Lymphohistiocytosis (HLH). <i>Blood</i> , 2013, 122, 3479-3479.	1.4	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. <i>Blood</i> , 2013, 122, 228-228.	1.4	0
77	Targeted Deep Sequencing of Genetic Alterations Identified By Whole Exome Sequencing Reveals Clonal Evolution in Pediatric T-Lymphoblastic Leukemia. <i>Blood</i> , 2014, 124, 491-491.	1.4	0
78	Gene Panel Sequencing of Primary and Relapsed Pediatric T-ALL Shows That Relapse-Specific Mutations Are Diverse and Mostly Non-Recurrent. <i>Blood</i> , 2015, 126, 1428-1428.	1.4	0
79	Identification of an Ultra High-Risk and Targetable Molecular Signature in Relapsed Pediatric T-ALL. <i>Blood</i> , 2016, 128, 1084-1084.	1.4	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. <i>Blood</i> , 2018, 132, 2826-2826.	1.4	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. <i>Blood</i> , 2018, 132, 1545-1545.	1.4	0
83	MBCL-21. GERMLINE ELONGATOR MUTATIONS IN SONIC HEDGEHOG MEDULLOBLASTOMA. <i>Neuro-Oncology</i> , 2020, 22, iii392-iii393.	1.2	0