

# Jörg Hackermüller

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

12,100  
citations

172207

29  
h-index

133063

59  
g-index

66  
all docs

66  
docs citations

66  
times ranked

19134  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
2	RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. <i>Science</i> , 2007, 316, 1484-1488.	6.0	2,250
3	The primary transcriptome of the major human pathogen <i>Helicobacter pylori</i> . <i>Nature</i> , 2010, 464, 250-255.	13.7	1,115
4	Interleukin-6-dependent survival of multiple myeloma cells involves the Stat3-mediated induction of microRNA-21 through a highly conserved enhancer. <i>Blood</i> , 2007, 110, 1330-1333.	0.6	597
5	Fast Mapping of Short Sequences with Mismatches, Insertions and Deletions Using Index Structures. <i>PLoS Computational Biology</i> , 2009, 5, e1000502.	1.5	487
6	Thermodynamics of RNA-RNA binding. <i>Bioinformatics</i> , 2006, 22, 1177-1182.	1.8	338
7	A multi-split mapping algorithm for circular RNA, splicing, trans-splicing and fusion detection. <i>Genome Biology</i> , 2014, 15, R34.	13.9	242
8	MiR-130a, miR-203 and miR-205 jointly repress key oncogenic pathways and are downregulated in prostate carcinoma. <i>Oncogene</i> , 2013, 32, 277-285.	2.6	198
9	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007, 17, 852-864.	2.4	150
10	From the exposome to mechanistic understanding of chemical-induced adverse effects. <i>Environment International</i> , 2017, 99, 97-106.	4.8	146
11	Prospects and challenges of multi-omics data integration in toxicology. <i>Archives of Toxicology</i> , 2020, 94, 371-388.	1.9	142
12	Evolution of Vault RNAs. <i>Molecular Biology and Evolution</i> , 2009, 26, 1975-1991.	3.5	130
13	HLA-DRB1*0401 and HLA-DRB1*0408 Are Strongly Associated with the Development of Antibodies against Interferon- $\beta$ Therapy in Multiple Sclerosis. <i>American Journal of Human Genetics</i> , 2008, 83, 219-227.	2.6	114
14	mRNA Openers and Closers: Modulating AU-Rich Element-Controlled mRNA Stability by a Molecular Switch in mRNA Secondary Structure. <i>ChemBioChem</i> , 2004, 5, 1432-1447.	1.3	112
15	Applying 'omics technologies in chemicals risk assessment: Report of an ECETOC workshop. <i>Regulatory Toxicology and Pharmacology</i> , 2017, 91, S3-S13.	1.3	102
16	Detection of small RNAs in <i>Pseudomonas aeruginosa</i> by RNomics and structure-based bioinformatic tools. <i>Microbiology (United Kingdom)</i> , 2008, 154, 3175-3187.	0.7	99
17	Dissecting the genetics of the human transcriptome identifies novel trait-related <i>trans</i> -eQTLs and corroborates the regulatory relevance of non-protein coding loci. <i>Human Molecular Genetics</i> , 2015, 24, 4746-4763.	1.4	94
18	The challenge of the application of 'omics technologies in chemicals risk assessment: Background and outlook. <i>Regulatory Toxicology and Pharmacology</i> , 2017, 91, S14-S26.	1.3	92

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19	Maternal phthalate exposure promotes allergic airway inflammation over 2 generations through epigenetic modifications. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 741-753.	1.5	92
20	CD31, EDNRB and TSPAN7 are promising prognostic markers in clear cell renal cell carcinoma revealed by genome-wide expression analyses of primary tumors and metastases. <i>International Journal of Cancer</i> , 2012, 131, E693-704.	2.3	72
21	multiGSEA: a GSEA-based pathway enrichment analysis for multi-omics data. <i>BMC Bioinformatics</i> , 2020, 21, 561.	1.2	70
22	The effect of RNA secondary structures on RNA-ligand binding and the modifier RNA mechanism: a quantitative model. <i>Gene</i> , 2005, 345, 3-12.	1.0	49
23	RNAs everywhere: genome-wide annotation of structured RNAs. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007, 308B, 1-25.	0.6	46
24	Roquin targets mRNAs in a 3' UTR-specific manner by different modes of regulation. <i>Nature Communications</i> , 2018, 9, 3810.	5.8	40
25	Computational RNomics of Drosophilids. <i>BMC Genomics</i> , 2007, 8, 406.	1.2	38
26	Cell cycle, oncogenic and tumor suppressor pathways regulate numerous long and macro non-protein-coding RNAs. <i>Genome Biology</i> , 2014, 15, R48.	13.9	37
27	A generic Transcriptomics Reporting Framework (TRF) for omics data processing and analysis. <i>Regulatory Toxicology and Pharmacology</i> , 2017, 91, S36-S45.	1.3	35
28	Long Non-Coding RNAs Differentially Expressed between Normal versus Primary Breast Tumor Tissues Disclose Converse Changes to Breast Cancer-Related Protein-Coding Genes. <i>PLoS ONE</i> , 2014, 9, e106076.	1.1	35
29	Framework for the quality assurance of omics technologies considering GLP requirements. <i>Regulatory Toxicology and Pharmacology</i> , 2017, 91, S27-S35.	1.3	32
30	A first Glimpse at the genome of the Baikalian amphipod <i>Eulimnogammarus verrucosus</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2014, 322, 177-189.	0.6	27
31	Binding of NUFIP2 to Roquin promotes recognition and regulation of ICOS mRNA. <i>Nature Communications</i> , 2018, 9, 299.	5.8	27
32	STAT3-induced long noncoding RNAs in multiple myeloma cells display different properties in cancer. <i>Scientific Reports</i> , 2017, 7, 7976.	1.6	26
33	The EcoExposome Concept: Supporting an Integrated Assessment of Mixtures of Environmental Chemicals. <i>Environmental Toxicology and Chemistry</i> , 2022, 41, 30-45.	2.2	25
34	Computational discovery of human coding and non-coding transcripts with conserved splice sites. <i>Bioinformatics</i> , 2011, 27, 1894-1900.	1.8	24
35	Unravelling the chemical exposome in cohort studies: routes explored and steps to become comprehensive. <i>Environmental Sciences Europe</i> , 2021, 33, 17.	2.6	22
36	Generation of IL-8 and IL-9 Producing CD4+T Cells Is Affected by Th17 Polarizing Conditions and AHR Ligands. <i>Mediators of Inflammation</i> , 2014, 2014, 1-14.	1.4	21

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37	The complete genome of the tetrachloroethene-respiring Epsilonproteobacterium <i>Sulfurospirillum halorespirans</i> . <i>Journal of Biotechnology</i> , 2017, 255, 33-36.	1.9	20
38	A translational silencing function of MCP1/Regnase-1 specified by the target site context. <i>Nucleic Acids Research</i> , 2018, 46, 4256-4270.	6.5	20
39	NcDNAAlign: Plausible multiple alignments of non-protein-coding genomic sequences. <i>Genomics</i> , 2008, 92, 65-74.	1.3	18
40	Comparison between transcriptomic responses to short-term stress exposures of a common Holarctic and endemic Lake Baikal amphipods. <i>BMC Genomics</i> , 2019, 20, 712.	1.2	17
41	Specific induction of the unique GPR15 expression in heterogeneous blood lymphocytes by tobacco smoking. <i>Biomarkers</i> , 2019, 24, 217-224.	0.9	16
42	The Role of lncRNAs TAPIR-1 and -2 as Diagnostic Markers and Potential Therapeutic Targets in Prostate Cancer. <i>Cancers</i> , 2020, 12, 1122.	1.7	15
43	ProstaTrend – A Multivariable Prognostic RNA Expression Score for Aggressive Prostate Cancer. <i>European Urology</i> , 2020, 78, 452-459.	0.9	15
44	Comparison of quantitation methods in proteomics to define relevant toxicological information on AhR activation of HepG2 cells by BaP. <i>Toxicology</i> , 2021, 448, 152652.	2.0	15
45	uap: reproducible and robust HTS data analysis. <i>BMC Bioinformatics</i> , 2019, 20, 664.	1.2	14
46	Mouse Retinal Organoid Growth and Maintenance in Longer-Term Culture. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 645704.	1.8	13
47	A Multi-Omics Analysis of Mucosal-Associated-Invariant T Cells Reveals Key Drivers of Distinct Modes of Activation. <i>Frontiers in Immunology</i> , 2021, 12, 616967.	2.2	13
48	Detection of differentially expressed segments in tiling array data. <i>Bioinformatics</i> , 2012, 28, 1471-1479.	1.8	11
49	DUPLICATED RNA GENES IN TELEOST FISH GENOMES. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 1157-1175.	0.3	10
50	Alzheimer-related genes show accelerated evolution. <i>Molecular Psychiatry</i> , 2021, 26, 5790-5796.	4.1	10
51	Complete genome sequence of <i>Pseudoalteromonas</i> phage vB_PspS-H40/1 (formerly H40/1) that infects <i>Pseudoalteromonas</i> sp. strain H40 and is used as biological tracer in hydrological transport studies. <i>Standards in Genomic Sciences</i> , 2017, 12, 20.	1.5	8
52	The EU chemicals strategy for sustainability: an opportunity to develop new approaches for hazard and risk assessment. <i>Archives of Toxicology</i> , 2022, 96, 2381-2386.	1.9	7
53	Bioinformatics for RNomics. <i>Methods in Molecular Biology</i> , 2011, 719, 299-330.	0.4	2
54	CEM-Designer: Design of custom expression microarrays in the post-ENCODE Era. <i>Journal of Biotechnology</i> , 2014, 189, 154-156.	1.9	2

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55	Complete genome sequence of Pseudoalteromonas virus vB_PspP-H6/1 that infects Pseudoalteromonas sp. strain H6. <i>Marine Genomics</i> , 2019, 47, 100667.	0.4	2
56	Transcriptome-level effects of the model organic pollutant phenanthrene and its solvent acetone in three amphipod species. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 33, 100630.	0.4	2
57	Requirements and Perspectives for Integrating Metabolomics with other Omics Data. <i>Current Metabolomics</i> , 2012, 1, 15-27.	0.5	2
58	Requirements and Perspectives for Integrating Metabolomics with other Omics Data. <i>Current Metabolomics</i> , 2012, 1, 15-27.	0.5	1
59	HLA-DRB10401 and HLA-DRB10408 Are Strongly Associated with the Development of Antibodies against Interferon- $\beta$ Therapy in Multiple Sclerosis. <i>American Journal of Human Genetics</i> , 2008, 83, 541.	2.6	0
60	MPO2-03 NEXT-GENERATION SEQUENCING REVEALS TRANSCRIPT CLUSTERS WITH PROGNOSTIC POTENTIAL FOR PROSTATE CANCER. <i>Journal of Urology</i> , 2016, 195, .	0.2	0