Jörg Hackermüller

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
2	RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. Science, 2007, 316, 1484-1488.	12.6	2,250
3	The primary transcriptome of the major human pathogen Helicobacter pylori. Nature, 2010, 464, 250-255.	27.8	1,115
4	Interleukin-6–dependent survival of multiple myeloma cells involves the Stat3-mediated induction of microRNA-21 through a highly conserved enhancer. Blood, 2007, 110, 1330-1333.	1.4	597
5	Fast Mapping of Short Sequences with Mismatches, Insertions and Deletions Using Index Structures. PLoS Computational Biology, 2009, 5, e1000502.	3.2	487
6	Thermodynamics of RNA-RNA binding. Bioinformatics, 2006, 22, 1177-1182.	4.1	338
7	A multi-split mapping algorithm for circular RNA, splicing, trans-splicing and fusion detection. Genome Biology, 2014, 15, R34.	9.6	242
8	MiR-130a, miR-203 and miR-205 jointly repress key oncogenic pathways and are downregulated in prostate carcinoma. Oncogene, 2013, 32, 277-285.	5.9	198
9	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	5.5	150
10	From the exposome to mechanistic understanding of chemical-induced adverse effects. Environment International, 2017, 99, 97-106.	10.0	146
11	Prospects and challenges of multi-omics data integration in toxicology. Archives of Toxicology, 2020, 94, 371-388.	4.2	142
12	Evolution of Vault RNAs. Molecular Biology and Evolution, 2009, 26, 1975-1991.	8.9	130
13	HLA-DRB1â^—0401 and HLA-DRB1â^—0408 Are Strongly Associated with the Development of Antibodies against Interferon-β Therapy in Multiple Sclerosis. American Journal of Human Genetics, 2008, 83, 219-227.	6.2	114
14	mRNA Openers and Closers: Modulating AU-Rich Element-Controlled mRNA Stability by a Molecular Switch in mRNA Secondary Structure. ChemBioChem, 2004, 5, 1432-1447.	2.6	112
15	Applying 'omics technologies in chemicals risk assessment: Report of an ECETOC workshop. Regulatory Toxicology and Pharmacology, 2017, 91, S3-S13.	2.7	102
16	Detection of small RNAs in Pseudomonas aeruginosa by RNomics and structure-based bioinformatic tools. Microbiology (United Kingdom), 2008, 154, 3175-3187.	1.8	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. Human Molecular Genetics, 2015, 24, 4746-4763.	2.9	94
18	The challenge of the application of 'omics technologies in chemicals risk assessment: Background and outlook. Regulatory Toxicology and Pharmacology, 2017, 91, S14-S26.	2.7	92

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19	Maternal phthalate exposure promotes allergic airway inflammation over 2 generations through epigenetic modifications. Journal of Allergy and Clinical Immunology, 2018, 141, 741-753.	2.9	92
20	CD31, EDNRB and TSPAN7 are promising prognostic markers in clearâ€cell renal cell carcinoma revealed by genomeâ€wide expression analyses of primary tumors and metastases. International Journal of Cancer, 2012, 131, E693-704.	5.1	72
21	multiGSEA: a GSEA-based pathway enrichment analysis for multi-omics data. BMC Bioinformatics, 2020, 21, 561.	2.6	70
22	The effect of RNA secondary structures on RNA-ligand binding and the modifier RNA mechanism: a quantitative model. Gene, 2005, 345, 3-12.	2.2	49
23	RNAs everywhere: genome-wide annotation of structured RNAs. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 1-25.	1.3	46
24	Roquin targets mRNAs in a 3′-UTR-specific manner by different modes of regulation. Nature Communications, 2018, 9, 3810.	12.8	40
25	Computational RNomics of Drosophilids. BMC Genomics, 2007, 8, 406.	2.8	38
26	Cell cycle, oncogenic and tumor suppressor pathways regulate numerous long and macro non-protein-coding RNAs. Genome Biology, 2014, 15, R48.	9.6	37
27	A generic Transcriptomics Reporting Framework (TRF) for â€~omics data processing and analysis. Regulatory Toxicology and Pharmacology, 2017, 91, S36-S45.	2.7	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. PLoS ONE, 2014, 9, e106076.	2.5	35
29	Framework for the quality assurance of 'omics technologies considering GLP requirements. Regulatory Toxicology and Pharmacology, 2017, 91, S27-S35.	2.7	32
30	A first Glimpse at the genome of the Baikalian amphipod <i>Eulimnogammarus verrucosus</i> . Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2014, 322, 177-189.	1.3	27
31	Binding of NUFIP2 to Roquin promotes recognition and regulation of ICOS mRNA. Nature Communications, 2018, 9, 299.	12.8	27
32	STAT3-induced long noncoding RNAs in multiple myeloma cells display different properties in cancer. Scientific Reports, 2017, 7, 7976.	3.3	26
33	The Ecoâ€Exposome Concept: Supporting an Integrated Assessment of Mixtures of Environmental Chemicals. Environmental Toxicology and Chemistry, 2022, 41, 30-45.	4.3	25
34	Computational discovery of human coding and non-coding transcripts with conserved splice sites. Bioinformatics, 2011, 27, 1894-1900.	4.1	24
35	Unravelling the chemical exposome in cohort studies: routes explored and steps to become comprehensive. Environmental Sciences Europe, 2021, 33, 17.	5.5	22
36	Generation of IL-8 and IL-9 Producing CD4+T Cells Is Affected by Th17 Polarizing Conditions and AHR Ligands. Mediators of Inflammation, 2014, 2014, 1-14.	3.0	21

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37	The complete genome of the tetrachloroethene-respiring Epsilonproteobacterium Sulfurospirillum halorespirans. Journal of Biotechnology, 2017, 255, 33-36.	3.8	20
38	A translational silencing function of MCPIP1/Regnase-1 specified by the target site context. Nucleic Acids Research, 2018, 46, 4256-4270.	14.5	20
39	NcDNAlign: Plausible multiple alignments of non-protein-coding genomic sequences. Genomics, 2008, 92, 65-74.	2.9	18
40	Comparison between transcriptomic responses to short-term stress exposures of a common Holarctic and endemic Lake Baikal amphipods. BMC Genomics, 2019, 20, 712.	2.8	17
41	Specific induction of the unique GPR15 expression in heterogeneous blood lymphocytes by tobacco smoking. Biomarkers, 2019, 24, 217-224.	1.9	16
42	The Role of IncRNAs TAPIR-1 and -2 as Diagnostic Markers and Potential Therapeutic Targets in Prostate Cancers, 2020, 12, 1122.	3.7	15
43	ProstaTrend—A Multivariable Prognostic RNA Expression Score for Aggressive Prostate Cancer. European Urology, 2020, 78, 452-459.	1.9	15
44	Comparison of quantitation methods in proteomics to define relevant toxicological information on AhR activation of HepG2 cells by BaP. Toxicology, 2021, 448, 152652.	4.2	15
45	uap: reproducible and robust HTS data analysis. BMC Bioinformatics, 2019, 20, 664.	2.6	14
46	Mouse Retinal Organoid Growth and Maintenance in Longer-Term Culture. Frontiers in Cell and Developmental Biology, 2021, 9, 645704.	3.7	13
47	A Multi-Omics Analysis of Mucosal-Associated-Invariant T Cells Reveals Key Drivers of Distinct Modes of Activation. Frontiers in Immunology, 2021, 12, 616967.	4.8	13
48	Detection of differentially expressed segments in tiling array data. Bioinformatics, 2012, 28, 1471-1479.	4.1	11
49	DUPLICATED RNA GENES IN TELEOST FISH GENOMES. Journal of Bioinformatics and Computational Biology, 2008, 06, 1157-1175.	0.8	10
50	Alzheimer-related genes show accelerated evolution. Molecular Psychiatry, 2021, 26, 5790-5796.	7.9	10
51	Complete genome sequence of Pseudoalteromonas phage vB_PspS-H40/1 (formerly H40/1) that infects Pseudoalteromonas sp. strain H40 and is used as biological tracer in hydrological transport studies. Standards in Genomic Sciences, 2017, 12, 20.	1.5	8
52	The EU chemicals strategy for sustainability: an opportunity to develop new approaches for hazard and risk assessment. Archives of Toxicology, 2022, 96, 2381-2386.	4.2	7
53	Bioinformatics for RNomics. Methods in Molecular Biology, 2011, 719, 299-330.	0.9	2
54	CEM-Designer: Design of custom expression microarrays in the post-ENCODE Era. Journal of Biotechnology, 2014, 189, 154-156.	3.8	2

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55	Complete genome sequence of Pseudoalteromonas virus vB_PspP-H6/1 that infects Pseudoalteromonas sp. strain H6. Marine Genomics, 2019, 47, 100667.	1.1	2
56	Transcriptome-level effects of the model organic pollutant phenanthrene and its solvent acetone in three amphipod species. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2020, 33, 100630.	1.0	2
57	Requirements and Perspectives for Integrating Metabolomics with other Omics Data. Current Metabolomics, 2012, 1, 15-27.	0.5	2
58	Requirements and Perspectives for Integrating Metabolomics with other Omics Data. Current Metabolomics, 2012, 1, 15-27.	0.5	1
59	HLA-DRB10401 and HLA-DRB10408 Are Strongly Associated with the Development of Antibodies against Interferon-β Therapy in Multiple Sclerosis. American Journal of Human Genetics, 2008, 83, 541.	6.2	0
60	MP02-03 NEXT-GENERATION SEQUENCING REVEALS TRANSCRIPT CLUSTERS WITH PROGNOSTIC POTENTIAL FOR PROSTATE CANCER. Journal of Urology, 2016, 195, .	0.4	0