# Jörg Hackermüller

## List of Publications by Year
in descending order

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|---|---|---|---|
| 60<br>papers | 12,100<br>citations | 172207<br>29<br>h-index | 133063<br>59<br>g-index |
| 66<br>all docs | 66<br>docs citations | 66<br>times ranked | 19134<br>citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | The Eco‑Exposome Concept: Supporting an Integrated Assessment of Mixtures of Environmental Chemicals. Environmental Toxicology and Chemistry, 2022, 41, 30-45. | 2.2 | 25 |
| 2 | The EU chemicals strategy for sustainability: an opportunity to develop new approaches for hazard and risk assessment. Archives of Toxicology, 2022, 96, 2381-2386. | 1.9 | 7 |
| 3 | Alzheimer-related genes show accelerated evolution. Molecular Psychiatry, 2021, 26, 5790-5796. | 4.1 | 10 |
| 4 | Comparison of quantitation methods in proteomics to define relevant toxicological information on AhR activation of HepG2 cells by BaP. Toxicology, 2021, 448, 152652. | 2.0 | 15 |
| 5 | Unravelling the chemical exposome in cohort studies: routes explored and steps to become comprehensive. Environmental Sciences Europe, 2021, 33, 17. | 2.6 | 22 |
| 6 | Mouse Retinal Organoid Growth and Maintenance in Longer-Term Culture. Frontiers in Cell and Developmental Biology, 2021, 9, 645704. | 1.8 | 13 |
| 7 | A Multi-Omics Analysis of Mucosal-Associated-Invariant T Cells Reveals Key Drivers of Distinct Modes of Activation. Frontiers in Immunology, 2021, 12, 616967. | 2.2 | 13 |
| 8 | 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. | 0.4 | 2 |
| 9 | multiGSEA: a GSEA-based pathway enrichment analysis for multi-omics data. BMC Bioinformatics, 2020, 21, 561. | 1.2 | 70 |
| 10 | The Role of lncRNAs TAPIR-1 and -2 as Diagnostic Markers and Potential Therapeutic Targets in Prostate Cancer. Cancers, 2020, 12, 1122. | 1.7 | 15 |
| 11 | ProstaTrend—A Multivariable Prognostic RNA Expression Score for Aggressive Prostate Cancer. European Urology, 2020, 78, 452-459. | 0.9 | 15 |
| 12 | Prospects and challenges of multi-omics data integration in toxicology. Archives of Toxicology, 2020, 94, 371-388. | 1.9 | 142 |
| 13 | Comparison between transcriptomic responses to short-term stress exposures of a common Holarctic and endemic Lake Baikal amphipods. BMC Genomics, 2019, 20, 712. | 1.2 | 17 |
| 14 | Complete genome sequence of Pseudoalteromonas virus vB_PspP-H6/1 that infects Pseudoalteromonas sp. strain H6. Marine Genomics, 2019, 47, 100667. | 0.4 | 2 |
| 15 | uap: reproducible and robust HTS data analysis. BMC Bioinformatics, 2019, 20, 664. | 1.2 | 14 |
| 16 | Specific induction of the unique GPR15 expression in heterogeneous blood lymphocytes by tobacco smoking. Biomarkers, 2019, 24, 217-224. | 0.9 | 16 |
| 17 | A translational silencing function of MCPIP1/Regnase-1 specified by the target site context. Nucleic Acids Research, 2018, 46, 4256-4270. | 6.5 | 20 |
| 18 | Binding of NUFIP2 to Roquin promotes recognition and regulation of ICOS mRNA. Nature Communications, 2018, 9, 299. | 5.8 | 27 |

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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. | 1.5 | 92 |
| 20 | Roquin targets mRNAs in a 3â€²-UTR-specific manner by different modes of regulation. Nature Communications, 2018, 9, 3810. | 5.8 | 40 |
| 21 | From the exposome to mechanistic understanding of chemical-induced adverse effects. Environment International, 2017, 99, 97-106. | 4.8 | 146 |
| 22 | The challenge of the application of 'omics technologies in chemicals risk assessment: Background and outlook. Regulatory Toxicology and Pharmacology, 2017, 91, S14-S26. | 1.3 | 92 |
| 23 | Applying 'omics technologies in chemicals risk assessment: Report of an ECETOC workshop. Regulatory Toxicology and Pharmacology, 2017, 91, S3-S13. | 1.3 | 102 |
| 24 | Framework for the quality assurance of â€™omics technologies considering GLP requirements. Regulatory Toxicology and Pharmacology, 2017, 91, S27-S35. | 1.3 | 32 |
| 25 | STAT3-induced long noncoding RNAs in multiple myeloma cells display different properties in cancer. Scientific Reports, 2017, 7, 7976. | 1.6 | 26 |
| 26 | A generic Transcriptomics Reporting Framework (TRF) for â€˜omics data processing and analysis. Regulatory Toxicology and Pharmacology, 2017, 91, S36-S45. | 1.3 | 35 |
| 27 | The complete genome of the tetrachloroethene-respiring Epsilonproteobacterium Sulfurospirillum halorespirans. Journal of Biotechnology, 2017, 255, 33-36. | 1.9 | 20 |
| 28 | 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 |
| 29 | MP02-03 NEXT-GENERATION SEQUENCING REVEALS TRANSCRIPT CLUSTERS WITH PROGNOSTIC POTENTIAL FOR PROSTATE CANCER. Journal of Urology, 2016, 195, . | 0.2 | 0 |
| 30 | Dissecting the genetics of the human transcriptome identifies novel trait-related *trans*-eQTLs and corroborates the regulatory relevance of non-protein coding loci. Human Molecular Genetics, 2015, 24, 4746-4763. | 1.4 | 94 |
| 31 | 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. | 1.4 | 21 |
| 32 | Cell cycle, oncogenic and tumor suppressor pathways regulate numerous long and macro non-protein-coding RNAs. Genome Biology, 2014, 15, R48. | 13.9 | 37 |
| 33 | A first Glimpse at the genome of the Baikalian amphipod *Eulimnogammarus verrucosus*. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2014, 322, 177-189. | 0.6 | 27 |
| 34 | CEM-Designer: Design of custom expression microarrays in the post-ENCODE Era. Journal of Biotechnology, 2014, 189, 154-156. | 1.9 | 2 |
| 35 | A multi-split mapping algorithm for circular RNA, splicing, trans-splicing and fusion detection. Genome Biology, 2014, 15, R34. | 13.9 | 242 |
| 36 | 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. | 1.1 | 35 |

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|---|---------|-----|-----------|
| 37 | MiR-130a, miR-203 and miR-205 jointly repress key oncogenic pathways and are downregulated in prostate carcinoma. Oncogene, 2013, 32, 277-285. | 2.6 | 198 |
| 38 | Detection of differentially expressed segments in tiling array data. Bioinformatics, 2012, 28, 1471-1479. | 1.8 | 11 |
| 39 | Requirements and Perspectives for Integrating Metabolomics with other Omics Data. Current Metabolomics, 2012, 1, 15-27. | 0.5 | 1 |
| 40 | 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. International Journal of Cancer, 2012, 131, E693-704. | 2.3 | 72 |
| 41 | Requirements and Perspectives for Integrating Metabolomics with other Omics Data. Current Metabolomics, 2012, 1, 15-27. | 0.5 | 2 |
| 42 | Bioinformatics for RNomics. Methods in Molecular Biology, 2011, 719, 299-330. | 0.4 | 2 |
| 43 | Computational discovery of human coding and non-coding transcripts with conserved splice sites. Bioinformatics, 2011, 27, 1894-1900. | 1.8 | 24 |
| 44 | The primary transcriptome of the major human pathogen Helicobacter pylori. Nature, 2010, 464, 250-255. | 13.7 | 1,115 |
| 45 | Fast Mapping of Short Sequences with Mismatches, Insertions and Deletions Using Index Structures. PLoS Computational Biology, 2009, 5, e1000502. | 1.5 | 487 |
| 46 | Evolution of Vault RNAs. Molecular Biology and Evolution, 2009, 26, 1975-1991. | 3.5 | 130 |
| 47 | HLA-DRB1ˆ—0401 and HLA-DRB1ˆ—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. | 2.6 | 114 |
| 48 | 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. | 2.6 | 0 |
| 49 | DUPLICATED RNA GENES IN TELEOST FISH GENOMES. Journal of Bioinformatics and Computational Biology, 2008, 06, 1157-1175. | 0.3 | 10 |
| 50 | NcDNAlign: Plausible multiple alignments of non-protein-coding genomic sequences. Genomics, 2008, 92, 65-74. | 1.3 | 18 |
| 51 | Detection of small RNAs in Pseudomonas aeruginosa by RNomics and structure-based bioinformatic tools. Microbiology (United Kingdom), 2008, 154, 3175-3187. | 0.7 | 99 |
| 52 | 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. | 0.6 | 597 |
| 53 | Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864. | 2.4 | 150 |
| 54 | RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. Science, 2007, 316, 1484-1488. | 6.0 | 2,250 |

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|---|---------|----|-----------|
| 55 | RNAs everywhere: genome-wide annotation of structured RNAs. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 1-25. | 0.6 | 46 |
| 56 | Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816. | 13.7 | 4,709 |
| 57 | Computational RNomics of Drosophilids. BMC Genomics, 2007, 8, 406. | 1.2 | 38 |
| 58 | Thermodynamics of RNA-RNA binding. Bioinformatics, 2006, 22, 1177-1182. | 1.8 | 338 |
| 59 | The effect of RNA secondary structures on RNA-ligand binding and the modifier RNA mechanism: a quantitative model. Gene, 2005, 345, 3-12. | 1.0 | 49 |
| 60 | mRNA Openers and Closers: Modulating AU-Rich Element-Controlled mRNA Stability by a Molecular Switch in mRNA Secondary Structure. ChemBioChem, 2004, 5, 1432-1447. | 1.3 | 112 |