

Thomas Lengauer

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

7,300
citations

218592

26
h-index

95218

68
g-index

79
all docs

79
docs citations

79
times ranked

17012
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Rhinovirus prevalence as indicator for efficacy of measures against SARS-CoV-2. BMC Public Health, 2021, 21, 1178. | 1.2 | 13 |
| 2 | Identification of tissue-specific and common methylation quantitative trait loci in healthy individuals using MAGAR. Epigenetics and Chromatin, 2021, 14, 44. | 1.8 | 3 |
| 3 | Reference-free deconvolution, visualization and interpretation of complex DNA methylation data using DecompPipeline, MeDeCom and FactorViz. Nature Protocols, 2020, 15, 3240-3263. | 5.5 | 19 |
| 4 | Statistical Data Analysis in the Era of Big Data. Chemie-Ingenieur-Technik, 2020, 92, 831-841. | 0.4 | 6 |
| 5 | Quantitative comparison of within-sample heterogeneity scores for DNA methylation data. Nucleic Acids Research, 2020, 48, e46-e46. | 6.5 | 45 |
| 6 | Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. Nucleic Acids Research, 2019, 47, 10580-10596. | 6.5 | 31 |
| 7 | Near-Neighbor Interactions in the NS3-4A Protease of HCV Impact Replicative Fitness of Drug-Resistant Viral Variants. Journal of Molecular Biology, 2019, 431, 2354-2368. | 2.0 | 3 |
| 8 | Relative Principal Components Analysis: Application to Analyzing Biomolecular Conformational Changes. Journal of Chemical Theory and Computation, 2019, 15, 2166-2178. | 2.3 | 13 |
| 9 | RnBeads 2.0: comprehensive analysis of DNA methylation data. Genome Biology, 2019, 20, 55. | 3.8 | 223 |
| 10 | geno2pheno[ngs-freq]: a genotypic interpretation system for identifying viral drug resistance using next-generation sequencing data. Nucleic Acids Research, 2018, 46, W271-W277. | 6.5 | 37 |
| 11 | Exposure to the gut microbiota drives distinct methylome and transcriptome changes in intestinal epithelial cells during postnatal development. Genome Medicine, 2018, 10, 27. | 3.6 | 117 |
| 12 | Integrative analysis of single-cell expression data reveals distinct regulatory states in bidirectional promoters. Epigenetics and Chromatin, 2018, 11, 66. | 1.8 | 6 |
| 13 | A comprehensive analysis of 195 DNA methylomes reveals shared and cell-specific features of partially methylated domains. Genome Biology, 2018, 19, 150. | 3.8 | 71 |
| 14 | From hype to reality: data science enabling personalized medicine. BMC Medicine, 2018, 16, 150. | 2.3 | 278 |
| 15 | ISCB's initial reaction to <i>New England Journal of Medicine</i> editorial on data sharing. Bioinformatics, 2017, 33, 2968-2968. | 1.8 | 1 |
| 16 | Results of the first international HIV-1 coreceptor proficiency panel test. Journal of Clinical Virology, 2017, 93, 53-56. | 1.6 | 4 |
| 17 | DeepBlueR: large-scale epigenomic analysis in R. Bioinformatics, 2017, 33, 2063-2064. | 1.8 | 8 |
| 18 | Determination of Phenotypic Resistance Cutoffs From Routine Clinical Data. Journal of Acquired Immune Deficiency Syndromes (1999), 2017, 74, e129-e137. | 0.9 | 3 |

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|----|---|------|-----------|
| 19 | Combining transcription factor binding affinities with open-chromatin data for accurate gene expression prediction. <i>Nucleic Acids Research</i> , 2017, 45, 54-66. | 6.5 | 112 |
| 20 | Elucidating the energetic contributions to the binding free energy. <i>Journal of Chemical Physics</i> , 2017, 146, 014105. | 1.2 | 3 |
| 21 | Using drug exposure for predicting drug resistance – A data-driven genotypic interpretation tool. <i>PLoS ONE</i> , 2017, 12, e0174992. | 1.1 | 9 |
| 22 | Computing phylogenetic trees using topologically related minimum spanning trees. <i>Journal of Graph Algorithms and Applications</i> , 2017, 21, 1003-1025. | 0.4 | 1 |
| 23 | Geno2pheno[HCV] – A Web-based Interpretation System to Support Hepatitis C Treatment Decisions in the Era of Direct-Acting Antiviral Agents. <i>PLoS ONE</i> , 2016, 11, e0155869. | 1.1 | 101 |
| 24 | A genotypic method for determining HIV-2 coreceptor usage enables epidemiological studies and clinical decision support. <i>Retrovirology</i> , 2016, 13, 85. | 0.9 | 13 |
| 25 | Family-Joining: A Fast Distance-Based Method for Constructing Generally Labeled Trees. <i>Molecular Biology and Evolution</i> , 2016, 33, 2720-2734. | 3.5 | 4 |
| 26 | Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016, 9, 33. | 1.8 | 73 |
| 27 | Epigenomic Profiling of Human CD4+ T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. <i>Immunity</i> , 2016, 45, 1148-1161. | 6.6 | 174 |
| 28 | The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149. | 13.5 | 404 |
| 29 | DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. <i>Cell Stem Cell</i> , 2016, 19, 808-822. | 5.2 | 216 |
| 30 | Making sense of big data in health research: Towards an EU action plan. <i>Genome Medicine</i> , 2016, 8, 71. | 3.6 | 190 |
| 31 | DeepBlue epigenomic data server: programmatic data retrieval and analysis of epigenome region sets. <i>Nucleic Acids Research</i> , 2016, 44, W581-W586. | 6.5 | 60 |
| 32 | The Role of Conformational Changes in Molecular Recognition. <i>Journal of Physical Chemistry B</i> , 2016, 120, 2138-2144. | 1.2 | 10 |
| 33 | ISCB’s initial reaction to New England Journal of Medicine editorial on data sharing. <i>F1000Research</i> , 2016, 5, 157. | 0.8 | 1 |
| 34 | ISCB’s Initial Reaction to The New England Journal of Medicine Editorial on Data Sharing. <i>PLoS Computational Biology</i> , 2016, 12, e1004816. | 1.5 | 12 |
| 35 | Large oligomeric complex structures can be computationally assembled by efficiently combining docked interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1887-1899. | 1.5 | 3 |
| 36 | A general concept for consistent documentation of computational analyses. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav050. | 1.4 | 9 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | Sequence and Structure Analysis of Distantly-Related Viruses Reveals Extensive Gene Transfer between Viruses and Hosts and among Viruses. <i>Viruses</i> , 2015, 7, 5388-5409. | 1.5 | 16 |
| 38 | Parameters Influencing Baseline HIV-1 Genotypic Tropism Testing Related to Clinical Outcome in Patients on Maraviroc. <i>PLoS ONE</i> , 2015, 10, e0125502. | 1.1 | 7 |
| 39 | Message from the ISCB: ISCB Ebola award for important future research on the computational biology of Ebola virus. <i>Bioinformatics</i> , 2015, 31, 616-617. | 1.8 | 3 |
| 40 | Effects of sequence alterations on results from genotypic tropism testing. <i>Journal of Clinical Virology</i> , 2015, 65, 68-73. | 1.6 | 1 |
| 41 | Enthalpy-Entropy Compensation upon Molecular Conformational Changes. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 1410-1418. | 2.3 | 30 |
| 42 | How to Write a Presubmission Inquiry. <i>PLoS Computational Biology</i> , 2015, 11, e1004098. | 1.5 | 2 |
| 43 | How Molecular Conformational Changes Affect Changes in Free Energy. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 2945-2957. | 2.3 | 5 |
| 44 | ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. <i>PLoS Computational Biology</i> , 2015, 11, e1004087. | 1.5 | 2 |
| 45 | ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. <i>F1000Research</i> , 2015, 4, 12. | 0.8 | 1 |
| 46 | Proviral DNA as a Target for HIV-1 Resistance Analysis. <i>Intervirology</i> , 2015, 58, 184-189. | 1.2 | 26 |
| 47 | Improved therapy-success prediction with GSS estimated from clinical HIV-1 sequences. <i>Journal of the International AIDS Society</i> , 2014, 17, 19743. | 1.2 | 4 |
| 48 | Efficient computation of root mean square deviations under rigid transformations. <i>Journal of Computational Chemistry</i> , 2014, 35, 765-771. | 1.5 | 9 |
| 49 | Comprehensive analysis of DNA methylation data with RnBeads. <i>Nature Methods</i> , 2014, 11, 1138-1140. | 9.0 | 565 |
| 50 | Modelling binding between CCR5 and CXCR4 receptors and their ligands suggests the surface electrostatic potential of the co-receptor to be a key player in the HIV-1 tropism. <i>Retrovirology</i> , 2013, 10, 130. | 0.9 | 24 |
| 51 | Improving HIV coreceptor usage prediction in the clinic using hints from next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, i589-i595. | 1.8 | 18 |
| 52 | A DNA methylation fingerprint of 1628 human samples. <i>Genome Research</i> , 2012, 22, 407-419. | 2.4 | 341 |
| 53 | Predicting Response to Antiretroviral Treatment by Machine Learning: The EuResist Project. <i>Intervirology</i> , 2012, 55, 123-127. | 1.2 | 43 |
| 54 | BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226. | 9.4 | 323 |

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|----|---|------|-----------|
| 55 | Genotyping hepatitis B virus dual infections using population-based sequence data. <i>Journal of General Virology</i> , 2012, 93, 1899-1907. | 1.3 | 19 |
| 56 | Prediction of HIV-1 Coreceptor Usage (Tropism) by Sequence Analysis using a Genotypic Approach. <i>Journal of Visualized Experiments</i> , 2011, . . | 0.2 | 11 |
| 57 | BiQ Analyzer HT: locus-specific analysis of DNA methylation by high-throughput bisulfite sequencing. <i>Nucleic Acids Research</i> , 2011, 39, W551-W556. | 6.5 | 114 |
| 58 | Learning from Past Treatments and Their Outcome Improves Prediction of In Vivo Response to Anti-HIV Therapy. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, Article 6. | 0.2 | 16 |
| 59 | Advantages of predicted phenotypes and statistical learning models in inferring virological response to antiretroviral therapy from HIV genotype. <i>Antiviral Therapy</i> , 2009, 14, 273-83. | 0.6 | 5 |
| 60 | Advantages of predicted phenotypes and statistical learning models in inferring virological response to antiretroviral therapy from HIV genotype. <i>Antiviral Therapy</i> , 2009, 14, 273-283. | 0.6 | 10 |
| 61 | Selecting anti-HIV therapies based on a variety of genomic and clinical factors. <i>Bioinformatics</i> , 2008, 24, i399-i406. | 1.8 | 50 |
| 62 | Integrative Visual Analysis of the Effects of Alternative Splicing on Protein Domain Interaction Networks. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, . | 1.0 | 1 |
| 63 | Structural Descriptors of gp120 V3 Loop for the Prediction of HIV-1 Coreceptor Usage. <i>PLoS Computational Biology</i> , 2007, 3, e58. | 1.5 | 76 |
| 64 | Combined similarity and QSPR virtual screening for guest molecules of β -cyclodextrin. <i>New Journal of Chemistry</i> , 2007, 31, 1941. | 1.4 | 6 |
| 65 | Bioinformatics prediction of HIV coreceptor usage. <i>Nature Biotechnology</i> , 2007, 25, 1407-1410. | 9.4 | 289 |
| 66 | Bioinformatics-assisted anti-HIV therapy. <i>Nature Reviews Microbiology</i> , 2006, 4, 790-797. | 13.6 | 82 |
| 67 | ROCR: visualizing classifier performance in R. <i>Bioinformatics</i> , 2005, 21, 3940-3941. | 1.8 | 2,677 |
| 68 | Geno2pheno: estimating phenotypic drug resistance from HIV-1 genotypes. <i>Nucleic Acids Research</i> , 2003, 31, 3850-3855. | 6.5 | 213 |