

Thomas Lengauer

List of Publications by Year in descending order

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Version: 2024-02-01

68

papers

7,300

citations

218677

26

h-index

95266

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.	2.9	13
2	Identification of tissue-specific and common methylation quantitative trait loci in healthy individuals using MAGAR. Epigenetics and Chromatin, 2021, 14, 44.	3.9	3
3	Reference-free deconvolution, visualization and interpretation of complex DNA methylation data using DecompPipeline, MeDeCom and FactorViz. Nature Protocols, 2020, 15, 3240-3263.	12.0	19
4	Statistical Data Analysis in the Era of Big Data. Chemie-Ingenieur-Technik, 2020, 92, 831-841.	0.8	6
5	Quantitative comparison of within-sample heterogeneity scores for DNA methylation data. Nucleic Acids Research, 2020, 48, e46-e46.	14.5	45
6	Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. Nucleic Acids Research, 2019, 47, 10580-10596.	14.5	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.	4.2	3
8	Relative Principal Components Analysis: Application to Analyzing Biomolecular Conformational Changes. Journal of Chemical Theory and Computation, 2019, 15, 2166-2178.	5.3	13
9	RnBeads 2.0: comprehensive analysis of DNA methylation data. Genome Biology, 2019, 20, 55.	8.8	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.	14.5	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.	8.2	117
12	Integrative analysis of single-cell expression data reveals distinct regulatory states in bidirectional promoters. Epigenetics and Chromatin, 2018, 11, 66.	3.9	6
13	A comprehensive analysis of 195 DNA methylomes reveals shared and cell-specific features of partially methylated domains. Genome Biology, 2018, 19, 150.	8.8	71
14	From hype to reality: data science enabling personalized medicine. BMC Medicine, 2018, 16, 150.	5.5	278
15	ISCB's initial reaction to <i>New England Journal of Medicine</i> editorial on data sharing. Bioinformatics, 2017, 33, 2968-2968.	4.1	1
16	Results of the first international HIV-1 coreceptor proficiency panel test. Journal of Clinical Virology, 2017, 93, 53-56.	3.1	4
17	DeepBlueR: large-scale epigenomic analysis in R. Bioinformatics, 2017, 33, 2063-2064.	4.1	8
18	Determination of Phenotypic Resistance Cutoffs From Routine Clinical Data. Journal of Acquired Immune Deficiency Syndromes (1999), 2017, 74, e129-e137.	2.1	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.	14.5	112
20	Elucidating the energetic contributions to the binding free energy. <i>Journal of Chemical Physics</i> , 2017, 146, 014105.	3.0	3
21	Using drug exposure for predicting drug resistance – A data-driven genotypic interpretation tool. <i>PLoS ONE</i> , 2017, 12, e0174992.	2.5	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.	2.5	101
24	A genotypic method for determining HIV-2 coreceptor usage enables epidemiological studies and clinical decision support. <i>Retrovirology</i> , 2016, 13, 85.	2.0	13
25	Family-Joining: A Fast Distance-Based Method for Constructing Generally Labeled Trees. <i>Molecular Biology and Evolution</i> , 2016, 33, 2720-2734.	8.9	4
26	Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016, 9, 33.	3.9	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.	14.3	174
28	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
29	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. <i>Cell Stem Cell</i> , 2016, 19, 808-822.	11.1	216
30	Making sense of big data in health research: Towards an EU action plan. <i>Genome Medicine</i> , 2016, 8, 71.	8.2	190
31	DeepBlue epigenomic data server: programmatic data retrieval and analysis of epigenome region sets. <i>Nucleic Acids Research</i> , 2016, 44, W581-W586.	14.5	60
32	The Role of Conformational Changes in Molecular Recognition. <i>Journal of Physical Chemistry B</i> , 2016, 120, 2138-2144.	2.6	10
33	ISCB’s initial reaction to New England Journal of Medicine editorial on data sharing. <i>F1000Research</i> , 2016, 5, 157.	1.6	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.	3.2	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.	2.6	3
36	A general concept for consistent documentation of computational analyses. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav050.	3.0	9

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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.	3.3	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.	2.5	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.	4.1	3
40	Effects of sequence alterations on results from genotypic tropism testing. <i>Journal of Clinical Virology</i> , 2015, 65, 68-73.	3.1	1
41	Enthalpy–Entropy Compensation upon Molecular Conformational Changes. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 1410-1418.	5.3	30
42	How to Write a Presubmission Inquiry. <i>PLoS Computational Biology</i> , 2015, 11, e1004098.	3.2	2
43	How Molecular Conformational Changes Affect Changes in Free Energy. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 2945-2957.	5.3	5
44	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. <i>PLoS Computational Biology</i> , 2015, 11, e1004087.	3.2	2
45	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. <i>F1000Research</i> , 2015, 4, 12.	1.6	1
46	Proviral DNA as a Target for HIV-1 Resistance Analysis. <i>Intervirology</i> , 2015, 58, 184-189.	2.8	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.	3.0	4
48	Efficient computation of root mean square deviations under rigid transformations. <i>Journal of Computational Chemistry</i> , 2014, 35, 765-771.	3.3	9
49	Comprehensive analysis of DNA methylation data with RnBeads. <i>Nature Methods</i> , 2014, 11, 1138-1140.	19.0	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.	2.0	24
51	Improving HIV coreceptor usage prediction in the clinic using hints from next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, i589-i595.	4.1	18
52	A DNA methylation fingerprint of 1628 human samples. <i>Genome Research</i> , 2012, 22, 407-419.	5.5	341
53	Predicting Response to Antiretroviral Treatment by Machine Learning: The EuResist Project. <i>Intervirology</i> , 2012, 55, 123-127.	2.8	43
54	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	17.5	323

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55	Genotyping hepatitis B virus dual infections using population-based sequence data. Journal of General Virology, 2012, 93, 1899-1907.	2.9	19
56	Prediction of HIV-1 Coreceptor Usage (Tropism) by Sequence Analysis using a Genotypic Approach. Journal of Visualized Experiments, 2011, , .	0.3	11
57	BiQ Analyzer HT: locus-specific analysis of DNA methylation by high-throughput bisulfite sequencing. Nucleic Acids Research, 2011, 39, W551-W556.	14.5	114
58	Learning from Past Treatments and Their Outcome Improves Prediction of In Vivo Response to Anti-HIV Therapy. Statistical Applications in Genetics and Molecular Biology, 2011, 10, Article 6.	0.6	16
59	Advantages of predicted phenotypes and statistical learning models in inferring virological response to antiretroviral therapy from HIV genotype. Antiviral Therapy, 2009, 14, 273-83.	1.0	5
60	Advantages of predicted phenotypes and statistical learning models in inferring virological response to antiretroviral therapy from HIV genotype. Antiviral Therapy, 2009, 14, 273-283.	1.0	10
61	Selecting anti-HIV therapies based on a variety of genomic and clinical factors. Bioinformatics, 2008, 24, i399-i406.	4.1	50
62	Integrative Visual Analysis of the Effects of Alternative Splicing on Protein Domain Interaction Networks. Journal of Integrative Bioinformatics, 2008, 5, .	1.5	1
63	Structural Descriptors of gp120 V3 Loop for the Prediction of HIV-1 Coreceptor Usage. PLoS Computational Biology, 2007, 3, e58.	3.2	76
64	Combined similarity and QSPR virtual screening for guest molecules of β -cyclodextrin. New Journal of Chemistry, 2007, 31, 1941.	2.8	6
65	Bioinformatics prediction of HIV coreceptor usage. Nature Biotechnology, 2007, 25, 1407-1410.	17.5	289
66	Bioinformatics-assisted anti-HIV therapy. Nature Reviews Microbiology, 2006, 4, 790-797.	28.6	82
67	ROCR: visualizing classifier performance in R. Bioinformatics, 2005, 21, 3940-3941.	4.1	2,677
68	Geno2pheno: estimating phenotypic drug resistance from HIV-1 genotypes. Nucleic Acids Research, 2003, 31, 3850-3855.	14.5	213