

# Thomas Lengauer

## List of Publications by Year in descending order

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Version: 2024-02-01

68  
papers

7,300  
citations

249298

26  
h-index

107981

68  
g-index

79  
all docs

79  
docs citations

79  
times ranked

18827  
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

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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.	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 $\beta$ -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