

# Leonid Chindelevitch

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

1,852  
citations

758635

12  
h-index

476904

29  
g-index

57  
all docs

57  
docs citations

57  
times ranked

3085  
citing authors

#	ARTICLE	IF	CITATIONS
1	Inferring the effectiveness of government interventions against COVID-19. <i>Science</i> , 2021, 371, .	6.0	730
2	A standardised method for interpreting the association between mutations and phenotypic drug resistance in <i>Mycobacterium tuberculosis</i> . <i>European Respiratory Journal</i> , 2017, 50, 1701354.	3.1	273
3	Understanding the effectiveness of government interventions against the resurgence of COVID-19 in Europe. <i>Nature Communications</i> , 2021, 12, 5820.	5.8	135
4	The 2021 WHO catalogue of <i>Mycobacterium tuberculosis</i> complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	3.4	114
5	Integrating standardized whole genome sequence analysis with a global <i>Mycobacterium tuberculosis</i> antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018, 8, 15382.	1.6	75
6	MentaLiST – A fast MLST caller for large MLST schemes. <i>Microbial Genomics</i> , 2018, 4, .	1.0	55
7	Optimizing a global alignment of protein interaction networks. <i>Bioinformatics</i> , 2013, 29, 2765-2773.	1.8	53
8	Within-Host Heterogeneity of <i>Mycobacterium tuberculosis</i> Infection Is Associated With Poor Early Treatment Response: A Prospective Cohort Study. <i>Journal of Infectious Diseases</i> , 2016, 213, 1796-1799.	1.9	45
9	An exact arithmetic toolbox for a consistent and reproducible structural analysis of metabolic network models. <i>Nature Communications</i> , 2014, 5, 4893.	5.8	37
10	MetaMerge: scaling up genome-scale metabolic reconstructions, with application to <i>Mycobacterium tuberculosis</i> . <i>Genome Biology</i> , 2012, 13, R6.	13.9	31
11	LOCAL OPTIMIZATION FOR GLOBAL ALIGNMENT OF PROTEIN INTERACTION NETWORKS. , 2009, , 123-132.		25
12	ON THE INFERENCE OF PARSIMONIOUS INDEL EVOLUTIONARY SCENARIOS. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 721-744.	0.3	24
13	Inverting the Viterbi algorithm. , 2008, , .		14
14	ClassTR: Classifying Within-Host Heterogeneity Based on Tandem Repeats with Application to <i>Mycobacterium tuberculosis</i> Infections. <i>PLoS Computational Biology</i> , 2016, 12, e1004475.	1.5	14
15	Relatedness of the incidence decay with exponential adjustment (IDEA) model, –Farr's law–and SIR compartmental difference equation models. <i>Infectious Disease Modelling</i> , 2018, 3, 1-12.	1.2	14
16	Polyclonal Pulmonary Tuberculosis Infections and Risk for Multidrug Resistance, Lima, Peru. <i>Emerging Infectious Diseases</i> , 2017, 23, 1887-1890.	2.0	11
17	Evaluating the potential impact of enhancing HIV treatment and tuberculosis control programmes on the burden of tuberculosis. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150146.	1.5	9
18	Towards better prediction of <i>Mycobacterium tuberculosis</i> lineages from MIRU-VNTR data. <i>Infection, Genetics and Evolution</i> , 2019, 72, 59-66.	1.0	9

#	ARTICLE	IF	CITATIONS
19	INGOT-DR: an interpretable classifier for predicting drug resistance in <i>M. tuberculosis</i> . <i>Algorithms for Molecular Biology</i> , 2021, 16, 17.	0.3	9
20	Reply to "Do genome-scale models need exact solvers or clearer standards?". <i>Molecular Systems Biology</i> , 2015, 11, 830.	3.2	7
21	SplitStrains, a tool to identify and separate mixed <i>Mycobacterium tuberculosis</i> infections from WGS data. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
22	Network science inspires novel tree shape statistics. <i>PLoS ONE</i> , 2021, 16, e0259877.	1.1	7
23	Error analysis and preconditioning for an enhanced DtN-FE algorithm for exterior scattering problems. <i>Journal of Computational and Applied Mathematics</i> , 2007, 204, 493-504.	1.1	5
24	MCS2: minimal coordinated supports for fast enumeration of minimal cut sets in metabolic networks. <i>Bioinformatics</i> , 2019, 35, i615-i623.	1.8	4
25	A new resolution function to evaluate tree shape statistics. <i>PLoS ONE</i> , 2019, 14, e0224197.	1.1	4
26	On the rank-distance median of 3 permutations. <i>BMC Bioinformatics</i> , 2018, 19, 142.	1.2	3
27	Deconvoluting the diversity of within-host pathogen strains in a multi-locus sequence typing framework. <i>BMC Bioinformatics</i> , 2019, 20, 637.	1.2	3
28	Counting Sorting Scenarios and Intermediate Genomes for the Rank Distance. <i>Lecture Notes in Computer Science</i> , 2019, , 137-151.	1.0	1
29	Fast median computation for symmetric, orthogonal matrices under the rank distance. <i>Linear Algebra and Its Applications</i> , 2021, 614, 394-414.	0.4	1
30	Predicting drug resistance in <i>M. tuberculosis</i> using a long-term recurrent convolutional network. , 2021, , .		1
31	On the Rank-Distance Median of 3 Permutations. <i>Lecture Notes in Computer Science</i> , 2017, , 256-276.	1.0	1
32	Computing the distribution of the Robinson-Foulds distance. <i>Computational Biology and Chemistry</i> , 2020, 87, 107284.	1.1	1
33	Reply to Chen et al. <i>Journal of Infectious Diseases</i> , 2016, 214, 1287-1288.	1.9	0
34	The MONGOOSE Rational Arithmetic Toolbox. <i>Methods in Molecular Biology</i> , 2018, 1716, 77-99.	0.4	0
35	A Cubic Algorithm for the Generalized Rank Median of Three Genomes. <i>Lecture Notes in Computer Science</i> , 2018, , 3-27.	1.0	0
36	A cubic algorithm for the generalized rank median of three genomes. <i>Algorithms for Molecular Biology</i> , 2019, 14, 16.	0.3	0

#	ARTICLE	IF	CITATIONS
37	Generalizations of the Genomic Rank Distance to Indels. Lecture Notes in Computer Science, 2019, , 152-164.	1.0	0
38	Metabolic Network Analysis Demystified. Lecture Notes in Computer Science, 2011, , 31-33.	1.0	0
39	Vision Screening Results in a Cohort of Bhopal Gas Disaster Survivors. Current Science, 2017, 112, 2085.	0.4	0
40	PathOGiST: A Novel Method for Clustering Pathogen Isolates by Combining Multiple Genotyping Signals. Lecture Notes in Computer Science, 2020, , 108-124.	1.0	0
41	A new resolution function to evaluate tree shape statistics. , 2019, 14, e0224197.		0
42	A new resolution function to evaluate tree shape statistics. , 2019, 14, e0224197.		0
43	A new resolution function to evaluate tree shape statistics. , 2019, 14, e0224197.		0