

Lars Barquist

List of Publications by Citations

Source: <https://exaly.com/author-pdf/9446908/lars-barquist-publications-by-citations.pdf>
Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

55 papers	3,305 citations	27 h-index	57 g-index
76 ext. papers	4,497 ext. citations	11.5 avg, IF	5.41 L-index

#	Paper	IF	Citations
55	Rfam 11.0: 10 years of RNA families. <i>Nucleic Acids Research</i> , 2013 , 41, D226-32	20.1	596
54	Dual RNA-seq unveils noncoding RNA functions in host-pathogen interactions. <i>Nature</i> , 2016 , 529, 496-501	50.4	318
53	Global RNA recognition patterns of post-transcriptional regulators Hfq and CsrA revealed by UV crosslinking in vivo. <i>EMBO Journal</i> , 2016 , 35, 991-1011	13	205
52	Patterns of genome evolution that have accompanied host adaptation in Salmonella. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 863-8	11.5	154
51	Resolving host-pathogen interactions by dual RNA-seq. <i>PLoS Pathogens</i> , 2017 , 13, e1006033	7.6	153
50	Distinct Salmonella Enteritidis lineages associated with enterocolitis in high-income settings and invasive disease in low-income settings. <i>Nature Genetics</i> , 2016 , 48, 1211-1217	36.3	116
49	Parallel independent evolution of pathogenicity within the genus Yersinia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6768-73	11.5	114
48	Approaches to querying bacterial genomes with transposon-insertion sequencing. <i>RNA Biology</i> , 2013 , 10, 1161-9	4.8	107
47	High-throughput analysis of gene essentiality and sporulation in Clostridium difficile. <i>MBio</i> , 2015 , 6, e02383-14	7.8	102
46	The TraDIS toolkit: sequencing and analysis for dense transposon mutant libraries. <i>Bioinformatics</i> , 2016 , 32, 1109-11	7.2	98
45	Accelerating Discovery and Functional Analysis of Small RNAs with New Technologies. <i>Annual Review of Genetics</i> , 2015 , 49, 367-94	14.5	92
44	A comparison of dense transposon insertion libraries in the Salmonella serovars Typhi and Typhimurium. <i>Nucleic Acids Research</i> , 2013 , 41, 4549-64	20.1	86
43	Functional genomics reveals that Clostridium difficile Spo0A coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , 2014 , 15, 160	4.5	85
42	The agr locus regulates virulence and colonization genes in Clostridium difficile 027. <i>Journal of Bacteriology</i> , 2013 , 195, 3672-81	3.5	82
41	Signatures of adaptation in human invasive Salmonella Typhimurium ST313 populations from sub-Saharan Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003611	4.8	80
40	A decade of advances in transposon-insertion sequencing. <i>Nature Reviews Genetics</i> , 2020 , 21, 526-540	30.1	78
39	Global Maps of ProQ Binding In Vivo Reveal Target Recognition via RNA Structure and Stability Control at mRNA 3' Ends. <i>Molecular Cell</i> , 2018 , 70, 971-982.e6	17.6	75

38	A high-resolution view of genome-wide pneumococcal transformation. <i>PLoS Pathogens</i> , 2012 , 8, e1002745	45	74
37	RNA target profiles direct the discovery of virulence functions for the cold-shock proteins CspC and CspE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 6824-6829	11.5	72
36	Dominant role of nucleotide substitution in the diversification of serotype 3 pneumococci over decades and during a single infection. <i>PLoS Genetics</i> , 2013 , 9, e1003868	6	58
35	An amphipathic peptide with antibiotic activity against multidrug-resistant Gram-negative bacteria. <i>Nature Communications</i> , 2020 , 11, 3184	17.4	50
34	RNIE: genome-wide prediction of bacterial intrinsic terminators. <i>Nucleic Acids Research</i> , 2011 , 39, 5845-520.1	50.1	50
33	Genome and transcriptome adaptation accompanying emergence of the definitive type 2 host-restricted <i>Salmonella enterica</i> serovar Typhimurium pathovar. <i>MBio</i> , 2013 , 4, e00565-13	7.8	47
32	The primary transcriptome of <i>Neisseria meningitidis</i> and its interaction with the RNA chaperone Hfq. <i>Nucleic Acids Research</i> , 2017 , 45, 6147-6167	20.1	40
31	Machine learning identifies signatures of host adaptation in the bacterial pathogen <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2018 , 14, e1007333	6	40
30	Robust identification of noncoding RNA from transcriptomes requires phylogenetically-informed sampling. <i>PLoS Computational Biology</i> , 2014 , 10, e1003907	5	35
29	Noncanonical crRNAs derived from host transcripts enable multiplexable RNA detection by Cas9. <i>Science</i> , 2021 , 372, 941-948	33.3	30
28	RNA-seq reveals the RNA binding proteins, Hfq and RsmA, play various roles in virulence, antibiotic production and genomic flux in <i>Serratia</i> sp. ATCC 39006. <i>BMC Genomics</i> , 2013 , 14, 822	4.5	25
27	Global discovery of bacterial RNA-binding proteins by RNase-sensitive gradient profiles reports a new FinO domain protein. <i>Rna</i> , 2020 , 26, 1448-1463	5.8	21
26	A high-resolution transcriptome map identifies small RNA regulation of metabolism in the gut microbe <i>Bacteroides thetaiotaomicron</i> . <i>Nature Communications</i> , 2020 , 11, 3557	17.4	21
25	Transcriptional noise and exaptation as sources for bacterial sRNAs. <i>Biochemical Society Transactions</i> , 2019 , 47, 527-539	5.1	16
24	The minimal meningococcal ProQ protein has an intrinsic capacity for structure-based global RNA recognition. <i>Nature Communications</i> , 2020 , 11, 2823	17.4	16
23	A profile-based method for identifying functional divergence of orthologous genes in bacterial genomes. <i>Bioinformatics</i> , 2016 , 32, 3566-3574	7.2	16
22	Dual RNA-seq of <i>Orientia tsutsugamushi</i> informs on host-pathogen interactions for this neglected intracellular human pathogen. <i>Nature Communications</i> , 2020 , 11, 3363	17.4	14
21	Molecular phenotyping of infection-associated small non-coding RNAs. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016 , 371,	5.8	14

20	HandAlign: Bayesian multiple sequence alignment, phylogeny and ancestral reconstruction. <i>Bioinformatics</i> , 2012 , 28, 1170-1	7.2	12
19	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , 2018 , 8, 9868	4.9	11
18	A global data-driven census of <i>Salmonella</i> small proteins and their potential functions in bacterial virulence. <i>MicroLife</i> , 2020 , 1,	5	11
17	Studying RNA Homology and Conservation with Infernal: From Single Sequences to RNA Families. <i>Current Protocols in Bioinformatics</i> , 2016 , 54, 12.13.1-12.13.25	24.2	11
16	Evolutionary modeling and prediction of non-coding RNAs in <i>Drosophila</i> . <i>PLoS ONE</i> , 2009 , 4, e6478	3.7	10
15	Conditional Hfq Association with Small Noncoding RNAs in <i>Pseudomonas aeruginosa</i> Revealed through Comparative UV Cross-Linking Immunoprecipitation Followed by High-Throughput Sequencing. <i>MSystems</i> , 2019 , 4,	7.6	10
14	Characterization of the yehUT two-component regulatory system of <i>Salmonella enterica</i> Serovar Typhi and Typhimurium. <i>PLoS ONE</i> , 2013 , 8, e84567	3.7	7
13	A global genomic approach uncovers novel components for twitching motility-mediated biofilm expansion in <i>Pseudomonas aeruginosa</i> . <i>Microbial Genomics</i> , 2018 , 4,	4.4	6
12	Single-Nucleotide RNA Maps for the Two Major Nosocomial Pathogens and. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 600325	5.9	6
11	An RNA-centric global view of reveals broad activity of Hfq in a clinically important gram-positive bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	6
10	RNA landscape of the emerging cancer-associated microbe <i>Fusobacterium nucleatum</i> . <i>Nature Microbiology</i> , 2021 , 6, 1007-1020	26.6	5
9	Functional analysis of <i>Salmonella</i> Typhi adaptation to survival in water. <i>Environmental Microbiology</i> , 2018 , 20, 4079-4090	5.2	5
8	Rapid transcriptional responses to serum exposure are associated with sensitivity and resistance to antibody-mediated complement killing in invasive Typhimurium ST313. <i>Wellcome Open Research</i> , 2019 , 4, 74	4.8	4
7	The in vitro and in vivo effects of constitutive light expression on a bioluminescent strain of the mouse enteropathogen <i>Citrobacter rodentium</i> . <i>PeerJ</i> , 2016 , 4, e2130	3.1	4
6	Global RNA profiles show target selectivity and physiological effects of peptide-delivered antisense antibiotics. <i>Nucleic Acids Research</i> , 2021 , 49, 4705-4724	20.1	4
5	xREI: a phylo-grammar visualization webserver. <i>Nucleic Acids Research</i> , 2008 , 36, W65-9	20.1	2
4	Global identification of RsmA/N binding sites in by UV CLIP-seq. <i>RNA Biology</i> , 2021 , 18, 2401-2416	4.8	2
3	Role of and in Susceptibility to Antibody-Mediated Complement-Dependent Killing and Virulence of <i>Salmonella enterica</i> Serovar Typhimurium. <i>Infection and Immunity</i> , 2017 , 85,	3.7	1

2	Global identification of RsmA/N binding sites in <i>Pseudomonas aeruginosa</i> by in vivo UV CLIP-seq	1
1	Comparative genomics provides structural and functional insights into <i>Bacteroides</i> RNA biology. <i>Molecular Microbiology</i> , 2021 ,	4.1 1