

Lars Barquist

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

5,109
citations

147726

31
h-index

133188

59
g-index

76
all docs

76
docs citations

76
times ranked

7505
citing authors

#	ARTICLE	IF	CITATIONS
1	Rfam 11.0: 10 years of RNA families. <i>Nucleic Acids Research</i> , 2013, 41, D226-D232.	6.5	745
2	Dual RNA-seq unveils noncoding RNA functions in host–pathogen interactions. <i>Nature</i> , 2016, 529, 496-501.	13.7	450
3	Global RNA recognition patterns of posttranscriptional regulators Hfq and CsrA revealed by UV crosslinking <i>in vivo</i> . <i>EMBO Journal</i> , 2016, 35, 991-1011.	3.5	296
4	Resolving host–pathogen interactions by dual RNA-seq. <i>PLoS Pathogens</i> , 2017, 13, e1006033.	2.1	245
5	A decade of advances in transposon-insertion sequencing. <i>Nature Reviews Genetics</i> , 2020, 21, 526-540.	7.7	228
6	Patterns of genome evolution that have accompanied host adaptation in <i>Salmonella</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 863-868.	3.3	213
7	Distinct <i>Salmonella</i> Enteritidis lineages associated with enterocolitis in high-income settings and invasive disease in low-income settings. <i>Nature Genetics</i> , 2016, 48, 1211-1217.	9.4	191
8	The TraDIS toolkit: sequencing and analysis for dense transposon mutant libraries. <i>Bioinformatics</i> , 2016, 32, 1109-1111.	1.8	167
9	High-Throughput Analysis of Gene Essentiality and Sporulation in <i>Clostridium difficile</i> . <i>MBio</i> , 2015, 6, e02383.	1.8	157
10	Parallel independent evolution of pathogenicity within the genus <i>Yersinia</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6768-6773.	3.3	154
11	Functional genomics reveals that <i>Clostridium difficile</i> SpoOA coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , 2014, 15, 160.	1.2	145
12	Approaches to querying bacterial genomes with transposon-insertion sequencing. <i>RNA Biology</i> , 2013, 10, 1161-1169.	1.5	132
13	Global Maps of ProQ Binding <i>In Vivo</i> Reveal Target Recognition via RNA Structure and Stability Control at mRNA 3' Ends. <i>Molecular Cell</i> , 2018, 70, 971-982.e6.	4.5	129
14	Accelerating Discovery and Functional Analysis of Small RNAs with New Technologies. <i>Annual Review of Genetics</i> , 2015, 49, 367-394.	3.2	118
15	Signatures of Adaptation in Human Invasive <i>Salmonella</i> Typhimurium ST313 Populations from Sub-Saharan Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003611.	1.3	116
16	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.	3.3	110
17	A comparison of dense transposon insertion libraries in the <i>Salmonella</i> serovars Typhi and Typhimurium. <i>Nucleic Acids Research</i> , 2013, 41, 4549-4564.	6.5	108
18	An amphipathic peptide with antibiotic activity against multidrug-resistant Gram-negative bacteria. <i>Nature Communications</i> , 2020, 11, 3184.	5.8	105

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19	The <i>agr</i> Locus Regulates Virulence and Colonization Genes in <i>Clostridium difficile</i> 027. <i>Journal of Bacteriology</i> , 2013, 195, 3672-3681.	1.0	99
20	A High-Resolution View of Genome-Wide Pneumococcal Transformation. <i>PLoS Pathogens</i> , 2012, 8, e1002745.	2.1	98
21	Noncanonical crRNAs derived from host transcripts enable multiplexable RNA detection by Cas9. <i>Science</i> , 2021, 372, 941-948.	6.0	83
22	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.	1.5	81
23	Machine learning identifies signatures of host adaptation in the bacterial pathogen <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2018, 14, e1007333.	1.5	73
24	RNIE: genome-wide prediction of bacterial intrinsic terminators. <i>Nucleic Acids Research</i> , 2011, 39, 5845-5852.	6.5	71
25	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.	6.5	67
26	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.	1.8	57
27	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.	1.2	50
28	Robust Identification of Noncoding RNA from Transcriptomes Requires Phylogenetically-Informed Sampling. <i>PLoS Computational Biology</i> , 2014, 10, e1003907.	1.5	49
29	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.	5.8	44
30	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.	5.8	39
31	Transcriptional noise and exaptation as sources for bacterial sRNAs. <i>Biochemical Society Transactions</i> , 2019, 47, 527-539.	1.6	38
32	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.	1.6	34
33	A global data-driven census of <i>Salmonella</i> small proteins and their potential functions in bacterial virulence. <i>MicroLife</i> , 2020, 1, .	1.0	34
34	An RNA-centric global view of <i>Clostridioides difficile</i> 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, .	3.3	33
35	The minimal meningococcal ProQ protein has an intrinsic capacity for structure-based global RNA recognition. <i>Nature Communications</i> , 2020, 11, 2823.	5.8	31
36	A profile-based method for identifying functional divergence of orthologous genes in bacterial genomes. <i>Bioinformatics</i> , 2016, 32, 3566-3574.	1.8	25

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37	RNA landscape of the emerging cancer-associated microbe <i>Fusobacterium nucleatum</i> . <i>Nature Microbiology</i> , 2021, 6, 1007-1020.	5.9	23
38	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.	25.8	21
39	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , 2018, 8, 9868.	1.6	20
40	Global RNA profiles show target selectivity and physiological effects of peptide-delivered antisense antibiotics. <i>Nucleic Acids Research</i> , 2021, 49, 4705-4724.	6.5	20
41	HandAlign: Bayesian multiple sequence alignment, phylogeny and ancestral reconstruction. <i>Bioinformatics</i> , 2012, 28, 1170-1171.	1.8	18
42	Comprehensive analysis of PNA-based antisense antibiotics targeting various essential genes in uropathogenic <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2022, 50, 6435-6452.	6.5	18
43	Functional analysis of <i>Salmonella</i> Typhi adaptation to survival in water. <i>Environmental Microbiology</i> , 2018, 20, 4079-4090.	1.8	17
44	A global genomic approach uncovers novel components for twitching motility-mediated biofilm expansion in <i>Pseudomonas aeruginosa</i> . <i>Microbial Genomics</i> , 2018, 4, .	1.0	17
45	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, .	1.7	17
46	Characterization of the yehUT Two-Component Regulatory System of <i>Salmonella enterica</i> Serovar Typhi and Typhimurium. <i>PLoS ONE</i> , 2013, 8, e84567.	1.1	16
47	Single-Nucleotide RNA Maps for the Two Major Nosocomial Pathogens <i>Enterococcus faecalis</i> and <i>Enterococcus faecium</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 600325.	1.8	16
48	Molecular phenotyping of infection-associated small non-coding RNAs. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20160081.	1.8	15
49	Evolutionary Modeling and Prediction of Non-Coding RNAs in <i>Drosophila</i> . <i>PLoS ONE</i> , 2009, 4, e6478.	1.1	13
50	Cellular RNA Targets of Cold Shock Proteins CspC and CspE and Their Importance for Serum Resistance in Septicemic <i>Escherichia coli</i> . <i>MSystems</i> , 2022, 7, .	1.7	11
51	Rapid transcriptional responses to serum exposure are associated with sensitivity and resistance to antibody-mediated complement killing in invasive <i>Salmonella</i> Typhimurium ST313. <i>Wellcome Open Research</i> , 2019, 4, 74.	0.9	8
52	Global identification of RsmA/N binding sites in <i>Pseudomonas aeruginosa</i> by <i>in vivo</i> UV CLIP-seq. <i>RNA Biology</i> , 2021, 18, 2401-2416.	1.5	6
53	The <i>in vitro</i> and <i>in vivo</i> effects of constitutive light expression on a bioluminescent strain of the mouse enteropathogen <i>Citrobacter rodentium</i> . <i>PeerJ</i> , 2016, 4, e2130.	0.9	6
54	Comparative genomics provides structural and functional insights into <i>Bacteroides</i> RNA biology. <i>Molecular Microbiology</i> , 2022, 117, 67-85.	1.2	5

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55	xREI: a phylo-grammar visualization webserver. <i>Nucleic Acids Research</i> , 2008, 36, W65-W69.	6.5	3
56	Functional analysis of colonization factor antigen I positive enterotoxigenic <i>Escherichia coli</i> identifies genes implicated in survival in water and host colonization. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
57	Role of <i>sapA</i> and <i>yfgA</i> in Susceptibility to Antibody-Mediated Complement-Dependent Killing and Virulence of <i>Salmonella enterica</i> Serovar Typhimurium. <i>Infection and Immunity</i> , 2017, 85, .	1.0	1
58	Plugging Small RNAs into the Network. <i>MSystems</i> , 2020, 5, .	1.7	0