

# Lars Barquist

## List of Publications by Year in Descending Order

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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	Global RNA profiles show target selectivity and physiological effects of peptide-delivered antisense antibiotics. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 4705-4724	20.1	4
54	Global identification of RsmA/N binding sites in by UV CLIP-seq. <i>RNA Biology</i> , <b>2021</b> , 18, 2401-2416	4.8	2
53	Noncanonical crRNAs derived from host transcripts enable multiplexable RNA detection by Cas9. <i>Science</i> , <b>2021</b> , 372, 941-948	33.3	30
52	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> , <b>2021</b> , 118,	11.5	6
51	RNA landscape of the emerging cancer-associated microbe <i>Fusobacterium nucleatum</i> . <i>Nature Microbiology</i> , <b>2021</b> , 6, 1007-1020	26.6	5
50	Comparative genomics provides structural and functional insights into <i>Bacteroides</i> RNA biology. <i>Molecular Microbiology</i> , <b>2021</b> ,	4.1	1
49	A decade of advances in transposon-insertion sequencing. <i>Nature Reviews Genetics</i> , <b>2020</b> , 21, 526-540	30.1	78
48	An amphipathic peptide with antibiotic activity against multidrug-resistant Gram-negative bacteria. <i>Nature Communications</i> , <b>2020</b> , 11, 3184	17.4	50
47	The minimal meningococcal ProQ protein has an intrinsic capacity for structure-based global RNA recognition. <i>Nature Communications</i> , <b>2020</b> , 11, 2823	17.4	16
46	Dual RNA-seq of <i>Orientia tsutsugamushi</i> informs on host-pathogen interactions for this neglected intracellular human pathogen. <i>Nature Communications</i> , <b>2020</b> , 11, 3363	17.4	14
45	Global discovery of bacterial RNA-binding proteins by RNase-sensitive gradient profiles reports a new FinO domain protein. <i>Rna</i> , <b>2020</b> , 26, 1448-1463	5.8	21
44	A high-resolution transcriptome map identifies small RNA regulation of metabolism in the gut microbe <i>Bacteroides thetaiotaomicron</i> . <i>Nature Communications</i> , <b>2020</b> , 11, 3557	17.4	21
43	Single-Nucleotide RNA Maps for the Two Major Nosocomial Pathogens and. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2020</b> , 10, 600325	5.9	6
42	A global data-driven census of <i>Salmonella</i> small proteins and their potential functions in bacterial virulence. <i>MicroLife</i> , <b>2020</b> , 1,	5	11
41	Transcriptional noise and exaptation as sources for bacterial sRNAs. <i>Biochemical Society Transactions</i> , <b>2019</b> , 47, 527-539	5.1	16
40	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> , <b>2019</b> , 4,	7.6	10
39	Rapid transcriptional responses to serum exposure are associated with sensitivity and resistance to antibody-mediated complement killing in invasive <i>Typhimurium</i> ST313. <i>Wellcome Open Research</i> , <b>2019</b> , 4, 74	4.8	4

38	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , <b>2018</b> , 8, 9868	4.9	11
37	A global genomic approach uncovers novel components for twitching motility-mediated biofilm expansion in <i>Pseudomonas aeruginosa</i> . <i>Microbial Genomics</i> , <b>2018</b> , 4,	4.4	6
36	Functional analysis of <i>Salmonella</i> Typhi adaptation to survival in water. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 4079-4090	5.2	5
35	Global Maps of ProQ Binding In Vivo Reveal Target Recognition via RNA Structure and Stability Control at mRNA 3' Ends. <i>Molecular Cell</i> , <b>2018</b> , 70, 971-982.e6	17.6	75
34	Machine learning identifies signatures of host adaptation in the bacterial pathogen <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007333	6	40
33	The primary transcriptome of <i>Neisseria meningitidis</i> and its interaction with the RNA chaperone Hfq. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 6147-6167	20.1	40
32	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> , <b>2017</b> , 114, 6824-6829	11.5	72
31	Resolving host-pathogen interactions by dual RNA-seq. <i>PLoS Pathogens</i> , <b>2017</b> , 13, e1006033	7.6	153
30	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> , <b>2017</b> , 85,	3.7	1
29	Distinct <i>Salmonella</i> Enteritidis lineages associated with enterocolitis in high-income settings and invasive disease in low-income settings. <i>Nature Genetics</i> , <b>2016</b> , 48, 1211-1217	36.3	116
28	Dual RNA-seq unveils noncoding RNA functions in host-pathogen interactions. <i>Nature</i> , <b>2016</b> , 529, 496-501	50.4	318
27	The TraDIS toolkit: sequencing and analysis for dense transposon mutant libraries. <i>Bioinformatics</i> , <b>2016</b> , 32, 1109-11	7.2	98
26	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> , <b>2016</b> , 4, e2130	3.1	4
25	A profile-based method for identifying functional divergence of orthologous genes in bacterial genomes. <i>Bioinformatics</i> , <b>2016</b> , 32, 3566-3574	7.2	16
24	Studying RNA Homology and Conservation with Infernal: From Single Sequences to RNA Families. <i>Current Protocols in Bioinformatics</i> , <b>2016</b> , 54, 12.13.1-12.13.25	24.2	11
23	Global RNA recognition patterns of post-transcriptional regulators Hfq and CsrA revealed by UV crosslinking in vivo. <i>EMBO Journal</i> , <b>2016</b> , 35, 991-1011	13	205
22	Molecular phenotyping of infection-associated small non-coding RNAs. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2016</b> , 371,	5.8	14
21	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> , <b>2015</b> , 112, 863-8	11.5	154

20	High-throughput analysis of gene essentiality and sporulation in <i>Clostridium difficile</i> . <i>MBio</i> , <b>2015</b> , 6, e02383	102
19	Signatures of adaptation in human invasive <i>Salmonella</i> Typhimurium ST313 populations from sub-Saharan Africa. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003611	4.8 80
18	Accelerating Discovery and Functional Analysis of Small RNAs with New Technologies. <i>Annual Review of Genetics</i> , <b>2015</b> , 49, 367-94	14.5 92
17	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> , <b>2014</b> , 111, 6768-73	11.5 114
16	Functional genomics reveals that <i>Clostridium difficile</i> Spo0A coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , <b>2014</b> , 15, 160	4.5 85
15	Robust identification of noncoding RNA from transcriptomes requires phylogenetically-informed sampling. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003907	5 35
14	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> , <b>2013</b> , 14, 822	4.5 25
13	The <i>agr</i> locus regulates virulence and colonization genes in <i>Clostridium difficile</i> 027. <i>Journal of Bacteriology</i> , <b>2013</b> , 195, 3672-81	3.5 82
12	Genome and transcriptome adaptation accompanying emergence of the definitive type 2 host-restricted <i>Salmonella enterica</i> serovar Typhimurium pathovar. <i>MBio</i> , <b>2013</b> , 4, e00565-13	7.8 47
11	Dominant role of nucleotide substitution in the diversification of serotype 3 pneumococci over decades and during a single infection. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003868	6 58
10	Rfam 11.0: 10 years of RNA families. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D226-32	20.1 596
9	A comparison of dense transposon insertion libraries in the <i>Salmonella</i> serovars Typhi and Typhimurium. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 4549-64	20.1 86
8	Approaches to querying bacterial genomes with transposon-insertion sequencing. <i>RNA Biology</i> , <b>2013</b> , 10, 1161-9	4.8 107
7	Characterization of the yehUT two-component regulatory system of <i>Salmonella enterica</i> Serovar Typhi and Typhimurium. <i>PLoS ONE</i> , <b>2013</b> , 8, e84567	3.7 7
6	A high-resolution view of genome-wide pneumococcal transformation. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002745	15 74
5	HandAlign: Bayesian multiple sequence alignment, phylogeny and ancestral reconstruction. <i>Bioinformatics</i> , <b>2012</b> , 28, 1170-1	7.2 12
4	RNIE: genome-wide prediction of bacterial intrinsic terminators. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, 5845-52	20.1 50
3	Evolutionary modeling and prediction of non-coding RNAs in <i>Drosophila</i> . <i>PLoS ONE</i> , <b>2009</b> , 4, e6478	3.7 10

2      xREI: a phylo-grammar visualization webserver. *Nucleic Acids Research*, **2008**, 36, W65-9      20.1      2

1      Global identification of RsmA/N binding sites in *Pseudomonas aeruginosa* by in vivo UV CLIP-seq      1