

Konrad U Frstner

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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.

94 papers	8,519 citations	29 h-index	92 g-index
101 ext. papers	10,973 ext. citations	9.9 avg, IF	5.47 L-index

#	Paper	IF	Citations
94	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
93	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. <i>Cell</i> , 2020 , 182, 1419-1440.e23	36.2	558
92	Dual RNA-seq unveils noncoding RNA functions in host-pathogen interactions. <i>Nature</i> , 2016 , 529, 496-504	50.4	318
91	Global transcriptional start site mapping using differential RNA sequencing reveals novel antisense RNAs in Escherichia coli. <i>Journal of Bacteriology</i> , 2015 , 197, 18-28	3.5	207
90	High-resolution transcriptome maps reveal strain-specific regulatory features of multiple Campylobacter jejuni isolates. <i>PLoS Genetics</i> , 2013 , 9, e1003495	6	201
89	Environments shape the nucleotide composition of genomes. <i>EMBO Reports</i> , 2005 , 6, 1208-13	6.5	200
88	Grad-seq guides the discovery of ProQ as a major small RNA-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 11591-11596	11.5	193
87	InVivo Cleavage Map Illuminates the Central Role of RNase E in Coding and Non-coding RNA Pathways. <i>Molecular Cell</i> , 2017 , 65, 39-51	17.6	159
86	The primary transcriptome of barley chloroplasts: numerous noncoding RNAs and the dominating role of the plastid-encoded RNA polymerase. <i>Plant Cell</i> , 2012 , 24, 123-36	11.6	155
85	Differential RNA-seq of Vibrio cholerae identifies the VqmR small RNA as a regulator of biofilm formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E766-75	11.5	141
84	The sigmaB regulon in Staphylococcus aureus and its regulation. <i>International Journal of Medical Microbiology</i> , 2006 , 296, 237-58	3.7	133
83	Evolution of resistance to a last-resort antibiotic in Staphylococcus aureus via bacterial competition. <i>Cell</i> , 2014 , 158, 1060-1071	56.2	129
82	Get the most out of your metagenome: computational analysis of environmental sequence data. <i>Current Opinion in Microbiology</i> , 2007 , 10, 490-8	7.9	127
81	READemption-a tool for the computational analysis of deep-sequencing-based transcriptome data. <i>Bioinformatics</i> , 2014 , 30, 3421-3	7.2	102
80	Genome organization and DNA accessibility control antigenic variation in trypanosomes. <i>Nature</i> , 2018 , 563, 121-125	50.4	84
79	Functional high-throughput screening identifies the miR-15 microRNA family as cellular restriction factors for Salmonella infection. <i>Nature Communications</i> , 2014 , 5, 4718	17.4	82
78	Genome-wide identification of transcriptional start sites in the haloarchaeon Haloferax volcanii based on differential RNA-Seq (dRNA-Seq). <i>BMC Genomics</i> , 2016 , 17, 629	4.5	78

77	SmashCommunity: a metagenomic annotation and analysis tool. <i>Bioinformatics</i> , 2010 , 26, 2977-8	7.2	77
76	Primary transcriptome map of the hyperthermophilic archaeon <i>Thermococcus kodakarensis</i> . <i>BMC Genomics</i> , 2014 , 15, 684	4.5	69
75	Splicing factors stimulate polyadenylation via USEs at non-canonical 3' end formation signals. <i>EMBO Journal</i> , 2007 , 26, 2658-69	13	65
74	Natural mutations in a <i>Staphylococcus aureus</i> virulence regulator attenuate cytotoxicity but permit bacteremia and abscess formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E3101-10	11.5	61
73	Insights into Microalga and Bacteria Interactions of Selected Phycosphere Biofilms Using Metagenomic, Transcriptomic, and Proteomic Approaches. <i>Frontiers in Microbiology</i> , 2017 , 8, 1941	5.7	53
72	The Major RNA-Binding Protein ProQ Impacts Virulence Gene Expression in <i>Salmonella enterica</i> Serovar Typhimurium. <i>MBio</i> , 2019 , 10,	7.8	51
71	Integrative "omics"-approach discovers dynamic and regulatory features of bacterial stress responses. <i>PLoS Genetics</i> , 2013 , 9, e1003576	6	50
70	Regulation of transcription termination by glucosylated hydroxymethyluracil, base J, in <i>Leishmania major</i> and <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2014 , 42, 9717-29	20.1	46
69	GT-rich promoters can drive RNA pol II transcription and deposition of H2A.Z in African trypanosomes. <i>EMBO Journal</i> , 2017 , 36, 2581-2594	13	43
68	Target recognition, RNA methylation activity and transcriptional regulation of the <i>Dictyostelium discoideum</i> Dnmt2-homologue (DnmA). <i>Nucleic Acids Research</i> , 2013 , 41, 8615-27	20.1	39
67	Genome-wide transcription start site mapping of <i>Bradyrhizobium japonicum</i> grown free-living or in symbiosis - a rich resource to identify new transcripts, proteins and to study gene regulation. <i>BMC Genomics</i> , 2016 , 17, 302	4.5	38
66	Role of oxygen and the OxyR protein in the response to iron limitation in <i>Rhodobacter sphaeroides</i> . <i>BMC Genomics</i> , 2014 , 15, 794	4.5	32
65	A computational screen for type I polyketide synthases in metagenomics shotgun data. <i>PLoS ONE</i> , 2008 , 3, e3515	3.7	29
64	RNA sequencing analysis of the broad-host-range strain <i>Sinorhizobium fredii</i> NGR234 identifies a large set of genes linked to quorum sensing-dependent regulation in the background of a <i>tral</i> and <i>ngrI</i> deletion mutant. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 5655-71	4.8	26
63	sRNA a newly identified regulator of nitrogen fixation in <i>Methanosarcina mazei</i> strain G1. <i>RNA Biology</i> , 2017 , 14, 1544-1558	4.8	25
62	Grad-seq in a Gram-positive bacterium reveals exonucleolytic sRNA activation in competence control. <i>EMBO Journal</i> , 2020 , 39, e103852	13	25
61	Induced Pluripotent Stem Cell-Derived Brain Endothelial Cells as a Cellular Model to Study Infection. <i>Frontiers in Microbiology</i> , 2019 , 10, 1181	5.7	24
60	Genome-wide transcription start site profiling in biofilm-grown <i>Burkholderia cenocepacia</i> J2315. <i>BMC Genomics</i> , 2015 , 16, 775	4.5	24

59	Profound impact of Hfq on nutrient acquisition, metabolism and motility in the plant pathogen <i>Agrobacterium tumefaciens</i> . <i>PLoS ONE</i> , 2014 , 9, e110427	3.7	24
58	Functional characterization of the RNA chaperone Hfq in the opportunistic human pathogen <i>Stenotrophomonas maltophilia</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 5864-74	3.5	24
57	ANNOgesic: a Swiss army knife for the RNA-seq based annotation of bacterial/archaeal genomes. <i>GigaScience</i> , 2018 , 7,	7.6	23
56	dRNA-Seq Reveals Genomewide TSSs and Noncoding RNAs of Plant Beneficial Rhizobacterium <i>Bacillus amyloliquefaciens</i> FZB42. <i>PLoS ONE</i> , 2015 , 10, e0142002	3.7	22
55	Comparative analysis of environmental sequences: potential and challenges. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 519-23	5.8	22
54	A nitrile hydratase in the eukaryote <i>Monosiga brevicollis</i> . <i>PLoS ONE</i> , 2008 , 3, e3976	3.7	21
53	An Open Science Peer Review Oath. <i>F1000Research</i> , 2014 , 3, 271	3.6	21
52	The small non-coding RNA RsaE influences extracellular matrix composition in <i>Staphylococcus epidermidis</i> biofilm communities. <i>PLoS Pathogens</i> , 2019 , 15, e1007618	7.6	20
51	cis-Encoded Small RNAs, a Conserved Mechanism for Repression of Polysaccharide Utilization in <i>Bacteroides</i> . <i>Journal of Bacteriology</i> , 2016 , 198, 2410-8	3.5	20
50	Effect of Shear Stress on <i>Pseudomonas aeruginosa</i> Isolated from the Cystic Fibrosis Lung. <i>MBio</i> , 2016 , 7,	7.8	20
49	Transcription Profiling of Cells Infected with AR9, a Giant Phage Encoding Two Multisubunit RNA Polymerases. <i>MBio</i> , 2017 , 8,	7.8	18
48	Sensory profiles and immune-related expression patterns of patients with and without neuropathic pain after peripheral nerve lesion. <i>Pain</i> , 2019 , 160, 2316-2327	8	18
47	A non-coding RNA from the intercellular adhesion (ica) locus of <i>Staphylococcus epidermidis</i> controls polysaccharide intercellular adhesion (PIA)-mediated biofilm formation. <i>Molecular Microbiology</i> , 2019 , 111, 1571-1591	4.1	17
46	Grad-seq shines light on unrecognized RNA and protein complexes in the model bacterium <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2020 , 48, 9301-9319	20.1	17
45	An RpoHI-Dependent Response Promotes Outgrowth after Extended Stationary Phase in the Alphaproteobacterium <i>Rhodobacter sphaeroides</i> . <i>Journal of Bacteriology</i> , 2017 , 199,	3.5	16
44	Characterization of the transcriptome of <i>Haloferax volcanii</i> , grown under four different conditions, with mixed RNA-Seq. <i>PLoS ONE</i> , 2019 , 14, e0215986	3.7	16
43	A conserved RNA seed-pairing domain directs small RNA-mediated stress resistance in enterobacteria. <i>EMBO Journal</i> , 2019 , 38, e101650	13	16
42	A molecular study of microbe transfer between distant environments. <i>PLoS ONE</i> , 2008 , 3, e2607	3.7	16

41	YBEY is an essential biogenesis factor for mitochondrial ribosomes. <i>Nucleic Acids Research</i> , 2020 , 48, 9762-9786	20.1	15
40	APRICOT: an integrated computational pipeline for the sequence-based identification and characterization of RNA-binding proteins. <i>Nucleic Acids Research</i> , 2017 , 45, e96	20.1	14
39	Gene autoregulation by 3'UTR-derived bacterial small RNAs. <i>ELife</i> , 2020 , 9,	8.9	14
38	dRNA-seq transcriptional profiling of the FK506 biosynthetic gene cluster in <i>Streptomyces tsukubaensis</i> NRRL18488 and general analysis of the transcriptome. <i>RNA Biology</i> , 2017 , 14, 1617-1626	4.8	13
37	RNase E cleavage shapes the transcriptome of and strongly impacts phototrophic growth. <i>Life Science Alliance</i> , 2018 , 1, e201800080	5.8	12
36	Phenotypic Heterogeneity Affects <i>Stenotrophomonas maltophilia</i> K279a Colony Morphotypes and β -Lactamase Expression. <i>Frontiers in Microbiology</i> , 2015 , 6, 1373	5.7	11
35	The open science peer review oath. <i>F1000Research</i> , 2014 , 3, 271	3.6	11
34	The primary transcriptome of the <i>Escherichia coli</i> O104:H4 pAA plasmid and novel insights into its virulence gene expression and regulation. <i>Scientific Reports</i> , 2016 , 6, 35307	4.9	10
33	Cross-cleavage activity of Cas6b in crRNA processing of two different CRISPR-Cas systems in <i>Methanosarcina mazei</i> G1. <i>RNA Biology</i> , 2019 , 16, 492-503	4.8	10
32	Differences in the Transcriptomic Response of and to Heat Stress. <i>Frontiers in Microbiology</i> , 2020 , 11, 523	5.7	9
31	SuhB, a small non-coding RNA involved in catabolite repression of tetralin degradation genes in <i>Sphingopyxis granuli</i> strain TFA. <i>Environmental Microbiology</i> , 2018 , 20, 3671-3683	5.2	9
30	Analysis of the Microprocessor in <i>Dictyostelium</i> : The Role of RbdB, a dsRNA Binding Protein. <i>PLoS Genetics</i> , 2016 , 12, e1006057	6	9
29	Post-transcriptional gene regulation by an Hfq-independent small RNA in <i>Caulobacter crescentus</i> . <i>Nucleic Acids Research</i> , 2018 , 46, 10969-10982	20.1	9
28	The Probiotic Strain Nissle 1917 Combats Lambdaoid Bacteriophages and β - <i>Frontiers in Microbiology</i> , 2018 , 9, 929	5.7	8
27	A New Bioactive Compound From the Marine Sponge-Derived sp. SBT348 Inhibits Staphylococcal Growth and Biofilm Formation. <i>Frontiers in Microbiology</i> , 2018 , 9, 1473	5.7	8
26	RNase J is required for processing of a small number of RNAs in <i>Rhodobacter sphaeroides</i> . <i>RNA Biology</i> , 2014 , 11, 855-64	4.8	8
25	Argonaute proteins affect siRNA levels and accumulation of a novel extrachromosomal DNA from the <i>Dictyostelium</i> retrotransposon DIRS-1. <i>Journal of Biological Chemistry</i> , 2014 , 289, 35124-38	5.4	8
24	IL-12 from endogenous cDC1, and not vaccine DC, is required for Th1 induction. <i>JCI Insight</i> , 2020 , 5,	9.9	8

23	A Novel Mechanism of Inactivating Antibacterial Nitro Compounds in the Human Pathogen <i>Staphylococcus aureus</i> by Overexpression of a NADH-Dependent Flavin Nitroreductase. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	8
22	The RNase YbeY Is Vital for Ribosome Maturation, Stress Resistance, and Virulence of the Natural Genetic Engineer. <i>Journal of Bacteriology</i> , 2019 , 201,	3.5	6
21	READemption - A tool for the computational analysis of deep-sequencing-based transcriptome data		6
20	The Absence of the N-acyl-homoserine-lactone Autoinducer Synthase Genes and Increases the Copy Number of the Symbiotic Plasmid in NGR234. <i>Frontiers in Microbiology</i> , 2016 , 7, 1858	5.7	6
19	Identification of Cholecystokinin by Genome-Wide Profiling as Potential Mediator of Serotonin-Dependent Behavioral Effects of Maternal Separation in the Amygdala. <i>Frontiers in Neuroscience</i> , 2019 , 13, 460	5.1	5
18	The Leader Peptide peTrpL Forms Antibiotic-Containing Ribonucleoprotein Complexes for Posttranscriptional Regulation of Multiresistance Genes. <i>MBio</i> , 2020 , 11,	7.8	5
17	Novel molecular cues for dental defects in hypophosphatasia. <i>Experimental Cell Research</i> , 2020 , 392, 112026	4.2	5
16	Wikis in scholarly publishing*. <i>Information Services and Use</i> , 2011 , 31, 53-59	0.5	4
15	Tetrachloroethene respiration in <i>Sulfurospirillum</i> species is regulated by a two-component system as unraveled by comparative genomics, transcriptomics, and regulator binding studies. <i>MicrobiologyOpen</i> , 2020 , 9, e1138	3.4	4
14	The small DUF1127 protein CcaF1 from <i>Rhodobacter sphaeroides</i> is an RNA-binding protein involved in sRNA maturation and RNA turnover. <i>Nucleic Acids Research</i> , 2021 , 49, 3003-3019	20.1	4
13	Collaborative platforms for streamlining workflows in Open Science. <i>Nature Precedings</i> , 2011 ,		3
12	Reprogramming of sRNA target specificity by the leader peptide peTrpL in response to antibiotic exposure. <i>Nucleic Acids Research</i> , 2021 , 49, 2894-2915	20.1	3
11	Computational Analysis of RNA-Protein Interactions via Deep Sequencing. <i>Methods in Molecular Biology</i> , 2018 , 1751, 171-182	1.4	2
10	ANNOgesic: A Swiss army knife for the RNA-Seq based annotation of bacterial/archaeal genomes		2
9	CoxBase: an online platform for epidemiological surveillance, visualization, analysis and typing of <i>Coxiella burnetii</i> genomic sequences		2
8	The bacterial leader peptide peTrpL has a conserved function in antibiotic-dependent posttranscriptional regulation of ribosomal genes		2
7	The CARF Protein MM_0565 Affects Transcription of the Casposon-Encoded Gene in <i>G1</i> . <i>Biomolecules</i> , 2020 , 10,	5.9	2
6	The induction of natural competence adapts staphylococcal metabolism to infection.. <i>Nature Communications</i> , 2022 , 13, 1525	17.4	2

5	Data Literacy for Libraries – A Local Perspective on Library Carpentry. <i>Bibliothek: Forschung Und Praxis</i> , 2020 , 44, 485-489	0.1	1
4	Trans-acting role of the leader peptide peTrpL in posttranscriptional regulation of multiresistance		1
3	Identification of BvgA-Dependent and BvgA-Independent Small RNAs (sRNAs) in <i>Bordetella pertussis</i> Using the Prokaryotic sRNA Prediction Toolkit ANNOgesic. <i>Microbiology Spectrum</i> , 2021 , 9, e0004421	8.9	1
2	CoxBase: an Online Platform for Epidemiological Surveillance, Visualization, Analysis, and Typing of <i>Coxiella burnetii</i> Genomic Sequences.. <i>MSystems</i> , 2021 , 6, e0040321	7.6	1
1	Cytosolic Sensing of Intracellular by Mast Cells Elicits a Type I IFN Response That Enhances Cell-Autonomous Immunity.. <i>Journal of Immunology</i> , 2022 , 208, 1675-1685	5.3	