## Konrad U Frstner

# 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.

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

#	Paper	IF	Citations
94	Cytosolic Sensing of Intracellular by Mast Cells Elicits a Type I IFN Response That Enhances Cell-Autonomous Immunity <i>Journal of Immunology</i> , <b>2022</b> , 208, 1675-1685	5.3	
93	The induction of natural competence adapts staphylococcal metabolism to infection <i>Nature Communications</i> , <b>2022</b> , 13, 1525	17.4	2
92	The small DUF1127 protein CcaF1 from Rhodobacter sphaeroides is an RNA-binding protein involved in sRNA maturation and RNA turnover. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 3003-3019	20.1	4
91	Reprograming of sRNA target specificity by the leader peptide peTrpL in response to antibiotic exposure. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 2894-2915	20.1	3
90	Identification of BvgA-Dependent and BvgA-Independent Small RNAs (sRNAs) in Bordetella pertussis Using the Prokaryotic sRNA Prediction Toolkit ANNOgesic. <i>Microbiology Spectrum</i> , <b>2021</b> , 9, e0004421	8.9	1
89	CoxBase: an Online Platform for Epidemiological Surveillance, Visualization, Analysis, and Typing of Coxiella burnetii Genomic Sequences <i>MSystems</i> , <b>2021</b> , 6, e0040321	7.6	1
88	The Leader Peptide peTrpL Forms Antibiotic-Containing Ribonucleoprotein Complexes for Posttranscriptional Regulation of Multiresistance Genes. <i>MBio</i> , <b>2020</b> , 11,	7.8	5
87	YBEY is an essential biogenesis factor for mitochondrial ribosomes. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 9762-9786	20.1	15
86	Differences in the Transcriptomic Response of and to Heat Stress. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 523	5.7	9
85	Novel molecular cues for dental defects in hypophosphatasia. <i>Experimental Cell Research</i> , <b>2020</b> , 392, 112026	4.2	5
84	IL-12 from endogenous cDC1, and not vaccine DC, is required for Th1 induction. JCI Insight, 2020, 5,	9.9	8
83	Grad-seq in a Gram-positive bacterium reveals exonucleolytic sRNA activation in competence control. <i>EMBO Journal</i> , <b>2020</b> , 39, e103852	13	25
82	Data Literacy for Libraries A Local Perspective on Library Carpentry. <i>Bibliothek: Forschung Und Praxis</i> , <b>2020</b> , 44, 485-489	0.1	1
81	Gene autoregulation by 3RUTR-derived bacterial small RNAs. ELife, 2020, 9,	8.9	14
80	Tetrachloroethene respiration in Sulfurospirillum species is regulated by a two-component system as unraveled by comparative genomics, transcriptomics, and regulator binding studies. <i>MicrobiologyOpen</i> , <b>2020</b> , 9, e1138	3.4	4
79	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. <i>Cell</i> , <b>2020</b> , 182, 1419-1440.6	<b>23</b> 6.2	558
78	Grad-seq shines light on unrecognized RNA and protein complexes in the model bacterium Escherichia coli. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 9301-9319	20.1	17

### (2018-2020)

77	The CARF Protein MM_0565 Affects Transcription of the Casposon-Encoded Gene in G1. <i>Biomolecules</i> , <b>2020</b> , 10,	5.9	2
76	Induced Pluripotent Stem Cell-Derived Brain Endothelial Cells as a Cellular Model to Study Infection. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1181	5.7	24
75	Characterization of the transcriptome of Haloferax volcanii, grown under four different conditions, with mixed RNA-Seq. <i>PLoS ONE</i> , <b>2019</b> , 14, e0215986	3.7	16
74	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> , <b>2019</b> , 13, 460	5.1	5
73	The RNase YbeY Is Vital for Ribosome Maturation, Stress Resistance, and Virulence of the Natural Genetic Engineer. <i>Journal of Bacteriology</i> , <b>2019</b> , 201,	3.5	6
72	A non-coding RNA from the intercellular adhesion (ica) locus of Staphylococcus epidermidis controls polysaccharide intercellular adhesion (PIA)-mediated biofilm formation. <i>Molecular Microbiology</i> , <b>2019</b> , 111, 1571-1591	4.1	17
71	The small non-coding RNA RsaE influences extracellular matrix composition in Staphylococcus epidermidis biofilm communities. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007618	7.6	20
70	A conserved RNA seed-pairing domain directs small RNA-mediated stress resistance in enterobacteria. <i>EMBO Journal</i> , <b>2019</b> , 38, e101650	13	16
69	Sensory profiles and immune-related expression patterns of patients with and without neuropathic pain after peripheral nerve lesion. <i>Pain</i> , <b>2019</b> , 160, 2316-2327	8	18
68	Cross-cleavage activity of Cas6b in crRNA processing of two different CRISPR-Cas systems in Methanosarcina mazei Ga. RNA Biology, <b>2019</b> , 16, 492-503	4.8	10
67	The Major RNA-Binding Protein ProQ Impacts Virulence Gene Expression in Salmonella enterica Serovar Typhimurium. <i>MBio</i> , <b>2019</b> , 10,	7.8	51
66	Computational Analysis of RNA-Protein Interactions via Deep Sequencing. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1751, 171-182	1.4	2
65	SuhB, a small non-coding RNA involved in catabolite repression of tetralin degradation genes in Sphingopyxis granuli strain TFA. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 3671-3683	5.2	9
64	The Probiotic Strain Nissle 1917 Combats Lambdoid Bacteriophages and [[Frontiers in Microbiology, 2018, 9, 929]	5.7	8
63	A New Bioactive Compound From the Marine Sponge-Derived sp. SBT348 Inhibits Staphylococcal Growth and Biofilm Formation. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1473	5.7	8
62	RNase E cleavage shapes the transcriptome of and strongly impacts phototrophic growth. <i>Life Science Alliance</i> , <b>2018</b> , 1, e201800080	5.8	12
61	A Novel Mechanism of Inactivating Antibacterial Nitro Compounds in the Human Pathogen Staphylococcus aureus by Overexpression of a NADH-Dependent Flavin Nitroreductase. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2018</b> , 62,	5.9	8
60	Genome organization and DNA accessibility control antigenic variation in trypanosomes. <i>Nature</i> , <b>2018</b> , 563, 121-125	50.4	84

59	ANNOgesic: a Swiss army knife for the RNA-seq based annotation of bacterial/archaeal genomes. <i>GigaScience</i> , <b>2018</b> , 7,	7.6	23
58	Post-transcriptional gene regulation by an Hfq-independent small RNA in Caulobacter crescentus. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 10969-10982	20.1	9
57	In [Vivo Cleavage Map Illuminates the Central Role of RNase E in Coding and Non-coding RNA Pathways. <i>Molecular Cell</i> , <b>2017</b> , 65, 39-51	17.6	159
56	Transcription Profiling of Cells Infected with AR9, a Giant Phage Encoding Two Multisubunit RNA Polymerases. <i>MBio</i> , <b>2017</b> , 8,	7.8	18
55	An RpoHI-Dependent Response Promotes Outgrowth after Extended Stationary Phase in the Alphaproteobacterium Rhodobacter sphaeroides. <i>Journal of Bacteriology</i> , <b>2017</b> , 199,	3.5	16
54	APRICOT: an integrated computational pipeline for the sequence-based identification and characterization of RNA-binding proteins. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e96	20.1	14
53	sRNA a newly identified regulator of nitrogen fixation in Methanosarcina mazei strain GI. <i>RNA Biology</i> , <b>2017</b> , 14, 1544-1558	4.8	25
52	GT-rich promoters can drive RNA pol II transcription and deposition of H2A.Z in African trypanosomes. <i>EMBO Journal</i> , <b>2017</b> , 36, 2581-2594	13	43
51	dRNA-seq transcriptional profiling of the FK506 biosynthetic gene cluster in Streptomyces tsukubaensis NRRL18488 and general analysis of the transcriptome. <i>RNA Biology</i> , <b>2017</b> , 14, 1617-1626	4.8	13
50	Insights into Microalga and Bacteria Interactions of Selected Phycosphere Biofilms Using Metagenomic, Transcriptomic, and Proteomic Approaches. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 1941	5.7	53
49	The primary transcriptome of the Escherichia coli O104:H4 pAA plasmid and novel insights into its virulence gene expression and regulation. <i>Scientific Reports</i> , <b>2016</b> , 6, 35307	4.9	10
48	Dual RNA-seq unveils noncoding RNA functions in host-pathogen interactions. <i>Nature</i> , <b>2016</b> , 529, 496-5	6 <b>05</b> 10.4	318
47	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> , <b>2016</b> , 7, 1858	5.7	6
46	Analysis of the Microprocessor in Dictyostelium: The Role of RbdB, a dsRNA Binding Protein. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006057	6	9
45	cis-Encoded Small RNAs, a Conserved Mechanism for Repression of Polysaccharide Utilization in Bacteroides. <i>Journal of Bacteriology</i> , <b>2016</b> , 198, 2410-8	3.5	20
44	Effect of Shear Stress on Pseudomonas aeruginosa Isolated from the Cystic Fibrosis Lung. <i>MBio</i> , <b>2016</b> , 7,	7.8	20
43	Genome-wide identification of transcriptional start sites in the haloarchaeon Haloferax volcanii based on differential RNA-Seq (dRNA-Seq). <i>BMC Genomics</i> , <b>2016</b> , 17, 629	4.5	78
42	Natural mutations in a Staphylococcus aureus 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> , <b>2016</b> , 113, E3101-10	11.5	61

#### (2014-2016)

41	Genome-wide transcription start site mapping of Bradyrhizobium japonicum grown free-living or in symbiosis - a rich resource to identify new transcripts, proteins and to study gene regulation. <i>BMC Genomics</i> , <b>2016</b> , 17, 302	4.5	38
40	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> , <b>2016</b> , 113, 11591-11596	11.5	193
39	Global transcriptional start site mapping using differential RNA sequencing reveals novel antisense RNAs in Escherichia coli. <i>Journal of Bacteriology</i> , <b>2015</b> , 197, 18-28	3.5	207
38	Genome-wide transcription start site profiling in biofilm-grown Burkholderia cenocepacia J2315. <i>BMC Genomics</i> , <b>2015</b> , 16, 775	4.5	24
37	Phenotypic Heterogeneity Affects Stenotrophomonas maltophilia K279a Colony Morphotypes and Lactamase Expression. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1373	5.7	11
36	dRNA-Seq Reveals Genomewide TSSs and Noncoding RNAs of Plant Beneficial Rhizobacterium Bacillus amyloliquefaciens FZB42. <i>PLoS ONE</i> , <b>2015</b> , 10, e0142002	3.7	22
35	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> , <b>2015</b> , 112, E766-75	11.5	141
34	RNA sequencing analysis of the broad-host-range strain Sinorhizobium fredii NGR234 identifies a large set of genes linked to quorum sensing-dependent regulation in the background of a tral and ngrI deletion mutant. <i>Applied and Environmental Microbiology</i> , <b>2014</b> , 80, 5655-71	4.8	26
33	READemption-a tool for the computational analysis of deep-sequencing-based transcriptome data. <i>Bioinformatics</i> , <b>2014</b> , 30, 3421-3	7.2	102
32	Evolution of resistance to a last-resort antibiotic in Staphylococcus aureus via bacterial competition. <i>Cell</i> , <b>2014</b> , 158, 1060-1071	56.2	129
31	Functional high-throughput screening identifies the miR-15 microRNA family as cellular restriction factors for Salmonella infection. <i>Nature Communications</i> , <b>2014</b> , 5, 4718	17.4	82
30	Profound impact of Hfq on nutrient acquisition, metabolism and motility in the plant pathogen Agrobacterium tumefaciens. <i>PLoS ONE</i> , <b>2014</b> , 9, e110427	3.7	24
29	RNase J is required for processing of a small number of RNAs in Rhodobacter sphaeroides. <i>RNA Biology</i> , <b>2014</b> , 11, 855-64	4.8	8
28	Role of oxygen and the OxyR protein in the response to iron limitation in Rhodobacter sphaeroides. <i>BMC Genomics</i> , <b>2014</b> , 15, 794	4.5	32
27	Argonaute proteins affect siRNA levels and accumulation of a novel extrachromosomal DNA from the Dictyostelium retrotransposon DIRS-1. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 35124-38	5.4	8
26	Primary transcriptome map of the hyperthermophilic archaeon Thermococcus kodakarensis. <i>BMC Genomics</i> , <b>2014</b> , 15, 684	4.5	69
25	Regulation of transcription termination by glucosylated hydroxymethyluracil, base J, in Leishmania major and Trypanosoma brucei. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 9717-29	20.1	46
24	The open science peer review oath. <i>F1000Research</i> , <b>2014</b> , 3, 271	3.6	11

23	An Open Science Peer Review Oath. <i>F1000Research</i> , <b>2014</b> , 3, 271	3.6	21
22	High-resolution transcriptome maps reveal strain-specific regulatory features of multiple Campylobacter jejuni isolates. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003495	6	201
21	Target recognition, RNA methylation activity and transcriptional regulation of the Dictyostelium discoideum Dnmt2-homologue (DnmA). <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 8615-27	20.1	39
20	Integrative "omics"-approach discovers dynamic and regulatory features of bacterial stress responses. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003576	6	50
19	Functional characterization of the RNA chaperone Hfq in the opportunistic human pathogen Stenotrophomonas maltophilia. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 5864-74	3.5	24
18	The primary transcriptome of barley chloroplasts: numerous noncoding RNAs and the dominating role of the plastid-encoded RNA polymerase. <i>Plant Cell</i> , <b>2012</b> , 24, 123-36	11.6	155
17	Collaborative platforms for streamlining workflows in Open Science. <i>Nature Precedings</i> , <b>2011</b> ,		3
16	Enterotypes of the human gut microbiome. <i>Nature</i> , <b>2011</b> , 473, 174-80	50.4	4240
15	Wikis in scholarly publishing*. <i>Information Services and Use</i> , <b>2011</b> , 31, 53-59	0.5	4
14	SmashCommunity: a metagenomic annotation and analysis tool. <i>Bioinformatics</i> , <b>2010</b> , 26, 2977-8	7.2	77
13	A computational screen for type I polyketide synthases in metagenomics shotgun data. <i>PLoS ONE</i> , <b>2008</b> , 3, e3515	3.7	29
12	A nitrile hydratase in the eukaryote Monosiga brevicollis. <i>PLoS ONE</i> , <b>2008</b> , 3, e3976	3.7	21
11	A molecular study of microbe transfer between distant environments. PLoS ONE, 2008, 3, e2607	3.7	16
10	Splicing factors stimulate polyadenylation via USEs at non-canonical 3Rend formation signals. <i>EMBO Journal</i> , <b>2007</b> , 26, 2658-69	13	65
9	Get the most out of your metagenome: computational analysis of environmental sequence data. <i>Current Opinion in Microbiology</i> , <b>2007</b> , 10, 490-8	7.9	127
8	Comparative analysis of environmental sequences: potential and challenges. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2006</b> , 361, 519-23	5.8	22
7	The sigmaB regulon in Staphylococcus aureus and its regulation. <i>International Journal of Medical Microbiology</i> , <b>2006</b> , 296, 237-58	3.7	133
6	Environments shape the nucleotide composition of genomes. <i>EMBO Reports</i> , <b>2005</b> , 6, 1208-13	6.5	200

#### LIST OF PUBLICATIONS

5	READemption - A tool for the computational analysis of deep-sequencing-based transcriptome data	6
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2	The bacterial leader peptide peTrpL has a conserved function in antibiotic-dependent posttranscriptional regulation of ribosomal genes	2
1	Trans-acting role of the leader peptide peTrpL in posttranscriptional regulation of multiresistance	1