

# Fabian Amman

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

1,748  
citations

331538

21  
h-index

302012

39  
g-index

51  
all docs

51  
docs citations

51  
times ranked

2609  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dual RNA-seq unveils noncoding RNA functions in host–pathogen interactions. <i>Nature</i> , 2016, 529, 496-501.	13.7	450
2	Inosine induces context-dependent recoding and translational stalling. <i>Nucleic Acids Research</i> , 2019, 47, 3-14.	6.5	128
3	A high resolution A-to-I editing map in the mouse identifies editing events controlled by pre-mRNA splicing. <i>Genome Research</i> , 2019, 29, 1453-1463.	2.4	90
4	Viral variant-resolved wastewater surveillance of SARS-CoV-2 at national scale. <i>Nature Biotechnology</i> , 2022, 40, 1814-1822.	9.4	82
5	TSSAR: TSS annotation regime for dRNA-seq data. <i>BMC Bioinformatics</i> , 2014, 15, 89.	1.2	73
6	Archaeal Signal Transduction: Impact of Protein Phosphatase Deletions on Cell Size, Motility, and Energy Metabolism in <i>Sulfolobus acidocaldarius</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3908-3923.	2.5	69
7	Transcriptional Responses to IFN- $\beta$ Require Mediator Kinase-Dependent Pause Release and Mechanistically Distinct CDK8 and CDK19 Functions. <i>Molecular Cell</i> , 2019, 76, 485-499.e8.	4.5	52
8	Fast accessibility-based prediction of RNA–RNA interactions. <i>Bioinformatics</i> , 2011, 27, 1934-1940.	1.8	48
9	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <i>Scientific Reports</i> , 2016, 6, 34589.	1.6	47
10	Transcriptional profiling of <i>Bordetella pertussis</i> reveals requirement of RNA chaperone Hfq for Type III secretion system functionality. <i>RNA Biology</i> , 2015, 12, 175-185.	1.5	42
11	RNASeq Based Transcriptional Profiling of <i>Pseudomonas aeruginosa</i> PA14 after Short- and Long-Term Anoxic Cultivation in Synthetic Cystic Fibrosis Sputum Medium. <i>PLoS ONE</i> , 2016, 11, e0147811.	1.1	42
12	Impact of Hfq on the <i>Bacillus subtilis</i> Transcriptome. <i>PLoS ONE</i> , 2014, 9, e98661.	1.1	40
13	An internal deletion of ADAR rescued by MAVS deficiency leads to a minute phenotype. <i>Nucleic Acids Research</i> , 2020, 48, 3286-3303.	6.5	39
14	Functional characterization of the human tRNA methyltransferases TRMT10A and TRMT10B. <i>Nucleic Acids Research</i> , 2020, 48, 6157-6169.	6.5	38
15	2D Meets 4G: G-Quadruplexes in RNA Secondary Structure Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 832-844.	1.9	37
16	Accurate mapping of tRNA reads. <i>Bioinformatics</i> , 2018, 34, 1116-1124.	1.8	33
17	ViennaNGS: A toolbox for building efficient next-generation sequencing analysis pipelines. <i>F1000Research</i> , 2015, 4, 50.	0.8	33
18	Primary transcriptome analysis reveals importance of IS elements for the shaping of the transcriptional landscape of <i>Bordetella pertussis</i> . <i>RNA Biology</i> , 2018, 15, 967-975.	1.5	32

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19	ADAR-deficiency perturbs the global splicing landscape in mouse tissues. <i>Genome Research</i> , 2020, 30, 1107-1118.	2.4	32
20	ViennaNGS: A toolbox for building efficient next- generation sequencing analysis pipelines. <i>F1000Research</i> , 2015, 4, 50.	0.8	31
21	Adaptive sequence evolution is driven by biotic stress in a pair of orchid species ( <i>Dactylorhiza</i> ) with distinct ecological optima. <i>Molecular Ecology</i> , 2017, 26, 3649-3662.	2.0	25
22	The SmAP1/2 proteins of the crenarchaeon <i>Sulfolobus solfataricus</i> interact with the exosome and stimulate A-rich tailing of transcripts. <i>Nucleic Acids Research</i> , 2017, 45, 7938-7949.	6.5	24
23	Alterations of the Transcriptome of <i>Sulfolobus acidocaldarius</i> by Exoribonuclease aCPSF2. <i>PLoS ONE</i> , 2013, 8, e76569.	1.1	21
24	Detection and abundance of SARS-CoV-2 in wastewater in Liechtenstein, and the estimation of prevalence and impact of the B.1.1.7 variant. <i>Journal of Water and Health</i> , 2022, 20, 114-125.	1.1	18
25	Emergence of SARS-CoV-2 Alpha lineage and its correlation with quantitative wastewater-based epidemiology data. <i>Water Research</i> , 2022, 215, 118257.	5.3	17
26	Negative Control of RpoS Synthesis by the sRNA ReaL in <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2488.	1.5	16
27	Identification of RNA 3' ends and termination sites in <i>Haloferax volcanii</i> . <i>RNA Biology</i> , 2020, 17, 663-676.	1.5	16
28	Gene Expression Profiling of <i>Pseudomonas aeruginosa</i> Upon Exposure to Colistin and Tobramycin. <i>Frontiers in Microbiology</i> , 2021, 12, 626715.	1.5	16
29	Transcriptional profiling of human macrophages during infection with <i>Bordetella pertussis</i> . <i>RNA Biology</i> , 2020, 17, 731-742.	1.5	15
30	The Anaerobically Induced sRNA Pail Affects Denitrification in <i>Pseudomonas aeruginosa</i> PA14. <i>Frontiers in Microbiology</i> , 2017, 8, 2312.	1.5	14
31	Signal transduction-dependent small regulatory RNA is involved in glutamate metabolism of the human pathogen <i>Bordetella pertussis</i> . <i>Rna</i> , 2018, 24, 1530-1541.	1.6	14
32	Organ-wide profiling in mouse reveals high editing levels of Filamin B mRNA in the musculoskeletal system. <i>RNA Biology</i> , 2018, 15, 877-885.	1.5	13
33	Bioinformatics of prokaryotic RNAs. <i>RNA Biology</i> , 2014, 11, 470-483.	1.5	12
34	iRAPs curb antisense transcription in <i>E. coli</i> . <i>Nucleic Acids Research</i> , 2019, 47, 10894-10905.	6.5	12
35	Comparative Integrated Omics Analysis of the Hfq Regulon in <i>Bordetella pertussis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 3073.	1.8	11
36	Adaptor protein RapZ activates endoribonuclease RNase E by protein-protein interaction to cleave a small regulatory RNA. <i>Rna</i> , 2020, 26, 1198-1215.	1.6	10

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37	Comparative Omics Analysis of Historic and Recent Isolates of <i>Bordetella pertussis</i> and Effects of Genome Rearrangements on Evolution. <i>Emerging Infectious Diseases</i> , 2021, 27, 57-68.	2.0	10
38	Modelling Translation Initiation under the Influence of sRNA. <i>International Journal of Molecular Sciences</i> , 2012, 13, 16223-16240.	1.8	9
39	Comparative genomics of Czech vaccine strains of <i>Bordetella pertussis</i> . <i>Pathogens and Disease</i> , 2018, 76, .	0.8	7
40	The Trouble with Long-Range Base Pairs in RNA Folding. <i>Lecture Notes in Computer Science</i> , 2013, , 1-11.	1.0	7
41	RNA Folding Algorithms with G-Quadruplexes. <i>Lecture Notes in Computer Science</i> , 2012, , 49-60.	1.0	7
42	Rewiring of Gene Expression in <i>Pseudomonas aeruginosa</i> During Diauxic Growth Reveals an Indirect Regulation of the MexGHI-OpmD Efflux Pump by Hfq. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
43	Nascent RNA signaling to yeast RNA Pol II during transcription elongation. <i>PLoS ONE</i> , 2018, 13, e0194438.	1.1	2
44	Enhancing the Cell-Free Expression of Native Membrane Proteins by In Silico Optimization of the Coding Sequence—An Experimental Study of the Human Voltage-Dependent Anion Channel. <i>Membranes</i> , 2021, 11, 741.	1.4	2
45	MSF: Modulated Sub-graph Finder. <i>F1000Research</i> , 2018, 7, 1346.	0.8	1
46	MSF: Modulated Sub-graph Finder. <i>F1000Research</i> , 0, 7, 1346.	0.8	1
47	MSF: Modulated Sub-graph Finder. <i>F1000Research</i> , 2018, 7, 1346.	0.8	1