

Sven Findeiss

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

4,547
citations

186265

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144013

57
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59
all docs

59
docs citations

59
times ranked

6785
citing authors

#	ARTICLE	IF	CITATIONS
1	Synthetic Riboswitches for the Analysis of tRNA Processing by eukaryotic RNase P Enzymes. <i>Rna</i> , 2022, , rna.078814.121.	3.5	3
2	Insights into the secondary and tertiary structure of the Bovine Viral Diarrhea Virus Internal Ribosome Entry Site. <i>RNA Biology</i> , 2022, 19, 496-506.	3.1	3
3	RNA Design Principles for Riboswitches that Regulate RNase P-Mediated tRNA Processing. <i>Methods in Molecular Biology</i> , 2022, , 179-202.	0.9	1
4	Evolutionary traits of Tick-borne encephalitis virus: Pervasive non-coding RNA structure conservation and molecular epidemiology. <i>Virus Evolution</i> , 2022, 8, .	4.9	10
5	Beyond Plug and Pray: Context Sensitivity and <i>in silico</i> Design of Artificial Neomycin Riboswitches. <i>RNA Biology</i> , 2021, 18, 457-467.	3.1	6
6	Ligand-dependent tRNA processing by a rationally designed RNase P riboswitch. <i>Nucleic Acids Research</i> , 2021, 49, 1784-1800.	14.5	4
7	Dynamic Molecular Epidemiology Reveals Lineage-Associated Single-Nucleotide Variants That Alter RNA Structure in Chikungunya Virus. <i>Genes</i> , 2021, 12, 239.	2.4	7
8	An African tick flavivirus forming an independent clade exhibits unique exoribonuclease-resistant RNA structures in the genomic 3' untranslated region. <i>Scientific Reports</i> , 2021, 11, 4883.	3.3	4
9	Gene Expression Profiling of <i>Pseudomonas aeruginosa</i> Upon Exposure to Colistin and Tobramycin. <i>Frontiers in Microbiology</i> , 2021, 12, 626715.	3.5	16
10	Common Features in lncRNA Annotation and Classification: A Survey. <i>Non-coding RNA</i> , 2021, 7, 77.	2.6	13
11	Discoveries of Exoribonuclease-Resistant Structures of Insect-Specific Flaviviruses Isolated in Zambia. <i>Viruses</i> , 2020, 12, 1017.	3.3	11
12	Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	203
13	Distinctive Regulation of Carbapenem Susceptibility in <i>Pseudomonas aeruginosa</i> by Hfq. <i>Frontiers in Microbiology</i> , 2020, 11, 1001.	3.5	16
14	Updated Phylogeny of Chikungunya Virus Suggests Lineage-Specific RNA Architecture. <i>Viruses</i> , 2019, 11, 798.	3.3	32
15	Evolving methods for rational de novo design of functional RNA molecules. <i>Methods</i> , 2019, 161, 54-63.	3.8	6
16	Musashi binding elements in Zika and related Flavivirus 3' UTRs: A comparative study <i>in silico</i> . <i>Scientific Reports</i> , 2019, 9, 6911.	3.3	16
17	Functional RNA Structures in the 3' UTR of Tick-Borne, Insect-Specific and No-Known-Vector Flaviviruses. <i>Viruses</i> , 2019, 11, 298.	3.3	43
18	Indications for a moonlighting function of translation factor aIF5A in the crenarchaeum <i>Sulfolobus solfataricus</i> . <i>RNA Biology</i> , 2019, 16, 675-685.	3.1	11

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19	Interplay between the catabolite repression control protein Crc, Hfq and RNA in Hfq-dependent translational regulation in <i>Pseudomonas aeruginosa</i> . <i>Nucleic Acids Research</i> , 2018, 46, 1470-1485.	14.5	85
20	Efficient computation of co-transcriptional RNA-ligand interaction dynamics. <i>Methods</i> , 2018, 143, 70-76.	3.8	13
21	Harnessing Metabolic Regulation to Increase Hfq-Dependent Antibiotic Susceptibility in <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2709.	3.5	27
22	In silico design of ligand triggered RNA switches. <i>Methods</i> , 2018, 143, 90-101.	3.8	14
23	TERribly Difficult: Searching for Telomerase RNAs in <i>Saccharomycetes</i> . <i>Genes</i> , 2018, 9, 372.	2.4	12
24	Applicability of a computational design approach for synthetic riboswitches. <i>Nucleic Acids Research</i> , 2017, 45, gkw1267.	14.5	52
25	NMR Structural Profiling of Transcriptional Intermediates Reveals Riboswitch Regulation by Metastable RNA Conformations. <i>Journal of the American Chemical Society</i> , 2017, 139, 2647-2656.	13.7	43
26	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.	14.5	24
27	RNAblueprint: flexible multiple target nucleic acid sequence design. <i>Bioinformatics</i> , 2017, 33, 2850-2858.	4.1	17
28	Design of Artificial Riboswitches as Biosensors. <i>Sensors</i> , 2017, 17, 1990.	3.8	50
29	The Anaerobically Induced sRNA Pail Affects Denitrification in <i>Pseudomonas aeruginosa</i> PA14. <i>Frontiers in Microbiology</i> , 2017, 8, 2312.	3.5	14
30	SHAPE directed RNA folding. <i>Bioinformatics</i> , 2016, 32, 145-147.	4.1	91
31	Cross-regulation by CrcZ RNA controls anoxic biofilm formation in <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2016, 6, 39621.	3.3	45
32	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <i>Scientific Reports</i> , 2016, 6, 34589.	3.3	47
33	Predicting RNA secondary structures from sequence and probing data. <i>Methods</i> , 2016, 103, 86-98.	3.8	110
34	Transcriptome-wide effects of inverted SINEs on gene expression and their impact on RNA polymerase II activity. <i>Genome Biology</i> , 2016, 17, 220.	8.8	20
35	The MazF-regulon: a toolbox for the post-transcriptional stress response in <i>Escherichia coli</i> .	14.5	45
36	Design of Transcription Regulating Riboswitches. <i>Methods in Enzymology</i> , 2015, 550, 1-22.	1.0	8

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37	General and MicroRNA-Mediated mRNA Degradation Occurs on Ribosome Complexes in <i>Drosophila</i> Cells. <i>Molecular and Cellular Biology</i> , 2015, 35, 2309-2320.	2.3	41
38	Design criteria for synthetic riboswitches acting on transcription. <i>RNA Biology</i> , 2015, 12, 221-231.	3.1	41
39	ViennaNGS: A toolbox for building efficient next-generation sequencing analysis pipelines. <i>F1000Research</i> , 2015, 4, 50.	1.6	31
40	Bioinformatics of prokaryotic RNAs. <i>RNA Biology</i> , 2014, 11, 470-483.	3.1	12
41	Memory-efficient RNA energy landscape exploration. <i>Bioinformatics</i> , 2014, 30, 2584-2591.	4.1	10
42	TSSAR: TSS annotation regime for dRNA-seq data. <i>BMC Bioinformatics</i> , 2014, 15, 89.	2.6	73
43	Identification of new protein coding sequences and signal peptidase cleavage sites of <i>Helicobacter pylori</i> strain 26695 by proteogenomics. <i>Journal of Proteomics</i> , 2013, 86, 27-42.	2.4	37
44	De novo design of a synthetic riboswitch that regulates transcription termination. <i>Nucleic Acids Research</i> , 2013, 41, 2541-2551.	14.5	163
45	Genome-wide transcriptome analysis of the plant pathogen <i>Xanthomonas</i> identifies sRNAs with putative virulence functions. <i>Nucleic Acids Research</i> , 2012, 40, 2020-2031.	14.5	93
46	Traces of post-transcriptional RNA modifications in deep sequencing data. <i>Biological Chemistry</i> , 2011, 392, 305-13.	2.5	54
47	Protein-coding structured RNAs: A computational survey of conserved RNA secondary structures overlapping coding regions in drosophilids. <i>Biochimie</i> , 2011, 93, 2019-2023.	2.6	9
48	Proteinortho: Detection of (Co-)orthologs in large-scale analysis. <i>BMC Bioinformatics</i> , 2011, 12, 124.	2.6	1,091
49	The small RNA Aar in <i>Acinetobacter baylyi</i> : a putative regulator of amino acid metabolism. <i>Archives of Microbiology</i> , 2010, 192, 691-702.	2.2	12
50	Optimization of parameters for coverage of low molecular weight proteins. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 398, 2867-2881.	3.7	43
51	The primary transcriptome of the major human pathogen <i>Helicobacter pylori</i> . <i>Nature</i> , 2010, 464, 250-255.	27.8	1,115
52	BarMap: RNA folding on dynamic energy landscapes. <i>Rna</i> , 2010, 16, 1308-1316.	3.5	53
53	RNAz 2.0: improved noncoding RNA detection. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2010, , 69-79.	0.7	135
54	RNAZ 2.0., 2009, , 69-79.		68

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55	Folding Kinetics of Large RNAs. <i>Journal of Molecular Biology</i> , 2008, 379, 160-173.	4.2	77
56	Computational RNomics of Drosophilids. <i>BMC Genomics</i> , 2007, 8, 406.	2.8	38
57	Efficient computation of RNA folding dynamics. <i>Journal of Physics A</i> , 2004, 37, 4731-4741.	1.6	99
58	Barrier Trees of Degenerate Landscapes. <i>Zeitschrift Fur Physikalische Chemie</i> , 2002, 216, .	2.8	130