

Sven Findeiss

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

4,547
citations

186265

28
h-index

144013

57
g-index

59
all docs

59
docs citations

59
times ranked

6785
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | The primary transcriptome of the major human pathogen <i>Helicobacter pylori</i> . <i>Nature</i> , 2010, 464, 250-255. | 27.8 | 1,115 |
| 2 | Proteinortho: Detection of (Co-)orthologs in large-scale analysis. <i>BMC Bioinformatics</i> , 2011, 12, 124. | 2.6 | 1,091 |
| 3 | 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 |
| 4 | De novo design of a synthetic riboswitch that regulates transcription termination. <i>Nucleic Acids Research</i> , 2013, 41, 2541-2551. | 14.5 | 163 |
| 5 | RNAz 2.0: improved noncoding RNA detection. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2010, , 69-79. | 0.7 | 135 |
| 6 | Barrier Trees of Degenerate Landscapes. <i>Zeitschrift Fur Physikalische Chemie</i> , 2002, 216, . | 2.8 | 130 |
| 7 | Predicting RNA secondary structures from sequence and probing data. <i>Methods</i> , 2016, 103, 86-98. | 3.8 | 110 |
| 8 | Efficient computation of RNA folding dynamics. <i>Journal of Physics A</i> , 2004, 37, 4731-4741. | 1.6 | 99 |
| 9 | 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 |
| 10 | SHAPE directed RNA folding. <i>Bioinformatics</i> , 2016, 32, 145-147. | 4.1 | 91 |
| 11 | 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 |
| 12 | Folding Kinetics of Large RNAs. <i>Journal of Molecular Biology</i> , 2008, 379, 160-173. | 4.2 | 77 |
| 13 | TSSAR: TSS annotation regime for dRNA-seq data. <i>BMC Bioinformatics</i> , 2014, 15, 89. | 2.6 | 73 |
| 14 | RNAZ 2.0: , 2009, , 69-79. | | 68 |
| 15 | Traces of post-transcriptional RNA modifications in deep sequencing data. <i>Biological Chemistry</i> , 2011, 392, 305-13. | 2.5 | 54 |
| 16 | BarMap: RNA folding on dynamic energy landscapes. <i>Rna</i> , 2010, 16, 1308-1316. | 3.5 | 53 |
| 17 | Applicability of a computational design approach for synthetic riboswitches. <i>Nucleic Acids Research</i> , 2017, 45, gkw1267. | 14.5 | 52 |
| 18 | Design of Artificial Riboswitches as Biosensors. <i>Sensors</i> , 2017, 17, 1990. | 3.8 | 50 |

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|----|---|------|-----------|
| 19 | Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <i>Scientific Reports</i> , 2016, 6, 34589. | 3.3 | 47 |
| 20 | Cross-regulation by CrcZ RNA controls anoxic biofilm formation in <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2016, 6, 39621. | 3.3 | 45 |
| 21 | The MazF-regulon: a toolbox for the post-transcriptional stress response in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2016, 44, 6660-6675. | 14.5 | 45 |
| 22 | Optimization of parameters for coverage of low molecular weight proteins. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 398, 2867-2881. | 3.7 | 43 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | Design criteria for synthetic riboswitches acting on transcription. <i>RNA Biology</i> , 2015, 12, 221-231. | 3.1 | 41 |
| 27 | Computational RNomics of <i>Drosophilids</i> . <i>BMC Genomics</i> , 2007, 8, 406. | 2.8 | 38 |
| 28 | 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 |
| 29 | Updated Phylogeny of Chikungunya Virus Suggests Lineage-Specific RNA Architecture. <i>Viruses</i> , 2019, 11, 798. | 3.3 | 32 |
| 30 | ViennaNGS: A toolbox for building efficient next-generation sequencing analysis pipelines. <i>F1000Research</i> , 2015, 4, 50. | 1.6 | 31 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | RNAblueprint: flexible multiple target nucleic acid sequence design. <i>Bioinformatics</i> , 2017, 33, 2850-2858. | 4.1 | 17 |
| 35 | Musashi binding elements in Zika and related Flavivirus 3'UTRs: A comparative study in silico. <i>Scientific Reports</i> , 2019, 9, 6911. | 3.3 | 16 |
| 36 | Distinctive Regulation of Carbapenem Susceptibility in <i>Pseudomonas aeruginosa</i> by Hfq. <i>Frontiers in Microbiology</i> , 2020, 11, 1001. | 3.5 | 16 |

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|----|--|------|-----------|
| 37 | 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 |
| 38 | The Anaerobically Induced sRNA Pail Affects Denitrification in <i>Pseudomonas aeruginosa</i> PA14. <i>Frontiers in Microbiology</i> , 2017, 8, 2312. | 3.5 | 14 |
| 39 | In silico design of ligand triggered RNA switches. <i>Methods</i> , 2018, 143, 90-101. | 3.8 | 14 |
| 40 | Efficient computation of co-transcriptional RNA-ligand interaction dynamics. <i>Methods</i> , 2018, 143, 70-76. | 3.8 | 13 |
| 41 | Common Features in lncRNA Annotation and Classification: A Survey. <i>Non-coding RNA</i> , 2021, 7, 77. | 2.6 | 13 |
| 42 | 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 |
| 43 | Bioinformatics of prokaryotic RNAs. <i>RNA Biology</i> , 2014, 11, 470-483. | 3.1 | 12 |
| 44 | TERribly Difficult: Searching for Telomerase RNAs in <i>Saccharomyces</i> . <i>Genes</i> , 2018, 9, 372. | 2.4 | 12 |
| 45 | 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 |
| 46 | Discoveries of Exoribonuclease-Resistant Structures of Insect-Specific Flaviviruses Isolated in Zambia. <i>Viruses</i> , 2020, 12, 1017. | 3.3 | 11 |
| 47 | Memory-efficient RNA energy landscape exploration. <i>Bioinformatics</i> , 2014, 30, 2584-2591. | 4.1 | 10 |
| 48 | 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 |
| 49 | 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 |
| 50 | Design of Transcription Regulating Riboswitches. <i>Methods in Enzymology</i> , 2015, 550, 1-22. | 1.0 | 8 |
| 51 | 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 |
| 52 | Evolving methods for rational de novo design of functional RNA molecules. <i>Methods</i> , 2019, 161, 54-63. | 3.8 | 6 |
| 53 | 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 |
| 54 | Ligand-dependent tRNA processing by a rationally designed RNase P riboswitch. <i>Nucleic Acids Research</i> , 2021, 49, 1784-1800. | 14.5 | 4 |

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|----|---|-----|-----------|
| 55 | 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 |
| 56 | Synthetic Riboswitches for the Analysis of tRNA Processing by eukaryotic RNase P Enzymes. <i>Rna</i> , 2022, , rna.078814.121. | 3.5 | 3 |
| 57 | 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 |
| 58 | RNA Design Principles for Riboswitches that Regulate RNase P-Mediated tRNA Processing. <i>Methods in Molecular Biology</i> , 2022, , 179-202. | 0.9 | 1 |