

# Jana Hertel

## List of Publications by Year in descending order

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44  
papers

10,090  
citations

257101

24  
h-index

243296

44  
g-index

49  
all docs

49  
docs citations

49  
times ranked

15548  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution and Phylogeny of MicroRNAs â€” Protocols, Pitfalls, and Problems. <i>Methods in Molecular Biology</i> , 2022, 2257, 211-233.	0.4	2
2	Mouse Retinal Organoid Growth and Maintenance in Longer-Term Culture. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 645704.	1.8	13
3	A Multi-Omics Analysis of Mucosal-Associated-Invariant T Cells Reveals Key Drivers of Distinct Modes of Activation. <i>Frontiers in Immunology</i> , 2021, 12, 616967.	2.2	13
4	Potential Co-Factors of an Intraoral Contact Allergyâ€”A Cross-Sectional Study. <i>Dentistry Journal</i> , 2020, 8, 83.	0.9	5
5	A probabilistic version of Sankoffâ€™s maximum parsimony algorithm. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050004.	0.3	1
6	Prospects and challenges of multi-omics data integration in toxicology. <i>Archives of Toxicology</i> , 2020, 94, 371-388.	1.9	142
7	uap: reproducible and robust HTS data analysis. <i>BMC Bioinformatics</i> , 2019, 20, 664.	1.2	14
8	Specific induction of the unique GPR15 expression in heterogeneous blood lymphocytes by tobacco smoking. <i>Biomarkers</i> , 2019, 24, 217-224.	0.9	16
9	The fungal snoRNAome. <i>Rna</i> , 2018, 24, 342-360.	1.6	10
10	Towards a Consistent, Quantitative Evaluation of MicroRNA Evolution. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	7
11	Evolution of Fungal U3 snoRNAs: Structural Variation and Introns. <i>Non-coding RNA</i> , 2017, 3, 3.	1.3	4
12	SnoReport 2.0: new features and a refined Support Vector Machine to improve snoRNA identification. <i>BMC Bioinformatics</i> , 2016, 17, 464.	1.2	21
13	Phylogenetic distribution of plant snoRNA families. <i>BMC Genomics</i> , 2016, 17, 969.	1.2	15
14	An updated human snoRNAome. <i>Nucleic Acids Research</i> , 2016, 44, 5068-5082.	6.5	216
15	U6 snRNA intron insertion occurred multiple times during fungi evolution. <i>RNA Biology</i> , 2016, 13, 119-127.	1.5	7
16	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. <i>Nature Genetics</i> , 2016, 48, 427-437.	9.4	545
17	Conservation and Losses of Non-Coding RNAs in Avian Genomes. <i>PLoS ONE</i> , 2015, 10, e0121797.	1.1	18
18	The Expansion of Animal MicroRNA Families Revisited. <i>Life</i> , 2015, 5, 905-920.	1.1	44

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19	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	0.6	97
20	23 RNA in phylogenetic reconstruction. , 2014, , 531-538.		1
21	<tt>snoStrip</tt>: a snoRNA annotation pipeline. <i>Bioinformatics</i> , 2014, 30, 115-116.	1.8	23
22	Matching of Soulmates: Coevolution of snoRNAs and Their Targets. <i>Molecular Biology and Evolution</i> , 2014, 31, 455-467.	3.5	51
23	The Coilin Interactome Identifies Hundreds of Small Noncoding RNAs that Traffic through Cajal Bodies. <i>Molecular Cell</i> , 2014, 56, 389-399.	4.5	88
24	Computational Prediction of MicroRNA Genes. <i>Methods in Molecular Biology</i> , 2014, 1097, 437-456.	0.4	15
25	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. <i>Current Biology</i> , 2013, 23, 1388.	1.8	1
26	Evolution of the let-7 microRNA Family. <i>RNA Biology</i> , 2012, 9, 231-241.	1.5	115
27	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. <i>Current Biology</i> , 2012, 22, 1309-1313.	1.8	140
28	MicroRNA or Not MicroRNA?. <i>Lecture Notes in Computer Science</i> , 2011, , 1-9.	1.0	14
29	<tt>RNAsnoop</tt>: efficient target prediction for H/ACA snoRNAs. <i>Bioinformatics</i> , 2010, 26, 610-616.	1.8	49
30	Non-coding RNA annotation of the genome of <i>Trichoplax adhaerens</i> . <i>Nucleic Acids Research</i> , 2009, 37, 1602-1615.	6.5	56
31	Accurate and efficient reconstruction of deep phylogenies from structured RNAs. <i>Nucleic Acids Research</i> , 2009, 37, 6184-6193.	6.5	108
32	Evidence for human microRNA-offset RNAs in small RNA sequencing data. <i>Bioinformatics</i> , 2009, 25, 2298-2301.	1.8	120
33	Homology-based annotation of non-coding RNAs in the genomes of <i>Schistosoma mansoni</i> and <i>Schistosoma japonicum</i> . <i>BMC Genomics</i> , 2009, 10, 464.	1.2	51
34	NcDNAAlign: Plausible multiple alignments of non-protein-coding genomic sequences. <i>Genomics</i> , 2008, 92, 65-74.	1.3	18
35	<tt>SnoReport</tt>: computational identification of snoRNAs with unknown targets. <i>Bioinformatics</i> , 2008, 24, 158-164.	1.8	116
36	Small ncRNA transcriptome analysis from <i>Aspergillus fumigatus</i> suggests a novel mechanism for regulation of protein synthesis. <i>Nucleic Acids Research</i> , 2008, 36, 2677-2689.	6.5	162

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37	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007, 17, 852-864.	2.4	150
38	RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. <i>Science</i> , 2007, 316, 1484-1488.	6.0	2,250
39	RNAs everywhere: genome-wide annotation of structured RNAs. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007, 308B, 1-25.	0.6	46
40	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
41	Computational RNomics of Drosophilids. <i>BMC Genomics</i> , 2007, 8, 406.	1.2	38
42	Variations on RNA folding and alignment: lessons from Benasque. <i>Journal of Mathematical Biology</i> , 2007, 56, 129-144.	0.8	65
43	The expansion of the metazoan microRNA repertoire. <i>BMC Genomics</i> , 2006, 7, 25.	1.2	304
44	Hairpins in a Haystack: recognizing microRNA precursors in comparative genomics data. <i>Bioinformatics</i> , 2006, 22, e197-e202.	1.8	180