

# Jana Hertel

## List of Publications by Year in descending order

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Version: 2024-02-01

44  
papers

10,090  
citations

257450

24  
h-index

243625

44  
g-index

49  
all docs

49  
docs citations

49  
times ranked

15548  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
2	RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. <i>Science</i> , 2007, 316, 1484-1488.	12.6	2,250
3	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. <i>Nature Genetics</i> , 2016, 48, 427-437.	21.4	545
4	The expansion of the metazoan microRNA repertoire. <i>BMC Genomics</i> , 2006, 7, 25.	2.8	304
5	An updated human snoRNAome. <i>Nucleic Acids Research</i> , 2016, 44, 5068-5082.	14.5	216
6	Hairpins in a Haystack: recognizing microRNA precursors in comparative genomics data. <i>Bioinformatics</i> , 2006, 22, e197-e202.	4.1	180
7	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.	14.5	162
8	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007, 17, 852-864.	5.5	150
9	Prospects and challenges of multi-omics data integration in toxicology. <i>Archives of Toxicology</i> , 2020, 94, 371-388.	4.2	142
10	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. <i>Current Biology</i> , 2012, 22, 1309-1313.	3.9	140
11	Evidence for human microRNA-offset RNAs in small RNA sequencing data. <i>Bioinformatics</i> , 2009, 25, 2298-2301.	4.1	120
12	<tt>SnoReport</tt>: computational identification of snoRNAs with unknown targets. <i>Bioinformatics</i> , 2008, 24, 158-164.	4.1	116
13	Evolution of the let-7 microRNA Family. <i>RNA Biology</i> , 2012, 9, 231-241.	3.1	115
14	Accurate and efficient reconstruction of deep phylogenies from structured RNAs. <i>Nucleic Acids Research</i> , 2009, 37, 6184-6193.	14.5	108
15	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	1.1	97
16	The Coilin Interactome Identifies Hundreds of Small Noncoding RNAs that Traffic through Cajal Bodies. <i>Molecular Cell</i> , 2014, 56, 389-399.	9.7	88
17	Variations on RNA folding and alignment: lessons from Benasque. <i>Journal of Mathematical Biology</i> , 2007, 56, 129-144.	1.9	65
18	Non-coding RNA annotation of the genome of <i>Trichoplax adhaerens</i> . <i>Nucleic Acids Research</i> , 2009, 37, 1602-1615.	14.5	56

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19	Homology-based annotation of non-coding RNAs in the genomes of <i>Schistosoma mansoni</i> and <i>Schistosoma japonicum</i> . BMC Genomics, 2009, 10, 464.	2.8	51
20	Matching of Soulmates: Coevolution of snoRNAs and Their Targets. Molecular Biology and Evolution, 2014, 31, 455-467.	8.9	51
21	<tt>RNAsnoop</tt>: efficient target prediction for H/ACA snoRNAs. Bioinformatics, 2010, 26, 610-616.	4.1	49
22	RNAs everywhere: genome-wide annotation of structured RNAs. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 1-25.	1.3	46
23	The Expansion of Animal MicroRNA Families Revisited. Life, 2015, 5, 905-920.	2.4	44
24	Computational RNomics of Drosophilids. BMC Genomics, 2007, 8, 406.	2.8	38
25	<tt>snoStrip</tt>: a snoRNA annotation pipeline. Bioinformatics, 2014, 30, 115-116.	4.1	23
26	SnoReport 2.0: new features and a refined Support Vector Machine to improve snoRNA identification. BMC Bioinformatics, 2016, 17, 464.	2.6	21
27	NcDNAAlign: Plausible multiple alignments of non-protein-coding genomic sequences. Genomics, 2008, 92, 65-74.	2.9	18
28	Conservation and Losses of Non-Coding RNAs in Avian Genomes. PLoS ONE, 2015, 10, e0121797.	2.5	18
29	Specific induction of the unique GPR15 expression in heterogeneous blood lymphocytes by tobacco smoking. Biomarkers, 2019, 24, 217-224.	1.9	16
30	Phylogenetic distribution of plant snoRNA families. BMC Genomics, 2016, 17, 969.	2.8	15
31	Computational Prediction of MicroRNA Genes. Methods in Molecular Biology, 2014, 1097, 437-456.	0.9	15
32	MicroRNA or Not MicroRNA?. Lecture Notes in Computer Science, 2011, , 1-9.	1.3	14
33	uap: reproducible and robust HTS data analysis. BMC Bioinformatics, 2019, 20, 664.	2.6	14
34	Mouse Retinal Organoid Growth and Maintenance in Longer-Term Culture. Frontiers in Cell and Developmental Biology, 2021, 9, 645704.	3.7	13
35	A Multi-Omics Analysis of Mucosal-Associated-Invariant T Cells Reveals Key Drivers of Distinct Modes of Activation. Frontiers in Immunology, 2021, 12, 616967.	4.8	13
36	The fungal snoRNAome. Rna, 2018, 24, 342-360.	3.5	10

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37	U6 snRNA intron insertion occurred multiple times during fungi evolution. RNA Biology, 2016, 13, 119-127.	3.1	7
38	Towards a Consistent, Quantitative Evaluation of MicroRNA Evolution. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	7
39	Potential Co-Factors of an Intraoral Contact Allergyâ€”A Cross-Sectional Study. Dentistry Journal, 2020, 8, 83.	2.3	5
40	Evolution of Fungal U3 snoRNAs: Structural Variation and Introns. Non-coding RNA, 2017, 3, 3.	2.6	4
41	Evolution and Phylogeny of MicroRNAs â€” Protocols, Pitfalls, and Problems. Methods in Molecular Biology, 2022, 2257, 211-233.	0.9	2
42	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. Current Biology, 2013, 23, 1388.	3.9	1
43	23 RNA in phylogenetic reconstruction. , 2014, , 531-538.		1
44	A probabilistic version of Sankoffâ€™s maximum parsimony algorithm. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050004.	0.8	1