Peter F F Stadler

List of Publications by Citations

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654 papers	43,000 citations	88 h-index	196 g-index
732 ext. papers	51,467 ext. citations	5.5 avg, IF	7.85 L-index

#	Paper	IF	Citations
654	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
653	MITOS: improved de novo metazoan mitochondrial genome annotation. *Molecular Phylogenetics and Evolution*, **2013**, 69, 313-9	4.1	2362
652	ViennaRNA Package 2.0. *Algorithms for Molecular Biology*, **2011**, 6, 26	1.8	2351
651	RNA maps reveal new RNA classes and a possible function for pervasive transcription. *Science*, **2007** , 316, 1484-8	33.3	1903
650	Fast folding and comparison of RNA secondary structures. *Monatshefte F� Chemie*, **1994**, 125, 167-188	1.4	1541
649	Analyses of pig genomes provide insight into porcine demography and evolution. *Nature*, **2012**, 491, 393-8	50.4	928
648	The primary transcriptome of the major human pathogen Helicobacter pylori. *Nature*, **2010**, 464, 250-5	50.4	891
647	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
646	Proteinortho: detection of (co-)orthologs in large-scale analysis. *BMC Bioinformatics*, **2011**, 12, 124	3.6	720
645	Comparative genomics reveals insights into avian genome evolution and adaptation. *Science*, **2014**, 346, 1311-20	33.3	628
644	tRNAdb 2009: compilation of tRNA sequences and tRNA genes. *Nucleic Acids Research*, **2009**, 37, D159-62	20.1	592
643	Interleukin-6 dependent survival of multiple myeloma cells involves the Stat3-mediated induction of microRNA-21 through a highly conserved enhancer. *Blood*, **2007**, 110, 1330-3	2.2	535
642	Fast and reliable prediction of noncoding RNAs. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 2454-9	11.5	518
641	Secondary structure prediction for aligned RNA sequences. *Journal of Molecular Biology*, **2002**, 319, 1059-66	6.5	490
640	The African coelacanth genome provides insights into tetrapod evolution. *Nature*, **2013**, 496, 311-6	50.4	488
639	Molecular evolution of a microRNA cluster. *Journal of Molecular Biology*, **2004**, 339, 327-35	6.5	483
638	Smoothness within ruggedness: the role of neutrality in adaptation. *Proceedings of the National Academy of Sciences of the United States of America*, **1996**, 93, 397-401	11.5	423

637	RNAalifold: improved consensus structure prediction for RNA alignments. *BMC Bioinformatics*, **2008** , 9, 474	3.6	390
636	Fast mapping of short sequences with mismatches, insertions and deletions using index structures. *PLoS Computational Biology*, **2009**, 5, e1000502	5	384
635	The genome of the recently domesticated crop plant sugar beet (Beta vulgaris). *Nature*, **2014**, 505, 546-9	50.4	365
634	Inferring noncoding RNA families and classes by means of genome-scale structure-based clustering. *PLoS Computational Biology*, **2007**, 3, e65	5	355
633	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. *Nature Genetics*, **2016**, 48, 427-37	36.3	352
632	The reality of pervasive transcription. *PLoS Biology*, **2011**, 9, e1000625; discussion e1001102	9.7	325
631	Mapping of conserved RNA secondary structures predicts thousands of functional noncoding RNAs in the human genome. *Nature Biotechnology*, **2005**, 23, 1383-90	44.5	324
630	Dual RNA-seq unveils noncoding RNA functions in host-pathogen interactions. *Nature*, **2016**, 529, 496-501	50.4	318
629	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. *Nature Genetics*, **2012**, 44, 1316-20	36.3	317
628	Multi-platform next-generation sequencing of the domestic turkey (Meleagris gallopavo): genome assembly and analysis. *PLoS Biology*, **2010**, 8, e1000475	9.7	311
627	Alu elements in ANRIL non-coding RNA at chromosome 9p21 modulate atherogenic cell functions through trans-regulation of gene networks. *PLoS Genetics*, **2013**, 9, e1003588	6	272
626	The expansion of the metazoan microRNA repertoire. *BMC Genomics*, **2006**, 7, 25	4.5	272
625	Thermodynamics of RNA-RNA binding. *Bioinformatics*, **2006**, 22, 1177-82	7.2	272
624	Evolution. Transitions from nonliving to living matter. *Science*, **2004**, 303, 963-5	33.3	253
623	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. *Nature Genetics*, **2013**, 45, 776-783	36.3	240
622	Statistics of RNA secondary structures. *Biopolymers*, **1993**, 33, 1389-404	2.2	238
621	Centers of complex networks. *Journal of Theoretical Biology*, **2003**, 223, 45-53	2.3	237
620	LocARNA-P: accurate boundary prediction and improved detection of structural RNAs. *Rna*, **2012**, 18, 900-14	5.8	221

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618	Sound-meaning association biases evidenced across thousands of languages. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 10818-23	11.5	194
617	A multi-split mapping algorithm for circular RNA, splicing, trans-splicing and fusion detection. *Genome Biology*, **2014**, 15, R34	18.3	188
616	CREx: inferring genomic rearrangements based on common intervals. *Bioinformatics*, **2007**, 23, 2957-8	7.2	188
615	Partition function and base pairing probabilities of RNA heterodimers. *Algorithms for Molecular Biology*, **2006**, 1, 3	1.8	183
614	Landscapes and their correlation functions. *Journal of Mathematical Chemistry*, **1996**, 20, 1-45	2.1	182
613	miRNAMap: genomic maps of microRNA genes and their target genes in mammalian genomes. *Nucleic Acids Research*, **2006**, 34, D135-9	20.1	176
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611	RNA folding and combinatory landscapes. *Physical Review E*, **1993**, 47, 2083-2099	2.4	175
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609	Ecological plant epigenetics: Evidence from model and non-model species, and the way forward. *Ecology Letters*, **2017**, 20, 1576-1590	10	165
608	Local RNA base pairing probabilities in large sequences. *Bioinformatics*, **2006**, 22, 614-5	7.2	164
607	Combinatorial Landscapes. *SIAM Review*, **2002**, 44, 3-54	7.4	162
606	Spontaneous and engineered deletions in the 3' noncoding region of tick-borne encephalitis virus: construction of highly attenuated mutants of a flavivirus. *Journal of Virology*, **1998**, 72, 2132-40	6.6	161
605	metilene: fast and sensitive calling of differentially methylated regions from bisulfite sequencing data. *Genome Research*, **2016**, 26, 256-62	9.7	159
604	The "fish-specific" Hox cluster duplication is coincident with the origin of teleosts. *Molecular Biology and Evolution*, **2006**, 23, 121-36	8.3	156
603	Hairpins in a Haystack: recognizing microRNA precursors in comparative genomics data. *Bioinformatics*, **2006**, 22, e197-202	7.2	155
602	Genetic aspects of mitochondrial genome evolution. *Molecular Phylogenetics and Evolution*, **2013**, 69, 328-38	4.1	154

601	Improved systematic tRNA gene annotation allows new insights into the evolution of mitochondrial tRNA structures and into the mechanisms of mitochondrial genome rearrangements. *Nucleic Acids Research*, **2012**, 40, 2833-45	20.1	145
600	Conserved RNA secondary structures in Flaviviridae genomes. *Journal of General Virology*, **2004**, 85, 1113-1124	4.9	142
599	An updated human snoRNAome. *Nucleic Acids Research*, **2016**, 44, 5068-82	20.1	141
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597	A comprehensive analysis of bilaterian mitochondrial genomes and phylogeny. *Molecular Phylogenetics and Evolution*, **2013**, 69, 352-64	4.1	140
596	Small ncRNA transcriptome analysis from Aspergillus fumigatus suggests a novel mechanism for regulation of protein synthesis. *Nucleic Acids Research*, **2008**, 36, 2677-89	20.1	140
595	De novo design of a synthetic riboswitch that regulates transcription termination. *Nucleic Acids Research*, **2013**, 41, 2541-51	20.1	131
594	RNAcode: robust discrimination of coding and noncoding regions in comparative sequence data. *Rna*, **2011**, 17, 578-94	5.8	131
593	Structured RNAs in the ENCODE selected regions of the human genome. *Genome Research*, **2007**, 17, 852-64	9.7	131
592	RNAz 2.0: improved noncoding RNA detection. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2010**, 69-79	1.3	129
591	Widespread purifying selection on RNA structure in mammals. *Nucleic Acids Research*, **2013**, 41, 8220-36	20.1	126
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589	Prediction of locally stable RNA secondary structures for genome-wide surveys. *Bioinformatics*, **2004**, 20, 186-90	7.2	125
588	RNAcentral: a comprehensive database of non-coding RNA sequences. *Nucleic Acids Research*, **2017**, 45, D128-D134	20.1	119
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