Peter F F Stadler

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Synthetic Riboswitches for the Analysis of tRNA Processing by eukaryotic RNase P Enzymes.. *Rna*, **2022**,	5.8	3
653	Evolution of DNA Methylation Across Ecdysozoa.. *Journal of Molecular Evolution*, **2022**, 90, 56	3.1	0
652	Chromosome-level Thlaspi arvense genome provides new tools for translational research and for a newly domesticated cash cover crop of the cooler climates.. *Plant Biotechnology Journal*, **2022**,	11.6	2
651	PredicTF: prediction of bacterial transcription factors in complex microbial communities using deep learning.. *Environmental Microbiomes*, **2022**, 17, 7	5.6	0
650	From modular decomposition trees to rooted median graphs. *Discrete Applied Mathematics*, **2022**, 310, 1-9	1	1
649	Evolution and Phylogeny of MicroRNAs - Protocols, Pitfalls, and Problems. *Methods in Molecular Biology*, **2022**, 2257, 211-233	1.4	
648	44 Current Challenges in miRNomics. *Methods in Molecular Biology*, **2022**, 2257, 423-438	1.4	4
647	Small integral membrane protein 10 like 1 enhances differentiation of adipose progenitor cells.. *Biochemical and Biophysical Research Communications*, **2022**, 604, 57-62	3.4	
646	Compatibility of partitions with trees, hierarchies, and split systems. *Discrete Applied Mathematics*, **2022**, 314, 265-283	1	2
645	Cas1 and Fen1 Display Equivalent Functions During Archaeal DNA Repair.. *Frontiers in Microbiology*, **2022**, 13, 822304	5.7	0
644	The genomic and transcriptional landscape of primary central nervous system lymphoma.. *Nature Communications*, **2022**, 13, 2558	17.4	4
643	Bi-alignments with affine gaps costs.. *Algorithms for Molecular Biology*, **2022**, 17, 10	1.8	
642	Kosteneffektive hybride Genomassemblierung mit LazyB. *BioSpektrum*, **2022**, 28, 283-286	0.1	
641	Complete edge-colored permutation graphs. *Advances in Applied Mathematics*, **2022**, 139, 102377	0.8	0
640	RNA Design Principles for Riboswitches that Regulate RNase P-Mediated tRNA Processing. *Methods in Molecular Biology*, **2022**, 179-202	1.4	0
639	cyPhyRNA-seq: a genome-scale RNA-seq method to detect active self-cleaving ribozymes by capturing RNAs with 2’,3’ clic hosphates and 5’ droxyl ends.. *RNA Biology*, **2021**, 18, 818-831	4.8	3
638	A simpler linear-time algorithm for the common refinement of rooted phylogenetic trees on a common leaf set. *Algorithms for Molecular Biology*, **2021**, 16, 23	1.8	2

637	Combining Orthology and Xenology Data in a Common Phylogenetic Tree. *Lecture Notes in Computer Science*, **2021**, 53-64	0.9	1
636	Efficient Laplacian spectral density computations for networks with arbitrary degree distributions. *Network Science*, **2021**, 9, 312-327	2.9	0
635	Disturbance of phylogenetic layer-specific adaptation of human brain gene expression in Alzheimer's disease. *Scientific Reports*, **2021**, 11, 20200	4.9	
634	Compositional Properties of Alignments. *Mathematics in Computer Science*, **2021**, 15, 609	0.5	2
633	Arc-Completion of 2-Colored Best Match Graphs to Binary-Explainable Best Match Graphs. *Algorithms*, **2021**, 14, 110	1.8	1
632	Lifestyle weight-loss intervention may attenuate methylation aging: the CENTRAL MRI randomized controlled trial. *Clinical Epigenetics*, **2021**, 13, 48	7.7	2
631	Complexity of modification problems for best match graphs. *Theoretical Computer Science*, **2021**, 865, 63-84	1.1	5
630	A workflow to identify novel proteins based on the direct mapping of peptide-spectrum-matches to genomic locations. *BMC Bioinformatics*, **2021**, 22, 277	3.6	2
629	Effects of lifestyle interventions on epigenetic signatures of liver fat: Central randomized controlled trial. *Liver International*, **2021**, 41, 2101-2111	7.9	3
628	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. *Leukemia*, **2021**, 35, 2002-2016	10.7	3
627	LazyB: fast and cheap genome assembly. *Algorithms for Molecular Biology*, **2021**, 16, 8	1.8	0
626	Alignments of biomolecular contact maps. *Interface Focus*, **2021**, 11, 20200066	3.9	2
625	Superbubbles as an empirical characteristic of directed networks. *Network Science*, **2021**, 9, 49-58	2.9	
624	Proteomics reveals sex-specific heat shock response of Baikal amphipod Eulimnogammarus cyaneus. *Science of the Total Environment*, **2021**, 763, 143008	10.2	0
623	HumanMetagenomeDB: a public repository of curated and standardized metadata for human metagenomes. *Nucleic Acids Research*, **2021**, 49, D743-D750	20.1	4
622	Beyond Plug and Pray: Context Sensitivity and Design of Artificial Neomycin Riboswitches. *RNA Biology*, **2021**, 18, 457-467	4.8	2
621	MCPIP1 ribonuclease can bind and cleave mRNA in -amplified neuroblastoma cells. *RNA Biology*, **2021**, 18, 144-156	4.8	4
620	Efficient Algorithms for Co-folding of Multiple RNAs. *Communications in Computer and Information Science*, **2021**, 193-214	0.3	

619	Cut Vertex Transit Functions of Hypergraphs. *Lecture Notes in Computer Science*, **2021**, 222-233	0.9	
618	Ligand-dependent tRNA processing by a rationally designed RNase P riboswitch. *Nucleic Acids Research*, **2021**, 49, 1784-1800	20.1	4
617	Best Match Graphs with Binary Trees. *Lecture Notes in Computer Science*, **2021**, 82-93	0.9	1
616	Comprehensive benchmarking of software for mapping whole genome bisulfite data: from read alignment to DNA methylation analysis. *Briefings in Bioinformatics*, **2021**, 22,	13.4	3
615	Thermal reaction norms of key metabolic enzymes reflect divergent physiological and behavioral adaptations of closely related amphipod species. *Scientific Reports*, **2021**, 11, 4562	4.9	4
614	Weighted Consensus Segmentations. *Computation*, **2021**, 9, 17	2.2	
613	Complete Characterization of Incorrect Orthology Assignments in Best Match Graphs. *Journal of Mathematical Biology*, **2021**, 82, 20	2	6
612	Human pathways in animal models: possibilities and limitations. *Nucleic Acids Research*, **2021**, 49, 1859-1871	20.1	7
611	Indirect identification of horizontal gene transfer. *Journal of Mathematical Biology*, **2021**, 83, 10	2	0
610	PTEN regulates adipose progenitor cell growth, differentiation, and replicative aging. *Journal of Biological Chemistry*, **2021**, 297, 100968	5.4	1
609	Heuristic algorithms for best match graph editing. *Algorithms for Molecular Biology*, **2021**, 16, 19	1.8	
608	Different ways to play it cool: Transcriptomic analysis sheds light on different activity patterns of three amphipod species under long-term cold exposure. *Molecular Ecology*, **2021**, 30, 5735-5751	5.7	0
607	EpiDiverse Toolkit: a pipeline suite for the analysis of bisulfite sequencing data in ecological plant epigenetics. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab106	3.7	0
606	Are spliced ncRNA host genes distinct classes of lncRNAs?. *Theory in Biosciences*, **2020**, 139, 349-359	1.3	0
605	Intronic tRNAs of mitochondrial origin regulate constitutive and alternative splicing. *Genome Biology*, **2020**, 21, 299	18.3	2
604	A probabilistic version of Sankoff's maximum parsimony algorithm. *Journal of Bioinformatics and Computational Biology*, **2020**, 18, 2050004	1	1
603	Best match graphs and reconciliation of gene trees with species trees. *Journal of Mathematical Biology*, **2020**, 80, 1459-1495	2	9
602	Alzheimer-related genes show accelerated evolution. *Molecular Psychiatry*, **2020**,	15.1	1

601	A guide to naming human non-coding RNA genes. *EMBO Journal*, **2020**, 39, e103777	13	39
600	Distinct abdominal and gluteal adipose tissue transcriptome signatures are altered by exercise training in African women with obesity. *Scientific Reports*, **2020**, 10, 10240	4.9	7
599	Generalized Fitch graphs II: Sets of binary relations that are explained by edge-labeled trees. *Discrete Applied Mathematics*, **2020**, 283, 495-511	1	3
598	Master and servant: LINC00152 - a STAT3-induced long noncoding RNA regulates STAT3 in a positive feedback in human multiple myeloma. *BMC Medical Genomics*, **2020**, 13, 22	3.7	7
597	Identification of RNA 3′ends and termination sites in. *RNA Biology*, **2020**, 17, 663-676	4.8	8
596	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
595	TerrestrialMetagenomeDB: a public repository of curated and standardized metadata for terrestrial metagenomes. *Nucleic Acids Research*, **2020**, 48, D626-D632	20.1	4
594	Computational Simulations for Cyclizations Catalyzed by Plant Monoterpene Synthases. *Lecture Notes in Computer Science*, **2020**, 247-258	0.9	
593	Anti-CD3 Stimulated T Cell Transcriptome Reveals Novel ncRNAs and Correlates with a Suppressive Profile. *Lecture Notes in Computer Science*, **2020**, 180-191	0.9	
592	Cograph editing: Merging modules is equivalent to editing P_4s. *Art of Discrete and Applied Mathematics*, **2020**, 3, #P2.01	1.5	2
591	RNA Secondary Structures with Limited Base Pair Span: Exact Backtracking and an Application. *Genes*, **2020**, 12,	4.2	2
590	Bi-alignments as Models of Incongruent Evolution of RNA Sequence and Secondary Structure. *Lecture Notes in Computer Science*, **2020**, 159-170	0.9	1
589	LOTTE-seq (Long hairpin oligonucleotide based tRNA high-throughput sequencing): specific selection of tRNAs with 3’-CCA end for high-throughput sequencing. *RNA Biology*, **2020**, 17, 23-32	4.8	7
588	Reciprocal best match graphs. *Journal of Mathematical Biology*, **2020**, 80, 865-953	2	9
587	Transcriptome-level effects of the model organic pollutant phenanthrene and its solvent acetone in three amphipod species. *Comparative Biochemistry and Physiology Part D: Genomics and Proteomics*, **2020**, 33, 100630	2	1
586	Complexity of modification problems for reciprocal best match graphs. *Theoretical Computer Science*, **2020**, 809, 384-393	1.1	4
585	Enrichment and identification of small proteins in a simplified human gut microbiome. *Journal of Proteomics*, **2020**, 213, 103604	3.9	19
584	DNA methylation signature in blood mirrors successful weight-loss during lifestyle interventions: the CENTRAL trial. *Genome Medicine*, **2020**, 12, 97	14.4	9

583	Unusual Occurrence of Two Bona-Fide CCA-Adding Enzymes in. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	3
582	Exact-2-relation graphs. *Discrete Applied Mathematics*, **2020**, 285, 212-226	1	2
581	Convexity Deficit of Benzenoids. *Croatica Chemica Acta*, **2020**, 92, 457-466	0.8	2
580	Clustering Improves the Goemans–Williamson Approximation for the Max-Cut Problem. *Computation*, **2020**, 8, 75	2.2	
579	Splicing Endonuclease Is an Important Player in rRNA and tRNA Maturation in Archaea. *Frontiers in Microbiology*, **2020**, 11, 594838	5.7	3
578	Street Name Data as a Reflection of Migration and Settlement History. *Urban Science*, **2020**, 4, 74	2.2	
577	Average Fitness Differences on NK Landscapes. *Theory in Biosciences*, **2020**, 139, 1-7	1.3	3
576	Transit sets of -point crossover operators. *AKCE International Journal of Graphs and Combinatorics*, **2020**, 17, 519-533	0.5	
575	From pairs of most similar sequences to phylogenetic best matches. *Algorithms for Molecular Biology*, **2020**, 15, 5	1.8	8
574	Splicing conservation signals in plant long noncoding RNAs. *Rna*, **2020**, 26, 784-793	5.8	7
573	Developmentally Driven Changes in Adipogenesis in Different Fat Depots Are Related to Obesity. *Frontiers in Endocrinology*, **2020**, 11, 138	5.7	4
572	DREAM and RB cooperate to induce gene repression and cell-cycle arrest in response to p53 activation. *Nucleic Acids Research*, **2019**, 47, 9087-9103	20.1	32
571	A streamlined protocol for the detection of mRNA-sRNA interactions using AMT-crosslinking. *BioTechniques*, **2019**, 67, 178-183	2.5	3
570	Comparison between transcriptomic responses to short-term stress exposures of a common Holarctic and endemic Lake Baikal amphipods. *BMC Genomics*, **2019**, 20, 712	4.5	10
569	Description of strongly heat-inducible heat shock protein 70 transcripts from Baikal endemic amphipods. *Scientific Reports*, **2019**, 9, 8907	4.9	7
568	Best match graphs. *Journal of Mathematical Biology*, **2019**, 78, 2015-2057	2	14
567	Exploration of the chemical space and its three historical regimes. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 12660-12665	11.5	37
566	Direct Superbubble Detection. *Algorithms*, **2019**, 12, 81	1.8	1

565	The RNA workbench 2.0: next generation RNA data analysis. *Nucleic Acids Research*, **2019**, 47, W511-W515	20.1	7
564	Exploring Plant Sesquiterpene Diversity by Generating Chemical Networks. *Processes*, **2019**, 7, 240	2.9	3
563	Big Data Competence Center ScaDS Dresden/Leipzig: Overview and selected research activities. *Datenbank-Spektrum*, **2019**, 19, 5-16	0.6	2
562	Automatic curation of large comparative animal MicroRNA datasets. *Bioinformatics*, **2019**, 35, 4553-4559	7.2	2
561	Ry□□network-flow based transcriptome reconstruction. *BMC Bioinformatics*, **2019**, 20, 190	3.6	12
560	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. *Nature Communications*, **2019**, 10, 1459	17.4	49
559	SSS-test: a novel test for detecting positive selection on RNA secondary structure. *BMC Bioinformatics*, **2019**, 20, 151	3.6	7
558	Indication of ongoing amphipod speciation in Lake Baikal by genetic structures within endemic species. *BMC Evolutionary Biology*, **2019**, 19, 138	3	4
557	Gene expression profile of human T cells following a single stimulation of peripheral blood mononuclear cells with anti-CD3 antibodies. *BMC Genomics*, **2019**, 20, 593	4.5	7
556	Selection Pressures on RNA Sequences and Structures. *Evolutionary Bioinformatics*, **2019**, 15, 1176934319871919	2.9	5
555	Improved annotation of protein-coding genes boundaries in metazoan mitochondrial genomes. *Nucleic Acids Research*, **2019**, 47, 10543-10552	20.1	70
554	Within-Population Genome Size Variation is Mediated by Multiple Genomic Elements That Segregate Independently during Meiosis. *Genome Biology and Evolution*, **2019**, 11, 3424-3435	3.9	7
553	Genome analyses of a placozoan rickettsial endosymbiont show a combination of mutualistic and parasitic traits. *Scientific Reports*, **2019**, 9, 17561	4.9	8
552	flowEMMi: an automated model-based clustering tool for microbial cytometric data. *BMC Bioinformatics*, **2019**, 20, 643	3.6	10
551	RNApuzzler: efficient outerplanar drawing of RNA-secondary structures. *Bioinformatics*, **2019**, 35, 1342-1349	7.2	6
550	RNAcentral: a hub of information for non-coding RNA sequences. *Nucleic Acids Research*, **2019**, 47, D221-D229	20.1	90
549	Chemical Transformation Motifs-Modelling Pathways as Integer Hyperflows. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2019**, 16, 510-523	3	10
548	Divergent evolution in the genomes of closely related lacertids, Lacerta viridis and L. bilineata, and implications for speciation. *GigaScience*, **2019**, 8,	7.6	6

547	ceRNAs in plants: computational approaches and associated challenges for target mimic research. *Briefings in Bioinformatics*, **2018**, 19, 1273-1289	13.4	13
546	In vitro iCLIP-based modeling uncovers how the splicing factor U2AF2 relies on regulation by cofactors. *Genome Research*, **2018**, 28, 699-713	9.7	43
545	Toward a mechanistic explanation of phenotypic evolution: The need for a theory of theory integration. *Journal of Experimental Zoology Part B: Molecular and Developmental Evolution*, **2018**, 330, 5-14	1.8	10
544	The fungal snoRNAome. *Rna*, **2018**, 24, 342-360	5.8	7
543	Gene Phylogenies and Orthologous Groups. *Methods in Molecular Biology*, **2018**, 1704, 1-28	1.4	5
542	Comparative RNA Genomics. *Methods in Molecular Biology*, **2018**, 1704, 363-400	1.4	5
541	Expansion of gene clusters, circular orders, and the shortest Hamiltonian path problem. *Journal of Mathematical Biology*, **2018**, 77, 313-341	2	1
540	Accurate mapping of tRNA reads. *Bioinformatics*, **2018**, 34, 1116-1124	7.2	18
539	Tracing the evolution of the heterotrimeric G protein □subunit in Metazoa. *BMC Evolutionary Biology*, **2018**, 18, 51	3	6
538	Finding the K best synthesis plans. *Journal of Cheminformatics*, **2018**, 10, 19	8.6	5
537	Partially Local Multi-way Alignments. *Mathematics in Computer Science*, **2018**, 12, 207-234	0.5	4
536	The Sierra Platinum Service for generating peak-calls for replicated ChIP-seq experiments. *BMC Research Notes*, **2018**, 11, 512	2.3	2
535	TERribly Difficult: Searching for Telomerase RNAs in Saccharomycetes. *Genes*, **2018**, 9,	4.2	8
534	Nonprotein-Coding RNAs as Regulators of Development in Tunicates. *Results and Problems in Cell Differentiation*, **2018**, 65, 197-225	1.4	1
533	Cover-Encodings of Fitness Landscapes. *Bulletin of Mathematical Biology*, **2018**, 80, 2154-2176	2.1	
532	Time-consistent reconciliation maps and forbidden time travel. *Algorithms for Molecular Biology*, **2018**, 13, 2	1.8	7
531	Trichoplax genomes reveal profound admixture and suggest stable wild populations without bisexual reproduction. *Scientific Reports*, **2018**, 8, 11168	4.9	22
530	Beyond the 3'UTR binding-microRNA-induced protein truncation via DNA binding. *Oncotarget*, **2018** , 9, 32855-32867	3.3	8

529	A short note on undirected Fitch graphs. *Art of Discrete and Applied Mathematics*, **2018**, 1, #1.08	1.5	5
528	Temporal ordering of substitutions in RNA evolution: Uncovering the structural evolution of the Human Accelerated Region 1. *Journal of Theoretical Biology*, **2018**, 438, 143-150	2.3	7
527	Detailed secondary structure models of invertebrate 7SK RNAs. *RNA Biology*, **2018**, 15, 158-164	4.8	8
526	Inferring phylogenetic trees from the knowledge of rare evolutionary events. *Journal of Mathematical Biology*, **2018**, 76, 1623-1653	2	5
525	Identification and characterization of novel conserved RNA structures in Drosophila. *BMC Genomics*, **2018**, 19, 899	4.5	3
524	Superbubbles revisited. *Algorithms for Molecular Biology*, **2018**, 13, 16	1.8	3
523	Split-inducing indels in phylogenomic analysis. *Algorithms for Molecular Biology*, **2018**, 13, 12	1.8	10
522	Patterning the insect eye: From stochastic to deterministic mechanisms. *PLoS Computational Biology*, **2018**, 14, e1006363	5	5
521	Combined Experimental and System-Level Analyses Reveal the Complex Regulatory Network of miR-124 during Human Neurogenesis. *Cell Systems*, **2018**, 7, 438-452.e8	10.6	25
520	Coordinate systems for supergenomes. *Algorithms for Molecular Biology*, **2018**, 13, 15	1.8	8
519	Noncoding RNA Transcripts during Differentiation of Induced Pluripotent Stem Cells into Hepatocytes. *Stem Cells International*, **2018**, 2018, 5692840	5	3
518	Reconstructing gene trees from Fitch's xenology relation. *Journal of Mathematical Biology*, **2018**, 77, 1459-1491	2	15
517	Moderate weather extremes alter phytoplankton diversity A microcosm study. *Freshwater Biology* , **2018**, 63, 1211-1224	3.1	11
516	Studying language evolution in the age of big data. *Journal of Language Evolution*, **2018**, 3, 94-129	1.4	4
515	Phylogenetics beyond biology. *Theory in Biosciences*, **2018**, 137, 133-143	1.3	3
514	The complete mitochondrial genome of Lacerta bilineata and comparison with its closely related congener L. Viridis. *Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis*, **2017**, 28, 116-118	1.3	5
513	Towards a Consistent, Quantitative Evaluation of MicroRNA Evolution. *Journal of Integrative Bioinformatics*, **2017**, 14,	3.8	2
512	The RNA workbench: best practices for RNA and high-throughput sequencing bioinformatics in Galaxy. *Nucleic Acids Research*, **2017**, 45, W560-W566	20.1	33

511	RNA-bioinformatics: Tools, services and databases for the analysis of RNA-based regulation. *Journal of Biotechnology*, **2017**, 261, 76-84	3.7	17
510	The mathematics of xenology: di-cographs, symbolic ultrametrics, 2-structures and tree-representable systems of binary relations. *Journal of Mathematical Biology*, **2017**, 75, 199-237	2	22
509	Keeping it complicated: Mitochondrial genome plasticity across diplonemids. *Scientific Reports*, **2017**, 7, 14166	4.9	14
508	Similarity-Based Segmentation of Multi-Dimensional Signals. *Scientific Reports*, **2017**, 7, 12355	4.9	5
507	Ecological plant epigenetics: Evidence from model and non-model species, and the way forward. *Ecology Letters*, **2017**, 20, 1576-1590	10	165
506	RIsearch2: suffix array-based large-scale prediction of RNA-RNA interactions and siRNA off-targets. *Nucleic Acids Research*, **2017**, 45, e60	20.1	41
505	Uncovering missing pieces: duplication and deletion history of arrestins in deuterostomes. *BMC Evolutionary Biology*, **2017**, 17, 163	3	27
504	Partially local three-way alignments and the sequence signatures of mitochondrial genome rearrangements. *Algorithms for Molecular Biology*, **2017**, 12, 22	1.8	5
503	Tractable RNA-ligand interaction kinetics. *BMC Bioinformatics*, **2017**, 18, 424	3.6	8
502	SMORE: Synteny Modulator of Repetitive Elements. *Life*, **2017**, 7,	3	1
501	STAT3-induced long noncoding RNAs in multiple myeloma cells display different properties in cancer. *Scientific Reports*, **2017**, 7, 7976	4.9	24
500	An intermediate level of abstraction for computational systems chemistry. *Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences*, **2017**, 375,	3	5
499	Recent advances in RNA folding. *Journal of Biotechnology*, **2017**, 261, 97-104	3.7	38
498	Do genome size differences within (Rotifera, Monogononta) cause reproductive barriers among geographic populations?. *Hydrobiologia*, **2017**, 796, 59-75	2.4	10
497	Accurate annotation of protein-coding genes in mitochondrial genomes. *Molecular Phylogenetics and Evolution*, **2017**, 106, 209-216	4.1	13
496	Evolutionary clues in lncRNAs. *Wiley Interdisciplinary Reviews RNA*, **2017**, 8, e1376	9.3	36
495	RNAcentral: a comprehensive database of non-coding RNA sequences. *Nucleic Acids Research*, **2017**, 45, D128-D134	20.1	119
494	Evolution of Fungal U3 snoRNAs: Structural Variation and Introns. *Non-coding RNA*, **2017**, 3,	7.1	1

493	Rare Splice Variants in Long Non-Coding RNAs. *Non-coding RNA*, **2017**, 3,	7.1	5
492	Design of Artificial Riboswitches as Biosensors. *Sensors*, **2017**, 17,	3.8	38
491	A Support Vector Machine based method to distinguish long non-coding RNAs from protein coding transcripts. *BMC Genomics*, **2017**, 18, 804	4.5	31
490	Algebraic Dynamic Programming on Trees. *Algorithms*, **2017**, 10, 135	1.8	3
489	Chemical Graph Transformation with Stereo-Information. *Lecture Notes in Computer Science*, **2017**, 54-69	0.9	3
488	Applicability of a computational design approach for synthetic riboswitches. *Nucleic Acids Research*, **2017**, 45, 4108-4119	20.1	37
487	Pseudoknots in RNA folding landscapes. *Bioinformatics*, **2016**, 32, 187-94	7.2	12
486	Evolution of RNA-Based Networks. *Current Topics in Microbiology and Immunology*, **2016**, 392, 43-59	3.3	8
485	Associativity and Non-Associativity of Some Hypergraph Products. *Mathematics in Computer Science* , **2016**, 10, 403-408	0.5	0
484	Changes of bivalent chromatin coincide with increased expression of developmental genes in cancer. *Scientific Reports*, **2016**, 6, 37393	4.9	64
483	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
482	Design specifications for cellular regulation. *Theory in Biosciences*, **2016**, 135, 231-240	1.3	1
481	Phylogenetic distribution of plant snoRNA families. *BMC Genomics*, **2016**, 17, 969	4.5	11
480	An updated human snoRNAome. *Nucleic Acids Research*, **2016**, 44, 5068-82	20.1	141
479	Algebraic dynamic programming for multiple context-free grammars. *Theoretical Computer Science*, **2016**, 639, 91-109	1.1	6
478	The paralog-to-contig assignment problem: high quality gene models from fragmented assemblies. *Algorithms for Molecular Biology*, **2016**, 11, 1	1.8	16
477	Temperature-responsive in vitro RNA structurome of Yersinia pseudotuberculosis. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 7237-42	11.5	55
476	RNA folding with hard and soft constraints. *Algorithms for Molecular Biology*, **2016**, 11, 8	1.8	53

475	Read mapping. *IT - Information Technology*, **2016**, 58, 119-125	0.4	
474	Dual RNA-seq unveils noncoding RNA functions in host-pathogen interactions. *Nature*, **2016**, 529, 496-501	50.4	318
473	U6 snRNA intron insertion occurred multiple times during fungi evolution. *RNA Biology*, **2016**, 13, 119-27	4.8	6
472	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. *Nature Genetics*, **2016**, 48, 427-37	36.3	352
471	metilene: fast and sensitive calling of differentially methylated regions from bisulfite sequencing data. *Genome Research*, **2016**, 26, 256-62	9.7	159
470	Spectral classes of regular, random, and empirical graphs. *Linear Algebra and Its Applications*, **2016**, 489, 30-49	0.9	11
469	SHAPE directed RNA folding. *Bioinformatics*, **2016**, 32, 145-7	7.2	50
468	Orthologs, turn-over, and remolding of tRNAs in primates and fruit flies. *BMC Genomics*, **2016**, 17, 617	4.5	12
467	Never Ending Analysis of a Century Old Evolutionary Debate: Unringing the Urmetazoon Bell. *Frontiers in Ecology and Evolution*, **2016**, 4,	3.7	14
466	Automatic Inference of Graph Transformation Rules Using the Cyclic Nature of Chemical Reactions. *Lecture Notes in Computer Science*, **2016**, 206-222	0.9	2
465	A Software Package for Chemically Inspired Graph Transformation. *Lecture Notes in Computer Science*, **2016**, 73-88	0.9	20
464	Automated detection of ncRNAs in the draft genome sequence of a colonial tunicate: the carpet sea squirt Didemnum vexillum. *BMC Genomics*, **2016**, 17, 691	4.5	8
463	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. *Scientific Reports*, **2016**, 6, 34589	4.9	30
462	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. *Haematologica*, **2016**, 101, 1380-1389	6.6	31
461	Assessing Greenness of Chemical Reactions and Synthesis Plans through Posetic Landscapes. *ACS Sustainable Chemistry and Engineering*, **2016**, 4, 2191-2199	8.3	4
460	Prevalent and distinct spliceosomal 3'-end processing mechanisms for fungal telomerase RNA. *Nature Communications*, **2015**, 6, 6105	17.4	18
459	Kiwi genome provides insights into evolution of a nocturnal lifestyle. *Genome Biology*, **2015**, 16, 147	18.3	52
458	Third Report on Chicken Genes and Chromosomes 2015. *Cytogenetic and Genome Research*, **2015**, 145, 78-179	1.9	57

457	A simple data-adaptive probabilistic variant calling model. *Algorithms for Molecular Biology*, **2015**, 10, 10	1.8	2
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