

# Dmitri D Pervouchine

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

4,953  
citations

331670

21  
h-index

377865

34  
g-index

46  
all docs

46  
docs citations

46  
times ranked

12337  
citing authors

#	ARTICLE	IF	CITATIONS
1	Tandem Exon Duplications Expanding the Alternative Splicing Repertoire. , 2022, 14, 73-81.		0
2	Transcriptome analysis reveals high tumor heterogeneity with respect to re-activation of stemness and proliferation programs. PLoS ONE, 2022, 17, e0268626.	2.5	0
3	An extended catalogue of tandem alternative splice sites in human tissue transcriptomes. PLoS Computational Biology, 2021, 17, e1008329.	3.2	7
4	Conserved long-range base pairings are associated with pre-mRNA processing of human genes. Nature Communications, 2021, 12, 2300.	12.8	27
5	Multiple competing RNA structures dynamically control alternative splicing in the human ATE1 gene. Nucleic Acids Research, 2021, 49, 479-490.	14.5	22
6	Urinary biomarkers of latent inflammation and fibrosis in children with vesicoureteral reflux. International Urology and Nephrology, 2020, 52, 603-610.	1.4	10
7	A limited set of transcriptional programs define major cell types. Genome Research, 2020, 30, 1047-1059.	5.5	32
8	Circular exonic RNAs: When RNA structure meets topology. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 194384.	1.9	31
9	Integrative transcriptomic analysis suggests new autoregulatory splicing events coupled with nonsense-mediated mRNA decay. Nucleic Acids Research, 2019, 47, 5293-5306.	14.5	49
10	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in SCN1A. Npj Genomic Medicine, 2019, 4, 31.	3.8	27
11	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. Nature Communications, 2018, 9, 490.	12.8	198
12	Hypoxic renal injury in newborns with abdominal compartment syndrome (clinical and experimental) Tj ETQqO 0 0 rgBT /Overlock 10 Tf 5	2.3	8
13	An Evolutionary Mechanism for the Generation of Competing RNA Structures Associated with Mutually Exclusive Exons. Genes, 2018, 9, 356.	2.4	14
14	Towards Long-Range RNA Structure Prediction in Eukaryotic Genes. Genes, 2018, 9, 302.	2.4	24
15	Gene-specific patterns of expression variation across organs and species. Genome Biology, 2016, 17, 151.	8.8	89
16	A benchmark for RNA-seq quantification pipelines. Genome Biology, 2016, 17, 74.	8.8	160
17	Urinary cytokines as markers of latent inflammation in children with chronic pyelonephritis and anorectal malformations. Journal of Pediatric Urology, 2016, 12, 153.e1-153.e6.	1.1	7
18	Comparison of GENCODE and RefSeq gene annotation and the impact of reference geneset on variant effect prediction. BMC Genomics, 2015, 16, S2.	2.8	80

#	ARTICLE	IF	CITATIONS
19	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015, 6, 5903.	12.8	73
20	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	12.6	1,127
21	IRBIS: a systematic search for conserved complementarity. <i>Rna</i> , 2014, 20, 1519-1531.	3.5	16
22	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444
23	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448.	27.8	289
24	Intron-centric estimation of alternative splicing from RNA-seq data. <i>Bioinformatics</i> , 2013, 29, 273-274.	4.1	92
25	Evidence for widespread association of mammalian splicing and conserved long-range RNA structures. <i>Rna</i> , 2012, 18, 1-15.	3.5	58
26	Modulation of alternative splicing by long-range RNA structures in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2009, 37, 4533-4544.	14.5	71
27	RNAKINETICS: A WEB SERVER THAT MODELS SECONDARY STRUCTURE KINETICS OF AN ELONGATING RNA. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 589-596.	0.8	52
28	Low-Dimensional Maps Encoding Dynamics in Entorhinal Cortex and Hippocampus. <i>Neural Computation</i> , 2006, 18, 2617-2650.	2.2	43
29	Neuronal metabolism governs cortical network response state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5597-5601.	7.1	165
30	Slow and Fast Inhibition and an H-Current Interact to Create a Theta Rhythm in a Model of CA1 Interneuron Network. <i>Journal of Neurophysiology</i> , 2005, 94, 1509-1518.	1.8	150
31	Engineered riboregulators enable post-transcriptional control of gene expression. <i>Nature Biotechnology</i> , 2004, 22, 841-847.	17.5	513
32	IRIS: intermolecular RNA interaction search. <i>Genome Informatics</i> , 2004, 15, 92-101.	0.4	24
33	On the normalization of RNA equilibrium free energy to the length of the sequence. <i>Nucleic Acids Research</i> , 2003, 31, 49e-49.	14.5	16
34	Invariants and orbits of the standard $\$ (\mathrm{SL}_4(\mathbb{C}) \times \mathrm{SL}_4(\mathbb{C}))$ Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 T	0.6	1