

Svetlana A Shabalina

List of Publications by Year in descending order

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66
papers

6,972
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81900

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98798

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docs citations

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9073
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#	ARTICLE	IF	CITATIONS
1	Uncertainty-aware and interpretable evaluation of Cas9â€™gRNA and Cas12aâ€™gRNA specificity for fully matched and partially mismatched targets with Deep Kernel Learning. <i>Nucleic Acids Research</i> , 2022, 50, e11-e11.	14.5	5
2	Alternative Splicing of Opioid Receptor Genes Shows a Conserved Pattern for 6TM Receptor Variants. <i>Cellular and Molecular Neurobiology</i> , 2021, 41, 1039-1055.	3.3	5
3	The genomic structure of a human chromosome 22 nucleolar organizer region determined by TAR cloning. <i>Scientific Reports</i> , 2021, 11, 2997.	3.3	13
4	A vast pool of lineage-specific microproteins encoded by long non-coding RNAs in plants. <i>Nucleic Acids Research</i> , 2021, 49, 10328-10346.	14.5	33
5	Understanding off-target effects through hybridization kinetics and thermodynamics. <i>Cell Biology and Toxicology</i> , 2020, 36, 11-15.	5.3	10
6	Prospects for Using Expression Patterns of Paramyxovirus Receptors as Biomarkers for Oncolytic Virotherapy. <i>Cancers</i> , 2020, 12, 3659.	3.7	6
7	A small protein encoded by a putative lncRNA regulates apoptosis and tumorigenicity in human colorectal cancer cells. <i>ELife</i> , 2020, 9, .	6.0	43
8	Alternative Splicing of the Delta-Opioid Receptor Gene Suggests Existence of New Functional Isoforms. <i>Molecular Neurobiology</i> , 2019, 56, 2855-2869.	4.0	20
9	The small protein MgtS and small RNA MgrR modulate the PitA phosphate symporter to boost intracellular magnesium levels. <i>Molecular Microbiology</i> , 2019, 111, 131-144.	2.5	37
10	A unique insert in the genomes of high-risk human papillomaviruses with a predicted dual role in conferring oncogenic risk. <i>F1000Research</i> , 2019, 8, 1000.	1.6	10
11	Sequence characteristics define trade-offs between on-target and genome-wide off-target hybridization of oligoprobes. <i>PLoS ONE</i> , 2018, 13, e0199162.	2.5	3
12	Variation in human chromosome 21 ribosomal RNA genes characterized by TAR cloning and long-read sequencing. <i>Nucleic Acids Research</i> , 2018, 46, 6712-6725.	14.5	61
13	Adaptation of mRNA structure to control protein folding. <i>RNA Biology</i> , 2017, 14, 1649-1654.	3.1	23
14	Diverse functions of homologous actin isoforms are defined by their nucleotide, rather than their amino acid sequence. <i>ELife</i> , 2017, 6, .	6.0	44
15	Prosurvival long noncoding RNA PINCR regulates a subset of p53 targets in human colorectal cancer cells by binding to MatrIn 3. <i>ELife</i> , 2017, 6, .	6.0	68
16	Optimization of signal-to-noise ratio for efficient microarray probe design. <i>Bioinformatics</i> , 2016, 32, i552-i558.	4.1	11
17	Evolutionary switches between two serine codon sets are driven by selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13109-13113.	7.1	25
18	Role of mRNA structure in the control of protein folding. <i>Nucleic Acids Research</i> , 2016, 44, 10898-10911.	14.5	99

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19	Oncolysis by paramyxoviruses: multiple mechanisms contribute to therapeutic efficiency. <i>Molecular Therapy - Oncolytics</i> , 2015, 2, 15011.	4.4	42
20	Oncolysis by paramyxoviruses: preclinical and clinical studies. <i>Molecular Therapy - Oncolytics</i> , 2015, 2, 15017.	4.4	33
21	Growth differentiation factor-15 encodes a novel microRNA 3189 that functions as a potent regulator of cell death. <i>Cell Death and Differentiation</i> , 2015, 22, 1641-1653.	11.2	30
22	Arginylation regulates purine nucleotide biosynthesis by enhancing the activity of phosphoribosyl pyrophosphate synthase. <i>Nature Communications</i> , 2015, 6, 7517.	12.8	36
23	How do base-pairing small RNAs evolve?. <i>FEMS Microbiology Reviews</i> , 2015, 39, 379-391.	8.6	76
24	Evolution at protein ends: major contribution of alternative transcription initiation and termination to the transcriptome and proteome diversity in mammals. <i>Nucleic Acids Research</i> , 2014, 42, 7132-7144.	14.5	40
25	MicL, a new σ^E -dependent sRNA, combats envelope stress by repressing synthesis of Lpp, the major outer membrane lipoprotein. <i>Genes and Development</i> , 2014, 28, 1620-1634.	5.9	255
26	The Vast, Conserved Mammalian lincRNome. <i>PLoS Computational Biology</i> , 2013, 9, e1002917.	3.2	62
27	Sounds of silence: synonymous nucleotides as a key to biological regulation and complexity. <i>Nucleic Acids Research</i> , 2013, 41, 2073-2094.	14.5	241
28	Related Giant Viruses in Distant Locations and Different Habitats: <i>Acanthamoeba polyphaga</i> mousmouvirus Represents a Third Lineage of the Mimiviridae That Is Close to the Megavirus Lineage. <i>Genome Biology and Evolution</i> , 2012, 4, 1324-1330.	2.5	118
29	Optimized models for design of efficient miR30-based shRNAs. <i>Frontiers in Genetics</i> , 2012, 3, 163.	2.3	17
30	Viruses with More Than 1,000 Genes: Mamavirus, a New <i>Acanthamoeba polyphaga</i> mimivirus Strain, and Reannotation of Mimivirus Genes. <i>Genome Biology and Evolution</i> , 2011, 3, 737-742.	2.5	83
31	Negative Correlation between Expression Level and Evolutionary Rate of Long Intergenic Noncoding RNAs. <i>Genome Biology and Evolution</i> , 2011, 3, 1390-1404.	2.5	86
32	Disruptive mRNA folding increases translational efficiency of catechol-O-methyltransferase variant. <i>Nucleic Acids Research</i> , 2011, 39, 6201-6212.	14.5	51
33	Connections between Alternative Transcription and Alternative Splicing in Mammals. <i>Genome Biology and Evolution</i> , 2010, 2, 791-799.	2.5	31
34	Continuing Evolution of <i>Burkholderia mallei</i> Through Genome Reduction and Large-Scale Rearrangements. <i>Genome Biology and Evolution</i> , 2010, 2, 102-116.	2.5	106
35	Differential Arginylation of Actin Isoforms Is Regulated by Coding Sequence-Dependent Degradation. <i>Science</i> , 2010, 329, 1534-1537.	12.6	179
36	Distinct Patterns of Expression and Evolution of Intronless and Intron-Containing Mammalian Genes. <i>Molecular Biology and Evolution</i> , 2010, 27, 1745-1749.	8.9	116

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37	Abundance of type I toxin-antitoxin systems in bacteria: searches for new candidates and discovery of novel families. <i>Nucleic Acids Research</i> , 2010, 38, 3743-3759.	14.5	237
38	Optimization of Duplex Stability and Terminal Asymmetry for shRNA Design. <i>PLoS ONE</i> , 2010, 5, e10180.	2.5	36
39	Low Enzymatic Activity Haplotypes of the Human Catechol-O-Methyltransferase Gene: Enrichment for Marker SNPs. <i>PLoS ONE</i> , 2009, 4, e5237.	2.5	46
40	Expansion of the human μ -opioid receptor gene architecture: novel functional variants. <i>Human Molecular Genetics</i> , 2009, 18, 1037-1051.	2.9	150
41	Evolution of alternative and constitutive regions of mammalian 5'UTRs. <i>BMC Genomics</i> , 2009, 10, 162.	2.8	62
42	Origins and evolution of eukaryotic RNA interference. <i>Trends in Ecology and Evolution</i> , 2008, 23, 578-587.	8.7	442
43	Expression Patterns of Protein Kinases Correlate with Gene Architecture and Evolutionary Rates. <i>PLoS ONE</i> , 2008, 3, e3599.	2.5	20
44	Widespread Positive Selection in Synonymous Sites of Mammalian Genes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1821-1831.	8.9	86
45	Comparison of approaches for rational siRNA design leading to a new efficient and transparent method. <i>Nucleic Acids Research</i> , 2007, 35, e63-e63.	14.5	129
46	Association of Polymorphisms in Odorant-Binding Protein Genes With Variation in Olfactory Response to Benzaldehyde in <i>Drosophila</i> . <i>Genetics</i> , 2007, 177, 1655-1665.	2.9	43
47	Genetic architecture of human pain perception. <i>Trends in Genetics</i> , 2007, 23, 605-613.	6.7	207
48	A putative RNA-interference-based immune system in prokaryotes: computational analysis of the predicted enzymatic machinery, functional analogies with eukaryotic RNAi, and hypothetical mechanisms of action. <i>Biology Direct</i> , 2006, 1, 7.	4.6	961
49	Computational models with thermodynamic and composition features improve siRNA design. <i>BMC Bioinformatics</i> , 2006, 7, 65.	2.6	139
50	Three major haplotypes of the $\alpha 2$ adrenergic receptor define psychological profile, blood pressure, and the risk for development of a common musculoskeletal pain disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2006, 141B, 449-462.	1.7	169
51	A periodic pattern of mRNA secondary structure created by the genetic code. <i>Nucleic Acids Research</i> , 2006, 34, 2428-2437.	14.5	175
52	Analysis of internal loops within the RNA secondary structure in almost quadratic time. <i>Bioinformatics</i> , 2006, 22, 1317-1324.	4.1	53
53	Persistence Time of Loss-of-Function Mutations at Nonessential Loci Affecting Eye Color in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2005, 171, 2133-2138.	2.9	2
54	Genetic basis for individual variations in pain perception and the development of a chronic pain condition. <i>Human Molecular Genetics</i> , 2005, 14, 135-143.	2.9	1,134

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55	Identification of regions in multiple sequence alignments thermodynamically suitable for targeting by consensus oligonucleotides: application to HIV genome. <i>BMC Bioinformatics</i> , 2004, 5, 44.	2.6	3
56	Identification and functional analysis of 'hypothetical' genes expressed in <i>Haemophilus influenzae</i> . <i>Nucleic Acids Research</i> , 2004, 32, 2353-2361.	14.5	75
57	The mammalian transcriptome and the function of non-coding DNA sequences. <i>Genome Biology</i> , 2004, 5, 105.	9.6	137
58	Comparative analysis of orthologous eukaryotic mRNAs: potential hidden functional signals. <i>Nucleic Acids Research</i> , 2004, 32, 1774-1782.	14.5	82
59	A significant fraction of conserved noncoding DNA in human and mouse consists of predicted matrix attachment regions. <i>Trends in Genetics</i> , 2003, 19, 119-124.	6.7	83
60	Patterns in interspecies similarity correlate with nucleotide composition in mammalian 3'UTRs. <i>Nucleic Acids Research</i> , 2003, 31, 5433-5439.	14.5	17
61	Classification of common conserved sequences in mammalian intergenic regions. <i>Human Molecular Genetics</i> , 2002, 11, 669-674.	2.9	50
62	Analysis of similarity within 142 pairs of orthologous intergenic regions of <i>Caenorhabditis elegans</i> and <i>Caenorhabditis briggsae</i> . <i>Nucleic Acids Research</i> , 2002, 30, 1233-1239.	14.5	36
63	A hierarchical approach to aligning collinear regions of genomes. <i>Bioinformatics</i> , 2002, 18, 1673-1680.	4.1	8
64	OWEN: aligning long collinear regions of genomes. <i>Bioinformatics</i> , 2002, 18, 1703-1704.	4.1	51
65	Selective constraint in intergenic regions of human and mouse genomes. <i>Trends in Genetics</i> , 2001, 17, 373-376.	6.7	127
66	Pattern of selective constraint in <i>C. elegans</i> and <i>C. briggsae</i> genomes. <i>Genetical Research</i> , 1999, 74, 23-30.	0.9	93