

Andrey Grigoriev

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

2,058
citations

394421

19
h-index

434195

31
g-index

35
all docs

35
docs citations

35
times ranked

2677
citing authors

#	ARTICLE	IF	CITATIONS
1	Analyzing genomes with cumulative skew diagrams. <i>Nucleic Acids Research</i> , 1998, 26, 2286-2290.	14.5	401
2	High resolution cosmid and P1 maps spanning the 14 Mb genome of the fission yeast <i>S. pombe</i> . <i>Cell</i> , 1993, 73, 109-120.	28.9	271
3	A relationship between gene expression and protein interactions on the proteome scale: analysis of the bacteriophage T7 and the yeast <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2001, 29, 3513-3519.	14.5	209
4	On the number of protein-protein interactions in the yeast proteome. <i>Nucleic Acids Research</i> , 2003, 31, 4157-4161.	14.5	122
5	Protein domains correlate strongly with exons in multiple eukaryotic genomes – evidence of exon shuffling?. <i>Trends in Genetics</i> , 2004, 20, 399-403.	6.7	121
6	Structural variants in 3000 rice genomes. <i>Genome Research</i> , 2019, 29, 870-880.	5.5	112
7	Complete coverage of the <i>Schizosaccharomyces pombe</i> genome in yeast artificial chromosomes. <i>Nature Genetics</i> , 1992, 1, 273-277.	21.4	99
8	Algorithms and software tools for ordering clone libraries: application to the mapping of the genome of <i>Schizosaccharomyces pombe</i> . <i>Nucleic Acids Research</i> , 1993, 21, 1965-1974.	14.5	80
9	Age-driven modulation of tRNA-derived fragments in <i>Drosophila</i> and their potential targets. <i>Biology Direct</i> , 2015, 10, 51.	4.6	78
10	Codon and Amino Acid Usage in Retroviral Genomes Is Consistent with Virus-Specific Nucleotide Pressure. <i>AIDS Research and Human Retroviruses</i> , 2002, 18, 133-141.	1.1	69
11	Strand-specific compositional asymmetries in double-stranded DNA viruses. <i>Virus Research</i> , 1999, 60, 1-19.	2.2	61
12	Impact of age-associated increase in 2m ² -methylation of miRNAs on aging and neurodegeneration in <i>Drosophila</i> . <i>Genes and Development</i> , 2014, 28, 44-57.	5.9	55
13	Significant expansion of exon-bordering protein domains during animal proteome evolution. <i>Nucleic Acids Research</i> , 2005, 33, 95-105.	14.5	48
14	Mutations induced by bacteriophage T7 RNA polymerase and their effects on the composition of the T7 genome Edited by M. Gottesman. <i>Journal of Molecular Biology</i> , 2000, 300, 1057-1065.	4.2	46
15	Dynamics of tRNA fragments and their targets in aging mammalian brain. <i>F1000Research</i> , 2016, 5, 2758.	1.6	46
16	Inferring targeting modes of Argonaute-loaded tRNA fragments. <i>RNA Biology</i> , 2020, 17, 1070-1080.	3.1	44
17	Computational meta-analysis of ribosomal RNA fragments: potential targets and interaction mechanisms. <i>Nucleic Acids Research</i> , 2021, 49, 4085-4103.	14.5	29
18	GROM-RD: resolving genomic biases to improve read depth detection of copy number variants. <i>PeerJ</i> , 2015, 3, e836.	2.0	29

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19	Identification and autonomous replication capability of a chromosomal replication origin from the archaeon <i>Sulfolobus solfataricus</i> . <i>Extremophiles</i> , 2004, 8, 385-391.	2.3	21
20	Evolutionary adaptation revealed by comparative genome analysis of woolly mammoths and elephants. <i>DNA Research</i> , 2017, 24, 359-369.	3.4	16
21	Metagenome Sequencing of Prokaryotic Microbiota Collected from Byron Glacier, Alaska. <i>Genome Announcements</i> , 2013, 1, e0009913.	0.8	15
22	Comparative metagenome analysis of an Alaskan glacier. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1441003.	0.8	15
23	Age-dependent patterns of microRNA RISC loading. <i>Aging</i> , 2014, 6, 705-706.	3.1	15
24	ARIADNA: machine learning method for ancient DNA variant discovery. <i>DNA Research</i> , 2018, 25, 619-627.	3.4	14
25	Lightning-fast genome variant detection with GROM. <i>GigaScience</i> , 2017, 6, 1-7.	6.4	13
26	Age-Related Argonaute Loading of Ribosomal RNA Fragments. <i>MicroRNA (Sharjah, United Arab Emirates)</i> , 2017, 1, 1-11.	1.2	11
27	Phylogenetic Heatmaps Highlight Composition Biases in Sequenced Reads. <i>Microorganisms</i> , 2017, 5, 4.	3.6	6
28	Large-Scale Computational Discovery of Binding Motifs in tRNA Fragments. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 647449.	3.5	4
29	Visualization of nucleotide substitutions in the (micro)transcriptome. <i>BMC Genomics</i> , 2014, 15, S9.	2.8	3
30	Transfer RNA and Origins of RNA Interference. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 708984.	3.5	3
31	Sequences of SARS-CoV-2 "Hybrids" with the Human Genome: Signs of Non-coding RNA?. <i>Journal of Virology</i> , 2021, , JVI0146221.	3.4	1
32	RNA fragments and brain aging. , 2021, , 37-47.		0