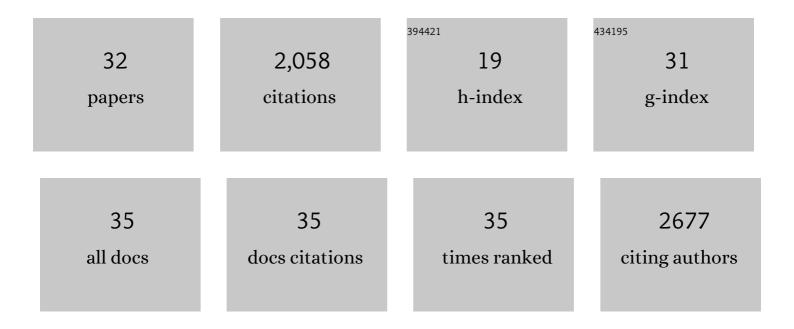
## Andrey Grigoriev

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3940948/publications.pdf

Version: 2024-02-01



#	Article	IF	CITATIONS
1	Analyzing genomes with cumulative skew diagrams. Nucleic Acids Research, 1998, 26, 2286-2290.	14.5	401
2	High resolution cosmid and P1 maps spanning the 14 Mb genome of the fission yeast S. pombe. Cell, 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 Saccharomyces cerevisiae. Nucleic Acids Research, 2001, 29, 3513-3519.	14.5	209
4	On the number of protein-protein interactions in the yeast proteome. Nucleic Acids Research, 2003, 31, 4157-4161.	14.5	122
5	Protein domains correlate strongly with exons in multiple eukaryotic genomes – evidence of exon shuffling?. Trends in Genetics, 2004, 20, 399-403.	6.7	121
6	Structural variants in 3000 rice genomes. Genome Research, 2019, 29, 870-880.	5.5	112
7	Complete coverage of the Schizosaccharomyces pombe genome in yeast artificial chromosomes. Nature Genetics, 1992, 1, 273-277.	21.4	99
8	Algorithms and software tools for ordering clone libraries: application to the mapping of the genome ofSchizosaccharomyces pombe. Nucleic Acids Research, 1993, 21, 1965-1974.	14.5	80
9	Age-driven modulation of tRNA-derived fragments in Drosophila and their potential targets. Biology Direct, 2015, 10, 51.	4.6	78
10	Codon and Amino Acid Usage in Retroviral Genomes Is Consistent with Virus-Specific Nucleotide Pressure. AIDS Research and Human Retroviruses, 2002, 18, 133-141.	1.1	69
11	Strand-specific compositional asymmetries in double-stranded DNA viruses. Virus Research, 1999, 60, 1-19.	2.2	61
12	Impact of age-associated increase in 2′- <i>O</i> -methylation of miRNAs on aging and neurodegeneration in <i>Drosophila</i> . Genes and Development, 2014, 28, 44-57.	5.9	55
13	Significant expansion of exon-bordering protein domains during animal proteome evolution. Nucleic Acids Research, 2005, 33, 95-105.	14.5	48
14	Mutations induced by bacteriophage T7 RNA polymerase and their effects on the composition of the T7 genome11Edited by M. Gottesman. Journal of Molecular Biology, 2000, 300, 1057-1065.	4.2	46
15	Dynamics of tRNA fragments and their targets in aging mammalian brain. F1000Research, 2016, 5, 2758.	1.6	46
16	Inferring targeting modes of Argonaute-loaded tRNA fragments. RNA Biology, 2020, 17, 1070-1080.	3.1	44
17	Computational meta-analysis of ribosomal RNA fragments: potential targets and interaction mechanisms. Nucleic Acids Research, 2021, 49, 4085-4103.	14.5	29
18	GROM-RD: resolving genomic biases to improve read depth detection of copy number variants. PeerJ, 2015, 3, e836.	2.0	29

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#	Article	IF	CITATIONS
19	Identification and autonomous replication capability of a chromosomal replication origin from the archaeon Sulfolobus solfataricus. Extremophiles, 2004, 8, 385-391.	2.3	21
20	Evolutionary adaptation revealed by comparative genome analysis of woolly mammoths and elephants. DNA Research, 2017, 24, 359-369.	3.4	16
21	Metagenome Sequencing of Prokaryotic Microbiota Collected from Byron Glacier, Alaska. Genome Announcements, 2013, 1, e0009913.	0.8	15
22	Comparative metagenome analysis of an Alaskan glacier. Journal of Bioinformatics and Computational Biology, 2014, 12, 1441003.	0.8	15
23	Age-dependent patterns of microRNA RISC loading. Aging, 2014, 6, 705-706.	3.1	15
24	ARIADNA: machine learning method for ancient DNA variant discovery. DNA Research, 2018, 25, 619-627.	3.4	14
25	Lightning-fast genome variant detection with GROM. GigaScience, 2017, 6, 1-7.	6.4	13
26	Age-Related Argonaute Loading of Ribosomal RNA Fragments. MicroRNA (Shariqah, United Arab) Tj ETQq0 0 0 rg	gBT_/Overlo 1.2	ock 10 Tf 50
27	Phylogenetic Heatmaps Highlight Composition Biases in Sequenced Reads. Microorganisms, 2017, 5, 4.	3.6	6
28	Large-Scale Computational Discovery of Binding Motifs in tRNA Fragments. Frontiers in Molecular Biosciences, 2021, 8, 647449.	3.5	4

29	Visualization of nucleotide substitutions in the (micro)transcriptome. BMC Genomics, 2014, 15, S9.	2.8	3
30	Transfer RNA and Origins of RNA Interference. Frontiers in Molecular Biosciences, 2021, 8, 708984.	3.5	3
31	Sequences of SARS-CoV-2 "Hybrids―with the Human Genome: Signs of Non-coding RNA?. Journal of Virology, 2021, , JVI0146221.	3.4	1

RNA fragments and brain aging. , 2021, , 37-47. 32