

Georgi K Marinov

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

29,681
citations

117625

34
h-index

118850

62
g-index

78
all docs

78
docs citations

78
times ranked

50386
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
2	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	27.8	4,484
3	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	5.5	1,708
4	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444
5	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	5.6	1,257
6	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6131-6138.	7.1	635
7	From single-cell to cell-pool transcriptomes: Stochasticity in gene expression and RNA splicing. <i>Genome Research</i> , 2014, 24, 496-510.	5.5	470
8	Piwi induces piRNA-guided transcriptional silencing and establishment of a repressive chromatin state. <i>Genes and Development</i> , 2013, 27, 390-399.	5.9	429
9	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418.	9.6	410
10	The bioenergetic costs of a gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15690-15695.	7.1	405
11	Transgenerationally inherited piRNAs trigger piRNA biogenesis by changing the chromatin of piRNA clusters and inducing precursor processing. <i>Genes and Development</i> , 2014, 28, 1667-1680.	5.9	204
12	An NF- κ B-microRNA regulatory network tunes macrophage inflammatory responses. <i>Nature Communications</i> , 2017, 8, 851.	12.8	191
13	Effects of sequence variation on differential allelic transcription factor occupancy and gene expression. <i>Genome Research</i> , 2012, 22, 860-869.	5.5	150
14	Single-Cell Transcriptome Analysis Reveals Dynamic Changes in lncRNA Expression during Reprogramming. <i>Cell Stem Cell</i> , 2015, 16, 88-101.	11.1	146
15	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. <i>Nature</i> , 2020, 583, 760-767.	27.8	131
16	Large-Scale Quality Analysis of Published ChIP-seq Data. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 209-223.	1.8	125
17	Inducible RasGEF1B circular RNA is a positive regulator of ICAM-1 in the TLR4/LPS pathway. <i>RNA Biology</i> , 2016, 13, 861-871.	3.1	123
18	Antitumor activity of a pyrrole-imidazole polyamide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1863-1868.	7.1	111

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19	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. <i>Nature Communications</i> , 2019, 10, 4063.	12.8	104
20	MIWI2 and MILI Have Differential Effects on piRNA Biogenesis and DNA Methylation. <i>Cell Reports</i> , 2015, 12, 1234-1243.	6.4	98
21	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	95
22	Long-range single-molecule mapping of chromatin accessibility in eukaryotes. <i>Nature Methods</i> , 2020, 17, 319-327.	19.0	93
23	Increased Expression of System xc ⁻ in Glioblastoma Confers an Altered Metabolic State and Temozolomide Resistance. <i>Molecular Cancer Research</i> , 2016, 14, 1229-1242.	3.4	85
24	The MicroRNA-132 and MicroRNA-212 Cluster Regulates Hematopoietic Stem Cell Maintenance and Survival with Age by Buffering FOXO3 Expression. <i>Immunity</i> , 2015, 42, 1021-1032.	14.3	84
25	The microRNA-212/132 cluster regulates B cell development by targeting Sox4. <i>Journal of Experimental Medicine</i> , 2015, 212, 1679-1692.	8.5	72
26	Splicing-independent loading of TREX on nascent RNA is required for efficient expression of dual-strand piRNA clusters in <i>Drosophila</i> . <i>Genes and Development</i> , 2016, 30, 840-855.	5.9	71
27	High-Throughput Discovery and Characterization of Human Transcriptional Effectors. <i>Cell</i> , 2020, 183, 2020-2035.e16.	28.9	71
28	<i>SLC7A11</i> Overexpression in Glioblastoma Is Associated with Increased Cancer Stem Cell-Like Properties. <i>Stem Cells and Development</i> , 2017, 26, 1236-1246.	2.1	66
29	Deciphering regulatory DNA sequences and noncoding genetic variants using neural network models of massively parallel reporter assays. <i>PLoS ONE</i> , 2019, 14, e0218073.	2.5	61
30	Membranes, energetics, and evolution across the prokaryote-eukaryote divide. <i>ELife</i> , 2017, 6, .	6.0	60
31	Genome-Wide Analysis Reveals Coating of the Mitochondrial Genome by TFAM. <i>PLoS ONE</i> , 2013, 8, e74513.	2.5	57
32	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. <i>Genome Research</i> , 2013, 23, 2136-2148.	5.5	51
33	A Transgenerational Process Defines piRNA Biogenesis in <i>Drosophila virilis</i> . <i>Cell Reports</i> , 2014, 8, 1617-1623.	6.4	49
34	Gene expression changes in a tumor xenograft by a pyrrole-imidazole polyamide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16041-16045.	7.1	42
35	Transcriptional and chromatin-based partitioning mechanisms uncouple protein scaling from cell size. <i>Molecular Cell</i> , 2021, 81, 4861-4875.e7.	9.7	42
36	Evidence for Site-Specific Occupancy of the Mitochondrial Genome by Nuclear Transcription Factors. <i>PLoS ONE</i> , 2014, 9, e84713.	2.5	38

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37	Diversity and Divergence of Dinoflagellate Histone Proteins. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 397-422.	1.8	38
38	Transcription-dependent domain-scale three-dimensional genome organization in the dinoflagellate <i>Breviolum minutum</i> . <i>Nature Genetics</i> , 2021, 53, 613-617.	21.4	38
39	G ₁ cyclin ¹ Cdk promotes cell cycle entry through localized phosphorylation of RNA polymerase II. <i>Science</i> , 2021, 374, 347-351.	12.6	36
40	Population Genomics of <i>Paramecium</i> Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 1194-1216.	8.9	35
41	Fully automated high-throughput chromatin immunoprecipitation for ChIP-seq: Identifying ChIP-quality p300 monoclonal antibodies. <i>Scientific Reports</i> , 2014, 4, 5152.	3.3	34
42	Transcriptomic analysis of the role of RasGEF1B circular RNA in the TLR4/LPS pathway. <i>Scientific Reports</i> , 2017, 7, 12227.	3.3	34
43	Pitfalls of Mapping High-Throughput Sequencing Data to Repetitive Sequences: Piwi's Genomic Targets Still Not Identified. <i>Developmental Cell</i> , 2015, 32, 765-771.	7.0	26
44	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3366.	7.1	25
45	Population Genetics of <i>Paramecium</i> Mitochondrial Genomes: Recombination, Mutation Spectrum, and Efficacy of Selection. <i>Genome Biology and Evolution</i> , 2019, 11, 1398-1416.	2.5	22
46	Reply to Lane and Martin: Mitochondria do not boost the bioenergetic capacity of eukaryotic cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E667-8.	7.1	20
47	On the design and prospects of direct RNA sequencing. <i>Briefings in Functional Genomics</i> , 2017, 16, 326-335.	2.7	18
48	The demographic and geographic impact of the COVID pandemic in Bulgaria and Eastern Europe in 2020. <i>Scientific Reports</i> , 2022, 12, 6333.	3.3	15
49	Genome Sequence of <i>Magnetospirillum magnetotacticum</i> Strain MS-1. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
50	Interrogating the Accessible Chromatin Landscape of Eukaryote Genomes Using ATAC-seq. <i>Methods in Molecular Biology</i> , 2021, 2243, 183-226.	0.9	13
51	Conservation and divergence of the histone code in nucleomorphs. <i>Biology Direct</i> , 2016, 11, 18.	4.6	12
52	Identification and characterization of a novel Epstein-Barr Virus-encoded circular RNA from LMP-2 Gene. <i>Scientific Reports</i> , 2021, 11, 14392.	3.3	10
53	ChIP-seq for the Identification of Functional Elements in the Human Genome. <i>Methods in Molecular Biology</i> , 2017, 1543, 3-18.	0.9	9
54	Draft Whole-Genome Sequence of <i>Haemophilus ducreyi</i> Strain AUSPNG1, Isolated from a Cutaneous Ulcer of a Child from Papua New Guinea. <i>Genome Announcements</i> , 2016, 4, .	0.8	8

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55	A decade of ChIP-seq. Briefings in Functional Genomics, 2018, 17, 77-79.	2.7	8
56	ChIP-ping the branches of the tree: functional genomics and the evolution of eukaryotic gene regulation. Briefings in Functional Genomics, 2018, 17, 116-137.	2.7	5
57	In Humans, Sex is Binary and Immutable. Academic Questions, 2020, 33, 279-288.	0.0	5
58	Response to Martin and colleagues: mitochondria do not boost the bioenergetic capacity of eukaryotic cells. Biology Direct, 2018, 13, 26.	4.6	4
59	The chromatin organization of a chlorarachniophyte nucleomorph genome. Genome Biology, 2022, 23, 65.	8.8	4
60	An optimized ATAC-seq protocol for genome-wide mapping of active regulatory elements in primary mouse cortical neurons. STAR Protocols, 2021, 2, 100854.	1.2	3
61	Identification of Candidate Functional Elements in the Genome from ChIP-seq Data. Methods in Molecular Biology, 2017, 1543, 19-43.	0.9	2
62	Single-Molecule Multikilobase-Scale Profiling of Chromatin Using m6A-SMAC-Seq and m6A-CpG-GpC-SMAC-Seq. Methods in Molecular Biology, 2022, 2458, 269-298.	0.9	1
63	A deeper confusion. Evolution: Education and Outreach, 2015, 8, .	0.8	0
64	The elephant in the room. EMBO Reports, 2015, 16, 399-403.	4.5	0