

Georgi K Marinov

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

68 papers	21,827 citations	31 h-index	78 g-index
78 ext. papers	26,975 ext. citations	12.8 avg, IF	8.19 L-index

#	Paper	IF	Citations
68	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
67	Landscape of transcription in human cells. <i>Nature</i> , 2012 , 489, 101-8	50.4	3544
66	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012 , 22, 1813-31	9.7	1211
65	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
64	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014 , 515, 355-64	50.4	1026
63	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, 6131-8	11.5	490
62	From single-cell to cell-pool transcriptomes: stochasticity in gene expression and RNA splicing. <i>Genome Research</i> , 2014 , 24, 496-510	9.7	363
61	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012 , 13, 418	18.3	340
60	Piwi induces piRNA-guided transcriptional silencing and establishment of a repressive chromatin state. <i>Genes and Development</i> , 2013 , 27, 390-9	12.6	329
59	The bioenergetic costs of a gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 15690-5	11.5	242
58	Transgenerationally inherited piRNAs trigger piRNA biogenesis by changing the chromatin of piRNA clusters and inducing precursor processing. <i>Genes and Development</i> , 2014 , 28, 1667-80	12.6	138
57	An NF- κ B-microRNA regulatory network tunes macrophage inflammatory responses. <i>Nature Communications</i> , 2017 , 8, 851	17.4	127
56	Single-cell transcriptome analysis reveals dynamic changes in lncRNA expression during reprogramming. <i>Cell Stem Cell</i> , 2015 , 16, 88-101	18	113
55	Effects of sequence variation on differential allelic transcription factor occupancy and gene expression. <i>Genome Research</i> , 2012 , 22, 860-9	9.7	113
54	Antitumor activity of a pyrrole-imidazole polyamide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 1863-8	11.5	97
53	Inducible RasGEF1B circular RNA is a positive regulator of ICAM-1 in the TLR4/LPS pathway. <i>RNA Biology</i> , 2016 , 13, 861-71	4.8	93
52	Large-scale quality analysis of published ChIP-seq data. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 209-23	3.2	90

51	MIWI2 and MILI Have Differential Effects on piRNA Biogenesis and DNA Methylation. <i>Cell Reports</i> , 2015 , 12, 1234-43	10.6	73
50	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, 1021-32	32.3	69
49	The microRNA-212/132 cluster regulates B cell development by targeting Sox4. <i>Journal of Experimental Medicine</i> , 2015 , 212, 1679-92	16.6	53
48	Increased Expression of System xc- in Glioblastoma Confers an Altered Metabolic State and Temozolomide Resistance. <i>Molecular Cancer Research</i> , 2016 , 14, 1229-1242	6.6	51
47	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. <i>Nature Communications</i> , 2019 , 10, 4063	17.4	49
46	Splicing-independent loading of TREX on nascent RNA is required for efficient expression of dual-strand piRNA clusters in Drosophila. <i>Genes and Development</i> , 2016 , 30, 840-55	12.6	46
45	SLC7A11 Overexpression in Glioblastoma Is Associated with Increased Cancer Stem Cell-Like Properties. <i>Stem Cells and Development</i> , 2017 , 26, 1236-1246	4.4	44
44	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. <i>Genome Research</i> , 2013 , 23, 2136-48	9.7	39
43	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, 16041-5	11.5	39
42	Genome-wide analysis reveals coating of the mitochondrial genome by TFAM. <i>PLoS ONE</i> , 2013 , 8, e74513	3.7	39
41	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. <i>Nature</i> , 2020 , 583, 760-767	50.4	39
40	Long-range single-molecule mapping of chromatin accessibility in eukaryotes. <i>Nature Methods</i> , 2020 , 17, 319-327	21.6	36
39	A transgenerational process defines piRNA biogenesis in Drosophila virilis. <i>Cell Reports</i> , 2014 , 8, 1617-1623	23.6	36
38	Membranes, energetics, and evolution across the prokaryote-eukaryote divide. <i>ELife</i> , 2017 , 6,	8.9	35
37	Fully automated high-throughput chromatin immunoprecipitation for ChIP-seq: identifying ChIP-quality p300 monoclonal antibodies. <i>Scientific Reports</i> , 2014 , 4, 5152	4.9	30
36	Deciphering regulatory DNA sequences and noncoding genetic variants using neural network models of massively parallel reporter assays. <i>PLoS ONE</i> , 2019 , 14, e0218073	3.7	27
35	Transcriptomic analysis of the role of RasGEF1B circular RNA in the TLR4/LPS pathway. <i>Scientific Reports</i> , 2017 , 7, 12227	4.9	25
34	Evidence for site-specific occupancy of the mitochondrial genome by nuclear transcription factors. <i>PLoS ONE</i> , 2014 , 9, e84713	3.7	25

33	Diversity and Divergence of Dinoflagellate Histone Proteins. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 6, 397-422	22
32	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	11.5 22
31	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021 , 1,	21
30	Population Genomics of Paramecium Species. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1194-1216	8.3 18
29	On the design and prospects of direct RNA sequencing. <i>Briefings in Functional Genomics</i> , 2017 , 16, 326-335	15
28	Pitfalls of mapping high-throughput sequencing data to repetitive sequences: Piwi genomic targets still not identified. <i>Developmental Cell</i> , 2015 , 32, 765-71	10.2 14
27	Genome Sequence of Magnetospirillum magnetotacticum Strain MS-1. <i>Genome Announcements</i> , 2015 , 3,	14
26	High-Throughput Discovery and Characterization of Human Transcriptional Effectors. <i>Cell</i> , 2020 , 183, 2020-2035.e16	56.2 14
25	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	11.5 13
24	Population Genetics of Paramecium Mitochondrial Genomes: Recombination, Mutation Spectrum, and Efficacy of Selection. <i>Genome Biology and Evolution</i> , 2019 , 11, 1398-1416	3.9 12
23	Transcription-dependent domain-scale three-dimensional genome organization in the dinoflagellate Breviolum minutum. <i>Nature Genetics</i> , 2021 , 53, 613-617	36.3 10
22	Conservation and divergence of the histone code in nucleomorphs. <i>Biology Direct</i> , 2016 , 11, 18	7.2 7
21	ChIP-seq for the Identification of Functional Elements in the Human Genome. <i>Methods in Molecular Biology</i> , 2017 , 1543, 3-18	1.4 6
20	Draft Whole-Genome Sequence of Haemophilus ducreyi Strain AUSPNG1, Isolated from a Cutaneous Ulcer of a Child from Papua New Guinea. <i>Genome Announcements</i> , 2016 , 4,	6
19	Transcriptional and chromatin-based partitioning mechanisms uncouple protein scaling from cell size. <i>Molecular Cell</i> , 2021 , 81, 4861-4875.e7	17.6 6
18	G cyclin-Cdk promotes cell cycle entry through localized phosphorylation of RNA polymerase II. <i>Science</i> , 2021 , 374, 347-351	33.3 5
17	ChIP-ping the branches of the tree: functional genomics and the evolution of eukaryotic gene regulation. <i>Briefings in Functional Genomics</i> , 2018 , 17, 116-137	4.9 4
16	Response to Martin and colleagues: mitochondria do not boost the bioenergetic capacity of eukaryotic cells. <i>Biology Direct</i> , 2018 , 13, 26	7.2 4

15	In Humans, Sex is Binary and Immutable. <i>Academic Questions</i> , 2020 , 33, 279-288	0.9	3
14	Size-independent mRNA synthesis and chromatin-based partitioning mechanisms generate and maintain constant amounts of protein per cell		3
13	Identification and characterization of a novel Epstein-Barr Virus-encoded circular RNA from LMP-2 Gene. <i>Scientific Reports</i> , 2021 , 11, 14392	4.9	3
12	Interrogating the Accessible Chromatin Landscape of Eukaryote Genomes Using ATAC-seq. <i>Methods in Molecular Biology</i> , 2021 , 2243, 183-226	1.4	3
11	Transcription-dependent domain-scale 3D genome organization in dinoflagellates		2
10	Epigenomic reprogramming of repetitive noncoding RNAs and IFN-stimulated genes by mutant KRAS		2
9	The demographic and geographic impact of the COVID pandemic in Bulgaria and Eastern Europe in 2020.. <i>Scientific Reports</i> , 2022 , 12, 6333	4.9	2
8	Identification and mitigation of pervasive off-target activity in CRISPR-Cas9 screens for essential non-coding elements		1
7	The demographic and geographic impact of the COVID pandemic in Bulgaria and Eastern Europe in 2020		1
6	Increasing cell size remodels the proteome and promotes senescence		1
5	The chromatin organization of a chlorarachniophyte nucleomorph genome.. <i>Genome Biology</i> , 2022 , 23, 65	18.3	1
4	Identification of Candidate Functional Elements in the Genome from ChIP-seq Data. <i>Methods in Molecular Biology</i> , 2017 , 1543, 19-43	1.4	0
3	An optimized ATAC-seq protocol for genome-wide mapping of active regulatory elements in primary mouse cortical neurons. <i>STAR Protocols</i> , 2021 , 2, 100854	1.4	0
2	The elephant in the room: Advertising science as a driver of economic growth is a long-term losing strategy. <i>EMBO Reports</i> , 2015 , 16, 399-403	6.5	
1	Single-Molecule Multikilobase-Scale Profiling of Chromatin Accessibility Using m6A-SMAC-Seq and m6A-CpG-GpC-SMAC-Seq.. <i>Methods in Molecular Biology</i> , 2022 , 2458, 269-298	1.4	