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List of Publications by Year
in descending order

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20 papers	2,967 citations	516215 16 h-index	794141 19 g-index
23 all docs	23 docs citations	23 times ranked	4349 citing authors

#	Article	IF	Citations
1	The medaka draft genome and insights into vertebrate genome evolution. Nature, 2007, 447, 714-719.	13.7	1,037
2	The genome of a lepidopteran model insect, the silkworm Bombyx mori. Insect Biochemistry and Molecular Biology, 2008, 38, 1036-1045.	1.2	592
3	Reconstruction of the vertebrate ancestral genome reveals dynamic genome reorganization in early vertebrates. Genome Research, 2007, 17, 1254-1265.	2.4	444
4	High-dimensional and large-scale phenotyping of yeast mutants. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 19015-19020.	3.3	276
5	Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. Science, 2009, 323, 401-404.	6.0	122
6	Reconstruction of proto-vertebrate, proto-cyclostome and proto-gnathostome genomes provides new insights into early vertebrate evolution. Nature Communications, 2021, 12, 4489.	5.8	88
7	Comprehensive Genomic Profiling of Neuroendocrine Carcinomas of the Gastrointestinal System. Cancer Discovery, 2022, 12, 692-711.	7.7	58
8	Coordinated Changes in DNA Methylation in Antigen-Specific Memory CD4 T Cells. Journal of Immunology, 2013, 190, 4076-4091.	0.4	46
9	Genome-wide profiling of DNA methylation in human cancer cells. Genomics, 2011, 98, 280-287.	1.3	42
10	High-Resolution Analysis of the 5â€²-End Transcriptome Using a Next Generation DNA Sequencer. PLoS ONE, 2009, 4, e4108.	1.1	42
11	Genome-wide genetic variations are highly correlated with proximal DNA methylation patterns. Genome Research, 2012, 22, 1419-1425.	2.4	41
12	Macrosynteny analysis shows the absence of ancient whole-genome duplication in lepidopteran insects. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1816-1818.	3.3	37
13	CTCF looping is established during gastrulation in medaka embryos. Genome Research, 2021, 31, 968-980.	2.4	37
14	UTGB/medaka: genomic resource database for medaka biology. Nucleic Acids Research, 2007, 36, D747-D752.	6.5	32
15	Diversity of Ca2+-Induced Morphology Revealed by Morphological Phenotyping of Ca2+-Sensitive Mutants of Saccharomyces cerevisiae. Eukaryotic Cell, 2007, 6, 817-830.	3.4	24
16	Genomes as documents of evolutionary history: a probabilistic macrosynteny model for the reconstruction of ancestral genomes. Bioinformatics, 2017, 33, i369-i378.	1.8	24
17	Data mining tools for the Saccharomyces cerevisiae morphological database. Nucleic Acids Research, 2005, 33, W753-W757.	6.5	15
18	Associations between nucleosome phasing, sequence asymmetry, and tissue-specific expression in a set of inbred Medaka species. BMC Genomics, 2015, 16, 978.	1.2	3

#	ARTICLE	IF	CITATIONS
19	Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. , 2011, , 39-47.		1
20	Reconstruction of the Vertebrate Ancestral Genome Reveals Dynamic Genome Reorganization in Early Vertebrates. , 2011, , 307-322.		1