Xin Li

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1594559/publications.pdf

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30	3,610	18	29
papers	citations	h-index	g-index
32	32	32	7822
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. Nature Biotechnology, 2012, 30, 105-111.	17.5	818
2	A comparison of non-integrating reprogramming methods. Nature Biotechnology, 2015, 33, 58-63.	17.5	424
3	Epigenomic reprogramming during pancreatic cancer progression links anabolic glucose metabolism to distant metastasis. Nature Genetics, 2017, 49, 367-376.	21.4	365
4	Single base–resolution methylome of the silkworm reveals a sparse epigenomic map. Nature Biotechnology, 2010, 28, 516-520.	17.5	349
5	The DNA Methylome of Human Peripheral Blood Mononuclear Cells. PLoS Biology, 2010, 8, e1000533.	5.6	290
6	Single-base resolution maps of cultivated and wild rice methylomes and regulatory roles of DNA methylation in plant gene expression. BMC Genomics, 2012, 13, 300.	2.8	266
7	On the origin of new genes in <i>Drosophila</i> . Genome Research, 2008, 18, 1446-1455.	5.5	240
8	Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. Genome Biology, 2015, 16, 80.	8.8	111
9	GeMes, Clusters of DNA Methylation under Genetic Control, Can Inform Genetic and Epigenetic Analysis of Disease. American Journal of Human Genetics, 2014, 94, 485-495.	6.2	93
10	Whole-genome analysis of the methylome and hydroxymethylome in normal and malignant lung and liver. Genome Research, 2016, 26, 1730-1741.	5.5	91
11	A Selective Phenelzine Analogue Inhibitor of Histone Demethylase LSD1. ACS Chemical Biology, 2014, 9, 1284-1293.	3.4	88
12	Repetitive Element-Mediated Recombination as a Mechanism for New Gene Origination in Drosophila. PLoS Genetics, 2008, 4, e3.	3.5	80
13	Short Homologous Sequences Are Strongly Associated with the Generation of Chimeric RNAs in Eukaryotes. Journal of Molecular Evolution, 2009, 68, 56-65.	1.8	77
14	Genome and Comparative Transcriptomics of African Wild Rice Oryza longistaminata Provide Insights into Molecular Mechanism of Rhizomatousness and Self-Incompatibility. Molecular Plant, 2015, 8, 1683-1686.	8.3	49
15	Comparative methylomics between domesticated and wild silkworms implies possible epigenetic influences on silkworm domestication. BMC Genomics, 2013, 14, 646.	2.8	47
16	Analysis of elite variety tag SNPs reveals an important allele in upland rice. Nature Communications, 2013, 4, 2138.	12.8	43
17	A genomic perspective on the important genetic mechanisms of upland adaptation of rice. BMC Plant Biology, 2014, 14, 160.	3.6	39
18	Comparative transcriptome analyses on silk glands of six silkmoths imply the genetic basis of silk structure and coloration. BMC Genomics, 2015, 16, 203.	2.8	24

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19	Strategies for identification of mutations induced by carbon-ion beam irradiation in Arabidopsis thaliana by whole genome re-sequencing. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2018, 807, 21-30.	1.0	18
20	Arioc: GPU-accelerated alignment of short bisulfite-treated reads. Bioinformatics, 2018, 34, 2673-2675.	4.1	17
21	ISL2 modulates angiogenesis through transcriptional regulation of ANGPT2 to promote cell proliferation and malignant transformation in oligodendroglioma. Oncogene, 2020, 39, 5964-5978.	5.9	16
22	Functional consequences of new exon acquisition in mammalian chromodomain Y-like (CDYL) genes. Trends in Genetics, 2007, 23, 427-431.	6.7	15
23	Single-cell transcriptome of early hematopoiesis guides arterial endothelial-enhanced functional T cell generation from human PSCs. Science Advances, 2021, 7, eabi9787.	10.3	13
24	Evolutionary Patterns of RNA-Based Duplication in Non-Mammalian Chordates. PLoS ONE, 2011, 6, e21466.	2.5	13
25	Tight junction protein 1 promotes vasculature remodeling via regulating USP2/TWIST1 in bladder cancer. Oncogene, 2022, 41, 502-514.	5.9	10
26	Origin and evolution of new exons in the rodent zinc finger protein 39 gene. Science Bulletin, 2005, 50, 1126.	1.7	2
27	Origin and evolution of new genes. Science Bulletin, 2004, 49, 1681-1686.	1.7	1
28	Whole-genome resequencing of the wheat A subgenome progenitor Triticum urartu provides insights into its demographic history and geographic adaptation. Plant Communications, 2022, , 100345.	7.7	1
29	Origin and evolution of new genes. Science Bulletin, 2004, 49, 1681.	1.7	0
30	Evolutionary characteristics of exons expressed at different abundance levels in mammals. Science Bulletin, 2009, 54, 3546-3554.	9.0	0