Hyo Sik Jang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Transposable elements drive widespread expression of oncogenes in human cancers. Nature Genetics, 2019, 51, 611-617.	21.4	253
2	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. Nature Genetics, 2017, 49, 1052-1060.	21.4	235
3	Evolution of Epigenetic Regulation in Vertebrate Genomes. Trends in Genetics, 2016, 32, 269-283.	6.7	86
4	Tissue-specific DNA methylation is conserved across human, mouse, and rat, and driven by primary sequence conservation. BMC Genomics, 2017, 18, 724.	2.8	71
5	Regenerating zebrafish fin epigenome is characterized by stable lineage-specific DNA methylation and dynamic chromatin accessibility. Genome Biology, 2020, 21, 52.	8.8	44
6	Transcription Start Site Evolution in Drosophila. Molecular Biology and Evolution, 2013, 30, 1966-1974.	8.9	29
7	Genome-Wide Characterization of Genetic Variation in the Unicellular, Green Alga Chlamydomonas reinhardtii. PLoS ONE, 2012, 7, e41307.	2.5	21
8	DeepH&M: Estimating single-CpG hydroxymethylation and methylation levels from enrichment and restriction enzyme sequencing methods. Science Advances, 2020, 6, .	10.3	8
9	Epigenetic dynamics shaping melanophore and iridophore cell fate in zebrafish. Genome Biology, 2021, 22, 282.	8.8	8
10	Abstract 2225: Transposable elements are an abundant and pan-cancer source of shared tumor-specific antigens and membrane targets. , 2021, , .		0