Michael Pheasant

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2289861/publications.pdf

Version: 2024-02-01

		687363	1058476
15	3,742 citations	13	14
papers	citations	h-index	g-index
15	15	15	6771
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Ultraconserved Elements in the Human Genome. Science, 2004, 304, 1321-1325.	12.6	1,496
2	The relationship between non-protein-coding DNA and eukaryotic complexity. BioEssays, 2007, 29, 288-299.	2.5	578
3	The UCSC Genome Browser database: update 2010. Nucleic Acids Research, 2010, 38, D613-D619.	14.5	537
4	ENCODE whole-genome data in the UCSC Genome Browser. Nucleic Acids Research, 2010, 38, D620-D625.	14.5	218
5	Raising the estimate of functional human sequences: Figure 1 Genome Research, 2007, 17, 1245-1253.	5.5	217
6	Genomics: The amazing complexity of the human transcriptome. European Journal of Human Genetics, 2005, 13, 894-897.	2.8	171
7	Genomics Virtual Laboratory: A Practical Bioinformatics Workbench for the Cloud. PLoS ONE, 2015, 10, e0140829.	2.5	119
8	Ultraconserved elements in insect genomes: A highly conserved intronic sequence implicated in the control of homothorax mRNA splicing. Genome Research, 2005, 15, 800-808.	5.5	112
9	Large-Scale Appearance of Ultraconserved Elements in Tetrapod Genomes and Slowdown of the Molecular Clock. Molecular Biology and Evolution, 2008, 25, 402-408.	8.9	103
10	Transposon-free regions in mammalian genomes. Genome Research, 2005, 16, 164-172.	5.5	102
11	Orthologous MicroRNA Genes Are Located in Cancer-Associated Genomic Regions in Human and Mouse. PLoS ONE, 2007, 2, e1133.	2.5	34
12	Maintenance of transposon-free regions throughout vertebrate evolution. BMC Genomics, 2007, 8, 470.	2.8	28
13	Comparison of Ultra-Conserved Elements in Drosophilids and Vertebrates. PLoS ONE, 2013, 8, e82362.	2.5	14
14	Evidence for Control of Splicing by Alternative RNA Secondary Structures in Dipteran Homothorax Pre-mRNA. RNA Biology, 2006, 3, 36-39.	3.1	13
15	Quality assurance study of real-time targeted massive parallel sequencing (MPS) comprehensive cancer panel (CCP) and network pathway analysis in early breast cancer (EBC) Journal of Clinical Oncology, 2014, 32, 11092-11092.	1.6	0