

Michele Clamp

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

40,199
citations

318942

23
h-index

685536

24
g-index

25
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25
docs citations

25
times ranked

47656
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-Genome Analyses Resolve the Phylogeny of Flightless Birds (Palaeognathae) in the Presence of an Empirical Anomaly Zone. <i>Systematic Biology</i> , 2019, 68, 937-955.	2.7	88
2	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019, 364, 74-78.	6.0	189
3	Three Periods of Regulatory Innovation During Vertebrate Evolution. <i>Science</i> , 2011, 333, 1019-1024.	6.0	127
4	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	13.7	1,016
5	Identifying novel constrained elements by exploiting biased substitution patterns. <i>Bioinformatics</i> , 2009, 25, i54-i62.	1.8	296
6	Distinguishing protein-coding and noncoding genes in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19428-19433.	3.3	503
7	Initial sequence and comparative analysis of the cat genome. <i>Genome Research</i> , 2007, 17, 1675-1689.	2.4	311
8	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	2.4	184
9	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	13.7	661
10	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	13.7	2,215
11	An initial strategy for the systematic identification of functional elements in the human genome by low-redundancy comparative sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4795-4800.	3.3	107
12	The Ensembl Automatic Gene Annotation System. <i>Genome Research</i> , 2004, 14, 942-950.	2.4	352
13	ESTGenes: Alternative Splicing From ESTs in Ensembl. <i>Genome Research</i> , 2004, 14, 976-987.	2.4	76
14	The Ensembl Core Software Libraries. <i>Genome Research</i> , 2004, 14, 929-933.	2.4	116
15	The Otter Annotation System. <i>Genome Research</i> , 2004, 14, 963-970.	2.4	51
16	An Overview of Ensembl. <i>Genome Research</i> , 2004, 14, 925-928.	2.4	391
17	The Ensembl Analysis Pipeline. <i>Genome Research</i> , 2004, 14, 934-941.	2.4	99
18	GeneWise and Genomewise. <i>Genome Research</i> , 2004, 14, 988-995.	2.4	2,128

#	ARTICLE	IF	CITATIONS
19	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
20	Biopipe: A Flexible Framework for Protocol-Based Bioinformatics Analysis. <i>Genome Research</i> , 2003, 13, 1904-15.	2.4	65
21	DATABASES AND TOOLS FOR BROW SING GENOMES. <i>Annual Review of Genomics and Human Genetics</i> , 2002, 3, 293-310.	2.5	23
22	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	6.0	1,859
23	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
24	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074