

Martin Krzywinski

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

20,660
citations

136885

32
h-index

276775

41
g-index

43
all docs

43
docs citations

43
times ranked

40167
citing authors

#	ARTICLE	IF	CITATIONS
1	Circos: An information aesthetic for comparative genomics. <i>Genome Research</i> , 2009, 19, 1639-1645.	2.4	9,003
2	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
3	<i>Fusobacterium nucleatum</i> infection is prevalent in human colorectal carcinoma. <i>Genome Research</i> , 2012, 22, 299-306.	2.4	1,582
4	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011, 476, 298-303.	13.7	1,428
5	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 279-284.	9.4	990
6	Visualizing samples with box plots. <i>Nature Methods</i> , 2014, 11, 119-120.	9.0	415
7	Model selection and overfitting. <i>Nature Methods</i> , 2016, 13, 703-704.	9.0	407
8	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. <i>BioTechniques</i> , 2008, 45, 81-94.	0.8	355
9	A physical map of the mouse genome. <i>Nature</i> , 2002, 418, 743-750.	13.7	316
10	Classification evaluation. <i>Nature Methods</i> , 2016, 13, 603-604.	9.0	274
11	Oligonucleotide Microarray Analysis of Genomic Imbalance in Children with Mental Retardation. <i>American Journal of Human Genetics</i> , 2006, 79, 500-513.	2.6	261
12	Association, correlation and causation. <i>Nature Methods</i> , 2015, 12, 899-900.	9.0	227
13	The curse(s) of dimensionality. <i>Nature Methods</i> , 2018, 15, 399-400.	9.0	216
14	Error bars. <i>Nature Methods</i> , 2013, 10, 921-922.	9.0	205
15	A physical map of the chicken genome. <i>Nature</i> , 2004, 432, 761-764.	13.7	200
16	Machine learning: supervised methods. <i>Nature Methods</i> , 2018, 15, 5-6.	9.0	190
17	Hive plots--rational approach to visualizing networks. <i>Briefings in Bioinformatics</i> , 2012, 13, 627-644.	3.2	187
18	Classification and regression trees. <i>Nature Methods</i> , 2017, 14, 757-758.	9.0	185

#	ARTICLE	IF	CITATIONS
19	Fast Diploidization in Close Mesopolyploid Relatives of <i>Arabidopsis</i> . <i>Plant Cell</i> , 2010, 22, 2277-2290.	3.1	168
20	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. <i>Genome Research</i> , 2008, 18, 1906-1917.	2.4	163
21	Ensemble methods: bagging and random forests. <i>Nature Methods</i> , 2017, 14, 933-934.	9.0	134
22	A set of BAC clones spanning the human genome. <i>Nucleic Acids Research</i> , 2004, 32, 3651-3660.	6.5	119
23	Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. <i>Genome Biology</i> , 2015, 16, 18.	3.8	107
24	Machine learning: a primer. <i>Nature Methods</i> , 2017, 14, 1119-1120.	9.0	104
25	P values and the search for significance. <i>Nature Methods</i> , 2017, 14, 3-4.	9.0	100
26	Simple linear regression. <i>Nature Methods</i> , 2015, 12, 999-1000.	9.0	88
27	Multiple linear regression. <i>Nature Methods</i> , 2015, 12, 1103-1104.	9.0	86
28	PICS: Probabilistic Inference for ChIP-seq. <i>Biometrics</i> , 2011, 67, 151-163.	0.8	62
29	Integrated and Sequence-Ordered BAC- and YAC-Based Physical Maps for the Rat Genome. <i>Genome Research</i> , 2004, 14, 766-779.	2.4	44
30	Regularization. <i>Nature Methods</i> , 2016, 13, 803-804.	9.0	30
31	Physical map-assisted whole-genome shotgun sequence assemblies. <i>Genome Research</i> , 2006, 16, 768-775.	2.4	27
32	Automated ordering of fingerprinted clones. <i>Bioinformatics</i> , 2004, 20, 1264-1271.	1.8	18
33	A BAC clone fingerprinting approach to the detection of human genome rearrangements. <i>Genome Biology</i> , 2007, 8, R224.	13.9	10
34	Study Design for Sequencing Studies. <i>Methods in Molecular Biology</i> , 2016, 1418, 39-66.	0.4	6
35	Enhancing knowledge discovery from cancer genomics data with Galaxy. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	6
36	Predicting with confidence and tolerance. <i>Nature Methods</i> , 2018, 15, 843-845.	9.0	5

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37	Second-Generation Sequencing for Cancer Genome Analysis. , 2014, , 13-30.		2
38	Differential Hive Plots: Seeing Networks Change. Leonardo, 2017, 50, 504-504.	0.2	1
39	Hive Panel Explorer: an interactive network visualization tool. Bioinformatics, 2021, 37, 436-437.	1.8	1