

JosÃ© Manuel RodrÃ­guez

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7156526/publications.pdf>

Version: 2024-02-01

30
papers

23,118
citations

331259

21
h-index

552369

26
g-index

32
all docs

32
docs citations

32
times ranked

45603
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
2	GENCODE: The reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012, 22, 1760-1774.	2.4	4,217
3	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	2.6	1,257
4	Multiple evidence strands suggest that there may be as few as 19 000 human protein-coding genes. <i>Human Molecular Genetics</i> , 2014, 23, 5866-5878.	1.4	463
5	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	3.8	261
6	APPRIS: annotation of principal and alternative splice isoforms. <i>Nucleic Acids Research</i> , 2013, 41, D110-D117.	6.5	205
7	APPRIS 2017: principal isoforms for multiple gene sets. <i>Nucleic Acids Research</i> , 2018, 46, D213-D217.	6.5	134
8	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016, 17, 251.	3.8	131
9	Most Highly Expressed Protein-Coding Genes Have a Single Dominant Isoform. <i>Journal of Proteome Research</i> , 2015, 14, 1880-1887.	1.8	106
10	Interoperability with Moby 1.0-It's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , 2008, 9, 220-231.	3.2	91
11	De Novo Assembly and Functional Annotation of the Olive (<i>Olea europaea</i>) Transcriptome. <i>DNA Research</i> , 2013, 20, 93-108.	1.5	84
12	Alternatively Spliced Homologous Exons Have Ancient Origins and Are Highly Expressed at the Protein Level. <i>PLoS Computational Biology</i> , 2015, 11, e1004325.	1.5	80
13	Comparative Proteomics Reveals a Significant Bias Toward Alternative Protein Isoforms with Conserved Structure and Function. <i>Molecular Biology and Evolution</i> , 2012, 29, 2265-2283.	3.5	71
14	PanDrugs: a novel method to prioritize anticancer drug treatments according to individual genomic data. <i>Genome Medicine</i> , 2018, 10, 41.	3.6	63
15	Loose ends: almost one in five human genes still have unresolved coding status. <i>Nucleic Acids Research</i> , 2018, 46, 7070-7084.	6.5	62
16	SanXoT: a modular and versatile package for the quantitative analysis of high-throughput proteomics experiments. <i>Bioinformatics</i> , 2019, 35, 1594-1596.	1.8	59
17	An analysis of tissue-specific alternative splicing at the protein level. <i>PLoS Computational Biology</i> , 2020, 16, e1008287.	1.5	55
18	firestar â€”advances in the prediction of functionally important residues. <i>Nucleic Acids Research</i> , 2011, 39, W235-W241.	6.5	52

#	ARTICLE	IF	CITATIONS
19	The EMBRACE web service collection. <i>Nucleic Acids Research</i> , 2010, 38, W683-W688.	6.5	40
20	Comprehensive Quantification of the Modified Proteome Reveals Oxidative Heart Damage in Mitochondrial Heteroplasmy. <i>Cell Reports</i> , 2018, 23, 3685-3697.e4.	2.9	39
21	APPRIS: selecting functionally important isoforms. <i>Nucleic Acids Research</i> , 2022, 50, D54-D59.	6.5	29
22	Characterization of the European Sea Bass (<i>Dicentrarchus labrax</i>) Gonadal Transcriptome During Sexual Development. <i>Marine Biotechnology</i> , 2019, 21, 359-373.	1.1	28
23	Unbiased plasma proteomics discovery of biomarkers for improved detection of subclinical atherosclerosis. <i>EBioMedicine</i> , 2022, 76, 103874.	2.7	23
24	APPRIS WebServer and WebServices. <i>Nucleic Acids Research</i> , 2015, 43, W455-W459.	6.5	19
25	CARGO: a web portal to integrate customized biological information. <i>Nucleic Acids Research</i> , 2007, 35, W16-W20.	6.5	16
26	Assessing the functional relevance of splice isoforms. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab044.	1.5	13
27	An analysis of tissue-specific alternative splicing at the protein level. , 2020, 16, e1008287.		0
28	An analysis of tissue-specific alternative splicing at the protein level. , 2020, 16, e1008287.		0
29	An analysis of tissue-specific alternative splicing at the protein level. , 2020, 16, e1008287.		0
30	An analysis of tissue-specific alternative splicing at the protein level. , 2020, 16, e1008287.		0