

James C Wright

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

3,780
citations

516710

16
h-index

713466

21
g-index

23
all docs

23
docs citations

23
times ranked

9493
citing authors

#	ARTICLE	IF	CITATIONS
1	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	14.5	2,350
2	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923.	14.5	633
3	Shotgun proteomics aids discovery of novel protein-coding genes, alternative splicing, and resurrected pseudogenes in the mouse genome. <i>Genome Research</i> , 2011, 21, 756-767.	5.5	113
4	The PRoteomics IDentification (PRIDE) Converter 2 Framework: An Improved Suite of Tools to Facilitate Data Submission to the PRIDE Database and the ProteomeXchange Consortium. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1682-1689.	3.8	105
5	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. <i>Cell Reports</i> , 2017, 20, 2201-2214.	6.4	95
6	Improving GENCODE reference gene annotation using a high-stringency proteogenomics workflow. <i>Nature Communications</i> , 2016, 7, 11778.	12.8	68
7	<i>Citrobacter rodentium</i> Subverts ATP Flux and Cholesterol Homeostasis in Intestinal Epithelial Cells In Vivo. <i>Cell Metabolism</i> , 2017, 26, 738-752.e6.	16.2	67
8	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. <i>Genome Research</i> , 2019, 29, 2073-2087.	5.5	52
9	Interferon-driven alterations of the host's amino acid metabolism in the pathogenesis of typhoid fever. <i>Journal of Experimental Medicine</i> , 2016, 213, 1061-1077.	8.5	45
10	Exploiting proteomic data for genome annotation and gene model validation in <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2009, 10, 61.	2.8	35
11	Enhanced Peptide Identification by Electron Transfer Dissociation Using an Improved Mascot Percolator. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 478-491.	3.8	34
12	Confident and sensitive phosphoproteomics using combinations of collision induced dissociation and electron transfer dissociation. <i>Journal of Proteomics</i> , 2014, 103, 1-14.	2.4	34
13	Evidence for a novel overlapping coding sequence in POLG initiated at a CUG start codon. <i>BMC Genetics</i> , 2020, 21, 25.	2.7	30
14	DecoyPyrat: Fast Non-redundant Hybrid Decoy Sequence Generation for Large Scale Proteomics. <i>Journal of Proteomics and Bioinformatics</i> , 2016, 09, 176-180.	0.4	24
15	The <i>Citrobacter rodentium</i> type III secretion system effector EspO affects mucosal damage repair and antimicrobial responses. <i>PLoS Pathogens</i> , 2018, 14, e1007406.	4.7	23
16	Cross Species Proteomics. <i>Methods in Molecular Biology</i> , 2010, 604, 123-135.	0.9	23
17	Recent Developments in Proteome Informatics for Mass Spectrometry Analysis. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2009, 12, 194-202.	1.1	14
18	The <sc>OMSSAP</sc>ercolator: <sc>A</sc>n automated tool to validate <sc>OMSSA</sc> results. <i>Proteomics</i> , 2014, 14, 1011-1014.	2.2	13

#	ARTICLE	IF	CITATIONS
19	Flexible Data Analysis Pipeline for High-Confidence Proteogenomics. Journal of Proteome Research, 2016, 15, 4686-4695.	3.7	11
20	Using Deep Learning to Extrapolate Protein Expression Measurements. Proteomics, 2020, 20, e2000009.	2.2	9
21	Chapter 4. PSM Scoring and Validation. New Developments in Mass Spectrometry, 2016, , 69-92.	0.2	1