James C Wright

List of Publications by Year
in descending order

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 2021. Nucleic Acids Research, 2021, 49, D916-D923.	14.5	633
2	Using Deep Learning to Extrapolate Protein Expression Measurements. Proteomics, 2020, 20, e2000009.	2.2	9
3	Evidence for a novel overlapping coding sequence in POLG initiated at a CUG start codon. BMC Genetics, 2020, 21, 25.	2.7	30
4	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. Genome Research, 2019, 29, 2073-2087.	5.5	52
5	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	14.5	2,350
6	The Citrobacter rodentium type III secretion system effector EspO affects mucosal damage repair and antimicrobial responses. PLoS Pathogens, 2018, 14, e1007406.	4.7	23
7	Citrobacter rodentium Subverts ATP Flux and Cholesterol Homeostasis in Intestinal Epithelial Cells InÂVivo. Cell Metabolism, 2017, 26, 738-752.e6.	16.2	67
8	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. Cell Reports, 2017, 20, 2201-2214.	6.4	95
9	DecoyPyrat: Fast Non-redundant Hybrid Decoy Sequence Generation for Large Scale Proteomics. Journal of Proteomics and Bioinformatics, 2016, 09, 176-180.	0.4	24
10	Interferon-driven alterations of the host's amino acid metabolism in the pathogenesis of typhoid fever. Journal of Experimental Medicine, 2016, 213, 1061-1077.	8.5	45
11	Improving GENCODE reference gene annotation using a high-stringency proteogenomics workflow. Nature Communications, 2016, 7, 11778.	12.8	68
12	Flexible Data Analysis Pipeline for High-Confidence Proteogenomics. Journal of Proteome Research, 2016, 15, 4686-4695.	3.7	11
13	Chapter 4. PSM Scoring and Validation. New Developments in Mass Spectrometry, 2016, , 69-92.	0.2	1
14	The <scp>OMSSAP</scp>ercolator: <scp>A</scp>n automated tool to validate <scp>OMSSA</scp> results. Proteomics, 2014, 14, 1011-1014.	2.2	13
15	Confident and sensitive phosphoproteomics using combinations of collision induced dissociation and electron transfer dissociation. Journal of Proteomics, 2014, 103, 1-14.	2.4	34
16	The PRoteomics IDEntification (PRIDE) Converter 2 Framework: An Improved Suite of Tools to Facilitate Data Submission to the PRIDE Database and the ProteomeXchange Consortium. Molecular and Cellular Proteomics, 2012, 11, 1682-1689.	3.8	105
17	Enhanced Peptide Identification by Electron Transfer Dissociation Using an Improved Mascot Percolator. Molecular and Cellular Proteomics, 2012, 11, 478-491.	3.8	34
18	Shotgun proteomics aids discovery of novel protein-coding genes, alternative splicing, and "resurrected" pseudogenes in the mouse genome. Genome Research, 2011, 21, 756-767.	5.5	113

#	Article	IF	Citations
19	Cross Species Proteomics. Methods in Molecular Biology, 2010, 604, 123-135.	0.9	23
20	Recent Developments in Proteome Informatics for Mass Spectrometry Analysis. Combinatorial Chemistry and High Throughput Screening, 2009, 12, 194-202.	1.1	14
21	Exploiting proteomic data for genome annotation and gene model validation in Aspergillus niger. BMC Genomics, 2009, 10, 61.	2.8	35