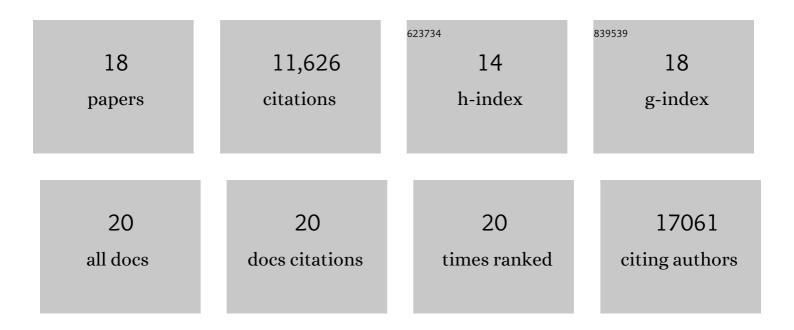
Pavel Pevzner

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10688821/publications.pdf Version: 2024-02-01



DAVIEL DEVIZNED

#	Article	IF	CITATIONS
1	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
2	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. Nature Biotechnology, 2016, 34, 828-837.	17.5	2,802
3	PepNovo:  De Novo Peptide Sequencing via Probabilistic Network Modeling. Analytical Chemistry, 2005, 77, 964-973.	6.5	615
4	American Gut: an Open Platform for Citizen Science Microbiome Research. MSystems, 2018, 3, .	3.8	604
5	Human and mouse genomic sequences reveal extensive breakpoint reuse in mammalian evolution. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7672-7677.	7.1	322
6	Genome Rearrangements in Mammalian Evolution: Lessons From Human and Mouse Genomes. Genome Research, 2003, 13, 37-45.	5.5	302
7	Peptide Sequence Tags for Fast Database Search in Mass-Spectrometry. Journal of Proteome Research, 2005, 4, 1287-1295.	3.7	131
8	Automated de novo protein sequencing of monoclonal antibodies. Nature Biotechnology, 2008, 26, 1336-1338.	17.5	114
9	Whole-Genome Sequencing and Assembly with High-Throughput, Short-Read Technologies. PLoS ONE, 2007, 2, e484.	2.5	112
10	Sequence similarityâ€driven proteomics in organisms with unknown genomes by LCâ€MS/MS and automated <i>de novo</i> sequencing. Proteomics, 2007, 7, 2318-2329.	2.2	98
11	The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome. Nucleic Acids Research, 2004, 32, 3977-3983.	14.5	77
12	Rapid Validation of Protein Identifications with the Borderline Statistical Confidence via De Novo Sequencing and MS BLAST Searches. Journal of Proteome Research, 2006, 5, 2448-2456.	3.7	40
13	Reconstructing the genomic architecture of mammalian ancestors using multispecies comparative maps. Human Genomics, 2003, 1, 30.	2.9	29
14	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. Marine Drugs, 2021, 19, 20.	4.6	19
15	MODELING AND CHARACTERIZATION OF MULTI-CHARGE MASS SPECTRA FOR PEPTIDE SEQUENCING. Journal of Bioinformatics and Computational Biology, 2006, 04, 1329-1352.	0.8	7
16	Peptide Sequence Tags for Fast Database Search in Mass-Spectrometry. Lecture Notes in Computer Science, 2005, , 326-341.	1.3	6
17	Application of <i>de novo</i> sequencing tools to study abiogenic peptide formations by tandem mass spectrometry. The case of homoâ€peptides from glutamic acid complicated by substitutions of hydrogen by sodium or potassium atoms. Rapid Communications in Mass Spectrometry, 2014, 28, 33-41.	1.5	2
18	CHARACTERIZATION OF MULTI-CHARGE MASS SPECTRA FOR PEPTIDE SEQUENCING. , 2005, , .		1