

Pavel Pevzner

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10688821/publications.pdf>

Version: 2024-02-01

18
papers

11,626
citations

623188

14
h-index

839053

18
g-index

20
all docs

20
docs citations

20
times ranked

17061
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
2	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. <i>Nature Biotechnology</i> , 2016, 34, 828-837.	9.4	2,802
3	PepNovo: De Novo Peptide Sequencing via Probabilistic Network Modeling. <i>Analytical Chemistry</i> , 2005, 77, 964-973.	3.2	615
4	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
5	Human and mouse genomic sequences reveal extensive breakpoint reuse in mammalian evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7672-7677.	3.3	322
6	Genome Rearrangements in Mammalian Evolution: Lessons From Human and Mouse Genomes. <i>Genome Research</i> , 2003, 13, 37-45.	2.4	302
7	Peptide Sequence Tags for Fast Database Search in Mass-Spectrometry. <i>Journal of Proteome Research</i> , 2005, 4, 1287-1295.	1.8	131
8	Automated de novo protein sequencing of monoclonal antibodies. <i>Nature Biotechnology</i> , 2008, 26, 1336-1338.	9.4	114
9	Whole-Genome Sequencing and Assembly with High-Throughput, Short-Read Technologies. <i>PLoS ONE</i> , 2007, 2, e484.	1.1	112
10	Sequence similarity-driven proteomics in organisms with unknown genomes by LC-MS/MS and automated de novo sequencing. <i>Proteomics</i> , 2007, 7, 2318-2329.	1.3	98
11	The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome. <i>Nucleic Acids Research</i> , 2004, 32, 3977-3983.	6.5	77
12	Rapid Validation of Protein Identifications with the Borderline Statistical Confidence via De Novo Sequencing and MS BLAST Searches. <i>Journal of Proteome Research</i> , 2006, 5, 2448-2456.	1.8	40
13	Reconstructing the genomic architecture of mammalian ancestors using multispecies comparative maps. <i>Human Genomics</i> , 2003, 1, 30.	1.4	29
14	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	2.2	19
15	MODELING AND CHARACTERIZATION OF MULTI-CHARGE MASS SPECTRA FOR PEPTIDE SEQUENCING. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 1329-1352.	0.3	7
16	Peptide Sequence Tags for Fast Database Search in Mass-Spectrometry. <i>Lecture Notes in Computer Science</i> , 2005, , 326-341.	1.0	6
17	Application of de novo sequencing tools to study abiogenic peptide formations by tandem mass spectrometry. The case of homo-peptides from glutamic acid complicated by substitutions of hydrogen by sodium or potassium atoms. <i>Rapid Communications in Mass Spectrometry</i> , 2014, 28, 33-41.	0.7	2
18	CHARACTERIZATION OF MULTI-CHARGE MASS SPECTRA FOR PEPTIDE SEQUENCING. , 2005, , .		1