List of Publications by Year in descending order

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ΗΛΙΧΗ ΤΑΝΟ

#	Article	IF	CITATIONS
1	The Ecoresponsive Genome of <i>Daphnia pulex</i> . Science, 2011, 331, 555-561.	12.6	1,086
2	FragGeneScan: predicting genes in short and error-prone reads. Nucleic Acids Research, 2010, 38, e191-e191.	14.5	760
3	Rate and molecular spectrum of spontaneous mutations in the bacterium <i>Escherichia coli</i> as determined by whole-genome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2774-83.	7.1	595
4	RAPSearch2: a fast and memory-efficient protein similarity search tool for next-generation sequencing data. Bioinformatics, 2012, 28, 125-126.	4.1	386
5	ISEScan: automated identification of insertion sequence elements in prokaryotic genomes. Bioinformatics, 2017, 33, 3340-3347.	4.1	272
6	The transcriptional diversity of 25 <i>Drosophila</i> cell lines. Genome Research, 2011, 21, 301-314.	5.5	235
7	Identification of Pol IV and RDR2-dependent precursors of 24 nt siRNAs guiding de novo DNA methylation in Arabidopsis. ELife, 2015, 4, e09591.	6.0	228
8	De Novo Repeat Classification and Fragment Assembly. Genome Research, 2004, 14, 1786-1796.	5.5	195
9	Ancestral reconstruction of segmental duplications reveals punctuated cores of human genome evolution. Nature Genetics, 2007, 39, 1361-1368.	21.4	192
10	Leaky Cauldron on the Dark Land. , 2017, 2017, 2421-2434.		169
11	A computational approach toward label-free protein quantification using predicted peptide detectability. Bioinformatics, 2006, 22, e481-e488.	4.1	166
12	MOGONET integrates multi-omics data using graph convolutional networks allowing patient classification and biomarker identification. Nature Communications, 2021, 12, 3445.	12.8	152
13	Learning your identity and disease from research papers. , 2009, , .		147
14	Spatial and functional relationships among Pol V-associated loci, Pol IV-dependent siRNAs, and cytosine methylation in the <i>Arabidopsis</i> epigenome. Genes and Development, 2012, 26, 1825-1836.	5.9	137
15	Determinants of spontaneous mutation in the bacterium <i>Escherichia coli</i> as revealed by whole-genome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5990-9.	7.1	135
16	RAPSearch: a fast protein similarity search tool for short reads. BMC Bioinformatics, 2011, 12, 159.	2.6	128
17	Regulation of adjacent yeast genes. Trends in Genetics, 2000, 16, 109-111.	6.7	127
18	Diverse CRISPRs Evolving in Human Microbiomes. PLoS Genetics, 2012, 8, e1002441.	3.5	125

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19	Whole-Genome Sequencing and Assembly with High-Throughput, Short-Read Technologies. PLoS ONE, 2007, 2, e484.	2.5	112
20	A novel method for multiple alignment of sequences with repeated and shuffled elements. Genome Research, 2004, 14, 2336-2346.	5.5	106
21	Insertion sequence-caused large-scale rearrangements in the genome of <i>Escherichia coli</i> . Nucleic Acids Research, 2016, 44, gkw647.	14.5	104
22	Interlaboratory Study on Differential Analysis of Protein Glycosylation by Mass Spectrometry: The ABRF Glycoprotein Research Multi-Institutional Study 2012. Molecular and Cellular Proteomics, 2013, 12, 2935-2951.	3.8	103
23	Automated interpretation of MS/MS spectra of oligosaccharides. Bioinformatics, 2005, 21, i431-i439.	4.1	101
24	Fragment assembly with double-barreled data. Bioinformatics, 2001, 17, S225-S233.	4.1	97
25	A Two-Step Process for Epigenetic Inheritance in Arabidopsis. Molecular Cell, 2014, 54, 30-42.	9.7	96
26	Strand-biased cytosine deamination at the replication fork causes cytosine to thymine mutations in <i>Escherichia coli</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2176-2181.	7.1	94
27	Computational Framework for Identification of Intact Glycopeptides in Complex Samples. Analytical Chemistry, 2014, 86, 453-463.	6.5	92
28	Quantitative Glycomics Strategies. Molecular and Cellular Proteomics, 2013, 12, 874-884.	3.8	86
29	Efficient Genome-Wide, Privacy-Preserving Similar Patient Query based on Private Edit Distance. , 2015, ,		76
30	On the Mutational Topology of the Bacterial Genome. G3: Genes, Genomes, Genetics, 2013, 3, 399-407.	1.8	75
31	De novo identification of LTR retrotransposons in eukaryotic genomes. BMC Genomics, 2007, 8, 90.	2.8	73
32	A Bayesian Approach to Protein Inference Problem in Shotgun Proteomics. Journal of Computational Biology, 2009, 16, 1183-1193.	1.6	72
33	MGEScan-non-LTR: computational identification and classification of autonomous non-LTR retrotransposons in eukaryotic genomes. Nucleic Acids Research, 2009, 37, e143-e143.	14.5	67
34	Improving confidence in detection and characterization of protein Nâ€glycosylation sites and microheterogeneity. Rapid Communications in Mass Spectrometry, 2011, 25, 2007-2019.	1.5	64
35	Quantitative Measurement of Phosphoproteome Response to Osmotic Stress in Arabidopsis Based on Library-Assisted eXtracted Ion Chromatogram (LAXIC). Molecular and Cellular Proteomics, 2013, 12, 2354-2369.	3.8	62
36	Addressing Beacon re-identification attacks: quantification and mitigation of privacy risks. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 799-805.	4.4	62

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37	Utilizing de Bruijn graph of metagenome assembly for metatranscriptome analysis. Bioinformatics, 2016, 32, 1001-1008.	4.1	59
38	Background Mutational Features of the Radiation-Resistant Bacterium <i>Deinococcus radiodurans</i> . Molecular Biology and Evolution, 2015, 32, 2383-2392.	8.9	58
39	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. Nature Communications, 2020, 11, 5281.	12.8	57
40	A Novel Alignment Method and Multiple Filters for Exclusion of Unqualified Peptides To Enhance Label-Free Quantification Using Peptide Intensity in LC–MS/MS. Journal of Proteome Research, 2011, 10, 4799-4812.	3.7	55
41	BuildSummary: Using a Group-Based Approach To Improve the Sensitivity of Peptide/Protein Identification in Shotgun Proteomics. Journal of Proteome Research, 2012, 11, 1494-1502.	3.7	52
42	Testosterone Affects Neural Gene Expression Differently in Male and Female Juncos: A Role for Hormones in Mediating Sexual Dimorphism and Conflict. PLoS ONE, 2013, 8, e61784.	2.5	52
43	Full-Spectrum Prediction of Peptides Tandem Mass Spectra using Deep Neural Network. Analytical Chemistry, 2020, 92, 4275-4283.	6.5	48
44	Shotgun Protein Sequencing by Tandem Mass Spectra Assembly. Analytical Chemistry, 2004, 76, 7221-7233.	6.5	47
45	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. Nature Microbiology, 2021, 6, 123-135.	13.3	47
46	N-Glycan Profiling by Microchip Electrophoresis to Differentiate Disease States Related to Esophageal Adenocarcinoma. Analytical Chemistry, 2012, 84, 3621-3627.	6.5	46
47	On the Accuracy and Limits of Peptide Fragmentation Spectrum Prediction. Analytical Chemistry, 2011, 83, 790-796.	6.5	45
48	Glycoproteomics: Identifying the Glycosylation of Prostate Specific Antigen at Normal and High Isoelectric Points by LC–MS/MS. Journal of Proteome Research, 2014, 13, 5570-5580.	3.7	44
49	Protecting genomic data analytics in the cloud: state of the art and opportunities. BMC Medical Genomics, 2016, 9, 63.	1.5	43
50	Adaptation of Escherichia coli to Long-Term Serial Passage in Complex Medium: Evidence of Parallel Evolution. MSystems, 2017, 2, .	3.8	42
51	RNAMotifScan: automatic identification of RNA structural motifs using secondary structural alignment. Nucleic Acids Research, 2010, 38, e176-e176.	14.5	41
52	The Importance of Peptide Detectability for Protein Identification, Quantification, and Experiment Design in MS/MS Proteomics. Journal of Proteome Research, 2010, 9, 6288-6297.	3.7	41
53	Mapping siteâ€specific protein Nâ€glycosylations through liquid chromatography/mass spectrometry and targeted tandem mass spectrometry. Rapid Communications in Mass Spectrometry, 2010, 24, 965-972.	1.5	39
54	Label-Free Glycopeptide Quantification for Biomarker Discovery in Human Sera. Journal of Proteome Research, 2014, 13, 4821-4832.	3.7	39

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55	A Graph-Centric Approach for Metagenome-Guided Peptide and Protein Identification in Metaproteomics. PLoS Computational Biology, 2016, 12, e1005224.	3.2	36
56	Automated annotation and quantitation of glycans by liquid chromatography/electrospray ionization mass spectrometric analysis using the MultiGlycanâ€ESI computational tool. Rapid Communications in Mass Spectrometry, 2015, 29, 135-142.	1.5	35
57	AN ORFOME ASSEMBLY APPROACH TO METAGENOMICS SEQUENCES ANALYSIS. Journal of Bioinformatics and Computational Biology, 2009, 07, 455-471.	0.8	33
58	A community effort to protect genomic data sharing, collaboration and outsourcing. Npj Genomic Medicine, 2017, 2, 33.	3.8	33
59	Identifying repeat domains in large genomes. Genome Biology, 2006, 7, R7.	9.6	31
60	Automated Glycan Sequencing from Tandem Mass Spectra of N-Linked Glycopeptides. Analytical Chemistry, 2016, 88, 5725-5732.	6.5	31
61	Determinants of Base-Pair Substitution Patterns Revealed by Whole-Genome Sequencing of DNA Mismatch Repair Defective <i>Escherichia coli</i> . Genetics, 2018, 209, 1029-1042.	2.9	31
62	Potential for sexual conflict assessed via testosterone-mediated transcriptional changes in liver and muscle of a songbird. Journal of Experimental Biology, 2014, 217, 507-17.	1.7	28
63	8-plex LC–MS/MS Analysis of Permethylated <i>N</i> -Glycans Achieved by Using Stable Isotopic Iodomethane. Analytical Chemistry, 2019, 91, 11794-11802.	6.5	24
64	Rational design of a more stable penicillin G acylase against organic cosolvent. Journal of Molecular Catalysis B: Enzymatic, 2002, 18, 285-290.	1.8	23
65	Genome Assembly, Rearrangement, and Repeats. Chemical Reviews, 2007, 107, 3391-3406.	47.7	23
66	A machine-learning approach to combined evidence validation of genome assemblies. Bioinformatics, 2008, 24, 744-750.	4.1	23
67	LTR retroelements in the genome of Daphnia pulex. BMC Genomics, 2010, 11, 425.	2.8	23
68	Choosing blindly but wisely: differentially private solicitation of DNA datasets for disease marker discovery. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 100-108.	4.4	22
69	iDASH secure genome analysis competition 2018: blockchain genomic data access logging, homomorphic encryption on GWAS, and DNA segment searching. BMC Medical Genomics, 2020, 13, 98.	1.5	22
70	ADVANCEMENT IN PROTEIN INFERENCE FROM SHOTGUN PROTEOMICS USING PEPTIDE DETECTABILITY. , 2006, , .		22
71	Proteomic Changes in the Photoreceptor Outer Segment upon Intense Light Exposure. Journal of Proteome Research, 2010, 9, 1173-1181.	3.7	21
72	A machine learning approach to predicting peptide fragmentation spectra. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 219-30.	0.7	21

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73	The Spectrum of Replication Errors in the Absence of Error Correction Assayed Across the Whole Genome of <i>Escherichia coli</i> . Genetics, 2018, 209, 1043-1054.	2.9	20
74	The Symmetrical Wave Pattern of Base-Pair Substitution Rates across the Escherichia coli Chromosome Has Multiple Causes. MBio, 2019, 10, .	4.1	20
75	Characterization of the Glycosylation Site of Human PSA Prompted by Missense Mutation using LC–MS/MS. Journal of Proteome Research, 2015, 14, 2872-2883.	3.7	19
76	msCRUSH: Fast Tandem Mass Spectral Clustering Using Locality Sensitive Hashing. Journal of Proteome Research, 2019, 18, 147-158.	3.7	19
77	A <i>de Bruijn</i> Graph Approach to the Quantification of Closely-Related Genomes in a Microbial Community. Journal of Computational Biology, 2012, 19, 814-825.	1.6	18
78	Probabilistic Inference of Biochemical Reactions in Microbial Communities from Metagenomic Sequences. PLoS Computational Biology, 2013, 9, e1002981.	3.2	17
79	Insertion sequence elements-mediated structural variations in bacterial genomes. Mobile DNA, 2018, 9, 29.	3.6	17
80	A Meta-proteogenomic Approach to Peptide Identification Incorporating Assembly Uncertainty and Genomic Variation. Molecular and Cellular Proteomics, 2019, 18, S183-S192.	3.8	17
81	Combinatorial Libraries of Synthetic Peptides as a Model for Shotgun Proteomics. Analytical Chemistry, 2010, 82, 6559-6568.	6.5	16
82	DNA sequence templates adjacent nucleosome and ORC sites at gene amplification origins in <i>Drosophila</i> . Nucleic Acids Research, 2015, 43, 8746-8761.	14.5	15
83	XLSearch: a Probabilistic Database Search Algorithm for Identifying Cross-Linked Peptides. Journal of Proteome Research, 2016, 15, 1830-1841.	3.7	15
84	Insertion polymorphisms of mobile genetic elements in sexual and asexual populations of Daphnia pulex. Genome Biology and Evolution, 2017, 9, evw302.	2.5	15
85	iDASH secure genome analysis competition 2017. BMC Medical Genomics, 2018, 11, 85.	1.5	15
86	Privacy-preserving construction of generalized linear mixed model for biomedical computation. Bioinformatics, 2020, 36, i128-i135.	4.1	15
87	Detection of Structural Variants Involving Repetitive Regions in the Reference Genome. Journal of Computational Biology, 2014, 21, 219-233.	1.6	14
88	STRScan: targeted profiling of short tandem repeats in whole-genome sequencing data. BMC Bioinformatics, 2017, 18, 398.	2.6	14
89	Independent Mammalian Genome Contractions Following the KT Boundary. Genome Biology and Evolution, 2009, 1, 2-12.	2.5	13
90	Identification of Glycopeptides with Multiple Hydroxylysine O-Glycosylation Sites by Tandem Mass Spectrometry. Journal of Proteome Research, 2015, 14, 5099-5108.	3.7	13

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91	Adaptation of Escherichia coli to long-term batch culture in various rich media. Research in Microbiology, 2018, 169, 145-156.	2.1	13
92	A New Estimator of Significance of Correlation in Time Series Data. Journal of Computational Biology, 2001, 8, 463-470.	1.6	12
93	Computational Methods in Mass Spectrometry-Based Proteomics. Advances in Experimental Medicine and Biology, 2016, 939, 63-89.	1.6	12
94	On the estimation of false positives in peptide identifications using decoy search strategy. Proteomics, 2009, 9, 194-204.	2.2	11
95	A Fast and Memoryâ€Efficient Spectral Library Search Algorithm Using Localityâ€Sensitive Hashing. Proteomics, 2020, 20, e2000002.	2.2	10
96	Correcting Base-Assignment Errors in Repeat Regions of Shotgun Assembly. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 54-64.	3.0	9
97	Extending the coverage of spectral libraries: A neighbor-based approach to predicting intensities of peptide fragmentation spectra. Proteomics, 2013, 13, 756-765.	2.2	9
98	Bioinformatics Protocols in Glycomics and Glycoproteomics. Current Protocols in Protein Science, 2014, 76, 2.15.1-2.15.7.	2.8	9
99	New complexities of SOS-induced "untargeted―mutagenesis in Escherichia coli as revealed by mutation accumulation and whole-genome sequencing. DNA Repair, 2020, 90, 102852.	2.8	9
100	GlycoHybridSeq: Automated Identification of N-Linked Glycopeptides Using Electron Transfer/High-Energy Collision Dissociation (EThcD). Journal of Proteome Research, 2021, 20, 3345-3352.	3.7	9
101	Impact of Amidination on Peptide Fragmentation and Identification in Shotgun Proteomics. Journal of Proteome Research, 2016, 15, 3656-3665.	3.7	8
102	Computational identification of micro-structural variations and their proteogenomic consequences in cancer. Bioinformatics, 2018, 34, 1672-1681.	4.1	8
103	Protein identification problem from a Bayesian point of view. Statistics and Its Interface, 2012, 5, 21-37.	0.3	8
104	Algorithmic approaches to clonal reconstruction in heterogeneous cell populations. Quantitative Biology, 2019, 7, 255-265.	0.5	7
105	Constrained De Novo Sequencing of neo-Epitope Peptides Using Tandem Mass Spectrometry. Lecture Notes in Computer Science, 2018, 10812, 138-153.	1.3	6
106	Clonal reconstruction from time course genomic sequencing data. BMC Genomics, 2019, 20, 1002.	2.8	6
107	A computational approach to characterizing bond linkages of glycan isomers using matrixâ€assisted laser desorption/ionization tandem timeâ€ofâ€flight mass spectrometry. Rapid Communications in Mass Spectrometry, 2008, 22, 3561-3569	1.5	4
108	A Secure Alignment Algorithm for Mapping Short Reads to Human Genome. Journal of Computational Biology, 2018, 25, 529-540.	1.6	4

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109 Haplotype-based membership inference from summary genomic data. Bioinformatics, 2021, 37, i161-i168.		
	4.1	4
110 Improving phosphopeptide identification in shotgun proteomics by supervised filtering of peptide-spectrum matches. , 2013, , .		3
Characterization of microbial associations in human oral microbiome. Bio-Medical Materials and Engineering, 2014, 24, 3737-3744.	0.6	3
Overlap detection on long, error-prone sequencing reads via smooth <i>q</i> -gram. Bioinformatics, 2020, 36, 4838-4845.	4.1	3
A Computational Approach for the Identification of Site-Specific Protein Glycosylations Through Ion-Trap Mass Spectrometry. Lecture Notes in Computer Science, 2007, , 96-107.	1.3	3
On the privacy risks of sharing clinical proteomics data. AMIA Summits on Translational Science Proceedings, 2016, 2016, 122-31.	0.4	3
A Maximum-Likelihood Approach to Estimating the Insertion Frequencies of Transposable Elements from Population Sequencing Data. Molecular Biology and Evolution, 2018, 35, 2560-2571.	8.9	2
116 Identification of Nâ€ŧerminal protein processing sites by chemical labeling mass spectrometry. Rapid Communications in Mass Spectrometry, 2019, 33, 1015-1023.	1.5	2
HySec-Flow: Privacy-Preserving Genomic Computing with SGX-based Big-Data Analytics Framework. , 2021, , .		2
Secure Genomic Computation through Site-Wise Encryption. AMIA Summits on Translational Science Proceedings, 2015, 2015, 227-31.	0.4	2
Real-time Protection of Genomic Data Sharing in Beacon Services. AMIA Summits on Translational Science Proceedings, 2018, 2017, 45-54.	0.4	2
Locality-Sensitive Hashing-Based k-Mer Clustering for Identification of Differential Microbial Markers Related to Host Phenotype. Journal of Computational Biology, 2022, 29, 738-751.	1.6	2
Bioinformatic Approaches in Glycomics and Glycoproteomics. Current Proteomics, 2011, 8, 309-324.	0.3	1
122 GlycanGUI: Automated Glycan Annotation and Quantification Using Glucose Unit Index. Frontiers in Chemistry, 2021, 9, 707382.	3.6	1
Improving de novo metatranscriptome assembly via machine learning algorithms. International Journal of Computational Biology and Drug Design, 2017, 10, 91.	0.3	1
A Reciprocal Best-hit Approach to Characterize Isomeric <i>N</i> -Glycans Using Tandem Mass Spectrometry. Analytical Chemistry, 2022, 94, 10003-10010.	6.5	1
A Community Effort to Protect Genomic Data Sharing, Collaboration and Outsourcing. SSRN Electronic Journal, 2017, , .	0.4	0