

Haixu Tang

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1899162/haixu-tang-publications-by-year.pdf>

Version: 2024-04-29

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

121
papers

6,269
citations

40
h-index

77
g-index

130
ext. papers

7,732
ext. citations

7.2
avg, IF

5.85
L-index

#	Paper	IF	Citations
121	GlycoHybridSeq: Automated Identification of N-Linked Glycopeptides Using Electron Transfer/High-Energy Collision Dissociation (ETHcD). <i>Journal of Proteome Research</i> , 2021 , 20, 3345-3352	5.6	4
120	MOGONET integrates multi-omics data using graph convolutional networks allowing patient classification and biomarker identification. <i>Nature Communications</i> , 2021 , 12, 3445	17.4	17
119	GlycanGUI: Automated Glycan Annotation and Quantification Using Glucose Unit Index. <i>Frontiers in Chemistry</i> , 2021 , 9, 707382	5	0
118	Haplotype-based membership inference from summary genomic data. <i>Bioinformatics</i> , 2021 , 37, i161-i168	7.2	1
117	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. <i>Nature Microbiology</i> , 2021 , 6, 123-135	26.6	16
116	A Fast and Memory-Efficient Spectral Library Search Algorithm Using Locality-Sensitive Hashing. <i>Proteomics</i> , 2020 , 20, e2000002	4.8	0
115	Full-Spectrum Prediction of Peptides Tandem Mass Spectra using Deep Neural Network. <i>Analytical Chemistry</i> , 2020 , 92, 4275-4283	7.8	17
114	New complexities of SOS-induced "untargeted" mutagenesis in Escherichia coli as revealed by mutation accumulation and whole-genome sequencing. <i>DNA Repair</i> , 2020 , 90, 102852	4.3	4
113	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. <i>Nature Communications</i> , 2020 , 11, 5281	17.4	19
112	Privacy-preserving construction of generalized linear mixed model for biomedical computation. <i>Bioinformatics</i> , 2020 , 36, i128-i135	7.2	2
111	Overlap detection on long, error-prone sequencing reads via smooth q-gram. <i>Bioinformatics</i> , 2020 , 36, 4838-4845	7.2	
110	A Meta-proteogenomic Approach to Peptide Identification Incorporating Assembly Uncertainty and Genomic Variation. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, S183-S192	7.6	11
109	Identification of N-terminal protein processing sites by chemical labeling mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2019 , 33, 1015-1023	2.2	2
108	The Symmetrical Wave Pattern of Base-Pair Substitution Rates across the Escherichia coli Chromosome Has Multiple Causes. <i>MBio</i> , 2019 , 10,	7.8	9
107	8-plex LC-MS/MS Analysis of Permethylated -Glycans Achieved by Using Stable Isotopic Iodomethane. <i>Analytical Chemistry</i> , 2019 , 91, 11794-11802	7.8	18
106	Clonal reconstruction from time course genomic sequencing data. <i>BMC Genomics</i> , 2019 , 20, 1002	4.5	5
105	Algorithmic approaches to clonal reconstruction in heterogeneous cell populations. <i>Quantitative Biology</i> , 2019 , 7, 255-265	3.9	1

104	msCRUSH: Fast Tandem Mass Spectral Clustering Using Locality Sensitive Hashing. <i>Journal of Proteome Research</i> , 2019 , 18, 147-158	5.6	10
103	Constrained Sequencing of neo-Epitope Peptides using Tandem Mass Spectrometry. <i>Lecture Notes in Computer Science</i> , 2018 , 10812, 138-153	0.9	4
102	Adaptation of Escherichia coli to long-term batch culture in various rich media. <i>Research in Microbiology</i> , 2018 , 169, 145-156	4	8
101	Computational identification of micro-structural variations and their proteogenomic consequences in cancer. <i>Bioinformatics</i> , 2018 , 34, 1672-1681	7.2	4
100	The Spectrum of Replication Errors in the Absence of Error Correction Assayed Across the Whole Genome of. <i>Genetics</i> , 2018 , 209, 1043-1054	4	10
99	A Secure Alignment Algorithm for Mapping Short Reads to Human Genome. <i>Journal of Computational Biology</i> , 2018 , 25, 529-540	1.7	2
98	A Maximum-Likelihood Approach to Estimating the Insertion Frequencies of Transposable Elements from Population Sequencing Data. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2560-2571	8.3	1
97	Determinants of Base-Pair Substitution Patterns Revealed by Whole-Genome Sequencing of DNA Mismatch Repair Defective. <i>Genetics</i> , 2018 , 209, 1029-1042	4	19
96	Real-time Protection of Genomic Data Sharing in Beacon Services. <i>AMIA Summits on Translational Science Proceedings</i> , 2018 , 2017, 45-54	1.1	2
95	iDASH secure genome analysis competition 2017. <i>BMC Medical Genomics</i> , 2018 , 11, 85	3.7	9
94	Insertion sequence elements-mediated structural variations in bacterial genomes. <i>Mobile DNA</i> , 2018 , 9, 29	4.4	6
93	Insertion Polymorphisms of Mobile Genetic Elements in Sexual and Asexual Populations of <i>Daphnia pulex</i> . <i>Genome Biology and Evolution</i> , 2017 , 9, 362-374	3.9	14
92	Addressing Beacon re-identification attacks: quantification and mitigation of privacy risks. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2017 , 24, 799-805	8.6	43
91	Adaptation of to Long-Term Serial Passage in Complex Medium: Evidence of Parallel Evolution. <i>MSystems</i> , 2017 , 2,	7.6	30
90	STRScan: targeted profiling of short tandem repeats in whole-genome sequencing data. <i>BMC Bioinformatics</i> , 2017 , 18, 398	3.6	11
89	A community effort to protect genomic data sharing, collaboration and outsourcing. <i>Npj Genomic Medicine</i> , 2017 , 2, 33	6.2	22
88	Leaky Cauldron on the Dark Land: Understanding Memory Side-Channel Hazards in SGX 2017 , 2017, 2421-2434	97	
87	ISEScan: automated identification of insertion sequence elements in prokaryotic genomes. <i>Bioinformatics</i> , 2017 , 33, 3340-3347	7.2	82

86	Impact of Amidination on Peptide Fragmentation and Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2016 , 15, 3656-3665	5.6	7
85	Computational Methods in Mass Spectrometry-Based Proteomics. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 939, 63-89	3.6	7
84	Utilizing de Bruijn graph of metagenome assembly for metatranscriptome analysis. <i>Bioinformatics</i> , 2016 , 32, 1001-8	7.2	29
83	Strand-biased cytosine deamination at the replication fork causes cytosine to thymine mutations in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 2176-81	11.5	58
82	A Graph-Centric Approach for Metagenome-Guided Peptide and Protein Identification in Metaproteomics. <i>PLoS Computational Biology</i> , 2016 , 12, e1005224	5	29
81	On the privacy risks of sharing clinical proteomics data. <i>AMIA Summits on Translational Science Proceedings</i> , 2016 , 2016, 122-31	1.1	3
80	Protecting genomic data analytics in the cloud: state of the art and opportunities. <i>BMC Medical Genomics</i> , 2016 , 9, 63	3.7	30
79	XLSearch: a Probabilistic Database Search Algorithm for Identifying Cross-Linked Peptides. <i>Journal of Proteome Research</i> , 2016 , 15, 1830-41	5.6	14
78	Automated Glycan Sequencing from Tandem Mass Spectra of N-Linked Glycopeptides. <i>Analytical Chemistry</i> , 2016 , 88, 5725-32	7.8	27
77	Insertion sequence-caused large-scale rearrangements in the genome of <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2016 , 44, 7109-19	20.1	49
76	Characterization of the Glycosylation Site of Human PSA Prompted by Missense Mutation using LC-MS/MS. <i>Journal of Proteome Research</i> , 2015 , 14, 2872-83	5.6	19
75	Background Mutational Features of the Radiation-Resistant Bacterium <i>Deinococcus radiodurans</i> . <i>Molecular Biology and Evolution</i> , 2015 , 32, 2383-92	8.3	45
74	DNA sequence templates adjacent nucleosome and ORC sites at gene amplification origins in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2015 , 43, 8746-61	20.1	10
73	Choosing blindly but wisely: differentially private solicitation of DNA datasets for disease marker discovery. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015 , 22, 100-8	8.6	18
72	Determinants of spontaneous mutation in the bacterium <i>Escherichia coli</i> as revealed by whole-genome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E5990-9	11.5	76
71	Identification of Glycopeptides with Multiple Hydroxylysine O-Glycosylation Sites by Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2015 , 14, 5099-108	5.6	8
70	Automated annotation and quantitation of glycans by liquid chromatography/electrospray ionization mass spectrometric analysis using the MultiGlycan-ESI computational tool. <i>Rapid Communications in Mass Spectrometry</i> , 2015 , 29, 135-42	2.2	31
69	Efficient Genome-Wide, Privacy-Preserving Similar Patient Query based on Private Edit Distance 2015 ,		55

68	Identification of Pol IV and RDR2-dependent precursors of 24 nt siRNAs guiding de novo DNA methylation in Arabidopsis. <i>ELife</i> , 2015 , 4, e09591	8.9	146
67	Secure Genomic Computation through Site-Wise Encryption. <i>AMIA Summits on Translational Science Proceedings</i> , 2015 , 2015, 227-31	1.1	2
66	A two-step process for epigenetic inheritance in Arabidopsis. <i>Molecular Cell</i> , 2014 , 54, 30-42	17.6	78
65	Computational framework for identification of intact glycopeptides in complex samples. <i>Analytical Chemistry</i> , 2014 , 86, 453-63	7.8	79
64	Label-free glycopeptide quantification for biomarker discovery in human sera. <i>Journal of Proteome Research</i> , 2014 , 13, 4821-32	5.6	34
63	Characterization of microbial associations in human oral microbiome. <i>Bio-Medical Materials and Engineering</i> , 2014 , 24, 3737-44	1	3
62	Detection of structural variants involving repetitive regions in the reference genome. <i>Journal of Computational Biology</i> , 2014 , 21, 219-33	1.7	13
61	Glycoproteomics: identifying the glycosylation of prostate specific antigen at normal and high isoelectric points by LC-MS/MS. <i>Journal of Proteome Research</i> , 2014 , 13, 5570-80	5.6	38
60	Bioinformatics protocols in glycomics and glycoproteomics. <i>Current Protocols in Protein Science</i> , 2014 , 76, 2.15.1-2.15.7	3.1	9
59	Potential for sexual conflict assessed via testosterone-mediated transcriptional changes in liver and muscle of a songbird. <i>Journal of Experimental Biology</i> , 2014 , 217, 507-17	3	24
58	Improving phosphopeptide identification in shotgun proteomics by supervised filtering of peptide-spectrum matches 2013 ,		2
57	On the mutational topology of the bacterial genome. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 399-407	3.2	53
56	Probabilistic inference of biochemical reactions in microbial communities from metagenomic sequences. <i>PLoS Computational Biology</i> , 2013 , 9, e1002981	5	12
55	Quantitative glycomics strategies. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 874-84	7.6	76
54	Extending the coverage of spectral libraries: a neighbor-based approach to predicting intensities of peptide fragmentation spectra. <i>Proteomics</i> , 2013 , 13, 756-65	4.8	9
53	Quantitative measurement of phosphoproteome response to osmotic stress in arabidopsis based on Library-Assisted eXtracted Ion Chromatogram (LAXIC). <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2354-69	7.6	55
52	Interlaboratory study on differential analysis of protein glycosylation by mass spectrometry: the ABRF glycoprotein research multi-institutional study 2012. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2935-51	7.6	92
51	Testosterone affects neural gene expression differently in male and female juncos: a role for hormones in mediating sexual dimorphism and conflict. <i>PLoS ONE</i> , 2013 , 8, e61784	3.7	42

50	Spatial and functional relationships among Pol V-associated loci, Pol IV-dependent siRNAs, and cytosine methylation in the Arabidopsis epigenome. <i>Genes and Development</i> , 2012 , 26, 1825-36	12.6	115
49	N-glycan profiling by microchip electrophoresis to differentiate disease states related to esophageal adenocarcinoma. <i>Analytical Chemistry</i> , 2012 , 84, 3621-7	7.8	40
48	BuildSummary: using a group-based approach to improve the sensitivity of peptide/protein identification in shotgun proteomics. <i>Journal of Proteome Research</i> , 2012 , 11, 1494-502	5.6	42
47	Diverse CRISPRs evolving in human microbiomes. <i>PLoS Genetics</i> , 2012 , 8, e1002441	6	100
46	RAPSearch2: a fast and memory-efficient protein similarity search tool for next-generation sequencing data. <i>Bioinformatics</i> , 2012 , 28, 125-6	7.2	292
45	Rate and molecular spectrum of spontaneous mutations in the bacterium <i>Escherichia coli</i> as determined by whole-genome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E2774-83	11.5	418
44	A de Bruijn graph approach to the quantification of closely-related genomes in a microbial community. <i>Journal of Computational Biology</i> , 2012 , 19, 814-25	1.7	11
43	Protein identification problem from a Bayesian point of view. <i>Statistics and Its Interface</i> , 2012 , 5, 21-37	0.4	8
42	A novel alignment method and multiple filters for exclusion of unqualified peptides to enhance label-free quantification using peptide intensity in LC-MS/MS. <i>Journal of Proteome Research</i> , 2011 , 10, 4799-812	5.6	54
41	The ecoresponsive genome of <i>Daphnia pulex</i> . <i>Science</i> , 2011 , 331, 555-61	33.3	924
40	RAPSearch: a fast protein similarity search tool for short reads. <i>BMC Bioinformatics</i> , 2011 , 12, 159	3.6	92
39	Improving confidence in detection and characterization of protein N-glycosylation sites and microheterogeneity. <i>Rapid Communications in Mass Spectrometry</i> , 2011 , 25, 2007-19	2.2	61
38	On the accuracy and limits of peptide fragmentation spectrum prediction. <i>Analytical Chemistry</i> , 2011 , 83, 790-6	7.8	40
37	Bioinformatic Approaches in Glycomics and Glycoproteomics. <i>Current Proteomics</i> , 2011 , 8, 309-324	0.7	1
36	The transcriptional diversity of 25 <i>Drosophila</i> cell lines. <i>Genome Research</i> , 2011 , 21, 301-14	9.7	171
35	RNAMotifScan: automatic identification of RNA structural motifs using secondary structural alignment. <i>Nucleic Acids Research</i> , 2010 , 38, e176	20.1	29
34	FragGeneScan: predicting genes in short and error-prone reads. <i>Nucleic Acids Research</i> , 2010 , 38, e191	20.1	535
33	The importance of peptide detectability for protein identification, quantification, and experiment design in MS/MS proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 6288-97	5.6	31

32	Combinatorial libraries of synthetic peptides as a model for shotgun proteomics. <i>Analytical Chemistry</i> , 2010 , 82, 6559-68	7.8	14
31	Proteomic changes in the photoreceptor outer segment upon intense light exposure. <i>Journal of Proteome Research</i> , 2010 , 9, 1173-81	5.6	17
30	LTR retroelements in the genome of <i>Daphnia pulex</i> . <i>BMC Genomics</i> , 2010 , 11, 425	4.5	21
29	Mapping site-specific protein N-glycosylations through liquid chromatography/mass spectrometry and targeted tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2010 , 24, 965-72	2.2	36
28	An ORFome assembly approach to metagenomics sequences analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2009 , 7, 455-71	1	31
27	A bayesian approach to protein inference problem in shotgun proteomics. <i>Journal of Computational Biology</i> , 2009 , 16, 1183-93	1.7	55
26	Learning your identity and disease from research papers 2009 ,		113
25	MGEScan-non-LTR: computational identification and classification of autonomous non-LTR retrotransposons in eukaryotic genomes. <i>Nucleic Acids Research</i> , 2009 , 37, e143	20.1	52
24	On the estimation of false positives in peptide identifications using decoy search strategy. <i>Proteomics</i> , 2009 , 9, 194-204	4.8	9
23	Independent mammalian genome contractions following the KT boundary. <i>Genome Biology and Evolution</i> , 2009 , 1, 2-12	3.9	12
22	A machine-learning approach to combined evidence validation of genome assemblies. <i>Bioinformatics</i> , 2008 , 24, 744-50	7.2	20
21	A computational approach to characterizing bond linkages of glycan isomers using matrix-assisted laser desorption/ionization tandem time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2008 , 22, 3561-9	2.2	3
20	Genome assembly, rearrangement, and repeats. <i>Chemical Reviews</i> , 2007 , 107, 3391-406	68.1	19
19	Ancestral reconstruction of segmental duplications reveals punctuated cores of human genome evolution. <i>Nature Genetics</i> , 2007 , 39, 1361-8	36.3	162
18	De novo identification of LTR retrotransposons in eukaryotic genomes. <i>BMC Genomics</i> , 2007 , 8, 90	4.5	64
17	Whole-genome sequencing and assembly with high-throughput, short-read technologies. <i>PLoS ONE</i> , 2007 , 2, e484	3.7	94
16	Correcting base-assignment errors in repeat regions of shotgun assembly. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007 , 4, 54-64	3	6
15	A Computational Approach for the Identification of Site-Specific Protein Glycosylations Through Ion-Trap Mass Spectrometry. <i>Lecture Notes in Computer Science</i> , 2007 , 96-107	0.9	3

14	Identifying repeat domains in large genomes. <i>Genome Biology</i> , 2006 , 7, R7	18.3	23
13	A computational approach toward label-free protein quantification using predicted peptide detectability. <i>Bioinformatics</i> , 2006 , 22, e481-8	7.2	141
12	ADVANCEMENT IN PROTEIN INFERENCE FROM SHOTGUN PROTEOMICS USING PEPTIDE DETECTABILITY 2006 ,		12
11	A machine learning approach to predicting peptide fragmentation spectra. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006 , 219-30	1.3	19
10	Automated interpretation of MS/MS spectra of oligosaccharides. <i>Bioinformatics</i> , 2005 , 21 Suppl 1, i431-97.2		89
9	A novel method for multiple alignment of sequences with repeated and shuffled elements. <i>Genome Research</i> , 2004 , 14, 2336-46	9.7	83
8	De novo repeat classification and fragment assembly. <i>Genome Research</i> , 2004 , 14, 1786-96	9.7	157
7	Shotgun protein sequencing by tandem mass spectra assembly. <i>Analytical Chemistry</i> , 2004 , 76, 7221-33	7.8	44
6	Rational design of a more stable penicillin G acylase against organic cosolvent. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2002 , 18, 285-290		21
5	Fragment assembly with double-barreled data. <i>Bioinformatics</i> , 2001 , 17 Suppl 1, S225-33	7.2	79
4	A new estimator of significance of correlation in time series data. <i>Journal of Computational Biology</i> , 2001 , 8, 463-70	1.7	11
3	Regulation of adjacent yeast genes. <i>Trends in Genetics</i> , 2000 , 16, 109-11	8.5	99
2	The symmetrical pattern of base-pair substitutions rates across the chromosome in Escherichia coli has multiple causes		1
1	Clonal reconstruction from time course genomic sequencing data		1