

# Ming Li

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

13,473  
citations

279798

23  
h-index

206112

48  
g-index

57  
all docs

57  
docs citations

57  
times ranked

14641  
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	27.8	6,319
2	PEAKS: powerful software for peptide <i>de novo</i> sequencing by tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2003, 17, 2337-2342.	1.5	1,156
3	An Introduction to Kolmogorov Complexity and Its Applications. , 1997, , .		1,072
4	The Similarity Metric. <i>IEEE Transactions on Information Theory</i> , 2004, 50, 3250-3264.	2.4	766
5	PatternHunter: faster and more sensitive homology search. <i>Bioinformatics</i> , 2002, 18, 440-445.	4.1	713
6	An Introduction to Kolmogorov Complexity and Its Applications. <i>Texts in Computer Science</i> , 2008, , .	0.7	682
7	Information distance. <i>IEEE Transactions on Information Theory</i> , 1998, 44, 1407-1423.	2.4	377
8	De novo peptide sequencing by deep learning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8247-8252.	7.1	278
9	RAPTOR: OPTIMAL PROTEIN THREADING BY LINEAR PROGRAMMING. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 95-117.	0.8	245
10	Deep learning enables de novo peptide sequencing from data-independent-acquisition mass spectrometry. <i>Nature Methods</i> , 2019, 16, 63-66.	19.0	235
11	On the closest string and substring problems. <i>Journal of the ACM</i> , 2002, 49, 157-171.	2.2	205
12	ZOOM! Zillions of oligos mapped. <i>Bioinformatics</i> , 2008, 24, 2431-2437.	4.1	187
13	Shared Information and Program Plagiarism Detection. <i>IEEE Transactions on Information Theory</i> , 2004, 50, 1545-1551.	2.4	180
14	PATTERNHUNTER II: HIGHLY SENSITIVE AND FAST HOMOLOGY SEARCH. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 417-439.	0.8	170
15	On spaced seeds for similarity search. <i>Discrete Applied Mathematics</i> , 2004, 138, 253-263.	0.9	110
16	Chain Letters and Evolutionary Histories. <i>Scientific American</i> , 2003, 288, 76-81.	1.0	88
17	Complete De Novo Assembly of Monoclonal Antibody Sequences. <i>Scientific Reports</i> , 2016, 6, 31730.	3.3	85
18	PICKY: a novel SVD-based NMR spectra peak picking method. <i>Bioinformatics</i> , 2009, 25, i268-i275.	4.1	61

#	ARTICLE	IF	CITATIONS
19	Fragmentâ€HMM: A new approach to protein structure prediction. <i>Protein Science</i> , 2008, 17, 1925-1934.	7.6	57
20	DeepIso: A Deep Learning Model for Peptide Feature Detection from LC-MS map. <i>Scientific Reports</i> , 2019, 9, 17168.	3.3	53
21	Computing exact P-values for DNA motifs. <i>Bioinformatics</i> , 2007, 23, 531-537.	4.1	38
22	On the complexity of the spaced seeds. <i>Journal of Computer and System Sciences</i> , 2007, 73, 1024-1034.	1.2	38
23	Computationally instrument-resolution-independent de novo peptide sequencing for high-resolution devices. <i>Nature Machine Intelligence</i> , 2021, 3, 420-425.	16.0	35
24	A streamlined platform for analyzing tera-scale DDA and DIA mass spectrometry data enables highly sensitive immunopeptidomics. <i>Nature Communications</i> , 2022, 13, .	12.8	34
25	Information distance from a question to an answer. , 2007, , .		23
26	Personalized deep learning of individual immunopeptidomes to identify neoantigens for cancer vaccines. <i>Nature Machine Intelligence</i> , 2020, 2, 764-771.	16.0	22
27	PatternHunter II: highly sensitive and fast homology search. <i>Genome Informatics</i> , 2003, 14, 164-75.	0.4	22
28	Optimizing Multiple Spaced Seeds for Homology Search. <i>Lecture Notes in Computer Science</i> , 2004, , 47-58.	1.3	21
29	New Information Distance Measure and Its Application in Question Answering System. <i>Journal of Computer Science and Technology</i> , 2008, 23, 557-572.	1.5	19
30	PROTEIN SECONDARY STRUCTURE PREDICTION USING NMR CHEMICAL SHIFT DATA. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 867-884.	0.8	19
31	ERROR TOLERANT NMR BACKBONE RESONANCE ASSIGNMENT AND AUTOMATED STRUCTURE GENERATION. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 15-41.	0.8	18
32	Optimizing Multiple Spaced Seeds for Homology Search. <i>Journal of Computational Biology</i> , 2006, 13, 1355-1368.	1.6	17
33	Knowledge map construction for question and answer archives. <i>Expert Systems With Applications</i> , 2020, 141, 112923.	7.6	16
34	INFORMATION DISTANCE AND ITS APPLICATIONS. <i>International Journal of Foundations of Computer Science</i> , 2007, 18, 669-681.	1.1	15
35	Designing succinct structural alphabets. <i>Bioinformatics</i> , 2008, 24, i182-i189.	4.1	11
36	Enhanced question understanding with dynamic memory networks for textual question answering. <i>Expert Systems With Applications</i> , 2017, 80, 39-45.	7.6	11

#	ARTICLE	IF	CITATIONS
37	Question Classification by Approximating Semantics. , 2015, , .		8
38	A New Multiword Expression Metric and Its Applications. Journal of Computer Science and Technology, 2011, 26, 3-13.	1.5	7
39	Merge-Weighted Dynamic Time Warping for Speech Recognition. Journal of Computer Science and Technology, 2014, 29, 1072-1082.	1.5	7
40	A tale of solving two computational challenges in protein science: neoantigen prediction and protein structure prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	7
41	Can We Determine a Protein Structure Quickly?. Journal of Computer Science and Technology, 2010, 25, 95-106.	1.5	6
42	Protein Threading by Linear Programming: Theoretical Analysis and Computational Results. Journal of Combinatorial Optimization, 2004, 8, 403-418.	1.3	5
43	Towards Automated Structure-Based NMR Resonance Assignment. Lecture Notes in Computer Science, 2010, , 189-207.	1.3	5
44	A note on the single genotype resolution problem. Journal of Computer Science and Technology, 2004, 19, 254-257.	1.5	4
45	Deep Omics. Proteomics, 2018, 18, 1700319.	2.2	4
46	Deep neural network for detecting arbitrary precision peptide features through attention based segmentation. Scientific Reports, 2021, 11, 18249.	3.3	4
47	Information distance between what I said and what it heard. Communications of the ACM, 2013, 56, 70-77.	4.5	3
48	JBCB, the first decade. Journal of Bioinformatics and Computational Biology, 2014, 12, 1401001.	0.8	1
49	Deep Learning Deciphers Proteinâ€™RNA Interaction. Genomics, Proteomics and Bioinformatics, 2019, 17, 475-477.	6.9	1
50	Partial Match Distance. Lecture Notes in Computer Science, 2013, , 55-64.	1.3	1
51	Information Distance and Its Extensions. Lecture Notes in Computer Science, 2011, , 18-28.	1.3	1
52	ChimST: An Efficient Spectral Library Search Tool for Peptide Identification from Chimeric Spectra in Data-Dependent Acquisition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1416-1425.	3.0	0
53	Invited Talk: Modern Homology Search. , 2007, , 145-145.		0