

# Ming Li

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

13,473  
citations

279487

23  
h-index

205818

48  
g-index

57  
all docs

57  
docs citations

57  
times ranked

14641  
citing authors

#	ARTICLE	IF	CITATIONS
1	A tale of solving two computational challenges in protein science: neoantigen prediction and protein structure prediction. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	7
2	A streamlined platform for analyzing tera-scale DDA and DIA mass spectrometry data enables highly sensitive immunopeptidomics. <i>Nature Communications</i> , 2022, 13, .	5.8	34
3	ChimST: An Efficient Spectral Library Search Tool for Peptide Identification from Chimeric Spectra in Data-Dependent Acquisition. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1416-1425.	1.9	0
4	Computationally instrument-resolution-independent de novo peptide sequencing for high-resolution devices. <i>Nature Machine Intelligence</i> , 2021, 3, 420-425.	8.3	35
5	Deep neural network for detecting arbitrary precision peptide features through attention based segmentation. <i>Scientific Reports</i> , 2021, 11, 18249.	1.6	4
6	Knowledge map construction for question and answer archives. <i>Expert Systems With Applications</i> , 2020, 141, 112923.	4.4	16
7	Personalized deep learning of individual immunopeptidomes to identify neoantigens for cancer vaccines. <i>Nature Machine Intelligence</i> , 2020, 2, 764-771.	8.3	22
8	DeepIso: A Deep Learning Model for Peptide Feature Detection from LC-MS map. <i>Scientific Reports</i> , 2019, 9, 17168.	1.6	53
9	Deep Learning Deciphers Protein-RNA Interaction. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 475-477.	3.0	1
10	Deep learning enables de novo peptide sequencing from data-independent-acquisition mass spectrometry. <i>Nature Methods</i> , 2019, 16, 63-66.	9.0	235
11	Deep Omics. <i>Proteomics</i> , 2018, 18, 1700319.	1.3	4
12	Enhanced question understanding with dynamic memory networks for textual question answering. <i>Expert Systems With Applications</i> , 2017, 80, 39-45.	4.4	11
13	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.	3.3	278
14	Complete De Novo Assembly of Monoclonal Antibody Sequences. <i>Scientific Reports</i> , 2016, 6, 31730.	1.6	85
15	Question Classification by Approximating Semantics. , 2015, , .		8
16	JBCB, the first decade. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1401001.	0.3	1
17	Merge-Weighted Dynamic Time Warping for Speech Recognition. <i>Journal of Computer Science and Technology</i> , 2014, 29, 1072-1082.	0.9	7
18	Information distance between what I said and what it heard. <i>Communications of the ACM</i> , 2013, 56, 70-77.	3.3	3

#	ARTICLE	IF	CITATIONS
19	Partial Match Distance. Lecture Notes in Computer Science, 2013, , 55-64.	1.0	1
20	A New Multiword Expression Metric and Its Applications. Journal of Computer Science and Technology, 2011, 26, 3-13.	0.9	7
21	ERROR TOLERANT NMR BACKBONE RESONANCE ASSIGNMENT AND AUTOMATED STRUCTURE GENERATION. Journal of Bioinformatics and Computational Biology, 2011, 09, 15-41.	0.3	18
22	Information Distance and Its Extensions. Lecture Notes in Computer Science, 2011, , 18-28.	1.0	1
23	Can We Determine a Protein Structure Quickly?. Journal of Computer Science and Technology, 2010, 25, 95-106.	0.9	6
24	PROTEIN SECONDARY STRUCTURE PREDICTION USING NMR CHEMICAL SHIFT DATA. Journal of Bioinformatics and Computational Biology, 2010, 08, 867-884.	0.3	19
25	Towards Automated Structure-Based NMR Resonance Assignment. Lecture Notes in Computer Science, 2010, , 189-207.	1.0	5
26	PICKY: a novel SVD-based NMR spectra peak picking method. Bioinformatics, 2009, 25, i268-i275.	1.8	61
27	New Information Distance Measure and Its Application in Question Answering System. Journal of Computer Science and Technology, 2008, 23, 557-572.	0.9	19
28	Fragmentâ€HMM: A new approach to protein structure prediction. Protein Science, 2008, 17, 1925-1934.	3.1	57
29	ZOOM! Zillions of oligos mapped. Bioinformatics, 2008, 24, 2431-2437.	1.8	187
30	Designing succinct structural alphabets. Bioinformatics, 2008, 24, i182-i189.	1.8	11
31	An Introduction to Kolmogorov Complexity and Its Applications. Texts in Computer Science, 2008, , .	0.5	682
32	INFORMATION DISTANCE AND ITS APPLICATIONS. International Journal of Foundations of Computer Science, 2007, 18, 669-681.	0.8	15
33	Computing exact P-values for DNA motifs. Bioinformatics, 2007, 23, 531-537.	1.8	38
34	Information distance from a question to an answer. , 2007, , .		23
35	On the complexity of the spaced seeds. Journal of Computer and System Sciences, 2007, 73, 1024-1034.	0.9	38
36	Invited Talk: Modern Homology Search. , 2007, , 145-145.		0

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37	Optimizing Multiple Spaced Seeds for Homology Search. Journal of Computational Biology, 2006, 13, 1355-1368.	0.8	17
38	PATTERNHUNTER II: HIGHLY SENSITIVE AND FAST HOMOMOLOGY SEARCH. Journal of Bioinformatics and Computational Biology, 2004, 02, 417-439.	0.3	170
39	Shared Information and Program Plagiarism Detection. IEEE Transactions on Information Theory, 2004, 50, 1545-1551.	1.5	180
40	The Similarity Metric. IEEE Transactions on Information Theory, 2004, 50, 3250-3264.	1.5	766
41	A note on the single genotype resolution problem. Journal of Computer Science and Technology, 2004, 19, 254-257.	0.9	4
42	Protein Threading by Linear Programming: Theoretical Analysis and Computational Results. Journal of Combinatorial Optimization, 2004, 8, 403-418.	0.8	5
43	On spaced seeds for similarity search. Discrete Applied Mathematics, 2004, 138, 253-263.	0.5	110
44	Optimizing Multiple Spaced Seeds for Homology Search. Lecture Notes in Computer Science, 2004, , 47-58.	1.0	21
45	PEAKS: powerful software for peptidede novo sequencing by tandem mass spectrometry. Rapid Communications in Mass Spectrometry, 2003, 17, 2337-2342.	0.7	1,156
46	Chain Letters and Evolutionary Histories. Scientific American, 2003, 288, 76-81.	1.0	88
47	RAPTOR: OPTIMAL PROTEIN THREADING BY LINEAR PROGRAMMING. Journal of Bioinformatics and Computational Biology, 2003, 01, 95-117.	0.3	245
48	PatternHunter II: highly sensitive and fast homology search. Genome Informatics, 2003, 14, 164-75.	0.4	22
49	On the closest string and substring problems. Journal of the ACM, 2002, 49, 157-171.	1.8	205
50	PatternHunter: faster and more sensitive homology search. Bioinformatics, 2002, 18, 440-445.	1.8	713
51	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
52	Information distance. IEEE Transactions on Information Theory, 1998, 44, 1407-1423.	1.5	377
53	An Introduction to Kolmogorov Complexity and Its Applications. , 1997, , ,		1,072