

# Louxin Zhang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7305384/publications.pdf>

Version: 2024-02-01

125  
papers

2,797  
citations

279798

23  
h-index

214800

47  
g-index

133  
all docs

133  
docs citations

133  
times ranked

2718  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence for transmission of COVID-19 prior to symptom onset. <i>ELife</i> , 2020, 9, .	6.0	259
2	Reconstructing contiguous regions of an ancestral genome. <i>Genome Research</i> , 2006, 16, 1557-1565.	5.5	246
3	Distinguishing string selection problems. <i>Information and Computation</i> , 2003, 185, 41-55.	0.7	198
4	Perfect Phylogenetic Networks with Recombination. <i>Journal of Computational Biology</i> , 2001, 8, 69-78.	1.6	187
5	From Gene Trees to Species Trees. <i>SIAM Journal on Computing</i> , 2000, 30, 729-752.	1.0	153
6	On a Mirkin-Muchnik-Smith Conjecture for Comparing Molecular Phylogenies. <i>Journal of Computational Biology</i> , 1997, 4, 177-187.	1.6	120
7	Improved anticancer drug response prediction in cell lines using matrix factorization with similarity regularization. <i>BMC Cancer</i> , 2017, 17, 513.	2.6	118
8	On the Nearest Neighbour Interchange Distance Between Evolutionary Trees. <i>Journal of Theoretical Biology</i> , 1996, 182, 463-467.	1.7	76
9	Good spaced seeds for homology search. <i>Bioinformatics</i> , 2004, 20, 1053-1059.	4.1	69
10	Sensitivity analysis and efficient method for identifying optimal spaced seeds. <i>Journal of Computer and System Sciences</i> , 2004, 68, 22-40.	1.2	66
11	More Taxa Are Not Necessarily Better for the Reconstruction of Ancestral Character States. <i>Systematic Biology</i> , 2008, 57, 647-653.	5.6	53
12	Counting motifs in the human interactome. <i>Nature Communications</i> , 2013, 4, 2241.	12.8	52
13	DUPCAR: Reconstructing Contiguous Ancestral Regions with Duplications. <i>Journal of Computational Biology</i> , 2008, 15, 1007-1027.	1.6	51
14	From Gene Trees to Species Trees II: Species Tree Inference by Minimizing Deep Coalescence Events. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1685-1691.	3.0	48
15	Genome-scale analysis of positional clustering of mouse testis-specific genes. <i>BMC Genomics</i> , 2005, 6, 7.	2.8	47
16	Divide-and-conquer approach for the exemplar breakpoint distance. <i>Bioinformatics</i> , 2005, 21, 2171-2176.	4.1	42
17	A survey and systematic assessment of computational methods for drug response prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, 232-246.	6.5	42
18	Recent Applications of Hidden Markov Models in Computational Biology. <i>Genomics, Proteomics and Bioinformatics</i> , 2004, 2, 84-96.	6.9	41

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19	On Tree-Based Phylogenetic Networks. <i>Journal of Computational Biology</i> , 2016, 23, 553-565.	1.6	41
20	Greedy method for inferring tandem duplication history. <i>Bioinformatics</i> , 2003, 19, 1497-1504.	4.1	33
21	Approximating the Spanning Star Forest Problem and Its Application to Genomic Sequence Alignment. <i>SIAM Journal on Computing</i> , 2008, 38, 946-962.	1.0	32
22	On reconstructing species trees from gene trees in term of duplications and losses. , 1998, , .		28
23	Positive correlation between gene coexpression and positional clustering in the zebrafish genome. <i>BMC Genomics</i> , 2009, 10, 42.	2.8	26
24	Conjugacy in special monoids. <i>Journal of Algebra</i> , 1991, 143, 487-497.	0.7	25
25	Predicting chemotherapeutic drug combinations through gene network profiling. <i>Scientific Reports</i> , 2016, 6, 18658.	3.3	24
26	Superiority and complexity of the spaced seeds. , 2006, , .		24
27	Translation initiation sites prediction with mixture Gaussian models in human cDNA sequences. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2005, 17, 1152-1160.	5.7	23
28	RecPhyloXML: a format for reconciled gene trees. <i>Bioinformatics</i> , 2018, 34, 3646-3652.	4.1	22
29	Fitness Profiling Links Topoisomerase II Regulation of Centromeric Integrity to Doxorubicin Resistance in Fission Yeast. <i>Scientific Reports</i> , 2015, 5, 8400.	3.3	21
30	A decomposition theorem and two algorithms for reticulation-visible networks. <i>Information and Computation</i> , 2017, 252, 161-175.	0.7	21
31	Decision problems for finite special string-rewriting systems that are confluent on some congruence class. <i>Acta Informatica</i> , 1991, 28, 477-510.	0.5	20
32	Transcriptome Analysis of Cold Syndrome Using Microarray. <i>The American Journal of Chinese Medicine</i> , 2007, 35, 609-620.	3.8	19
33	Profiling the transcription factor regulatory networks of human cell types. <i>Nucleic Acids Research</i> , 2014, 42, 12380-12387.	14.5	19
34	Run Probabilities of Seed-Like Patterns and Identifying Good Transition Seeds. <i>Journal of Computational Biology</i> , 2008, 15, 1295-1313.	1.6	16
35	Structural properties of the reconciliation space and their applications in enumerating nearly-optimal reconciliations between a gene tree and a species tree. <i>BMC Bioinformatics</i> , 2011, 12, S7.	2.6	16
36	Counting and enumerating tree-child networks and their subclasses. <i>Journal of Computer and System Sciences</i> , 2020, 114, 84-104.	1.2	16

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37	The Consecutive Ones Submatrix Problem for Sparse Matrices. <i>Algorithmica</i> , 2007, 48, 287-299.	1.3	15
38	Locating a Tree in a Phylogenetic Network in Quadratic Time. <i>Lecture Notes in Computer Science</i> , 2015, , 96-107.	1.3	15
39	Applying rewriting methods to special monoids. <i>Mathematical Proceedings of the Cambridge Philosophical Society</i> , 1992, 112, 495-505.	0.4	14
40	Reconciliation with Non-binary Gene Trees Revisited. <i>Lecture Notes in Computer Science</i> , 2014, , 418-432.	1.3	14
41	Quick, Practical Selection of Effective Seeds for Homology Search. <i>Journal of Computational Biology</i> , 2005, 12, 1137-1152.	1.6	13
42	Superiority of Spaced Seeds for Homology Search. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 496-505.	3.0	13
43	Solving the tree containment problem in linear time for nearly stable phylogenetic networks. <i>Discrete Applied Mathematics</i> , 2018, 246, 62-79.	0.9	13
44	A short proof of a theorem of Adjan. <i>Proceedings of the American Mathematical Society</i> , 1992, 116, 1-1.	0.8	13
45	Fitting Distances by Tree Metrics with Increment Error. <i>Journal of Combinatorial Optimization</i> , 1999, 3, 213-225.	1.3	12
46	Twistâ€“Rotation Transformations of Binary Trees and Arithmetic Expressions. <i>Journal of Algorithms</i> , 1999, 32, 155-166.	0.9	12
47	Conversion events in gene clusters. <i>BMC Evolutionary Biology</i> , 2011, 11, 226.	3.2	12
48	A program for verification of phylogenetic network models. <i>Bioinformatics</i> , 2016, 32, i503-i510.	4.1	12
49	How much can deep learning improve prediction of the responses to drugs in cancer cell lines?. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	12
50	ON THE CONJUGACY PROBLEM FOR ONE-RELATOR MONOIDS WITH ELEMENTS OF FINITE ORDER. <i>International Journal of Algebra and Computation</i> , 1992, 02, 209-220.	0.5	11
51	A program to compute the soft Robinsonâ€“Foulds distance between phylogenetic networks. <i>BMC Genomics</i> , 2017, 18, 111.	2.8	11
52	On the asymptotic growth of the number of tree-child networks. <i>European Journal of Combinatorics</i> , 2021, 93, 103278.	0.8	11
53	Existence of Inverted Profile in Chemically Responsive Molecular Pathways in the Zebrafish Liver. <i>PLoS ONE</i> , 2011, 6, e27819.	2.5	11
54	A post-processing method for optimizing synthesis strategy for oligonucleotide microarrays. <i>Nucleic Acids Research</i> , 2005, 33, e144-e144.	14.5	10

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55	CAGE: Combinatorial Analysis of Gene-Cluster Evolution. Journal of Computational Biology, 2010, 17, 1227-1242.	1.6	10
56	Clusters, Trees, and Phylogenetic Network Classes. Computational Biology, 2019, , 277-315.	0.2	10
57	Counting and enumerating galled networks. Discrete Applied Mathematics, 2020, 283, 644-654.	0.9	10
58	Reconstructing Recombination Network from Sequence Data: The Small Parsimony Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 394-402.	3.0	9
59	Greedy Selection of Species for Ancestral State Reconstruction on Phylogenies: Elimination Is Better than Insertion. PLoS ONE, 2010, 5, e8985.	2.5	9
60	Revealing Mammalian Evolutionary Relationships by Comparative Analysis of Gene Clusters. Genome Biology and Evolution, 2012, 4, 586-601.	2.5	9
61	Maximum Likelihood Inference of the Evolutionary History of a PPI Network from the Duplication History of Its Proteins. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1412-1421.	3.0	9
62	Optimal Bounds for Matching Routing on Trees. SIAM Journal on Discrete Mathematics, 1999, 12, 64-77.	0.8	8
63	Analyzing the Fitch Method for Reconstructing Ancestral States on Ultrametric Phylogenetic Trees. Bulletin of Mathematical Biology, 2010, 72, 1760-1782.	1.9	8
64	Algorithmic and Complexity Issues of Three Clustering Methods in Microarray Data Analysis. Algorithmica, 2007, 48, 203-219.	1.3	7
65	A Polynomial Algebra Method for Computing Exemplar Breakpoint Distance. Lecture Notes in Computer Science, 2011, , 297-305.	1.3	7
66	Many-to-one packet routing via matchings. Lecture Notes in Computer Science, 1997, , 11-17.	1.3	6
67	SEPARATING AUXILIARY ARITY HIERARCHY OF FIRST-ORDER INCREMENTAL EVALUATION SYSTEMS USING (3K+1)-ary INPUT RELATIONS. International Journal of Foundations of Computer Science, 2000, 11, 573-578.	1.1	6
68	On Counting Tandem Duplication Trees. Molecular Biology and Evolution, 2004, 21, 1160-1163.	8.9	6
69	Efficient estimation of the accuracy of the maximum likelihood method for ancestral state reconstruction. Journal of Combinatorial Optimization, 2011, 21, 409-422.	1.3	6
70	Effect of Incomplete Lineage Sorting On Tree-Reconciliation-Based Inference of Gene Duplication. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 477-485.	3.0	6
71	S-Cluster++: a fast program for solving the cluster containment problem for phylogenetic networks. Bioinformatics, 2018, 34, i680-i686.	4.1	6
72	The Bourque distances for mutation trees of cancers. Algorithms for Molecular Biology, 2021, 16, 9.	1.2	6

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73	Routing on trees via matchings. Lecture Notes in Computer Science, 1995, , 251-262.	1.3	6
74	An Efficient Method for DNA-Based Species Assignment via Gene Tree and Species Tree Reconciliation. Lecture Notes in Computer Science, 2010, , 300-311.	1.3	6
75	Detecting molecular subtypes from multi-omics datasets using SUMO. Cell Reports Methods, 2022, 2, 100152.	2.9	6
76	Inverted Expression Profiles of Sex-Biased Genes in Response to Toxicant Perturbations and Diseases. PLoS ONE, 2013, 8, e56668.	2.5	5
77	Are the Duplication Cost and Robinson-Foulds Distance Equivalent?. Journal of Computational Biology, 2014, 21, 578-590.	1.6	5
78	Compression of Phylogenetic Networks and Algorithm for the Tree Containment Problem. Journal of Computational Biology, 2019, 26, 285-294.	1.6	5
79	Computing Distances between Evolutionary Trees. , 1998, , 781-822.		5
80	On the approximation of longest common nonsupersequences and shortest common nonsubsequences. Theoretical Computer Science, 1995, 143, 353-362.	0.9	4
81	Network model and efficient method for detecting relative duplications or horizontal gene transfers. , 2011, , .		4
82	Generating normal networks via leaf insertion and nearest neighbor interchange. BMC Bioinformatics, 2019, 20, 642.	2.6	4
83	Controlling Size When Aligning Multiple Genomic Sequences with Duplications. Lecture Notes in Computer Science, 2006, , 138-149.	1.3	4
84	A Linear-Time Algorithm for Reconciliation of Non-binary Gene Tree and Binary Species Tree. Lecture Notes in Computer Science, 2013, , 190-201.	1.3	4
85	Toxicogenomic Analysis Suggests Chemical-Induced Sexual Dimorphism in the Expression of Metabolic Genes in Zebrafish Liver. PLoS ONE, 2012, 7, e51971.	2.5	4
86	Asymptotic enumeration and distributional properties of galled networks. Journal of Combinatorial Theory - Series A, 2022, 189, 105599.	0.8	4
87	Rational strong codes and structure of rational group languages. Semigroup Forum, 1986, 35, 181-193.	0.6	3
88	Small weight bases for hamming codes. Theoretical Computer Science, 1997, 181, 337-345.	0.9	3
89	Addition in $\log_2 n + O(1)$ steps on average a simple analysis. Theoretical Computer Science, 1998, 191, 245-248.	0.9	3
90	A new clustering method for microarray data analysis. , 0, , .		3

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91	Translation Initiation Sites Prediction with Mixture Gaussian Models. Lecture Notes in Computer Science, 2004, , 338-349.	1.3	3
92	A stable iterative method for refining discriminative gene clusters. BMC Genomics, 2008, 9, S18.	2.8	3
93	Spectrum-Based <i>De Novo</i> Repeat Detection in Genomic Sequences. Journal of Computational Biology, 2008, 15, 469-488.	1.6	3
94	MOTIF DISCOVERY WITH DATA MINING IN 3D PROTEIN STRUCTURE DATABASES: DISCOVERY, VALIDATION AND PREDICTION OF THE U-SHAPE ZINC BINDING ("HUF-ZINC") MOTIF. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340008.	0.8	3
95	Efficient Methods for Inferring Tandem Duplication History. Lecture Notes in Computer Science, 2002, , 97-111.	1.3	3
96	Approximation Algorithms for the Consecutive Ones Submatrix Problem on Sparse Matrices. Lecture Notes in Computer Science, 2004, , 835-846.	1.3	3
97	Some properties of finite special string-rewriting systems. Journal of Symbolic Computation, 1992, 14, 359-369.	0.8	2
98	The pre-NTS property is undecidable for context-free grammars. Information Processing Letters, 1992, 44, 181-184.	0.6	2
99	A PTAS For The $k$ -Consensus Structures Problem Under Squared Euclidean Distance. Algorithms, 2008, 1, 43-51.	2.1	2
100	Reconciliation With Nonbinary Gene Trees Revisited. Journal of the ACM, 2017, 64, 1-28.	2.2	2
101	Superiority and Complexity of the Spaced Seeds. , 2016, , 2166-2170.		2
102	Effect of Incomplete Lineage Sorting on Tree-Reconciliation-Based Inference of Gene Duplication. Lecture Notes in Computer Science, 2013, , 261-272.	1.3	2
103	On the descriptive power of special Thue systems. Discrete Mathematics, 1996, 160, 291-297.	0.7	1
104	ANALYSIS OF SPACED SEED TECHNIQUE IN SEQUENCE ALIGNMENT. Cosmos, 2005, 01, 57-73.	0.4	1
105	Models and Methods in Comparative Genomics. Advances in Computers, 2006, 68, 59-104.	1.6	1
106	APPROXIMATING THE SPANNING $k$ -TREE FOREST PROBLEM. International Journal of Foundations of Computer Science, 2012, 23, 1543-1554.	1.1	1
107	Two combinatorial optimization problems for SNP discovery using base-specific cleavage and mass spectrometry. BMC Systems Biology, 2012, 6, S5.	3.0	1
108	ZDOG: zooming in on dominating genes with mutations in cancer pathways. BMC Bioinformatics, 2019, 20, 740.	2.6	1

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109	Inferring the Recent Duplication History of a Gene Cluster. Lecture Notes in Computer Science, 2009, , 111-125.	1.3	1
110	A Heuristic Algorithm for Reconstructing Ancestral Gene Orders with Duplications. Lecture Notes in Computer Science, 2007, , 122-135.	1.3	1
111	Selecting Genomes for Reconstruction of Ancestral Genomes. Lecture Notes in Computer Science, 2007, , 110-121.	1.3	1
112	Computing Distances Between Evolutionary Trees. , 2013, , 747-781.		1
113	COMPUTING AND COMBINATORICS CONFERENCE " COCOON'02. International Journal of Foundations of Computer Science, 2004, 15, 1-1.	1.1	0
114	Expression Profile of Immunogenes in Cold Constitution. , 2007, , .		0
115	A Robust Method for Generating Discriminative Gene Clusters. , 2007, , .		0
116	Online buffer management for transmitting packets with processing cycles. Theoretical Computer Science, 2018, 723, 73-83.	0.9	0
117	Stage-specific protein-domain mutational profile of invasive ductal breast cancer. BMC Medical Genomics, 2020, 13, 150.	1.5	0
118	RUN PROBABILITY OF HIGH-ORDER SEED PATTERNS AND ITS APPLICATIONS TO FINDING GOOD TRANSITION SEEDS. , 2007, , .		0
119	A Tool for Non-binary Tree Reconciliation. Lecture Notes in Computer Science, 2013, , 40-51.	1.3	0
120	Superiority and Complexity of the Spaced Seeds. , 2015, , 1-5.		0
121	Recent Progresses in the Combinatorial and Algorithmic Study of Rooted Phylogenetic Networks. Lecture Notes in Computer Science, 2020, , 22-27.	1.3	0
122	A PTAS for the k-Consensus Structures Problem Under Euclidean Squared Distance. , 2008, , 35-44.		0
123	A new clustering method for microarray data analysis. Proceedings, 2002, 1, 268-75.	0.1	0
124	Guest Editorial for the 17th Asia Pacific Bioinformatics Conference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2123-2124.	3.0	0
125	Introduction to the Special Issue of the 18th Annual International RECOMB Satellite Workshop on Comparative Genomics. Journal of Bioinformatics and Computational Biology, 2021, 19, 2102003.	0.8	0