Teresa M Przytycka

List of Publications by Year
in descending order

99 papers	5,731 citations	76326 40 h-index	88630 70 g-index
110 all docs	110 docs citations	110 times ranked	8194 citing authors

#	Article	IF	Citations
1	Fly Cell Atlas: A single-nucleus transcriptomic atlas of the adult fruit fly. Science, 2022, 375, eabk2432.	12.6	295
2	DNA Aptamers for Early Detection of Ebolavirus. FASEB Journal, 2021, 35, .	0.5	2
3	Mutational Signatures: From Methods to Mechanisms. Annual Review of Biomedical Data Science, 2021, 4, 189-206.	6.5	19
4	ISMB/ECCB 2021 proceedings. Bioinformatics, 2021, 37, i7-i8.	4.1	2
5	RepairSig: Deconvolution of DNA damage and repair contributions to the mutational landscape of cancer. Cell Systems, 2021, 12, 994-1003.e4.	6.2	6
6	The language of a virus. Science, 2021, 371, 233-234.	12.6	4
7	Bioinformatics pipeline using JUDI: <i>Just Do It!</i>. Bioinformatics, 2020, 36, 2572-2574.	4.1	5
8	Embedding gene sets in low-dimensional space. Nature Machine Intelligence, 2020, 2, 367-368.	16.0	2
9	Identifying Drug Sensitivity Subnetworks with NETPHIX. IScience, 2020, 23, 101619.	4.1	5
10	Direct, Competitive Comparison of Linear, Monocyclic, and Bicyclic Libraries Using mRNA Display. ACS Combinatorial Science, 2020, 22, 306-310.	3.8	13
11	Network-based approaches elucidate differences within APOBEC and clock-like signatures in breast cancer. Genome Medicine, 2020, 12, 52.	8.2	20
12	AptaBlocks Online: A Web-Based Toolkit for the In Silico Design of Oligonucleotide Sticky Bridges. Journal of Computational Biology, 2020, 27, 356-360.	1.6	0
13	A Sticky Multinomial Mixture Model of Strand-Coordinated Mutational Processes in Cancer. IScience, 2020, 23, 100900.	4.1	5
14	Reconstruction of Gene Regulatory Networks by Integrating Biological Model and a Recommendation System. Lecture Notes in Computer Science, 2020, , 274-275.	1.3	1
15	DNA Repair Footprint Uncovers Contribution of DNA Repair Mechanism to Mutational Signatures. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 262-273.	0.7	2
16	Hidden Markov models lead to higher resolution maps of mutation signature activity in cancer. Genome Medicine, 2019, 11, 49.	8.2	22
17	Co-SELECT reveals sequence non-specific contribution of DNA shape to transcription factor binding in vitro. Nucleic Acids Research, 2019, 47, 6632-6641.	14.5	15
18	Subpopulation Detection and Their Comparative Analysis across Single-Cell Experiments with scPopCorn. Cell Systems, 2019, 8, 506-513.e5.	6.2	13

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19	Session Introduction: Mutational Signatures: Etiology, Properties, and Role in Cancer. , 2019, , .		0
20	Detecting presence of mutational signatures in cancer with confidence. Bioinformatics, 2018, 34, 330-337.	4.1	86
21	Mapping DNA Breaks by Next-Generation Sequencing. Methods in Molecular Biology, 2018, 1672, 155-166.	0.9	6
22	Dosage-Dependent Expression Variation Suppressed on the <i>Drosophila</i> Male <i>X</i> Chromosome. G3: Genes, Genomes, Genetics, 2018, 8, 587-598.	1.8	9
23	Reprogramming of regulatory network using expression uncovers sex-specific gene regulation in Drosophila. Nature Communications, 2018, 9, 4061.	12.8	23
24	AptaSUITE: A Full-Featured Bioinformatics Framework for the Comprehensive Analysis of Aptamers from HT-SELEX Experiments. Molecular Therapy - Nucleic Acids, 2018, 11, 515-517.	5.1	54
25	AptaBlocks: Designing RNA complexes and accelerating RNA-based drug delivery systems. Nucleic Acids Research, 2018, 46, 8133-8142.	14.5	8
26	A 2â€²FY-RNA Motif Defines an Aptamer for Ebolavirus Secreted Protein. Scientific Reports, 2018, 8, 12373.	3.3	23
27	WeSME: uncovering mutual exclusivity of cancer drivers and beyond. Bioinformatics, 2017, 33, 814-821.	4.1	79
28	Highly Constrained Bicyclic Scaffolds for the Discovery of Protease-Stable Peptides <i>via</i> mRNA Display. ACS Chemical Biology, 2017, 12, 795-804.	3.4	53
29	Permanganate/S1 Nuclease Footprinting Reveals Non-B DNA Structures with Regulatory Potential across a Mammalian Genome. Cell Systems, 2017, 4, 344-356.e7.	6.2	169
30	Aptamer-Drug Conjugates of Active Metabolites of Nucleoside Analogs and Cytotoxic Agents Inhibit Pancreatic Tumor Cell Growth. Molecular Therapy - Nucleic Acids, 2017, 6, 80-88.	5.1	65
31	BeWith: A Between-Within method to discover relationships between cancer modules via integrated analysis of mutual exclusivity, co-occurrence and functional interactions. PLoS Computational Biology, 2017, 13, e1005695.	3.2	38
32	ISMB 2016 Proceedings. Bioinformatics, 2016, 32, i1-i2.	4.1	15
33	RNA Polymerase II Regulates Topoisomerase 1 Activity to Favor Efficient Transcription. Cell, 2016, 165, 357-371.	28.9	211
34	AptaPLEX â€" A dedicated, multithreaded demultiplexer for HT-SELEX data. Methods, 2016, 106, 82-85.	3.8	16
35	AptaTRACE Elucidates RNA Sequence-Structure Motifs from Selection Trends in HT-SELEX Experiments. Cell Systems, 2016, 3, 62-70.	6.2	55
36	Generalized logical model based on network topology to capture the dynamical trends of cellular signaling pathways. BMC Systems Biology, 2016, 10, 7.	3.0	2

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37	Understanding Genotype-Phenotype Effects in Cancer via Network Approaches. PLoS Computational Biology, 2016, 12, e1004747.	3.2	51
38	Ups and Downs of Poised RNA Polymerase II in B-Cells. PLoS Computational Biology, 2016, 12, e1004821.	3.2	2
39	Effects of Gene Dose, Chromatin, and Network Topology on Expression in Drosophila melanogaster. PLoS Genetics, 2016, 12, e1006295.	3.5	38
40	AptaGUIâ€"A Graphical User Interface for the Efficient Analysis of HT-SELEX Data. Molecular Therapy - Nucleic Acids, 2015, 4, e257.	5.1	18
41	Identifying high-affinity aptamer ligands with defined cross-reactivity using high-throughput guided systematic evolution of ligands by exponential enrichment. Nucleic Acids Research, 2015, 43, e82-e82.	14.5	61
42	MEMCover: integrated analysis of mutual exclusivity and functional network reveals dysregulated pathways across multiple cancer types. Bioinformatics, 2015, 31, i284-i292.	4.1	87
43	Shapely DNA attracts the right partner. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4516-4517.	7.1	3
44	Large scale analysis of the mutational landscape in HT-SELEX improves aptamer discovery. Nucleic Acids Research, 2015, 43, 5699-5707.	14.5	97
45	Genome-wide detection of DNase I hypersensitive sites in single cells and FFPE tissue samples. Nature, 2015, 528, 142-146.	27.8	303
46	Transcription Factor Networks in Drosophila melanogaster. Cell Reports, 2014, 8, 2031-2043.	6.4	83
47	DNA copy number evolution in Drosophila cell lines. Genome Biology, 2014, 15, R70.	8.8	96
48	Sex- and Tissue-Specific Functions of Drosophila Doublesex Transcription Factor Target Genes. Developmental Cell, 2014, 31, 761-773.	7.0	122
49	DNA Break Mapping Reveals Topoisomerase II Activity Genome-Wide. International Journal of Molecular Sciences, 2014, 15, 13111-13122.	4.1	70
50	Potential non-B DNA regions in the human genome are associated with higher rates of nucleotide mutation and expression variation. Nucleic Acids Research, 2014, 42, 12367-12379.	14.5	45
51	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. Genome Research, 2014, 24, 1209-1223.	5.5	147
52	AptaCluster â€" A Method to Cluster HT-SELEX Aptamer Pools and Lessons from Its Application. Lecture Notes in Computer Science, 2014, 8394, 115-128.	1.3	71
53	A Gene-Specific Method for Predicting Hemophilia-Causing Point Mutations. Journal of Molecular Biology, 2013, 425, 4023-4033.	4.2	30
54	Endogenous factor VIII synthesis from the intron 22â€"inverted F8 locus may modulate the immunogenicity of replacement therapy for hemophilia A. Nature Medicine, 2013, 19, 1318-1324.	30.7	59

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55	Dissecting cancer heterogeneity with a probabilistic genotype-phenotype model. Nucleic Acids Research, 2013, 41, 8011-8020.	14.5	17
56	Transcription-dependent dynamic supercoiling is a short-range genomic force. Nature Structural and Molecular Biology, 2013, 20, 396-403.	8.2	270
57	Global Regulation of Promoter Melting in Naive Lymphocytes. Cell, 2013, 153, 988-999.	28.9	145
58	The genome-wide distribution of non-B DNA motifs is shaped by operon structure and suggests the transcriptional importance of non-B DNA structures in Escherichia coli. Nucleic Acids Research, 2013, 41, 5965-5977.	14.5	55
59	Sensitive measurement of single-nucleotide polymorphism-induced changes of RNA conformation: application to disease studies. Nucleic Acids Research, 2013, 41, 44-53.	14.5	86
60	eQTL Epistasis â€" Challenges and Computational Approaches. Frontiers in Genetics, 2013, 4, 51.	2.3	22
61	Module cover - a new approach to genotype-phenotype studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 135-46.	0.7	14
62	Chapter 5: Network Biology Approach to Complex Diseases. PLoS Computational Biology, 2012, 8, e1002820.	3.2	239
63	Phylogenetic Analysis of Mitochondrial Outer Membrane Î²-Barrel Channels. Genome Biology and Evolution, 2012, 4, 110-125.	2.5	14
64	MODELING CELL HETEROGENEITY: FROM SINGLE-CELL VARIATIONS TO MIXED CELLS. , 2012, , .		1
65	Mediation of Drosophila autosomal dosage effects and compensation by network interactions. Genome Biology, 2012, 13, R28.	9.6	98
66	Crystal Structures of the Outer Membrane Domain of Intimin and Invasin from Enterohemorrhagic E. coli and Enteropathogenic Y. pseudotuberculosis. Structure, 2012, 20, 1233-1243.	3.3	82
67	Teasing Apart Translational and Transcriptional Components of Stochastic Variations in Eukaryotic Gene Expression. PLoS Computational Biology, 2012, 8, e1002644.	3.2	21
68	Characterization of Coding Synonymous and Non-Synonymous Variants in ADAMTS13 Using Ex Vivo and In Silico Approaches. PLoS ONE, 2012, 7, e38864.	2.5	61
69	MODULE COVER â€" A NEW APPROACH TO GENOTYPE-PHENOTYPE STUDIES. , 2012, , .		12
70	Evolution of domain promiscuity in eukaryotic genomesâ€"a perspective from the inferred ancestral domain architectures. Molecular BioSystems, 2011, 7, 784-792.	2.9	17
71	Identifying Causal Genes and Dysregulated Pathways in Complex Diseases. PLoS Computational Biology, 2011, 7, e1001095.	3.2	163
72	Network integration meets network dynamics. BMC Biology, 2010, 8, 48.	3.8	29

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73	Systems-biology dissection of eukaryotic cell growth. BMC Biology, 2010, 8, 62.	3.8	4
74	Toward the dynamic interactome: it's about time. Briefings in Bioinformatics, 2010, 11, 15-29.	6.5	230
75	Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture. Molecular Systems Biology, 2009, 5, 294.	7.2	146
76	Selection for minimization of translational frameshifting errors as a factor in the evolution of codon usage. Nucleic Acids Research, 2009, 37, 6799-6810.	14.5	34
77	Recursive domains in proteins. Protein Science, 2009, 11, 409-417.	7.6	38
78	Correlated Evolution of Interacting Proteins: Looking Behind the Mirrortree. Journal of Molecular Biology, 2009, 385, 91-98.	4.2	54
79	Differences in evolutionary pressure acting within highly conserved ortholog groups. BMC Evolutionary Biology, 2008, 8, 208.	3.2	4
80	Why Do Hubs in the Yeast Protein Interaction Network Tend To Be Essential: Reexamining the Connection between the Network Topology and Essentiality. PLoS Computational Biology, 2008, 4, e1000140.	3.2	373
81	Improving Strand Pairing Prediction through Exploring Folding Cooperativity. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 484-491.	3.0	9
82	DYNAMICS OF BIOLOGICAL NETWORKS â€" SESSION INTRODUCTION. , 2008, , .		0
83	Support for the Coelomata Clade of Animals from a Rigorous Analysis of the Pattern of Intron Conservation. Molecular Biology and Evolution, 2007, 24, 2583-2592.	8.9	68
84	Stability of Characters and Construction of Phylogenetic Trees. Journal of Computational Biology, 2007, 14, 539-549.	1.6	32
85	Computational Approaches to Predict Protein-Protein and Domain-Domain Interactions. , 2007, , 465-491.		3
86	Graph Theoretical Approaches to Delineate Dynamics of Biological Processes. , 2007, , 29-54.		0
87	Predicting protein domain interactions from coevolution of conserved regions. Proteins: Structure, Function and Bioinformatics, 2007, 67, 811-820.	2.6	42
88	Co-evolutionary Analysis of Domains in Interacting Proteins Reveals Insights into Domainâ€"Domain Interactions Mediating Proteinâ€"Protein Interactions. Journal of Molecular Biology, 2006, 362, 861-875.	4.2	123
89	Refining multiple sequence alignments with conserved core regions. Nucleic Acids Research, 2006, 34, 2598-2606.	14.5	33
90	Graph Theoretical Insights into Evolution of Multidomain Proteins. Journal of Computational Biology, 2006, 13, 351-363.	1.6	76

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91	Significance of conformational biases in Monte Carlo simulations of protein folding: Lessons from Metropolis-Hastings approach. Proteins: Structure, Function and Bioinformatics, 2004, 57, 338-344.	2.6	6
92	Scale-free networks versus evolutionary drift. Computational Biology and Chemistry, 2004, 28, 257-264.	2.3	16
93	An O(nlog n) Algorithm for the Maximum Agreement Subtree Problem for Binary Trees. SIAM Journal on Computing, 2000, 30, 1385-1404.	1.0	76
94	A protein taxonomy based on secondary structure. Nature Structural Biology, 1999, 6, 672-682.	9.7	105
95	The Optimal Alphabetic Tree Problem Revisited. Journal of Algorithms, 1998, 28, 1-20.	0.9	6
96	On the complexity of string folding. Discrete Applied Mathematics, 1996, 71, 217-230.	0.9	27
97	On the agreement of many trees. Information Processing Letters, 1995, 55, 297-301.	0.6	105
98	Constructing Huffman Trees in Parallel. SIAM Journal on Computing, 1995, 24, 1163-1169.	1.0	21
99	A Fast Algorithm For Optimum Height-Limited Alphabetic Binary Trees. SIAM Journal on Computing, 1994, 23, 1283-1312.	1.0	23