

Anna Gambin

List of Publications by Year in descending order

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Version: 2024-02-01

85
papers

1,888
citations

257357

24
h-index

289141

40
g-index

91
all docs

91
docs citations

91
times ranked

3748
citing authors

#	ARTICLE	IF	CITATIONS
1	Applying dynamic Bayesian networks to perturbed gene expression data. <i>BMC Bioinformatics</i> , 2006, 7, 249.	1.2	133
2	NAHR-mediated copy-number variants in a clinical population: Mechanistic insights into both genomic disorders and Mendelizing traits. <i>Genome Research</i> , 2013, 23, 1395-1409.	2.4	120
3	Gene Expression Profile of the Clinically Aggressive Micropapillary Variant of Bladder Cancer. <i>European Urology</i> , 2016, 70, 611-620.	0.9	120
4	Jaccard/Tanimoto similarity test and estimation methods for biological presence-absence data. <i>BMC Bioinformatics</i> , 2019, 20, 644.	1.2	114
5	Predicting the outcomes of organic reactions via machine learning: are current descriptors sufficient?. <i>Scientific Reports</i> , 2017, 7, 3582.	1.6	95
6	Leaf and Plant Age Affects Photosynthetic Performance and Photoprotective Capacity. <i>Plant Physiology</i> , 2017, 175, 1634-1648.	2.3	88
7	Genomic Hypomethylation in the Human Germline Associates with Selective Structural Mutability in the Human Genome. <i>PLoS Genetics</i> , 2012, 8, e1002692.	1.5	80
8	Genome-wide analyses of LINE-mediated nonallelic homologous recombination. <i>Nucleic Acids Research</i> , 2015, 43, 2188-2198.	6.5	79
9	Human endogenous retroviral elements promote genome instability via non-allelic homologous recombination. <i>BMC Biology</i> , 2014, 12, 74.	1.7	60
10	Automatic mapping of atoms across both simple and complex chemical reactions. <i>Nature Communications</i> , 2019, 10, 1434.	5.8	57
11	Application of array comparative genomic hybridization in 102 patients with epilepsy and additional neurodevelopmental disorders. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012, 159B, 760-771.	1.1	48
12	Inverted Low-Copy Repeats and Genome Instability-A Genome-Wide Analysis. <i>Human Mutation</i> , 2013, 34, 210-220.	1.1	48
13	Modelling the efficacy of hyperthermia treatment. <i>Journal of the Royal Society Interface</i> , 2013, 10, 20130527.	1.5	42
14	Recurrent HERV-H-Mediated 3q13.2-q13.31 Deletions Cause a Syndrome of Hypotonia and Motor, Language, and Cognitive Delays. <i>Human Mutation</i> , 2013, 34, 1415-1423.	1.1	40
15	BRAIN: A Universal Tool for High-Throughput Calculations of the Isotopic Distribution for Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 1991-1994.	3.2	38
16	Application of custom-designed oligonucleotide array CGH in 145 patients with autistic spectrum disorders. <i>European Journal of Human Genetics</i> , 2013, 21, 620-625.	1.4	37
17	Application of array comparative genomic hybridization in 256 patients with developmental delay or intellectual disability. <i>Journal of Applied Genetics</i> , 2014, 55, 125-144.	1.0	37
18	On consensus biomarker selection. <i>BMC Bioinformatics</i> , 2007, 8, S5.	1.2	32

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19	IsoSpec: Hyperfast Fine Structure Calculator. <i>Analytical Chemistry</i> , 2017, 89, 3272-3277.	3.2	32
20	Risk assessment of COVID-19 epidemic resurgence in relation to SARS-CoV-2 variants and vaccination passes. <i>Communications Medicine</i> , 2022, 2, .	1.9	32
21	Comparative Analyses of Lung Transcriptomes in Patients with Alveolar Capillary Dysplasia with Misalignment of Pulmonary Veins and in <i>Foxf1</i> Heterozygous Knockout Mice. <i>PLoS ONE</i> , 2014, 9, e94390.	1.1	31
22	Population dynamics of miniature inverted-repeat transposable elements (MITEs) in <i>Medicago truncatula</i> . <i>Gene</i> , 2009, 448, 214-220.	1.0	30
23	Genomic parasites or symbionts? Modeling the effects of environmental pressure on transposition activity in asexual populations. <i>Theoretical Population Biology</i> , 2013, 90, 145-151.	0.5	27
24	Conformational Space and Stability of ETD Charge Reduction Products of Ubiquitin. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 69-76.	1.2	27
25	Diversity and structure of PIF/Harbinger-like elements in the genome of <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2007, 8, 409.	1.2	25
26	Chromosome conformation capture-on-chip analysis of long-range cis-interactions of the <i>SOX9</i> promoter. <i>Chromosome Research</i> , 2013, 21, 781-788.	1.0	23
27	On Subset Seeds for Protein Alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 483-494.	1.9	20
28	Computational models of the JAK1/2-STAT1 signaling. <i>Jak-stat</i> , 2013, 2, e24672.	2.2	20
29	Understanding reaction pathways in top-down ETD by dissecting isotope distributions: A mammoth task. <i>International Journal of Mass Spectrometry</i> , 2015, 390, 146-154.	0.7	20
30	Lethal lung hypoplasia and vascular defects in mice with conditional <i>Foxf1</i> overexpression. <i>Biology Open</i> , 2016, 5, 1595-1606.	0.6	20
31	Automated reduction and interpretation of multidimensional mass spectra for analysis of complex peptide mixtures. <i>International Journal of Mass Spectrometry</i> , 2007, 260, 20-30.	0.7	16
32	Computational modeling of sphingolipid metabolism. <i>BMC Systems Biology</i> , 2015, 9, 47.	3.0	16
33	Harvest time affects antioxidant capacity, total polyphenol and flavonoid content of Polish St John's wort (Hypericum perforatum L.) flowers. <i>Scientific Reports</i> , 2021, 11, 3989.	1.6	16
34	LINE- and <i>Alu</i> -containing genomic instability hotspot at 16q24.1 associated with recurrent and nonrecurrent CNV deletions causative for ACDMPV. <i>Human Mutation</i> , 2018, 39, 1916-1925.	1.1	14
35	Mapping of breakpoints in balanced chromosomal translocations by shallow whole-genome sequencing points to <i>EFNA5</i> , <i>BAHD1</i> and <i>PPP2R5E</i> as novel candidates for genes causing human Mendelian disorders. <i>Journal of Medical Genetics</i> , 2019, 56, 104-112.	1.5	13
36	Assessment of the role of copy-number variants in 150 patients with congenital heart defects. , 2012, 16, 175-82.		12

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37	Modeling Exopeptidase Activity from LC-MS Data. <i>Journal of Computational Biology</i> , 2009, 16, 395-406.	0.8	11
38	Molecular and clinical analyses of 16q24.1 duplications involving FOXF1 identify an evolutionarily unstable large minisatellite. <i>BMC Medical Genetics</i> , 2014, 15, 128.	2.1	11
39	Hierarchical clustering based upon contextual alignment of proteins: a different way to approach phylogeny. <i>Comptes Rendus - Biologies</i> , 2005, 328, 11-22.	0.1	10
40	On the Fine Isotopic Distribution and Limits to Resolution in Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1732-1745.	1.2	10
41	RESEARCH PAPER Sensitivity analysis of mathematical models of signaling pathways. <i>Biotechnologia</i> , 2012, 3, 291-308.	0.3	10
42	Improvement of the k-nn Entropy Estimator with Applications in Systems Biology. <i>Entropy</i> , 2016, 18, 13.	1.1	9
43	Model-based selection of the robust JAK-STAT activation mechanism. <i>Journal of Theoretical Biology</i> , 2012, 309, 34-46.	0.8	8
44	MuTAnT: a family of Mutator-like transposable elements targeting TA microsatellites in <i>Medicago truncatula</i> . <i>Genetica</i> , 2015, 143, 433-440.	0.5	8
45	Knot_pull python package for biopolymer smoothing and knot detection. <i>Bioinformatics</i> , 2020, 36, 953-955.	1.8	8
46	Data-driven case fatality rate estimation for the primary lineage of SARS-CoV-2 in Poland. <i>Methods</i> , 2022, , .	1.9	8
47	TIRfinder: A Web Tool for Mining Class II Transposons Carrying Terminal Inverted Repeats. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S10619.	0.6	7
48	masstodon: A Tool for Assigning Peaks and Modeling Electron Transfer Reactions in Top-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 1801-1807.	3.2	7
49	Masserstein: Linear regression of mass spectra by optimal transport. <i>Rapid Communications in Mass Spectrometry</i> , 2020, , e8956.	0.7	7
50	TADeus2: a web server facilitating the clinical diagnosis by pathogenicity assessment of structural variations disarranging 3D chromatin structure. <i>Nucleic Acids Research</i> , 2022, 50, W744-W752.	6.5	7
51	Contextual alignment of biological sequences (Extended abstract). <i>Bioinformatics</i> , 2002, 18, S116-S127.	1.8	6
52	CTX-BLAST: context sensitive version of protein BLAST. <i>Bioinformatics</i> , 2007, 23, 1686-1688.	1.8	6
53	Towards automated discrimination of lipids versus peptides from full scan mass spectra. <i>EuPA Open Proteomics</i> , 2014, 4, 87-100.	2.5	6
54	Alignment with Context Dependent Scoring Function. <i>Journal of Computational Biology</i> , 2006, 13, 81-101.	0.8	5

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55	Aggregation Algorithms for Perturbed Markov Chains with Applications to Networks Modeling. SIAM Journal of Scientific Computing, 2008, 31, 45-73.	1.3	5
56	Two-Stage Model-Based Clustering for Liquid Chromatography Mass Spectrometry Data Analysis. Statistical Applications in Genetics and Molecular Biology, 2009, 8, 1-34.	0.2	5
57	Classification of peptide mass fingerprint data by novel no-regret boosting method. Computers in Biology and Medicine, 2009, 39, 460-473.	3.9	5
58	Tav4SB: integrating tools for analysis of kinetic models of biological systems. BMC Systems Biology, 2012, 6, 25.	3.0	5
59	StochDecomp – Matlab package for noise decomposition in stochastic biochemical systems. Bioinformatics, 2014, 30, 137-138.	1.8	5
60	Inferring serum proteolytic activity from LC-MS/MS data. BMC Bioinformatics, 2012, 13, S7.	1.2	4
61	Functional performance of aCGH design for clinical cytogenetics. Computers in Biology and Medicine, 2013, 43, 775-785.	3.9	4
62	Breakpoint Mapping of Symptomatic Balanced Translocations Links the EPHA6, KLF13 and UBR3 Genes to Novel Disease Phenotype. Journal of Clinical Medicine, 2020, 9, 1245.	1.0	4
63	Confounding by Repetitive Elements and CpG Islands Does Not Explain the Association between Hypomethylation and Genomic Instability. PLoS Genetics, 2013, 9, e1003333.	1.5	3
64	Inferring Molecular Processes Heterogeneity from Transcriptional Data. BioMed Research International, 2017, 2017, 1-14.	0.9	3
65	TADeus-a tool for clinical interpretation of structural variants modifying chromatin organization. , 2018, , .		3
66	MIND: A Double-Linear Model To Accurately Determine Monoisotopic Precursor Mass in High-Resolution Top-Down Proteomics. Analytical Chemistry, 2019, 91, 10310-10319.	3.2	3
67	Biologically sound formal model of Hsp70 heat induction. Journal of Theoretical Biology, 2019, 478, 74-101.	0.8	3
68	Truncated Robust Principal Component Analysis and Noise Reduction for Single Cell RNA Sequencing Data. Journal of Computational Biology, 2019, 26, 782-793.	0.8	3
69	Contextual Multiple Sequence Alignment. Journal of Biomedicine and Biotechnology, 2005, 2005, 124-131.	3.0	2
70	Modeling Proteolysis from Mass Spectrometry Proteomic Data. Fundamenta Informaticae, 2010, 103, 89-104.	0.3	2
71	Multiple samples aCGH analysis for rare CNVs detection. Journal of Clinical Bioinformatics, 2013, 3, 12.	1.2	2
72	Inferring transposons activity chronology by TRANScendence – TEs database and de-novo mining tool. BMC Bioinformatics, 2017, 18, 422.	1.2	2

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73	Estimation of Rates of Reactions Triggered by Electron Transfer in Top-Down Mass Spectrometry. <i>Journal of Computational Biology</i> , 2018, 25, 282-301.	0.8	2
74	Low Entropy Sub-Networks Prevent the Integration of Metabolomic and Transcriptomic Data. <i>Entropy</i> , 2020, 22, 1238.	1.1	1
75	Efficient Model-Based Clustering for LC-MS Data. <i>Lecture Notes in Computer Science</i> , 2006, , 32-43.	1.0	1
76	Efficient Seeding Techniques for Protein Similarity Search. <i>Communications in Computer and Information Science</i> , 2008, , 466-478.	0.4	1
77	Almost FPRAS for Lattice Models of Protein Folding. <i>Lecture Notes in Computer Science</i> , 2005, , 534-544.	1.0	0
78	The model of proteolysis. <i>Nature Precedings</i> , 2010, , .	0.1	0
79	Efficient Multiple Samples aCGH Analysis for Rare CNVs Detection. , 2011, , .		0
80	Inferring serum proteolytic activity from LC-MS/MS data. , 2011, , .		0
81	PCA-like Methods for the Integration of Single Cell RNA-seq Data with Metabolic Networks. , 2018, , .		0
82	Truncated Robust Principal Component Analysis and Noise Reduction for Single Cell RNA-seq Data. <i>Lecture Notes in Computer Science</i> , 2018, , 335-346.	1.0	0
83	On the semantics of multistage interconnection networks. <i>Lecture Notes in Computer Science</i> , 1996, , 359-368.	1.0	0
84	Randomized Gossiping by Packets in Faulty Networks. <i>Lecture Notes in Computer Science</i> , 1999, , 387-394.	1.0	0
85	Estimation of Rates of Reactions Triggered by Electron Transfer in Top-Down Mass Spectrometry. <i>Lecture Notes in Computer Science</i> , 2017, , 96-107.	1.0	0