Anna Gambin

List of Publications by Year
in descending order

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	Data-driven case fatality rate estimation for the primary lineage of SARS-CoV-2 in Poland. Methods, 2022, , .	1.9	8
2	Risk assessment of COVID-19 epidemic resurgence in relation to SARS-CoV-2 variants and vaccination passes. Communications Medicine, 2022, 2, .	1.9	32
3	<tt>TADeus2</tt>: a web server facilitating the clinical diagnosis by pathogenicity assessment of structural variations disarranging 3D chromatin structure. Nucleic Acids Research, 2022, 50, W744-W752.	6.5	7
4	Harvest time affects antioxidant capacity, total polyphenol and flavonoid content of Polish St John's wort's (Hypericum perforatum L.) flowers. Scientific Reports, 2021, 11, 3989.	1.6	16
5	Knot_pull—python package for biopolymer smoothing and knot detection. Bioinformatics, 2020, 36, 953-955.	1.8	8
6	Low Entropy Sub-Networks Prevent the Integration of Metabolomic and Transcriptomic Data. Entropy, 2020, 22, 1238.	1.1	1
7	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
8	Masserstein: Linear regression of mass spectra by optimal transport. Rapid Communications in Mass Spectrometry, 2020, , e8956.	0.7	7
9	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
10	Biologically sound formal model of Hsp70 heat induction. Journal of Theoretical Biology, 2019, 478, 74-101.	0.8	3
11	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
12	Automatic mapping of atoms across both simple and complex chemical reactions. Nature Communications, 2019, 10, 1434.	5.8	57
13	Jaccard/Tanimoto similarity test and estimation methods for biological presence-absence data. BMC Bioinformatics, 2019, 20, 644.	1.2	114
14	masstodon: A Tool for Assigning Peaks and Modeling Electron Transfer Reactions in Top-Down Mass Spectrometry. Analytical Chemistry, 2019, 91, 1801-1807.	3.2	7
15	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. Journal of Medical Genetics, 2019, 56, 104-112.	1.5	13
16	Estimation of Rates of Reactions Triggered by Electron Transfer in Top-Down Mass Spectrometry. Journal of Computational Biology, 2018, 25, 282-301.	0.8	2
17	TADeus-a tool for clinical interpretation of structural variants modifying chromatin organization. , 2018, , .		3
18	PCA-like Methods for the Integration of Single Cell RNA-seq Data with Metabolic Networks. , 2018, , .		0

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19	Truncated Robust Principal Component Analysis and Noise Reduction for Single Cell RNA-seq Data. Lecture Notes in Computer Science, 2018, , 335-346.	1.0	0
20	LINE- and *Alu*-containing genomic instability hotspot at 16q24.1 associated with recurrent and nonrecurrent CNV deletions causative for ACDMPV. Human Mutation, 2018, 39, 1916-1925.	1.1	14
21	IsoSpec: Hyperfast Fine Structure Calculator. Analytical Chemistry, 2017, 89, 3272-3277.	3.2	32
22	Predicting the outcomes of organic reactions via machine learning: are current descriptors sufficient?. Scientific Reports, 2017, 7, 3582.	1.6	95
23	Leaf and Plant Age Affects Photosynthetic Performance and Photoprotective Capacity. Plant Physiology, 2017, 175, 1634-1648.	2.3	88
24	Conformational Space and Stability of ETD Charge Reduction Products of Ubiquitin. Journal of the American Society for Mass Spectrometry, 2017, 28, 69-76.	1.2	27
25	Inferring Molecular Processes Heterogeneity from Transcriptional Data. BioMed Research International, 2017, 2017, 1-14.	0.9	3
26	Inferring transposons activity chronology by TRANScendence â€" TEs database and de-novo mining tool. BMC Bioinformatics, 2017, 18, 422.	1.2	2
27	Estimation of Rates of Reactions Triggered by Electron Transfer in Top-Down Mass Spectrometry. Lecture Notes in Computer Science, 2017, , 96-107.	1.0	0
28	Improvement of the k-nn Entropy Estimator with Applications in Systems Biology. Entropy, 2016, 18, 13.	1.1	9
29	Gene Expression Profile of the Clinically Aggressive Micropapillary Variant of Bladder Cancer. European Urology, 2016, 70, 611-620.	0.9	120
30	Lethal lung hypoplasia and vascular defects in mice with conditional *Foxf1* overexpression. Biology Open, 2016, 5, 1595-1606.	0.6	20
31	MuTAnT: a family of Mutator-like transposable elements targeting TA microsatellites in Medicago truncatula. Genetica, 2015, 143, 433-440.	0.5	8
32	On the Fine Isotopic Distribution and Limits to Resolution in Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2015, 26, 1732-1745.	1.2	10
33	Genome-wide analyses of LINEâ€"LINE-mediated nonallelic homologous recombination. Nucleic Acids Research, 2015, 43, 2188-2198.	6.5	79
34	Understanding reaction pathways in top-down ETD by dissecting isotope distributions: A mammoth task. International Journal of Mass Spectrometry, 2015, 390, 146-154.	0.7	20
35	Computational modeling of sphingolipid metabolism. BMC Systems Biology, 2015, 9, 47.	3.0	16
36	Human endogenous retroviral elements promote genome instability via non-allelic homologous recombination. BMC Biology, 2014, 12, 74.	1.7	60

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37	Molecular and clinical analyses of 16q24.1 duplications involving FOXF1 identify an evolutionarily unstable large minisatellite. BMC Medical Genetics, 2014, 15, 128.	2.1	11
38	Application of array comparative genomic hybridization in 256 patients with developmental delay or intellectual disability. Journal of Applied Genetics, 2014, 55, 125-144.	1.0	37
39	StochDecomp—Matlab package for noise decomposition in stochastic biochemical systems. Bioinformatics, 2014, 30, 137-138.	1.8	5
40	Towards automated discrimination of lipids versus peptides from full scan mass spectra. EuPA Open Proteomics, 2014, 4, 87-100.	2.5	6
41	Comparative Analyses of Lung Transcriptomes in Patients with Alveolar Capillary Dysplasia with Misalignment of Pulmonary Veins and in Foxf1 Heterozygous Knockout Mice. PLoS ONE, 2014, 9, e94390.	1.1	31
42	Multiple samples aCGH analysis for rare CNVs detection. Journal of Clinical Bioinformatics, 2013, 3, 12.	1.2	2
43	Functional performance of aCGH design for clinical cytogenetics. Computers in Biology and Medicine, 2013, 43, 775-785.	3.9	4
44	Recurrent HERV-H-Mediated 3q13.2-q13.31 Deletions Cause a Syndrome of Hypotonia and Motor, Language, and Cognitive Delays. Human Mutation, 2013, 34, 1415-1423.	1.1	40
45	Inverted Low-Copy Repeats and Genome Instability-A Genome-Wide Analysis. Human Mutation, 2013, 34, 210-220.	1.1	48
46	Genomic parasites or symbionts? Modeling the effects of environmental pressure on transposition activity in asexual populations. Theoretical Population Biology, 2013, 90, 145-151.	0.5	27
47	Application of custom-designed oligonucleotide array CGH in 145 patients with autistic spectrum disorders. European Journal of Human Genetics, 2013, 21, 620-625.	1.4	37
48	BRAIN: A Universal Tool for High-Throughput Calculations of the Isotopic Distribution for Mass Spectrometry. Analytical Chemistry, 2013, 85, 1991-1994.	3.2	38
49	Chromosome conformation capture-on-chip analysis of long-range cis-interactions of the SOX9 promoter. Chromosome Research, 2013, 21, 781-788.	1.0	23
50	TIRfinder: A Web Tool for Mining Class II Transposons Carrying Terminal Inverted Repeats. Evolutionary Bioinformatics, 2013, 9, EBO.S10619.	0.6	7
51	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
52	Modelling the efficacy of hyperthermia treatment. Journal of the Royal Society Interface, 2013, 10, 20130527.	1.5	42
53	Computational models of the JAK1/2-STAT1 signaling. Jak-stat, 2013, 2, e24672.	2.2	20
54	NAHR-mediated copy-number variants in a clinical population: Mechanistic insights into both genomic disorders and Mendelizing traits. Genome Research, 2013, 23, 1395-1409.	2.4	120

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55	Genomic Hypomethylation in the Human Germline Associates with Selective Structural Mutability in the Human Genome. PLoS Genetics, 2012, 8, e1002692.	1.5	80
56	Tav4SB: integrating tools for analysis of kinetic models of biological systems. BMC Systems Biology, 2012, 6, 25.	3.0	5
57	Application of array comparative genomic hybridization in 102 patients with epilepsy and additional neurodevelopmental disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 760-771.	1.1	48
58	Model-based selection of the robust JAK-STAT activation mechanism. Journal of Theoretical Biology, 2012, 309, 34-46.	0.8	8
59	Inferring serum proteolytic activity from LC-MS/MS data. BMC Bioinformatics, 2012, 13, S7.	1.2	4
60	RESEARCH PAPER Sensitivity analysis of mathematical models of signaling pathways. Biotechnologia, 2012, 3, 291-308.	0.3	10
61	Assessment of the role of copy-number variants in 150 patients with congenital heart defects. , 2012, 16, 175-82.		12
62	Efficient Multiple Samples aCGH Analysis for Rare CNVs Detection. , 2011, , .		0
63	Inferring serum proteolytic activity from LC-MS/MS data. , 2011, , .		0
64	Modeling Proteolysis from Mass Spectrometry Proteomic Data. Fundamenta Informaticae, 2010, 103, 89-104.	0.3	2
65	The model of proteolysis. Nature Precedings, 2010, , .	0.1	0
66	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
67	Classification of peptide mass fingerprint data by novel no-regret boosting method. Computers in Biology and Medicine, 2009, 39, 460-473.	3.9	5
68	On Subset Seeds for Protein Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 483-494.	1.9	20
69	Population dynamics of miniature inverted-repeat transposable elements (MITEs) in Medicago truncatula. Gene, 2009, 448, 214-220.	1.0	30
70	Modeling Exopeptidase Activity from LC-MS Data. Journal of Computational Biology, 2009, 16, 395-406.	0.8	11
71	Aggregation Algorithms for Perturbed Markov Chains with Applications to Networks Modeling. SIAM Journal of Scientific Computing, 2008, 31, 45-73.	1.3	5
72	Efficient Seeding Techniques for Protein Similarity Search. Communications in Computer and Information Science, 2008, , 466-478.	0.4	1

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73	CTX-BLAST: context sensitive version of protein BLAST. Bioinformatics, 2007, 23, 1686-1688.	1.8	6
74	Automated reduction and interpretation of multidimensional mass spectra for analysis of complex peptide mixtures. International Journal of Mass Spectrometry, 2007, 260, 20-30.	0.7	16
75	On consensus biomarker selection. BMC Bioinformatics, 2007, 8, S5.	1.2	32
76	Diversity and structure of PIF/Harbinger-like elements in the genome of Medicago truncatula. BMC Genomics, 2007, 8, 409.	1.2	25
77	Applying dynamic Bayesian networks to perturbed gene expression data. BMC Bioinformatics, 2006, 7, 249.	1.2	133
78	Alignment with Context Dependent Scoring Function. Journal of Computational Biology, 2006, 13, 81-101.	0.8	5
79	Efficient Model-Based Clustering for LC-MS Data. Lecture Notes in Computer Science, 2006, , 32-43.	1.0	1
80	Contextual Multiple Sequence Alignment. Journal of Biomedicine and Biotechnology, 2005, 2005, 124-131.	3.0	2
81	Almost FPRAS for Lattice Models of Protein Folding. Lecture Notes in Computer Science, 2005, , 534-544.	1.0	0
82	Hierarchical clustering based upon contextual alignment of proteins: a different way to approach phylogeny. Comptes Rendus - Biologies, 2005, 328, 11-22.	0.1	10
83	Contextual alignment of biological sequences (Extended abstract). Bioinformatics, 2002, 18, S116-S127.	1.8	6
84	Randomized Gossiping by Packets in Faulty Networks. Lecture Notes in Computer Science, 1999, , 387-394.	1.0	0
85	On the semantics of multistage interconnection networks. Lecture Notes in Computer Science, 1996, , 359-368.	1.0	0