Sorin Draghici

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A systems biology approach for pathway level analysis. Genome Research, 2007, 17, 1537-1545.	5.5	1,036
2	A novel signaling pathway impact analysis. Bioinformatics, 2009, 25, 75-82.	4.1	950
3	Ontological analysis of gene expression data: current tools, limitations, and open problems. Bioinformatics, 2005, 21, 3587-3595.	4.1	766
4	Global functional profiling of gene expressionâ~†â~†This work was funded in part by a Sun Microsystems grant awarded to S.D., NIH Grant HD36512 to S.A.K., a Wayne State University SOM Dean's Post-Doctoral Fellowship, and an NICHD Contraception and Infertility Loan to G.C.O. Support from the WSU MCBI mode is gratefully appreciated Genomics, 2003, 81, 98-104.	2.9	544
5	Use and misuse of the gene ontology annotations. Nature Reviews Genetics, 2008, 9, 509-515.	16.3	518
6	Reliability and reproducibility issues in DNA microarray measurements. Trends in Genetics, 2006, 22, 101-109.	6.7	516
7	Machine Learning and Its Applications to Biology. PLoS Computational Biology, 2007, 3, e116.	3.2	490
8	NetPath: a public resource of curated signal transduction pathways. Genome Biology, 2010, 11, R3.	9.6	456
9	Profiling Gene Expression Using Onto-Express. Genomics, 2002, 79, 266-270.	2.9	429
10	Distinct subsets of microRNAs are expressed differentially in the human placentas of patients with preeclampsia. American Journal of Obstetrics and Gynecology, 2007, 196, 261.e1-261.e6.	1.3	373
11	A survey of small RNAs in human sperm. Human Reproduction, 2011, 26, 3401-3412.	0.9	366
12	Onto-Tools, the toolkit of the modern biologist: Onto-Express, Onto-Compare, Onto-Design and Onto-Translate. Nucleic Acids Research, 2003, 31, 3775-3781.	14.5	319
13	Analysis of microarray experiments of gene expression profiling. American Journal of Obstetrics and Gynecology, 2006, 195, 373-388.	1.3	263
14	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
15	Diagnostic Markers of Ovarian Cancer by High-Throughput Antigen Cloning and Detection on Arrays. Cancer Research, 2006, 66, 1181-1190.	0.9	199
16	Villitis of Unknown Etiology Is Associated with a Distinct Pattern of Chemokine Up-Regulation in the Feto-Maternal and Placental Compartments: Implications for Conjoint Maternal Allograft Rejection and Maternal Anti-Fetal Graft-versus-Host Disease. Journal of Immunology, 2009, 182, 3919-3927.	0.8	176
17	Methods and approaches in the topology-based analysis of biological pathways. Frontiers in Physiology, 2013, 4, 278.	2.8	173
18	Characterization of the myometrial transcriptome and biological pathways of spontaneous human labor at term. Journal of Perinatal Medicine, 2010, 38, 617-43.	1.4	150

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19	Integrated Systems Biology Approach Identifies Novel Maternal and Placental Pathways of Preeclampsia. Frontiers in Immunology, 2018, 9, 1661.	4.8	146
20	Onto-Tools: an ensemble of web-accessible, ontology-based tools for the functional design and interpretation of high-throughput gene expression experiments. Nucleic Acids Research, 2004, 32, W449-W456.	14.5	139
21	A novel approach for data integration and disease subtyping. Genome Research, 2017, 27, 2025-2039.	5.5	139
22	Identifying significantly impacted pathways: a comprehensive review and assessment. Genome Biology, 2019, 20, 203.	8.8	136
23	Down-weighting overlapping genes improves gene set analysis. BMC Bioinformatics, 2012, 13, 136.	2.6	128
24	Epigenetic silencing of multiple interferon pathway genes after cellular immortalization. Oncogene, 2003, 22, 4118-4127.	5.9	127
25	miR-210 Targets Iron-Sulfur Cluster Scaffold Homologue in Human Trophoblast Cell Lines. American Journal of Pathology, 2011, 179, 590-602.	3.8	127
26	Analysis and correction of crosstalk effects in pathway analysis. Genome Research, 2013, 23, 1885-1893.	5.5	123
27	A Neural Network Based Artificial Vision System for Licence Plate Recognition. International Journal of Neural Systems, 1997, 08, 113-126.	5.2	122
28	Gene Expression Profiles Predict Survival and Progression of Pleural Mesothelioma. Clinical Cancer Research, 2004, 10, 849-859.	7.0	121
29	Predicting HIV drug resistance with neural networks. Bioinformatics, 2003, 19, 98-107.	4.1	119
30	ORIGINAL ARTICLE: The Transcriptome of the Fetal Inflammatory Response Syndrome. American Journal of Reproductive Immunology, 2010, 63, 73-92.	1.2	114
31	Recent additions and improvements to the Onto-Tools. Nucleic Acids Research, 2005, 33, W762-W765.	14.5	106
32	Statistical intelligence: effective analysis of high-density microarray data. Drug Discovery Today, 2002, 7, S55-S63.	6.4	94
33	Expression patterns of microRNAs in the chorioamniotic membranes: a role for microRNAs in human pregnancy and parturition. Journal of Pathology, 2009, 217, 113-121.	4.5	91
34	Onto-Tools: new additions and improvements in 2006. Nucleic Acids Research, 2007, 35, W206-W211.	14.5	87
35	A novel computational approach for drug repurposing using systems biology. Bioinformatics, 2018, 34, 2817-2825.	4.1	87
36	The transcriptome of cervical ripening in human pregnancy before the onset of labor at term: Identification of novel molecular functions involved in this process. Journal of Maternal-Fetal and Neonatal Medicine, 2009, 22, 1183-1193.	1.5	84

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37	A common pattern of persistent gene activation in human neocortical epileptic foci. Annals of Neurology, 2005, 58, 736-747.	5.3	83
38	PINSPlus: a tool for tumor subtype discovery in integrated genomic data. Bioinformatics, 2019, 35, 2843-2846.	4.1	82
39	The prediction of early preeclampsia: Results from a longitudinal proteomics study. PLoS ONE, 2019, 14, e0217273.	2.5	81
40	On the capabilities of neural networks using limited precision weights. Neural Networks, 2002, 15, 395-414.	5.9	80
41	Identifying Significantly Impacted Pathways and Putative Mechanisms with iPathwayGuide. Current Protocols in Bioinformatics, 2017, 57, 7.15.1-7.15.30.	25.8	70
42	Autoantibody Approach for Serum-Based Detection of Head and Neck Cancer. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 2396-2405.	2.5	69
43	A semantic analysis of the annotations of the human genome. Bioinformatics, 2005, 21, 3416-3421.	4.1	61
44	Region-Specific Gene Expression Profiling: Novel Evidence for Biological Heterogeneity of the Human Amnion1. Biology of Reproduction, 2008, 79, 954-961.	2.7	58
45	Noise sampling method: an ANOVA approach allowing robust selection of differentially regulated genes measured by DNA microarrays. Bioinformatics, 2003, 19, 1348-1359.	4.1	54
46	Increased Interaction With Insulin Receptor Substrate 1, a Novel Abnormality in Insulin Resistance and Type 2 Diabetes. Diabetes, 2014, 63, 1933-1947.	0.6	51
47	A survey of the approaches for identifying differential methylation using bisulfite sequencing data. Briefings in Bioinformatics, 2018, 19, 737-753.	6.5	51
48	Transforming function of the LSM1 oncogene in human breast cancers with the 8p11–12 amplicon. Oncogene, 2007, 26, 2104-2114.	5.9	50
49	Whole-genome microarray and targeted analysis of angiogenesis-regulating gene expression (ENG,) Tj ETQq1 1 C Maternal-Fetal and Neonatal Medicine, 2008, 21, 267-273.).784314 1.5	rgBT /Overloc 48
50	A Comprehensive Survey of Tools and Software for Active Subnetwork Identification. Frontiers in Genetics, 2019, 10, 155.	2.3	48
51	Signature pathways identified from gene expression profiles in the human uterine cervix before and after spontaneous term parturition. American Journal of Obstetrics and Gynecology, 2007, 197, 250.e1-250.e7.	1.3	47
52	MicroRNA expression profiling of the human uterine cervix after term labor and delivery. American Journal of Obstetrics and Gynecology, 2010, 202, 80.e1-80.e8.	1.3	47
53	Differential expression of microRNAs with progression of gestation and inflammation in the human chorioamniotic membranes. American Journal of Obstetrics and Gynecology, 2007, 197, 289.e1-289.e6.	1.3	45
54	Nuclear matrix association of the human Â-globin locus utilizing a novel approach to quantitative real-time PCR. Nucleic Acids Research, 2003, 31, 3257-3266.	14.5	43

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55	Accuracy of cDNA microarray methods to detect small gene expression changes induced by neuregulin on breast epithelial cells. BMC Bioinformatics, 2004, 5, 99.	2.6	43
56	Mitochondrial manganese superoxide dismutase mRNA expression in human chorioamniotic membranes and its association with labor, inflammation, and infection. Journal of Maternal-Fetal and Neonatal Medicine, 2009, 22, 1000-1013.	1.5	43
57	Characterization of the myometrial transcriptome in women with an arrest of dilatation during labor. Journal of Perinatal Medicine, 2013, 41, 665-681.	1.4	42
58	Identification of key signaling pathways induced by SARS-CoV2 that underlie thrombosis and vascular injury in COVID-19 patients. Journal of Leukocyte Biology, 2021, 109, 35-47.	3.3	42
59	Differential expression pattern of genes encoding for anti-microbial peptides in the fetal membranes of patients with spontaneous preterm labor and intact membranes and those with preterm prelabor rupture of the membranes. Journal of Maternal-Fetal and Neonatal Medicine, 2009, 22, 1103-1115.	1.5	41
60	Predicting Novel Human Gene Ontology Annotations Using Semantic Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 91-99.	3.0	41
61	Differences and similarities in the transcriptional profile of peripheral whole blood in early and late-onset preeclampsia: insights into the molecular basis of the phenotype of preeclampsia ^a . Journal of Perinatal Medicine, 2013, 41, 485-504.	1.4	40
62	Babel's tower revisited: a universal resource for cross-referencing across annotation databases. Bioinformatics, 2006, 22, 2934-2939.	4.1	39
63	Epitomics: serum screening for the early detection of cancer on microarrays using complex panels of tumor antigens. Expert Review of Molecular Diagnostics, 2005, 5, 735-743.	3.1	37
64	Surfactant Protein-A as an Anti-Inflammatory Component in the Amnion: Implications for Human Pregnancy. Journal of Immunology, 2010, 184, 6479-6491.	0.8	35
65	Networkâ€Based Approaches for Pathway Level Analysis. Current Protocols in Bioinformatics, 2018, 61, 8.25.1-8.25.24.	25.8	33
66	A new computational drug repurposing method using established disease–drug pair knowledge. Bioinformatics, 2019, 35, 3672-3678.	4.1	33
67	NEURAL NETWORKS IN ANALOG HARDWARE — DESIGN AND IMPLEMENTATION ISSUES. International Journal of Neural Systems, 2000, 10, 19-42.	5.2	31
68	A molecular signature of an arrest of descent in human parturition. American Journal of Obstetrics and Gynecology, 2011, 204, 177.e15-177.e33.	1.3	30
69	A novel bi-level meta-analysis approach: applied to biological pathway analysis. Bioinformatics, 2016, 32, 409-416.	4.1	30
70	Placenta-Specific Genes, Their Regulation During Villous Trophoblast Differentiation and Dysregulation in Preterm Preeclampsia. International Journal of Molecular Sciences, 2020, 21, 628.	4.1	30
71	Gene Expression Databases and Data Mining. BioTechniques, 2003, 34, S36-S44.	1.8	29
72	Identification of cell types from single cell data using stable clustering. Scientific Reports, 2020, 10, 12349.	3.3	28

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73	Epitomics: Global Profiling of Immune Response to Disease Using Protein Microarrays. OMICS A Journal of Integrative Biology, 2006, 10, 499-506.	2.0	25
74	Overcoming the matched-sample bottleneck: an orthogonal approach to integrate omic data. Scientific Reports, 2016, 6, 29251.	3.3	25
75	A Multi-Cohort and Multi-Omics Meta-Analysis Framework to Identify Network-Based Gene Signatures. Frontiers in Genetics, 2019, 10, 159.	2.3	25
76	DC-ATLAS: a systems biology resource to dissect receptor specific signal transduction in dendritic cells. Immunome Research, 2010, 6, 10.	0.1	23
77	Identification of Novel Type 2 Diabetes Candidate Genes Involved in the Crosstalk between the Mitochondrial and the Insulin Signaling Systems. PLoS Genetics, 2012, 8, e1003046.	3.5	23
78	Modeling time-dependent transcription effects of HER2 oncogene and discovery of a role for E2F2 in breast cancer cell-matrix adhesion. Bioinformatics, 2014, 30, 3036-3043.	4.1	23
79	DANUBE: Data-Driven Meta-ANalysis Using UnBiased Empirical Distributions—Applied to Biological Pathway Analysis. Proceedings of the IEEE, 2017, 105, 496-515.	21.3	23
80	Cross-Clustering: A Partial Clustering Algorithm with Automatic Estimation of the Number of Clusters. PLoS ONE, 2016, 11, e0152333.	2.5	22
81	The Biological Connection Markup Language: a SBGN-compliant format for visualization, filtering and analysis of biological pathways. Bioinformatics, 2011, 27, 2127-2133.	4.1	21
82	COVID-19: disease pathways and gene expression changes predict methylprednisolone can improve outcome in severe cases. Bioinformatics, 2021, 37, 2691-2698.	4.1	21
83	The peripheral whole-blood transcriptome of acute pyelonephritis in human pregnancy ^a . Journal of Perinatal Medicine, 2014, 42, 31-53.	1.4	20
84	CPA: a web-based platform for consensus pathway analysis and interactive visualization. Nucleic Acids Research, 2021, 49, W114-W124.	14.5	20
85	SPATIAL: A System-level PAThway Impact AnaLysis approach. Nucleic Acids Research, 2016, 44, 5034-5044.	14.5	18
86	Platelets and renal failure in the SARS-CoV-2 syndrome. Platelets, 2021, 32, 130-137.	2.3	18
87	New Onto-Tools: Promoter-Express, nsSNPCounter and Onto-Translate. Nucleic Acids Research, 2006, 34, W626-W631.	14.5	17
88	Incorporating Gene Significance in the Impact Analysis of Signaling Pathways. , 2012, , .		16
89	GSMA: an approach to identify robust global and test Gene Signatures using Meta-Analysis. Bioinformatics, 2020, 36, 487-495.	4.1	13
90	Assessing the Functional Bias of Commercial Microarrays Using the Onto-Compare Database. BioTechniques, 2003, 34, S55-S61.	1.8	13

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91	The constraint based decomposition (CBD) training architecture. Neural Networks, 2001, 14, 527-550.	5.9	12
92	Gene expression profiling demonstrates a novel role for foetal fibrocytes and the umbilical vessels in human fetoplacental development. Journal of Cellular and Molecular Medicine, 2008, 12, 1317-1330.	3.6	12
93	Quantitative proteomics reveals novel protein interaction partners of PP2A catalytic subunit in pancreatic β-cells. Molecular and Cellular Endocrinology, 2016, 424, 1-11.	3.2	12
94	Application of an Objective Method for Localizing Bilateral Cortical FDG PET Abnormalities to Guide the Resection of Epileptic Foci. IEEE Transactions on Biomedical Engineering, 2005, 52, 1574-1581.	4.2	10
95	A Novel Pathway Analysis Approach Based on the Unexplained Disregulation of Genes. Proceedings of the IEEE, 2016, 105, 1-14.	21.3	10
96	NBIA: a network-based integrative analysis framework – applied to pathway analysis. Scientific Reports, 2020, 10, 4188.	3.3	10
97	Pathway crosstalk effects: shrinkage and disentanglement using a Bayesian hierarchical model. Statistics in Biosciences, 2016, 8, 374-394.	1.2	9
98	MICRORNA-AUGMENTED PATHWAYS (mirAP) AND THEIR APPLICATIONS TO PATHWAY ANALYSIS AND DISEASE SUBTYPING. , 2017, 22, 390-401.		9
99	Novel T7 Phage Display Library Detects Classifiers for Active Mycobacterium Tuberculosis Infection. Viruses, 2018, 10, 375.	3.3	9
100	Kinome Profiling Reveals Abnormal Activity of Kinases in Skeletal Muscle From Adults With Obesity and Insulin Resistance. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 644-659.	3.6	9
101	Distilled single-cell genome sequencing and <i>de novo</i> assembly for sparse microbial communities. Bioinformatics, 2013, 29, 2395-2401.	4.1	8
102	Serum prognostic biomarkers in head and neck cancer patients. Laryngoscope, 2014, 124, 1819-1826.	2.0	7
103	An approach to infer putative disease-specific mechanisms using neighboring gene networks. Bioinformatics, 2017, 33, 1987-1994.	4.1	7
104	Detection of Cystic Fibrosis Serological Biomarkers Using a T7 Phage Display Library. Scientific Reports, 2017, 7, 17745.	3.3	7
105	Integrating 5hmC and gene expression data to infer regulatory mechanisms. Bioinformatics, 2018, 34, 1441-1447.	4.1	7
106	MDAsim: A multiple displacement amplification simulator. , 2012, , .		6
107	A systems biology approach for the identification of significantly perturbed genes. , 2015, , .		6
108	Detecting Phenotype-Specific Interactions between Biological Processes from Microarray Data and Annotations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1399-1409.	3.0	5

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109	Detecting qualitative changes in biological systems. Scientific Reports, 2020, 10, 8146.	3.3	5
110	Developing Classifiers for the Detection of Cancer Using Multi-Analytes. Methods in Molecular Biology, 2009, 520, 259-272.	0.9	5
111	Integration of Multimodal Data from Disparate Sources for Identifying Disease Subtypes. Biology, 2022, 11, 360.	2.8	5
112	KUTE-BASE: storing, downloading and exporting MIAME-compliant microarray experiments in minutes rather than hours. Bioinformatics, 2008, 24, 738-740.	4.1	4
113	Signaling pathways coupling phenomena. , 2010, , .		4
114	MAGPEL: an autoMated pipeline for inferring vAriant-driven Gene PanEls from the full-length biomedical literature. Scientific Reports, 2020, 10, 12365.	3.3	4
115	Identifying biologically relevant putative mechanisms in a given phenotype comparison. PLoS ONE, 2017, 12, e0176950.	2.5	4
116	Ontologies for Bioinformatics. , 2014, , 441-461.		4
117	Assessing co-regulation of directly linked genes in biological networks using microarray time series analysis. BioSystems, 2013, 114, 149-154.	2.0	3
118	A Systems Biology Approach for Unsupervised Clustering of High-Dimensional Data. Lecture Notes in Computer Science, 2016, , 193-203.	1.3	3
119	Autoantibodies against cytoskeletons and lysosomal trafficking discriminate sarcoidosis from healthy controls, tuberculosis and lung cancers. Molecular Biomedicine, 2022, 3, 3.	4.4	3
120	Mining HIV dynamics using independent component analysis. Bioinformatics, 2003, 19, 981-986.	4.1	2
121	Discovering Document Semantics QBYS: A System for Querying the WWW by Semantics. Multimedia Tools and Applications, 2004, 24, 155-188.	3.9	2
122	Identifying uncertainty regions in Support Vector Machines using geometric margin and convex hulls. , 2008, , .		2
123	A method for analysis and correction of cross-talk effects in pathway analysis. , 2012, , .		2
124	Zâ€BAG: A CLASSIFICATION ENSEMBLE SYSTEM WITH POSTERIOR PROBABILISTIC OUTPUTS. Computational Intelligence, 2013, 29, 310-330.	3.2	2
125	TOMAS., 2016,,.		2
126	Automated Assay of a Four-Protein Biomarker Panel for Improved Detection of Ovarian Cancer. Cancers, 2021, 13, 325.	3.7	2

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127	On the computational power of limited precision weights neural networks in classification problems: How to calculate the weight range so that a solution will exist. Lecture Notes in Computer Science, 1999, , 401-412.	1.3	1
128	666 The Biological Connection Markup Language – a Data Format to Visualize, Annotate and Analyze Biological Pathways. European Journal of Cancer, 2012, 48, S158.	2.8	1
129	A genetic algorithms framework for estimating individual gene contributions in signaling pathways. , 2013, , .		1
130	Intelligent Informatics in Translational Medicine. BioMed Research International, 2015, 2015, 1-2.	1.9	1
131	Intelligent Informatics in Translational Medicine 2016. BioMed Research International, 2017, 2017, 1-2.	1.9	1
132	Disease Subtyping using Somatic Variant Data. , 2018, , .		1
133	75: The molecular basis for sonographic cervical shortening: identification of differentially expressed genes as a function of cervical length. American Journal of Obstetrics and Gynecology, 2009, 201, S42.	1.3	Ο
134	The International Society of Computational Biology presents: the Great Lakes Bioinformatics Conference, May 16-18, 2014, Cincinnati, Ohio. Bioinformatics, 2014, 30, 148-149.	4.1	0
135	On the complexity of VLSI-friendly neural networks for classification problems. Lecture Notes in Computer Science, 1998, , 285-297.	1.3	0