

# Sorin Draghici

## List of Publications by Year in descending order

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135  
papers

12,365  
citations

47004

47  
h-index

26610

107  
g-index

138  
all docs

138  
docs citations

138  
times ranked

16407  
citing authors

#	ARTICLE	IF	CITATIONS
1	A systems biology approach for pathway level analysis. <i>Genome Research</i> , 2007, 17, 1537-1545.	5.5	1,036
2	A novel signaling pathway impact analysis. <i>Bioinformatics</i> , 2009, 25, 75-82.	4.1	950
3	Ontological analysis of gene expression data: current tools, limitations, and open problems. <i>Bioinformatics</i> , 2005, 21, 3587-3595.	4.1	766
4	Global functional profiling of gene expression—††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.. <i>Genomics</i> , 2003, 81, 98-104.	2.9	544
5	Use and misuse of the gene ontology annotations. <i>Nature Reviews Genetics</i> , 2008, 9, 509-515.	16.3	518
6	Reliability and reproducibility issues in DNA microarray measurements. <i>Trends in Genetics</i> , 2006, 22, 101-109.	6.7	516
7	Machine Learning and Its Applications to Biology. <i>PLoS Computational Biology</i> , 2007, 3, e116.	3.2	490
8	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010, 11, R3.	9.6	456
9	Profiling Gene Expression Using Onto-Express. <i>Genomics</i> , 2002, 79, 266-270.	2.9	429
10	Distinct subsets of microRNAs are expressed differentially in the human placentas of patients with preeclampsia. <i>American Journal of Obstetrics and Gynecology</i> , 2007, 196, 261.e1-261.e6.	1.3	373
11	A survey of small RNAs in human sperm. <i>Human Reproduction</i> , 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. <i>Nucleic Acids Research</i> , 2003, 31, 3775-3781.	14.5	319
13	Analysis of microarray experiments of gene expression profiling. <i>American Journal of Obstetrics and Gynecology</i> , 2006, 195, 373-388.	1.3	263
14	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.	12.8	240
15	Diagnostic Markers of Ovarian Cancer by High-Throughput Antigen Cloning and Detection on Arrays. <i>Cancer Research</i> , 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. <i>Journal of Immunology</i> , 2009, 182, 3919-3927.	0.8	176
17	Methods and approaches in the topology-based analysis of biological pathways. <i>Frontiers in Physiology</i> , 2013, 4, 278.	2.8	173
18	Characterization of the myometrial transcriptome and biological pathways of spontaneous human labor at term. <i>Journal of Perinatal Medicine</i> , 2010, 38, 617-43.	1.4	150

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

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37	A common pattern of persistent gene activation in human neocortical epileptic foci. <i>Annals of Neurology</i> , 2005, 58, 736-747.	5.3	83
38	PINSPlus: a tool for tumor subtype discovery in integrated genomic data. <i>Bioinformatics</i> , 2019, 35, 2843-2846.	4.1	82
39	The prediction of early preeclampsia: Results from a longitudinal proteomics study. <i>PLoS ONE</i> , 2019, 14, e0217273.	2.5	81
40	On the capabilities of neural networks using limited precision weights. <i>Neural Networks</i> , 2002, 15, 395-414.	5.9	80
41	Identifying Significantly Impacted Pathways and Putative Mechanisms with iPathwayGuide. <i>Current Protocols in Bioinformatics</i> , 2017, 57, 7.15.1-7.15.30.	25.8	70
42	Autoantibody Approach for Serum-Based Detection of Head and Neck Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007, 16, 2396-2405.	2.5	69
43	A semantic analysis of the annotations of the human genome. <i>Bioinformatics</i> , 2005, 21, 3416-3421.	4.1	61
44	Region-Specific Gene Expression Profiling: Novel Evidence for Biological Heterogeneity of the Human Amnion1. <i>Biology of Reproduction</i> , 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. <i>Bioinformatics</i> , 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. <i>Diabetes</i> , 2014, 63, 1933-1947.	0.6	51
47	A survey of the approaches for identifying differential methylation using bisulfite sequencing data. <i>Briefings in Bioinformatics</i> , 2018, 19, 737-753.	6.5	51
48	Transforming function of the LSM1 oncogene in human breast cancers with the 8p11â€“12 amplicon. <i>Oncogene</i> , 2007, 26, 2104-2114.	5.9	50
49	Whole-genome microarray and targeted analysis of angiogenesis-regulating gene expression (ENG, Tj ETQq1 1 0.784314 rgBT /Overlaid Maternal-Fetal and Neonatal Medicine, 2008, 21, 267-273.	1.5	48
50	A Comprehensive Survey of Tools and Software for Active Subnetwork Identification. <i>Frontiers in Genetics</i> , 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. <i>American Journal of Obstetrics and Gynecology</i> , 2007, 197, 250.e1-250.e7.	1.3	47
52	MicroRNA expression profiling of the human uterine cervix after term labor and delivery. <i>American Journal of Obstetrics and Gynecology</i> , 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. <i>American Journal of Obstetrics and Gynecology</i> , 2007, 197, 289.e1-289.e6.	1.3	45
54	Nuclear matrix association of the human $\hat{\alpha}$ -globin locus utilizing a novel approach to quantitative real-time PCR. <i>Nucleic Acids Research</i> , 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. <i>BMC Bioinformatics</i> , 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. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2009, 22, 1000-1013.	1.5	43
57	Characterization of the myometrial transcriptome in women with an arrest of dilatation during labor. <i>Journal of Perinatal Medicine</i> , 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. <i>Journal of Leukocyte Biology</i> , 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. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2009, 22, 1103-1115.	1.5	41
60	Predicting Novel Human Gene Ontology Annotations Using Semantic Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 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. <i>Journal of Perinatal Medicine</i> , 2013, 41, 485-504.	1.4	40
62	Babel's tower revisited: a universal resource for cross-referencing across annotation databases. <i>Bioinformatics</i> , 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. <i>Expert Review of Molecular Diagnostics</i> , 2005, 5, 735-743.	3.1	37
64	Surfactant Protein-A as an Anti-Inflammatory Component in the Amnion: Implications for Human Pregnancy. <i>Journal of Immunology</i> , 2010, 184, 6479-6491.	0.8	35
65	Network-Based Approaches for Pathway Level Analysis. <i>Current Protocols in Bioinformatics</i> , 2018, 61, 8.25.1-8.25.24.	25.8	33
66	A new computational drug repurposing method using established disease-drug pair knowledge. <i>Bioinformatics</i> , 2019, 35, 3672-3678.	4.1	33
67	NEURAL NETWORKS IN ANALOG HARDWARE DESIGN AND IMPLEMENTATION ISSUES. <i>International Journal of Neural Systems</i> , 2000, 10, 19-42.	5.2	31
68	A molecular signature of an arrest of descent in human parturition. <i>American Journal of Obstetrics and Gynecology</i> , 2011, 204, 177.e15-177.e33.	1.3	30
69	A novel bi-level meta-analysis approach: applied to biological pathway analysis. <i>Bioinformatics</i> , 2016, 32, 409-416.	4.1	30
70	Placenta-Specific Genes, Their Regulation During Villous Trophoblast Differentiation and Dysregulation in Preterm Preeclampsia. <i>International Journal of Molecular Sciences</i> , 2020, 21, 628.	4.1	30
71	Gene Expression Databases and Data Mining. <i>BioTechniques</i> , 2003, 34, S36-S44.	1.8	29
72	Identification of cell types from single cell data using stable clustering. <i>Scientific Reports</i> , 2020, 10, 12349.	3.3	28

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73	Epitomics: Global Profiling of Immune Response to Disease Using Protein Microarrays. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 499-506.	2.0	25
74	Overcoming the matched-sample bottleneck: an orthogonal approach to integrate omic data. <i>Scientific Reports</i> , 2016, 6, 29251.	3.3	25
75	A Multi-Cohort and Multi-Omics Meta-Analysis Framework to Identify Network-Based Gene Signatures. <i>Frontiers in Genetics</i> , 2019, 10, 159.	2.3	25
76	DC-ATLAS: a systems biology resource to dissect receptor specific signal transduction in dendritic cells. <i>Immunome Research</i> , 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. <i>PLoS Genetics</i> , 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. <i>Bioinformatics</i> , 2014, 30, 3036-3043.	4.1	23
79	DANUBE: Data-Driven Meta-Analysis Using UnBiased Empirical Distributions Applied to Biological Pathway Analysis. <i>Proceedings of the IEEE</i> , 2017, 105, 496-515.	21.3	23
80	Cross-Clustering: A Partial Clustering Algorithm with Automatic Estimation of the Number of Clusters. <i>PLoS ONE</i> , 2016, 11, e0152333.	2.5	22
81	The Biological Connection Markup Language: a SBGN-compliant format for visualization, filtering and analysis of biological pathways. <i>Bioinformatics</i> , 2011, 27, 2127-2133.	4.1	21
82	COVID-19: disease pathways and gene expression changes predict methylprednisolone can improve outcome in severe cases. <i>Bioinformatics</i> , 2021, 37, 2691-2698.	4.1	21
83	The peripheral whole-blood transcriptome of acute pyelonephritis in human pregnancy<sup>a</sup>. <i>Journal of Perinatal Medicine</i> , 2014, 42, 31-53.	1.4	20
84	CPA: a web-based platform for consensus pathway analysis and interactive visualization. <i>Nucleic Acids Research</i> , 2021, 49, W114-W124.	14.5	20
85	SPATIAL: A System-level PATHway Impact Analysis approach. <i>Nucleic Acids Research</i> , 2016, 44, 5034-5044.	14.5	18
86	Platelets and renal failure in the SARS-CoV-2 syndrome. <i>Platelets</i> , 2021, 32, 130-137.	2.3	18
87	New Onto-Tools: Promoter-Express, nsSNPCounter and Onto-Translate. <i>Nucleic Acids Research</i> , 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. <i>Bioinformatics</i> , 2020, 36, 487-495.	4.1	13
90	Assessing the Functional Bias of Commercial Microarrays Using the Onto-Compare Database. <i>BioTechniques</i> , 2003, 34, S55-S61.	1.8	13

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91	The constraint based decomposition (CBD) training architecture. <i>Neural Networks</i> , 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. <i>Journal of Cellular and Molecular Medicine</i> , 2008, 12, 1317-1330.	3.6	12
93	Quantitative proteomics reveals novel protein interaction partners of PP2A catalytic subunit in pancreatic $\beta^2$ -cells. <i>Molecular and Cellular Endocrinology</i> , 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. <i>IEEE Transactions on Biomedical Engineering</i> , 2005, 52, 1574-1581.	4.2	10
95	A Novel Pathway Analysis Approach Based on the Unexplained Disregulation of Genes. <i>Proceedings of the IEEE</i> , 2016, 105, 1-14.	21.3	10
96	NBIA: a network-based integrative analysis framework “ applied to pathway analysis. <i>Scientific Reports</i> , 2020, 10, 4188.	3.3	10
97	Pathway crosstalk effects: shrinkage and disentanglement using a Bayesian hierarchical model. <i>Statistics in Biosciences</i> , 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. <i>Viruses</i> , 2018, 10, 375.	3.3	9
100	Kinome Profiling Reveals Abnormal Activity of Kinases in Skeletal Muscle From Adults With Obesity and Insulin Resistance. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 644-659.	3.6	9
101	Distilled single-cell genome sequencing and <i>de novo</i> assembly for sparse microbial communities. <i>Bioinformatics</i> , 2013, 29, 2395-2401.	4.1	8
102	Serum prognostic biomarkers in head and neck cancer patients. <i>Laryngoscope</i> , 2014, 124, 1819-1826.	2.0	7
103	An approach to infer putative disease-specific mechanisms using neighboring gene networks. <i>Bioinformatics</i> , 2017, 33, 1987-1994.	4.1	7
104	Detection of Cystic Fibrosis Serological Biomarkers Using a T7 Phage Display Library. <i>Scientific Reports</i> , 2017, 7, 17745.	3.3	7
105	Integrating 5hmC and gene expression data to infer regulatory mechanisms. <i>Bioinformatics</i> , 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. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1399-1409.	3.0	5

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109	Detecting qualitative changes in biological systems. <i>Scientific Reports</i> , 2020, 10, 8146.	3.3	5
110	Developing Classifiers for the Detection of Cancer Using Multi-Analytes. <i>Methods in Molecular Biology</i> , 2009, 520, 259-272.	0.9	5
111	Integration of Multimodal Data from Disparate Sources for Identifying Disease Subtypes. <i>Biology</i> , 2022, 11, 360.	2.8	5
112	KUTE-BASE: storing, downloading and exporting MIAME-compliant microarray experiments in minutes rather than hours. <i>Bioinformatics</i> , 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. <i>Scientific Reports</i> , 2020, 10, 12365.	3.3	4
115	Identifying biologically relevant putative mechanisms in a given phenotype comparison. <i>PLoS ONE</i> , 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. <i>BioSystems</i> , 2013, 114, 149-154.	2.0	3
118	A Systems Biology Approach for Unsupervised Clustering of High-Dimensional Data. <i>Lecture Notes in Computer Science</i> , 2016, , 193-203.	1.3	3
119	Autoantibodies against cytoskeletons and lysosomal trafficking discriminate sarcoidosis from healthy controls, tuberculosis and lung cancers. <i>Molecular Biomedicine</i> , 2022, 3, 3.	4.4	3
120	Mining HIV dynamics using independent component analysis. <i>Bioinformatics</i> , 2003, 19, 981-986.	4.1	2
121	Discovering Document Semantics QBYS: A System for Querying the WWW by Semantics. <i>Multimedia Tools and Applications</i> , 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	Z&EAG: A CLASSIFICATION ENSEMBLE SYSTEM WITH POSTERIOR PROBABILISTIC OUTPUTS. <i>Computational Intelligence</i> , 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. <i>Cancers</i> , 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	0
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