

# Sorin Draghici

## List of Publications by Citations

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127  
papers

9,555  
citations

43  
h-index

97  
g-index

138  
ext. papers

11,314  
ext. citations

6.8  
avg, IF

6.02  
L-index

#	Paper	IF	Citations
127	A systems biology approach for pathway level analysis. <i>Genome Research</i> , <b>2007</b> , 17, 1537-45	9.7	796
126	A novel signaling pathway impact analysis. <i>Bioinformatics</i> , <b>2009</b> , 25, 75-82	7.2	715
125	Ontological analysis of gene expression data: current tools, limitations, and open problems. <i>Bioinformatics</i> , <b>2005</b> , 21, 3587-95	7.2	669
124	Global functional profiling of gene expression. <i>Genomics</i> , <b>2003</b> , 81, 98-104	4.3	479
123	Reliability and reproducibility issues in DNA microarray measurements. <i>Trends in Genetics</i> , <b>2006</b> , 22, 101-9.5	4.5	459
122	Profiling gene expression using onto-express. <i>Genomics</i> , <b>2002</b> , 79, 266-70	4.3	398
121	Use and misuse of the gene ontology annotations. <i>Nature Reviews Genetics</i> , <b>2008</b> , 9, 509-15	30.1	390
120	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , <b>2010</b> , 11, R3	18.3	331
119	Distinct subsets of microRNAs are expressed differentially in the human placentas of patients with preeclampsia. <i>American Journal of Obstetrics and Gynecology</i> , <b>2007</b> , 196, 261.e1-6	6.4	327
118	A survey of small RNAs in human sperm. <i>Human Reproduction</i> , <b>2011</b> , 26, 3401-12	5.7	290
117	Onto-Tools, the toolkit of the modern biologist: Onto-Express, Onto-Compare, Onto-Design and Onto-Translate. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3775-81	20.1	280
116	Diagnostic markers of ovarian cancer by high-throughput antigen cloning and detection on arrays. <i>Cancer Research</i> , <b>2006</b> , 66, 1181-90	10.1	189
115	Analysis of microarray experiments of gene expression profiling. <i>American Journal of Obstetrics and Gynecology</i> , <b>2006</b> , 195, 373-88	6.4	177
114	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> , <b>2009</b> , 182, 3919-27	5.3	143
113	Methods and approaches in the topology-based analysis of biological pathways. <i>Frontiers in Physiology</i> , <b>2013</b> , 4, 278	4.6	136
112	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> , <b>2004</b> , 32, W449-56	20.1	120
111	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , <b>2019</b> , 10, 2674	17.4	119

110	Epigenetic silencing of multiple interferon pathway genes after cellular immortalization. <i>Oncogene</i> , <b>2003</b> , 22, 4118-27	9.2	112
109	Characterization of the myometrial transcriptome and biological pathways of spontaneous human labor at term. <i>Journal of Perinatal Medicine</i> , <b>2010</b> , 38, 617-43	2.7	111
108	Gene expression profiles predict survival and progression of pleural mesothelioma. <i>Clinical Cancer Research</i> , <b>2004</b> , 10, 849-59	12.9	108
107	The transcriptome of the fetal inflammatory response syndrome. <i>American Journal of Reproductive Immunology</i> , <b>2010</b> , 63, 73-92	3.8	105
106	miR-210 targets iron-sulfur cluster scaffold homologue in human trophoblast cell lines: siderosis of interstitial trophoblasts as a novel pathology of preterm preeclampsia and small-for-gestational-age pregnancies. <i>American Journal of Pathology</i> , <b>2011</b> , 179, 590-602	5.8	103
105	Recent additions and improvements to the Onto-Tools. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, W762-5	20.1	101
104	Predicting HIV drug resistance with neural networks. <i>Bioinformatics</i> , <b>2003</b> , 19, 98-107	7.2	92
103	Down-weighting overlapping genes improves gene set analysis. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 136	3.6	86
102	Analysis and correction of crosstalk effects in pathway analysis. <i>Genome Research</i> , <b>2013</b> , 23, 1885-93	9.7	84
101	Onto-Tools: new additions and improvements in 2006. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W206-11	20.1	84
100	Statistical intelligence: effective analysis of high-density microarray data. <i>Drug Discovery Today</i> , <b>2002</b> , 7, S55-63	8.8	81
99	Integrated Systems Biology Approach Identifies Novel Maternal and Placental Pathways of Preeclampsia. <i>Frontiers in Immunology</i> , <b>2018</b> , 9, 1661	8.4	79
98	A neural network based artificial vision system for licence plate recognition. <i>International Journal of Neural Systems</i> , <b>1997</b> , 8, 113-26	6.2	79
97	A novel approach for data integration and disease subtyping. <i>Genome Research</i> , <b>2017</b> , 27, 2025-2039	9.7	78
96	A common pattern of persistent gene activation in human neocortical epileptic foci. <i>Annals of Neurology</i> , <b>2005</b> , 58, 736-47	9.4	74
95	On the capabilities of neural networks using limited precision weights. <i>Neural Networks</i> , <b>2002</b> , 15, 395-404	9.4	70
94	Expression patterns of microRNAs in the chorioamniotic membranes: a role for microRNAs in human pregnancy and parturition. <i>Journal of Pathology</i> , <b>2009</b> , 217, 113-21	9.4	69
93	Autoantibody approach for serum-based detection of head and neck cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2007</b> , 16, 2396-405	4	64

92	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> , <b>2009</b> , 22, 1183-93	2	59
91	A novel computational approach for drug repurposing using systems biology. <i>Bioinformatics</i> , <b>2018</b> , 34, 2817-2825	7.2	55
90	A semantic analysis of the annotations of the human genome. <i>Bioinformatics</i> , <b>2005</b> , 21, 3416-21	7.2	55
89	Noise sampling method: an ANOVA approach allowing robust selection of differentially regulated genes measured by DNA microarrays. <i>Bioinformatics</i> , <b>2003</b> , 19, 1348-59	7.2	52
88	Identifying significantly impacted pathways: a comprehensive review and assessment. <i>Genome Biology</i> , <b>2019</b> , 20, 203	18.3	50
87	Region-specific gene expression profiling: novel evidence for biological heterogeneity of the human amnion. <i>Biology of Reproduction</i> , <b>2008</b> , 79, 954-61	3.9	48
86	Whole-genome microarray and targeted analysis of angiogenesis-regulating gene expression (ENG, FLT1, VEGF, PlGF) in placentas from pre-eclamptic and small-for-gestational-age pregnancies. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , <b>2008</b> , 21, 267-73	2	45
85	Nuclear matrix association of the human beta-globin locus utilizing a novel approach to quantitative real-time PCR. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3257-66	20.1	43
84	The prediction of early preeclampsia: Results from a longitudinal proteomics study. <i>PLoS ONE</i> , <b>2019</b> , 14, e0217273	3.7	41
83	MicroRNA expression profiling of the human uterine cervix after term labor and delivery. <i>American Journal of Obstetrics and Gynecology</i> , <b>2010</b> , 202, 80.e1-8	6.4	41
82	Transforming function of the LSM1 oncogene in human breast cancers with the 8p11-12 amplicon. <i>Oncogene</i> , <b>2007</b> , 26, 2104-14	9.2	41
81	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> , <b>2007</b> , 197, 250.e1-7	6.4	40
80	Increased interaction with insulin receptor substrate 1, a novel abnormality in insulin resistance and type 2 diabetes. <i>Diabetes</i> , <b>2014</b> , 63, 1933-47	0.9	39
79	Differential expression of microRNAs with progression of gestation and inflammation in the human chorioamniotic membranes. <i>American Journal of Obstetrics and Gynecology</i> , <b>2007</b> , 197, 289.e1-6	6.4	39
78	A survey of the approaches for identifying differential methylation using bisulfite sequencing data. <i>Briefings in Bioinformatics</i> , <b>2018</b> , 19, 737-753	13.4	36
77	Identifying Significantly Impacted Pathways and Putative Mechanisms with iPathwayGuide. <i>Current Protocols in Bioinformatics</i> , <b>2017</b> , 57, 7.15.1-7.15.30	24.2	36
76	Accuracy of cDNA microarray methods to detect small gene expression changes induced by neuregulin on breast epithelial cells. <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 99	3.6	36
75	Surfactant protein-A as an anti-inflammatory component in the amnion: implications for human pregnancy. <i>Journal of Immunology</i> , <b>2010</b> , 184, 6479-91	5.3	34

74	Epitomics: serum screening for the early detection of cancer on microarrays using complex panels of tumor antigens. <i>Expert Review of Molecular Diagnostics</i> , <b>2005</b> , 5, 735-43	3.8	34
73	Characterization of the myometrial transcriptome in women with an arrest of dilatation during labor. <i>Journal of Perinatal Medicine</i> , <b>2013</b> , 41, 665-81	2.7	33
72	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> , <b>2009</b> , 22, 1103-15	2	33
71	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> , <b>2009</b> , 22, 1000-13	2	33
70	Babel tower revisited: a universal resource for cross-referencing across annotation databases. <i>Bioinformatics</i> , <b>2006</b> , 22, 2934-9	7.2	33
69	PINSPlus: a tool for tumor subtype discovery in integrated genomic data. <i>Bioinformatics</i> , <b>2019</b> , 35, 2843-2846	3.8	32
68	Predicting novel human gene ontology annotations using semantic analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2010</b> , 7, 91-9	3	31
67	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> , <b>2013</b> , 41, 485-504	2.7	27
66	A Comprehensive Survey of Tools and Software for Active Subnetwork Identification. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 155	4.5	25
65	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> , <b>2021</b> , 109, 35-47	6.5	23
64	A molecular signature of an arrest of descent in human parturition. <i>American Journal of Obstetrics and Gynecology</i> , <b>2011</b> , 204, 177.e15-33	6.4	21
63	Epitomics: global profiling of immune response to disease using protein microarrays. <i>OMICS A Journal of Integrative Biology</i> , <b>2006</b> , 10, 499-506	3.8	21
62	Network-Based Approaches for Pathway Level Analysis. <i>Current Protocols in Bioinformatics</i> , <b>2018</b> , 61, 8.25.1-8.25.24	24.2	20
61	DC-ATLAS: a systems biology resource to dissect receptor specific signal transduction in dendritic cells. <i>Immunome Research</i> , <b>2010</b> , 6, 10		20
60	The Biological Connection Markup Language: a SBGN-compliant format for visualization, filtering and analysis of biological pathways. <i>Bioinformatics</i> , <b>2011</b> , 27, 2127-33	7.2	20
59	Cross-Clustering: A Partial Clustering Algorithm with Automatic Estimation of the Number of Clusters. <i>PLoS ONE</i> , <b>2016</b> , 11, e0152333	3.7	19
58	Neural networks in analog hardware--design and implementation issues. <i>International Journal of Neural Systems</i> , <b>2000</b> , 10, 19-42	6.2	18
57	A novel bi-level meta-analysis approach: applied to biological pathway analysis. <i>Bioinformatics</i> , <b>2016</b> , 32, 409-16	7.2	17

56	Modeling time-dependent transcription effects of HER2 oncogene and discovery of a role for E2F2 in breast cancer cell-matrix adhesion. <i>Bioinformatics</i> , <b>2014</b> , 30, 3036-43	7.2	17
55	Identification of novel type 2 diabetes candidate genes involved in the crosstalk between the mitochondrial and the insulin signaling systems. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003046	6	17
54	New Onto-Tools: Promoter-Express, nsSNPCounter and Onto-Translate. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W626-31	20.1	17
53	Overcoming the matched-sample bottleneck: an orthogonal approach to integrate omic data. <i>Scientific Reports</i> , <b>2016</b> , 6, 29251	4.9	16
52	The peripheral whole-blood transcriptome of acute pyelonephritis in human pregnancy. <i>Journal of Perinatal Medicine</i> , <b>2014</b> , 42, 31-53	2.7	16
51	DANUBE: Data-driven meta-ANalysis using UnBiased Empirical distributions-applied to biological pathway analysis. <i>Proceedings of the IEEE</i> , <b>2017</b> , 105, 496-515	14.3	15
50	A new computational drug repurposing method using established disease-drug pair knowledge. <i>Bioinformatics</i> , <b>2019</b> , 35, 3672-3678	7.2	14
49	SPATIAL: A System-level PATHway Impact AnaLysis approach. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 5034-44	20.1	14
48	Gene Expression Databases and Data Mining. <i>BioTechniques</i> , <b>2003</b> , 34, S36-S44	2.5	14
47	<b>2012</b> ,		13
46	A Multi-Cohort and Multi-Omics Meta-Analysis Framework to Identify Network-Based Gene Signatures. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 159	4.5	12
45	Placenta-Specific Genes, Their Regulation During Villous Trophoblast Differentiation and Dysregulation in Preterm Preeclampsia. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	12
44	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> , <b>2008</b> , 12, 1317-30	5.6	12
43	The constraint based decomposition (CBD) training architecture. <i>Neural Networks</i> , <b>2001</b> , 14, 527-50	9.1	12
42	Identification of cell types from single cell data using stable clustering. <i>Scientific Reports</i> , <b>2020</b> , 10, 12342	4.9	10
41	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> , <b>2005</b> , 52, 1574-81	5	9
40	Assessing the Functional Bias of Commercial Microarrays Using the Onto-Compare Database. <i>BioTechniques</i> , <b>2003</b> , 34, S55-S61	2.5	8
39	Quantitative proteomics reveals novel protein interaction partners of PP2A catalytic subunit in pancreatic cells. <i>Molecular and Cellular Endocrinology</i> , <b>2016</b> , 424, 1-11	4.4	7

38	Serum prognostic biomarkers in head and neck cancer patients. <i>Laryngoscope</i> , <b>2014</b> , 124, 1819-26	3.6	7
37	A novel pathway analysis approach based on the unexplained dysregulation of genes. <i>Proceedings of the IEEE</i> , <b>2017</b> , 105, 482-495	14.3	7
36	GSMA: an approach to identify robust global and test Gene Signatures using Meta-Analysis. <i>Bioinformatics</i> , <b>2020</b> , 36, 487-495	7.2	7
35	Platelets and renal failure in the SARS-CoV-2 syndrome. <i>Platelets</i> , <b>2021</b> , 32, 130-137	3.6	7
34	Distilled single-cell genome sequencing and de novo assembly for sparse microbial communities. <i>Bioinformatics</i> , <b>2013</b> , 29, 2395-401	7.2	6
33	An approach to infer putative disease-specific mechanisms using neighboring gene networks. <i>Bioinformatics</i> , <b>2017</b> , 33, 1987-1994	7.2	5
32	Integrating 5hmC and gene expression data to infer regulatory mechanisms. <i>Bioinformatics</i> , <b>2018</b> , 34, 1441-1447	7.2	5
31	Novel T7 Phage Display Library Detects Classifiers for Active Mycobacterium Tuberculosis Infection. <i>Viruses</i> , <b>2018</b> , 10,	6.2	5
30	Detection of Cystic Fibrosis Serological Biomarkers Using a T7 Phage Display Library. <i>Scientific Reports</i> , <b>2017</b> , 7, 17745	4.9	5
29	Detecting phenotype-specific interactions between biological processes from microarray data and annotations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2012</b> , 9, 1399-409	3	5
28	Developing classifiers for the detection of cancer using multi-analytes. <i>Methods in Molecular Biology</i> , <b>2009</b> , 520, 259-72	1.4	5
27	COVID-19: disease pathways and gene expression changes predict methylprednisolone can improve outcome in severe cases. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	5
26	MICRORNA-AUGMENTED PATHWAYS (mirAP) AND THEIR APPLICATIONS TO PATHWAY ANALYSIS AND DISEASE SUBTYPING. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2017</b> , 22, 390-401	1.3	4
25	A systems biology approach for the identification of significantly perturbed genes <b>2015</b> ,		4
24	Detecting qualitative changes in biological systems. <i>Scientific Reports</i> , <b>2020</b> , 10, 8146	4.9	4
23	NBIA: a network-based integrative analysis framework - applied to pathway analysis. <i>Scientific Reports</i> , <b>2020</b> , 10, 4188	4.9	4
22	MDAsim: A multiple displacement amplification simulator <b>2012</b> ,		4
21	KUTE-BASE: storing, downloading and exporting MIAME-compliant microarray experiments in minutes rather than hours. <i>Bioinformatics</i> , <b>2008</b> , 24, 738-40	7.2	4

20	CPA: a web-based platform for consensus pathway analysis and interactive visualization. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, W114-W124	20.1	4
19	Pathway crosstalk effects: Shrinkage and disentanglement using a Bayesian hierarchical model. <i>Statistics in Biosciences</i> , <b>2016</b> , 8, 374-394	1.5	4
18	Assessing co-regulation of directly linked genes in biological networks using microarray time series analysis. <i>BioSystems</i> , <b>2013</b> , 114, 149-54	1.9	3
17	Signaling pathways coupling phenomena <b>2010</b> ,		3
16	MAGPEL: an autoMated pipeline for inferring vAriant-driven Gene PanEls from the full-length biomedical literature. <i>Scientific Reports</i> , <b>2020</b> , 10, 12365	4.9	3
15	Z-BAG: A CLASSIFICATION ENSEMBLE SYSTEM WITH POSTERIOR PROBABILISTIC OUTPUTS. <i>Computational Intelligence</i> , <b>2013</b> , 29, 310-330	2.5	2
14	A method for analysis and correction of cross-talk effects in pathway analysis <b>2012</b> ,		2
13	Mining HIV dynamics using independent component analysis. <i>Bioinformatics</i> , <b>2003</b> , 19, 981-6	7.2	2
12	Identifying biologically relevant putative mechanisms in a given phenotype comparison. <i>PLoS ONE</i> , <b>2017</b> , 12, e0176950	3.7	2
11	A Systems Biology Approach for Unsupervised Clustering of High-Dimensional Data. <i>Lecture Notes in Computer Science</i> , <b>2016</b> , 193-203	0.9	2
10	TOMAS <b>2016</b> ,		2
9	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> , <b>2020</b> , 105,	5.6	1
8	A genetic algorithms framework for estimating individual gene contributions in signaling pathways <b>2013</b> ,		1
7	Identifying uncertainty regions in Support Vector Machines using geometric margin and convex hulls <b>2008</b> ,		1
6	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. <i>Lecture Notes in Computer Science</i> , <b>1999</b> , 401-412	0.9	1
5	Ontologies for Bioinformatics <b>2014</b> , 441-461		1
4	Discovering Document Semantics QBYS: A System for Querying the WWW by Semantics. <i>Multimedia Tools and Applications</i> , <b>2004</b> , 24, 155-188	2.5	0
3	Autoantibodies against cytoskeletons and lysosomal trafficking discriminate sarcoidosis from healthy controls, tuberculosis and lung cancers.. <i>Molecular Biomedicine</i> , <b>2022</b> , 3, 3	3.1	0



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|---|--|-----|
| 2 | The International Society of Computational Biology presents: the Great Lakes Bioinformatics Conference, May 16-18, 2014, Cincinnati, Ohio. <i>Bioinformatics</i> , <b>2014</b> , 30, 148-149 | 7.2 |
| 1 | On the complexity of VLSI-friendly neural networks for classification problems. <i>Lecture Notes in Computer Science</i> , <b>1998</b> , 285-297   | 0.9 |