

# Igor Jurisica

## List of Publications by Year in descending order

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247  
papers

20,919  
citations

10986

71  
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11308

136  
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281  
all docs

281  
docs citations

281  
times ranked

30566  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene expression-based survival prediction in lung adenocarcinoma: a multi-site, blinded validation study. <i>Nature Medicine</i> , 2008, 14, 822-827.	30.7	1,015
2	Stem cell gene expression programs influence clinical outcome in human leukemia. <i>Nature Medicine</i> , 2011, 17, 1086-1093.	30.7	894
3	Isolation of Single Human Hematopoietic Stem Cells Capable of Long-Term Multilineage Engraftment. <i>Science</i> , 2011, 333, 218-221.	12.6	717
4	High-Throughput Mapping of a Dynamic Signaling Network in Mammalian Cells. <i>Science</i> , 2005, 307, 1621-1625.	12.6	651
5	Protein complex prediction via cost-based clustering. <i>Bioinformatics</i> , 2004, 20, 3013-3020.	4.1	620
6	Online Predicted Human Interaction Database. <i>Bioinformatics</i> , 2005, 21, 2076-2082.	4.1	557
7	Modeling interactome: scale-free or geometric?. <i>Bioinformatics</i> , 2004, 20, 3508-3515.	4.1	544
8	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. <i>Nature Methods</i> , 2012, 9, 345-350.	19.0	500
9	The c-Myc Oncogene Directly Induces the H19 Noncoding RNA by Allele-Specific Binding to Potentiate Tumorigenesis. <i>Cancer Research</i> , 2006, 66, 5330-5337.	0.9	451
10	mirDIP 4.1-integrative database of human microRNA target predictions. <i>Nucleic Acids Research</i> , 2018, 46, D360-D370.	14.5	430
11	Prognostic and Predictive Gene Signature for Adjuvant Chemotherapy in Resected Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2010, 28, 4417-4424.	1.6	405
12	Functional topology in a network of protein interactions. <i>Bioinformatics</i> , 2004, 20, 340-348.	4.1	388
13	TAp73 knockout shows genomic instability with infertility and tumor suppressor functions. <i>Genes and Development</i> , 2008, 22, 2677-2691.	5.9	378
14	Comprehensive MicroRNA Profiling for Head and Neck Squamous Cell Carcinomas. <i>Clinical Cancer Research</i> , 2010, 16, 1129-1139.	7.0	353
15	Molecular Evidence of Placental Hypoxia in Preeclampsia. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2005, 90, 4299-4308.	3.6	343
16	Dysregulation of the mevalonate pathway promotes transformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15051-15056.	7.1	323
17	Prognostic gene-expression signature of carcinoma-associated fibroblasts in non-small cell lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7160-7165.	7.1	317
18	Unequal evolutionary conservation of human protein interactions in interologous networks. <i>Genome Biology</i> , 2007, 8, R95.	9.6	308

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19	Tumour genomic and microenvironmental heterogeneity for integrated prediction of 5-year biochemical recurrence of prostate cancer: a retrospective cohort study. <i>Lancet Oncology</i> , The, 2014, 15, 1521-1532.	10.7	291
20	Validation of a Histology-Independent Prognostic Gene Signature for Early-Stage, Non-Small-Cell Lung Cancer Including Stage IA Patients. <i>Journal of Thoracic Oncology</i> , 2014, 9, 59-64.	1.1	243
21	Hypoxia Predicts Aggressive Growth and Spontaneous Metastasis Formation from Orthotopically Grown Primary Xenografts of Human Pancreatic Cancer. <i>Cancer Research</i> , 2011, 71, 3110-3120.	0.9	241
22	NAViGaTOR: Network Analysis, Visualization and Graphing Toronto. <i>Bioinformatics</i> , 2009, 25, 3327-3329.	4.1	234
23	mRNA transcript quantification in archival samples using multiplexed, color-coded probes. <i>BMC Biotechnology</i> , 2011, 11, 46.	3.3	234
24	Three-Gene Prognostic Classifier for Early-Stage Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2007, 25, 5562-5569.	1.6	226
25	Fundamentals of protein interaction network mapping. <i>Molecular Systems Biology</i> , 2015, 11, 848.	7.2	226
26	Identification of a microRNA signature associated with progression of leukoplakia to oral carcinoma. <i>Human Molecular Genetics</i> , 2009, 18, 4818-4829.	2.9	223
27	Robust global micro-RNA profiling with formalin-fixed paraffin-embedded breast cancer tissues. <i>Laboratory Investigation</i> , 2009, 89, 597-606.	3.7	221
28	Integrated interactions database: tissue-specific view of the human and model organism interactomes. <i>Nucleic Acids Research</i> , 2016, 44, D536-D541.	14.5	212
29	NAViGaTing the Micronome – Using Multiple MicroRNA Prediction Databases to Identify Signalling Pathway-Associated MicroRNAs. <i>PLoS ONE</i> , 2011, 6, e17429.	2.5	207
30	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. <i>Nature Communications</i> , 2019, 10, 10.	12.8	193
31	Molecular profiling of non-small cell lung cancer and correlation with disease-free survival. <i>Cancer Research</i> , 2002, 62, 3005-8.	0.9	183
32	Prognostic gene signatures for non-small-cell lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2824-2828.	7.1	182
33	Alterations in mitochondrial membrane potential during preimplantation stages of mouse and human embryo development. <i>Molecular Human Reproduction</i> , 2004, 10, 23-32.	2.8	172
34	IID 2018 update: context-specific physical protein-protein interactions in human, model organisms and domesticated species. <i>Nucleic Acids Research</i> , 2019, 47, D581-D589.	14.5	164
35	Knowledge Discovery and interactive Data Mining in Bioinformatics - State-of-the-Art, future challenges and research directions. <i>BMC Bioinformatics</i> , 2014, 15, 11.	2.6	161
36	Ontologies for Knowledge Management: An Information Systems Perspective. <i>Knowledge and Information Systems</i> , 2004, 6, 380-401.	3.2	155

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37	Comparative systems biology of human and mouse as a tool to guide the modeling of human placental pathology. <i>Molecular Systems Biology</i> , 2009, 5, 279.	7.2	151
38	The mammalian-membrane two-hybrid assay (MaMTH) for probing membrane-protein interactions in human cells. <i>Nature Methods</i> , 2014, 11, 585-592.	19.0	149
39	In silico prediction of physical protein interactions and characterization of interactome orphans. <i>Nature Methods</i> , 2015, 12, 79-84.	19.0	148
40	Integrin $\alpha 11$ regulates IGF2 expression in fibroblasts to enhance tumorigenicity of human non-small-cell lung cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11754-11759.	7.1	141
41	Regulation of Epidermal Growth Factor Receptor Trafficking by Lysine Deacetylase HDAC6. <i>Science Signaling</i> , 2009, 2, ra84.	3.6	140
42	Integrin $\alpha 11 \beta 1$ regulates cancer stromal stiffness and promotes tumorigenicity and metastasis in non-small cell lung cancer. <i>Oncogene</i> , 2016, 35, 1899-1908.	5.9	138
43	A Proteome Resource of Ovarian Cancer Ascites: Integrated Proteomic and Bioinformatic Analyses To Identify Putative Biomarkers. <i>Journal of Proteome Research</i> , 2008, 7, 339-351.	3.7	134
44	Gene Expression Profiling in Cervical Cancer: An Exploration of Intratumor Heterogeneity. <i>Clinical Cancer Research</i> , 2006, 12, 5632-5640.	7.0	131
45	A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome. <i>Molecular Cell</i> , 2017, 65, 347-360.	9.7	123
46	Programmed cell death 4 loss increases tumor cell invasion and is regulated by miR-21 in oral squamous cell carcinoma. <i>Molecular Cancer</i> , 2010, 9, 238.	19.2	121
47	A gene signature in histologically normal surgical margins is predictive of oral carcinoma recurrence. <i>BMC Cancer</i> , 2011, 11, 437.	2.6	117
48	BioID identifies novel c-MYC interacting partners in cultured cells and xenograft tumors. <i>Journal of Proteomics</i> , 2015, 118, 95-111.	2.4	112
49	Efficient estimation of graphlet frequency distributions in protein-protein interaction networks. <i>Bioinformatics</i> , 2006, 22, 974-980.	4.1	109
50	Copy number alterations of <i>c-MYC</i> and <i>PTEN</i> are prognostic factors for relapse after prostate cancer radiotherapy. <i>Cancer</i> , 2012, 118, 4053-4062.	4.1	105
51	pathDIP: an annotated resource for known and predicted human gene-pathway associations and pathway enrichment analysis. <i>Nucleic Acids Research</i> , 2017, 45, D419-D426.	14.5	105
52	The Murine Caecal MicroRNA Signature Depends on the Presence of the Endogenous Microbiota. <i>International Journal of Biological Sciences</i> , 2012, 8, 171-186.	6.4	102
53	Myc and its interactors take shape. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 469-483.	1.9	102
54	The non-coding RNA interactome in joint health and disease. <i>Nature Reviews Rheumatology</i> , 2021, 17, 692-705.	8.0	102

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55	Information fusion as an integrative cross-cutting enabler to achieve robust, explainable, and trustworthy medical artificial intelligence. <i>Information Fusion</i> , 2022, 79, 263-278.	19.1	100
56	Identification of synovial fluid microRNA signature in knee osteoarthritis: differentiating early- and late-stage knee osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2016, 24, 1577-1586.	1.3	98
57	Mechanical Stiffness Controls Dendritic Cell Metabolism and Function. <i>Cell Reports</i> , 2021, 34, 108609.	6.4	98
58	Clinical Utility of Patient-Derived Xenografts to Determine Biomarkers of Prognosis and Map Resistance Pathways in EGFR-Mutant Lung Adenocarcinoma. <i>Journal of Clinical Oncology</i> , 2015, 33, 2472-2480.	1.6	94
59	Sex-specific differences in placental global gene expression in pregnancies complicated by asthma. <i>Placenta</i> , 2011, 32, 570-578.	1.5	92
60	CpG Island microarray probe sequences derived from a physical library are representative of CpG Islands annotated on the human genome. <i>Nucleic Acids Research</i> , 2005, 33, 2952-2961.	14.5	89
61	Case-based reasoning in IVF: prediction and knowledge mining. <i>Artificial Intelligence in Medicine</i> , 1998, 12, 1-24.	6.5	88
62	Network-based characterization of drug-regulated genes, drug targets, and toxicity. <i>Methods</i> , 2012, 57, 499-507.	3.8	88
63	Multiple dysregulated pathways in nasopharyngeal carcinoma revealed by gene expression profiling. <i>International Journal of Cancer</i> , 2006, 119, 2467-2475.	5.1	87
64	Impaired tRNA Nuclear Export Links DNA Damage and Cell-Cycle Checkpoint. <i>Cell</i> , 2007, 131, 915-926.	28.9	83
65	In silico cancer research towards 3R. <i>BMC Cancer</i> , 2018, 18, 408.	2.6	83
66	Exploiting the mevalonate pathway to distinguish statin-sensitive multiple myeloma. <i>Blood</i> , 2010, 115, 4787-4797.	1.4	81
67	Data mining for case-based reasoning in high-dimensional biological domains. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2005, 17, 1127-1137.	5.7	78
68	The Emerging Role of the RAB25 Small GTPase in Cancer. <i>Traffic</i> , 2009, 10, 1561-1568.	2.7	78
69	Knowledge Discovery and Data Mining in Biomedical Informatics: The Future Is in Integrative, Interactive Machine Learning Solutions. <i>Lecture Notes in Computer Science</i> , 2014, , 1-18.	1.3	78
70	Macromolecular crystallization in a high throughput laboratory—the search phase. <i>Journal of Crystal Growth</i> , 2001, 232, 591-595.	1.5	76
71	The complex landscape of microRNAs in articular cartilage: biology, pathology, and therapeutic targets. <i>JCI Insight</i> , 2018, 3, .	5.0	76
72	Systematic identification of SH3 domain-mediated human protein–protein interactions by peptide array target screening. <i>Proteomics</i> , 2007, 7, 1775-1785.	2.2	74

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73	The FlowVizMenu and Parallel Scatterplot Matrix: Hybrid Multidimensional Visualizations for Network Exploration. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2010, 16, 1100-1108.	4.4	74
74	Autoantibodies targeting GPCRs and RAS-related molecules associate with COVID-19 severity. <i>Nature Communications</i> , 2022, 13, 1220.	12.8	74
75	In-Depth Proteomics of Ovarian Cancer Ascites: Combining Shotgun Proteomics and Selected Reaction Monitoring Mass Spectrometry. <i>Journal of Proteome Research</i> , 2011, 10, 2286-2299.	3.7	72
76	Transcriptional targets of hepatocyte growth factor signaling and Ki-ras oncogene activation in colorectal cancer. <i>Oncogene</i> , 2006, 25, 91-102.	5.9	71
77	Why imaging data alone is not enough: AI-based integration of imaging, omics, and clinical data. <i>European Journal of Nuclear Medicine and Molecular Imaging</i> , 2019, 46, 2722-2730.	6.4	69
78	Molecular heterogeneity of non-small cell lung carcinoma patient-derived xenografts closely reflect their primary tumors. <i>International Journal of Cancer</i> , 2017, 140, 662-673.	5.1	67
79	Determinants of sensitivity to lovastatin-induced apoptosis in multiple myeloma. <i>Molecular Cancer Therapeutics</i> , 2007, 6, 1886-1897.	4.1	65
80	Role of Pirh2 in Mediating the Regulation of p53 and c-Myc. <i>PLoS Genetics</i> , 2011, 7, e1002360.	3.5	65
81	Integrated proteomic and transcriptomic profiling of mouse lung development and Nmyc target genes. <i>Molecular Systems Biology</i> , 2007, 3, 109.	7.2	64
82	Genomic markers for malignant progression in pulmonary adenocarcinoma with bronchioloalveolar features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10155-10160.	7.1	64
83	Evaluation of linguistic features useful in extraction of interactions from PubMed; Application to annotating known, high-throughput and predicted interactions in I2D. <i>Bioinformatics</i> , 2010, 26, 111-119.	4.1	63
84	Systematic protein-protein interaction mapping for clinically relevant human GPCR</sc>s. <i>Molecular Systems Biology</i> , 2017, 13, 918.	7.2	63
85	The histone deacetylase inhibitor valproic acid alters sensitivity towards all trans retinoic acid in acute myeloblastic leukemia cells. <i>Leukemia</i> , 2005, 19, 1161-1168.	7.2	61
86	Identification of microRNA-181a-5p and microRNA-4454 as mediators of facet cartilage degeneration. <i>JCI Insight</i> , 2016, 1, e86820.	5.0	60
87	Understanding Prognostic Gene Expression Signatures in Lung Cancer. <i>Clinical Lung Cancer</i> , 2009, 10, 331-340.	2.6	59
88	Molecular classification of oral cancer by cDNA microarrays identifies overexpressed genes correlated with nodal metastasis. <i>International Journal of Cancer</i> , 2004, 110, 857-868.	5.1	57
89	MicroRNA-34a-5p Promotes Joint Destruction During Osteoarthritis. <i>Arthritis and Rheumatology</i> , 2021, 73, 426-439.	5.6	56
90	STAT3 pathway regulates lung-derived brain metastasis initiating cell capacity through miR-21 activation. <i>Oncotarget</i> , 2015, 6, 27461-27477.	1.8	55

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91	Inhibition of the Sodium/Potassium ATPase Impairs <i>N</i> -Glycan Expression and Function. <i>Cancer Research</i> , 2008, 68, 6688-6697.	0.9	54
92	Interaction Techniques for Selecting and Manipulating Subgraphs in Network Visualizations. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2009, 15, 937-944.	4.4	51
93	Flotillin-2 deficiency leads to reduced lung metastases in a mouse breast cancer model. <i>Oncogene</i> , 2013, 32, 4989-4994.	5.9	51
94	The ablation of the matricellular protein EMILIN2 causes defective vascularization due to impaired EGFR-dependent IL-8 production affecting tumor growth. <i>Oncogene</i> , 2018, 37, 3399-3414.	5.9	51
95	<i>CUL7</i> Is a Novel Antiapoptotic Oncogene. <i>Cancer Research</i> , 2007, 67, 9616-9622.	0.9	50
96	Inferring the functions of longevity genes with modular subnetwork biomarkers of <i>Caenorhabditis elegans</i> aging. <i>Genome Biology</i> , 2010, 11, R13.	9.6	50
97	A functional biological network centered on XRCC3: a new possible marker of chemoradiotherapy resistance in rectal cancer patients. <i>Cancer Biology and Therapy</i> , 2015, 16, 1160-1171.	3.4	49
98	Towards a unified open access dataset of molecular interactions. <i>Nature Communications</i> , 2020, 11, 6144.	12.8	49
99	Integrative transcriptome analysis identifies deregulated microRNA-transcription factor networks in lung adenocarcinoma. <i>Oncotarget</i> , 2016, 7, 28920-28934.	1.8	49
100	L1 Cell Adhesion Molecule Promotes Tumorigenicity and Metastatic Potential in Non-Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2012, 18, 1914-1924.	7.0	48
101	Identification of pathways associated with invasive behavior by ovarian cancer cells using multidimensional protein identification technology (MudPIT). <i>Molecular BioSystems</i> , 2008, 4, 762.	2.9	47
102	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. <i>BMC Bioinformatics</i> , 2018, 19, 134.	2.6	47
103	Recurrent genomic alterations in sequential progressive leukoplakia and oral cancer: drivers of oral tumorigenesis?. <i>Human Molecular Genetics</i> , 2014, 23, 2618-2628.	2.9	46
104	Differential roles of cyclin D1 and D3 in pancreatic ductal adenocarcinoma. <i>Molecular Cancer</i> , 2010, 9, 24.	19.2	45
105	An integrative approach for the identification of prognostic and predictive biomarkers in rectal cancer. <i>Oncotarget</i> , 2015, 6, 32561-32574.	1.8	45
106	Intelligent decision support for protein crystal growth. <i>IBM Systems Journal</i> , 2001, 40, 394-409.	3.0	44
107	Automatic classification of sub-microlitre protein-crystallization trials in 1536-well plates. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1619-1627.	2.5	43
108	Stability and Heterogeneity of Expression Profiles in Lung Cancer Specimens Harvested Following Surgical Resection. <i>Neoplasia</i> , 2004, 6, 761-767.	5.3	43

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109	<i>NKX3.1</i> Haploinsufficiency Is Prognostic for Prostate Cancer Relapse following Surgery or Image-Guided Radiotherapy. <i>Clinical Cancer Research</i> , 2012, 18, 308-316.	7.0	43
110	Sequencing identifies a distinct signature of circulating microRNAs in early radiographic knee osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2020, 28, 1471-1481.	1.3	43
111	Developmental transcription factor NFIB is a putative target of oncofetal miRNAs and is associated with tumour aggressiveness in lung adenocarcinoma. <i>Journal of Pathology</i> , 2016, 240, 161-172.	4.5	42
112	Protein interactome mining defines melatonin <i>MT<sub>1</sub></i> receptors as integral component of presynaptic protein complexes of neurons. <i>Journal of Pineal Research</i> , 2016, 60, 95-108.	7.4	42
113	Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRASG13D. <i>Nature Communications</i> , 2020, 11, 499.	12.8	42
114	Smoking status impacts microRNA mediated prognosis and lung adenocarcinoma biology. <i>BMC Cancer</i> , 2014, 14, 778.	2.6	41
115	Epithelial tumor suppressor ELF3 is a lineage-specific amplified oncogene in lung adenocarcinoma. <i>Nature Communications</i> , 2019, 10, 5438.	12.8	41
116	Protein crystallization analysis on the World Community Grid. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 61-69.	1.2	40
117	Protease nexin 1 inhibits hedgehog signaling in prostate adenocarcinoma. <i>Journal of Clinical Investigation</i> , 2012, 122, 4025-4036.	8.2	39
118	pathDIP 4: an extended pathway annotations and enrichment analysis resource for human, model organisms and domesticated species. <i>Nucleic Acids Research</i> , 2020, 48, D479-D488.	14.5	38
119	IID 2021: towards context-specific protein interaction analyses by increased coverage, enhanced annotation and enrichment analysis. <i>Nucleic Acids Research</i> , 2022, 50, D640-D647.	14.5	38
120	MicroRNA Signature Obtained From the Comparison of Aggressive With Indolent Non-Hodgkin Lymphomas: Potential Prognostic Value in Mantle-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2013, 31, 2903-2911.	1.6	37
121	Integration, visualization and analysis of human interactome. <i>Biochemical and Biophysical Research Communications</i> , 2014, 445, 757-773.	2.1	37
122	MYC interaction with the tumor suppressive SWI/SNF complex member INI1 regulates transcription and cellular transformation. <i>Cell Cycle</i> , 2016, 15, 1693-1705.	2.6	37
123	Differentially androgen-modulated genes in ovarian epithelial cells from BRCA mutation carriers and control patients predict ovarian cancer survival and disease progression. <i>Oncogene</i> , 2007, 26, 198-214.	5.9	36
124	Prioritizing Therapeutics for Lung Cancer: An Integrative Meta-analysis of Cancer Gene Signatures and Chemogenomic Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004068.	3.2	36
125	An Integrated Approach Identifies Mediators of Local Recurrence in Head and Neck Squamous Carcinoma. <i>Clinical Cancer Research</i> , 2017, 23, 3769-3780.	7.0	36
126	Automated Microinjection of Recombinant BCL-X into Mouse Zygotes Enhances Embryo Development. <i>PLoS ONE</i> , 2011, 6, e21687.	2.5	36



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127	Therapeutic Targeting of the Premetastatic Stage in Human Lung-to-Brain Metastasis. <i>Cancer Research</i> , 2018, 78, 5124-5134.	0.9	35
128	The IMEx coronavirus interactome: an evolving map of <i>Coronaviridae</i> host molecular interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	34
129	Genomic amplicons target vesicle recycling in breast cancer. <i>Journal of Clinical Investigation</i> , 2009, 119, 2123-7.	8.2	34
130	Split Intein-Mediated Protein Ligation for detecting protein-protein interactions and their inhibition. <i>Nature Communications</i> , 2020, 11, 2440.	12.8	33
131	Automatic Classification and Pattern Discovery in High-throughput Protein Crystallization Trials. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 195-202.	1.2	32
132	Phenotypic and Transcriptional Plasticity Directed by a Yeast Mitogen-Activated Protein Kinase Network. <i>Genetics</i> , 2003, 165, 997-1015.	2.9	32
133	Modeling of lung cancer by an orthotopically growing H460SM variant cell line reveals novel candidate genes for systemic metastasis. <i>Oncogene</i> , 2004, 23, 6316-6324.	5.9	31
134	Prognostic Gene Expression Signature for Squamous Cell Carcinoma of Lung. <i>Clinical Cancer Research</i> , 2010, 16, 5038-5047.	7.0	31
135	Ubiquitin ligase RNF8 suppresses Notch signaling to regulate mammary development and tumorigenesis. <i>Journal of Clinical Investigation</i> , 2018, 128, 4525-4542.	8.2	31
136	<i>NBN</i> gain is predictive for adverse outcome following image-guided radiotherapy for localized prostate cancer. <i>Oncotarget</i> , 2014, 5, 11081-11090.	1.8	30
137	Circulating plant miRNAs can regulate human gene expression in vitro. <i>Scientific Reports</i> , 2016, 6, 32773.	3.3	29
138	<i>TP53</i> mutations in high grade serous ovarian cancer and impact on clinical outcomes: a comparison of next generation sequencing and bioinformatics analyses. <i>International Journal of Gynecological Cancer</i> , 2019, 29, 346-352.	2.5	29
139	Extracellular Matrix Injury of Kidney Allografts in Antibody-Mediated Rejection: A Proteomics Study. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 2705-2724.	6.1	29
140	Identification of GAS-dependent interferon-sensitive target genes whose transcription is STAT2-dependent but ISGF3-independent. <i>FEBS Journal</i> , 2006, 273, 1569-1581.	4.7	28
141	Optimization of experimental design parameters for high-throughput chromatin immunoprecipitation studies. <i>Nucleic Acids Research</i> , 2008, 36, e144-e144.	14.5	28
142	Integrative computational biology for cancer research. <i>Human Genetics</i> , 2011, 130, 465-481.	3.8	28
143	Macrophage migration inhibitory factor drives pathology in a mouse model of spondyloarthritis and is associated with human disease. <i>Science Translational Medicine</i> , 2021, 13, eabg1210.	12.4	28
144	Primary Tumor Xenografts of Human Lung Adeno and Squamous Cell Carcinoma Express Distinct Proteomic Signatures. <i>Journal of Proteome Research</i> , 2011, 10, 161-174.	3.7	27

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145	Severe COVID-19 Shares a Common Neutrophil Activation Signature with Other Acute Inflammatory States. <i>Cells</i> , 2022, 11, 847.	4.1	27
146	RNAi screen identifies essential regulators of human brain metastasis-initiating cells. <i>Acta Neuropathologica</i> , 2017, 134, 923-940.	7.7	26
147	Establishing a training set through the visual analysis of crystallization trials. Part I: 150,000 images. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1123-1130.	2.5	25
148	A stemness screen reveals C3orf54/INKA1 as a promoter of human leukemia stem cell latency. <i>Blood</i> , 2019, 133, 2198-2211.	1.4	25
149	Quantification of angiotensin II-regulated proteins in urine of patients with polycystic and other chronic kidney diseases by selected reaction monitoring. <i>Clinical Proteomics</i> , 2016, 13, 16.	2.1	24
150	SCRIPDB: a portal for easy access to syntheses, chemicals and reactions in patents. <i>Nucleic Acids Research</i> , 2012, 40, D428-D433.	14.5	22
151	Systematic Identification of Oncogenic EGFR Interaction Partners. <i>Journal of Molecular Biology</i> , 2017, 429, 280-294.	4.2	22
152	Physiological Tau Interactome in Brain and Its Link to Tauopathies. <i>Journal of Proteome Research</i> , 2020, 19, 2429-2442.	3.7	22
153	An Integrative Genomic and Transcriptomic Analysis Reveals Potential Targets Associated with Cell Proliferation in Uterine Leiomyomas. <i>PLoS ONE</i> , 2013, 8, e57901.	2.5	22
154	Comparative network analysis via differential graphlet communities. <i>Proteomics</i> , 2015, 15, 608-617.	2.2	21
155	Current Applications of Microarrays in Head and Neck Cancer Research. <i>Laryngoscope</i> , 2004, 114, 241-248.	2.0	19
156	Visual Data Mining of Biological Networks: One Size Does Not Fit All. <i>PLoS Computational Biology</i> , 2013, 9, e1002833.	3.2	19
157	BioPAX-Parser: parsing and enrichment analysis of BioPAX pathways. <i>Bioinformatics</i> , 2020, 36, 4377-4378.	4.1	19
158	Loss of coordinated androgen regulation in nonmalignant ovarian epithelial cells with BRCA1/2 mutations and ovarian cancer cells. <i>Cancer Research</i> , 2003, 63, 2416-24.	0.9	19
159	Establishing a training set through the visual analysis of crystallization trials. Part II: crystal examples. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1131-1137.	2.5	18
160	Kinome-wide screening of HER2+ breast cancer cells for molecules that mediate cell proliferation or sensitize cells to trastuzumab therapy. <i>Oncogenesis</i> , 2014, 3, e133-e133.	4.9	18
161	Prediction of Protein-Protein Interactions. <i>Current Protocols in Bioinformatics</i> , 2017, 60, 8.2.1-8.2.14.	25.8	18
162	Incremental Iterative Retrieval and Browsing for Efficient Conversational CBR Systems. <i>Applied Intelligence</i> , 2000, 12, 251-268.	5.3	17

#	ARTICLE	IF	CITATIONS
163	CHIP-MYTH: A novel interactive proteomics method for the assessment of agonist-dependent interactions of the human $\beta$ 2-adrenergic receptor. <i>Biochemical and Biophysical Research Communications</i> , 2014, 445, 746-756.	2.1	17
164	Visual Data Mining: Effective Exploration of the Biological Universe. <i>Lecture Notes in Computer Science</i> , 2014, , 19-33.	1.3	17
165	The relationship between cytokine and neutrophil gene network distinguishes SARS-CoV-2â€infecte patients by sex and age. <i>JCI Insight</i> , 2021, 6, .	5.0	17
166	Lung cancer: Developmental networks gone awry?. <i>Cancer Biology and Therapy</i> , 2009, 8, 312-318.	3.4	16
167	Exploiting the noise: improving biomarkers with ensembles of data analysis methodologies. <i>Genome Medicine</i> , 2012, 4, 84.	8.2	15
168	A 4-gene signature from histologically normal surgical margins predicts local recurrence in patients with oral carcinoma: clinical validation. <i>Scientific Reports</i> , 2020, 10, 1713.	3.3	15
169	A comprehensive catalogue of functional genetic variations in the EGFR pathway: Proteinâ€protein interaction analysis reveals novel genes and polymorphisms important for cancer research. <i>International Journal of Cancer</i> , 2009, 125, 1257-1265.	5.1	13
170	NAVIGATOR: Large Scalable and Interactive Navigation and Analysis of Large Graphs. <i>Internet Mathematics</i> , 2011, 7, 314-347.	0.7	13
171	Novel semantic similarity measure improves an integrative approach to predicting gene functional associations. <i>BMC Systems Biology</i> , 2013, 7, 22.	3.0	13
172	Integrating RAS Status into Prognostic Signatures for Adenocarcinomas of the Lung. <i>Clinical Cancer Research</i> , 2015, 21, 1477-1486.	7.0	13
173	Uninterrupted Sedentary Behavior Downregulates <i>BRCA1</i> Gene Expression. <i>Cancer Prevention Research</i> , 2016, 9, 83-88.	1.5	13
174	Differentially expressed microRNAs in lung adenocarcinoma invert effects of copy number aberrations of prognostic genes. <i>Oncotarget</i> , 2018, 9, 9137-9155.	1.8	13
175	CFTR interactome mapping using the mammalian membrane twoâ€hybrid highâ€throughput screening system. <i>Molecular Systems Biology</i> , 2022, 18, e10629.	7.2	13
176	Improving Performance of Case-Based Classification Using Context-Based Relevance. <i>International Journal on Artificial Intelligence Tools</i> , 1997, 06, 511-536.	1.0	12
177	Advances in ovarian cancer proteomics: the quest for biomarkers and improved therapeutic interventions. <i>Expert Review of Proteomics</i> , 2008, 5, 551-560.	3.0	12
178	GSOAP: a tool for visualization of gene set over-representation analysis. <i>Bioinformatics</i> , 2020, 36, 2923-2925.	4.1	12
179	Informed Use of Proteinâ€Protein Interaction Data: A Focus on the Integrated Interactions Database (IID). <i>Methods in Molecular Biology</i> , 2020, 2074, 125-134.	0.9	12
180	Estrogen Receptor 1â€Inhibition of Wnt/ $\beta$ -Catenin Signalingâ€Contributes to Sex Differences in Hepatocarcinogenesis. <i>Frontiers in Oncology</i> , 2021, 11, 777834.	2.8	12

#	ARTICLE	IF	CITATIONS
181	Circulating microRNAs differentiate fast-progressing from slow-progressing and non-progressing knee osteoarthritis in the Osteoarthritis Initiative cohort. <i>Therapeutic Advances in Musculoskeletal Disease</i> , 2022, 14, 1759720X2210829.	2.7	12
182	Robust quantitative scratch assay. <i>Bioinformatics</i> , 2016, 32, 1439-1440.	4.1	11
183	Immune-enrichment of non-small cell lung cancer baseline biopsies for multiplex profiling define prognostic immune checkpoint combinations for patient stratification. , 2019, 7, 86.		11
184	Case-based classification using similarity-based retrieval. , 0, , .		10
185	Allelic loss of the loci containing the androgen synthesis gene, <i>StAR</i> , is prognostic for relapse in intermediate-risk prostate cancer. <i>Prostate</i> , 2012, 72, 1295-1305.	2.3	10
186	Tumor cell endogenous HIF-1 $\alpha$ activity induces aberrant angiogenesis and interacts with TRAF6 pathway required for colorectal cancer development. <i>Neoplasia</i> , 2020, 22, 745-758.	5.3	9
187	Increased Autoantibodies Against Ro/SS-A, CENP-B, and La/SS-B in Patients With Kidney Allograft Antibody-mediated Rejection. <i>Transplantation Direct</i> , 2021, 7, e768.	1.6	9
188	Mapping the Phospho-dependent ALK Interactome to Identify Novel Components in ALK Signaling. <i>Journal of Molecular Biology</i> , 2021, 433, 167283.	4.2	9
189	NetwoRx: connecting drugs to networks and phenotypes in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2012, 41, D720-D727.	14.5	8
190	SDREGION. , 2018, , .		8
191	Urine Angiotensin II Signature Proteins as Markers of Fibrosis in Kidney Transplant Recipients. <i>Transplantation</i> , 2019, 103, e146-e158.	1.0	8
192	Construction of New Medicines via Game Proof Search. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2012, 26, 1564-1570.	4.9	8
193	Re: Gene Expression-Based Prognostic Signatures in Lung Cancer: Ready for Clinical Use?. <i>Journal of the National Cancer Institute</i> , 2010, 102, 1677-1678.	6.3	7
194	Machine Learning for In Silico Modeling of Tumor Growth. <i>Lecture Notes in Computer Science</i> , 2016, , 415-434.	1.3	7
195	Modeling tumor progression via the comparison of stage-specific graphs. <i>Methods</i> , 2018, 132, 34-41.	3.8	7
196	<i>HABP2</i> p.G534E variant in patients with family history of thyroid and breast cancer. <i>Oncotarget</i> , 2017, 8, 40896-40905.	1.8	7
197	Contribution of <i>MicroRNA-27b</i> to Synovial Fibrotic Responses in Knee Osteoarthritis. <i>Arthritis and Rheumatology</i> , 2022, 74, 1928-1942.	5.6	7
198	Urinary proteomics links keratan sulfate degradation and lysosomal enzymes to early type 1 diabetes. <i>PLoS ONE</i> , 2020, 15, e0233639.	2.5	6

#	ARTICLE	IF	CITATIONS
199	Normothermic Ex-vivo Kidney Perfusion in a Porcine Auto-Transplantation Model Preserves the Expression of Key Mitochondrial Proteins: An Unbiased Proteomics Analysis. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100101.	3.8	6
200	Changes in circulating microRNAs following head impacts in soccer. <i>Brain Injury</i> , 2022, 36, 560-571.	1.2	6
201	Potential role of <i>CC</i> chemokine receptor 6 in prediction of late-onset cytomegalovirus infection following solid organ transplant. <i>Clinical Transplantation</i> , 2015, 29, 492-498.	1.6	5
202	Two Decades of Biological Pathway Databases: Results and Challenges. , 2019, , 1071-1084.		5
203	The network interplay of interferon and Toll-like receptor signaling pathways in the anti-Candida immune response. <i>Scientific Reports</i> , 2021, 11, 20281.	3.3	5
204	Algorithms for Systematic Identification of Small Subgraphs. <i>Methods in Molecular Biology</i> , 2012, 804, 219-244.	0.9	5
205	Case-Based Reasoning for Biomedical Informatics and Medicine. , 2014, , 207-221.		5
206	Comprehensive pathway enrichment analysis workflows: COVID-19 case study. <i>Briefings in Bioinformatics</i> , 2021, 22, 676-689.	6.5	5
207	A Network Biology Approach to Understanding the Tissue-Specific Roles of Non-Coding RNAs in Arthritis. <i>Frontiers in Endocrinology</i> , 2021, 12, 744747.	3.5	5
208	Failed immune responses across multiple pathologies share pan-tumor and circulating lymphocytic targets. <i>Journal of Clinical Investigation</i> , 2019, 129, 2463-2479.	8.2	4
209	Peripheral microRNA alteration and pathway signaling after mild traumatic brain injur. <i>General Physiology and Biophysics</i> , 2021, 40, 523-539.	0.9	4
210	Sportomics suggests that albuminuria is a sensitive biomarker of hydration in cross combat. <i>Scientific Reports</i> , 2022, 12, 8150.	3.3	4
211	Comparison of Machine Learning and Pattern Discovery Algorithms for the Prediction of Human Single Nucleotide Polymorphisms. , 2007, , .		3
212	High-throughput protein crystallization on the World Community Grid and the GPU. <i>Journal of Physics: Conference Series</i> , 2012, 341, 012027.	0.4	3
213	Protein-Protein Interaction Databases. , 2019, , 988-996.		3
214	CD40L modulates transcriptional signatures of neutrophils in the bone marrow associated with development and trafficking. <i>JCI Insight</i> , 2021, 6, .	5.0	3
215	Motivators, barriers, and opportunity for eHealth to encourage physical activity in axial spondyloarthritis: a qualitative descriptive study. <i>Arthritis Care and Research</i> , 2022, 74, 50-58.	3.4	3
216	Germline Mutation in MUS81 Resulting in Impaired Protein Stability is Associated with Familial Breast and Thyroid Cancer. <i>Cancers</i> , 2020, 12, 1289.	3.7	3

#	ARTICLE	IF	CITATIONS
217	Osteoarthritis Data Integration Portal (OsteoDIP): A web-based gene and non-coding RNA expression database. <i>Osteoarthritis and Cartilage Open</i> , 2022, 4, 100237.	2.0	3
218	sbv IMPROVER Diagnostic Signature Challenge. <i>Systems Biomedicine (Austin, Tex )</i> , 2013, 1, 208-216.	0.7	2
219	Where are we at regarding species translation? A review of the sbv IMPROVER challenge. <i>Bioinformatics</i> , 2015, 31, 451-452.	4.1	2
220	Visualization of Biomedical Networks. , 2019, , 1016-1035.		2
221	<i>Citrobacter rodentium</i> alters the mouse colonic miRNome. <i>Genes and Immunity</i> , 2019, 20, 207-213.	4.1	2
222	Zinc finger protein-440 promotes cartilage degenerative mechanisms in human facet and knee osteoarthritis chondrocytes. <i>Osteoarthritis and Cartilage</i> , 2021, 29, 372-379.	1.3	2
223	The KBMS Project and Beyond. <i>Lecture Notes in Computer Science</i> , 2009, , 466-482.	1.3	2
224	P2.11-19 MicroRNAs as Liquid Biopsy Biomarkers for Early Detection in Lung Cancer.. <i>Journal of Thoracic Oncology</i> , 2018, 13, S785-S786.	1.1	1
225	Effect of autotaxin inhibition in a surgically-induced mouse model of osteoarthritis. <i>Osteoarthritis and Cartilage Open</i> , 2020, 2, 100080.	2.0	1
226	miRAnnoâ€”network-based functional microRNA annotation. <i>Bioinformatics</i> , 2021, , .	4.1	1
227	Precision Medicine for Osteoarthritis. , 2015, , 257-270.		1
228	Abstract 4912: Systematic, comparative network analysis on non-small cell lung cancer. <i>Cancer Research</i> , 2012, 72, 4912-4912.	0.9	1
229	Cancer informatics in the post genomic era. Toward information-based medicine. <i>Cancer Treatment and Research</i> , 2007, 137, 1-178.	0.5	1
230	Multiple Dysregulated Pathways in Nasopharyngeal Carcinoma Revealed by Gene Expression Profiling. <i>International Journal of Radiation Oncology Biology Physics</i> , 2005, 63, S373-S374.	0.8	0
231	Comparison of Machine Learning and Pattern Discovery Algorithms for the Prediction of Human Single Nucleotide Polymorphisms. , 2007, , .		0
232	Ensembles of caseâ€”based reasoning classifiers in highâ€”dimensional biological domains. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2011, 1, 164-171.	6.8	0
233	P2.01-037 Molecular Biology Underlying COPD and Lung Cancer Converge on FOXM1 Network. <i>Journal of Thoracic Oncology</i> , 2017, 12, S807-S808.	1.1	0
234	P3.01-049 ELF3 Overexpression Leads to Oncogenic Reprogramming of Protein Interactions Exposing Therapeutically Actionable Targets. <i>Journal of Thoracic Oncology</i> , 2017, 12, S1149-S1150.	1.1	0

#	ARTICLE	IF	CITATIONS
235	MAO2.03 Expression of Oncofetal miRNAs Inactivates NFIB, a Developmental Transcription Factor Linked to Tumor Aggressiveness in Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2017, 12, S349-S350.	1.1	0
236	Competitive in vivo screening of 64 candidate leukemia stem cell self-renewal regulators selects for genes protracting stem cell latency. <i>Experimental Hematology</i> , 2017, 53, S91.	0.4	0
237	P3.02-094 Identification of Oncofetal piRNAs in Lung. <i>Journal of Thoracic Oncology</i> , 2017, 12, S2271-S2272.	1.1	0
238	Unique circulating microRNA profile identified in early radiographic knee osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2020, 28, S55-S56.	1.3	0
239	Integrative analysis of layers of data in hepatocellular carcinoma reveals pathway dependencies. <i>World Journal of Hepatology</i> , 2021, 13, 94-108.	2.0	0
240	Reactivation of Multiple Fetal miRNAs in Lung Adenocarcinoma. <i>Cancers</i> , 2021, 13, 2686.	3.7	0
241	D6-05: Genomic profile of invasion in lung adenocarcinoma with bronchioloalveolar features (AWBF). <i>Journal of Thoracic Oncology</i> , 2007, 2, S408.	1.1	0
242	Comparing MicroRNA Expression In Aggressive and Indolent Non-Hodgkin Lymphomas Identifies a Prognostic Signature for Mantle Cell Lymphoma. <i>Blood</i> , 2010, 116, 800-800.	1.4	0
243	A 7-Gene MicroRNA Signature Characteristic of Mantle Cell Lymphoma Reveals Focal Adhesion and Integrin Signalling, Proteasome-Mediated Degradation, and the PI3K Signalling Cascade As Important to MCL Pathogenesis. <i>Blood</i> , 2012, 120, 1586-1586.	1.4	0
244	Prediction and knowledge mining with in vitro fertilization data. <i>ACM SIGBIO Newsletter</i> , 1998, 18, 11-11.	0.1	0
245	Proteomics and Bioinformatics in Biomedical Research. <i>Cancer Genomics and Proteomics</i> , 2006, 3, 11-28.	2.0	0
246	Pathway Enrichment Analysis of Microarray Data. <i>Methods in Molecular Biology</i> , 2022, 2401, 147-159.	0.9	0
247	Improving Analysis and Annotation of Microarray Data with Protein Interactions. <i>Methods in Molecular Biology</i> , 2022, 2401, 51-68.	0.9	0