Igor Jurisica

List of Publications by Year
in descending order

247 papers	20,919 citations	10986 71 h-index	11308 136 g-index
281 all docs	281 docs citations	281 times ranked	30566 citing authors

#	Article	IF	Citations
1	Motivators, barriers, and opportunity for e‐health to encourage physical activity in axial spondyloarthritis: a qualitative descriptive study. Arthritis Care and Research, 2022, 74, 50-58.	3.4	3
2	IID 2021: towards context-specific protein interaction analyses by increased coverage, enhanced annotation and enrichment analysis. Nucleic Acids Research, 2022, 50, D640-D647.	14.5	38
3	Information fusion as an integrative cross-cutting enabler to achieve robust, explainable, and trustworthy medical artificial intelligence. Information Fusion, 2022, 79, 263-278.	19.1	100
4	Osteoarthritis Data Integration Portal (OsteoDIP): A web-based gene and non-coding RNA expression database. Osteoarthritis and Cartilage Open, 2022, 4, 100237.	2.0	3
5	Circulating microRNAs differentiate fast-progressing from slow-progressing and non-progressing knee osteoarthritis in the Osteoarthritis Initiative cohort. Therapeutic Advances in Musculoskeletal Disease, 2022, 14, 1759720X2210829.	2.7	12
6	CFTR interactome mapping using the mammalian membrane two‐hybrid high‐throughput screening system. Molecular Systems Biology, 2022, 18, e10629.	7.2	13
7	Changes in circulating microRNAs following head impacts in soccer. Brain Injury, 2022, 36, 560-571.	1.2	6
8	Severe COVID-19 Shares a Common Neutrophil Activation Signature with Other Acute Inflammatory States. Cells, 2022, 11, 847.	4.1	27
9	Autoantibodies targeting GPCRs and RAS-related molecules associate with COVID-19 severity. Nature Communications, 2022, 13, 1220.	12.8	74
10	Pathway Enrichment Analysis of Microarray Data. Methods in Molecular Biology, 2022, 2401, 147-159.	0.9	0
11	Improving Analysis and Annotation of Microarray Data with Protein Interactions. Methods in Molecular Biology, 2022, 2401, 51-68.	0.9	0
12	Sportomics suggests that albuminuria is a sensitive biomarker of hydration in cross combat. Scientific Reports, 2022, 12, 8150.	3.3	4
13	Contribution of <scp>MicroRNA</scp>‐27b‐3p to Synovial Fibrotic Responses in Knee Osteoarthritis. Arthritis and Rheumatology, 2022, 74, 1928-1942.	5.6	7
14	MicroRNA‐34a‐5p Promotes Joint Destruction During Osteoarthritis. Arthritis and Rheumatology, 2021, 73, 426-439.	5.6	56
15	Integrative analysis of layers of data in hepatocellular carcinoma reveals pathway dependencies. World Journal of Hepatology, 2021, 13, 94-108.	2.0	0
16	Normothermic Ex-vivo Kidney Perfusion in a Porcine Auto-Transplantation Model Preserves the Expression of Key Mitochondrial Proteins: An Unbiased Proteomics Analysis. Molecular and Cellular Proteomics, 2021, 20, 100101.	3.8	6
17	Zinc finger protein-440 promotes cartilage degenerative mechanisms in human facet and knee osteoarthritis chondrocytes. Osteoarthritis and Cartilage, 2021, 29, 372-379.	1.3	2
18	The relationship between cytokine and neutrophil gene network distinguishes SARS-CoV-2‐infected patients by sex and age. JCI Insight, 2021, 6, .	5.0	17

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19	Reactivation of Multiple Fetal miRNAs in Lung Adenocarcinoma. Cancers, 2021, 13, 2686.	3.7	0
20	miRAnno—network-based functional microRNA annotation. Bioinformatics, 2021, , .	4.1	1
21	CD40L modulates transcriptional signatures of neutrophils in the bone marrow associated with development and trafficking. JCI Insight, 2021, 6, .	5.0	3
22	Increased Autoantibodies Against Ro/SS-A, CENP-B, and La/SS-B in Patients With Kidney Allograft Antibody-mediated Rejection. Transplantation Direct, 2021, 7, e768.	1.6	9
23	The non-coding RNA interactome in joint health and disease. Nature Reviews Rheumatology, 2021, 17, 692-705.	8.0	102
24	Mapping the Phospho-dependent ALK Interactome to Identify Novel Components in ALK Signaling. Journal of Molecular Biology, 2021, 433, 167283.	4.2	9
25	Mechanical Stiffness Controls Dendritic Cell Metabolism and Function. Cell Reports, 2021, 34, 108609.	6.4	98
26	The network interplay of interferon and Toll-like receptor signaling pathways in the anti-Candida immune response. Scientific Reports, 2021, 11, 20281.	3.3	5
27	Macrophage migration inhibitory factor drives pathology in a mouse model of spondyloarthritis and is associated with human disease. Science Translational Medicine, 2021, 13, eabg1210.	12.4	28
28	Comprehensive pathway enrichment analysis workflows: COVID-19 case study. Briefings in Bioinformatics, 2021, 22, 676-689.	6.5	5
29	A Network Biology Approach to Understanding the Tissue-Specific Roles of Non-Coding RNAs in Arthritis. Frontiers in Endocrinology, 2021, 12, 744747.	3.5	5
30	Estrogen Receptor 1 Inhibition of Wnt/β-Catenin Signaling Contributes to Sex Differences in Hepatocarcinogenesis. Frontiers in Oncology, 2021, 11, 777834.	2.8	12
31	Peripheral microRNA alteration and pathway signaling after mild traumatic brain injur. General Physiology and Biophysics, 2021, 40, 523-539.	0.9	4
32	pathDIP 4: an extended pathway annotations and enrichment analysis resource for human, model organisms and domesticated species. Nucleic Acids Research, 2020, 48, D479-D488.	14.5	38
33	Extracellular Matrix Injury of Kidney Allografts in Antibody-Mediated Rejection: A Proteomics Study. Journal of the American Society of Nephrology: JASN, 2020, 31, 2705-2724.	6.1	29
34	Towards a unified open access dataset of molecular interactions. Nature Communications, 2020, 11, 6144.	12.8	49
35	Effect of autotaxin inhibition in a surgically-induced mouse model of osteoarthritis. Osteoarthritis and Cartilage Open, 2020, 2, 100080.	2.0	1
36	Sequencing identifies a distinct signature of circulating microRNAs in early radiographic knee osteoarthritis. Osteoarthritis and Cartilage, 2020, 28, 1471-1481.	1.3	43

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37	Tumor cell endogenous HIF-1Î± activity induces aberrant angiogenesis and interacts with TRAF6 pathway required for colorectal cancer development. Neoplasia, 2020, 22, 745-758.	5.3	9
38	Split Intein-Mediated Protein Ligation for detecting protein-protein interactions and their inhibition. Nature Communications, 2020, 11, 2440.	12.8	33
39	Unique circulating microrna profile identified in early radiographic knee osteoarthritis. Osteoarthritis and Cartilage, 2020, 28, S55-S56.	1.3	0
40	Urinary proteomics links keratan sulfate degradation and lysosomal enzymes to early type 1 diabetes. PLoS ONE, 2020, 15, e0233639.	2.5	6
41	A 4-gene signature from histologically normal surgical margins predicts local recurrence in patients with oral carcinoma: clinical validation. Scientific Reports, 2020, 10, 1713.	3.3	15
42	Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRASG13D. Nature Communications, 2020, 11, 499.	12.8	42
43	GSOAP: a tool for visualization of gene set over-representation analysis. Bioinformatics, 2020, 36, 2923-2925.	4.1	12
44	Physiological Tau Interactome in Brain and Its Link to Tauopathies. Journal of Proteome Research, 2020, 19, 2429-2442.	3.7	22
45	Informed Use of Proteinâ€"Protein Interaction Data: A Focus on the Integrated Interactions Database (IID). Methods in Molecular Biology, 2020, 2074, 125-134.	0.9	12
46	BioPAX-Parser: parsing and enrichment analysis of BioPAX pathways. Bioinformatics, 2020, 36, 4377-4378.	4.1	19
47	The IMEx coronavirus interactome: an evolving map of *Coronaviridae*â€"host molecular interactions. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	34
48	Germline Mutation in MUS81 Resulting in Impaired Protein Stability is Associated with Familial Breast and Thyroid Cancer. Cancers, 2020, 12, 1289.	3.7	3
49	Visualization of Biomedical Networks. , 2019, , 1016-1035.		2
50	Two Decades of Biological Pathway Databases: Results and Challenges. , 2019, , 1071-1084.		5
51	Proteinâ€"Protein Interaction Databases. , 2019, , 988-996.		3
52	Citrobacter rodentium alters the mouse colonic miRNome. Genes and Immunity, 2019, 20, 207-213.	4.1	2
53	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. Nature Communications, 2019, 10, 10.	12.8	193
54	Why imaging data alone is not enough: AI-based integration of imaging, omics, and clinical data. European Journal of Nuclear Medicine and Molecular Imaging, 2019, 46, 2722-2730.	6.4	69

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55	*TP53* mutations in high grade serous ovarian cancer and impact on clinical outcomes: a comparison of next generation sequencing and bioinformatics analyses. International Journal of Gynecological Cancer, 2019, 29, 346-352.	2.5	29
56	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
57	A stemness screen reveals C3orf54/INKA1 as a promoter of human leukemia stem cell latency. Blood, 2019, 133, 2198-2211.	1.4	25
58	Urine Angiotensin II Signature Proteins as Markers of Fibrosis in Kidney Transplant Recipients. Transplantation, 2019, 103, e146-e158.	1.0	8
59	Epithelial tumor suppressor ELF3 is a lineage-specific amplified oncogene in lung adenocarcinoma. Nature Communications, 2019, 10, 5438.	12.8	41
60	IID 2018 update: context-specific physical protein–protein interactions in human, model organisms and domesticated species. Nucleic Acids Research, 2019, 47, D581-D589.	14.5	164
61	Failed immune responses across multiple pathologies share pan-tumor and circulating lymphocytic targets. Journal of Clinical Investigation, 2019, 129, 2463-2479.	8.2	4
62	The ablation of the matricellular protein EMILIN2 causes defective vascularization due to impaired EGFR-dependent IL-8 production affecting tumor growth. Oncogene, 2018, 37, 3399-3414.	5.9	51
63	mirDIP 4.1—integrative database of human microRNA target predictions. Nucleic Acids Research, 2018, 46, D360-D370.	14.5	430
64	In silico cancer research towards 3R. BMC Cancer, 2018, 18, 408.	2.6	83
65	Modeling tumor progression via the comparison of stage-specific graphs. Methods, 2018, 132, 34-41.	3.8	7
66	Differentially expressed microRNAs in lung adenocarcinoma invert effects of copy number aberrations of prognostic genes. Oncotarget, 2018, 9, 9137-9155.	1.8	13
67	P2.11-19 MicroRNAs as Liquid Biopsy Biomarkers for Early Detection in Lung Cancer.. Journal of Thoracic Oncology, 2018, 13, S785-S786.	1.1	1
68	Therapeutic Targeting of the Premetastatic Stage in Human Lung-to-Brain Metastasis. Cancer Research, 2018, 78, 5124-5134.	0.9	35
69	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. BMC Bioinformatics, 2018, 19, 134.	2.6	47
70	SDREGION. , 2018, , .		8
71	The complex landscape of microRNAs in articular cartilage: biology, pathology, and therapeutic targets. JCI Insight, 2018, 3, .	5.0	76
72	Ubiquitin ligase RNF8 suppresses Notch signaling to regulate mammary development and tumorigenesis. Journal of Clinical Investigation, 2018, 128, 4525-4542.	8.2	31

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73	Systematic Identification of Oncogenic EGFR Interaction Partners. Journal of Molecular Biology, 2017, 429, 280-294.	4.2	22
74	P2.01-037 Molecular Biology Underlying COPD and Lung Cancer Converge on FOXM1 Network. Journal of Thoracic Oncology, 2017, 12, S807-S808.	1.1	0
75	An Integrated Approach Identifies Mediators of Local Recurrence in Head and Neck Squamous Carcinoma. Clinical Cancer Research, 2017, 23, 3769-3780.	7.0	36
76	P3.01-049 ELF3 Overexpression Leads to Oncogenic Reprogramming of Protein Interactions Exposing Therapeutically Actionable Targets. Journal of Thoracic Oncology, 2017, 12, S1149-S1150.	1.1	0
77	MA02.03 Expression of Oncofetal miRNAs Inactivates NFIB, a Developmental Transcription Factor Linked to Tumor Aggressiveness in Lung Adenocarcinoma. Journal of Thoracic Oncology, 2017, 12, S349-S350.	1.1	0
78	Systematic protein–protein interaction mapping for clinically relevant human GPCRs. Molecular Systems Biology, 2017, 13, 918.	7.2	63
79	A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome. Molecular Cell, 2017, 65, 347-360.	9.7	123
80	Competitive in vivo screening of 64 candidate leukemia stem cell self-renewal regulators selects for genes protracting stem cell latency. Experimental Hematology, 2017, 53, S91.	0.4	0
81	RNAi screen identifies essential regulators of human brain metastasis-initiating cells. Acta Neuropathologica, 2017, 134, 923-940.	7.7	26
82	Prediction of Protein–Protein Interactions. Current Protocols in Bioinformatics, 2017, 60, 8.2.1-8.2.14.	25.8	18
83	Molecular heterogeneity of non-small cell lung carcinoma patient-derived xenografts closely reflect their primary tumors. International Journal of Cancer, 2017, 140, 662-673.	5.1	67
84	P3.02-094 Identification of Oncofetal piRNAs in Lung. Journal of Thoracic Oncology, 2017, 12, S2271-S2272.	1.1	0
85	pathDIP: an annotated resource for known and predicted human gene-pathway associations and pathway enrichment analysis. Nucleic Acids Research, 2017, 45, D419-D426.	14.5	105
86	HABP2 p.G534E variant in patients with family history of thyroid and breast cancer. Oncotarget, 2017, 8, 40896-40905.	1.8	7
87	Machine Learning for In Silico Modeling of Tumor Growth. Lecture Notes in Computer Science, 2016, , 415-434.	1.3	7
88	Identification of synovial fluid microRNA signature in knee osteoarthritis: differentiating early- and late-stage knee osteoarthritis. Osteoarthritis and Cartilage, 2016, 24, 1577-1586.	1.3	98
89	Integrated interactions database: tissue-specific view of the human and model organism interactomes. Nucleic Acids Research, 2016, 44, D536-D541.	14.5	212
90	Robust quantitative scratch assay. Bioinformatics, 2016, 32, 1439-1440.	4.1	11

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91	Developmental transcription factor NFIB is a putative target of oncofetal miRNAs and is associated with tumour aggressiveness in lung adenocarcinoma. Journal of Pathology, 2016, 240, 161-172.	4.5	42
92	Circulating plant miRNAs can regulate human gene expression in vitro. Scientific Reports, 2016, 6, 32773.	3.3	29
93	Quantification of angiotensin II-regulated proteins in urine of patients with polycystic and other chronic kidney diseases by selected reaction monitoring. Clinical Proteomics, 2016, 13, 16.	2.1	24
94	MYC interaction with the tumor suppressive SWI/SNF complex member INI1 regulates transcription and cellular transformation. Cell Cycle, 2016, 15, 1693-1705.	2.6	37
95	Uninterrupted Sedentary Behavior Downregulates *BRCA1* Gene Expression. Cancer Prevention Research, 2016, 9, 83-88.	1.5	13
96	Protein interactome mining defines melatonin MT$_1$ receptors as integral component of presynaptic protein complexes of neurons. Journal of Pineal Research, 2016, 60, 95-108.	7.4	42
97	Integrin α11β1 regulates cancer stromal stiffness and promotes tumorigenicity and metastasis in non-small cell lung cancer. Oncogene, 2016, 35, 1899-1908.	5.9	138
98	Identification of microRNA-181a-5p and microRNA-4454 as mediators of facet cartilage degeneration. JCI Insight, 2016, 1, e86820.	5.0	60
99	Integrative transcriptome analysis identifies deregulated microRNA-transcription factor networks in lung adenocarcinoma. Oncotarget, 2016, 7, 28920-28934.	1.8	49
100	Comparative network analysis via differential graphlet communities. Proteomics, 2015, 15, 608-617.	2.2	21
101	Fundamentals of protein interaction network mapping. Molecular Systems Biology, 2015, 11, 848.	7.2	226
102	Potential role of CC chemokine receptor 6 in prediction of late-onset cytomegalovirus infection following solid organ transplant. Clinical Transplantation, 2015, 29, 492-498.	1.6	5
103	An integrative approach for the identification of prognostic and predictive biomarkers in rectal cancer. Oncotarget, 2015, 6, 32561-32574.	1.8	45
104	Integrating RAS Status into Prognostic Signatures for Adenocarcinomas of the Lung. Clinical Cancer Research, 2015, 21, 1477-1486.	7.0	13
105	Where are we at regarding species translation? A review of the sbv IMPROVER challenge. Bioinformatics, 2015, 31, 451-452.	4.1	2
106	Clinical Utility of Patient-Derived Xenografts to Determine Biomarkers of Prognosis and Map Resistance Pathways in *EGFR*-Mutant Lung Adenocarcinoma. Journal of Clinical Oncology, 2015, 33, 2472-2480.	1.6	94
107	A functional biological network centered on XRCC3: a new possible marker of chemoradiotherapy resistance in rectal cancer patients. Cancer Biology and Therapy, 2015, 16, 1160-1171.	3.4	49
108	Prioritizing Therapeutics for Lung Cancer: An Integrative Meta-analysis of Cancer Gene Signatures and Chemogenomic Data. PLoS Computational Biology, 2015, 11, e1004068.	3.2	36

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109	BioID identifies novel c-MYC interacting partners in cultured cells and xenograft tumors. Journal of Proteomics, 2015, 118, 95-111.	2.4	112
110	In silico prediction of physical protein interactions and characterization of interactome orphans. Nature Methods, 2015, 12, 79-84.	19.0	148
111	Myc and its interactors take shape. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2015, 1849, 469-483.	1.9	102
112	Precision Medicine for Osteoarthritis. , 2015, , 257-270.		1
113	STAT3 pathway regulates lung-derived brain metastasis initiating cell capacity through miR-21 activation. Oncotarget, 2015, 6, 27461-27477.	1.8	55
114	Tumour genomic and microenvironmental heterogeneity for integrated prediction of 5-year biochemical recurrence of prostate cancer: a retrospective cohort study. Lancet Oncology, The, 2014, 15, 1521-1532.	10.7	291
115	Smoking status impacts microRNA mediated prognosis and lung adenocarcinoma biology. BMC Cancer, 2014, 14, 778.	2.6	41
116	Kinome-wide screening of HER2+ breast cancer cells for molecules that mediate cell proliferation or sensitize cells to trastuzumab therapy. Oncogenesis, 2014, 3, e133-e133.	4.9	18
117	Knowledge Discovery and interactive Data Mining in Bioinformatics - State-of-the-Art, future challenges and research directions. BMC Bioinformatics, 2014, 15, I1.	2.6	161
118	Validation of a Histology-Independent Prognostic Gene Signature for Early-Stage, Non–Small-Cell Lung Cancer Including Stage IA Patients. Journal of Thoracic Oncology, 2014, 9, 59-64.	1.1	243
119	Recurrent genomic alterations in sequential progressive leukoplakia and oral cancer: drivers of oral tumorigenesis?. Human Molecular Genetics, 2014, 23, 2618-2628.	2.9	46
120	CHIP-MYTH: A novel interactive proteomics method for the assessment of agonist-dependent interactions of the human β2-adrenergic receptor. Biochemical and Biophysical Research Communications, 2014, 445, 746-756.	2.1	17
121	The mammalian-membrane two-hybrid assay (MaMTH) for probing membrane-protein interactions in human cells. Nature Methods, 2014, 11, 585-592.	19.0	149
122	Visual Data Mining: Effective Exploration of the Biological Universe. Lecture Notes in Computer Science, 2014, , 19-33.	1.3	17
123	Integration, visualization and analysis of human interactome. Biochemical and Biophysical Research Communications, 2014, 445, 757-773.	2.1	37
124	Knowledge Discovery and Data Mining in Biomedical Informatics: The Future Is in Integrative, Interactive Machine Learning Solutions. Lecture Notes in Computer Science, 2014, , 1-18.	1.3	78
125	<i>NBN</i>gain is predictive for adverse outcome following image-guided radiotherapy for localized prostate cancer. Oncotarget, 2014, 5, 11081-11090.	1.8	30
126	Case-Based Reasoning for Biomedical Informatics and Medicine. , 2014, , 207-221.		5

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127	Novel semantic similarity measure improves an integrative approach to predicting gene functional associations. BMC Systems Biology, 2013, 7, 22.	3.0	13
128	MicroRNA Signature Obtained From the Comparison of Aggressive With Indolent Non-Hodgkin Lymphomas: Potential Prognostic Value in Mantle-Cell Lymphoma. Journal of Clinical Oncology, 2013, 31, 2903-2911.	1.6	37
129	Flotillin-2 deficiency leads to reduced lung metastases in a mouse breast cancer model. Oncogene, 2013, 32, 4989-4994.	5.9	51
130	Visual Data Mining of Biological Networks: One Size Does Not Fit All. PLoS Computational Biology, 2013, 9, e1002833.	3.2	19
131	sbv IMPROVER Diagnostic Signature Challenge. Systems Biomedicine (Austin, Tex), 2013, 1, 208-216.	0.7	2
132	An Integrative Genomic and Transcriptomic Analysis Reveals Potential Targets Associated with Cell Proliferation in Uterine Leiomyomas. PLoS ONE, 2013, 8, e57901.	2.5	22
133	L1 Cell Adhesion Molecule Promotes Tumorigenicity and Metastatic Potential in Non–Small Cell Lung Cancer. Clinical Cancer Research, 2012, 18, 1914-1924.	7.0	48
134	NetwoRx: connecting drugs to networks and phenotypes in Saccharomyces cerevisiae. Nucleic Acids Research, 2012, 41, D720-D727.	14.5	8
135	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	19.0	500
136	*NKX3.1* Haploinsufficiency Is Prognostic for Prostate Cancer Relapse following Surgery or Image-Guided Radiotherapy. Clinical Cancer Research, 2012, 18, 308-316.	7.0	43
137	SCRIPDB: a portal for easy access to syntheses, chemicals and reactions in patents. Nucleic Acids Research, 2012, 40, D428-D433.	14.5	22
138	High-throughput protein crystallization on the World Community Grid and the GPU. Journal of Physics: Conference Series, 2012, 341, 012027.	0.4	3
139	Network-based characterization of drug-regulated genes, drug targets, and toxicity. Methods, 2012, 57, 499-507.	3.8	88
140	Exploiting the noise: improving biomarkers with ensembles of data analysis methodologies. Genome Medicine, 2012, 4, 84.	8.2	15
141	The Murine Caecal MicroRNA Signature Depends on the Presence of the Endogenous Microbiota. International Journal of Biological Sciences, 2012, 8, 171-186.	6.4	102
142	Allelic loss of the loci containing the androgen synthesis gene, *StAR*, is prognostic for relapse in intermediate-risk prostate cancer. Prostate, 2012, 72, 1295-1305.	2.3	10
143	Copy number alterations of *c-MYC* and *PTEN* are prognostic factors for relapse after prostate cancer radiotherapy. Cancer, 2012, 118, 4053-4062.	4.1	105
144	Abstract 4912: Systematic, comparative network analysis on non-small cell lung cancer. Cancer Research, 2012, 72, 4912-4912.	0.9	1

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145	Protease nexin 1 inhibits hedgehog signaling in prostate adenocarcinoma. Journal of Clinical Investigation, 2012, 122, 4025-4036.	8.2	39
146	Algorithms for Systematic Identification of Small Subgraphs. Methods in Molecular Biology, 2012, 804, 219-244.	0.9	5
147	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. Blood, 2012, 120, 1586-1586.	1.4	0
148	Construction of New Medicines via Game Proof Search. Proceedings of the AAAI Conference on Artificial Intelligence, 2012, 26, 1564-1570.	4.9	8
149	NAViGaTOR: Large Scalable and Interactive Navigation and Analysis of Large Graphs. Internet Mathematics, 2011, 7, 314-347.	0.7	13
150	Primary Tumor Xenografts of Human Lung Adeno and Squamous Cell Carcinoma Express Distinct Proteomic Signatures. Journal of Proteome Research, 2011, 10, 161-174.	3.7	27
151	Isolation of Single Human Hematopoietic Stem Cells Capable of Long-Term Multilineage Engraftment. Science, 2011, 333, 218-221.	12.6	717
152	Stem cell gene expression programs influence clinical outcome in human leukemia. Nature Medicine, 2011, 17, 1086-1093.	30.7	894
153	Sex-specific differences in placental global gene expression in pregnancies complicated by asthma. Placenta, 2011, 32, 570-578.	1.5	92
154	In-Depth Proteomics of Ovarian Cancer Ascites: Combining Shotgun Proteomics and Selected Reaction Monitoring Mass Spectrometry. Journal of Proteome Research, 2011, 10, 2286-2299.	3.7	72
155	Ensembles of caseâ€based reasoning classifiers in highâ€dimensional biological domains. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2011, 1, 164-171.	6.8	0
156	Integrative computational biology for cancer research. Human Genetics, 2011, 130, 465-481.	3.8	28
157	A gene signature in histologically normal surgical margins is predictive of oral carcinoma recurrence. BMC Cancer, 2011, 11, 437.	2.6	117
158	mRNA transcript quantification in archival samples using multiplexed, color-coded probes. BMC Biotechnology, 2011, 11, 46.	3.3	234
159	Prognostic gene-expression signature of carcinoma-associated fibroblasts in non-small cell lung cancer. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7160-7165.	7.1	317
160	Hypoxia Predicts Aggressive Growth and Spontaneous Metastasis Formation from Orthotopically Grown Primary Xenografts of Human Pancreatic Cancer. Cancer Research, 2011, 71, 3110-3120.	0.9	241
161	Role of Pirh2 in Mediating the Regulation of p53 and c-Myc. PLoS Genetics, 2011, 7, e1002360.	3.5	65
162	NAViGaTing the Micronome â€" Using Multiple MicroRNA Prediction Databases to Identify Signalling Pathway-Associated MicroRNAs. PLoS ONE, 2011, 6, e17429.	2.5	207

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163	Automated Microinjection of Recombinant BCL-X into Mouse Zygotes Enhances Embryo Development. PLoS ONE, 2011, 6, e21687.	2.5	36
164	Exploiting the mevalonate pathway to distinguish statin-sensitive multiple myeloma. Blood, 2010, 115, 4787-4797.	1.4	81
165	Protein crystallization analysis on the World Community Grid. Journal of Structural and Functional Genomics, 2010, 11, 61-69.	1.2	40
166	Evaluation of linguistic features useful in extraction of interactions from PubMed; Application to annotating known, high-throughput and predicted interactions in I2D. Bioinformatics, 2010, 26, 111-119.	4.1	63
167	Re: Gene Expression-Based Prognostic Signatures in Lung Cancer: Ready for Clinical Use?. Journal of the National Cancer Institute, 2010, 102, 1677-1678.	6.3	7
168	Prognostic and Predictive Gene Signature for Adjuvant Chemotherapy in Resected Non–Small-Cell Lung Cancer. Journal of Clinical Oncology, 2010, 28, 4417-4424.	1.6	405
169	Dysregulation of the mevalonate pathway promotes transformation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15051-15056.	7.1	323
170	Prognostic Gene Expression Signature for Squamous Cell Carcinoma of Lung. Clinical Cancer Research, 2010, 16, 5038-5047.	7.0	31
171	Programmed cell death 4 loss increases tumor cell invasion and is regulated by miR-21 in oral squamous cell carcinoma. Molecular Cancer, 2010, 9, 238.	19.2	121
172	Differential roles of cyclin D1 and D3 in pancreatic ductal adenocarcinoma. Molecular Cancer, 2010, 9, 24.	19.2	45
173	The FlowVizMenu and Parallel Scatterplot Matrix: Hybrid Multidimensional Visualizations for Network Exploration. IEEE Transactions on Visualization and Computer Graphics, 2010, 16, 1100-1108.	4.4	74
174	Inferring the functions of longevity genes with modular subnetwork biomarkers of Caenorhabditis elegans aging. Genome Biology, 2010, 11, R13.	9.6	50
175	Comprehensive MicroRNA Profiling for Head and Neck Squamous Cell Carcinomas. Clinical Cancer Research, 2010, 16, 1129-1139.	7.0	353
176	Comparing MicroRNA Expression In Aggressive and Indolent Non-Hodgkin Lymphomas Identifies a Prognostic Signature for Mantle Cell Lymphoma. Blood, 2010, 116, 800-800.	1.4	0
177	Identification of a microRNA signature associated with progression of leukoplakia to oral carcinoma. Human Molecular Genetics, 2009, 18, 4818-4829.	2.9	223
178	Prognostic gene signatures for non-small-cell lung cancer. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2824-2828.	7.1	182
179	NAViGaTOR: Network Analysis, Visualization and Graphing Toronto. Bioinformatics, 2009, 25, 3327-3329.	4.1	234
180	Lung cancer: Developmental networks gone awry?. Cancer Biology and Therapy, 2009, 8, 312-318.	3.4	16

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181	Regulation of Epidermal Growth Factor Receptor Trafficking by Lysine Deacetylase HDAC6. Science Signaling, 2009, 2, ra84.	3.6	140
182	A comprehensive catalogue of functional genetic variations in the EGFR pathway: Protein–protein interaction analysis reveals novel genes and polymorphisms important for cancer research. International Journal of Cancer, 2009, 125, 1257-1265.	5.1	13
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