Igor Jurisica

List of Publications by Year
in descending order

247 papers	20,919 citations	10956 71 h-index	11288 136 g-index
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. Nature Medicine, 2008, 14, 822-827.	15.2	1,015
2	Stem cell gene expression programs influence clinical outcome in human leukemia. Nature Medicine, 2011, 17, 1086-1093.	15.2	894
3	Isolation of Single Human Hematopoietic Stem Cells Capable of Long-Term Multilineage Engraftment. Science, 2011, 333, 218-221.	6.0	717
4	High-Throughput Mapping of a Dynamic Signaling Network in Mammalian Cells. Science, 2005, 307, 1621-1625.	6.0	651
5	Protein complex prediction via cost-based clustering. Bioinformatics, 2004, 20, 3013-3020.	1.8	620
6	Online Predicted Human Interaction Database. Bioinformatics, 2005, 21, 2076-2082.	1.8	557
7	Modeling interactome: scale-free or geometric?. Bioinformatics, 2004, 20, 3508-3515.	1.8	544
8	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	9.0	500
9	The c-Myc Oncogene Directly Induces the H19 Noncoding RNA by Allele-Specific Binding to Potentiate Tumorigenesis. Cancer Research, 2006, 66, 5330-5337.	0.4	451
10	mirDIP 4.1–integrative database of human microRNA target predictions. Nucleic Acids Research, 2018, 46, D360-D370.	6.5	430
11	Prognostic and Predictive Gene Signature for Adjuvant Chemotherapy in Resected Non–Small-Cell Lung Cancer. Journal of Clinical Oncology, 2010, 28, 4417-4424.	0.8	405
12	Functional topology in a network of protein interactions. Bioinformatics, 2004, 20, 340-348.	1.8	388
13	TAp73 knockout shows genomic instability with infertility and tumor suppressor functions. Genes and Development, 2008, 22, 2677-2691.	2.7	378
14	Comprehensive MicroRNA Profiling for Head and Neck Squamous Cell Carcinomas. Clinical Cancer Research, 2010, 16, 1129-1139.	3.2	353
15	Molecular Evidence of Placental Hypoxia in Preeclampsia. Journal of Clinical Endocrinology and Metabolism, 2005, 90, 4299-4308.	1.8	343
16	Dysregulation of the mevalonate pathway promotes transformation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15051-15056.	3.3	323
17	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.	3.3	317
18	Unequal evolutionary conservation of human protein interactions in interologous networks. Genome Biology, 2007, 8, R95.	13.9	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. Lancet Oncology, The, 2014, 15, 1521-1532.	5.1	291
20	Validation of a Histology-Independent Prognostic Gene Signature for Early-Stage, Nonâ€"Small-Cell Lung Cancer Including Stage IA Patients. Journal of Thoracic Oncology, 2014, 9, 59-64.	0.5	243
21	Hypoxia Predicts Aggressive Growth and Spontaneous Metastasis Formation from Orthotopically Grown Primary Xenografts of Human Pancreatic Cancer. Cancer Research, 2011, 71, 3110-3120.	0.4	241
22	NAViGaTOR: Network Analysis, Visualization and Graphing Toronto. Bioinformatics, 2009, 25, 3327-3329.	1.8	234
23	mRNA transcript quantification in archival samples using multiplexed, color-coded probes. BMC Biotechnology, 2011, 11, 46.	1.7	234
24	Three-Gene Prognostic Classifier for Early-Stage Nonâ€"Small-Cell Lung Cancer. Journal of Clinical Oncology, 2007, 25, 5562-5569.	0.8	226
25	Fundamentals of protein interaction network mapping. Molecular Systems Biology, 2015, 11, 848.	3.2	226
26	Identification of a microRNA signature associated with progression of leukoplakia to oral carcinoma. Human Molecular Genetics, 2009, 18, 4818-4829.	1.4	223
27	Robust global micro-RNA profiling with formalin-fixed paraffin-embedded breast cancer tissues. Laboratory Investigation, 2009, 89, 597-606.	1.7	221
28	Integrated interactions database: tissue-specific view of the human and model organism interactomes. Nucleic Acids Research, 2016, 44, D536-D541.	6.5	212
29	NAViGaTing the Micronome â€" Using Multiple MicroRNA Prediction Databases to Identify Signalling Pathway-Associated MicroRNAs. PLoS ONE, 2011, 6, e17429.	1.1	207
30	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. Nature Communications, 2019, 10, 10.	5.8	193
31	Molecular profiling of non-small cell lung cancer and correlation with disease-free survival. Cancer Research, 2002, 62, 3005-8.	0.4	183
32	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.	3.3	182
33	Alterations in mitochondrial membrane potential during preimplantation stages of mouse and human embryo development. Molecular Human Reproduction, 2004, 10, 23-32.	1.3	172
34	IID 2018 update: context-specific physical proteinâ€"protein interactions in human, model organisms and domesticated species. Nucleic Acids Research, 2019, 47, D581-D589.	6.5	164
35	Knowledge Discovery and interactive Data Mining in Bioinformatics - State-of-the-Art, future challenges and research directions. BMC Bioinformatics, 2014, 15, I1.	1.2	161
36	Ontologies for Knowledge Management: An Information Systems Perspective. Knowledge and Information Systems, 2004, 6, 380-401.	2.1	155

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37	Comparative systems biology of human and mouse as a tool to guide the modeling of human placental pathology. Molecular Systems Biology, 2009, 5, 279.	3.2	151
38	The mammalian-membrane two-hybrid assay (MaMTH) for probing membrane-protein interactions in human cells. Nature Methods, 2014, 11, 585-592.	9.0	149
39	In silico prediction of physical protein interactions and characterization of interactome orphans. Nature Methods, 2015, 12, 79-84.	9.0	148
40	Integrin Â11 regulates IGF2 expression in fibroblasts to enhance tumorigenicity of human non-small-cell lung cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11754-11759.	3.3	141
41	Regulation of Epidermal Growth Factor Receptor Trafficking by Lysine Deacetylase HDAC6. Science Signaling, 2009, 2, ra84.	1.6	140
42	Integrin Î±11Î²1 regulates cancer stromal stiffness and promotes tumorigenicity and metastasis in non-small cell lung cancer. Oncogene, 2016, 35, 1899-1908.	2.6	138
43	A Proteome Resource of Ovarian Cancer Ascites: Integrated Proteomic and Bioinformatic Analyses To Identify Putative Biomarkers. Journal of Proteome Research, 2008, 7, 339-351.	1.8	134
44	Gene Expression Profiling in Cervical Cancer: An Exploration of Intratumor Heterogeneity. Clinical Cancer Research, 2006, 12, 5632-5640.	3.2	131
45	A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome. Molecular Cell, 2017, 65, 347-360.	4.5	123
46	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.	7.9	121
47	A gene signature in histologically normal surgical margins is predictive of oral carcinoma recurrence. BMC Cancer, 2011, 11, 437.	1.1	117
48	BioID identifies novel c-MYC interacting partners in cultured cells and xenograft tumors. Journal of Proteomics, 2015, 118, 95-111.	1.2	112
49	Efficient estimation of graphlet frequency distributions in protein-protein interaction networks. Bioinformatics, 2006, 22, 974-980.	1.8	109
50	Copy number alterations of <i>câ€MYC</i> and <i>PTEN</i> are prognostic factors for relapse after prostate cancer radiotherapy. Cancer, 2012, 118, 4053-4062.	2.0	105
51	pathDIP: an annotated resource for known and predicted human gene-pathway associations and pathway enrichment analysis. Nucleic Acids Research, 2017, 45, D419-D426.	6.5	105
52	The Murine Caecal MicroRNA Signature Depends on the Presence of the Endogenous Microbiota. International Journal of Biological Sciences, 2012, 8, 171-186.	2.6	102
53	Myc and its interactors take shape. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2015, 1849, 469-483.	0.9	102
54	The non-coding RNA interactome in joint health and disease. Nature Reviews Rheumatology, 2021, 17, 692-705.	3.5	102

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55	Information fusion as an integrative cross-cutting enabler to achieve robust, explainable, and trustworthy medical artificial intelligence. Information Fusion, 2022, 79, 263-278.	11.7	100
56	Identification of synovial fluid microRNA signature in knee osteoarthritis: differentiating early- and late-stage knee osteoarthritis. Osteoarthritis and Cartilage, 2016, 24, 1577-1586.	0.6	98
57	Mechanical Stiffness Controls Dendritic Cell Metabolism and Function. Cell Reports, 2021, 34, 108609.	2.9	98
58	Clinical Utility of Patient-Derived Xenografts to Determine Biomarkers of Prognosis and Map Resistance Pathways in <i>EGFR</i>-Mutant Lung Adenocarcinoma. Journal of Clinical Oncology, 2015, 33, 2472-2480.	0.8	94
59	Sex-specific differences in placental global gene expression in pregnancies complicated by asthma. Placenta, 2011, 32, 570-578.	0.7	92
60	CpG Island microarray probe sequences derived from a physical library are representative of CpG Islands annotated on the human genome. Nucleic Acids Research, 2005, 33, 2952-2961.	6.5	89
61	Case-based reasoning in IVF: prediction and knowledge mining. Artificial Intelligence in Medicine, 1998, 12, 1-24.	3.8	88
62	Network-based characterization of drug-regulated genes, drug targets, and toxicity. Methods, 2012, 57, 499-507.	1.9	88
63	Multiple dysregulated pathways in nasopharyngeal carcinoma revealed by gene expression profiling. International Journal of Cancer, 2006, 119, 2467-2475.	2.3	87
64	Impaired tRNA Nuclear Export Links DNA Damage and Cell-Cycle Checkpoint. Cell, 2007, 131, 915-926.	13.5	83
65	In silico cancer research towards 3R. BMC Cancer, 2018, 18, 408.	1.1	83
66	Exploiting the mevalonate pathway to distinguish statin-sensitive multiple myeloma. Blood, 2010, 115, 4787-4797.	0.6	81
67	Data mining for case-based reasoning in high-dimensional biological domains. IEEE Transactions on Knowledge and Data Engineering, 2005, 17, 1127-1137.	4.0	78
68	The Emerging Role of the RAB25 Small GTPase in Cancer. Traffic, 2009, 10, 1561-1568.	1.3	78
69	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.	1.0	78
70	Macromolecular crystallization in a high throughput laboratory—the search phase. Journal of Crystal Growth, 2001, 232, 591-595.	0.7	76
71	The complex landscape of microRNAs in articular cartilage: biology, pathology, and therapeutic targets. JCI Insight, 2018, 3, .	2.3	76
72	Systematic identification of SH3 domain-mediated human protein—protein interactions by peptide array target screening. Proteomics, 2007, 7, 1775-1785.	1.3	74

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73	The FlowVizMenu and Parallel Scatterplot Matrix: Hybrid Multidimensional Visualizations for Network Exploration. IEEE Transactions on Visualization and Computer Graphics, 2010, 16, 1100-1108.	2.9	74
74	Autoantibodies targeting GPCRs and RAS-related molecules associate with COVID-19 severity. Nature Communications, 2022, 13, 1220.	5.8	74
75	In-Depth Proteomics of Ovarian Cancer Ascites: Combining Shotgun Proteomics and Selected Reaction Monitoring Mass Spectrometry. Journal of Proteome Research, 2011, 10, 2286-2299.	1.8	72
76	Transcriptional targets of hepatocyte growth factor signaling and Ki-ras oncogene activation in colorectal cancer. Oncogene, 2006, 25, 91-102.	2.6	71
77	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.	3.3	69
78	Molecular heterogeneity of non-small cell lung carcinoma patient-derived xenografts closely reflect their primary tumors. International Journal of Cancer, 2017, 140, 662-673.	2.3	67
79	Determinants of sensitivity to lovastatin-induced apoptosis in multiple myeloma. Molecular Cancer Therapeutics, 2007, 6, 1886-1897.	1.9	65
80	Role of Pirh2 in Mediating the Regulation of p53 and c-Myc. PLoS Genetics, 2011, 7, e1002360.	1.5	65
81	Integrated proteomic and transcriptomic profiling of mouse lung development and Nmyc target genes. Molecular Systems Biology, 2007, 3, 109.	3.2	64
82	Genomic markers for malignant progression in pulmonary adenocarcinoma with bronchioloalveolar features. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10155-10160.	3.3	64
83	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.	1.8	63
84	Systematic protein–protein interaction mapping for clinically relevant human <scp>GPCR</scp>s. Molecular Systems Biology, 2017, 13, 918.	3.2	63
85	The histone deacetylase inhibitor valproic acid alters sensitivity towards all trans retinoic acid in acute myeloblastic leukemia cells. Leukemia, 2005, 19, 1161-1168.	3.3	61
86	Identification of microRNA-181a-5p and microRNA-4454 as mediators of facet cartilage degeneration. JCI Insight, 2016, 1, e86820.	2.3	60
87	Understanding Prognostic Gene Expression Signatures in Lung Cancer. Clinical Lung Cancer, 2009, 10, 331-340.	1.1	59
88	Molecular classification of oral cancer by cDNA microarrays identifies overexpressed genes correlated with nodal metastasis. International Journal of Cancer, 2004, 110, 857-868.	2.3	57
89	MicroRNA‑34a‑5p Promotes Joint Destruction During Osteoarthritis. Arthritis and Rheumatology, 2021, 73, 426-439.	2.9	56
90	STAT3 pathway regulates lung-derived brain metastasis initiating cell capacity through miR-21 activation. Oncotarget, 2015, 6, 27461-27477.	0.8	55

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91	Inhibition of the Sodium/Potassium ATPase Impairs *N*-Glycan Expression and Function. Cancer Research, 2008, 68, 6688-6697.	0.4	54
92	Interaction Techniques for Selecting and Manipulating Subgraphs in Network Visualizations. IEEE Transactions on Visualization and Computer Graphics, 2009, 15, 937-944.	2.9	51
93	Flotillin-2 deficiency leads to reduced lung metastases in a mouse breast cancer model. Oncogene, 2013, 32, 4989-4994.	2.6	51
94	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.	2.6	51
95	*CUL7* Is a Novel Antiapoptotic Oncogene. Cancer Research, 2007, 67, 9616-9622.	0.4	50
96	Inferring the functions of longevity genes with modular subnetwork biomarkers of Caenorhabditis elegans aging. Genome Biology, 2010, 11, R13.	13.9	50
97	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.	1.5	49
98	Towards a unified open access dataset of molecular interactions. Nature Communications, 2020, 11, 6144.	5.8	49
99	Integrative transcriptome analysis identifies deregulated microRNA-transcription factor networks in lung adenocarcinoma. Oncotarget, 2016, 7, 28920-28934.	0.8	49
100	L1 Cell Adhesion Molecule Promotes Tumorigenicity and Metastatic Potential in Non–Small Cell Lung Cancer. Clinical Cancer Research, 2012, 18, 1914-1924.	3.2	48
101	Identification of pathways associated with invasive behavior by ovarian cancer cells using multidimensional protein identification technology (MudPIT). Molecular BioSystems, 2008, 4, 762.	2.9	47
102	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. BMC Bioinformatics, 2018, 19, 134.	1.2	47
103	Recurrent genomic alterations in sequential progressive leukoplakia and oral cancer: drivers of oral tumorigenesis?. Human Molecular Genetics, 2014, 23, 2618-2628.	1.4	46
104	Differential roles of cyclin D1 and D3 in pancreatic ductal adenocarcinoma. Molecular Cancer, 2010, 9, 24.	7.9	45
105	An integrative approach for the identification of prognostic and predictive biomarkers in rectal cancer. Oncotarget, 2015, 6, 32561-32574.	0.8	45
106	Intelligent decision support for protein crystal growth. IBM Systems Journal, 2001, 40, 394-409.	3.1	44
107	Automatic classification of sub-microlitre protein-crystallization trials in 1536-well plates. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1619-1627.	2.5	43
108	Stability and Heterogeneity of Expression Profiles in Lung Cancer Specimens Harvested Following Surgical Resection. Neoplasia, 2004, 6, 761-767.	2.3	43

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109	*NKX3.1* Haploinsufficiency Is Prognostic for Prostate Cancer Relapse following Surgery or Image-Guided Radiotherapy. Clinical Cancer Research, 2012, 18, 308-316.	3.2	43
110	Sequencing identifies a distinct signature of circulating microRNAs in early radiographic knee osteoarthritis. Osteoarthritis and Cartilage, 2020, 28, 1471-1481.	0.6	43
111	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.	2.1	42
112	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.	3.4	42
113	Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRASG13D. Nature Communications, 2020, 11, 499.	5.8	42
114	Smoking status impacts microRNA mediated prognosis and lung adenocarcinoma biology. BMC Cancer, 2014, 14, 778.	1.1	41
115	Epithelial tumor suppressor ELF3 is a lineage-specific amplified oncogene in lung adenocarcinoma. Nature Communications, 2019, 10, 5438.	5.8	41
116	Protein crystallization analysis on the World Community Grid. Journal of Structural and Functional Genomics, 2010, 11, 61-69.	1.2	40
117	Protease nexin 1 inhibits hedgehog signaling in prostate adenocarcinoma. Journal of Clinical Investigation, 2012, 122, 4025-4036.	3.9	39
118	pathDIP 4: an extended pathway annotations and enrichment analysis resource for human, model organisms and domesticated species. Nucleic Acids Research, 2020, 48, D479-D488.	6.5	38
119	IID 2021: towards context-specific protein interaction analyses by increased coverage, enhanced annotation and enrichment analysis. Nucleic Acids Research, 2022, 50, D640-D647.	6.5	38
120	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.	0.8	37
121	Integration, visualization and analysis of human interactome. Biochemical and Biophysical Research Communications, 2014, 445, 757-773.	1.0	37
122	MYC interaction with the tumor suppressive SWI/SNF complex member INI1 regulates transcription and cellular transformation. Cell Cycle, 2016, 15, 1693-1705.	1.3	37
123	Differentially androgen-modulated genes in ovarian epithelial cells from BRCA mutation carriers and control patients predict ovarian cancer survival and disease progression. Oncogene, 2007, 26, 198-214.	2.6	36
124	Prioritizing Therapeutics for Lung Cancer: An Integrative Meta-analysis of Cancer Gene Signatures and Chemogenomic Data. PLoS Computational Biology, 2015, 11, e1004068.	1.5	36
125	An Integrated Approach Identifies Mediators of Local Recurrence in Head and Neck Squamous Carcinoma. Clinical Cancer Research, 2017, 23, 3769-3780.	3.2	36
126	Automated Microinjection of Recombinant BCL-X into Mouse Zygotes Enhances Embryo Development. PLoS ONE, 2011, 6, e21687.	1.1	36

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127	Therapeutic Targeting of the Premetastatic Stage in Human Lung-to-Brain Metastasis. Cancer Research, 2018, 78, 5124-5134.	0.4	35
128	The IMEx coronavirus interactome: an evolving map of *Coronaviridae*â€"host molecular interactions. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	34
129	Genomic amplicons target vesicle recycling in breast cancer. Journal of Clinical Investigation, 2009, 119, 2123-7.	3.9	34
130	Split Intein-Mediated Protein Ligation for detecting protein-protein interactions and their inhibition. Nature Communications, 2020, 11, 2440.	5.8	33
131	Automatic Classification and Pattern Discovery in High-throughput Protein Crystallization Trials. Journal of Structural and Functional Genomics, 2005, 6, 195-202.	1.2	32
132	Phenotypic and Transcriptional Plasticity Directed by a Yeast Mitogen-Activated Protein Kinase Network. Genetics, 2003, 165, 997-1015.	1.2	32
133	Modeling of lung cancer by an orthotopically growing H460SM variant cell line reveals novel candidate genes for systemic metastasis. Oncogene, 2004, 23, 6316-6324.	2.6	31
134	Prognostic Gene Expression Signature for Squamous Cell Carcinoma of Lung. Clinical Cancer Research, 2010, 16, 5038-5047.	3.2	31
135	Ubiquitin ligase RNF8 suppresses Notch signaling to regulate mammary development and tumorigenesis. Journal of Clinical Investigation, 2018, 128, 4525-4542.	3.9	31
136	*NBN* gain is predictive for adverse outcome following image-guided radiotherapy for localized prostate cancer. Oncotarget, 2014, 5, 11081-11090.	0.8	30
137	Circulating plant miRNAs can regulate human gene expression in vitro. Scientific Reports, 2016, 6, 32773.	1.6	29
138	*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.	1.2	29
139	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.	3.0	29
140	Identification of GAS-dependent interferon-sensitive target genes whose transcription is STAT2-dependent but ISGF3-independent. FEBS Journal, 2006, 273, 1569-1581.	2.2	28
141	Optimization of experimental design parameters for high-throughput chromatin immunoprecipitation studies. Nucleic Acids Research, 2008, 36, e144-e144.	6.5	28
142	Integrative computational biology for cancer research. Human Genetics, 2011, 130, 465-481.	1.8	28
143	Macrophage migration inhibitory factor drives pathology in a mouse model of spondyloarthritis and is associated with human disease. Science Translational Medicine, 2021, 13, eabg1210.	5.8	28
144	Primary Tumor Xenografts of Human Lung Adeno and Squamous Cell Carcinoma Express Distinct Proteomic Signatures. Journal of Proteome Research, 2011, 10, 161-174.	1.8	27

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145	Severe COVID-19 Shares a Common Neutrophil Activation Signature with Other Acute Inflammatory States. Cells, 2022, 11, 847.	1.8	27
146	RNAi screen identifies essential regulators of human brain metastasis-initiating cells. Acta Neuropathologica, 2017, 134, 923-940.	3.9	26
147	Establishing a training set through the visual analysis of crystallization trials. Part I: â^¼150â€¦000 images. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1123-1130.	2.5	25
148	A stemness screen reveals C3orf54/INKA1 as a promoter of human leukemia stem cell latency. Blood, 2019, 133, 2198-2211.	0.6	25
149	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.	1.1	24
150	SCRIPDB: a portal for easy access to syntheses, chemicals and reactions in patents. Nucleic Acids Research, 2012, 40, D428-D433.	6.5	22
151	Systematic Identification of Oncogenic EGFR Interaction Partners. Journal of Molecular Biology, 2017, 429, 280-294.	2.0	22
152	Physiological Tau Interactome in Brain and Its Link to Tauopathies. Journal of Proteome Research, 2020, 19, 2429-2442.	1.8	22
153	An Integrative Genomic and Transcriptomic Analysis Reveals Potential Targets Associated with Cell Proliferation in Uterine Leiomyomas. PLoS ONE, 2013, 8, e57901.	1.1	22
154	Comparative network analysis via differential graphlet communities. Proteomics, 2015, 15, 608-617.	1.3	21
155	Current Applications of Microarrays in Head and Neck Cancer Research. Laryngoscope, 2004, 114, 241-248.	1.1	19
156	Visual Data Mining of Biological Networks: One Size Does Not Fit All. PLoS Computational Biology, 2013, 9, e1002833.	1.5	19
157	BioPAX-Parser: parsing and enrichment analysis of BioPAX pathways. Bioinformatics, 2020, 36, 4377-4378.	1.8	19
158	Loss of coordinated androgen regulation in nonmalignant ovarian epithelial cells with BRCA1/2 mutations and ovarian cancer cells. Cancer Research, 2003, 63, 2416-24.	0.4	19
159	Establishing a training set through the visual analysis of crystallization trials. Part II: crystal examples. Acta Crystallographica Section D: Biological Crystallography, 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. Oncogenesis, 2014, 3, e133-e133.	2.1	18
161	Prediction of Proteinâ€Protein Interactions. Current Protocols in Bioinformatics, 2017, 60, 8.2.1-8.2.14.	25.8	18
162	Incremental Iterative Retrieval and Browsing for Efficient Conversational CBR Systems. Applied Intelligence, 2000, 12, 251-268.	3.3	17

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163	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.	1.0	17
164	Visual Data Mining: Effective Exploration of the Biological Universe. Lecture Notes in Computer Science, 2014, , 19-33.	1.0	17
165	The relationship between cytokine and neutrophil gene network distinguishes SARS-CoV-2–infected patients by sex and age. JCI Insight, 2021, 6, .	2.3	17
166	Lung cancer: Developmental networks gone awry?. Cancer Biology and Therapy, 2009, 8, 312-318.	1.5	16
167	Exploiting the noise: improving biomarkers with ensembles of data analysis methodologies. Genome Medicine, 2012, 4, 84.	3.6	15
168	A 4-gene signature from histologically normal surgical margins predicts local recurrence in patients with oral carcinoma: clinical validation. Scientific Reports, 2020, 10, 1713.	1.6	15
169	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.	2.3	13
170	NAViGaTOR: Large Scalable and Interactive Navigation and Analysis of Large Graphs. Internet Mathematics, 2011, 7, 314-347.	0.7	13
171	Novel semantic similarity measure improves an integrative approach to predicting gene functional associations. BMC Systems Biology, 2013, 7, 22.	3.0	13
172	Integrating RAS Status into Prognostic Signatures for Adenocarcinomas of the Lung. Clinical Cancer Research, 2015, 21, 1477-1486.	3.2	13
173	Uninterrupted Sedentary Behavior Downregulates <i>BRCA1</i> Gene Expression. Cancer Prevention Research, 2016, 9, 83-88.	0.7	13
174	Differentially expressed microRNAs in lung adenocarcinoma invert effects of copy number aberrations of prognostic genes. Oncotarget, 2018, 9, 9137-9155.	0.8	13
175	CFTR interactome mapping using the mammalian membrane two–hybrid high–throughput screening system. Molecular Systems Biology, 2022, 18, e10629.	3.2	13
176	Improving Performance of Case-Based Classification Using Context-Based Relevance. International Journal on Artificial Intelligence Tools, 1997, 06, 511-536.	0.7	12
177	Advances in ovarian cancer proteomics: the quest for biomarkers and improved therapeutic interventions. Expert Review of Proteomics, 2008, 5, 551-560.	1.3	12
178	GSOAP: a tool for visualization of gene set over-representation analysis. Bioinformatics, 2020, 36, 2923-2925.	1.8	12
179	Informed Use of Protein–Protein Interaction Data: A Focus on the Integrated Interactions Database (IID). Methods in Molecular Biology, 2020, 2074, 125-134.	0.4	12
180	Estrogen Receptor 1 Inhibition of Wnt/β-Catenin Signaling Contributes to Sex Differences in Hepatocarcinogenesis. Frontiers in Oncology, 2021, 11, 777834.	1.3	12

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181	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.	1.2	12
182	Robust quantitative scratch assay. Bioinformatics, 2016, 32, 1439-1440.	1.8	11
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