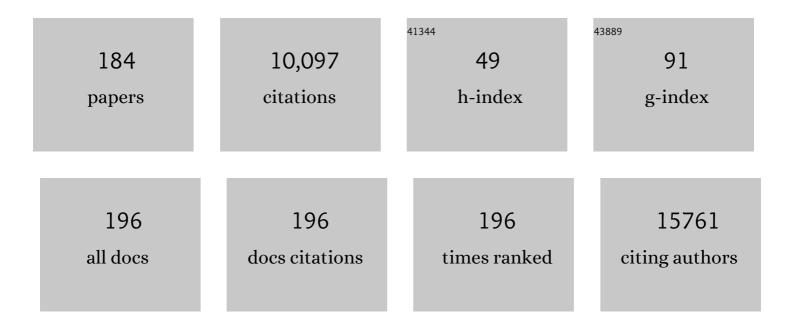
Javier De Las Rivas

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A Proteome-Scale Map of the Human Interactome Network. Cell, 2014, 159, 1212-1226.	28.9	1,199
2	A reference map of the human binary protein interactome. Nature, 2020, 580, 402-408.	27.8	724
3	Protein–Protein Interactions Essentials: Key Concepts to Building and Analyzing Interactome Networks. PLoS Computational Biology, 2010, 6, e1000807.	3.2	496
4	The minimum information required for reporting a molecular interaction experiment (MIMIx). Nature Biotechnology, 2007, 25, 894-898.	17.5	274
5	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529.	19.0	274
6	Human Gene Coexpression Landscape: Confident Network Derived from Tissue Transcriptomic Profiles. PLoS ONE, 2008, 3, e3911.	2.5	213
7	APID: Agile Protein Interaction DataAnalyzer. Nucleic Acids Research, 2006, 34, W298-W302.	14.5	209
8	Deregulation of microRNA expression in the different genetic subtypes of multiple myeloma and correlation with gene expression profiling. Leukemia, 2010, 24, 629-637.	7.2	188
9	Gene expression profiling of B lymphocytes and plasma cells from Waldenström's macroglobulinemia: comparison with expression patterns of the same cell counterparts from chronic lymphocytic leukemia, multiple myeloma and normal individuals. Leukemia, 2007, 21, 541-549.	7.2	187
10	Responses of Sugar Beet Roots to Iron Deficiency. Changes in Carbon Assimilation and Oxygen Use. Plant Physiology, 2000, 124, 885-898.	4.8	157
11	The 90S Preribosome Is a Multimodular Structure That Is Assembled through a Hierarchical Mechanism. Molecular and Cellular Biology, 2007, 27, 5414-5429.	2.3	155
12	miRNA cargo within exosomeâ€like vesicle transfer influences metastatic bone colonization. Molecular Oncology, 2014, 8, 689-703.	4.6	155
13	A functional model for the role of cytochrome b559 in the protection against donor and acceptor side photoinhibition. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 10942-10946.	7.1	149
14	Î ² -Carotene within the isolated Photosystem II reaction centre: photooxidation and irreversible bleaching of this chromophore by oxidised P680. Biochimica Et Biophysica Acta - Bioenergetics, 1991, 1060, 106-114.	1.0	140
15	A New Reversed Phase-HPLC Method Resolving All Major Higher Plant Photosynthetic Pigments. Plant Physiology, 1989, 91, 190-192.	4.8	121
16	Analysis of the Structure of the PsbO Protein and its Implications. Photosynthesis Research, 2004, 81, 329-343.	2.9	117
17	Infection Exposure Is a Causal Factor in B-cell Precursor Acute Lymphoblastic Leukemia as a Result of <i>Pax5</i> -Inherited Susceptibility. Cancer Discovery, 2015, 5, 1328-1343.	9.4	117
18	APID database: redefining protein–protein interaction experimental evidences and binary interactomes. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	113

#	Article	IF	CITATIONS
19	APID interactomes: providing proteome-based interactomes with controlled quality for multiple species and derived networks. Nucleic Acids Research, 2016, 44, W529-W535.	14.5	112
20	Dynamic flexibility in the structure and function of photosystem II in higher plant thylakoid membranes: the grana enigma. Photosynthesis Research, 2008, 98, 575-587.	2.9	110
21	Two sites of primary degradation of the D1-protein induced by acceptor or donor side photo-inhibition in photosystem II core complexes. FEBS Letters, 1992, 301, 246-252.	2.8	108
22	Comparative Analysis of Chloroplast Genomes: Functional Annotation, Genome-Based Phylogeny, and Deduced Evolutionary Patterns. Genome Research, 2002, 12, 567-583.	5.5	106
23	Cancer immunotherapy resistance based on immune checkpoints inhibitors: Targets, biomarkers, and remedies. Drug Resistance Updates, 2020, 53, 100718.	14.4	103
24	Two coupled Î ² -carotene molecules protect P680 from photodamage in isolated Photosystem II reaction centres. Biochimica Et Biophysica Acta - Bioenergetics, 1993, 1142, 155-164.	1.0	100
25	Systematic comparison and assessment of RNA-seq procedures for gene expression quantitative analysis. Scientific Reports, 2020, 10, 19737.	3.3	99
26	Proteomic profiles of thylakoid membranes and changes in response to iron deficiency. Photosynthesis Research, 2006, 89, 141-155.	2.9	98
27	Evolution of oxygenic photosynthesis: genome-wide analysis of the OEC extrinsic proteins. Trends in Plant Science, 2004, 9, 18-25.	8.8	95
28	Hypoxia as a driver of resistance to immunotherapy. Drug Resistance Updates, 2021, 59, 100787.	14.4	94
29	Cancer drug resistance induced by EMT:Ânovel therapeutic strategies. Archives of Toxicology, 2021, 95, 2279-2297.	4.2	92
30	A Novel Lung Cancer Signature Mediates Metastatic Bone Colonization by a Dual Mechanism. Cancer Research, 2008, 68, 2275-2285.	0.9	89
31	Crebbp loss cooperates with Bcl2 overexpression to promote lymphoma in mice. Blood, 2017, 129, 2645-2656.	1.4	84
32	Impaired expression of DICER, DROSHA, SBDS and some microRNAs in mesenchymal stromal cells from myelodysplastic syndrome patients. Haematologica, 2012, 97, 1218-1224.	3.5	83
33	Functional Gene Networks: R/Bioc package to generate and analyse gene networks derived from functional enrichment and clustering. Bioinformatics, 2015, 31, 1686-1688.	4.1	81
34	Structure and Thermal Stability of Photosystem II Reaction Centers Studied by Infrared Spectroscopyâ€. Biochemistry, 1997, 36, 8897-8903.	2.5	79
35	Infection Exposure Promotes <i>ETV6-RUNX1</i> Precursor B-cell Leukemia via Impaired H3K4 Demethylases. Cancer Research, 2017, 77, 4365-4377.	0.9	76
36	GATExplorer: Genomic and Transcriptomic Explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics, 2010, 11, 221.	2.6	75

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37	Comparison of Primary Charge Separation in the Photosystem II Reaction Center Complex Isolated from Wild-type and D1-130 Mutants of the Cyanobacterium Synechocystis PCC 6803. Journal of Biological Chemistry, 1996, 271, 2093-2101.	3.4	74
38	Protein-protein interaction networks: unraveling the wiring of molecular machines within the cell. Briefings in Functional Genomics, 2012, 11, 489-496.	2.7	74
39	APID2NET: unified interactome graphic analyzer. Bioinformatics, 2007, 23, 2495-2497.	4.1	72
40	Microvesicles from Mesenchymal Stromal Cells Are Involved in HPC-Microenvironment Crosstalk in Myelodysplastic Patients. PLoS ONE, 2016, 11, e0146722.	2.5	70
41	ColoLipidGene: signature of lipid metabolism-related genes to predict prognosis in stage-II colon cancer patients. Oncotarget, 2015, 6, 7348-7363.	1.8	69
42	Resistance to Tyrosine Kinase Inhibitors in Chronic Myeloid Leukemia—From Molecular Mechanisms to Clinical Relevance. Cancers, 2021, 13, 4820.	3.7	65
43	An intact gut microbiome protects genetically predisposed mice against leukemia. Blood, 2020, 136, 2003-2017.	1.4	64
44	Acceptor side mechanism of photoinduced proteolysis of the D1 protein in photosystem II reaction centers. Biochemistry, 1993, 32, 6944-6950.	2.5	62
45	A novel molecular mechanism involved in multiple myeloma development revealed by targeting MafB to haematopoietic progenitors. EMBO Journal, 2012, 31, 3704-3717.	7.8	62
46	The 1.49Ã Resolution Crystal Structure of PsbQ from Photosystem II of Spinacia oleracea Reveals a PPII Structure in the N-terminal Region. Journal of Molecular Biology, 2005, 350, 1051-1060.	4.2	60
47	A high number of losses in 13q14 chromosome band is associated with a worse outcome and biological differences in patients with B-cell chronic lymphoid leukemia. Haematologica, 2009, 94, 364-371.	3.5	59
48	Transcriptomic portrait of human Mesenchymal Stromal/Stem cells isolated from bone marrow and placenta. BMC Genomics, 2014, 15, 910.	2.8	59
49	Maximizing binary interactome mapping with a minimal number of assays. Nature Communications, 2019, 10, 3907.	12.8	57
50	Insights into the human mesenchymal stromal/stem cell identity through integrative transcriptomic profiling. BMC Genomics, 2016, 17, 944.	2.8	55
51	Evidence for Cu(I)-thiolate ligation and prediction of a putative copper-binding site in the Escherichia coli NADH dehydrogenase-2. Archives of Biochemistry and Biophysics, 2002, 405, 87-94.	3.0	54
52	GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training. PLoS Computational Biology, 2015, 11, e1004143.	3.2	52
53	Bioinformatics training: a review of challenges, actions and support requirements. Briefings in Bioinformatics, 2010, 11, 544-551.	6.5	51
54	Best practices in bioinformatics training for life scientists. Briefings in Bioinformatics, 2013, 14, 528-537.	6.5	51

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55	Three-dimensional Electron Cryo-microscopy Study of the Extrinsic Domains of the Oxygen-evolving Complex of Spinach. Journal of Biological Chemistry, 2002, 277, 15006-15012.	3.4	49
56	Survival marker genes of colorectal cancer derived from consistent transcriptomic profiling. BMC Genomics, 2018, 19, 857.	2.8	48
57	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. BMC Bioinformatics, 2018, 19, 134.	2.6	47
58	Laser microdissection and microarray analysis of the hippocampus of Ras-GRF1 knockout mice reveals gene expression changes affecting signal transduction pathways related to memory and learning. Neuroscience, 2007, 146, 272-285.	2.3	45
59	Oxygen-evolving extrinsic proteins (PsbO,P,Q,R): Bioinformatic and functional analysis. Biochimica Et Biophysica Acta - Bioenergetics, 2007, 1767, 575-582.	1.0	45
60	Receptor of Activated Protein C Promotes Metastasis and Correlates with Clinical Outcome in Lung Adenocarcinoma. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 96-105.	5.6	45
61	Cancer-associated fibroblast-derived gene signatures determine prognosis in colon cancer patients. Molecular Cancer, 2021, 20, 73.	19.2	44
62	Functional Analysis beyond Enrichment: Non-Redundant Reciprocal Linkage of Genes and Biological Terms. PLoS ONE, 2011, 6, e24289.	2.5	44
63	Mobilisation with G-CSF in healthy donors promotes a high but temporal deregulation of genes. Leukemia, 2005, 19, 1088-1091.	7.2	43
64	Transcriptomic profile induced in bone marrow mesenchymal stromal cells after interaction with multiple myeloma cells: implications in myeloma progression and myeloma bone disease. Oncotarget, 2014, 5, 8284-8305.	1.8	43
65	Matrix-Gla protein promotes osteosarcoma lung metastasis and associates with poor prognosis. Journal of Pathology, 2016, 239, 438-449.	4.5	42
66	Computational approaches in cancer multidrug resistance research: Identification of potential biomarkers, drug targets and drug-target interactions. Drug Resistance Updates, 2020, 48, 100662.	14.4	42
67	Calcium-Dependent Conformational Change and Thermal Stability of the Isolated PsbO Protein Detected by FTIR Spectroscopy. Biochemistry, 2003, 42, 11831-11838.	2.5	41
68	RasGRF1 disruption causes retinal photoreception defects and associated transcriptomic alterations. Journal of Neurochemistry, 2009, 110, 641-652.	3.9	40
69	Molecular Characterization of Chronic Lymphocytic Leukemia Patients with a High Number of Losses in 13q14. PLoS ONE, 2012, 7, e48485.	2.5	37
70	Loss of Pax5 Exploits Sca1-BCR-ABLp190 Susceptibility to Confer the Metabolic Shift Essential for pB-ALL. Cancer Research, 2018, 78, 2669-2679.	0.9	37
71	Photosynthetic pigments and mineral composition of iron deficient pear leaves. Journal of Plant Nutrition, 1989, 12, 827-838.	1.9	36
72	A gene signature of bone metastatic colonization sensitizes for tumor-induced osteolysis and predicts survival in lung cancer. Oncogene, 2014, 33, 5090-5099.	5.9	35

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73	Micro <scp>RNA</scp> (miR)â€203 and miRâ€205 expression patterns identify subgroups of prognosis in cutaneous squamous cell carcinoma. British Journal of Dermatology, 2017, 177, 168-178.	1.5	35
74	Integrating literature-constrained and data-driven inference of signalling networks. Bioinformatics, 2012, 28, 2311-2317.	4.1	34
75	Profiling of Chemonaive Osteosarcoma and Paired-Normal Cells Identifies EBF2 as a Mediator of Osteoprotegerin Inhibition to Tumor Necrosis Factor–Related Apoptosis-Inducing Ligand–Induced Apoptosis. Clinical Cancer Research, 2009, 15, 5082-5091.	7.0	32
76	Unique genetic profile of sporadic colorectal cancer liver metastasis versus primary tumors as defined by high-density single-nucleotide polymorphism arrays. Modern Pathology, 2012, 25, 590-601.	5.5	32
77	Regulatory motifs found in the small heat shock protein (sHSP) gene family in tomato. BMC Genomics, 2018, 19, 860.	2.8	32
78	Lmo2 expression defines tumor cell identity during T ell leukemogenesis. EMBO Journal, 2018, 37, .	7.8	32
79	Transcriptional networks of knockout cell lines identify functional specificities of H-Ras and N-Ras: significant involvement of N-Ras in biotic and defense responses. Oncogene, 2007, 26, 917-933.	5.9	31
80	Genome-wide profiling of methylation identifies novel targets with aberrant hypermethylation and reduced expression in low-risk myelodysplastic syndromes. Leukemia, 2013, 27, 610-618.	7.2	31
81	Transcriptome Analysis in Prenatal IGF1-Deficient Mice Identifies Molecular Pathways and Target Genes Involved in Distal Lung Differentiation. PLoS ONE, 2013, 8, e83028.	2.5	31
82	Interactome Data and Databases: Different Types of Protein Interaction. Comparative and Functional Genomics, 2004, 5, 173-178.	2.0	30
83	Ten Simple Rules for Developing a Short Bioinformatics Training Course. PLoS Computational Biology, 2011, 7, e1002245.	3.2	29
84	Structure and evolution of the extrinsic proteins that stabilize the oxygen-evolving engine. Photochemical and Photobiological Sciences, 2005, 4, 1003.	2.9	27
85	RHOB influences lung adenocarcinoma metastasis and resistance in a hostâ€sensitive manner. Molecular Oncology, 2014, 8, 196-206.	4.6	27
86	Isolation of a yellow carotenoprotein from carrot. Phytochemistry, 1991, 30, 1535-1537.	2.9	25
87	Structural and functional properties of Escherichia coli -derived nucleoplasmin. FEBS Journal, 2001, 268, 1739-1748.	0.2	25
88	Linking amyotrophic lateral sclerosis and spinal muscular atrophy through <scp>RNA</scp> â€ŧranscriptome homeostasis: a genomics perspective. Journal of Neurochemistry, 2017, 141, 12-30.	3.9	25
89	40 Years of RAS—A Historic Overview. Genes, 2021, 12, 681.	2.4	24
90	Segmentation of genomic and transcriptomic microarrays data reveals major correlation between DNA copy number aberrations and gene–loci expression. Genomics, 2011, 97, 86-93.	2.9	23

#	Article	IF	CITATIONS
91	Bioinformatics Training Network (BTN): a community resource for bioinformatics trainers. Briefings in Bioinformatics, 2012, 13, 383-389.	6.5	23
92	Unraveling heterogeneous susceptibility and the evolution of breast cancer using a systems biology approach. Genome Biology, 2015, 16, 40.	8.8	23
93	Cystatin D Locates in the Nucleus at Sites of Active Transcription and Modulates Gene and Protein Expression. Journal of Biological Chemistry, 2015, 290, 26533-26548.	3.4	23
94	Screening and Validation of Novel Biomarkers in Osteoarticular Pathologies by Comprehensive Combination of Protein Array Technologies. Journal of Proteome Research, 2017, 16, 1890-1899.	3.7	23
95	Transcriptomic landscape, gene signatures and regulatory profile of aging in the human brain. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194491.	1.9	23
96	Title is missing!. , 1999, 61, 11-21.		22
97	Structural Analysis of the PsbQ Protein of Photosystem II by Fourier Transform Infrared and Circular Dichroic Spectroscopy and by Bioinformatic Methodsâ€. Biochemistry, 2003, 42, 1000-1007.	2.5	22
98	Algorithm to find gene expression profiles of deregulation and identify families of disease-altered genes. Bioinformatics, 2006, 22, 1103-1110.	4.1	22
99	Mapping of Genetic Abnormalities of Primary Tumours from Metastatic CRC by High-Resolution SNP Arrays. PLoS ONE, 2010, 5, e13752.	2.5	22
100	Structural domain–domain interactions: Assessment and comparison with protein–protein interaction data to improve the interactome. Proteins: Structure, Function and Bioinformatics, 2010, 78, 109-117.	2.6	21
101	Deregulation of Genes Related to Iron and Mitochondrial Metabolism in Refractory Anemia with Ring Sideroblasts. PLoS ONE, 2015, 10, e0126555.	2.5	21
102	Infectious stimuli promote malignant B-cell acute lymphoblastic leukemia in the absence of AID. Nature Communications, 2019, 10, 5563.	12.8	21
103	pH sensitivity of the redox state of cytochrome b559 may regulate its function as a protectant against donor and acceptor side photoinhibition. Photosynthesis Research, 1995, 46, 193-202.	2.9	20
104	Threading structural model of the manganese-stabilizing protein PsbO reveals presence of two possible ?-sandwich domains. Proteins: Structure, Function and Bioinformatics, 2001, 45, 372-381.	2.6	20
105	Functional Integrative Levels in the Human Interactome Recapitulate Organ Organization. PLoS ONE, 2011, 6, e22051.	2.5	20
106	Cortactin (CTTN) overexpression in osteosarcoma correlates with advanced stage and reduced survival. Cancer Biomarkers, 2012, 10, 35-41.	1.7	19
107	Mesenchymal stromal cells (MSC) from JAK2+ myeloproliferative neoplasms differ from normal MSC and contribute to the maintenance of neoplastic hematopoiesis. PLoS ONE, 2017, 12, e0182470.	2.5	19
108	Phycomyces blakesleeanus car B mutants: Their use in assays of phytoene desaturase. Phytochemistry, 1991, 30, 3971-3976.	2.9	18

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109	Prognostic Impact of del(17p) and del(22q) as Assessed by Interphase FISH in Sporadic Colorectal Carcinomas. PLoS ONE, 2012, 7, e42683.	2.5	18
110	Fluorescence induction of Photosystem II membranes shows the steps till reduction and protonation of the quinone pool. Journal of Plant Physiology, 2003, 160, 1499-1506.	3.5	17
111	Identification of a characteristic copy number alteration profile by highâ€resolution single nucleotide polymorphism arrays associated with metastatic sporadic colorectal cancer. Cancer, 2014, 120, 1948-1959.	4.1	17
112	Analyse multiple disease subtypes and build associated gene networks using genome-wide expression profiles. BMC Genomics, 2015, 16, S3.	2.8	17
113	Stromal SNAI2 Is Required for ERBB2 Breast Cancer Progression. Cancer Research, 2020, 80, 5216-5230.	0.9	17
114	Interleukin-12 inhibits liver-specific drug-inducible systems in vivo. Gene Therapy, 2008, 15, 277-288.	4.5	16
115	Transcriptomic Effects of Tet-On and Mifepristone-Inducible Systems in Mouse Liver. Human Gene Therapy, 2008, 19, 1233-1248.	2.7	16
116	Integration of Proteomics and Transcriptomics Data Sets for the Analysis of a Lymphoma B-Cell Line in the Context of the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 3530-3540.	3.7	16
117	Single mutations of residues outside the active center of the xylanase Xys1Δ fromStreptomyces halstediiJM8 affect its activity. FEMS Microbiology Letters, 2004, 240, 237-243.	1.8	15
118	Transcriptional repression of the tumor suppressor DRO1 by AIB1. FEBS Letters, 2011, 585, 3041-3046.	2.8	15
119	Identification of expression patterns in the progression of disease stages by integration of transcriptomic data. BMC Bioinformatics, 2016, 17, 432.	2.6	15
120	Searching the overlap between network modules with specific betweeness (S2B) and its application to cross-disease analysis. Scientific Reports, 2018, 8, 11555.	3.3	15
121	Inhibition of inflammatory signaling in Pax5 mutant cells mitigates B-cell leukemogenesis. Scientific Reports, 2020, 10, 19189.	3.3	15
122	Effect of Photosystem II inhibitor K-15 on photochemical reactions of the isolated D1/D2 cytochrome b559 complex. Photosynthesis Research, 1995, 44, 67-74.	2.9	14
123	Serum-dependent transcriptional networks identify distinct functional roles for H-Ras and N-Ras during initial stages of the cell cycle. Genome Biology, 2009, 10, R123.	9.6	14
124	SARS-CoV-2 Infection Triggers Auto-Immune Response in ARDS. Frontiers in Immunology, 2022, 13, 732197.	4.8	14
125	Identification of a novel recurrent gain on 20q13 in chronic lymphocytic leukemia by array CGH and gene expression profiling. Annals of Oncology, 2012, 23, 2138-2146.	1.2	13
126	Protein Interactions: Mapping Interactome Networks to Support Drug Target Discovery and Selection. Methods in Molecular Biology, 2012, 910, 279-296.	0.9	13

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127	Combining dissimilarity based classifiers for cancer prediction using gene expression profiles. BMC Bioinformatics, 2007, 8, .	2.6	12
128	A robust estimation of exon expression to identify alternative spliced genes applied to human tissues and cancer samples. BMC Genomics, 2014, 15, 879.	2.8	12
129	<i>TET2</i> Overexpression in Chronic Lymphocytic Leukemia Is Unrelated to the Presence of <i>TET2</i> Variations. BioMed Research International, 2014, 2014, 1-6.	1.9	12
130	Epidermal Growth Factor Signaling towards Proliferation: Modeling and Logic Inference Using Forward and Backward Search. BioMed Research International, 2017, 2017, 1-11.	1.9	12
131	In Vitro Transcription/Translation System: A Versatile Tool in the Search for Missing Proteins. Journal of Proteome Research, 2015, 14, 3441-3451.	3.7	11
132	The single tryptophan of the PsbQ protein of photosystem II is at the end of a 4-α-helical bundle domain. FEBS Journal, 2003, 270, 3916-3927.	0.2	10
133	Human Interactomics: Comparative Analysis of Different Protein Interaction Resources and Construction of a Cancer Protein–Drug Bipartite Network. Advances in Protein Chemistry and Structural Biology, 2018, 111, 263-282.	2.3	10
134	Bioinformatics in Latin America and SolBio impact, a tale of spin-off and expansion around genomes and protein structures. Briefings in Bioinformatics, 2019, 20, 390-397.	6.5	10
135	Transcriptomic analysis of patients with immune thrombocytopenia treated with eltrombopag. Platelets, 2020, 31, 993-1000.	2.3	10
136	Determination of carotenoid pigments in several tree leaves by reversed-phase high-performance liquid chromatography. Journal of Chromatography A, 1991, 585, 168-172.	3.7	9
137	Linear array of conserved sequence motifs to discriminate protein subfamilies: study on pyridine nucleotide-disulfide reductases. BMC Bioinformatics, 2007, 8, 96.	2.6	9
138	Proteomic and Transcriptomic Profiling Identifies Early Developmentally Regulated Proteins in Dictyostelium Discoideum. Cells, 2019, 8, 1187.	4.1	9
139	Mining Drug-Target Associations in Cancer: Analysis of Gene Expression and Drug Activity Correlations. Biomolecules, 2020, 10, 667.	4.0	9
140	Transient Inhibition of the JAK/STAT Pathway Prevents B-ALL Development in Genetically Predisposed Mice. Cancer Research, 2022, 82, 1098-1109.	0.9	9
141	Structural and functional properties of Escherichia coli-derived nucleoplasmin. A comparative study of recombinant and natural proteins. FEBS Journal, 2001, 268, 1739-48.	0.2	9
142	Methylseleninic acid enhances the effect of etoposide to inhibit prostate cancer growthin vivo. International Journal of Cancer, 2007, 121, 1197-1204.	5.1	8
143	Deciphering Master Gene Regulators and Associated Networks of Human Mesenchymal Stromal Cells. Biomolecules, 2020, 10, 557.	4.0	8
144	Deepening into Intracellular Signaling Landscape through Integrative Spatial Proteomics and Transcriptomics in a Lymphoma Model. Biomolecules, 2021, 11, 1776.	4.0	8

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145	Long-lived primary radical pair state detected by time-resolved fluorescence and absorption spectroscopy in an isolated Photosystem two core. Photosynthesis Research, 1992, 34, 419-431.	2.9	7
146	Role of electrostatics on membrane binding, aggregation and destabilization induced by NAD(P)H dehydrogenases. Implication in membrane fusion. Biophysical Chemistry, 2008, 137, 126-132.	2.8	7
147	Combining Dissimilarities in a Hyper Reproducing Kernel Hilbert Space for Complex Human Cancer Prediction. Journal of Biomedicine and Biotechnology, 2009, 2009, 1-9.	3.0	7
148	Combined analysis of genome-wide expression and copy number profiles to identify key altered genomic regions in cancer. BMC Genomics, 2012, 13, S5.	2.8	7
149	DECO: decompose heterogeneous population cohorts for patient stratification and discovery of sample biomarkers using omic data profiling. Bioinformatics, 2019, 35, 3651-3662.	4.1	7
150	Ten simple rules for forming a scientific professional society. PLoS Computational Biology, 2017, 13, e1005226.	3.2	7
151	Further studies on the blue carotenoprotein from Astacus leptodactylus. Comparative Biochemistry and Physiology Part B: Comparative Biochemistry, 1988, 89, 65-68.	0.2	6
152	iAnn: an event sharing platform for the life sciences. Bioinformatics, 2013, 29, 1919-1921.	4.1	6
153	JAMI: a Java library for molecular interactions and data interoperability. BMC Bioinformatics, 2018, 19, 133.	2.6	6
154	Interactomic analysis of the sHSP family during tomato fruit ripening. Plant Gene, 2020, 21, 100208.	2.3	6
155	Conditional expression of HGAL leads to the development of diffuse large B-cell lymphoma in mice. Blood, 2021, 137, 1741-1753.	1.4	6
156	A Logic Computational Framework to Query Dynamics on Complex Biological Pathways. Advances in Intelligent Systems and Computing, 2014, , 207-214.	0.6	6
157	Improving k-NN for Human Cancer Classification Using the Gene Expression Profiles. Lecture Notes in Computer Science, 2009, , 107-118.	1.3	6
158	Characterization of a blue astaxanthin protein from the carapace of the crayfish Astacus leptodactylus. Comparative Biochemistry and Physiology Part B: Comparative Biochemistry, 1986, 83, 855-859.	0.2	5
159	Indirect reduction of cytochrome b559 in isolated reaction centres of photosystem II by exogenous flavins. Bioelectrochemistry, 1995, 38, 9-14.	1.0	5
160	Joining European Scientific Forces to Face Pandemics. Trends in Microbiology, 2021, 29, 92-97.	7.7	5
161	Challenges and Considerations for Delivering Bioinformatics Training in LMICs: Perspectives From Pan-African and Latin American Bioinformatics Networks. Frontiers in Education, 2021, 6, .	2.1	5
162	Expression of cysteine proteinase mRNA in chickpea (Cicer arietinum L.) is localized to provascular cells in the developing root. Journal of Plant Physiology, 2001, 158, 1463-1469.	3.5	4

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163	Structural Stability of the PsbQ Protein of Higher Plant Photosystem IIâ€. Biochemistry, 2004, 43, 14171-14179.	2.5	4
164	Evolutionary hallmarks of the human proteome: chasing the age and coregulation of protein-coding genes. BMC Genomics, 2016, 17, 725.	2.8	4
165	Ten simple rules for organizing a bioinformatics training course in low- and middle-income countries. PLoS Computational Biology, 2021, 17, e1009218.	3.2	4
166	Ensemble of Support Vector Machines to Improve the Cancer Class Prediction Based on the Gene Expression Profiles. Advances in Intelligent and Soft Computing, 2007, , 393-400.	0.2	4
167	Exomes of Ductal Luminal Breast Cancer Patients from Southwest Colombia: Gene Mutational Profile and Related Expression Alterations. Biomolecules, 2020, 10, 698.	4.0	4
168	Extracellular Vesicles Play an Important Role in Intercellular Communication Between Bone Marrow Stroma and Hematopoietic Progenitor Cells in Myeloproliferative Neoplasms. Blood, 2016, 128, 1957-1957.	1.4	3
169	A Gene Signature Derived from the Loss of CDKN1A (p21) Is Associated with CMS4 Colorectal Cancer. Cancers, 2022, 14, 136.	3.7	3
170	Gene Expression Analysis and Profiling of Microarrays Data and RNA-Sequencing Data. Comprehensive Analytical Chemistry, 2014, 63, 355-384.	1.3	2
171	Stroma-Mediated Resistance to S63845 and Venetoclax through MCL-1 and BCL-2 Expression Changes Induced by miR-193b-3p and miR-21-5p Dysregulation in Multiple Myeloma. Cells, 2021, 10, 559.	4.1	2
172	A comparison of the photochemical activity of two forms of Photosystem II reaction centre isolated from sugar beet. Biochimica Et Biophysica Acta - Bioenergetics, 1994, 1185, 85-91.	1.0	1
173	Path2enet: generation of human pathway-derived networks in an expression specific context. BMC Genomics, 2016, 17, 731.	2.8	1
174	CREBBP Loss Cooperates with BCL2 Over-Expression to Promote Lymphoma in Mice. Blood, 2016, 128, 458-458.	1.4	1
175	A High Number of Losses in 13q14 Chromosome Is Associated with a Worse Outcome and Biological Differences in Patients with B Chronic Lymphoid Leukemia Blood, 2008, 112, 2073-2073.	1.4	1
176	Kernel Alignment k-NN for Human Cancer Classification Using the Gene Expression Profiles. Lecture Notes in Computer Science, 2009, , 195-204.	1.3	1
177	Ensemble of Kernel Based Classifiers to Improve the Human Cancer Prediction using DNA Microarrays. , 2007, , .		0
178	Classification of multiple cancer types in a Hyper Reproducing Kernel Hilbert Space. , 2008, , .		0
179	Combining Dissimilarities in a Hyper Reproducing Kernel Hilbert Space for Complex Human Cancer Prediction. , 2008, , .		0
180	Lenalidomide Differentially Modifies the Genomic Profile and miRNA Expression of Mesenchymal Stromal Cells From Patients with 5q- Syndrome,. Blood, 2011, 118, 3810-3810.	1.4	0

#	Article	IF	CITATIONS
181	Epigenetic Silencing of BCL2, ETS1, IL27RA and DICER1 in Low-Risk MDS Patients. Blood, 2012, 120, 1704-1704.	1.4	0
182	Secondary Structure of Photosystem II Reaction Centre Determined by FTIR Spectroscopy. , 1997, , 105-106.		0
183	A New ETV6-RUNX1 In Vivo Model Produces a Phenocopy of the Human Pb-ALL. Blood, 2015, 126, 3658-3658.	1.4	0
184	A Tumor Suppressor Role for Bank1 in B-Cell Precursor Acute Lymphoblastic Leukemia. Blood, 2018, 132, 1333-1333.	1.4	0