

Javier De Las Rivas

List of Publications by Year in descending order

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184
papers

10,097
citations

41344

49
h-index

43889

91
g-index

196
all docs

196
docs citations

196
times ranked

15761
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 Infection Triggers Auto-Immune Response in ARDS. <i>Frontiers in Immunology</i> , 2022, 13, 732197.	4.8	14
2	Transient Inhibition of the JAK/STAT Pathway Prevents B-ALL Development in Genetically Predisposed Mice. <i>Cancer Research</i> , 2022, 82, 1098-1109.	0.9	9
3	A Gene Signature Derived from the Loss of CDKN1A (p21) Is Associated with CMS4 Colorectal Cancer. <i>Cancers</i> , 2022, 14, 136.	3.7	3
4	Conditional expression of HGAL leads to the development of diffuse large B-cell lymphoma in mice. <i>Blood</i> , 2021, 137, 1741-1753.	1.4	6
5	Joining European Scientific Forces to Face Pandemics. <i>Trends in Microbiology</i> , 2021, 29, 92-97.	7.7	5
6	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. <i>Cells</i> , 2021, 10, 559.	4.1	2
7	Cancer-associated fibroblast-derived gene signatures determine prognosis in colon cancer patients. <i>Molecular Cancer</i> , 2021, 20, 73.	19.2	44
8	Cancer drug resistance induced by EMT: A novel therapeutic strategies. <i>Archives of Toxicology</i> , 2021, 95, 2279-2297.	4.2	92
9	40 Years of RAS: A Historic Overview. <i>Genes</i> , 2021, 12, 681.	2.4	24
10	Challenges and Considerations for Delivering Bioinformatics Training in LMICs: Perspectives From Pan-African and Latin American Bioinformatics Networks. <i>Frontiers in Education</i> , 2021, 6, .	2.1	5
11	Ten simple rules for organizing a bioinformatics training course in low- and middle-income countries. <i>PLoS Computational Biology</i> , 2021, 17, e1009218.	3.2	4
12	Resistance to Tyrosine Kinase Inhibitors in Chronic Myeloid Leukemia: From Molecular Mechanisms to Clinical Relevance. <i>Cancers</i> , 2021, 13, 4820.	3.7	65
13	Hypoxia as a driver of resistance to immunotherapy. <i>Drug Resistance Updates</i> , 2021, 59, 100787.	14.4	94
14	Deepening into Intracellular Signaling Landscape through Integrative Spatial Proteomics and Transcriptomics in a Lymphoma Model. <i>Biomolecules</i> , 2021, 11, 1776.	4.0	8
15	Interactomic analysis of the sHSP family during tomato fruit ripening. <i>Plant Gene</i> , 2020, 21, 100208.	2.3	6
16	Computational approaches in cancer multidrug resistance research: Identification of potential biomarkers, drug targets and drug-target interactions. <i>Drug Resistance Updates</i> , 2020, 48, 100662.	14.4	42
17	Transcriptomic analysis of patients with immune thrombocytopenia treated with eltrombopag. <i>Platelets</i> , 2020, 31, 993-1000.	2.3	10
18	Stromal SNAI2 Is Required for ERBB2 Breast Cancer Progression. <i>Cancer Research</i> , 2020, 80, 5216-5230.	0.9	17

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19	Cancer immunotherapy resistance based on immune checkpoints inhibitors: Targets, biomarkers, and remedies. <i>Drug Resistance Updates</i> , 2020, 53, 100718.	14.4	103
20	Systematic comparison and assessment of RNA-seq procedures for gene expression quantitative analysis. <i>Scientific Reports</i> , 2020, 10, 19737.	3.3	99
21	An intact gut microbiome protects genetically predisposed mice against leukemia. <i>Blood</i> , 2020, 136, 2003-2017.	1.4	64
22	Inhibition of inflammatory signaling in Pax5 mutant cells mitigates B-cell leukemogenesis. <i>Scientific Reports</i> , 2020, 10, 19189.	3.3	15
23	Transcriptomic landscape, gene signatures and regulatory profile of aging in the human brain. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194491.	1.9	23
24	Mining Drug-Target Associations in Cancer: Analysis of Gene Expression and Drug Activity Correlations. <i>Biomolecules</i> , 2020, 10, 667.	4.0	9
25	A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408.	27.8	724
26	Deciphering Master Gene Regulators and Associated Networks of Human Mesenchymal Stromal Cells. <i>Biomolecules</i> , 2020, 10, 557.	4.0	8
27	Exomes of Ductal Luminal Breast Cancer Patients from Southwest Colombia: Gene Mutational Profile and Related Expression Alterations. <i>Biomolecules</i> , 2020, 10, 698.	4.0	4
28	Maximizing binary interactome mapping with a minimal number of assays. <i>Nature Communications</i> , 2019, 10, 3907.	12.8	57
29	Proteomic and Transcriptomic Profiling Identifies Early Developmentally Regulated Proteins in <i>Dictyostelium Discoideum</i> . <i>Cells</i> , 2019, 8, 1187.	4.1	9
30	DECO: decompose heterogeneous population cohorts for patient stratification and discovery of sample biomarkers using omic data profiling. <i>Bioinformatics</i> , 2019, 35, 3651-3662.	4.1	7
31	APID database: redefining protein-protein interaction experimental evidences and binary interactomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	113
32	Infectious stimuli promote malignant B-cell acute lymphoblastic leukemia in the absence of AID. <i>Nature Communications</i> , 2019, 10, 5563.	12.8	21
33	Bioinformatics in Latin America and SolBio impact, a tale of spin-off and expansion around genomes and protein structures. <i>Briefings in Bioinformatics</i> , 2019, 20, 390-397.	6.5	10
34	Loss of Pax5 Exploits Sca1-BCR-ABLp190 Susceptibility to Confer the Metabolic Shift Essential for pB-ALL. <i>Cancer Research</i> , 2018, 78, 2669-2679.	0.9	37
35	Regulatory motifs found in the small heat shock protein (sHSP) gene family in tomato. <i>BMC Genomics</i> , 2018, 19, 860.	2.8	32
36	Survival marker genes of colorectal cancer derived from consistent transcriptomic profiling. <i>BMC Genomics</i> , 2018, 19, 857.	2.8	48

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37	Human Interactomics: Comparative Analysis of Different Protein Interaction Resources and Construction of a Cancer Protein-Drug Bipartite Network. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018, 111, 263-282.	2.3	10
38	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
39	JAMI: a Java library for molecular interactions and data interoperability. <i>BMC Bioinformatics</i> , 2018, 19, 133.	2.6	6
40	Searching the overlap between network modules with specific betweenness (S2B) and its application to cross-disease analysis. <i>Scientific Reports</i> , 2018, 8, 11555.	3.3	15
41	Lmo2 expression defines tumor cell identity during T-cell leukemogenesis. <i>EMBO Journal</i> , 2018, 37, .	7.8	32
42	A Tumor Suppressor Role for Bank1 in B-Cell Precursor Acute Lymphoblastic Leukemia. <i>Blood</i> , 2018, 132, 1333-1333.	1.4	0
43	Linking amyotrophic lateral sclerosis and spinal muscular atrophy through <i>scRNA</i> -transcriptome homeostasis: a genomics perspective. <i>Journal of Neurochemistry</i> , 2017, 141, 12-30.	3.9	25
44	Infection Exposure Promotes <i>ETV6-RUNX1</i> Precursor B-cell Leukemia via Impaired H3K4 Demethylases. <i>Cancer Research</i> , 2017, 77, 4365-4377.	0.9	76
45	Screening and Validation of Novel Biomarkers in Osteoarticular Pathologies by Comprehensive Combination of Protein Array Technologies. <i>Journal of Proteome Research</i> , 2017, 16, 1890-1899.	3.7	23
46	Crebbp loss cooperates with Bcl2 overexpression to promote lymphoma in mice. <i>Blood</i> , 2017, 129, 2645-2656.	1.4	84
47	Micro <i>scRNA</i> (miR)-203 and miR-205 expression patterns identify subgroups of prognosis in cutaneous squamous cell carcinoma. <i>British Journal of Dermatology</i> , 2017, 177, 168-178.	1.5	35
48	Epidermal Growth Factor Signaling towards Proliferation: Modeling and Logic Inference Using Forward and Backward Search. <i>BioMed Research International</i> , 2017, 2017, 1-11.	1.9	12
49	Ten simple rules for forming a scientific professional society. <i>PLoS Computational Biology</i> , 2017, 13, e1005226.	3.2	7
50	Mesenchymal stromal cells (MSC) from JAK2+ myeloproliferative neoplasms differ from normal MSC and contribute to the maintenance of neoplastic hematopoiesis. <i>PLoS ONE</i> , 2017, 12, e0182470.	2.5	19
51	Microvesicles from Mesenchymal Stromal Cells Are Involved in HPC-Microenvironment Crosstalk in Myelodysplastic Patients. <i>PLoS ONE</i> , 2016, 11, e0146722.	2.5	70
52	Identification of expression patterns in the progression of disease stages by integration of transcriptomic data. <i>BMC Bioinformatics</i> , 2016, 17, 432.	2.6	15
53	Path2enet: generation of human pathway-derived networks in an expression specific context. <i>BMC Genomics</i> , 2016, 17, 731.	2.8	1
54	Insights into the human mesenchymal stromal/stem cell identity through integrative transcriptomic profiling. <i>BMC Genomics</i> , 2016, 17, 944.	2.8	55

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55	Evolutionary hallmarks of the human proteome: chasing the age and coregulation of protein-coding genes. <i>BMC Genomics</i> , 2016, 17, 725.	2.8	4
56	APID interactomes: providing proteome-based interactomes with controlled quality for multiple species and derived networks. <i>Nucleic Acids Research</i> , 2016, 44, W529-W535.	14.5	112
57	Matrix-Gla protein promotes osteosarcoma lung metastasis and associates with poor prognosis. <i>Journal of Pathology</i> , 2016, 239, 438-449.	4.5	42
58	Extracellular Vesicles Play an Important Role in Intercellular Communication Between Bone Marrow Stroma and Hematopoietic Progenitor Cells in Myeloproliferative Neoplasms. <i>Blood</i> , 2016, 128, 1957-1957.	1.4	3
59	CREBBP Loss Cooperates with BCL2 Over-Expression to Promote Lymphoma in Mice. <i>Blood</i> , 2016, 128, 458-458.	1.4	1
60	Analyse multiple disease subtypes and build associated gene networks using genome-wide expression profiles. <i>BMC Genomics</i> , 2015, 16, S3.	2.8	17
61	Deregulation of Genes Related to Iron and Mitochondrial Metabolism in Refractory Anemia with Ring Sideroblasts. <i>PLoS ONE</i> , 2015, 10, e0126555.	2.5	21
62	Functional Gene Networks: R/Bioc package to generate and analyse gene networks derived from functional enrichment and clustering. <i>Bioinformatics</i> , 2015, 31, 1686-1688.	4.1	81
63	GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training. <i>PLoS Computational Biology</i> , 2015, 11, e1004143.	3.2	52
64	Unraveling heterogeneous susceptibility and the evolution of breast cancer using a systems biology approach. <i>Genome Biology</i> , 2015, 16, 40.	8.8	23
65	Infection Exposure Is a Causal Factor in B-cell Precursor Acute Lymphoblastic Leukemia as a Result of <i>Pax5</i> -Inherited Susceptibility. <i>Cancer Discovery</i> , 2015, 5, 1328-1343.	9.4	117
66	Cystatin D Locates in the Nucleus at Sites of Active Transcription and Modulates Gene and Protein Expression. <i>Journal of Biological Chemistry</i> , 2015, 290, 26533-26548.	3.4	23
67	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. <i>Journal of Proteome Research</i> , 2015, 14, 3530-3540.	3.7	16
68	In Vitro Transcription/Translation System: A Versatile Tool in the Search for Missing Proteins. <i>Journal of Proteome Research</i> , 2015, 14, 3441-3451.	3.7	11
69	ColoLipidGene: signature of lipid metabolism-related genes to predict prognosis in stage-II colon cancer patients. <i>Oncotarget</i> , 2015, 6, 7348-7363.	1.8	69
70	A New ETV6-RUNX1 In Vivo Model Produces a Phenocopy of the Human Pb-ALL. <i>Blood</i> , 2015, 126, 3658-3658.	1.4	0
71	A robust estimation of exon expression to identify alternative spliced genes applied to human tissues and cancer samples. <i>BMC Genomics</i> , 2014, 15, 879.	2.8	12
72	A gene signature of bone metastatic colonization sensitizes for tumor-induced osteolysis and predicts survival in lung cancer. <i>Oncogene</i> , 2014, 33, 5090-5099.	5.9	35

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73	Gene Expression Analysis and Profiling of Microarrays Data and RNA-Sequencing Data. Comprehensive Analytical Chemistry, 2014, 63, 355-384.	1.3	2
74	Identification of a characteristic copy number alteration profile by high-resolution single nucleotide polymorphism arrays associated with metastatic sporadic colorectal cancer. Cancer, 2014, 120, 1948-1959.	4.1	17
75	Transcriptomic portrait of human Mesenchymal Stromal/Stem cells isolated from bone marrow and placenta. BMC Genomics, 2014, 15, 910.	2.8	59
76	TET2 Overexpression in Chronic Lymphocytic Leukemia Is Unrelated to the Presence of TET2 Variations. BioMed Research International, 2014, 2014, 1-6.	1.9	12
77	miRNA cargo within exosome-like vesicle transfer influences metastatic bone colonization. Molecular Oncology, 2014, 8, 689-703.	4.6	155
78	A Proteome-Scale Map of the Human Interactome Network. Cell, 2014, 159, 1212-1226.	28.9	1,199
79	RHOB influences lung adenocarcinoma metastasis and resistance in a host-sensitive manner. Molecular Oncology, 2014, 8, 196-206.	4.6	27
80	A Logic Computational Framework to Query Dynamics on Complex Biological Pathways. Advances in Intelligent Systems and Computing, 2014, , 207-214.	0.6	6
81	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
82	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
83	Best practices in bioinformatics training for life scientists. Briefings in Bioinformatics, 2013, 14, 528-537.	6.5	51
84	iAnn: an event sharing platform for the life sciences. Bioinformatics, 2013, 29, 1919-1921.	4.1	6
85	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
86	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
87	Integrating literature-constrained and data-driven inference of signalling networks. Bioinformatics, 2012, 28, 2311-2317.	4.1	34
88	Bioinformatics Training Network (BTN): a community resource for bioinformatics trainers. Briefings in Bioinformatics, 2012, 13, 383-389.	6.5	23
89	Protein-protein interaction networks: unraveling the wiring of molecular machines within the cell. Briefings in Functional Genomics, 2012, 11, 489-496.	2.7	74
90	Cortactin (CTTN) overexpression in osteosarcoma correlates with advanced stage and reduced survival. Cancer Biomarkers, 2012, 10, 35-41.	1.7	19

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91	Impaired expression of DICER, DROSHA, SBDS and some microRNAs in mesenchymal stromal cells from myelodysplastic syndrome patients. <i>Haematologica</i> , 2012, 97, 1218-1224.	3.5	83
92	Molecular Characterization of Chronic Lymphocytic Leukemia Patients with a High Number of Losses in 13q14. <i>PLoS ONE</i> , 2012, 7, e48485.	2.5	37
93	Identification of a novel recurrent gain on 20q13 in chronic lymphocytic leukemia by array CGH and gene expression profiling. <i>Annals of Oncology</i> , 2012, 23, 2138-2146.	1.2	13
94	Protein Interactions: Mapping Interactome Networks to Support Drug Target Discovery and Selection. <i>Methods in Molecular Biology</i> , 2012, 910, 279-296.	0.9	13
95	Combined analysis of genome-wide expression and copy number profiles to identify key altered genomic regions in cancer. <i>BMC Genomics</i> , 2012, 13, S5.	2.8	7
96	Prognostic Impact of del(17p) and del(22q) as Assessed by Interphase FISH in Sporadic Colorectal Carcinomas. <i>PLoS ONE</i> , 2012, 7, e42683.	2.5	18
97	Receptor of Activated Protein C Promotes Metastasis and Correlates with Clinical Outcome in Lung Adenocarcinoma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012, 186, 96-105.	5.6	45
98	Unique genetic profile of sporadic colorectal cancer liver metastasis versus primary tumors as defined by high-density single-nucleotide polymorphism arrays. <i>Modern Pathology</i> , 2012, 25, 590-601.	5.5	32
99	Epigenetic Silencing of BCL2, ETS1, IL27RA and DICER1 in Low-Risk MDS Patients. <i>Blood</i> , 2012, 120, 1704-1704.	1.4	0
100	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	19.0	274
101	Segmentation of genomic and transcriptomic microarrays data reveals major correlation between DNA copy number aberrations and gene loci expression. <i>Genomics</i> , 2011, 97, 86-93.	2.9	23
102	Functional Integrative Levels in the Human Interactome Recapitulate Organ Organization. <i>PLoS ONE</i> , 2011, 6, e22051.	2.5	20
103	Transcriptional repression of the tumor suppressor DRO1 by AIB1. <i>FEBS Letters</i> , 2011, 585, 3041-3046.	2.8	15
104	Ten Simple Rules for Developing a Short Bioinformatics Training Course. <i>PLoS Computational Biology</i> , 2011, 7, e1002245.	3.2	29
105	Functional Analysis beyond Enrichment: Non-Redundant Reciprocal Linkage of Genes and Biological Terms. <i>PLoS ONE</i> , 2011, 6, e24289.	2.5	44
106	Lenalidomide Differentially Modifies the Genomic Profile and miRNA Expression of Mesenchymal Stromal Cells From Patients with 5q- Syndrome. <i>Blood</i> , 2011, 118, 3810-3810.	1.4	0
107	GATEplorer: Genomic and Transcriptomic Explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. <i>BMC Bioinformatics</i> , 2010, 11, 221.	2.6	75
108	Structural domain domain interactions: Assessment and comparison with protein protein interaction data to improve the interactome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 109-117.	2.6	21

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109	Deregulation of microRNA expression in the different genetic subtypes of multiple myeloma and correlation with gene expression profiling. <i>Leukemia</i> , 2010, 24, 629-637.	7.2	188
110	Bioinformatics training: a review of challenges, actions and support requirements. <i>Briefings in Bioinformatics</i> , 2010, 11, 544-551.	6.5	51
111	Protein-Protein Interactions Essentials: Key Concepts to Building and Analyzing Interactome Networks. <i>PLoS Computational Biology</i> , 2010, 6, e1000807.	3.2	496
112	Mapping of Genetic Abnormalities of Primary Tumours from Metastatic CRC by High-Resolution SNP Arrays. <i>PLoS ONE</i> , 2010, 5, e13752.	2.5	22
113	Combining Dissimilarities in a Hyper Reproducing Kernel Hilbert Space for Complex Human Cancer Prediction. <i>Journal of Biomedicine and Biotechnology</i> , 2009, 2009, 1-9.	3.0	7
114	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. <i>Clinical Cancer Research</i> , 2009, 15, 5082-5091.	7.0	32
115	RasGRF1 disruption causes retinal photoreception defects and associated transcriptomic alterations. <i>Journal of Neurochemistry</i> , 2009, 110, 641-652.	3.9	40
116	Serum-dependent transcriptional networks identify distinct functional roles for H-Ras and N-Ras during initial stages of the cell cycle. <i>Genome Biology</i> , 2009, 10, R123.	9.6	14
117	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. <i>Haematologica</i> , 2009, 94, 364-371.	3.5	59
118	Improving k-NN for Human Cancer Classification Using the Gene Expression Profiles. <i>Lecture Notes in Computer Science</i> , 2009, , 107-118.	1.3	6
119	Kernel Alignment k-NN for Human Cancer Classification Using the Gene Expression Profiles. <i>Lecture Notes in Computer Science</i> , 2009, , 195-204.	1.3	1
120	Dynamic flexibility in the structure and function of photosystem II in higher plant thylakoid membranes: the grana enigma. <i>Photosynthesis Research</i> , 2008, 98, 575-587.	2.9	110
121	Role of electrostatics on membrane binding, aggregation and destabilization induced by NAD(P)H dehydrogenases. Implication in membrane fusion. <i>Biophysical Chemistry</i> , 2008, 137, 126-132.	2.8	7
122	Interleukin-12 inhibits liver-specific drug-inducible systems in vivo. <i>Gene Therapy</i> , 2008, 15, 277-288.	4.5	16
123	Classification of multiple cancer types in a Hyper Reproducing Kernel Hilbert Space. , 2008, , .		0
124	Transcriptomic Effects of Tet-On and Mifepristone-Inducible Systems in Mouse Liver. <i>Human Gene Therapy</i> , 2008, 19, 1233-1248.	2.7	16
125	Combining Dissimilarities in a Hyper Reproducing Kernel Hilbert Space for Complex Human Cancer Prediction. , 2008, , .		0
126	A Novel Lung Cancer Signature Mediates Metastatic Bone Colonization by a Dual Mechanism. <i>Cancer Research</i> , 2008, 68, 2275-2285.	0.9	89

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127	Human Gene Coexpression Landscape: Confident Network Derived from Tissue Transcriptomic Profiles. PLoS ONE, 2008, 3, e3911.	2.5	213
128	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
129	APID2NET: unified interactome graphic analyzer. Bioinformatics, 2007, 23, 2495-2497.	4.1	72
130	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
131	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
132	Ensemble of Kernel Based Classifiers to Improve the Human Cancer Prediction using DNA Microarrays. , 2007, , .		0
133	Oxygen-evolving extrinsic proteins (PsbO,P,Q,R): Bioinformatic and functional analysis. Biochimica Et Biophysica Acta - Bioenergetics, 2007, 1767, 575-582.	1.0	45
134	Methylseleninic acid enhances the effect of etoposide to inhibit prostate cancer growth in vivo. International Journal of Cancer, 2007, 121, 1197-1204.	5.1	8
135	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
136	The minimum information required for reporting a molecular interaction experiment (MIMIx). Nature Biotechnology, 2007, 25, 894-898.	17.5	274
137	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
138	Linear array of conserved sequence motifs to discriminate protein subfamilies: study on pyridine nucleotide-disulfide reductases. BMC Bioinformatics, 2007, 8, 96.	2.6	9
139	Combining dissimilarity based classifiers for cancer prediction using gene expression profiles. BMC Bioinformatics, 2007, 8, .	2.6	12
140	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
141	APID: Agile Protein Interaction DataAnalyzer. Nucleic Acids Research, 2006, 34, W298-W302.	14.5	209
142	Proteomic profiles of thylakoid membranes and changes in response to iron deficiency. Photosynthesis Research, 2006, 89, 141-155.	2.9	98
143	Algorithm to find gene expression profiles of deregulation and identify families of disease-altered genes. Bioinformatics, 2006, 22, 1103-1110.	4.1	22
144	Mobilisation with G-CSF in healthy donors promotes a high but temporal deregulation of genes. Leukemia, 2005, 19, 1088-1091.	7.2	43

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145	The 1.49Å... Resolution Crystal Structure of PsbQ from Photosystem II of Spinacia oleracea Reveals a PPII Structure in the N-terminal Region. <i>Journal of Molecular Biology</i> , 2005, 350, 1051-1060.	4.2	60
146	Structure and evolution of the extrinsic proteins that stabilize the oxygen-evolving engine. <i>Photochemical and Photobiological Sciences</i> , 2005, 4, 1003.	2.9	27
147	Analysis of the Structure of the PsbO Protein and its Implications. <i>Photosynthesis Research</i> , 2004, 81, 329-343.	2.9	117
148	Single mutations of residues outside the active center of the xylanase Xys1AŽŽ” from <i>Streptomyces halstedii</i> M8 affect its activity. <i>FEMS Microbiology Letters</i> , 2004, 240, 237-243.	1.8	15
149	Interactome Data and Databases: Different Types of Protein Interaction. <i>Comparative and Functional Genomics</i> , 2004, 5, 173-178.	2.0	30
150	Structural Stability of the PsbQ Protein of Higher Plant Photosystem II. <i>Biochemistry</i> , 2004, 43, 14171-14179.	2.5	4
151	Evolution of oxygenic photosynthesis: genome-wide analysis of the OEC extrinsic proteins. <i>Trends in Plant Science</i> , 2004, 9, 18-25.	8.8	95
152	The single tryptophan of the PsbQ protein of photosystem II is at the end of a 4-ŕ±-helical bundle domain. <i>FEBS Journal</i> , 2003, 270, 3916-3927.	0.2	10
153	Structural Analysis of the PsbQ Protein of Photosystem II by Fourier Transform Infrared and Circular Dichroic Spectroscopy and by Bioinformatic Methods. <i>Biochemistry</i> , 2003, 42, 1000-1007.	2.5	22
154	Calcium-Dependent Conformational Change and Thermal Stability of the Isolated PsbO Protein Detected by FTIR Spectroscopy. <i>Biochemistry</i> , 2003, 42, 11831-11838.	2.5	41
155	Fluorescence induction of Photosystem II membranes shows the steps till reduction and protonation of the quinone pool. <i>Journal of Plant Physiology</i> , 2003, 160, 1499-1506.	3.5	17
156	Three-dimensional Electron Cryo-microscopy Study of the Extrinsic Domains of the Oxygen-evolving Complex of Spinach. <i>Journal of Biological Chemistry</i> , 2002, 277, 15006-15012.	3.4	49
157	Comparative Analysis of Chloroplast Genomes: Functional Annotation, Genome-Based Phylogeny, and Deduced Evolutionary Patterns. <i>Genome Research</i> , 2002, 12, 567-583.	5.5	106
158	Evidence for Cu(I)-thiolate ligation and prediction of a putative copper-binding site in the <i>Escherichia coli</i> NADH dehydrogenase-2. <i>Archives of Biochemistry and Biophysics</i> , 2002, 405, 87-94.	3.0	54
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