

Carlos Prieto

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

2,156
citations

304602

22
h-index

233338

45
g-index

47
all docs

47
docs citations

47
times ranked

4323
citing authors

#	ARTICLE	IF	CITATIONS
1	Effects of copy number variations on brain structure and risk for psychiatric illness: Large-scale studies from the ENIGMA working groups on CNVs. <i>Human Brain Mapping</i> , 2022, 43, 300-328.	1.9	30
2	SingleCAnalyzer: Interactive Analysis of Single Cell RNA-Seq Data on the Cloud. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	14
3	Aripiprazole as a Candidate Treatment of COVID-19 Identified Through Genomic Analysis. <i>Frontiers in Pharmacology</i> , 2021, 12, 646701.	1.6	24
4	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. <i>Translational Psychiatry</i> , 2021, 11, 182.	2.4	24
5	Whole-Exome Sequencing Reveals Recurrent but Heterogeneous Mutational Profiles in Sporadic WHO Grade 1 Meningiomas. <i>Frontiers in Oncology</i> , 2021, 11, 740782.	1.3	5
6	RaNA-Seq: interactive RNA-Seq analysis from FASTQ files to functional analysis. <i>Bioinformatics</i> , 2020, 36, 1955-1956.	1.8	64
7	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. <i>Molecular Psychiatry</i> , 2020, 25, 584-602.	4.1	49
8	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. <i>JAMA Psychiatry</i> , 2020, 77, 420.	6.0	54
9	Frequency and prognostic impact of KIT and other genetic variants in indolent systemic mastocytosis. <i>Blood</i> , 2019, 134, 456-468.	0.6	44
10	Time dependent expression of the blood biomarkers EIF2D and TOX in patients with schizophrenia. <i>Brain, Behavior, and Immunity</i> , 2019, 80, 909-915.	2.0	3
11	Sex differences in gene expression related to antipsychotic induced weight gain. <i>PLoS ONE</i> , 2019, 14, e0215477.	1.1	13
12	Altered gene expression in antipsychotic-induced weight gain. <i>NPJ Schizophrenia</i> , 2019, 5, 7.	2.0	16
13	Defects in memory B-cell and plasma cell subsets expressing different immunoglobulin-subclasses in patients with CVID and immunoglobulin subclass deficiencies. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 809-824.	1.5	55
14	The biological age linked to oxidative stress modifies breast cancer aggressiveness. <i>Free Radical Biology and Medicine</i> , 2018, 120, 133-146.	1.3	17
15	RJSplot: Interactive Graphs with R. <i>Molecular Informatics</i> , 2018, 37, 1700090.	1.4	6
16	Defining the Species <i>Micromonospora saelicesensis</i> and <i>Micromonospora noduli</i> Under the Framework of Genomics. <i>Frontiers in Microbiology</i> , 2018, 9, 1360.	1.5	32
17	Blood Gene Expression Profile Predicts Response to Antipsychotics. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 73.	1.4	18
18	Supplementary data for the biological age linked to oxidative stress modifies breast cancer aggressiveness. <i>Data in Brief</i> , 2018, 18, 1172-1184.	0.5	2

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19	D3GB: An Interactive Genome Browser for R, Python, and WordPress. <i>Journal of Computational Biology</i> , 2017, 24, 447-449.	0.8	12
20	Gene clustering for time-series microarray with production outputs. <i>Soft Computing</i> , 2016, 20, 4301-4312.	2.1	5
21	APID interactomes: providing proteome-based interactomes with controlled quality for multiple species and derived networks. <i>Nucleic Acids Research</i> , 2016, 44, W529-W535.	6.5	112
22	Comparative blood transcriptome analysis in idiopathic and LRRK2 G2019S-associated Parkinson's disease. <i>Neurobiology of Aging</i> , 2016, 38, 214.e1-214.e5.	1.5	31
23	Characterization of Nonribosomal Peptide Synthetases with NRPSp. <i>Methods in Molecular Biology</i> , 2016, 1401, 273-278.	0.4	7
24	Identification of candidate genes for Parkinson's disease through blood transcriptome analysis in LRRK2-G2019S carriers, idiopathic cases, and controls. <i>Neurobiology of Aging</i> , 2015, 36, 1105-1109.	1.5	31
25	Schizophrenia Gene Expression Profile Reverted to Normal Levels by Antipsychotics. <i>International Journal of Neuropsychopharmacology</i> , 2015, 18, .	1.0	37
26	PcFKH1, a novel regulatory factor from the forkhead family, controls the biosynthesis of penicillin in <i>Penicillium chrysogenum</i> . <i>Biochimie</i> , 2015, 115, 162-176.	1.3	12
27	A CLUSTER MERGING METHOD FOR TIME SERIES MICROARRAY WITH PRODUCTION VALUES. <i>International Journal of Neural Systems</i> , 2014, 24, 1450018.	3.2	13
28	Gene Clustering in Time Series Microarray Analysis. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 289-298.	0.5	1
29	Gimatecan and other camptothecin derivatives poison <i>Leishmania</i> DNA-topoisomerase IB leading to a strong leishmanicidal effect. <i>Biochemical Pharmacology</i> , 2013, 85, 1433-1440.	2.0	43
30	Draft Genome of <i>Streptomyces tsukubaensis</i> NRRL 18488, the Producer of the Clinically Important Immunosuppressant Tacrolimus (FK506). <i>Journal of Bacteriology</i> , 2012, 194, 3756-3757.	1.0	46
31	The regulatory factor PcRFX1 controls the expression of the three genes of β -lactam biosynthesis in <i>Penicillium chrysogenum</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 866-881.	0.9	22
32	NRPSp: non-ribosomal peptide synthase substrate predictor. <i>Bioinformatics</i> , 2012, 28, 426-427.	1.8	95
33	A pentapeptide signature motif plays a pivotal role in <i>Leishmania</i> DNA topoisomerase IB activity and camptothecin sensitivity. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2012, 1820, 2062-2071.	1.1	14
34	Protein Interactions: Mapping Interactome Networks to Support Drug Target Discovery and Selection. <i>Methods in Molecular Biology</i> , 2012, 910, 279-296.	0.4	13
35	Merge Method for Shape-Based Clustering in Time Series Microarray Analysis. <i>Lecture Notes in Computer Science</i> , 2012, , 834-841.	1.0	0
36	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	9.0	274

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37	Functional Integrative Levels in the Human Interactome Recapitulate Organ Organization. PLoS ONE, 2011, 6, e22051.	1.1	20
38	Cross-talk of global nutritional regulators in the control of primary and secondary metabolism in <i>Streptomyces</i> . Microbial Biotechnology, 2011, 4, 165-174.	2.0	80
39	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.	1.5	21
40	Human Gene Coexpression Landscape: Confident Network Derived from Tissue Transcriptomic Profiles. PLoS ONE, 2008, 3, e3911.	1.1	213
41	APID2NET: unified interactome graphic analyzer. Bioinformatics, 2007, 23, 2495-2497.	1.8	72
42	The minimum information required for reporting a molecular interaction experiment (MIMIx). Nature Biotechnology, 2007, 25, 894-898.	9.4	274
43	APID: Agile Protein Interaction DataAnalyzer. Nucleic Acids Research, 2006, 34, W298-W302.	6.5	209
44	Algorithm to find gene expression profiles of deregulation and identify families of disease-altered genes. Bioinformatics, 2006, 22, 1103-1110.	1.8	22