Carlos Prieto

List of Publications by Year
in descending order

44 papers	2,156 citations	304743 22 h-index
47 all docs	47 docs citations	47 times ranked

233421 45 g-index
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<scp>ENIGMA</scp>working groups on<scp>CNVs</scp>. Human Brain Mapping, 2022, 43, 300-328.	3.6	30
2	SingleCAnalyzer: Interactive Analysis of Single Cell RNA-Seq Data on the Cloud. Frontiers in Bioinformatics, 2022, 2, .	2.1	14
3	Aripiprazole as a Candidate Treatment of COVID-19 Identified Through Genomic Analysis. Frontiers in Pharmacology, 2021, 12, 646701.	3.5	24
4	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	4.8	24
5	Whole-Exome Sequencing Reveals Recurrent but Heterogeneous Mutational Profiles in Sporadic WHO Grade 1 Meningiomas. Frontiers in Oncology, 2021, 11, 740782.	2.8	5
6	RaNA-Seq: interactive RNA-Seq analysis from FASTQ files to functional analysis. Bioinformatics, 2020, 36, 1955-1956.	4.1	64
7	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. Molecular Psychiatry, 2020, 25, 584-602.	7.9	49
8	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420.	11.0	54
9	Frequency and prognostic impact of KIT and other genetic variants in indolent systemic mastocytosis. Blood, 2019, 134, 456-468.	1.4	44
10	Time dependent expression of the blood biomarkers EIF2D and TOX in patients with schizophrenia. Brain, Behavior, and Immunity, 2019, 80, 909-915.	4.1	3
11	Sex differences in gene expression related to antipsychotic induced weight gain. PLoS ONE, 2019, 14, e0215477.	2.5	13
12	Altered gene expression in antipsychotic-induced weight gain. NPJ Schizophrenia, 2019, 5, 7.	3.6	16
13	Defects in memory B-cell and plasma cell subsets expressing different immunoglobulin-subclasses in patients with CVID and immunoglobulin subclass deficiencies. Journal of Allergy and Clinical Immunology, 2019, 144, 809-824.	2.9	55
14	The biological age linked to oxidative stress modifies breast cancer aggressiveness. Free Radical Biology and Medicine, 2018, 120, 133-146.	2.9	17
15	RJSplot: Interactive Graphs with R. Molecular Informatics, 2018, 37, 1700090.	2.5	6
16	Defining the Species Micromonospora saelicesensis and Micromonospora noduli Under the Framework of Genomics. Frontiers in Microbiology, 2018, 9, 1360.	3.5	32
17	Blood Gene Expression Profile Predicts Response to Antipsychotics. Frontiers in Molecular Neuroscience, 2018, 11, 73.	2.9	18
18	Supplementary data for the biological age linked to oxidative stress modifies breast cancer aggressiveness. Data in Brief, 2018, 18, 1172-1184.	1.0	2

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19	D3GB: An Interactive Genome Browser for R, Python, and WordPress. Journal of Computational Biology, 2017, 24, 447-449.	1.6	12
20	Gene clustering for time-series microarray with production outputs. Soft Computing, 2016, 20, 4301-4312.	3.6	5
21	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
22	Comparative blood transcriptome analysis in idiopathic and LRRK2 G2019S–associated Parkinson's disease. Neurobiology of Aging, 2016, 38, 214.e1-214.e5.	3.1	31
23	Characterization of Nonribosomal Peptide Synthetases with NRPSsp. Methods in Molecular Biology, 2016, 1401, 273-278.	0.9	7
24	Identification of candidate genes for Parkinson's disease through blood transcriptome analysis in LRRK2-G2019S carriers, idiopathic cases, and controls. Neurobiology of Aging, 2015, 36, 1105-1109.	3.1	31
25	Schizophrenia Gene Expression Profile Reverted to Normal Levels by Antipsychotics. International Journal of Neuropsychopharmacology, 2015, 18, .	2.1	37
26	PcFKH1, a novel regulatory factor from the forkhead family, controls the biosynthesis of penicillin in Penicillium chrysogenum. Biochimie, 2015, 115, 162-176.	2.6	12
27	A CLUSTER MERGING METHOD FOR TIME SERIES MICROARRAY WITH PRODUCTION VALUES. International Journal of Neural Systems, 2014, 24, 1450018.	5.2	13
28	Gene Clustering in Time Series Microarray Analysis. Advances in Intelligent Systems and Computing, 2014, , 289-298.	0.6	1
29	Gimatecan and other camptothecin derivatives poison Leishmania DNA-topoisomerase IB leading to a strong leishmanicidal effect. Biochemical Pharmacology, 2013, 85, 1433-1440.	4.4	43
30	Draft Genome of Streptomyces tsukubaensis NRRL 18488, the Producer of the Clinically Important Immunosuppressant Tacrolimus (FK506). Journal of Bacteriology, 2012, 194, 3756-3757.	2.2	46
31	The regulatory factor PcRFX1 controls the expression of the three genes of β-lactam biosynthesis in Penicillium chrysogenum. Fungal Genetics and Biology, 2012, 49, 866-881.	2.1	22
32	NRPSsp: non-ribosomal peptide synthase substrate predictor. Bioinformatics, 2012, 28, 426-427.	4.1	95
33	A pentapeptide signature motif plays a pivotal role in Leishmania DNA topoisomerase IB activity and camptothecin sensitivity. Biochimica Et Biophysica Acta - General Subjects, 2012, 1820, 2062-2071.	2.4	14
34	Protein Interactions: Mapping Interactome Networks to Support Drug Target Discovery and Selection. Methods in Molecular Biology, 2012, 910, 279-296.	0.9	13
35	Merge Method for Shape-Based Clustering in Time Series Microarray Analysis. Lecture Notes in Computer Science, 2012, , 834-841.	1.3	0
36	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529.	19.0	274

#	ARTICLE	IF	CITATIONS
37	Functional Integrative Levels in the Human Interactome Recapitulate Organ Organization. PLoS ONE, 2011, 6, e22051.	2.5	20
38	Crossâ€talk of global nutritional regulators in the control of primary and secondary metabolism in <i>Streptomyces</i>. Microbial Biotechnology, 2011, 4, 165-174.	4.2	80
39	Structural domainâ€"domain interactions: Assessment and comparison with proteinâ€"protein interaction data to improve the interactome. Proteins: Structure, Function and Bioinformatics, 2010, 78, 109-117.	2.6	21
40	Human Gene Coexpression Landscape: Confident Network Derived from Tissue Transcriptomic Profiles. PLoS ONE, 2008, 3, e3911.	2.5	213
41	APID2NET: unified interactome graphic analyzer. Bioinformatics, 2007, 23, 2495-2497.	4.1	72
42	The minimum information required for reporting a molecular interaction experiment (MIMIx). Nature Biotechnology, 2007, 25, 894-898.	17.5	274
43	APID: Agile Protein Interaction DataAnalyzer. Nucleic Acids Research, 2006, 34, W298-W302.	14.5	209
44	Algorithm to find gene expression profiles of deregulation and identify families of disease-altered genes. Bioinformatics, 2006, 22, 1103-1110.	4.1	22