

# Carlos Prieto

## List of Publications by Year in descending order

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Version: 2024-02-01

44  
papers

2,156  
citations

331259

21  
h-index

233125

45  
g-index

47  
all docs

47  
docs citations

47  
times ranked

4323  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | The minimum information required for reporting a molecular interaction experiment (MIMiX). <i>Nature Biotechnology</i> , 2007, 25, 894-898.   | 9.4 | 274       |
| 2  | PSICQUIC and PSIScore: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.  | 9.0 | 274       |
| 3  | Human Gene Coexpression Landscape: Confident Network Derived from Tissue Transcriptomic Profiles. <i>PLoS ONE</i> , 2008, 3, e3911.   | 1.1 | 213       |
| 4  | APID: Agile Protein Interaction DataAnalyzer. <i>Nucleic Acids Research</i> , 2006, 34, W298-W302.  | 6.5 | 209       |
| 5  | 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       |
| 6  | NRPSp: non-ribosomal peptide synthase substrate predictor. <i>Bioinformatics</i> , 2012, 28, 426-427.   | 1.8 | 95        |
| 7  | Crosstalk of global nutritional regulators in the control of primary and secondary metabolism in <i>Streptomyces</i> . <i>Microbial Biotechnology</i> , 2011, 4, 165-174.   | 2.0 | 80        |
| 8  | APID2NET: unified interactome graphic analyzer. <i>Bioinformatics</i> , 2007, 23, 2495-2497.  | 1.8 | 72        |
| 9  | RaNA-Seq: interactive RNA-Seq analysis from FASTQ files to functional analysis. <i>Bioinformatics</i> , 2020, 36, 1955-1956.  | 1.8 | 64        |
| 10 | 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        |
| 11 | 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        |
| 12 | 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        |
| 13 | 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        |
| 14 | Frequency and prognostic impact of KIT and other genetic variants in indolent systemic mastocytosis. <i>Blood</i> , 2019, 134, 456-468.   | 0.6 | 44        |
| 15 | 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        |
| 16 | Schizophrenia Gene Expression Profile Reverted to Normal Levels by Antipsychotics. <i>International Journal of Neuropsychopharmacology</i> , 2015, 18, .  | 1.0 | 37        |
| 17 | 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        |
| 18 | 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        |

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|----|---|-----|-----------|
| 19 | 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        |
| 20 | 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        |
| 21 | Aripiprazole as a Candidate Treatment of COVID-19 Identified Through Genomic Analysis. <i>Frontiers in Pharmacology</i> , 2021, 12, 646701.   | 1.6 | 24        |
| 22 | 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        |
| 23 | Algorithm to find gene expression profiles of deregulation and identify families of disease-altered genes. <i>Bioinformatics</i> , 2006, 22, 1103-1110.   | 1.8 | 22        |
| 24 | The regulatory factor PcRFX1 controls the expression of the three genes of Î²-lactam biosynthesis in <i>Penicillium chrysogenum</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 866-881.                   | 0.9 | 22        |
| 25 | 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. | 1.5 | 21        |
| 26 | Functional Integrative Levels in the Human Interactome Recapitulate Organ Organization. <i>PLoS ONE</i> , 2011, 6, e22051.  | 1.1 | 20        |
| 27 | Blood Gene Expression Profile Predicts Response to Antipsychotics. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 73.   | 1.4 | 18        |
| 28 | 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        |
| 29 | Altered gene expression in antipsychotic-induced weight gain. <i>NPJ Schizophrenia</i> , 2019, 5, 7.  | 2.0 | 16        |
| 30 | A pentapeptide signature motif plays a pivotal role in Leishmania DNA topoisomerase IB activity and camptothecin sensitivity. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2012, 1820, 2062-2071.  | 1.1 | 14        |
| 31 | SingleCAnalyzer: Interactive Analysis of Single Cell RNA-Seq Data on the Cloud. <i>Frontiers in Bioinformatics</i> , 2022, 2, .   | 1.0 | 14        |
| 32 | 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        |
| 33 | A CLUSTER MERGING METHOD FOR TIME SERIES MICROARRAY WITH PRODUCTION VALUES. <i>International Journal of Neural Systems</i> , 2014, 24, 1450018.   | 3.2 | 13        |
| 34 | Sex differences in gene expression related to antipsychotic induced weight gain. <i>PLoS ONE</i> , 2019, 14, e0215477.  | 1.1 | 13        |
| 35 | 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        |
| 36 | D3GB: An Interactive Genome Browser for R, Python, and WordPress. <i>Journal of Computational Biology</i> , 2017, 24, 447-449.  | 0.8 | 12        |

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|----|--|-----|-----------|
| 37 | Characterization of Nonribosomal Peptide Synthetases with NRPSsp. <i>Methods in Molecular Biology</i> , 2016, 1401, 273-278.   | 0.4 | 7         |
| 38 | RJSplot: Interactive Graphs with R. <i>Molecular Informatics</i> , 2018, 37, 1700090.  | 1.4 | 6         |
| 39 | Gene clustering for time-series microarray with production outputs. <i>Soft Computing</i> , 2016, 20, 4301-4312.   | 2.1 | 5         |
| 40 | 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         |
| 41 | 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         |
| 42 | 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         |
| 43 | Gene Clustering in Time Series Microarray Analysis. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 289-298.  | 0.5 | 1         |
| 44 | Merge Method for Shape-Based Clustering in Time Series Microarray Analysis. <i>Lecture Notes in Computer Science</i> , 2012, , 834-841.                              | 1.0 | 0         |