

# David Gomez-Cabrero

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9185588/publications.pdf>

Version: 2024-02-01

105  
papers

7,355  
citations

147801

31  
h-index

64796

79  
g-index

124  
all docs

124  
docs citations

124  
times ranked

15378  
citing authors

#	ARTICLE	IF	CITATIONS
1	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	8.8	1,898
2	A beta-mixture quantile normalization method for correcting probe design bias in Illumina Infinium 450 k DNA methylation data. <i>Bioinformatics</i> , 2013, 29, 189-196.	4.1	1,295
3	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. <i>Science</i> , 2019, 365, .	12.6	710
4	Data integration in the era of omics: current and future challenges. <i>BMC Systems Biology</i> , 2014, 8, 11.	3.0	300
5	An evaluation of analysis pipelines for DNA methylation profiling using the Illumina HumanMethylation450 BeadChip platform. <i>Epigenetics</i> , 2013, 8, 333-346.	2.7	192
6	An integrative analysis reveals coordinated reprogramming of the epigenome and the transcriptome in human skeletal muscle after training. <i>Epigenetics</i> , 2014, 9, 1557-1569.	2.7	184
7	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. <i>Nature Communications</i> , 2018, 9, 2397.	12.8	147
8	Identification of novel markers in rheumatoid arthritis through integrated analysis of DNA methylation and microRNA expression. <i>Journal of Autoimmunity</i> , 2013, 41, 6-16.	6.5	144
9	Single-Cell RNA Sequencing Analysis Reveals a Crucial Role for CTHRC1 (Collagen Triple Helix Repeat) Tj ETQq1 1 0.784314 rgBT /Ove 1.6 132		
10	Therapeutic efficacy of dimethyl fumarate in relapsing-remitting multiple sclerosis associates with ROS pathway in monocytes. <i>Nature Communications</i> , 2019, 10, 3081.	12.8	97
11	Monozygotic twins discordant for common variable immunodeficiency reveal impaired DNA demethylation during naïve-to-memory B-cell transition. <i>Nature Communications</i> , 2015, 6, 7335.	12.8	81
12	Functional genomics analysis of vitamin D effects on CD4+ T cells in vivo in experimental autoimmune encephalomyelitis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1678-E1687.	7.1	81
13	Software for the Integration of Multiomics Experiments in Bioconductor. <i>Cancer Research</i> , 2017, 77, e39-e42.	0.9	80
14	Cesarean delivery and hematopoietic stem cell epigenetics in the newborn infant: implications for future health?. <i>American Journal of Obstetrics and Gynecology</i> , 2014, 211, 502.e1-502.e8.	1.3	67
15	Reconciling Coherent Oscillation with Modulation of Irregular Spiking Activity in Selective Attention: Gamma-Range Synchronization between Sensory and Executive Cortical Areas. <i>Journal of Neuroscience</i> , 2010, 30, 2856-2870.	3.6	66
16	Proposals for enhanced health risk assessment and stratification in an integrated care scenario. <i>BMJ Open</i> , 2016, 6, e010301.	1.9	61
17	Building gene regulatory networks from scATAC-seq and scRNA-seq using Linked Self Organizing Maps. <i>PLoS Computational Biology</i> , 2019, 15, e1006555.	3.2	56
18	EULAR points to consider for the use of big data in rheumatic and musculoskeletal diseases. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 69-76.	0.9	55

#	ARTICLE	IF	CITATIONS
19	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <i>Frontiers in Microbiology</i> , 2021, 12, 635781.	3.5	51
20	Abundance and diversity of resistomes differ between healthy human oral cavities and gut. <i>Nature Communications</i> , 2020, 11, 693.	12.8	49
21	Targeted lipidomics reveals extensive changes in circulating lipid mediators in patients with acutely decompensated cirrhosis. <i>Journal of Hepatology</i> , 2020, 73, 817-828.	3.7	48
22	Public data and open source tools for multi-assay genomic investigation of disease. <i>Briefings in Bioinformatics</i> , 2016, 17, 603-615.	6.5	46
23	Combining evidence from four immune cell types identifies DNA methylation patterns that implicate functionally distinct pathways during Multiple Sclerosis progression. <i>EBioMedicine</i> , 2019, 43, 411-423.	6.1	45
24	Serotonin Regulates Performance Nonmonotonically in a Spatial Working Memory Network. <i>Cerebral Cortex</i> , 2014, 24, 2449-2463.	2.9	44
25	Harmonization of quality metrics and power calculation in multi-omic studies. <i>Nature Communications</i> , 2020, 11, 3092.	12.8	43
26	Impact of genetic risk loci for multiple sclerosis on expression of proximal genes in patients. <i>Human Molecular Genetics</i> , 2018, 27, 912-928.	2.9	41
27	ChainRank, a chain prioritisation method for contextualisation of biological networks. <i>BMC Bioinformatics</i> , 2016, 17, 17.	2.6	38
28	Pre-B cell to macrophage transdifferentiation without significant promoter DNA methylation changes. <i>Nucleic Acids Research</i> , 2012, 40, 1954-1968.	14.5	37
29	Chronic Obstructive Pulmonary Disease heterogeneity: challenges for health risk assessment, stratification and management. <i>Journal of Translational Medicine</i> , 2014, 12, S3.	4.4	34
30	Epigenetic Alterations Associated With Early Prenatal Dexamethasone Treatment. <i>Journal of the Endocrine Society</i> , 2019, 3, 250-263.	0.2	34
31	Functional and transcriptomic analysis of extracellular vesicles identifies calprotectin as a new prognostic marker in peripheral arterial disease (PAD). <i>Journal of Extracellular Vesicles</i> , 2020, 9, 1729646.	12.2	34
32	Workflow for generating competing hypothesis from models with parameter uncertainty. <i>Interface Focus</i> , 2011, 1, 438-449.	3.0	33
33	Hypermethylation of <i>MIR21</i> in CD4+ T cells from patients with relapsing-remitting multiple sclerosis associates with lower miRNA-21 levels and concomitant up-regulation of its target genes. <i>Multiple Sclerosis Journal</i> , 2018, 24, 1288-1300.	3.0	33
34	Sex influences eQTL effects of SLE and Sjögren's syndrome-associated genetic polymorphisms. <i>Biology of Sex Differences</i> , 2017, 8, 34.	4.1	32
35	A robust machine learning framework to identify signatures for frailty: a nested case-control study in four aging European cohorts. <i>GeroScience</i> , 2021, 43, 1317-1329.	4.6	31
36	Current status of use of big data and artificial intelligence in RMDs: a systematic literature review informing EULAR recommendations. <i>RMD Open</i> , 2019, 5, e001004.	3.8	30

#	ARTICLE	IF	CITATIONS
37	ParkDB: a Parkinson's disease gene expression database. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar007-bar007.	3.0	28
38	High-specificity bioinformatics framework for epigenomic profiling of discordant twins reveals specific and shared markers for ACPA and ACPA-positive rheumatoid arthritis. Genome Medicine, 2016, 8, 124.	8.2	27
39	Patterns of circulating fat-soluble vitamins and carotenoids and risk of frailty in four European cohorts of older adults. European Journal of Nutrition, 2019, 58, 379-389.	3.9	27
40	The COPD Knowledge Base: enabling data analysis and computational simulation in translational COPD research. Journal of Translational Medicine, 2014, 12, S6.	4.4	26
41	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. Scientific Data, 2019, 6, 256.	5.3	26
42	Importance of mitochondrial $P$ in maximal $O_2$ transport and utilization: A theoretical analysis. Respiratory Physiology and Neurobiology, 2013, 189, 477-483.	0.6	25
43	Usability of human Infinium MethylationEPIC BeadChip for mouse DNA methylation studies. BMC Bioinformatics, 2017, 18, 486.	2.6	25
44	Neuronal methylome reveals CREB-associated neuro-axonal impairment in multiple sclerosis. Clinical Epigenetics, 2019, 11, 86.	4.1	24
45	STATegra: Multi-Omics Data Integration – A Conceptual Scheme With a Bioinformatics Pipeline. Frontiers in Genetics, 2021, 12, 620453.	2.3	24
46	Non-HLA genes PTPN22, CDK6 and PADI4 are associated with specific autoantibodies in HLA-defined subgroups of rheumatoid arthritis. Arthritis Research and Therapy, 2014, 16, 414.	3.5	23
47	Systems Medicine: from molecular features and models to the clinic in COPD. Journal of Translational Medicine, 2014, 12, S4.	4.4	23
48	Time-resolved transcriptome and proteome landscape of human regulatory T cell (Treg) differentiation reveals novel regulators of FOXP3. BMC Biology, 2018, 16, 47.	3.8	23
49	Network modules uncover mechanisms of skeletal muscle dysfunction in COPD patients. Journal of Translational Medicine, 2018, 16, 34.	4.4	22
50	Associations of fat-soluble micronutrients and redox biomarkers with frailty status in the FRAILOMIC initiative. Journal of Cachexia, Sarcopenia and Muscle, 2019, 10, 1339-1346.	7.3	22
51	Increased levels of soluble Receptor for Advanced Glycation End-products (RAGE) are associated with a higher risk of mortality in frail older adults. Age and Ageing, 2019, 48, 696-702.	1.6	22
52	Biomedical research in a Digital Health Framework. Journal of Translational Medicine, 2014, 12, S10.	4.4	21
53	From comorbidities of chronic obstructive pulmonary disease to identification of shared molecular mechanisms by data integration. BMC Bioinformatics, 2016, 17, 441.	2.6	20
54	STATegra EMS: an Experiment Management System for complex next-generation omics experiments. BMC Systems Biology, 2014, 8, S9.	3.0	19

#	ARTICLE	IF	CITATIONS
55	Synergy-COPD: a systems approach for understanding and managing chronic diseases. <i>Journal of Translational Medicine</i> , 2014, 12, S2.	4.4	19
56	Assessing the consistency of public human tissue RNA-seq data sets. <i>Briefings in Bioinformatics</i> , 2015, 16, 941-949.	6.5	19
57	Assessment of health status and program performance in patients on long-term oxygen therapy. <i>Respiratory Medicine</i> , 2015, 109, 500-509.	2.9	18
58	The role of overweight in the association between the Mediterranean diet and the risk of type 2 diabetes mellitus: a mediation analysis among 21,585 UK biobank participants. <i>International Journal of Epidemiology</i> , 2020, 49, 1582-1590.	1.9	18
59	Laboratory biomarkers and frailty: presentation of the FRAILOMIC initiative. <i>Clinical Chemistry and Laboratory Medicine</i> , 2015, 53, e253-5.	2.3	17
60	Optimization in Biology Parameter Estimation and the Associated Optimization Problem. <i>Studies in Mechanobiology, Tissue Engineering and Biomaterials</i> , 2016, , 177-197.	1.0	17
61	Phosphatase inhibitor PPP1R11 modulates resistance of human T cells toward Treg-mediated suppression of cytokine expression. <i>Journal of Leukocyte Biology</i> , 2019, 106, 413-430.	3.3	17
62	A comparative evaluation of data-merging and meta-analysis methods for reconstructing gene-gene interactions. <i>BMC Bioinformatics</i> , 2016, 17, 194.	2.6	16
63	Conditional Disease Development extracted from Longitudinal Health Care Cohort Data using Layered Network Construction. <i>Scientific Reports</i> , 2016, 6, 26170.	3.3	15
64	A perspective on bridging scales and design of models using low-dimensional manifolds and data-driven model inference. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016, 374, 20160144.	3.4	14
65	Oxygen Pathway Modeling Estimates High Reactive Oxygen Species Production above the Highest Permanent Human Habitation. <i>PLoS ONE</i> , 2014, 9, e111068.	2.5	14
66	Distribution of Human Papillomavirus Types in Women from Valencia, Spain, with Abnormal Cytology. <i>Acta Cytologica</i> , 2010, 54, 159-164.	1.3	13
67	Non-parametric combination analysis of multiple data types enables detection of novel regulatory mechanisms in T cells of multiple sclerosis patients. <i>Scientific Reports</i> , 2019, 9, 11996.	3.3	13
68	GeneSetCluster: a tool for summarizing and integrating gene-set analysis results. <i>BMC Bioinformatics</i> , 2020, 21, 443.	2.6	13
69	Challenges in the Multivariate Analysis of Mass Cytometry Data: The Effect of Randomization. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2019, 95, 1178-1190.	1.5	12
70	Predicting anti-PD-1 responders in malignant melanoma from the frequency of S100A9+ monocytes in the blood. , 2021, 9, e002171.		12
71	Workforce preparation: the Biohealth computing model for Master and PhD students. <i>Journal of Translational Medicine</i> , 2014, 12, S11.	4.4	11
72	Understanding the Adult Mammalian Heart at Single-Cell RNA-Seq Resolution. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 645276.	3.7	11

#	ARTICLE	IF	CITATIONS
73	Risk and temporal order of disease diagnosis of comorbidities in patients with COPD: a population health perspective. <i>BMJ Open Respiratory Research</i> , 2018, 5, e000302.	3.0	10
74	From Systems Understanding to Personalized Medicine: Lessons and Recommendations Based on a Multidisciplinary and Translational Analysis of COPD. <i>Methods in Molecular Biology</i> , 2016, 1386, 283-303.	0.9	10
75	DNA methylation changes in glial cells of the normal-appearing white matter in Multiple Sclerosis patients. <i>Epigenetics</i> , 2022, 17, 1311-1330.	2.7	10
76	Alterations in the Oral Microbiome Associated With Diabetes, Overweight, and Dietary Components. <i>Frontiers in Nutrition</i> , 0, 9, .	3.7	9
77	The Travelling Salesman&#x2019;s Problem: A self-adapting PSO-ACS algorithm. , 2007, , .		8
78	Implementation of the CDC translational informatics platform - from genetic variants to the national Swedish Rheumatology Quality Register. <i>Journal of Translational Medicine</i> , 2013, 11, 85.	4.4	8
79	Feedforward regulation of Myc coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. <i>PLoS Biology</i> , 2019, 17, e2006506.	5.6	8
80	Prevalence and distribution of human papillomavirus findings in swab specimens from gynaecology clinics of the east coast of Spain. <i>Scandinavian Journal of Infectious Diseases</i> , 2010, 42, 549-553.	1.5	7
81	Simulation environment and graphical visualization environment: a COPD use-case. <i>Journal of Translational Medicine</i> , 2014, 12, S7.	4.4	7
82	Guidelines for Developing Successful Short Advanced Courses in Systems Medicine and Systems Biology. <i>Cell Systems</i> , 2017, 5, 168-175.	6.2	7
83	Predictive medicine: outcomes, challenges and opportunities in the Synergy-COPD project. <i>Journal of Translational Medicine</i> , 2014, 12, S12.	4.4	6
84	An Introduction to Uncertainty in the Development of Computational Models of Biological Processes. <i>Studies in Mechanobiology, Tissue Engineering and Biomaterials</i> , 2016, , 3-11.	1.0	6
85	Short Communication Comparison of the prevalence and distribution of human papillomavirus infection and cervical lesions between urban and native habitants of an Amazonian region of Peru. <i>Genetics and Molecular Research</i> , 2012, 11, 2099-2106.	0.2	5
86	MYC as a driver of stochastic chromatin networks: implications for the fitness of cancer cells. <i>Nucleic Acids Research</i> , 2020, 48, 10867-10876.	14.5	5
87	Immunometabolic Network Interactions of the Kynurenine Pathway in Cutaneous Malignant Melanoma. <i>Frontiers in Oncology</i> , 2020, 10, 51.	2.8	5
88	Iterative Systems Biology for Medicine â€œ Time for advancing from network signatures to mechanistic equations. <i>Current Opinion in Systems Biology</i> , 2017, 3, 111-118.	2.6	4
89	The salivary proteome reflects some traits of dietary habits in diabetic and non-diabetic older adults. <i>European Journal of Nutrition</i> , 2021, 60, 4331-4344.	3.9	4
90	Deep characterization of paired chromatin and transcriptomes in four immune cell types from multiple sclerosis patients. <i>Epigenomics</i> , 2021, 13, 1607-1618.	2.1	4

#	ARTICLE	IF	CITATIONS
91	Computational Modeling Under Uncertainty: Challenges and Opportunities. <i>Studies in Mechanobiology, Tissue Engineering and Biomaterials</i> , 2016, , 467-476.	1.0	3
92	Higher sRAGE Levels Predict Mortality in Frail Older Adults with Cardiovascular Disease. <i>Gerontology</i> , 2021, 67, 202-210.	2.8	3
93	Health risk assessment and stratification in an integrated care scenario. <i>International Journal of Integrated Care</i> , 2016, 16, 322.	0.2	3
94	Introduction to Data Types in Epigenomics. <i>Translational Bioinformatics</i> , 2015, , 3-34.	0.0	2
95	Gene Regulatory Network of Human GM-CSF-Secreting T Helper Cells. <i>Journal of Immunology Research</i> , 2021, 2021, 1-24.	2.2	2
96	Deconvolution of the hematopoietic stem cell microenvironment reveals a high degree of specialization and conservation. <i>IScience</i> , 2022, 25, 104225.	4.1	2
97	Epigenetic alterations in autoimmune disease. <i>Journal of Translational Medicine</i> , 2011, 9, .	4.4	1
98	Unsupervised Cell Segmentation and Labelling in Neural Tissue Images. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 3733.	2.5	1
99	Genome-wide investigation of DNA methylation in congenital adrenal hyperplasia. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2020, 201, 105699.	2.5	1
100	Data-driven bioinformatics to disentangle cells within a tissue microenvironment. <i>Trends in Cell Biology</i> , 2022, 32, 467-469.	7.9	1
101	Non-HLA-DRB1 RA-associated risk alleles associate with anti-CCP and specific ACPA levels. <i>Annals of the Rheumatic Diseases</i> , 2011, 70, A20-A21.	0.9	0
102	Methylome characterization of CD4+ T cells in multiple sclerosis " Establishing a role for miR-21 in autoimmune disease. <i>Journal of Neuroimmunology</i> , 2014, 275, 112.	2.3	0
103	Comment on "Epigenetics in the pathogenesis of RA" <i>Seminars in Immunopathology</i> , 2017, 39, 421-422.	6.1	0
104	Transcriptomic Analysis Of Extracellular Vesicles For Biomarker Discovery In Peripheral Artery Disease (Pad). <i>Atherosclerosis</i> , 2019, 287, e65.	0.8	0
105	Network Biology Empowering Detection and Understanding of Interactions Between Genetic Factors in Development of Complex Phenotypes. , 2014, , 175-194.		0