

# David Gomez-Cabrero

## List of Publications by Year in descending order

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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	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
2	Deconvolution of the hematopoietic stem cell microenvironment reveals a high degree of specialization and conservation. <i>IScience</i> , 2022, 25, 104225.	4.1	2
3	Data-driven bioinformatics to disentangle cells within a tissue microenvironment. <i>Trends in Cell Biology</i> , 2022, 32, 467-469.	7.9	1
4	Higher sRAGE Levels Predict Mortality in Frail Older Adults with Cardiovascular Disease. <i>Gerontology</i> , 2021, 67, 202-210.	2.8	3
5	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
6	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <i>Frontiers in Microbiology</i> , 2021, 12, 635781.	3.5	51
7	STATegra: Multi-Omics Data Integration – A Conceptual Scheme With a Bioinformatics Pipeline. <i>Frontiers in Genetics</i> , 2021, 12, 620453.	2.3	24
8	Unsupervised Cell Segmentation and Labelling in Neural Tissue Images. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 3733.	2.5	1
9	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
10	Predicting anti-PD-1 responders in malignant melanoma from the frequency of S100A9+ monocytes in the blood. , 2021, 9, e002171.		12
11	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
12	Gene Regulatory Network of Human GM-CSF-Secreting T Helper Cells. <i>Journal of Immunology Research</i> , 2021, 2021, 1-24.	2.2	2
13	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
14	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
15	GeneSetCluster: a tool for summarizing and integrating gene-set analysis results. <i>BMC Bioinformatics</i> , 2020, 21, 443.	2.6	13
16	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
17	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
18	Harmonization of quality metrics and power calculation in multi-omic studies. <i>Nature Communications</i> , 2020, 11, 3092.	12.8	43

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19	Immunometabolic Network Interactions of the Kynurenine Pathway in Cutaneous Malignant Melanoma. <i>Frontiers in Oncology</i> , 2020, 10, 51.	2.8	5
20	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
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	Abundance and diversity of resistomes differ between healthy human oral cavities and gut. <i>Nature Communications</i> , 2020, 11, 693.	12.8	49
23	Single-Cell RNA Sequencing Analysis Reveals a Crucial Role for CTHRC1 (Collagen Triple Helix Repeat) Tj ETQq1 1 0.784314 rgBT /Over 1.6 132	1.6	132
24	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
25	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
26	Associations of fat-soluble micronutrients and redox biomarkers with frailty status in the FRAILOMIC initiative. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2019, 10, 1339-1346.	7.3	22
27	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
28	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. <i>Scientific Data</i> , 2019, 6, 256.	5.3	26
29	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
30	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
31	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
32	Transcriptomic Analysis Of Extracellular Vesicles For Biomarker Discovery In Peripheral Artery Disease (Pad). <i>Atherosclerosis</i> , 2019, 287, e65.	0.8	0
33	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. <i>Science</i> , 2019, 365, .	12.6	710
34	Increased levels of soluble Receptor for Advanced Glycation End-products (RAGE) are associated with a higher risk of mortality in frail older adults. <i>Age and Ageing</i> , 2019, 48, 696-702.	1.6	22
35	Neuronal methylome reveals CREB-associated neuro-axonal impairment in multiple sclerosis. <i>Clinical Epigenetics</i> , 2019, 11, 86.	4.1	24
36	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

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37	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
38	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
39	Epigenetic Alterations Associated With Early Prenatal Dexamethasone Treatment. <i>Journal of the Endocrine Society</i> , 2019, 3, 250-263.	0.2	34
40	Patterns of circulating fat-soluble vitamins and carotenoids and risk of frailty in four European cohorts of older adults. <i>European Journal of Nutrition</i> , 2019, 58, 379-389.	3.9	27
41	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
42	Network modules uncover mechanisms of skeletal muscle dysfunction in COPD patients. <i>Journal of Translational Medicine</i> , 2018, 16, 34.	4.4	22
43	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
44	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
45	Time-resolved transcriptome and proteome landscape of human regulatory T cell (Treg) differentiation reveals novel regulators of FOXP3. <i>BMC Biology</i> , 2018, 16, 47.	3.8	23
46	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
47	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
48	Comment on "Epigenetics in the pathogenesis of RA". <i>Seminars in Immunopathology</i> , 2017, 39, 421-422.	6.1	0
49	Guidelines for Developing Successful Short Advanced Courses in Systems Medicine and Systems Biology. <i>Cell Systems</i> , 2017, 5, 168-175.	6.2	7
50	Software for the Integration of Multiomics Experiments in Bioconductor. <i>Cancer Research</i> , 2017, 77, e39-e42.	0.9	80
51	Iterative Systems Biology for Medicine "Time for advancing from network signatures to mechanistic equations. <i>Current Opinion in Systems Biology</i> , 2017, 3, 111-118.	2.6	4
52	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
53	Usability of human Infinium MethylationEPIC BeadChip for mouse DNA methylation studies. <i>BMC Bioinformatics</i> , 2017, 18, 486.	2.6	25
54	Proposals for enhanced health risk assessment and stratification in an integrated care scenario. <i>BMJ Open</i> , 2016, 6, e010301.	1.9	61

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55	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
56	From comorbidities of chronic obstructive pulmonary disease to identification of shared molecular mechanisms by data integration. <i>BMC Bioinformatics</i> , 2016, 17, 441.	2.6	20
57	High-specificity bioinformatics framework for epigenomic profiling of discordant twins reveals specific and shared markers for ACPA and ACPA-positive rheumatoid arthritis. <i>Genome Medicine</i> , 2016, 8, 124.	8.2	27
58	Conditional Disease Development extracted from Longitudinal Health Care Cohort Data using Layered Network Construction. <i>Scientific Reports</i> , 2016, 6, 26170.	3.3	15
59	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
60	ChainRank, a chain prioritisation method for contextualisation of biological networks. <i>BMC Bioinformatics</i> , 2016, 17, 17.	2.6	38
61	Computational Modeling Under Uncertainty: Challenges and Opportunities. <i>Studies in Mechanobiology, Tissue Engineering and Biomaterials</i> , 2016, , 467-476.	1.0	3
62	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	8.8	1,898
63	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
64	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
65	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
66	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
67	Health risk assessment and stratification in an integrated care scenario. <i>International Journal of Integrated Care</i> , 2016, 16, 322.	0.2	3
68	Introduction to Data Types in Epigenomics. <i>Translational Bioinformatics</i> , 2015, , 3-34.	0.0	2
69	Laboratory biomarkers and frailty: presentation of the FRAILOMIC initiative. <i>Clinical Chemistry and Laboratory Medicine</i> , 2015, 53, e253-5.	2.3	17
70	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
71	Assessing the consistency of public human tissue RNA-seq data sets. <i>Briefings in Bioinformatics</i> , 2015, 16, 941-949.	6.5	19
72	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

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73	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
74	Non-HLA genes PTPN22, CDK6 and PADI4 are associated with specific autoantibodies in HLA-defined subgroups of rheumatoid arthritis. <i>Arthritis Research and Therapy</i> , 2014, 16, 414.	3.5	23
75	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
76	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
77	Serotonin Regulates Performance Nonmonotonically in a Spatial Working Memory Network. <i>Cerebral Cortex</i> , 2014, 24, 2449-2463.	2.9	44
78	Data integration in the era of omics: current and future challenges. <i>BMC Systems Biology</i> , 2014, 8, 11.	3.0	300
79	STATegra EMS: an Experiment Management System for complex next-generation omics experiments. <i>BMC Systems Biology</i> , 2014, 8, S9.	3.0	19
80	Systems Medicine: from molecular features and models to the clinic in COPD. <i>Journal of Translational Medicine</i> , 2014, 12, S4.	4.4	23
81	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
82	Biomedical research in a Digital Health Framework. <i>Journal of Translational Medicine</i> , 2014, 12, S10.	4.4	21
83	Workforce preparation: the Biohealth computing model for Master and PhD students. <i>Journal of Translational Medicine</i> , 2014, 12, S11.	4.4	11
84	Predictive medicine: outcomes, challenges and opportunities in the Synergy-COPD project. <i>Journal of Translational Medicine</i> , 2014, 12, S12.	4.4	6
85	Synergy-COPD: a systems approach for understanding and managing chronic diseases. <i>Journal of Translational Medicine</i> , 2014, 12, S2.	4.4	19
86	The COPD Knowledge Base: enabling data analysis and computational simulation in translational COPD research. <i>Journal of Translational Medicine</i> , 2014, 12, S6.	4.4	26
87	Simulation environment and graphical visualization environment: a COPD use-case. <i>Journal of Translational Medicine</i> , 2014, 12, S7.	4.4	7
88	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
89	Network Biology Empowering Detection and Understanding of Interactions Between Genetic Factors in Development of Complex Phenotypes. , 2014, , 175-194.		0
90	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

