

# Isidro Cortes-Ciriano

## List of Publications by Citations

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**Version:** 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

58

papers

3,213

citations

25

h-index

56

g-index

68

ext. papers

4,737

ext. citations

12.8

avg, IF

5.56

L-index

#	Paper	IF	Citations
58	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , <b>2018</b> , 173, 371-385.e18	56.2	854
57	A molecular portrait of microsatellite instability across multiple cancers. <i>Nature Communications</i> , <b>2017</b> , 8, 15180	17.4	288
56	Mechanisms and therapeutic implications of hypermutation in gliomas. <i>Nature</i> , <b>2020</b> , 580, 517-523	50.4	172
55	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , <b>2020</b> , 52, 331-341	36.3	168
54	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , <b>2018</b> , 173, 305-320.e10	56.2	166
53	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. <i>Science</i> , <b>2017</b> , 356,	33.3	152
52	Detecting the mutational signature of homologous recombination deficiency in clinical samples. <i>Nature Genetics</i> , <b>2019</b> , 51, 912-919	36.3	96
51	Experimental validation of in silico target predictions on synergistic protein targets. <i>Journal of Cheminformatics</i> , <b>2013</b> , 5,	8.6	78
50	Polypharmacology modelling using proteochemometrics (PCM): recent methodological developments, applications to target families, and future prospects. <i>MedChemComm</i> , <b>2015</b> , 6, 24-50	5	74
49	Prediction of the potency of mammalian cyclooxygenase inhibitors with ensemble proteochemometric modeling. <i>Journal of Cheminformatics</i> , <b>2015</b> , 7, 1	8.6	70
48	Improved large-scale prediction of growth inhibition patterns using the NCI60 cancer cell line panel. <i>Bioinformatics</i> , <b>2016</b> , 32, 85-95	7.2	60
47	The Impact of Environmental and Endogenous Damage on Somatic Mutation Load in Human Skin Fibroblasts. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006385	6	55
46	Benchmarking of protein descriptor sets in proteochemometric modeling (part 2): modeling performance of 13 amino acid descriptor sets. <i>Journal of Cheminformatics</i> , <b>2013</b> , 5, 42	8.6	48
45	Linked-read analysis identifies mutations in single-cell DNA-sequencing data. <i>Nature Genetics</i> , <b>2019</b> , 51, 749-754	36.3	42
44	Reconstructing the Lineage Histories and Differentiation Trajectories of Individual Cancer Cells in Myeloproliferative Neoplasms. <i>Cell Stem Cell</i> , <b>2021</b> , 28, 514-523.e9	18	42
43	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , <b>2020</b> , 11, 733	17.4	40
42	Deep Confidence: A Computationally Efficient Framework for Calculating Reliable Prediction Errors for Deep Neural Networks. <i>Journal of Chemical Information and Modeling</i> , <b>2019</b> , 59, 1269-1281	6.1	40

41	Artificial intelligence in drug discovery: what is realistic, what are illusions? Part 1: Ways to make an impact, and why we are not there yet. <i>Drug Discovery Today</i> , <b>2021</b> , 26, 511-524	8.8	39
40	Proteochemometric modeling in a Bayesian framework. <i>Journal of Cheminformatics</i> , <b>2014</b> , 6, 35	8.6	32
39	Chemically Aware Model Builder (camb): an R package for property and bioactivity modelling of small molecules. <i>Journal of Cheminformatics</i> , <b>2015</b> , 7, 45	8.6	31
38	KekuleScope: prediction of cancer cell line sensitivity and compound potency using convolutional neural networks trained on compound images. <i>Journal of Cheminformatics</i> , <b>2019</b> , 11, 41	8.6	29
37	Benchmarking the Predictive Power of Ligand Efficiency Indices in QSAR. <i>Journal of Chemical Information and Modeling</i> , <b>2016</b> , 56, 1576-87	6.1	28
36	Conformal Regression for Quantitative Structure-Activity Relationship Modeling-Quantifying Prediction Uncertainty. <i>Journal of Chemical Information and Modeling</i> , <b>2018</b> , 58, 1132-1140	6.1	27
35	Proteochemometric modelling coupled to in silico target prediction: an integrated approach for the simultaneous prediction of polypharmacology and binding affinity/potency of small molecules. <i>Journal of Cheminformatics</i> , <b>2015</b> , 7, 15	8.6	26
34	Improved Chemical Structure-Activity Modeling Through Data Augmentation. <i>Journal of Chemical Information and Modeling</i> , <b>2015</b> , 55, 2682-92	6.1	23
33	Modelling ligand selectivity of serine proteases using integrative proteochemometric approaches improves model performance and allows the multi-target dependent interpretation of features. <i>Integrative Biology (United Kingdom)</i> , <b>2014</b> , 6, 1023-33	3.7	23
32	Artificial intelligence in drug discovery: what is realistic, what are illusions? Part 2: a discussion of chemical and biological data. <i>Drug Discovery Today</i> , <b>2021</b> , 26, 1040-1052	8.8	22
31	Discovering Highly Potent Molecules from an Initial Set of Inactives Using Iterative Screening. <i>Journal of Chemical Information and Modeling</i> , <b>2018</b> , 58, 2000-2014	6.1	21
30	Comparing the Influence of Simulated Experimental Errors on 12 Machine Learning Algorithms in Bioactivity Modeling Using 12 Diverse Data Sets. <i>Journal of Chemical Information and Modeling</i> , <b>2015</b> , 55, 1413-25	6.1	21
29	Prediction of PARP Inhibition with Proteochemometric Modelling and Conformal Prediction. <i>Molecular Informatics</i> , <b>2015</b> , 34, 357-66	3.8	20
28	Accurate detection of mosaic variants in sequencing data without matched controls. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 314-319	44.5	20
27	Bioalerts: a python library for the derivation of structural alerts from bioactivity and toxicity data sets. <i>Journal of Cheminformatics</i> , <b>2016</b> , 8, 13	8.6	19
26	How Consistent are Publicly Reported Cytotoxicity Data? Large-Scale Statistical Analysis of the Concordance of Public Independent Cytotoxicity Measurements. <i>ChemMedChem</i> , <b>2016</b> , 11, 57-71	3.7	19
25	Reliable Prediction Errors for Deep Neural Networks Using Test-Time Dropout. <i>Journal of Chemical Information and Modeling</i> , <b>2019</b> , 59, 3330-3339	6.1	18
24	Extending in silico mechanism-of-action analysis by annotating targets with pathways: application to cellular cytotoxicity readouts. <i>Future Medicinal Chemistry</i> , <b>2014</b> , 6, 2029-56	4.1	16

23	QSAR-derived affinity fingerprints (part 1): fingerprint construction and modeling performance for similarity searching, bioactivity classification and scaffold hopping. <i>Journal of Cheminformatics</i> , <b>2020</b> , 12, 39	8.6	13
22	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing		12
21	Temperature Accelerated Molecular Dynamics with Soft-Ratcheting Criterion Orients Enhanced Sampling by Low-Resolution Information. <i>Journal of Chemical Theory and Computation</i> , <b>2015</b> , 11, 3446-54	6.4	11
20	Identification of binding sites and favorable ligand binding moieties by virtual screening and self-organizing map analysis. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 93	3.6	11
19	Current Trends in Drug Sensitivity Prediction. <i>Current Pharmaceutical Design</i> , <b>2016</b> , 22, 6918-6927	3.3	9
18	A decision-theoretic approach to the evaluation of machine learning algorithms in computational drug discovery. <i>Bioinformatics</i> , <b>2019</b> , 35, 4656-4663	7.2	7
17	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , <b>2020</b> , 11, 3400	17.4	7
16	QSAR-derived affinity fingerprints (part 2): modeling performance for potency prediction. <i>Journal of Cheminformatics</i> , <b>2020</b> , 12, 41	8.6	7
15	Experimental validation of in silico target predictions on synergistic protein targets. <i>MedChemComm</i> , <b>2013</b> , 4, 278-288	5	7
14	Improving the prediction of organism-level toxicity through integration of chemical, protein target and cytotoxicity qHTS data. <i>Toxicology Research</i> , <b>2016</b> , 5, 883-894	2.6	7
13	Genomics of MPNST (GeM) Consortium: Rationale and Study Design for Multi-Omic Characterization of NF1-Associated and Sporadic MPNSTs. <i>Genes</i> , <b>2020</b> , 11,	4.2	6
12	Reconstructing the Lineage Histories and Differentiation Trajectories of Individual Hematopoietic Stem Cells in JAK2-Mutant Myeloproliferative Neoplasms. <i>Blood</i> , <b>2020</b> , 136, 7-8	2.2	4
11	Applications of proteochemometrics - from species extrapolation to cell line sensitivity modelling. <i>BMC Bioinformatics</i> , <b>2015</b> , 16,	3.6	3
10	A user guide to the online resources for data exploration, visualization, and discovery for the Pan-Cancer Analysis of Whole Genomes project (PCAWG)		3
9	Abstract LB-378: Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing <b>2018</b> ,		2
8	A semi-supervised learning framework for quantitative structure-activity regression modelling. <i>Bioinformatics</i> , <b>2021</b> , 37, 342-350	7.2	2
7	Computational analysis of cancer genome sequencing data. <i>Nature Reviews Genetics</i> , <b>2021</b> ,	30.1	2
6	Elucidating Compound Mechanism of Action and Predicting Cytotoxicity Using Machine Learning Approaches, Taking Prediction Confidence into Account. <i>Current Protocols in Chemical Biology</i> , <b>2019</b> , 11, e73	1.8	1

5	Clonal diversification and histogenesis of malignant germ cell tumours		1
4	Reconstructing the lineage histories and differentiation trajectories of individual cancer cells in JAK2-mutant myeloproliferative neoplasms		1
3	Cancer Cell Line Profiler (CCLP): a webserver for the prediction of compound activity across the NCI60 panel		1
2	Rearrangement-mediated cis-regulatory alterations in advanced patient tumors reveal interactions with therapy. <i>Cell Reports</i> , <b>2021</b> , 37, 110023	10.6	0
1	Patient-derived models of brain metastases recapitulate human disseminated disease.. <i>Cell Reports Medicine</i> , <b>2022</b> , 3, 100623	18	0