

Francesco Iorio

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

15,311
citations

101543

36
h-index

106344

65
g-index

96
all docs

96
docs citations

96
times ranked

27723
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational estimation of quality and clinical relevance of cancer cell lines. <i>Molecular Systems Biology</i> , 2022, 18, .	7.2	12
2	Analysis of CRISPR-Cas9 screens identifies genetic dependencies in melanoma. <i>Pigment Cell and Melanoma Research</i> , 2021, 34, 122-131.	3.3	10
3	Project Score database: a resource for investigating cancer cell dependencies and prioritizing therapeutic targets. <i>Nucleic Acids Research</i> , 2021, 49, D1365-D1372.	14.5	54
4	Redefining false discoveries in cancer data analyses. <i>Nature Computational Science</i> , 2021, 1, 22-23.	8.0	1
5	Cancer research needs a better map. <i>Nature</i> , 2021, 589, 514-516.	27.8	57
6	Integrated cross-study datasets of genetic dependencies in cancer. <i>Nature Communications</i> , 2021, 12, 1661.	12.8	135
7	Functional Impact of Genomic Complexity on the Transcriptome of Multiple Myeloma. <i>Clinical Cancer Research</i> , 2021, 27, 6479-6490.	7.0	9
8	Minimal genome-wide human CRISPR-Cas9 library. <i>Genome Biology</i> , 2021, 22, 40.	8.8	40
9	Combinatorial CRISPR screen identifies fitness effects of gene paralogues. <i>Nature Communications</i> , 2021, 12, 1302.	12.8	59
10	CoRe: a robustly benchmarked R package for identifying core-fitness genes in genome-wide pooled CRISPR-Cas9 screens. <i>BMC Genomics</i> , 2021, 22, 828.	2.8	14
11	Identification of Intrinsic Drug Resistance and Its Biomarkers in High-Throughput Pharmacogenomic and CRISPR Screens. <i>Patterns</i> , 2020, 1, 100065.	5.9	6
12	CELLector: Genomics-Guided Selection of Cancer In Vitro Models. <i>Cell Systems</i> , 2020, 10, 424-432.e6.	6.2	35
13	Drug mechanism-action discovery through the integration of pharmacological and CRISPR screens. <i>Molecular Systems Biology</i> , 2020, 16, e9405.	7.2	63
14	JACKS: joint analysis of CRISPR/Cas9 knockout screens. <i>Genome Research</i> , 2019, 29, 464-471.	5.5	64
15	Functional linkage of gene fusions to cancer cell fitness assessed by pharmacological and CRISPR-Cas9 screening. <i>Nature Communications</i> , 2019, 10, 2198.	12.8	92
16	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. <i>Cell</i> , 2019, 176, 1282-1294.e20.	28.9	298
17	Prioritization of cancer therapeutic targets using CRISPR-Cas9 screens. <i>Nature</i> , 2019, 568, 511-516.	27.8	886
18	Structural rearrangements generate cell-specific, gene-independent CRISPR-Cas9 loss of fitness effects. <i>Genome Biology</i> , 2019, 20, 27.	8.8	35

#	ARTICLE	IF	CITATIONS
19	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. <i>Nature Communications</i> , 2019, 10, 5817.	12.8	160
20	Drug repurposing: progress, challenges and recommendations. <i>Nature Reviews Drug Discovery</i> , 2019, 18, 41-58.	46.4	2,689
21	GDSCTools for mining pharmacogenomic interactions in cancer. <i>Bioinformatics</i> , 2018, 34, 1226-1228.	4.1	45
22	Comprehensive Pharmacogenomic Profiling of Malignant Pleural Mesothelioma Identifies a Subgroup Sensitive to FGFR Inhibition. <i>Clinical Cancer Research</i> , 2018, 24, 84-94.	7.0	33
23	Transcription Factor Activities Enhance Markers of Drug Sensitivity in Cancer. <i>Cancer Research</i> , 2018, 78, 769-780.	0.9	161
24	CellMinerCDB for Integrative Cross-Database Genomics and Pharmacogenomics Analyses of Cancer Cell Lines. <i>IScience</i> , 2018, 10, 247-264.	4.1	117
25	Loss of functional BAP1 augments sensitivity to TRAIL in cancer cells. <i>ELife</i> , 2018, 7, .	6.0	20
26	Pathway-based dissection of the genomic heterogeneity of cancer hallmarksâ€™ acquisition with SLAPenrich. <i>Scientific Reports</i> , 2018, 8, 6713.	3.3	24
27	The germline genetic component of drug sensitivity in cancer cell lines. <i>Nature Communications</i> , 2018, 9, 3385.	12.8	38
28	Unsupervised correction of gene-independent cell responses to CRISPR-Cas9 targeting. <i>BMC Genomics</i> , 2018, 19, 604.	2.8	75
29	Genome-wide chemical mutagenesis screens allow unbiased saturation of the cancer genome and identification of drug resistance mutations. <i>Genome Research</i> , 2017, 27, 613-625.	5.5	20
30	Stem cell-like transcriptional reprogramming mediates metastatic resistance to mTOR inhibition. <i>Oncogene</i> , 2017, 36, 2737-2749.	5.9	34
31	Hemopoietic-specific Sf3b1-K700E knock-in mice display the splicing defect seen in human MDS but develop anemia without ring sideroblasts. <i>Leukemia</i> , 2017, 31, 720-727.	7.2	105
32	Abstract A44: A landscape of pharmacogenomic interactions in cancer. , 2017, , .		9
33	Integrated transcriptomic and proteomic analysis identifies protein kinase CK2 as a key signaling node in an inflammatory cytokine network in ovarian cancer cells. <i>Oncotarget</i> , 2016, 7, 15648-15661.	1.8	13
34	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016, 166, 740-754.	28.9	1,518
35	Multilevel models improve precision and speed of IC ₅₀ estimates. <i>Pharmacogenomics</i> , 2016, 17, 691-700.	1.3	57
36	Logic models to predict continuous outputs based on binary inputs with an application to personalized cancer therapy. <i>Scientific Reports</i> , 2016, 6, 36812.	3.3	43

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37	A CRISPR Dropout Screen Identifies Genetic Vulnerabilities and Therapeutic Targets in Acute Myeloid Leukemia. <i>Cell Reports</i> , 2016, 17, 1193-1205.	6.4	556
38	Efficient randomization of biological networks while preserving functional characterization of individual nodes. <i>BMC Bioinformatics</i> , 2016, 17, 542.	2.6	38
39	Transcriptional response networks for elucidating mechanisms of action of multitargeted agents. <i>Drug Discovery Today</i> , 2016, 21, 1063-1075.	6.4	28
40	Blood transcriptomics of drug-naïve sporadic Parkinson's disease patients. <i>BMC Genomics</i> , 2015, 16, 876.	2.8	64
41	A Semi-Supervised Approach for Refining Transcriptional Signatures of Drug Response and Repositioning Predictions. <i>PLoS ONE</i> , 2015, 10, e0139446.	2.5	39
42	BRAF inhibitor resistance mediated by the AKT pathway in an oncogenic BRAF mouse melanoma model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E536-45.	7.1	121
43	Identification of drug-specific pathways based on gene expression data: application to drug induced lung injury. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 904-920.	1.3	43
44	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. <i>Cell</i> , 2015, 161, 933-945.	28.9	1,710
45	Pharmacogenomic agreement between two cancer cell line data sets. <i>Nature</i> , 2015, 528, 84-87.	27.8	358
46	A Crispr/Cas9 Drop-out Screen Identifies Genome-Wide Genetic Vulnerabilities in Acute Myeloid Leukaemia. <i>Blood</i> , 2015, 126, 554-554.	1.4	1
47	Unravelling druggable signalling networks that control F508del-CFTR proteostasis. <i>ELife</i> , 2015, 4, .	6.0	22
48	Exploiting combinatorial patterns in cancer genomic data for personalized therapy and new target discovery. <i>Pharmacogenomics</i> , 2014, 15, 1943-1946.	1.3	5
49	Fast randomization of large genomic datasets while preserving alteration counts. <i>Bioinformatics</i> , 2014, 30, i617-i623.	4.1	36
50	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. <i>Nature Communications</i> , 2014, 5, 2997.	12.8	741
51	Abstract 2218: Genomic characterisation of 1015 cancer cell-lines. , 2014, , .		0
52	Phosphoproteomics data classify hematological cancer cell lines according to tumor type and sensitivity to kinase inhibitors. <i>Genome Biology</i> , 2013, 14, R37.	9.6	60
53	DvD: An R/Cytoscape pipeline for drug repurposing using public repositories of gene expression data. <i>Bioinformatics</i> , 2013, 29, 132-134.	4.1	64
54	Network based elucidation of drug response: from modulators to targets. <i>BMC Systems Biology</i> , 2013, 7, 139.	3.0	47

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55	Transcriptional data: a new gateway to drug repositioning?. Drug Discovery Today, 2013, 18, 350-357.	6.4	209
56	Machine Learning Prediction of Cancer Cell Sensitivity to Drugs Based on Genomic and Chemical Properties. PLoS ONE, 2013, 8, e61318.	2.5	406
57	Whole Exome Sequencing Of Multiple Myeloma Reveals An Heterogeneous Clonal Architecture and Genomic Evolution. Blood, 2013, 122, 399-399.	1.4	0
58	Cancer develops, progresses and responds to therapies through restricted perturbation of the protein-protein interaction network. Integrative Biology (United Kingdom), 2012, 4, 1038.	1.3	10
59	Systematic identification of genomic markers of drug sensitivity in cancer cells. Nature, 2012, 483, 570-575.	27.8	2,173
60	Abstract 49: Targeting the TNF network in human ovarian cancer - A systems biology approach. , 2012, , .		0
61	Artificial neural network analysis of circulating tumor cells in metastatic breast cancer patients. Breast Cancer Research and Treatment, 2011, 129, 451-458.	2.5	31
62	Transcriptional gene network inference from a massive dataset elucidates transcriptome organization and gene function. Nucleic Acids Research, 2011, 39, 8677-8688.	14.5	102
63	Discovery of drug mode of action and drug repositioning from transcriptional responses. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14621-14626.	7.1	813
64	Gene ontology fuzzy-enrichment analysis to investigate drug mode-of-action. , 2010, , .		0
65	Identification of small molecules enhancing autophagic function from drug network analysis. Autophagy, 2010, 6, 1204-1205.	9.1	58
66	NIReSt: A Tool for Gene Network and Mode of Action Inference. Annals of the New York Academy of Sciences, 2009, 1158, 257-264.	3.8	8
67	A Yeast Synthetic Network for In Vivo Assessment of Reverse-Engineering and Modeling Approaches. Cell, 2009, 137, 172-181.	28.9	348
68	Identifying Network of Drug Mode of Action by Gene Expression Profiling. Journal of Computational Biology, 2009, 16, 241-251.	1.6	94
69	Building Maps of Drugs Mode-of-Action from Gene Expression Data. Lecture Notes in Computer Science, 2009, , 56-65.	1.3	1
70	Interactive data analysis and clustering of genomic data. Neural Networks, 2008, 21, 368-378.	5.9	31
71	High-Throughput Analysis of the Drug Mode of Action of PB28, MC18 and MC70, Three Cyclohexylpiperazine Derivative New Molecules. Lecture Notes in Computer Science, 2008, , 1085-1092.	1.3	0
72	CellMinerCDB for Integrative Genomics and Pharmacogenomics Analyses of Cancer Cell Lines. SSRN Electronic Journal, 0, , .	0.4	0