Mathew J Garnett

List of Publications by Year
in descending order

55 papers	13,688 citations	117625 34 h-index	149698 56 g-index
79 all docs	79 docs citations	79 times ranked	19479 citing authors

#	Article	IF	Citations
1	Genomics of Drug Sensitivity in Cancer (GDSC): a resource for therapeutic biomarker discovery in cancer cells. Nucleic Acids Research, 2012, 41, D955-D961.	14.5	2,363
2	Systematic identification of genomic markers of drug sensitivity in cancer cells. Nature, 2012, 483, 570-575.	27.8	2,173
3	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	28.9	1,710
4	A Landscape of Pharmacogenomic Interactions in Cancer. Cell, 2016, 166, 740-754.	28.9	1,518
5	Human primary liver cancerâ€“derived organoid cultures for disease modeling and drug screening. Nature Medicine, 2017, 23, 1424-1435.	30.7	905
6	Prioritization of cancer therapeutic targets using CRISPRâ€“Cas9 screens. Nature, 2019, 568, 511-516.	27.8	886
7	Perturbation-response genes reveal signaling footprints in cancer gene expression. Nature Communications, 2018, 9, 20.	12.8	436
8	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. Cell, 2016, 167, 260-274.e22.	28.9	376
9	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. Cell, 2019, 176, 1282-1294.e20.	28.9	298
10	Pancreatic cancer organoids recapitulate disease and allow personalized drug screening. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26580-26590.	7.1	279
11	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
12	Organoid cultures recapitulate esophageal adenocarcinoma heterogeneity providing a model for clonality studies and precision therapeutics. Nature Communications, 2018, 9, 2983.	12.8	206
13	Transcription Factor Activities Enhance Markers of Drug Sensitivity in Cancer. Cancer Research, 2018, 78, 769-780.	0.9	161
14	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. Nature Communications, 2019, 10, 5817.	12.8	160
15	Effective drug combinations in breast, colon and pancreatic cancer cells. Nature, 2022, 603, 166-173.	27.8	154
16	Integrated cross-study datasets of genetic dependencies in cancer. Nature Communications, 2021, 12, 1661.	12.8	135
17	Cell Model Passportsâ€”a hub for clinical, genetic and functional datasets of preclinical cancer models. Nucleic Acids Research, 2019, 47, D923-D929.	14.5	118
18	Drug Resistance Mechanisms in Colorectal Cancer Dissected with Cell Typeâ€“Specific Dynamic Logic Models. Cancer Research, 2017, 77, 3364-3375.	0.9	101

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19	Functional linkage of gene fusions to cancer cell fitness assessed by pharmacological and CRISPR-Cas9 screening. Nature Communications, 2019, 10, 2198.	12.8	92
20	Unsupervised correction of gene-independent cell responses to CRISPR-Cas9 targeting. BMC Genomics, 2018, 19, 604.	2.8	75
21	Combinations of PARP Inhibitors with Temozolomide Drive PARP1 Trapping and Apoptosis in Ewingâ€™s Sarcoma. PLoS ONE, 2015, 10, e0140988.	2.5	72
22	Drug mechanismâ€ofâ€action discovery through the integration of pharmacological and <scp>CRISPR</scp> screens. Molecular Systems Biology, 2020, 16, e9405.	7.2	63
23	Patientâ€specific logic models of signaling pathways from screenings on cancer biopsies to prioritize personalized combination therapies. Molecular Systems Biology, 2020, 16, e8664.	7.2	60
24	Combinatorial CRISPR screen identifies fitness effects of gene paralogues. Nature Communications, 2021, 12, 1302.	12.8	59
25	Multilevel models improve precision and speed of IC₅₀ estimates. Pharmacogenomics, 2016, 17, 691-700.	1.3	57
26	Cancer research needs a better map. Nature, 2021, 589, 514-516.	27.8	57
27	Drug Sensitivity Assays of Human Cancer Organoid Cultures. Methods in Molecular Biology, 2016, 1576, 339-351.	0.9	54
28	Itraconazole targets cell cycle heterogeneity in colorectal cancer. Journal of Experimental Medicine, 2018, 215, 1891-1912.	8.5	54
29	Project Score database: a resource for investigating cancer cell dependencies and prioritizing therapeutic targets. Nucleic Acids Research, 2021, 49, D1365-D1372.	14.5	54
30	Pan-cancer proteomic map of 949 human cell lines. Cancer Cell, 2022, 40, 835-849.e8.	16.8	52
31	Werner Helicase Is a Synthetic-Lethal Vulnerability in Mismatch Repairâ€“Deficient Colorectal Cancer Refractory to Targeted Therapies, Chemotherapy, and Immunotherapy. Cancer Discovery, 2021, 11, 1923-1937.	9.4	48
32	GDSCTools for mining pharmacogenomic interactions in cancer. Bioinformatics, 2018, 34, 1226-1228.	4.1	45
33	Logic models to predict continuous outputs based on binary inputs with an application to personalized cancer therapy. Scientific Reports, 2016, 6, 36812.	3.3	43
34	Patient-Derived Xenografts and Matched Cell Lines Identify Pharmacogenomic Vulnerabilities in Colorectal Cancer. Clinical Cancer Research, 2019, 25, 6243-6259.	7.0	42
35	AZD4320, A Dual Inhibitor of Bcl-2 and Bcl-xL, Induces Tumor Regression in Hematologic Cancer Models without Dose-limiting Thrombocytopenia. Clinical Cancer Research, 2020, 26, 6535-6549.	7.0	42
36	Minimal genome-wide human CRISPR-Cas9 library. Genome Biology, 2021, 22, 40.	8.8	40

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37	The germline genetic component of drug sensitivity in cancer cell lines. Nature Communications, 2018, 9, 3385.	12.8	38
38	Structural rearrangements generate cell-specific, gene-independent CRISPR-Cas9 loss of fitness effects. Genome Biology, 2019, 20, 27.	8.8	35
39	CELLector: Genomics-Guided Selection of Cancer InÂVitro Models. Cell Systems, 2020, 10, 424-432.e6.	6.2	35
40	Discovery of Potent and Selective MRCK Inhibitors with Therapeutic Effect on Skin Cancer. Cancer Research, 2018, 78, 2096-2114.	0.9	31
41	Genome-wide CRISPR screens of oral squamous cell carcinoma reveal fitness genes in the Hippo pathway. ELife, 2020, 9, .	6.0	31
42	Genomics-guided pre-clinical development of cancer therapies. Nature Cancer, 2020, 1, 482-492.	13.2	23
43	Identification of differential PI3K pathway target dependencies in T-cell acute lymphoblastic leukemia through a large cancer cell panel screen. Oncotarget, 2016, 7, 22128-22139.	1.8	21
44	Use of preclinical models for malignant pleural mesothelioma. Thorax, 2021, 76, 1154-1162.	5.6	16
45	A statistical framework for assessing pharmacological responses and biomarkers using uncertainty estimates. ELife, 2020, 9, .	6.0	16
46	MTH1 Inhibitor TH1579 Induces Oxidative DNA Damage and Mitotic Arrest in Acute Myeloid Leukemia. Cancer Research, 2021, 81, 5733-5744.	0.9	15
47	CoRe: a robustly benchmarked R package for identifying core-fitness genes in genome-wide pooled CRISPR-Cas9 screens. BMC Genomics, 2021, 22, 828.	2.8	14
48	AZD0364 Is a Potent and Selective ERK1/2 Inhibitor That Enhances Antitumor Activity in KRAS-Mutant Tumor Models when Combined with the MEK Inhibitor, Selumetinib. Molecular Cancer Therapeutics, 2021, 20, 238-249.	4.1	13
49	What role could organoids play in the personalization of cancer treatment?. Pharmacogenomics, 2015, 16, 1523-1526.	1.3	11
50	High-throughput RNAi screen for essential genes and drug synergistic combinations in colorectal cancer. Scientific Data, 2017, 4, 170139.	5.3	11
51	NOTCH1 Represses MCL-1 Levels in GSI-resistant T-ALL, Making them Susceptible to ABT-263. Clinical Cancer Research, 2019, 25, 312-324.	7.0	11
52	A suspension technique for efficient large-scale cancer organoid culturing and perturbation screens. Scientific Reports, 2022, 12, 5571.	3.3	11
53	Can Drug Repurposing Accelerate Precision Oncology?. Cancer Discovery, 0, , OF1-OF8.	9.4	11
54	A Road Map for Precision Cancer Medicine Using Personalized Models. Cancer Discovery, 2017, 7, 456-458.	9.4	9

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55	Inferred Ancestral Origin of Cancer Cell Lines Associates with Differential Drug Response. International Journal of Molecular Sciences, 2021, 22, 10135.	4.1	2