Mathew J Garnett

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Effective drug combinations in breast, colon and pancreatic cancer cells. Nature, 2022, 603, 166-173.	27.8	154
2	A suspension technique for efficient large-scale cancer organoid culturing and perturbation screens. Scientific Reports, 2022, 12, 5571.	3.3	11
3	Pan-cancer proteomic map of 949 human cell lines. Cancer Cell, 2022, 40, 835-849.e8.	16.8	52
4	AZD0364 Is a Potent and Selective ERK1/2 Inhibitor That Enhances Antitumor Activity in <i>KRAS</i> -Mutant Tumor Models when Combined with the MEK Inhibitor, Selumetinib. Molecular Cancer Therapeutics, 2021, 20, 238-249.	4.1	13
5	Project Score database: a resource for investigating cancer cell dependencies and prioritizing therapeutic targets. Nucleic Acids Research, 2021, 49, D1365-D1372.	14.5	54
6	Cancer research needs a better map. Nature, 2021, 589, 514-516.	27.8	57
7	Integrated cross-study datasets of genetic dependencies in cancer. Nature Communications, 2021, 12, 1661.	12.8	135
8	Use of preclinical models for malignant pleural mesothelioma. Thorax, 2021, 76, 1154-1162.	5.6	16
9	Werner Helicase Is a Synthetic-Lethal Vulnerability in Mismatch Repair–Deficient Colorectal Cancer Refractory to Targeted Therapies, Chemotherapy, and Immunotherapy. Cancer Discovery, 2021, 11, 1923-1937.	9.4	48
10	MTH1 Inhibitor TH1579 Induces Oxidative DNA Damage and Mitotic Arrest in Acute Myeloid Leukemia. Cancer Research, 2021, 81, 5733-5744.	0.9	15
11	Inferred Ancestral Origin of Cancer Cell Lines Associates with Differential Drug Response. International Journal of Molecular Sciences, 2021, 22, 10135.	4.1	2
12	Minimal genome-wide human CRISPR-Cas9 library. Genome Biology, 2021, 22, 40.	8.8	40
13	Combinatorial CRISPR screen identifies fitness effects of gene paralogues. Nature Communications, 2021, 12, 1302.	12.8	59
14	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
15	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
16	CELLector: Genomics-Guided Selection of Cancer InÂVitro Models. Cell Systems, 2020, 10, 424-432.e6.	6.2	35
17	Genomics-guided pre-clinical development of cancer therapies. Nature Cancer, 2020, 1, 482-492.	13.2	23
18	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

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19	Drug mechanismâ€ofâ€action discovery through the integration of pharmacological and <scp>CRISPR</scp> screens. Molecular Systems Biology, 2020, 16, e9405.	7.2	63
20	Genome-wide CRISPR screens of oral squamous cell carcinoma reveal fitness genes in the Hippo pathway. ELife, 2020, 9, .	6.0	31
21	A statistical framework for assessing pharmacological responses and biomarkers using uncertainty estimates. ELife, 2020, 9, .	6.0	16
22	Patient-Derived Xenografts and Matched Cell Lines Identify Pharmacogenomic Vulnerabilities in Colorectal Cancer. Clinical Cancer Research, 2019, 25, 6243-6259.	7.0	42
23	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
24	Functional linkage of gene fusions to cancer cell fitness assessed by pharmacological and CRISPR-Cas9 screening. Nature Communications, 2019, 10, 2198.	12.8	92
25	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. Cell, 2019, 176, 1282-1294.e20.	28.9	298
26	Prioritization of cancer therapeutic targets using CRISPR–Cas9 screens. Nature, 2019, 568, 511-516.	27.8	886
27	Structural rearrangements generate cell-specific, gene-independent CRISPR-Cas9 loss of fitness effects. Genome Biology, 2019, 20, 27.	8.8	35
28	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. Nature Communications, 2019, 10, 5817.	12.8	160
29	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
30	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
31	Cell Model Passports—a hub for clinical, genetic and functional datasets of preclinical cancer models. Nucleic Acids Research, 2019, 47, D923-D929.	14.5	118
32	Discovery of Potent and Selective MRCK Inhibitors with Therapeutic Effect on Skin Cancer. Cancer Research, 2018, 78, 2096-2114.	0.9	31
33	GDSCTools for mining pharmacogenomic interactions in cancer. Bioinformatics, 2018, 34, 1226-1228.	4.1	45
34	Perturbation-response genes reveal signaling footprints in cancer gene expression. Nature Communications, 2018, 9, 20.	12.8	436
35	Transcription Factor Activities Enhance Markers of Drug Sensitivity in Cancer. Cancer Research, 2018, 78, 769-780.	0.9	161
36	Itraconazole targets cell cycle heterogeneity in colorectal cancer. Journal of Experimental Medicine, 2018, 215, 1891-1912.	8.5	54

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37	Organoid cultures recapitulate esophageal adenocarcinoma heterogeneity providing a model for clonality studies and precision therapeutics. Nature Communications, 2018, 9, 2983.	12.8	206
38	The germline genetic component of drug sensitivity in cancer cell lines. Nature Communications, 2018, 9, 3385.	12.8	38
39	Unsupervised correction of gene-independent cell responses to CRISPR-Cas9 targeting. BMC Genomics, 2018, 19, 604.	2.8	75
40	A Road Map for Precision Cancer Medicine Using Personalized Models. Cancer Discovery, 2017, 7, 456-458.	9.4	9
41	Drug Resistance Mechanisms in Colorectal Cancer Dissected with Cell Type–Specific Dynamic Logic Models. Cancer Research, 2017, 77, 3364-3375.	0.9	101
42	High-throughput RNAi screen for essential genes and drug synergistic combinations in colorectal cancer. Scientific Data, 2017, 4, 170139.	5.3	11
43	Human primary liver cancer–derived organoid cultures for disease modeling and drug screening. Nature Medicine, 2017, 23, 1424-1435.	30.7	905
44	A Landscape of Pharmacogenomic Interactions in Cancer. Cell, 2016, 166, 740-754.	28.9	1,518
45	Multilevel models improve precision and speed of IC ₅₀ estimates. Pharmacogenomics, 2016, 17, 691-700.	1.3	57
46	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
47	Drug Sensitivity Assays of Human Cancer Organoid Cultures. Methods in Molecular Biology, 2016, 1576, 339-351.	0.9	54
48	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. Cell, 2016, 167, 260-274.e22.	28.9	376
49	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
50	Combinations of PARP Inhibitors with Temozolomide Drive PARP1 Trapping and Apoptosis in Ewing's Sarcoma. PLoS ONE, 2015, 10, e0140988.	2.5	72
51	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	28.9	1,710
52	What role could organoids play in the personalization of cancer treatment?. Pharmacogenomics, 2015, 16, 1523-1526.	1.3	11
53	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
54	Systematic identification of genomic markers of drug sensitivity in cancer cells. Nature, 2012, 483, 570-575.	27.8	2,173

#	Article	IF	CITATIONS
55	Can Drug Repurposing Accelerate Precision Oncology?. Cancer Discovery, 0, , OF1-OF8.	9.4	11