## Nikhil Wagle

List of Publications by Year in descending order

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Version: 2024-02-01

71 13,619 44 72
papers citations h-index g-index

77 77 23073

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all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Somatic and Germline Genomic Alterations in Very Young Women with Breast Cancer. Clinical Cancer Research, 2022, 28, 2339-2348.	7.0	20
2	Hotspot <i>ESR1</i> Mutations Are Multimodal and Contextual Modulators of Breast Cancer Metastasis. Cancer Research, 2022, 82, 1321-1339.	0.9	30
3	Abstract PD1-05: Targeting the FRA1-dependent transcriptional nexus in high FOXA1-driven endocrine-resistant and metastatic breast cancer. Cancer Research, 2022, 82, PD1-05-PD1-05.	0.9	O
4	ESR1 mutant breast cancers show elevated basal cytokeratins and immune activation. Nature Communications, 2022, 13, 2011.	12.8	29
5	A Framework for Promoting Diversity, Equity, and Inclusion in Genetics and Genomics Research. JAMA Health Forum, 2022, 3, e220603.	2.2	13
6	Multidimensional Molecular Profiling of Metastatic Triple-Negative Breast Cancer and Immune Checkpoint Inhibitor Benefit. JCO Precision Oncology, 2022, , .	3.0	11
7	Genomic Characterization of <i>de novo</i> Metastatic Breast Cancer. Clinical Cancer Research, 2021, 27, 1105-1118.	7.0	24
8	Opposing immune and genetic mechanisms shape oncogenic programs in synovial sarcoma. Nature Medicine, 2021, 27, 289-300.	30.7	64
9	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. Science, 2021, 371, .	12.6	197
10	A phase II study of efficacy, toxicity, and the potential impact of genomic alterations on response to eribulin mesylate in combination with trastuzumab and pertuzumab in women with human epidermal growth factor receptor 2 (HER2)+ metastatic breast cancer. Breast Cancer Research and Treatment, 2021, 189, 411-423.	2.5	3
11	ER+ Breast Cancer Strongly Depends on MCL-1 and BCL-xL Anti-Apoptotic Proteins. Cells, 2021, 10, 1659.	4.1	16
12	Cell Line–Specific Network Models of ER+ Breast Cancer Identify Potential PI3Kα Inhibitor Resistance Mechanisms and Drug Combinations. Cancer Research, 2021, 81, 4603-4617.	0.9	13
13	cDNA-detector: detection and removal of cDNA contamination in DNA sequencing libraries. BMC Bioinformatics, 2021, 22, 611.	2.6	3
14	Acquired FGFR and FGF Alterations Confer Resistance to Estrogen Receptor (ER) Targeted Therapy in ER+ Metastatic Breast Cancer. Clinical Cancer Research, 2020, 26, 5974-5989.	7.0	87
15	TBCRC 048: Phase II Study of Olaparib for Metastatic Breast Cancer and Mutations in Homologous Recombination-Related Genes. Journal of Clinical Oncology, 2020, 38, 4274-4282.	1.6	276
16	Identification of a RAS-activating <i>TMEM87A–RASGRF1</i> Fusion in an Exceptional Responder to Sunitinib with Non–Small Cell Lung Cancer. Clinical Cancer Research, 2020, 26, 4072-4079.	7.0	13
17	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. Nature Medicine, 2020, 26, 792-802.	30.7	381
18	The Genomic Landscape of Intrinsic and Acquired Resistance to Cyclin-Dependent Kinase 4/6 Inhibitors in Patients with Hormone Receptor–Positive Metastatic Breast Cancer. Cancer Discovery, 2020, 10, 1174-1193.	9.4	176

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19	Sensitive Detection of Minimal Residual Disease in Patients Treated for Early-Stage Breast Cancer. Clinical Cancer Research, 2020, 26, 2556-2564.	7.0	109
20	The Angiosarcoma Project: enabling genomic and clinical discoveries in a rare cancer through patient-partnered research. Nature Medicine, 2020, 26, 181-187.	30.7	158
21	Tumor Mutational Burden and <i>PTEN</i> Alterations as Molecular Correlates of Response to PD-1/L1 Blockade in Metastatic Triple-Negative Breast Cancer. Clinical Cancer Research, 2020, 26, 2565-2572.	7.0	138
22	Subclonal cooperation drives metastasis by modulating local and systemic immune microenvironments. Nature Cell Biology, 2019, 21, 879-888.	10.3	114
23	MicroRNA-Mediated Suppression of the TGF-β Pathway Confers Transmissible and Reversible CDK4/6 Inhibitor Resistance. Cell Reports, 2019, 26, 2667-2680.e7.	6.4	101
24	FOXA1 upregulation promotes enhancer and transcriptional reprogramming in endocrine-resistant breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26823-26834.	7.1	103
25	Acquired HER2 mutations in ER+ metastatic breast cancer confer resistance to estrogen receptor–directed therapies. Nature Genetics, 2019, 51, 207-216.	21.4	170
26	Research Directions in the Clinical Implementation of Pharmacogenomics: An Overview of US Programs and Projects. Clinical Pharmacology and Therapeutics, 2018, 103, 778-786.	4.7	110
27	Phase I Trial of a Tablet Formulation of Pilaralisib, a Panâ€Class I PI3K Inhibitor, in Patients with Advanced Solid Tumors. Oncologist, 2018, 23, 401.	3.7	13
28	Allele-Specific Chromatin Recruitment and Therapeutic Vulnerabilities of ESR1 Activating Mutations. Cancer Cell, 2018, 33, 173-186.e5.	16.8	201
29	Characterizing reduced coverage regions through comparison of exome and genome sequencing data across 10 centers. Genetics in Medicine, 2018, 20, 855-866.	2.4	22
30	Association of Cell-Free DNA Tumor Fraction and Somatic Copy Number Alterations With Survival in Metastatic Triple-Negative Breast Cancer. Journal of Clinical Oncology, 2018, 36, 543-553.	1.6	162
31	KDM5 Histone Demethylase Activity Links Cellular Transcriptomic Heterogeneity to Therapeutic Resistance. Cancer Cell, 2018, 34, 939-953.e9.	16.8	170
32	Everolimus and pazopanib (E/P) benefit genomically selected patients with metastatic urothelial carcinoma. British Journal of Cancer, 2018, 119, 707-712.	6.4	28
33	Real-time Genomic Characterization of Advanced Pancreatic Cancer to Enable Precision Medicine. Cancer Discovery, 2018, 8, 1096-1111.	9.4	256
34	Assigning clinical meaning to somatic and germ-line whole-exome sequencing data in a prospective cancer precision medicine study. Genetics in Medicine, 2017, 19, 787-795.	2.4	46
35	The fuzzy world of precision medicine: deliberations of a precision medicine tumor board. Personalized Medicine, 2017, 14, 37-50.	1.5	15
36	Multiplexed Elimination of Wild-Type DNA and High-Resolution Melting Prior to Targeted Resequencing of Liquid Biopsies. Clinical Chemistry, 2017, 63, 1605-1613.	3.2	23

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37	Systematic genomic and translational efficiency studies of uveal melanoma. PLoS ONE, 2017, 12, e0178189.	2.5	34
38	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. American Journal of Human Genetics, 2016, 98, 1051-1066.	6.2	137
39	The impact of tumor profiling approaches and genomic data strategies for cancer precision medicine. Genome Medicine, 2016, 8, 79.	8.2	151
40	Oncologists' and cancer patients' views on whole-exome sequencing and incidental findings: results from the CanSeq study. Genetics in Medicine, 2016, 18, 1011-1019.	2.4	108
41	mTOR Inhibitors in Cancer: What Can We Learn from Exceptional Responses?. EBioMedicine, 2015, 2, 2-4.	6.1	15
42	Clinical Acquired Resistance to RAF Inhibitor Combinations in <i>BRAF</i> Hutant Colorectal Cancer through MAPK Pathway Alterations. Cancer Discovery, 2015, 5, 358-367.	9.4	265
43	Phase II study of tivantinib (ARQ 197) in patients with metastatic triple-negative breast cancer. Investigational New Drugs, 2015, 33, 1108-1114.	2.6	44
44	Genomic Correlate of Exceptional Erlotinib Response in Head and Neck Squamous Cell Carcinoma. JAMA Oncology, 2015, 1, 238.	7.1	44
45	Somatic <i>ERCC2</i> Mutations Correlate with Cisplatin Sensitivity in Muscle-Invasive Urothelial Carcinoma. Cancer Discovery, 2014, 4, 1140-1153.	9.4	506
46	Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5564-73.	7.1	355
47	The Genetic Landscape of Clinical Resistance to RAF Inhibition in Metastatic Melanoma. Cancer Discovery, 2014, 4, 94-109.	9.4	782
48	ERK Mutations Confer Resistance to Mitogen-Activated Protein Kinase Pathway Inhibitors. Cancer Research, 2014, 74, 7079-7089.	0.9	90
49	MAP Kinase Pathway Alterations in <i>BRAF</i> -Mutant Melanoma Patients with Acquired Resistance to Combined RAF/MEK Inhibition. Cancer Discovery, 2014, 4, 61-68.	9.4	419
50	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. Nature Medicine, 2014, 20, 682-688.	30.7	508
51	A phase II trial of AS1411 (a novel nucleolin-targeted DNA aptamer) in metastatic renal cell carcinoma. Investigational New Drugs, 2014, 32, 178-187.	2.6	302
52	Response and Acquired Resistance to Everolimus in Anaplastic Thyroid Cancer. New England Journal of Medicine, 2014, 371, 1426-1433.	27.0	290
53	Assessing the clinical utility of cancer genomic and proteomic data across tumor types. Nature Biotechnology, 2014, 32, 644-652.	17.5	257
54	Activating mTOR Mutations in a Patient with an Extraordinary Response on a Phase I Trial of Everolimus and Pazopanib. Cancer Discovery, 2014, 4, 546-553.	9.4	266

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55	Clinicopathological Features Among Patients With Advanced Human Epidermal Growth Factor–2-Positive Breast Cancer With Prolonged Clinical Benefit to First-Line Trastuzumab-Based Therapy: A Retrospective Cohort Study. Clinical Breast Cancer, 2013, 13, 254-263.	2.4	26
56	Clinical Analysis and Interpretation of Cancer Genome Data. Journal of Clinical Oncology, 2013, 31, 1825-1833.	1.6	123
57	Oncogenic mutations in cervical cancer. Cancer, 2013, 119, 3776-3783.	4.1	225
58	A Genome-Scale RNA Interference Screen Implicates NF1 Loss in Resistance to RAF Inhibition. Cancer Discovery, 2013, 3, 350-362.	9.4	299
59	Processes and preliminary outputs for identification of actionable genes as incidental findings in genomic sequence data in the Clinical Sequencing Exploratory Research Consortium. Genetics in Medicine, 2013, 15, 860-867.	2.4	99
60	Discordant Cellular Response to Presurgical Letrozole in Bilateral Synchronous ER+ Breast Cancers with a <i>KRAS</i> Mutation or <i>FGFR1</i> Gene Amplification. Molecular Cancer Therapeutics, 2012, 11, 2301-2305.	4.1	22
61	High-Throughput Detection of Actionable Genomic Alterations in Clinical Tumor Samples by Targeted, Massively Parallel Sequencing. Cancer Discovery, 2012, 2, 82-93.	9.4	484
62	Melanoma genome sequencing reveals frequent PREX2 mutations. Nature, 2012, 485, 502-506.	27.8	671
63	A Landscape of Driver Mutations in Melanoma. Cell, 2012, 150, 251-263.	28.9	2,247
64	Dissecting Therapeutic Resistance to RAF Inhibition in Melanoma by Tumor Genomic Profiling. Journal of Clinical Oncology, 2011, 29, 3085-3096.	1.6	890
65	Biomarker-Based Prediction of Response to Therapy for Colorectal Cancer. American Journal of Clinical Pathology, 2010, 134, 478-490.	0.7	69
66	Cardiac Presentation of Anaplastic Large-Cell Lymphoma. Journal of Clinical Oncology, 2010, 28, e314-e316.	1.6	5
67	A p53-Dependent Checkpoint Pathway Prevents Rereplication. Molecular Cell, 2003, 11, 997-1008.	9.7	379
68	Measuring the Incremental Cost of Clinical Cancer Research. Journal of Clinical Oncology, 2001, 19, 105-110.	1.6	27
69	Using Hospital Tumor Registries to Identify Research Subjects. Health Services and Outcomes Research Methodology, 2001, 2, 67-76.	1.8	1
70	Rvb1p and Rvb2p Are Essential Components of a Chromatin Remodeling Complex That Regulates Transcription of over 5% of Yeast Genes. Journal of Biological Chemistry, 2001, 276, 16279-16288.	3.4	103
71	Analysis of JNK, Mdm2 and p14ARF contribution to the regulation of mutant p53 stability. Journal of Molecular Biology, 2000, 295, 1009-1021.	4.2	35