

# Neekesh V Dharia

## List of Publications by Year in descending order

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43  
papers

5,014  
citations

201674

27  
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315739

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46  
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46  
docs citations

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times ranked

9162  
citing authors

#	ARTICLE	IF	CITATIONS
1	An <i>In Vivo</i> CRISPR Screening Platform for Prioritizing Therapeutic Targets in AML. <i>Cancer Discovery</i> , 2022, 12, 432-449.	9.4	32
2	EP300 Selectively Controls the Enhancer Landscape of <i>MYCN</i> -Amplified Neuroblastoma. <i>Cancer Discovery</i> , 2022, 12, 730-751.	9.4	64
3	A distinct core regulatory module enforces oncogene expression in <i>KMT2A</i> -rearranged leukemia. <i>Genes and Development</i> , 2022, 36, 368-389.	5.9	14
4	Unleashing Cell-Intrinsic Inflammation as a Strategy to Kill AML Blasts. <i>Cancer Discovery</i> , 2022, 12, 1760-1781.	9.4	15
5	Transcriptional Plasticity Drives Leukemia Immune Escape. <i>Blood Cancer Discovery</i> , 2022, 3, 394-409.	5.0	8
6	Network-based systems pharmacology reveals heterogeneity in <i>LCK</i> and <i>BCL2</i> signaling and therapeutic sensitivity of T-cell acute lymphoblastic leukemia. <i>Nature Cancer</i> , 2021, 2, 284-299.	13.2	70
7	Matched Targeted Therapy for Pediatric Patients with Relapsed, Refractory, or High-Risk Leukemias: A Report from the LEAP Consortium. <i>Cancer Discovery</i> , 2021, 11, 1424-1439.	9.4	16
8	A first-generation pediatric cancer dependency map. <i>Nature Genetics</i> , 2021, 53, 529-538.	21.4	76
9	Selective Modulation of a Pan-Essential Protein as a Therapeutic Strategy in Cancer. <i>Cancer Discovery</i> , 2021, 11, 2282-2299.	9.4	21
10	<i>STAG2</i> loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. <i>Cancer Cell</i> , 2021, 39, 827-844.e10.	16.8	49
11	Gene Fusions Create Partner and Collateral Dependencies Essential to Cancer Cell Survival. <i>Cancer Research</i> , 2021, 81, 3971-3984.	0.9	11
12	<i>TRIM8</i> modulates the <i>EWS/FLI</i> oncoprotein to promote survival in Ewing sarcoma. <i>Cancer Cell</i> , 2021, 39, 1262-1278.e7.	16.8	49
13	An <i>In Vivo</i> CRISPR Screening Platform to Identify New Therapeutic Targets in AML. <i>Blood</i> , 2021, 138, 266-266.	1.4	0
14	<i>SLC5A3</i> Transports Myo-Inositol to Support the Growth of Acute Myeloid Leukemia. <i>Blood</i> , 2021, 138, 3319-3319.	1.4	0
15	Unleashing Cell-Intrinsic Inflammation As a Strategy to Kill AML Blasts. <i>Blood</i> , 2021, 138, 3305-3305.	1.4	1
16	Synthetic Lethal Interaction between the ESCRT Paralog Enzymes <i>VPS4A</i> and <i>VPS4B</i> in Cancers Harboring Loss of Chromosome 18q or 16q. <i>Cell Reports</i> , 2020, 33, 108493.	6.4	28
17	Small-Molecule and CRISPR Screening Converge to Reveal Receptor Tyrosine Kinase Dependencies in Pediatric Rhabdoid Tumors. <i>Cell Reports</i> , 2019, 28, 2331-2344.e8.	6.4	24
18	Neuronal differentiation and cell-cycle programs mediate response to BET-bromodomain inhibition in <i>MYC</i> -driven medulloblastoma. <i>Nature Communications</i> , 2019, 10, 2400.	12.8	37

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19	MDM2 and MDM4 Are Therapeutic Vulnerabilities in Malignant Rhabdoid Tumors. <i>Cancer Research</i> , 2019, 79, 2404-2414.	0.9	43
20	CRISPR studies identify genes preferentially essential for myeloma cells vs. other neoplasias: implications for future therapies selective against MM. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e48-e49.	0.4	0
21	A Combination CDK4/6 and IGF1R Inhibitor Strategy for Ewing Sarcoma. <i>Clinical Cancer Research</i> , 2019, 25, 1343-1357.	7.0	69
22	EWS/FLI Confers Tumor Cell Synthetic Lethality to CDK12 Inhibition in Ewing Sarcoma. <i>Cancer Cell</i> , 2018, 33, 202-216.e6.	16.8	116
23	Precision Targeting of BFL-1/A1 and an ATM Co-dependency in Human Cancer. <i>Cell Reports</i> , 2018, 24, 3393-3403.e5.	6.4	15
24	Targetable vulnerabilities in T- and NK-cell lymphomas identified through preclinical models. <i>Nature Communications</i> , 2018, 9, 2024.	12.8	80
25	Genome-scale CRISPR-Cas9 screen identifies druggable dependencies in TP53 wild-type Ewing sarcoma. <i>Journal of Experimental Medicine</i> , 2018, 215, 2137-2155.	8.5	55
26	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. <i>Nature Genetics</i> , 2018, 50, 1240-1246.	21.4	199
27	Comparative proteomics reveals a diagnostic signature for pulmonary head&neck cancer metastasis. <i>EMBO Molecular Medicine</i> , 2018, 10, .	6.9	41
28	Esterase mutation is a mechanism of resistance to antimalarial compounds. <i>Nature Communications</i> , 2017, 8, 14240.	12.8	47
29	Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. <i>Nature Genetics</i> , 2017, 49, 1779-1784.	21.4	1,436
30	CRISPR-Cas9 screen reveals a MYCN-amplified neuroblastoma dependency on EZH2. <i>Journal of Clinical Investigation</i> , 2017, 128, 446-462.	8.2	117
31	Answer to May 2015 Photo Quiz. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1788-1788.	3.9	0
32	Photo Quiz: A Child with Fever after Hematopoietic Stem Cell Transplantation: FIG 1. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1463-1463.	3.9	0
33	Mitotic Evolution of <i>Plasmodium falciparum</i> Shows a Stable Core Genome but Recombination in Antigen Families. <i>PLoS Genetics</i> , 2013, 9, e1003293.	3.5	192
34	A Chemical Genomic Analysis of Decoquininate, a <i>Plasmodium falciparum</i> Cytochrome b Inhibitor. <i>ACS Chemical Biology</i> , 2011, 6, 1214-1222.	3.4	84
35	Imaging of <i>Plasmodium</i> Liver Stages to Drive Next-Generation Antimalarial Drug Discovery. <i>Science</i> , 2011, 334, 1372-1377.	12.6	308
36	Piperazine Resistance Is Associated with a Copy Number Variation on Chromosome 5 in Drug-Pressured <i>Plasmodium falciparum</i> Parasites. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 3908-3916.	3.2	102

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37	Validation of isoleucine utilization targets in <i>Plasmodium falciparum</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1627-1632.	7.1	123
38	Spiroindolones, a Potent Compound Class for the Treatment of Malaria. Science, 2010, 329, 1175-1180.	12.6	1,081
39	Whole-genome sequencing and microarray analysis of ex vivo <i>Plasmodium vivax</i> reveal selective pressure on putative drug resistance genes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20045-20050.	7.1	99
40	A Systems-Based Analysis of <i>Plasmodium vivax</i> Lifecycle Transcription from Human to Mosquito. PLoS Neglected Tropical Diseases, 2010, 4, e653.	3.0	96
41	Genome scanning of Amazonian <i>Plasmodium falciparum</i> shows subtelomeric instability and clindamycin-resistant parasites. Genome Research, 2010, 20, 1534-1544.	5.5	59
42	Genome-wide nucleosome mapping of <i>Plasmodium falciparum</i> reveals histone-rich coding and histone-poor intergenic regions and chromatin remodeling of core and subtelomeric genes. BMC Genomics, 2009, 10, 610.	2.8	67
43	Use of high-density tiling microarrays to identify mutations globally and elucidate mechanisms of drug resistance in <i>Plasmodium falciparum</i> . Genome Biology, 2009, 10, R21.	9.6	120