

Housheng Hansen He

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

9,669
citations

66336
42
h-index

79691
73
g-index

92
all docs

92
docs citations

92
times ranked

16836
citing authors

#	ARTICLE	IF	CITATIONS
1	Subpathologies and genomic classifier for treatment individualization of post-prostatectomy radiotherapy. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2022, 40, 5.e1-5.e13.	1.6	2
2	TRIM21 regulates pyroptotic cell death by promoting Gasdermin D oligomerization. <i>Cell Death and Differentiation</i> , 2022, 29, 439-450.	11.2	33
3	RB1 loss in castration-resistant prostate cancer confers vulnerability to LSD1 inhibition. <i>Oncogene</i> , 2022, 41, 852-864.	5.9	18
4	Exploiting the tumor-suppressive activity of the androgen receptor by CDK4/6 inhibition in castration-resistant prostate cancer. <i>Molecular Therapy</i> , 2022, 30, 1628-1644.	8.2	10
5	Neonatal LT1 ² R signaling is required for the accumulation of eosinophils in the inflamed adult mesenteric lymph node. <i>Mucosal Immunology</i> , 2022, , .	6.0	1
6	N6-Methyladenosine Reader YTHDF1 Promotes ARHGEF2 Translation and RhoA Signaling in Colorectal Cancer. <i>Gastroenterology</i> , 2022, 162, 1183-1196.	1.3	89
7	RNA N6-Methyladenosine Methyltransferase METTL3 Facilitates Colorectal Cancer by Activating the m6A-GLUT1-mTORC1 Axis and Is a Therapeutic Target. <i>Gastroenterology</i> , 2021, 160, 1284-1300.e16.	1.3	161
8	CRISPR screen identifies genes that sensitize AML cells to double-negative T-cell therapy. <i>Blood</i> , 2021, 137, 2171-2181.	1.4	23
9	Pioneer of prostate cancer: past, present and the future of FOXA1. <i>Protein and Cell</i> , 2021, 12, 29-38.	11.0	77
10	Single-cell analysis reveals transcriptomic remodellings in distinct cell types that contribute to human prostate cancer progression. <i>Nature Cell Biology</i> , 2021, 23, 87-98.	10.3	209
11	Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy. <i>Cell</i> , 2021, 184, 226-242.e21.	28.9	258
12	EZH2 inhibition activates a dsRNA-“STING”-interferon stress axis that potentiates response to PD-1 checkpoint blockade in prostate cancer. <i>Nature Cancer</i> , 2021, 2, 444-456.	13.2	118
13	CRISPRi screens reveal a DNA methylation-mediated 3D genome dependent causal mechanism in prostate cancer. <i>Nature Communications</i> , 2021, 12, 1781.	12.8	32
14	Uncovering the dosage-dependent roles of <i>Arid1a</i> in gastric tumorigenesis for combinatorial drug therapy. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	16
15	HNRNPM controls circRNA biogenesis and splicing fidelity to sustain cancer cell fitness. <i>ELife</i> , 2021, 10, .	6.0	27
16	SPOP mutation induces DNA methylation via stabilizing GLP/G9a. <i>Nature Communications</i> , 2021, 12, 5716.	12.8	19
17	An androgen receptor switch underlies lineage infidelity in treatment-resistant prostate cancer. <i>Nature Cell Biology</i> , 2021, 23, 1023-1034.	10.3	72
18	CRISPR screens identify cholesterol biosynthesis as a therapeutic target on stemness and drug resistance of colon cancer. <i>Oncogene</i> , 2021, 40, 6601-6613.	5.9	37

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19	ZNF545 loss promotes ribosome biogenesis and protein translation to initiate colorectal tumorigenesis in mice. <i>Oncogene</i> , 2021, 40, 6590-6600.	5.9	11
20	Somatic driver mutation prevalence in 1844 prostate cancers identifies ZNRF3 loss as a predictor of metastatic relapse. <i>Nature Communications</i> , 2021, 12, 6248.	12.8	15
21	Androgen receptor and MYC equilibration centralizes on developmental super-enhancer. <i>Nature Communications</i> , 2021, 12, 7308.	12.8	46
22	MAP9 Loss Triggers Chromosomal Instability, Initiates Colorectal Tumorigenesis, and Is Associated with Poor Survival of Patients with Colorectal Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 746-757.	7.0	11
23	The DNA methylation landscape of advanced prostate cancer. <i>Nature Genetics</i> , 2020, 52, 778-789.	21.4	198
24	Chromatin binding of FOXA1 is promoted by LSD1-mediated demethylation in prostate cancer. <i>Nature Genetics</i> , 2020, 52, 1011-1017.	21.4	78
25	Haploinsufficiency of RREB1 causes a Noonan-like RASopathy via epigenetic reprogramming of RAS-MAPK pathway genes. <i>Nature Communications</i> , 2020, 11, 4673.	12.8	19
26	Noncoding mutations target cis-regulatory elements of the FOXA1 plexus in prostate cancer. <i>Nature Communications</i> , 2020, 11, 441.	12.8	51
27	Forkhead domain mutations in FOXA1 drive prostate cancer progression. <i>Cell Research</i> , 2019, 29, 770-772.	12.0	25
28	DNA-Dependent Protein Kinase Drives Prostate Cancer Progression through Transcriptional Regulation of the Wnt Signaling Pathway. <i>Clinical Cancer Research</i> , 2019, 25, 5608-5622.	7.0	17
29	Landscape of Noncoding RNA in Prostate Cancer. <i>Trends in Genetics</i> , 2019, 35, 840-851.	6.7	114
30	N6-methyladenosine mRNA marking promotes selective translation of regulons required for human erythropoiesis. <i>Nature Communications</i> , 2019, 10, 4596.	12.8	42
31	Cistrome Partitioning Reveals Convergence of Somatic Mutations and Risk Variants on Master Transcription Regulators in Primary Prostate Tumors. <i>Cancer Cell</i> , 2019, 36, 674-689.e6.	16.8	52
32	ZBTB7A Mediates the Transcriptional Repression Activity of the Androgen Receptor in Prostate Cancer. <i>Cancer Research</i> , 2019, 79, 5260-5271.	0.9	19
33	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. <i>Nature Medicine</i> , 2019, 25, 1615-1626.	30.7	45
34	ONECUT2 is a driver of neuroendocrine prostate cancer. <i>Nature Communications</i> , 2019, 10, 278.	12.8	143
35	TMPRSS2-ERG activates NO-cGMP signaling in prostate cancer cells. <i>Oncogene</i> , 2019, 38, 4397-4411.	5.9	29
36	Widespread and Functional RNA Circularization in Localized Prostate Cancer. <i>Cell</i> , 2019, 176, 831-843.e22.	28.9	317

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37	Early-life programming of mesenteric lymph node stromal cell identity by the lymphotoxin pathway regulates adult mucosal immunity. <i>Science Immunology</i> , 2019, 4, .	11.9	23
38	Gastrointestinal transcription factors drive lineage-specific developmental programs in organ specification and cancer. <i>Science Advances</i> , 2019, 5, eaax8898.	10.3	26
39	Orphan noncoding RNAs: novel regulators and cancer biomarkers. <i>Annals of Translational Medicine</i> , 2019, 7, S21-S21.	1.7	1
40	Refined RIP-seq protocol for epitranscriptome analysis with low input materials. <i>PLoS Biology</i> , 2018, 16, e2006092.	5.6	112
41	LSD1 Ablation Stimulates Anti-tumor Immunity and Enables Checkpoint Blockade. <i>Cell</i> , 2018, 174, 549-563.e19.	28.9	473
42	Risk SNP-Mediated Promoter-Enhancer Switching Drives Prostate Cancer through lncRNA PCAT19. <i>Cell</i> , 2018, 174, 564-575.e18.	28.9	264
43	Genomic Hallmarks and Structural Variation in Metastatic Prostate Cancer. <i>Cell</i> , 2018, 174, 758-769.e9.	28.9	459
44	Reactivation of androgen receptor-regulated lipid biosynthesis drives the progression of castration-resistant prostate cancer. <i>Oncogene</i> , 2018, 37, 710-721.	5.9	69
45	Genomic hallmarks of localized, non-indolent prostate cancer. <i>Nature</i> , 2017, 541, 359-364.	27.8	462
46	Noncoding RNA for personalized prostate cancer treatment: utilizing the “dark matters”™ of the genome. <i>Personalized Medicine</i> , 2017, 14, 159-169.	1.5	0
47	K48-linked KLF4 ubiquitination by E3 ligase Mule controls T-cell proliferation and cell cycle progression. <i>Nature Communications</i> , 2017, 8, 14003.	12.8	25
48	Genome-wide CRISPR screen identifies HNRNPL as a prostate cancer dependency regulating RNA splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5207-E5215.	7.1	266
49	Transcriptional landscape of the human cell cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3473-3478.	7.1	110
50	LSD1-Mediated Epigenetic Reprogramming Drives CENPE Expression and Prostate Cancer Progression. <i>Cancer Research</i> , 2017, 77, 5479-5490.	0.9	71
51	Variant Set Enrichment: an R package to identify disease-associated functional genomic regions. <i>BioData Mining</i> , 2017, 10, 9.	4.0	17
52	Crucial role of noncoding RNA in driving prostate cancer development and progression. <i>Epigenomics</i> , 2017, 9, 1-3.	2.1	4
53	High-dimensional genomic data bias correction and data integration using MANCIE. <i>Nature Communications</i> , 2016, 7, 11305.	12.8	52
54	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. <i>Nature Genetics</i> , 2016, 48, 1142-1150.	21.4	196

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55	Modeling <i>cis</i> -regulation with a compendium of genome-wide histone H3K27ac profiles. <i>Genome Research</i> , 2016, 26, 1417-1429.	5.5	75
56	Androgen Receptor Tumor Suppressor Function Is Mediated by Recruitment of Retinoblastoma Protein. <i>Cell Reports</i> , 2016, 17, 966-976.	6.4	66
57	Integrative Analysis Reveals the Transcriptional Collaboration between EZH2 and E2F1 in the Regulation of Cancer-Related Gene Expression. <i>Molecular Cancer Research</i> , 2016, 14, 163-172.	3.4	34
58	Response and resistance to BET bromodomain inhibitors in triple-negative breast cancer. <i>Nature</i> , 2016, 529, 413-417.	27.8	490
59	SOX9 drives WNT pathway activation in prostate cancer. <i>Journal of Clinical Investigation</i> , 2016, 126, 1745-1758.	8.2	138
60	PLZF, a Tumor Suppressor Genetically Lost in Metastatic Castration-Resistant Prostate Cancer, Is a Mediator of Resistance to Androgen Deprivation Therapy. <i>Cancer Research</i> , 2015, 75, 1944-1948.	0.9	46
61	Lysine-Specific Demethylase 1 Has Dual Functions as a Major Regulator of Androgen Receptor Transcriptional Activity. <i>Cell Reports</i> , 2014, 9, 1618-1627.	6.4	115
62	Refined DNase-seq protocol and data analysis reveals intrinsic bias in transcription factor footprint identification. <i>Nature Methods</i> , 2014, 11, 73-78.	19.0	195
63	MiR-221 promotes the development of androgen independence in prostate cancer cells via downregulation of HECTD2 and RAB1A. <i>Oncogene</i> , 2014, 33, 2790-2800.	5.9	131
64	Digital Quantification of Gene Expression in Sequential Breast Cancer Biopsies Reveals Activation of an Immune Response. <i>PLoS ONE</i> , 2013, 8, e64225.	2.5	16
65	ERG induces androgen receptor-mediated regulation of SOX9 in prostate cancer. <i>Journal of Clinical Investigation</i> , 2013, 123, 1109-1122.	8.2	227
66	EZH2 Oncogenic Activity in Castration-Resistant Prostate Cancer Cells Is Polycomb-Independent. <i>Science</i> , 2012, 338, 1465-1469.	12.6	748
67	Tet3 CXXC Domain and Dioxygenase Activity Cooperatively Regulate Key Genes for <i>Xenopus</i> Eye and Neural Development. <i>Cell</i> , 2012, 151, 1200-1213.	28.9	227
68	Differential DNase I hypersensitivity reveals factor-dependent chromatin dynamics. <i>Genome Research</i> , 2012, 22, 1015-1025.	5.5	161
69	Systematic evaluation of factors influencing ChIP-seq fidelity. <i>Nature Methods</i> , 2012, 9, 609-614.	19.0	156
70	Androgen Receptor Gene Expression in Prostate Cancer Is Directly Suppressed by the Androgen Receptor Through Recruitment of Lysine-Specific Demethylase 1. <i>Cancer Cell</i> , 2011, 20, 457-471.	16.8	387
71	BINOCh: binding inference from nucleosome occupancy changes. <i>Bioinformatics</i> , 2011, 27, 1867-1868.	4.1	25
72	GlcNAcylation of histone H2B facilitates its monoubiquitination. <i>Nature</i> , 2011, 480, 557-560.	27.8	279

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73	Nucleosome dynamics define transcriptional enhancers. Nature Genetics, 2010, 42, 343-347.	21.4	426
74	8q24 prostate, breast, and colon cancer risk loci show tissue-specific long-range interaction with <i>MYC</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9742-9746.	7.1	353
75	Differentiation-Specific Histone Modifications Reveal Dynamic Chromatin Interactions and Partners for the Intestinal Transcription Factor CDX2. Developmental Cell, 2010, 19, 713-726.	7.0	192
76	Somatic Mutations and Risk-Variants Converge on Cis-Regulatory Elements to Reveal the Cancer Driver Transcription Regulators in Primary Prostate Tumors. SSRN Electronic Journal, 0, , .	0.4	2