

# Henry W Long

## List of Publications by Year in descending order

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Version: 2024-02-01

66  
papers

5,873  
citations

117625

34  
h-index

118850

62  
g-index

76  
all docs

76  
docs citations

76  
times ranked

11759  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Rb1</i> and <i>Trp53</i> cooperate to suppress prostate cancer lineage plasticity, metastasis, and antiandrogen resistance. <i>Science</i> , 2017, 355, 78-83.	12.6	767
2	A major chromatin regulator determines resistance of tumor cells to T cell-mediated killing. <i>Science</i> , 2018, 359, 770-775.	12.6	641
3	Response and resistance to BET bromodomain inhibitors in triple-negative breast cancer. <i>Nature</i> , 2016, 529, 413-417.	27.8	490
4	The androgen receptor cistrome is extensively reprogrammed in human prostate tumorigenesis. <i>Nature Genetics</i> , 2015, 47, 1346-1351.	21.4	363
5	Treatment-Induced Tumor Dormancy through YAP-Mediated Transcriptional Reprogramming of the Apoptotic Pathway. <i>Cancer Cell</i> , 2020, 37, 104-122.e12.	16.8	267
6	A Somatically Acquired Enhancer of the Androgen Receptor Is a Noncoding Driver in Advanced Prostate Cancer. <i>Cell</i> , 2018, 174, 422-432.e13.	28.9	234
7	The Public Repository of Xenografts Enables Discovery and Randomized Phase II-like Trials in Mice. <i>Cancer Cell</i> , 2016, 29, 574-586.	16.8	227
8	Broadly permissive intestinal chromatin underlies lateral inhibition and cell plasticity. <i>Nature</i> , 2014, 506, 511-515.	27.8	207
9	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. <i>Nature Genetics</i> , 2020, 52, 790-799.	21.4	174
10	VIPER: Visualization Pipeline for RNA-seq, a Snakemake workflow for efficient and complete RNA-seq analysis. <i>BMC Bioinformatics</i> , 2018, 19, 135.	2.6	156
11	ARv7 Represses Tumor-Suppressor Genes in Castration-Resistant Prostate Cancer. <i>Cancer Cell</i> , 2019, 35, 401-413.e6.	16.8	127
12	Enhancer signatures stratify and predict outcomes of non-functional pancreatic neuroendocrine tumors. <i>Nature Medicine</i> , 2019, 25, 1260-1265.	30.7	120
13	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
14	Synthetic Lethal and Resistance Interactions with BET Bromodomain Inhibitors in Triple-Negative Breast Cancer. <i>Molecular Cell</i> , 2020, 78, 1096-1113.e8.	9.7	114
15	Therapeutically Increasing MHC-I Expression Potentiates Immune Checkpoint Blockade. <i>Cancer Discovery</i> , 2021, 11, 1524-1541.	9.4	103
16	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. <i>BMC Bioinformatics</i> , 2016, 17, 404.	2.6	100
17	A Novel Mechanism Driving Poor-Prognosis Prostate Cancer: Overexpression of the DNA Repair Gene, Ribonucleotide Reductase Small Subunit M2 (RRM2). <i>Clinical Cancer Research</i> , 2019, 25, 4480-4492.	7.0	96
18	Enhanced Efficacy of Simultaneous PD-1 and PD-L1 Immune Checkpoint Blockade in High-Grade Serous Ovarian Cancer. <i>Cancer Research</i> , 2021, 81, 158-173.	0.9	85

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19	Embryonic transcription factor SOX9 drives breast cancer endocrine resistance. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4482-E4491.	7.1	83
20	InÂvivo CRISPR screens identify the E3 ligase Cop1 as a modulator of macrophage infiltration and cancer immunotherapy target. Cell, 2021, 184, 5357-5374.e22.	28.9	79
21	Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer. Nature Communications, 2021, 12, 1979.	12.8	70
22	Chromatin immunoprecipitation from fixed clinical tissues reveals tumor-specific enhancer profiles. Nature Medicine, 2016, 22, 685-691.	30.7	64
23	Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. IScience, 2019, 17, 242-255.	4.1	60
24	Enhancer-Mediated Oncogenic Function of the Menin Tumor Suppressor in Breast Cancer. Cell Reports, 2017, 18, 2359-2372.	6.4	59
25	Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. Nature Communications, 2021, 12, 5775.	12.8	59
26	Inhibition of CDK4/6 Promotes CD8 T-cell Memory Formation. Cancer Discovery, 2021, 11, 2564-2581.	9.4	58
27	MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. Nature Communications, 2022, 13, 2559.	12.8	56
28	Estrogen receptor signaling is reprogrammed during breast tumorigenesis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11437-11443.	7.1	55
29	Trisomy of a Down Syndrome Critical Region Globally Amplifies Transcription via HMGN1 Overexpression. Cell Reports, 2018, 25, 1898-1911.e5.	6.4	52
30	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. Human Molecular Genetics, 2015, 24, 5603-5618.	2.9	50
31	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
32	CDK4/6 inhibition reprograms the breast cancer enhancer landscape by stimulating AP-1 transcriptional activity. Nature Cancer, 2021, 2, 34-48.	13.2	48
33	TRPS1 Is a Lineage-Specific Transcriptional Dependency in Breast Cancer. Cell Reports, 2018, 25, 1255-1267.e5.	6.4	46
34	CREB5 Promotes Resistance to Androgen-Receptor Antagonists and Androgen Deprivation in Prostate Cancer. Cell Reports, 2019, 29, 2355-2370.e6.	6.4	45
35	Reprogramming of the esophageal squamous carcinoma epigenome by SOX2 promotes ADAR1 dependence. Nature Genetics, 2021, 53, 881-894.	21.4	44
36	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. JCI Insight, 2016, 1, .	5.0	42

#	ARTICLE	IF	CITATIONS
37	Perturbed myoepithelial cell differentiation in BRCA mutation carriers and in ductal carcinoma in situ. <i>Nature Communications</i> , 2019, 10, 4182.	12.8	37
38	CistromeMap: a knowledgebase and web server for CHIP-Seq and DNase-Seq studies in mouse and human. <i>Bioinformatics</i> , 2012, 28, 1411-1412.	4.1	35
39	Chromatin accessibility promotes hematopoietic and leukemia stem cell activity. <i>Nature Communications</i> , 2020, 11, 1406.	12.8	32
40	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021, 7, eabf6123.	10.3	30
41	Hdac3 is an epigenetic inhibitor of the cytotoxicity program in CD8 T cells. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	28
42	An Enhancer-Driven Stem Cell-Like Program Mediated by SOX9 Blocks Intestinal Differentiation in Colorectal Cancer. <i>Gastroenterology</i> , 2022, 162, 209-222.	1.3	27
43	FGFR-inhibitor-mediated dismissal of SWI/SNF complexes from YAP-dependent enhancers induces adaptive therapeutic resistance. <i>Nature Cell Biology</i> , 2021, 23, 1187-1198.	10.3	21
44	FiTAc-seq: fixed-tissue CHIP-seq for H3K27ac profiling and super-enhancer analysis of FFPE tissues. <i>Nature Protocols</i> , 2020, 15, 2503-2518.	12.0	20
45	CistromeFinder for CHIP-seq and DNase-seq data reuse. <i>Bioinformatics</i> , 2013, 29, 1352-1354.	4.1	18
46	CoBRA: Containerized Bioinformatics Workflow for Reproducible CHIP/ATAC-seq Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 652-661.	6.9	18
47	<i>BCOR</i> and <i>BCORL1</i> Mutations Drive Epigenetic Reprogramming and Oncogenic Signaling by Unlinking PRC1.1 from Target Genes. <i>Blood Cancer Discovery</i> , 2022, 3, 116-135.	5.0	18
48	Subependymal giant cell astrocytomas are characterized by mTORC1 hyperactivation, a very low somatic mutation rate, and a unique gene expression profile. <i>Modern Pathology</i> , 2021, 34, 264-279.	5.5	16
49	Clonal tracing reveals diverse patterns of response to immune checkpoint blockade. <i>Genome Biology</i> , 2020, 21, 263.	8.8	15
50	Pan-ERBB kinase inhibition augments CDK4/6 inhibitor efficacy in oesophageal squamous cell carcinoma. <i>Gut</i> , 2022, 71, 665-675.	12.1	15
51	MITF is a driver oncogene and potential therapeutic target in kidney angiomyolipoma tumors through transcriptional regulation of <i>CYR61</i> . <i>Oncogene</i> , 2021, 40, 112-126.	5.9	14
52	Androgen receptor splice variant 7 functions independently of the full length receptor in prostate cancer cells. <i>Cancer Letters</i> , 2021, 519, 172-184.	7.2	13
53	Non-muscle-invasive micropapillary bladder cancer has a distinct lncRNA profile associated with unfavorable prognosis. <i>British Journal of Cancer</i> , 2022, 127, 313-320.	6.4	13
54	p16INK4A-deficiency predicts response to combined HER2 and CDK4/6 inhibition in HER2+ breast cancer brain metastases. <i>Nature Communications</i> , 2022, 13, 1473.	12.8	10

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55	ERG-Mediated Coregulator Complex Formation Maintains Androgen Receptor Signaling in Prostate Cancer. <i>Cancer Research</i> , 2020, 80, 4612-4619.	0.9	9
56	YAP1 and PRDM14 converge to promote cell survival and tumorigenesis. <i>Developmental Cell</i> , 2022, 57, 212-227.e8.	7.0	9
57	Response to supraphysiological testosterone is predicted by a distinct androgen receptor cistrome. <i>JCI Insight</i> , 2022, 7, .	5.0	9
58	Androgen receptor reprogramming demarcates prognostic, context-dependent gene sets in primary and metastatic prostate cancer. <i>Clinical Epigenetics</i> , 2022, 14, 60.	4.1	8
59	Principles and methods of integrative chromatin analysis in primary tissues and tumors. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2020, 1873, 188333.	7.4	7
60	Nutritional Epigenetics in Cancer. <i>Advances in Nutrition</i> , 2022, 13, 1748-1761.	6.4	7
61	The nuclear receptor THRB facilitates differentiation of human PSCs into more mature hepatocytes. <i>Cell Stem Cell</i> , 2022, 29, 795-809.e11.	11.1	5
62	Transcriptomic analysis of micropapillary high grade T1 urothelial bladder cancer. <i>Scientific Reports</i> , 2020, 10, 20135.	3.3	4
63	CHIPS: A Snakemake pipeline for quality control and reproducible processing of chromatin profiling data. <i>F1000Research</i> , 0, 10, 517.	1.6	4
64	Distinct oncogenic signatures in malignant PEComa and leiomyosarcoma identified by integrative RNA-seq and H3K27ac ChIP-seq analysis.. <i>Journal of Clinical Oncology</i> , 2022, 40, 11552-11552.	1.6	1
65	<i>In vivo</i> CRISPR Screens Identify E3 Ligase Cop1 as a Modulator of Macrophage Infiltration and Cancer Immunotherapy Target. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
66	High-Resolution ATAC-Seq Analysis of Frozen Clinical Tissues. <i>Methods in Molecular Biology</i> , 2022, 2458, 259-267.	0.9	0