

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	Pan-ERBB kinase inhibition augments CDK4/6 inhibitor efficacy in oesophageal squamous cell carcinoma. <i>Gut</i> , 2022, 71, 665-675.	12.1	15
2	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
3	YAP1 and PRDM14 converge to promote cell survival and tumorigenesis. <i>Developmental Cell</i> , 2022, 57, 212-227.e8.	7.0	9
4	High-Resolution ATAC-Seq Analysis of Frozen Clinical Tissues. <i>Methods in Molecular Biology</i> , 2022, 2458, 259-267.	0.9	0
5	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
6	<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
7	Nutritional Epigenetics in Cancer. <i>Advances in Nutrition</i> , 2022, 13, 1748-1761.	6.4	7
8	The nuclear receptor THRβ facilitates differentiation of human PSCs into more mature hepatocytes. <i>Cell Stem Cell</i> , 2022, 29, 795-809.e11.	11.1	5
9	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
10	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
11	MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. <i>Nature Communications</i> , 2022, 13, 2559.	12.8	56
12	Response to supraphysiological testosterone is predicted by a distinct androgen receptor cisome. <i>JCI Insight</i> , 2022, 7, .	5.0	9
13	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
14	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
15	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
16	MITF is a driver oncogene and potential therapeutic target in kidney angiomyolipoma tumors through transcriptional regulation of CYR61. <i>Oncogene</i> , 2021, 40, 112-126.	5.9	14
17	CDK4/6 inhibition reprograms the breast cancer enhancer landscape by stimulating AP-1 transcriptional activity. <i>Nature Cancer</i> , 2021, 2, 34-48.	13.2	48
18	Therapeutically Increasing MHC-I Expression Potentiates Immune Checkpoint Blockade. <i>Cancer Discovery</i> , 2021, 11, 1524-1541.	9.4	103

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19	EZH2 inhibition activates a dsRNAâ€“STINGâ€“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
20	Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer. <i>Nature Communications</i> , 2021, 12, 1979.	12.8	70
21	Reprogramming of the esophageal squamous carcinoma epigenome by SOX2 promotes ADAR1 dependence. <i>Nature Genetics</i> , 2021, 53, 881-894.	21.4	44
22	Inhibition of CDK4/6 Promotes CD8 T-cell Memory Formation. <i>Cancer Discovery</i> , 2021, 11, 2564-2581.	9.4	58
23	CoBRA: Containerized Bioinformatics Workflow for Reproducible ChIP/ATAC-seq Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 652-661.	6.9	18
24	InÂvivo CRISPR screens identify the E3 ligase Cop1 as a modulator of macrophage infiltration and cancer immunotherapy target. <i>Cell</i> , 2021, 184, 5357-5374.e22.	28.9	79
25	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
26	Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. <i>Nature Communications</i> , 2021, 12, 5775.	12.8	59
27	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
28	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021, 7, eabf6123.	10.3	30
29	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
30	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. <i>Nature Genetics</i> , 2020, 52, 790-799.	21.4	174
31	Transcriptomic analysis of micropapillary high grade T1 urothelial bladder cancer. <i>Scientific Reports</i> , 2020, 10, 20135.	3.3	4
32	Clonal tracing reveals diverse patterns of response to immune checkpoint blockade. <i>Genome Biology</i> , 2020, 21, 263.	8.8	15
33	Hdac3 is an epigenetic inhibitor of the cytotoxicity program in CD8 T cells. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	28
34	ERG-Mediated Coregulator Complex Formation Maintains Androgen Receptor Signaling in Prostate Cancer. <i>Cancer Research</i> , 2020, 80, 4612-4619.	0.9	9
35	Chromatin accessibility promotes hematopoietic and leukemia stem cell activity. <i>Nature Communications</i> , 2020, 11, 1406.	12.8	32
36	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

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37	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
38	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
39	Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. <i>IScience</i> , 2019, 17, 242-255.	4.1	60
40	Enhancer signatures stratify and predict outcomes of non-functional pancreatic neuroendocrine tumors. <i>Nature Medicine</i> , 2019, 25, 1260-1265.	30.7	120
41	Perturbed myoepithelial cell differentiation in BRCA mutation carriers and in ductal carcinoma in situ. <i>Nature Communications</i> , 2019, 10, 4182.	12.8	37
42	Estrogen receptor signaling is reprogrammed during breast tumorigenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11437-11443.	7.1	55
43	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
44	ARv7 Represses Tumor-Suppressor Genes in Castration-Resistant Prostate Cancer. <i>Cancer Cell</i> , 2019, 35, 401-413.e6.	16.8	127
45	CREB5 Promotes Resistance to Androgen-Receptor Antagonists and Androgen Deprivation in Prostate Cancer. <i>Cell Reports</i> , 2019, 29, 2355-2370.e6.	6.4	45
46	A major chromatin regulator determines resistance of tumor cells to T cell-mediated killing. <i>Science</i> , 2018, 359, 770-775.	12.6	641
47	Trisomy of a Down Syndrome Critical Region Globally Amplifies Transcription via HMGN1 Overexpression. <i>Cell Reports</i> , 2018, 25, 1898-1911.e5.	6.4	52
48	TRPS1 Is a Lineage-Specific Transcriptional Dependency in Breast Cancer. <i>Cell Reports</i> , 2018, 25, 1255-1267.e5.	6.4	46
49	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
50	A Somatic 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
51	<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
52	Enhancer-Mediated Oncogenic Function of the Menin Tumor Suppressor in Breast Cancer. <i>Cell Reports</i> , 2017, 18, 2359-2372.	6.4	59
53	Embryonic transcription factor SOX9 drives breast cancer endocrine resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4482-E4491.	7.1	83
54	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. <i>BMC Bioinformatics</i> , 2016, 17, 404.	2.6	100

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55	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
56	Chromatin immunoprecipitation from fixed clinical tissues reveals tumor-specific enhancer profiles. <i>Nature Medicine</i> , 2016, 22, 685-691.	30.7	64
57	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. <i>Nature Communications</i> , 2016, 7, 10979.	12.8	50
58	Response and resistance to BET bromodomain inhibitors in triple-negative breast cancer. <i>Nature</i> , 2016, 529, 413-417.	27.8	490
59	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. <i>JCI Insight</i> , 2016, 1, .	5.0	42
60	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. <i>Human Molecular Genetics</i> , 2015, 24, 5603-5618.	2.9	50
61	The androgen receptor cistrome is extensively reprogrammed in human prostate tumorigenesis. <i>Nature Genetics</i> , 2015, 47, 1346-1351.	21.4	363
62	Broadly permissive intestinal chromatin underlies lateral inhibition and cell plasticity. <i>Nature</i> , 2014, 506, 511-515.	27.8	207
63	CistromeFinder for ChIP-seq and DNase-seq data reuse. <i>Bioinformatics</i> , 2013, 29, 1352-1354.	4.1	18
64	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
65	CHIPS: A Snakemake pipeline for quality control and reproducible processing of chromatin profiling data. <i>F1000Research</i> , 0, 10, 517.	1.6	4
66	<i>In vivo</i> CRISPR Screens Identify E3 Ligase <i>Cop1</i> as a Modulator of Macrophage Infiltration and Cancer Immunotherapy Target. <i>SSRN Electronic Journal</i> , 0, .	0.4	0