Hoon Kim

List of Publications by Year
in descending order

36 papers	23,641 citations	236925 25 h-index	477307 29 g-index
47 all docs	47 docs citations	47 times ranked	33830 citing authors

#	Article	IF	Citations
1	Live-Cell Imaging Shows Uneven Segregation of Extrachromosomal DNA Elements and Transcriptionally Active Extrachromosomal DNA Hubs in Cancer. Cancer Discovery, 2022, 12, 468-483.	9.4	63
2	Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. Cancer Cell, 2021, 39, 694-707.e7.	16.8	115
3	OMRT-3. Longitudinal analysis of diffuse glioma reveals cell state dynamics at recurrence associated with changes in genetics and the microenvironment. Neuro-Oncology Advances, 2021, 3, ii7-ii8.	0.7	1
4	Abstract 2084: Single-cell multimodal glioma analyses reveal epigenetic regulators of cellular plasticity and environmental stress response. , 2021, , .		0
5	Single-cell multimodal glioma analyses identify epigenetic regulators of cellular plasticity and environmental stress response. Nature Genetics, 2021, 53, 1456-1468.	21.4	111
6	MGMT genomic rearrangements contribute to chemotherapy resistance in gliomas. Nature Communications, 2020, 11, 3883.	12.8	110
7	Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers. Nature Genetics, 2020, 52, 891-897.	21.4	273
8	Comparative Molecular Life History of Spontaneous Canine and Human Gliomas. Cancer Cell, 2020, 37, 243-257.e7.	16.8	59
9	Extrachromosomal DNA (ecDNA) carrying amplified oncogenes as a biomarker for insensitivity to pembrolizumab treatment in gastric cancer patients.. Journal of Clinical Oncology, 2020, 38, 3123-3123.	1.6	5
10	EPCO-27. GLIOMA SINGLE CELL MULTI-OMIC ANALYSES REVEALS REGULATORS OF PLASTICITY AND ADAPTIVE STRESS RESPONSE. Neuro-Oncology, 2020, 22, ii75-ii75.	1.2	0
11	EPCO-08. TUMOR-IMMUNE INTERACTIONS ARE DYNAMIC AND INFLUENCE THE EVOLUTIONARY TRAJECTORY OF ADULT DIFFUSE GLIOMA. Neuro-Oncology, 2020, 22, ii70-ii71.	1.2	0
12	GENE-57. COMPARATIVE MOLECULAR LIFE HISTORY OF SPONTANEOUS CANINE AND HUMAN GLIOMA. Neuro-Oncology, 2019, 21, vi110-vi110.	1.2	0
13	Circular ecDNA promotes accessible chromatin and high oncogene expression. Nature, 2019, 575, 699-703.	27.8	343
14	Longitudinal molecular trajectories of diffuse glioma in adults. Nature, 2019, 576, 112-120.	27.8	320
15	Discordant inheritance of chromosomal and extrachromosomal DNA elements contributes to dynamic disease evolution in glioblastoma. Nature Genetics, 2018, 50, 708-717.	21.4	212
16	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. Neuro-Oncology, 2018, 20, 873-884.	1.2	119
17	COMP-07. COMPARATIVE MOLECULAR LIFE HISTORY OF SPONTANEOUS CANINE AND HUMAN GLIOMA. Neuro-Oncology, 2018, 20, vi64-vi65.	1.2	1
18	DRES-05. MOLECULAR EVOLUTION OF DIFFUSE GLIOMAS AND THE GLIOMA LONGITUDINAL ANALYSIS CONSORTIUM. Neuro-Oncology, 2018, 20, vi76-vi76.	1.2	0

#	Article	IF	Citations
19	Multigene signature for predicting prognosis of patients with 1p19q co-deletion diffuse glioma. Neuro-Oncology, 2017, 19, 786-795.	1.2	87
20	Exosomes from Glioma-Associated Mesenchymal Stem Cells Increase the Tumorigenicity of Glioma Stem-like Cells via Transfer of miR-1587. Cancer Research, 2017, 77, 5808-5819.	0.9	169
21	Tumor Evolution of Glioma-Intrinsic Gene Expression Subtypes Associates with Immunological Changes in the Microenvironment. Cancer Cell, 2017, 32, 42-56.e6.	16.8	1,282
22	TMOD-31. AN INFLAMMATION RESPONSE GENE SIGNATURE IS ASSOCIATED WITH PROGNOSIS OF GLIOMA PATIENTS WITH 1p/19q CO-DELETION TUMORS. Neuro-Oncology, 2016, 18, vi213-vi213.	1.2	0
23	TMOD-36. GENE EXPRESSION ANALYSIS OF SHORT AND LONG SURVIVAL GROUPS OF GLIOBLASTOMA PATIENT-DERIVED ORTHOTOPIC XENOGRAFTS. Neuro-Oncology, 2016, 18, vi214-vi214.	1.2	0
24	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
25	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. Genome Research, 2015, 25, 316-327.	5.5	343
26	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
27	Transcriptional mimicry by tumor-associated stroma. Nature Genetics, 2015, 47, 307-309.	21.4	14
28	The landscape and therapeutic relevance of cancer-associated transcript fusions. Oncogene, 2015, 34, 4845-4854.	5.9	398
29	Comparison of gene expression patterns across 12 tumor types identifies a cancer supercluster characterized by TP53 mutations and cell cycle defects. Oncogene, 2015, 34, 2732-2740.	5.9	46
30	Silent Mutations Make Some Noise. Cell, 2014, 156, 1129-1131.	28.9	33
31	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
32	Inferring tumour purity and stromal and immune cell admixture from expression data. Nature Communications, 2013, 4, 2612.	12.8	5,788
33	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	21.4	6,265
34	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
35	Biomarker Discovery Using Statistically Significant Gene Sets. Journal of Computational Biology, 2011, 18, 1329-1338.	1.6	11
36	Multi-cancer computational analysis reveals invasion-associated variant of desmoplastic reaction involving INHBA, THBS2 and COL11A1. BMC Medical Genomics, 2010, 3, 51.	1.5	156