Seungyeul Yoo

List of Publications by Year
in descending order

28 papers	2,786 citations	394421 19 h-index	526287 27 g-index
35 all docs	35 docs citations	35 times ranked	4476 citing authors

#	Article	IF	Citations
1	Early-Stage Lung Adenocarcinoma MDM2 Genomic Amplification Predicts Clinical Outcome and Response to Targeted Therapy. Cancers, 2022, 14, 708.	3.7	8
2	Integrative network analysis of early-stage lung adenocarcinoma identifies aurora kinase inhibition as interceptor of invasion and progression. Nature Communications, 2022, 13, 1592.	12.8	16
3	HBV genome-enriched single cell sequencing revealed heterogeneity in HBV-driven hepatocellular carcinoma (HCC). BMC Medical Genomics, 2022, 15, .	1.5	6
4	Transcriptional Circuitry of NKX2-1 and SOX1 Defines an Unrecognized Lineage Subtype of Small-Cell Lung Cancer. American Journal of Respiratory and Critical Care Medicine, 2022, 206, 1480-1494.	5.6	4
5	Prototypical oncogene family Myc defines unappreciated distinct lineage states of small cell lung cancer. Science Advances, 2021, 7, .	10.3	40
6	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	16.8	189
7	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	16.8	327
8	A community effort to identify and correct mislabeled samples in proteogenomic studies. Patterns, 2021, 2, 100245.	5.9	6
9	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	28.9	236
10	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	28.9	177
11	A reference profile-free deconvolution method to infer cancer cell-intrinsic subtypes and tumor-type-specific stromal profiles. Genome Medicine, 2020, 12, 24.	8.2	34
12	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	28.9	410
13	A probabilistic multi-omics data matching method for detecting sample errors in integrative analysis. GigaScience, 2019, 8, .	6.4	9
14	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	28.9	430
15	A Network Analysis of Multiple Myeloma Related Gene Signatures. Cancers, 2019, 11, 1452.	3.7	23
16	Epigenomic Profiling Discovers Trans-lineage SOX2 Partnerships Driving Tumor Heterogeneity in Lung Squamous Cell Carcinoma. Cancer Research, 2019, 79, 6084-6100.	0.9	24
17	Inching towards precision medicine for multiple myeloma with causal network models.. Journal of Clinical Oncology, 2019, 37, e19526-e19526.	1.6	0
18	Temporal genetic association and temporal genetic causality methods for dissecting complex networks. Nature Communications, 2018, 9, 3980.	12.8	5

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19	Oncogenic role of SFRP2 in p53-mutant osteosarcoma development via autocrine and paracrine mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11128-E11137.	7.1	38
20	A pilot systematic genomic comparison of recurrence risks of hepatitis B virus-associated hepatocellular carcinoma with low- and high-degree liver fibrosis. BMC Medicine, 2017, 15, 214.	5.5	64
21	Impact of non-neoplastic vs intratumoural hepatitis B viral DNA and replication on hepatocellular carcinoma recurrence. British Journal of Cancer, 2016, 115, 841-847.	6.4	12
22	Functional Characterization of DNA Methylation in the Oligodendrocyte Lineage. Cell Reports, 2016, 15, 748-760.	6.4	81
23	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. PLoS Genetics, 2015, 11, e1004898.	3.5	82
24	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. PLoS Computational Biology, 2014, 10, e1003790.	3.2	35
25	Epigenome-wide differences in pathology-free regions of multiple sclerosisâ€"affected brains. Nature Neuroscience, 2014, 17, 121-130.	14.8	239
26	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. Molecular Systems Biology, 2014, 10, 743.	7.2	182
27	Interferon Î± Has Varied Effects On CD34+ Cells From Patients With Polycythemia Vera. Blood, 2013, 122, 2840-2840.	1.4	0
28	SiteComp: a server for ligand binding site analysis in protein structures. Bioinformatics, 2012, 28, 1172-1173.	4.1	36