

Seungyeul Yoo

List of Publications by Year in descending order

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Version: 2024-02-01

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	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
2	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	28.9	410
3	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	16.8	327
4	Epigenome-wide differences in pathology-free regions of multiple sclerosis-affected brains. <i>Nature Neuroscience</i> , 2014, 17, 121-130.	14.8	239
5	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	28.9	236
6	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16.	16.8	189
7	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. <i>Molecular Systems Biology</i> , 2014, 10, 743.	7.2	182
8	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	28.9	177
9	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. <i>PLoS Genetics</i> , 2015, 11, e1004898.	3.5	82
10	Functional Characterization of DNA Methylation in the Oligodendrocyte Lineage. <i>Cell Reports</i> , 2016, 15, 748-760.	6.4	81
11	A pilot systematic genomic comparison of recurrence risks of hepatitis B virus-associated hepatocellular carcinoma with low- and high-degree liver fibrosis. <i>BMC Medicine</i> , 2017, 15, 214.	5.5	64
12	Prototypical oncogene family Myc defines unappreciated distinct lineage states of small cell lung cancer. <i>Science Advances</i> , 2021, 7, .	10.3	40
13	Oncogenic role of SFRP2 in p53-mutant osteosarcoma development via autocrine and paracrine mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11128-E11137.	7.1	38
14	SiteComp: a server for ligand binding site analysis in protein structures. <i>Bioinformatics</i> , 2012, 28, 1172-1173.	4.1	36
15	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003790.	3.2	35
16	A reference profile-free deconvolution method to infer cancer cell-intrinsic subtypes and tumor-type-specific stromal profiles. <i>Genome Medicine</i> , 2020, 12, 24.	8.2	34
17	Epigenomic Profiling Discovers Trans-lineage SOX2 Partnerships Driving Tumor Heterogeneity in Lung Squamous Cell Carcinoma. <i>Cancer Research</i> , 2019, 79, 6084-6100.	0.9	24
18	A Network Analysis of Multiple Myeloma Related Gene Signatures. <i>Cancers</i> , 2019, 11, 1452.	3.7	23

#	ARTICLE	IF	CITATIONS
19	Integrative network analysis of early-stage lung adenocarcinoma identifies aurora kinase inhibition as interceptor of invasion and progression. <i>Nature Communications</i> , 2022, 13, 1592.	12.8	16
20	Impact of non-neoplastic vs intratumoural hepatitis B viral DNA and replication on hepatocellular carcinoma recurrence. <i>British Journal of Cancer</i> , 2016, 115, 841-847.	6.4	12
21	A probabilistic multi-omics data matching method for detecting sample errors in integrative analysis. <i>GigaScience</i> , 2019, 8, .	6.4	9
22	Early-Stage Lung Adenocarcinoma MDM2 Genomic Amplification Predicts Clinical Outcome and Response to Targeted Therapy. <i>Cancers</i> , 2022, 14, 708.	3.7	8
23	A community effort to identify and correct mislabeled samples in proteogenomic studies. <i>Patterns</i> , 2021, 2, 100245.	5.9	6
24	HBV genome-enriched single cell sequencing revealed heterogeneity in HBV-driven hepatocellular carcinoma (HCC). <i>BMC Medical Genomics</i> , 2022, 15, .	1.5	6
25	Temporal genetic association and temporal genetic causality methods for dissecting complex networks. <i>Nature Communications</i> , 2018, 9, 3980.	12.8	5
26	Transcriptional Circuitry of NKX2-1 and SOX1 Defines an Unrecognized Lineage Subtype of Small-Cell Lung Cancer. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 206, 1480-1494.	5.6	4
27	Interferon $\hat{\pm}$ Has Varied Effects On CD34+ Cells From Patients With Polycythemia Vera. <i>Blood</i> , 2013, 122, 2840-2840.	1.4	0
28	Inching towards precision medicine for multiple myeloma with causal network models.. <i>Journal of Clinical Oncology</i> , 2019, 37, e19526-e19526.	1.6	0