Winnie S Liang

List of Publications by Year
in descending order

12	437	1040056 9	1199594 12
papers	citations	h-index	g-index

15	15	15	1268
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Hyperthermic Intraperitoneal Chemotherapyâ€“Induced Molecular Changes in Humans Validate Preclinical Data in Ovarian Cancer. JCO Precision Oncology, 2022, 6, e2100239.	3.0	10
2	Posterior cingulate cortex reveals an expression profile of resilience in cognitively intact elders. Brain Communications, 2022, 4, .	3.3	10
3	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. Nature Biotechnology, 2021, 39, 1151-1160.	17.5	39
4	ACValidator: A novel assembly-based approach for in silico verification of circular RNAs. Biology Methods and Protocols, 2020, 5, bpaa010.	2.2	3
5	Leveraging Spatial Variation in Tumor Purity for Improved Somatic Variant Calling of Archival Tumor Only Samples. Frontiers in Oncology, 2019, 9, 119.	2.8	15
6	A virome-wide clonal integration analysis platform for discovering cancer viral etiology. Genome Research, 2019, 29, 819-830.	5.5	47
7	Identification of therapeutic targets in chordoma through comprehensive genomic and transcriptomic analyses. Journal of Physical Education and Sports Management, 2018, 4, a003418.	1.2	13
8	Integrated genomic analyses reveal frequent TERT aberrations in acral melanoma. Genome Research, 2017, 27, 524-532.	5.5	122
9	Comprehensive molecular profiling of 718 Multiple Myelomas reveals significant differences in mutation frequencies between African and European descent cases. PLoS Genetics, 2017, 13, e1007087.	3.5	66
10	A somatic reference standard for cancer genome sequencing. Scientific Reports, 2016, 6, 24607.	3.3	64
11	Simultaneous Characterization of Somatic Events and HPV-18 Integration in a Metastatic Cervical Carcinoma Patient Using DNA and RNA Sequencing. International Journal of Gynecological Cancer, 2014, 24, 329-338.	2.5	14
12	Long insert whole genome sequencing for copy number variant and translocation detection. Nucleic Acids Research, 2014, 42, e8-e8.	14.5	23