## Lixing Yang

List of Publications by Year in descending order

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LIVING YANG

#	Article	IF	CITATIONS
1	A functional genomic approach to actionable gene fusions for precision oncology. Science Advances, 2022, 8, eabm2382.	10.3	9
2	Starfish infers signatures of complex genomic rearrangements across human cancers. Nature Cancer, 2022, 3, 1247-1259.	13.2	20
3	Dysregulation of cancer genes by recurrent intergenic fusions. Genome Biology, 2020, 21, 166.	8.8	22
4	An enhanced genetic model of colorectal cancer progression history. Genome Biology, 2019, 20, 168.	8.8	34
5	Global impact of somatic structural variation on the DNA methylome of human cancers. Genome Biology, 2019, 20, 209.	8.8	40
6	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	6.4	523
7	A Pan-Cancer Compendium of Genes Deregulated by Somatic Genomic Rearrangement across More Than 1,400 Cases. Cell Reports, 2018, 24, 515-527.	6.4	70
8	Engineering and Functional Characterization of Fusion Genes Identifies Novel Oncogenic Drivers of Cancer. Cancer Research, 2017, 77, 3502-3512.	0.9	31
9	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. Cancer Cell, 2017, 31, 820-832.e3.	16.8	433
10	Analyzing Somatic Genome Rearrangements in Human Cancers by Using Whole-Exome Sequencing. American Journal of Human Genetics, 2016, 98, 843-856.	6.2	33
11	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. Cell Reports, 2016, 14, 2476-2489.	6.4	298
12	Cell Lineage Analysis in Human Brain Using Endogenous Retroelements. Neuron, 2015, 85, 49-59.	8.1	234
13	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
14	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the United States of America, 2014, 111, 15544-15549.	7.1	317
15	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
16	Diverse Mechanisms of Somatic Structural Variations in Human Cancer Genomes. Cell, 2013, 153, 919-929.	28.9	308