## Toshihide Ueno

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4608950/publications.pdf

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361413 377865 1,763 35 20 34 citations h-index g-index papers 36 36 36 4190 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Recurrent DUX4 fusions in B cell acute lymphoblastic leukemia of adolescents and young adults. Nature Genetics, 2016, 48, 569-574.	21.4	198
2	A method of high-throughput functional evaluation of $\langle i \rangle$ EGFR $\langle i \rangle$ gene variants of unknown significance in cancer. Science Translational Medicine, 2017, 9, .	12.4	168
3	Genome-wide CRISPR screen identifies <i>TMEM41B</i> as a gene required for autophagosome formation. Journal of Cell Biology, 2018, 217, 3817-3828.	5.2	168
4	Genomic characterization of primary central nervous system lymphoma. Acta Neuropathologica, 2016, 131, 865-875.	7.7	138
5	An Oncogenic Alteration Creates a Microenvironment that Promotes Tumor Progression by Conferring a Metabolic Advantage to Regulatory T Cells. Immunity, 2020, 53, 187-203.e8.	14.3	119
6	miR-378a-3p modulates tamoxifen sensitivity in breast cancer MCF-7 cells through targeting GOLT1A. Scientific Reports, 2015, 5, 13170.	3.3	82
7	Uterine adenomyosis is an oligoclonal disorder associated with KRAS mutations. Nature Communications, 2019, 10, 5785.	12.8	82
8	Small-RNA asymmetry is directly driven by mammalian Argonautes. Nature Structural and Molecular Biology, 2015, 22, 512-521.	8.2	75
9	Recurrent CDC25C mutations drive malignant transformation in FPD/AML. Nature Communications, 2014, 5, 4770.	12.8	74
10	A Low Tumor Mutational Burden and <i>PTEN</i> Mutations Are Predictors of a Negative Response to PD-1 Blockade in MSI-H/dMMR Gastrointestinal Tumors. Clinical Cancer Research, 2021, 27, 3714-3724.	7.0	61
11	High-Throughput Functional Evaluation of Variants of Unknown Significance in <i>ERBB2</i> Cancer Research, 2018, 24, 5112-5122.	7.0	60
12	Fusion Kinases Identified by Genomic Analyses of Sporadic Microsatellite Instability–High Colorectal Cancers. Clinical Cancer Research, 2019, 25, 378-389.	7.0	49
13	Micro <scp>RNA</scp> â€31 is a positive modulator of endothelial–mesenchymal transition and associated secretory phenotype induced by <scp>TGF</scp> â€Î². Genes To Cells, 2016, 21, 99-116.	1.2	46
14	PD-1 blockade therapy promotes infiltration of tumor-attacking exhausted TÂcell clonotypes. Cell Reports, 2022, 38, 110331.	6.4	45
15	Multi-omic profiling of peritoneal metastases in gastric cancer identifies molecular subtypes and therapeutic vulnerabilities. Nature Cancer, 2021, 2, 962-977.	13.2	41
16	Integrative analysis of genomic alterations in triple-negative breast cancer in association with homologous recombination deficiency. PLoS Genetics, 2017, 13, e1006853.	3 <b>.</b> 5	39
17	High-throughput functional evaluation of BRCA2 variants of unknown significance. Nature Communications, 2020, 11, 2573.	12.8	38
18	Mutational Landscape and Antiproliferative Functions of ELF Transcription Factors in Human Cancer. Cancer Research, 2016, 76, 1814-1824.	0.9	31

#	Article	IF	Citations
19	Transcriptomic Profiling of MSI-H/dMMR Gastrointestinal Tumors to Identify Determinants of Responsiveness to Anti–PD-1 Therapy. Clinical Cancer Research, 2022, 28, 2110-2117.	<b>7.</b> 0	30
20	Inactivating mutations and hypermethylation of the <i>NKX2â€1/TTFâ€1</i> gene in nonâ€terminal respiratory unitâ€type lung adenocarcinomas. Cancer Science, 2017, 108, 1888-1896.	3.9	28
21	Oncogenic activity of <scp>BIRC</scp> 2 and <scp>BIRC</scp> 3 mutants independent of nuclear factorâ€PBâ€activating potential. Cancer Science, 2015, 106, 1137-1142.	3.9	24
22	Genomic profiles of colorectal carcinoma with liver metastases and newly identified fusion genes. Cancer Science, 2019, 110, 2973-2981.	3.9	23
23	A Hyperactive RelA/p65-Hexokinase 2 Signaling Axis Drives Primary Central Nervous System Lymphoma. Cancer Research, 2020, 80, 5330-5343.	0.9	19
24	Comprehensive functional evaluation of variants of fibroblast growth factor receptor genes in cancer. Npj Precision Oncology, 2021, 5, 66.	5.4	19
25	Transforming somatic mutations of mammalian target of rapamycin kinase in human cancer. Cancer Science, 2015, 106, 1687-1692.	3.9	18
26	Transcriptional activities of DUX4 fusions in B-cell acute lymphoblastic leukemia. Haematologica, 2018, 103, e522-e526.	3.5	17
27	Pediatric soft tissue tumor of the upper arm with LMNA-NTRK1 fusion. Human Pathology, 2018, 72, 167-173.	2.0	13
28	Transcript-targeted analysis reveals isoform alterations and double-hop fusions in breast cancer. Communications Biology, 2021, 4, 1320.	4.4	13
29	Targeting MEF2D-fusion Oncogenic Transcriptional Circuitries in B-cell Precursor Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 82-95.	5.0	12
30	A germline HLTF mutation in familial MDS induces DNA damage accumulation through impaired PCNA polyubiquitination. Leukemia, 2019, 33, 1773-1782.	7.2	11
31	Assessment of Predictive Biomarkers of the Response to Pazopanib Based on an Integrative Analysis of High-grade Soft-tissue Sarcomas: Analysis of a Tumor Sample from a Responder and Patients with Other Soft-tissue Sarcomas. Clinical Orthopaedics and Related Research, 2020, 478, 2461-2476.	1.5	9
32	Identification of candidates for driver oncogenes in scirrhousâ€type gastric cancer cell lines. Cancer Science, 2019, 110, 2643-2651.	3.9	8
33	Comparative Study on the Efficacy and Exposure of Molecular Target Agents in Non–small Cell Lung Cancer PDX Models with Driver Genetic Alterations. Molecular Cancer Therapeutics, 2022, 21, 359-370.	4.1	3
34	MicroSEC filters sequence errors for formalin-fixed and paraffin-embedded samples. Communications Biology, 2021, 4, 1396.	4.4	2
35	Targeting MEF2D-fusion Oncogenic Transcriptional Circuitries in B-cell Precursor Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 82-95.	5.0	0