Akihiro Fujimoto

List of Publications by Year in descending order

34 papers	3,192 citations	567281 15 h-index	526287 27 g-index
39 all docs	39 docs citations	39 times ranked	7354 citing authors

#	Article	IF	Citations
1	Likely pathogenic structural variants in genetically unsolved patients with retinitis pigmentosa revealed by long-read sequencing. Journal of Medical Genetics, 2022, 59, 1133-1138.	3.2	9
2	Whole-genome sequencing with long reads reveals complex structure and origin of structural variation in human genetic variations and somatic mutations in cancer. Genome Medicine, 2021, 13, 65.	8.2	43
3	Characterization of intermediate-sized insertions using whole-genome sequencing data and analysis of their functional impact on gene expression. Human Genetics, 2021, 140, 1201-1216.	3.8	3
4	Immunogenomic pan-cancer landscape reveals immune escape mechanisms and immunoediting histories. Scientific Reports, 2021, 11, 15713.	3.3	10
5	Clinical Impact of Detecting Low-Frequency Variants in Cell-Free DNA on Treatment of Castration-Resistant Prostate Cancer. Clinical Cancer Research, 2021, 27, 6164-6173.	7.0	10
6	Aberrant (pro)renin receptor expression induces genomic instability in pancreatic ductal adenocarcinoma through upregulation of SMARCA5/SNF2H. Communications Biology, 2020, 3, 724.	4.4	5
7	Multiregional wholeâ€genome sequencing of hepatocellular carcinoma with noduleâ€inâ€nodule appearance reveals stepwise cancer evolution. Journal of Pathology, 2020, 252, 398-410.	4.5	15
8	Comprehensive analysis of indels in whole-genome microsatellite regions and microsatellite instability across 21 cancer types. Genome Research, 2020, 30, 334-346.	5.5	56
9	Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. EBioMedicine, 2020, 53, 102659.	6.1	48
10	Systematic clustering algorithm for chromatin accessibility data and its application to hematopoietic cells. PLoS Computational Biology, 2020, 16, e1008422.	3.2	2
11	Title is missing!. , 2020, 16, e1008422.		0
12	Title is missing!. , 2020, 16, e1008422.		0
13	Title is missing!. , 2020, 16, e1008422.		0
14	Title is missing!. , 2020, 16, e1008422.		0
15	Title is missing!. , 2020, 16, e1008422.		0
16	Title is missing!. , 2020, 16, e1008422.		0
17	Title is missing!. , 2020, 16, e1008422.		0
18	Identification of intermediate-sized deletions and inference of their impact on gene expression in a human population. Genome Medicine, 2019, 11, 44.	8.2	9

#	Article	IF	Citations
19	eVIDENCE: a practical variant filtering for low-frequency variants detection in cell-free DNA. Scientific Reports, 2019, 9, 15017.	3.3	9
20	IMSindel: An accurate intermediate-size indel detection tool incorporating de novo assembly and gapped global-local alignment with split read analysis. Scientific Reports, 2018, 8, 5608.	3.3	20
21	Whole Genome Sequencing of a Vietnamese Family from a Dioxin Contamination Hotspot Reveals Novel Variants in the Son with Undiagnosed Intellectual Disability. International Journal of Environmental Research and Public Health, 2018, 15, 2629.	2.6	4
22	Whole genome sequencing and mutation rate analysis of trios with paternal dioxin exposure. Human Mutation, 2018, 39, 1384-1392.	2.5	14
23	Genomic landscape of colitis-associated cancer indicates the impact of chronic inflammation and its stratification by mutations in the Wnt signaling. Oncotarget, 2018, 9, 969-981.	1.8	34
24	A Highly Specific Genome-Wide Association Study Integrated with Transcriptome Data Reveals the Contribution of Copy Number Variations to Specialized Metabolites in Arabidopsis thaliana Accessions. Molecular Biology and Evolution, 2017, 34, 3111-3122.	8.9	14
25	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. Journal of Hepatology, 2017, 66, 363-373.	3.7	81
26	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. Nature Genetics, 2016, 48, 500-509.	21.4	596
27	Systematic analysis of mutation distribution in three dimensional protein structures identifies cancer driver genes. Scientific Reports, 2016, 6, 26483.	3.3	20
28	Mutational signatures associated with tobacco smoking in human cancer. Science, 2016, 354, 618-622.	12.6	842
29	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. Nature Communications, 2015, 6, 6120.	12.8	178
30	A practical method to detect SNVs and indels from whole genome and exome sequencing data. Scientific Reports, 2013, 3, 2161.	3.3	39
31	Whole-genome sequencing of liver cancers identifies etiological influences on mutation patterns and recurrent mutations in chromatin regulators. Nature Genetics, 2012, 44, 760-764.	21.4	781
32	Whole-genome sequencing and comprehensive variant analysis of a Japanese individual using massively parallel sequencing. Nature Genetics, 2010, 42, 931-936.	21.4	106
33	Appropriate data cleaning methods for genome-wide association study. Journal of Human Genetics, 2008, 53, 886-893.	2.3	40
34	A scan for genetic determinants of human hair morphology: EDAR is associated with Asian hair thickness. Human Molecular Genetics, 2008, 17, 835-843.	2.9	203