

# Xian Fan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11162411/publications.pdf>

Version: 2024-02-01

16  
papers

4,847  
citations

687363

13  
h-index

940533

16  
g-index

20  
all docs

20  
docs citations

20  
times ranked

11433  
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	27.8	1,994
2	Clonal Architecture of Secondary Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2012, 366, 1090-1098.	27.0	688
3	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	12.8	636
4	CREST maps somatic structural variation in cancer genomes with base-pair resolution. <i>Nature Methods</i> , 2011, 8, 652-654.	19.0	451
5	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020, 38, 1347-1355.	17.5	233
6	Background Mutations in Parental Cells Account for Most of the Genetic Heterogeneity of Induced Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2012, 10, 570-582.	11.1	199
7	BreakDancer: Identification of Genomic Structural Variation from Paired-End Read Mapping. <i>Current Protocols in Bioinformatics</i> , 2014, 45, 15.6.1-11.	25.8	135
8	novoBreak: local assembly for breakpoint detection in cancer genomes. <i>Nature Methods</i> , 2017, 14, 65-67.	19.0	93
9	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. <i>Journal of Clinical Investigation</i> , 2011, 121, 1445-1455.	8.2	91
10	Genome Modeling System: A Knowledge Management Platform for Genomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004274.	3.2	83
11	TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. <i>Genome Research</i> , 2014, 24, 310-317.	5.5	81
12	HySA: a Hybrid Structural variant Assembly approach using next-generation and single-molecule sequencing technologies. <i>Genome Research</i> , 2017, 27, 793-800.	5.5	32
13	BreakTrans: uncovering the genomic architecture of gene fusions. <i>Genome Biology</i> , 2013, 14, R87.	9.6	25
14	Towards accurate characterization of clonal heterogeneity based on structural variation. <i>BMC Bioinformatics</i> , 2014, 15, 299.	2.6	10
15	BreakPoint Surveyor: a pipeline for structural variant visualization. <i>Bioinformatics</i> , 2017, 33, 3121-3122.	4.1	5
16	Detecting Large Indels Using Optical Map Data. <i>Lecture Notes in Computer Science</i> , 2018, , 108-127.	1.3	3