

# Daehwan Kim

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7746971/publications.pdf>

Version: 2024-02-01

13  
papers

52,582  
citations

1163117

8  
h-index

1281871

11  
g-index

18  
all docs

18  
docs citations

18  
times ranked

80139  
citing authors

#	ARTICLE	IF	CITATIONS
1	HISAT: a fast spliced aligner with low memory requirements. <i>Nature Methods</i> , 2015, 12, 357-360.	19.0	16,262
2	TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. <i>Genome Biology</i> , 2013, 14, R36.	9.6	11,713
3	Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. <i>Nature Protocols</i> , 2012, 7, 562-578.	12.0	11,433
4	Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. <i>Nature Biotechnology</i> , 2019, 37, 907-915.	17.5	6,567
5	Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. <i>Nature Protocols</i> , 2016, 11, 1650-1667.	12.0	4,743
6	Centrifuge: rapid and sensitive classification of metagenomic sequences. <i>Genome Research</i> , 2016, 26, 1721-1729.	5.5	1,025
7	TopHat-Fusion: an algorithm for discovery of novel fusion transcripts. <i>Genome Biology</i> , 2011, 12, R72.	9.6	670
8	Rapid and accurate alignment of nucleotide conversion sequencing reads with HISAT-3N. <i>Genome Research</i> , 2021, 31, 1290-1295.	5.5	104
9	Genomic characterization of chromosome translocations in patients with T/myeloid mixed-phenotype acute leukemia. <i>Leukemia and Lymphoma</i> , 2018, 59, 1231-1238.	1.3	8
10	Automated classification of cytogenetic abnormalities in hematolymphoid neoplasms. <i>Bioinformatics</i> , 2022, 38, 1420-1426.	4.1	5
11	The novel fusion transcript NR5A2â€KLHL29FT is generated by an insertion at the KLHL29 locus. <i>Cancer</i> , 2017, 123, 1507-1515.	4.1	4
12	GG-08â€Immune repertoire and genetic risk alleles in healthy pediatric populations with autoimmune indicators. , 2018, , .		1
13	SeqWho: reliable, rapid determination of sequence file identity using <i>k</i> -mer frequencies in Random Forest classifiers. <i>Bioinformatics</i> , 2022, 38, 1830-1837.	4.1	0