

# Jaebum Kim

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3490850/publications.pdf>

Version: 2024-02-01

48  
papers

2,647  
citations

430874

18  
h-index

276875

41  
g-index

48  
all docs

48  
docs citations

48  
times ranked

4797  
citing authors

#	ARTICLE	IF	CITATIONS
1	DLEB: a web application for building deep learning models in biological research. <i>Nucleic Acids Research</i> , 2022, , .	14.5	1
2	Generation and application of pseudo-“long reads for metagenome assembly. <i>GigaScience</i> , 2022, 11, .	6.4	4
3	Integration of multi-omics approaches for functional characterization of muscle related selective sweep genes in Nanchukmacdon. <i>Scientific Reports</i> , 2021, 11, 7219.	3.3	8
4	Comparative methylation and RNA-seq expression analysis in CpG context to identify genes involved in Backfat vs. Liver diversification in Nanchukmacdon Pig. <i>BMC Genomics</i> , 2021, 22, 801.	2.8	4
5	Molecular mechanisms of embryonic tail development in the self-fertilizing mangrove killifish <i>Kryptolebias marmoratus</i> . <i>Development (Cambridge)</i> , 2021, 148, .	2.5	2
6	Unraveling the Genome-Wide Impact of Recombinant Baculovirus Infection in Mammalian Cells for Gene Delivery. <i>Genes</i> , 2020, 11, 1306.	2.4	6
7	Population analysis of the Korean native duck using whole-genome sequencing data. <i>BMC Genomics</i> , 2020, 21, 554.	2.8	5
8	TAMA: improved metagenomic sequence classification through meta-analysis. <i>BMC Bioinformatics</i> , 2020, 21, 185.	2.6	3
9	Evolutionary and Functional Analysis of Korean Native Pig Using Single Nucleotide Polymorphisms. <i>Molecules and Cells</i> , 2020, 43, 728-738.	2.6	0
10	An integrated chromosome-scale genome assembly of the Masai giraffe ( <i>Giraffa camelopardalis</i> ) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 3	6.4	13
11	Integrative Meta-Assembly Pipeline (IMAP): Chromosome-level genome assembler combining multiple de novo assemblies. <i>PLoS ONE</i> , 2019, 14, e0221858.	2.5	3
12	GMASS: a novel measure for genome assembly structural similarity. <i>BMC Bioinformatics</i> , 2019, 20, 147.	2.6	4
13	Markov chain Monte Carlo simulation of a Bayesian mixture model for gene network inference. <i>Genes and Genomics</i> , 2019, 41, 547-555.	1.4	8
14	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. <i>Genome Research</i> , 2019, 29, 576-589.	5.5	39
15	Using INTERSPIA to Explore the Dynamics of Protein-Protein Interactions Among Multiple Species. <i>Current Protocols in Bioinformatics</i> , 2019, 68, e88.	25.8	0
16	A near-chromosome-scale genome assembly of the gemsbok ( <i>Oryx gazella</i> ): an iconic antelope of the Kalahari desert. <i>GigaScience</i> , 2019, 8, .	6.4	138
17	The genome of the marine medaka <i>Oryzias melastigma</i> . <i>Molecular Ecology Resources</i> , 2018, 18, 656-665.	4.8	31
18	RWNetSig. , 2018, , .		0

#	ARTICLE	IF	CITATIONS
19	Reconstruction of avian ancestral karyotypes reveals differences in the evolutionary history of macro- and microchromosomes. <i>Genome Biology</i> , 2018, 19, 155.	8.8	44
20	mySyntenyPortal: an application package to construct websites for synteny block analysis. <i>BMC Bioinformatics</i> , 2018, 19, 216.	2.6	8
21	INTERSPIA: a web application for exploring the dynamics of protein-protein interactions among multiple species. <i>Nucleic Acids Research</i> , 2018, 46, W89-W94.	14.5	11
22	Construction of Red Fox Chromosomal Fragments from the Short-Read Genome Assembly. <i>Genes</i> , 2018, 9, 308.	2.4	14
23	Diversity, distribution, and significance of transposable elements in the genome of the only selfing hermaphroditic vertebrate <i>Kryptolebias marmoratus</i> . <i>Scientific Reports</i> , 2017, 7, 40121.	3.3	28
24	Reconstruction and evolutionary history of eutherian chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5379-E5388.	7.1	94
25	Phylogenetic analysis of two <i>Plectus</i> mitochondrial genomes (Nematoda: Plectida) supports a sister group relationship between Plectida and Rhabditida within Chromadorea. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 90-102.	2.7	39
26	Functional and evolutionary analysis of Korean bob-tailed native dog using whole-genome sequencing data. <i>Scientific Reports</i> , 2017, 7, 17303.	3.3	4
27	Identification of disease comorbidity through hidden molecular mechanisms. <i>Scientific Reports</i> , 2016, 6, 39433.	3.3	42
28	Synteny Portal: a web-based application portal for synteny block analysis. <i>Nucleic Acids Research</i> , 2016, 44, W35-W40.	14.5	42
29	Omics of the marine medaka ( <i>Oryzias melastigma</i> ) and its relevance to marine environmental research. <i>Marine Environmental Research</i> , 2016, 113, 141-152.	2.5	56
30	Evolutionary Analyses of Hanwoo (Korean Cattle)- Specific Single-Nucleotide Polymorphisms and Genes Using Whole-Genome Resequencing Data of a Hanwoo Population. <i>Molecules and Cells</i> , 2016, 39, 692-698.	2.6	6
31	Genome-wide analysis of DNA methylation in pigs using reduced representation bisulfite sequencing. <i>DNA Research</i> , 2015, 22, 343-355.	3.4	72
32	Structural Neuroimaging Genetics Interactions in Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2015, 48, 1051-1063.	2.6	36
33	FCMM: A comparative metagenomic approach for functional characterization of multiple metagenome samples. <i>Journal of Microbiological Methods</i> , 2015, 115, 121-128.	1.6	2
34	Metagenome assembly through clustering of next-generation sequencing data using protein sequences. <i>Journal of Microbiological Methods</i> , 2015, 109, 180-187.	1.6	1
35	Effects of omics data combinations on in silico tumor-normal tissue classification. <i>Genes and Genomics</i> , 2015, 37, 525-535.	1.4	1
36	Prevertebrate Local Gene Duplication Facilitated Expansion of the Neuropeptide GPCR Superfamily. <i>Molecular Biology and Evolution</i> , 2015, 32, 2803-2817.	8.9	54

#	ARTICLE	IF	CITATIONS
37	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014, 24, 2077-2089.	5.5	102
38	A clustering method for next-generation sequences of bacterial genomes through multiomics data mapping. <i>Genes and Genomics</i> , 2014, 36, 191-196.	1.4	1
39	Computational prediction of transcription factor binding sites based on an integrative approach incorporating genomic and epigenomic features. <i>Genes and Genomics</i> , 2014, 36, 25-30.	1.4	0
40	PSAR-Align: improving multiple sequence alignment using probabilistic sampling. <i>Bioinformatics</i> , 2014, 30, 1010-1012.	4.1	16
41	Estimating the number of species in metagenomes by clustering next-generation read sequences. , 2014, , .		0
42	Estimating the composition of species in metagenomes by clustering of next-generation read sequences. <i>Methods</i> , 2014, 69, 213-219.	3.8	2
43	Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , 2014, 5, 3966.	12.8	124
44	A Next-generation Sequence Clustering Method for E. Coli through Proteomics-genomics Data Mapping. <i>Procedia Computer Science</i> , 2013, 23, 96-101.	2.0	1
45	Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013, 4, 1858.	12.8	229
46	Reference-assisted chromosome assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1785-1790.	7.1	124
47	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	27.8	1,190
48	PSAR: measuring multiple sequence alignment reliability by probabilistic sampling. <i>Nucleic Acids Research</i> , 2011, 39, 6359-6368.	14.5	35