Osamu Ogasawara

List of Publications by Year
in descending order

17 papers	1,143 citations	623734 14 h-index	839539 18 g-index
20 all docs	20 docs citations	20 times ranked	2749 citing authors

#	Article	IF	Citations
1	Ch <scp>IP</scp> â€Atlas: a dataâ€mining suite powered by full integration of public Ch <scp>IP</scp> â€seq data. EMBO Reports, 2018, 19, .	4.5	544
2	DNA Data Bank of Japan. Nucleic Acids Research, 2017, 45, D25-D31.	14.5	78
3	DNA data bank of Japan (DDBJ) progress report. Nucleic Acids Research, 2016, 44, D51-D57.	14.5	76
4	The DDBJ Japanese Genotype-phenotype Archive for genetic and phenotypic human data. Nucleic Acids Research, 2015, 43, D18-D22.	14.5	57
5	RefEx, a reference gene expression dataset as a web tool for the functional analysis of genes. Scientific Data, 2017, 4, 170105.	5.3	55
6	DNA Data Bank of Japan: 30th anniversary. Nucleic Acids Research, 2018, 46, D30-D35.	14.5	51
7	DDBJ update: streamlining submission and access of human data. Nucleic Acids Research, 2021, 49, D71-D75.	14.5	38
8	DDBJ new system and service refactoring. Nucleic Acids Research, 2012, 41, D25-D29.	14.5	37
9	DDBJ update: the Genomic Expression Archive (GEA) for functional genomics data. Nucleic Acids Research, 2019, 47, D69-D73.	14.5	36
10	Practical guide for managing large-scale human genome data in research. Journal of Human Genetics, 2021, 66, 39-52.	2.3	31
11	DDBJ Database updates and computational infrastructure enhancement. Nucleic Acids Research, 2019, 48, D45-D50.	14.5	28
12	BodyMap-Xs: anatomical breakdown of 17 million animal ESTs for cross-species comparison of gene expression. Nucleic Acids Research, 2006, 34, D628-D631.	14.5	26
13	DNA Data Bank of Japan (DDBJ) update report 2021. Nucleic Acids Research, 2022, 50, D102-D105.	14.5	22
14	MACON: a web tool for computing DNA methylation data obtained by the Illumina Infinium Human DNA methylation BeadArray. Epigenomics, 2018, 10, 249-258.	2.1	21
15	Zipf's law and human transcriptomes: an explanation with an evolutionary model. Comptes Rendus - Biologies, 2003, 326, 1097-1101.	0.2	14
16	Accumulating computational resource usage of genomic data analysis workflow to optimize cloud computing instance selection. GigaScience, 2019, 8, .	6.4	8
17	On Theoretical Models of Gene Expression Evolution with Random Genetic Drift and Natural Selection. PLoS ONE, 2009, 4, e7943.	2.5	7