Kitty K Lo

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6889607/publications.pdf

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19 papers	1,106 citations	687363 13 h-index	888059 17 g-index
19 all docs	19 docs citations	19 times ranked	2339 citing authors

#	Article	IF	Citations
1	Abundant small RNAs in the reproductive tissues and eggs of the honey bee, Apis mellifera. BMC Genomics, 2022, 23, 257.	2.8	6
2	Investigating proteome changes between primary and metastatic cutaneous squamous cell carcinoma using SWATH mass spectrometry. Journal of Dermatological Science, 2020, 99, 119-127.	1.9	9
3	Development of RNA-seq-based molecular markers for characterizing Thinopyrum bessarabicum and Secale introgressions in wheat. Genome, 2020, 63, 525-534.	2.0	0
4	Altered serum protein levels in frontotemporal dementia and amyotrophic lateral sclerosis indicate calcium and immunity dysregulation. Scientific Reports, 2020, 10, 13741.	3.3	26
5	Sierra: discovery of differential transcript usage from polyA-captured single-cell RNA-seq data. Genome Biology, 2020, 21, 167.	8.8	59
6	Paternallyâ€biased gene expression follows kinâ€selected predictions in female honey bee embryos. Molecular Ecology, 2020, 29, 1523-1533.	3.9	16
7	MSH3 modifies somatic instability and disease severity in Huntingtonâ€™s and myotonic dystrophy type 1. Brain, 2019, 142, 1876-1886.	7.6	114
8	scMerge leverages factor analysis, stable expression, and pseudoreplication to merge multiple single-cell RNA-seq datasets. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9775-9784.	7.1	130
9	scDC: single cell differential composition analysis. BMC Bioinformatics, 2019, 20, 721.	2.6	29
10	scReClassify: post hoc cell type classification of single-cell rNA-seq data. BMC Genomics, 2019, 20, 913.	2.8	18
11	C06â€…Genetic variation in MSH3 that lowers its expression ameliorates disease course and limits repeat expansion in huntingtonâ€™s disease and myotonic dystrophy type 1. , 2018, , .		0
12	Identification of genetic variants associated with Huntington's disease progression: a genome-wide association study. Lancet Neurology, The, 2017, 16, 701-711.	10.2	248
13	Humanized mutant FUS drives progressive motor neuron degeneration without aggregation in â€˜FUSDelta14â€™ knockin mice. Brain, 2017, 140, 2797-2805.	7.6	95
14	RNA-Seq of Huntingtonâ€™s disease patient myeloid cells reveals innate transcriptional dysregulation associated with proinflammatory pathway activation. Human Molecular Genetics, 2016, 25, ddw142.	2.9	47
15	Limited Clinical Utility of Non-invasive Prenatal Testing for Subchromosomal Abnormalities. American Journal of Human Genetics, 2016, 98, 34-44.	6.2	101
16	AUTOCLASSIFICATION OF THE VARIABLE 3XMM SOURCES USING THE RANDOM FOREST MACHINE LEARNING ALGORITHM. Astrophysical Journal, 2015, 813, 28.	4.5	26
17	Susceptibility to tuberculosis is associated with variants in the ASAP1 gene encoding a regulator of dendritic cell migration. Nature Genetics, 2015, 47, 523-527.	21.4	156
18	AUTOMATIC CLASSIFICATION OF TIME-VARIABLE X-RAY SOURCES. Astrophysical Journal, 2014, 786, 20.	4.5	22

#	ARTICLE	IF	CITATIONS
19	Classification of ASKAP VAST Radio Light Curves. Proceedings of the International Astronomical Union, 2011, 7, 397-399.	0.0	4