Li Song

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10789484/publications.pdf

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| | | 933447 | 1372567 | |
|----------|-----------------|--------------|----------------|--|
| 10 | 2,464 citations | 10 | 10 | |
| papers | citations | h-index | g-index | |
| | | | | |
| | | | | |
| 10 | 10 | 10 | 4585 | |
| all docs | docs citations | times ranked | citing authors | |
| | | | | |

| # | Article | IF | Citations |
|----|--|------|-----------|
| 1 | A multi-sample approach increases the accuracy of transcript assembly. Nature Communications, 2019, 10, 5000. | 12.8 | 30 |
| 2 | Genomic differences between nasal Staphylococcus aureus from hog slaughterhouse workers and their communities. PLoS ONE, 2018, 13, e0193820. | 2.5 | 11 |
| 3 | Hybrid assembly with long and short reads improves discovery of gene family expansions. BMC Genomics, 2017, 18, 541. | 2.8 | 51 |
| 4 | Centrifuge: rapid and sensitive classification of metagenomic sequences. Genome Research, 2016, 26, 1721-1729. | 5.5 | 1,025 |
| 5 | CLASS2: accurate and efficient splice variant annotation from RNA-seq reads. Nucleic Acids Research, 2016, 44, e98-e98. | 14.5 | 70 |
| 6 | Rcorrector: efficient and accurate error correction for Illumina RNA-seq reads. GigaScience, 2015, 4, 48. | 6.4 | 381 |
| 7 | Lighter: fast and memory-efficient sequencing error correction without counting. Genome Biology, 2014, 15, 509. | 8.8 | 201 |
| 8 | CLASS: constrained transcript assembly of RNA-seq reads. BMC Bioinformatics, 2013, 14, S14. | 2.6 | 30 |
| 9 | Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. F1000Research, 2013, 2, 188. | 1.6 | 372 |
| 10 | Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. F1000Research, 2013, 2, 188. | 1.6 | 293 |