## Harry Taegyun Yang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1976536/publications.pdf

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|          |                | 1307594      | 1474206        |  |
|----------|----------------|--------------|----------------|--|
| 8        | 333            | 7            | 9              |  |
| papers   | citations      | h-index      | g-index        |  |
|          |                |              |                |  |
|          |                |              |                |  |
| 0        | 0              | 0            | 506            |  |
| 9        | 9              | 9            | 586            |  |
| all docs | docs citations | times ranked | citing authors |  |
|          |                |              |                |  |

| # | Article   | IF   | CITATIONS |
|---|---|------|-----------|
| 1 | Technology dictates algorithms: recent developments in read alignment. Genome Biology, 2021, 22, 249.   | 8.8  | 51        |
| 2 | Benchmarking of computational error-correction methods for next-generation sequencing data. Genome Biology, 2020, 21, 71.   | 8.8  | 26        |
| 3 | Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing. Nature Communications, 2020, $11$ , $3126$ .   | 12.8 | 44        |
| 4 | Regional Variation of Splicing QTLs in Human Brain. American Journal of Human Genetics, 2020, 107, 196-210.   | 6.2  | 26        |
| 5 | Pathway-guided analysis identifies Myc-dependent alternative pre-mRNA splicing in aggressive prostate cancers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5269-5279. | 7.1  | 44        |
| 6 | ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues. Genome Biology, 2018, 19, 36.   | 8.8  | 42        |
| 7 | Transcriptome analysis in whole blood reveals increased microbial diversity in schizophrenia.<br>Translational Psychiatry, 2018, 8, 96.   | 4.8  | 92        |
| 8 | Haplso: An Accurate Method for the Haplotype- Specific Isoforms Reconstruction From Long Single-Molecule Reads. IEEE Transactions on Nanobioscience, 2017, 16, 108-115.   | 3.3  | 6         |