

# Xinyuan Zhang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6647119/publications.pdf>

Version: 2024-02-01

8  
papers

195  
citations

1478505

6  
h-index

1720034

7  
g-index

10  
all docs

10  
docs citations

10  
times ranked

567  
citing authors

| # | ARTICLE   | IF   | CITATIONS |
|---|---|------|-----------|
| 1 | Exome-wide evaluation of rare coding variants using electronic health records identifies new gene-phenotype associations. <i>Nature Medicine</i> , 2021, 27, 66-72.   | 30.7 | 44        |
| 2 | Mendelian pathway analysis of laboratory traits reveals distinct roles for ciliary subcompartments in common disease pathogenesis. <i>American Journal of Human Genetics</i> , 2021, 108, 482-501.  | 6.2  | 7         |
| 3 | Statistical Impact of Sample Size and Imbalance on Multivariate Analysis and A Case Study in the UK Biobank. <i>AMIA ... Annual Symposium proceedings</i> , 2020, 2020, 1383-1391.  | 0.2  | 0         |
| 4 | Real world scenarios in rare variant association analysis: the impact of imbalance and sample size on the power in silico. <i>BMC Bioinformatics</i> , 2019, 20, 46.  | 2.6  | 20        |
| 5 | Genomics-First Evaluation of Heart Disease Associated With Titin-Truncating Variants. <i>Circulation</i> , 2019, 140, 42-54.  | 1.6  | 97        |
| 6 | Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 272-283. | 0.7  | 6         |
| 7 | Rare variants in drug target genes contributing to complex diseases, phenome-wide. <i>Scientific Reports</i> , 2018, 8, 4624.   | 3.3  | 13        |
| 8 | Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. , 2018, , .   |      | 6         |