# Qingbo S Wang

## List of Publications by Year in Descending Order



| | | | |
|---|---|---|---|
| 18 papers | 3,297 citations | 9 h-index | 22 g-index |
| 22 ext. papers | 6,440 ext. citations | 31.8 avg, IF | 3.39 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 18 | Methods for statistical fine-mapping and their applications to auto-immune diseases.. *Seminars in Immunopathology*, **2022**, 44, 101 | 12 | 0 |
| 17 | Centers for Mendelian Genomics: A decade of facilitating gene discovery.. *Genetics in Medicine*, **2022**, | 8.1 | 5 |
| 16 | High-resolution Slide-seqV2 spatial transcriptomics enables discovery of disease-specific cell neighborhoods and pathways.. *IScience*, **2022**, 25, 104097 | 6.1 | 1 |
| 15 | Principles of Spatial Transcriptomics Analysis: A Practical Walk-Through in Kidney Tissue.. *Frontiers in Physiology*, **2021**, 12, 809346 | 4.6 | 2 |
| 14 | Leveraging supervised learning for functionally informed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. *Nature Communications*, **2021**, 12, 3394 | 17.4 | 9 |
| 13 | Mapping the human genetic architecture of COVID-19. *Nature*, **2021**, | 50.4 | 162 |
| 12 | Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2021**, 597, E3-E4 | 50.4 | 3 |
| 11 | Evaluating drug targets through human loss-of-function genetic variation. *Nature*, **2020**, 581, 459-464 | 50.4 | 53 |
| 10 | The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443 | 50.4 | 2278 |
| 9 | Landscape of multi-nucleotide variants in 125,748 human exomes and 15,708 genomes. *Nature Communications*, **2020**, 11, 2539 | 17.4 | 51 |
| 8 | A structural variation reference for medical and population genetics. *Nature*, **2020**, 581, 444-451 | 50.4 | 223 |
| 7 | Transcript expression-aware annotation improves rare variant interpretation. *Nature*, **2020**, 581, 452-458 | 50.4 | 55 |
| 6 | The effect of LRRK2 loss-of-function variants in humans. *Nature Medicine*, **2020**, 26, 869-877 | 50.5 | 47 |
| 5 | High Resolution Slide-seqV2 Spatial Transcriptomics Enables Discovery of Disease-Specific Cell Neighborhoods and Pathways | | 3 |
| 4 | Leveraging supervised learning for functionally-informed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs | | 2 |
| 3 | The mutational constraint spectrum quantified from variation in 141,456 humans | | 381 |
| 2 | Landscape of multi-nucleotide variants in 125,748 human exomes and 15,708 genomes | | 3 |

# List of Publications