

# William W Greenwald

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5398522/publications.pdf>

Version: 2024-02-01

10  
papers

583  
citations

1040056

9  
h-index

1372567

10  
g-index

12  
all docs

12  
docs citations

12  
times ranked

1765  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Human iPSC-Derived Retinal Pigment Epithelium: A Model System for Prioritizing and Functionally Characterizing Causal Variants at AMD Risk Loci. <i>Stem Cell Reports</i> , 2019, 12, 1342-1353.                     | 4.8  | 32        |
| 2  | Subtle changes in chromatin loop contact propensity are associated with differential gene regulation and expression. <i>Nature Communications</i> , 2019, 10, 1054.  | 12.8 | 100       |
| 3  | Updated and standardized genome-scale reconstruction of <i>Mycobacterium tuberculosis</i> H37Rv, iEK1011, simulates flux states indicative of physiological conditions. <i>BMC Systems Biology</i> , 2018, 12, 25.   | 3.0  | 63        |
| 4  | Identification of Common and Rare Genetic Variation Associated With Plasma Protein Levels Using Whole-Exome Sequencing and Mass Spectrometry. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002170. | 3.6  | 26        |
| 5  | Insights into the Mutational Burden of Human Induced Pluripotent Stem Cells from an Integrative Multi-Omics Approach. <i>Cell Reports</i> , 2018, 24, 883-894.   | 6.4  | 85        |
| 6  | Decreased STARD10 Expression Is Associated with Defective Insulin Secretion in Humans and Mice. <i>American Journal of Human Genetics</i> , 2017, 100, 238-256.  | 6.2  | 60        |
| 7  | Utilization of defined microbial communities enables effective evaluation of meta-genomic assemblies. <i>BMC Genomics</i> , 2017, 18, 296.   | 2.8  | 21        |
| 8  | iPSCORE: A Resource of 222 iPSC Lines Enabling Functional Characterization of Genetic Variation across a Variety of Cell Types. <i>Stem Cell Reports</i> , 2017, 8, 1086-1100.                                       | 4.8  | 147       |
| 9  | Efficient Prioritization of Multiple Causal eQTL Variants via Sparse Polygenic Modeling. <i>Genetics</i> , 2017, 207, 1301-1312.   | 2.9  | 10        |
| 10 | Pgltools: a genomic arithmetic tool suite for manipulation of Hi-C peak and other chromatin interaction data. <i>BMC Bioinformatics</i> , 2017, 18, 207.   | 2.6  | 35        |