

# Robert Gerszten

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11083396/publications.pdf>

Version: 2024-02-01

8  
papers

1,876  
citations

1163117

8  
h-index

1588992

8  
g-index

9  
all docs

9  
docs citations

9  
times ranked

4296  
citing authors

| # | ARTICLE  | IF   | CITATIONS |
|---|--|------|-----------|
| 1 | Metabo-Endotypes of Asthma Reveal Differences in Lung Function: Discovery and Validation in Two TOPMed Cohorts. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 205, 288-299.      | 5.6  | 17        |
| 2 | Protein prediction for trait mapping in diverse populations. <i>PLoS ONE</i> , 2022, 17, e0264341.   | 2.5  | 13        |
| 3 | Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. <i>Nature Genetics</i> , 2022, 54, 263-273.   | 21.4 | 156       |
| 4 | Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.  | 27.8 | 1,069     |
| 5 | Genome sequencing unveils a regulatory landscape of platelet reactivity. <i>Nature Communications</i> , 2021, 12, 3626.  | 12.8 | 29        |
| 6 | A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.                          | 21.4 | 69        |
| 7 | Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.   | 27.8 | 376       |
| 8 | Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020, 52, 969-983. | 21.4 | 146       |