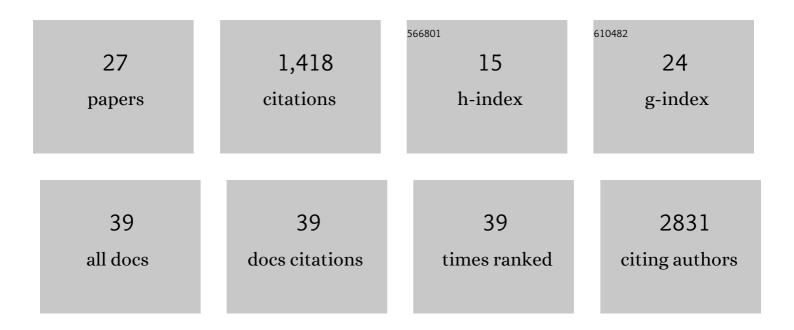
## Winston A Haynes

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3533179/publications.pdf Version: 2024-02-01



WINSTON & HAVNES

| #  | Article  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | High-affinity, neutralizing antibodies to SARS-CoV-2 can be made without T follicular helper cells.<br>Science Immunology, 2022, 7, .  | 5.6 | 28        |
| 2  | Case Study: Longitudinal immune profiling of a SARS-CoV-2 reinfection in a solid organ transplant recipient. , 2021, , .   |     | 3         |
| 3  | Phase Ib study of patients with metastatic castrate-resistant prostate cancer treated with different sequencing regimens of atezolizumab and sipuleucel-T. , 2021, 9, e002931.     |     | 18        |
| 4  | Immunogenic amino acid motifs and linear epitopes of COVID-19 mRNA vaccines. PLoS ONE, 2021, 16, e0252849.   | 1.1 | 11        |
| 5  | High-affinity, neutralizing antibodies to SARS-CoV-2 can be made without T follicular helper cells<br>Science Immunology, 2021, , eabl5652.  | 5.6 | 6         |
| 6  | Integrated, multicohort analysis reveals unified signature of systemic lupus erythematosus. JCI<br>Insight, 2020, 5, .   | 2.3 | 36        |
| 7  | Gene annotation bias impedes biomedical research. Scientific Reports, 2018, 8, 1362.   | 1.6 | 125       |
| 8  | Unsupervised Analysis of Transcriptomics in Bacterial Sepsis Across Multiple Datasets Reveals Three<br>Robust Clusters. Critical Care Medicine, 2018, 46, 915-925.                 | 0.4 | 219       |
| 9  | Leveraging heterogeneity across multiple datasets increases cell-mixture deconvolution accuracy and reduces biological and technical biases. Nature Communications, 2018, 9, 4735. | 5.8 | 128       |
| 10 | Interpretation of biological experiments changes with evolution of the Gene Ontology and its annotations. Scientific Reports, 2018, 8, 5115.                                       | 1.6 | 110       |
| 11 | Methods to increase reproducibility in differential gene expression via meta-analysis. Nucleic Acids<br>Research, 2017, 45, e1-e1.   | 6.5 | 137       |
| 12 | EMPOWERING MULTI-COHORT GENE EXPRESSION ANALYSIS TO INCREASE REPRODUCIBILITY. , 2017, 22, 144-153.   |     | 75        |
| 13 | A Case Study: Analyzing City Vitality with Four Pillars of Activity—Live, Work, Shop, and Play. Big Data,<br>2016, 4, 60-66.   | 2.1 | 8         |
| 14 | Development of Th17-associated interstitial kidney inflammation in lupus-prone mice lacking the gene<br>encoding STAT-1. Arthritis and Rheumatology, 2015, 68, n/a-n/a.            | 2.9 | 10        |
| 15 | Visualizing the Protein Sequence Universe. Concurrency Computation Practice and Experience, 2014, 26, 1313-1325.   | 1.4 | 5         |
| 16 | MOPED Enables Discoveries through Consistently Processed Proteomics Data. Journal of Proteome Research, 2014, 13, 107-113.   | 1.8 | 20        |
| 17 | Unraveling the Complexities of Life Sciences Data. Big Data, 2013, 1, 42-50.   | 2.1 | 46        |
| 18 | Integrative Analysis of Longitudinal Metabolomics Data from a Personal Multi-Omics Profile.<br>Metabolites, 2013, 3, 741-760.  | 1.3 | 56        |

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| #  | Article  | IF  | CITATIONS |
|----|--|-----|-----------|
| 19 | Differential Expression Analysis for Pathways. PLoS Computational Biology, 2013, 9, e1002967.  | 1.5 | 78        |
| 20 | MOPED: Model Organism Protein Expression Database. Nucleic Acids Research, 2012, 40, D1093-D1099.  | 6.5 | 106       |
| 21 | Visualizing the protein sequence universe. , 2012, , .   |     | 3         |
| 22 | Classifying Proteins into Functional Groups Based on All-versus-All BLAST of 10 Million Proteins.<br>OMICS A Journal of Integrative Biology, 2011, 15, 513-521.  | 1.0 | 11        |
| 23 | SPIRE: Systematic protein investigative research environment. Journal of Proteomics, 2011, 75, 122-126.  | 1.2 | 30        |
| 24 | IPM: An integrated protein model for false discovery rate estimation and identification in high-throughput proteomics. Journal of Proteomics, 2011, 75, 116-121. | 1.2 | 12        |
| 25 | Bioinformatics and Data-Intensive Scientific Discovery in the Beginning of the 21st Century. OMICS A<br>Journal of Integrative Biology, 2011, 15, 199-201.       | 1.0 | 15        |
| 26 | The United States of America and Scientific Research. PLoS ONE, 2010, 5, e12203.   | 1.1 | 30        |
| 27 | Meta-analysis for Protein Identification: A Case Study on Yeast Data. OMICS A Journal of Integrative<br>Biology, 2010, 14, 309-314.                              | 1.0 | 17        |