

# Winston A Haynes

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3533179/publications.pdf>

Version: 2024-02-01

27  
papers

1,418  
citations

566801

15  
h-index

610482

24  
g-index

39  
all docs

39  
docs citations

39  
times ranked

2831  
citing authors

#	ARTICLE	IF	CITATIONS
1	High-affinity, neutralizing antibodies to SARS-CoV-2 can be made without T follicular helper cells. <i>Science Immunology</i> , 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. <i>PLoS ONE</i> , 2021, 16, e0252849.	1.1	11
5	High-affinity, neutralizing antibodies to SARS-CoV-2 can be made without T follicular helper cells.. <i>Science Immunology</i> , 2021, , eabl5652.	5.6	6
6	Integrated, multicohort analysis reveals unified signature of systemic lupus erythematosus. <i>JCI Insight</i> , 2020, 5, .	2.3	36
7	Gene annotation bias impedes biomedical research. <i>Scientific Reports</i> , 2018, 8, 1362.	1.6	125
8	Unsupervised Analysis of Transcriptomics in Bacterial Sepsis Across Multiple Datasets Reveals Three Robust Clusters. <i>Critical Care Medicine</i> , 2018, 46, 915-925.	0.4	219
9	Leveraging heterogeneity across multiple datasets increases cell-mixture deconvolution accuracy and reduces biological and technical biases. <i>Nature Communications</i> , 2018, 9, 4735.	5.8	128
10	Interpretation of biological experiments changes with evolution of the Gene Ontology and its annotations. <i>Scientific Reports</i> , 2018, 8, 5115.	1.6	110
11	Methods to increase reproducibility in differential gene expression via meta-analysis. <i>Nucleic Acids Research</i> , 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 Activityâ€”Live, Work, Shop, and Play. <i>Big Data</i> , 2016, 4, 60-66.	2.1	8
14	Development of Th17-associated interstitial kidney inflammation in lupus-prone mice lacking the gene encoding STAT-1. <i>Arthritis and Rheumatology</i> , 2015, 68, n/a-n/a.	2.9	10
15	Visualizing the Protein Sequence Universe. <i>Concurrency Computation Practice and Experience</i> , 2014, 26, 1313-1325.	1.4	5
16	MOPED Enables Discoveries through Consistently Processed Proteomics Data. <i>Journal of Proteome Research</i> , 2014, 13, 107-113.	1.8	20
17	Unraveling the Complexities of Life Sciences Data. <i>Big Data</i> , 2013, 1, 42-50.	2.1	46
18	Integrative Analysis of Longitudinal Metabolomics Data from a Personal Multi-Omics Profile. <i>Metabolites</i> , 2013, 3, 741-760.	1.3	56

#	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. 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 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 Biology, 2010, 14, 309-314.	1.0	17