

# Brad T Sherman

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11508865/publications.pdf>

Version: 2024-02-01

18  
papers

66,739  
citations

586496

16  
h-index

939365

18  
g-index

19  
all docs

19  
docs citations

19  
times ranked

94807  
citing authors

#	ARTICLE	IF	CITATIONS
1	DAVID: a web server for functional enrichment analysis and functional annotation of gene lists (2021 update). <i>Nucleic Acids Research</i> , 2022, 50, W216-W221.	6.5	1,694
2	Profiles of Long Non-Coding RNAs and mRNA Expression in Human Macrophages Regulated by Interleukin-27. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6207.	1.8	12
3	A novel microRNA, hsa-miR-6852 differentially regulated by Interleukin-27 induces necrosis in cervical cancer cells by downregulating the FoxM1 expression. <i>Scientific Reports</i> , 2018, 8, 900.	1.6	31
4	Genome analysis of three <i>Pneumocystis</i> species reveals adaptation mechanisms to life exclusively in mammalian hosts. <i>Nature Communications</i> , 2016, 7, 10740.	5.8	153
5	Sequencing and characterization of the complete mitochondrial genomes of three <i>Pneumocystis</i> species provide new insights into divergence between human and rodent <i>Pneumocystis</i> . <i>FASEB Journal</i> , 2013, 27, 1962-1972.	0.2	40
6	Evolution of the Pygmy Phenotype: Evidence of Positive Selection from Genome-wide Scans in African, Asian, and Melanesian Pygmies. <i>Human Biology</i> , 2013, 85, 251.	0.4	12
7	DAVID-WS: a stateful web service to facilitate gene/protein list analysis. <i>Bioinformatics</i> , 2012, 28, 1805-1806.	1.8	955
8	Gene duplications in prokaryotes can be associated with environmental adaptation. <i>BMC Genomics</i> , 2010, 11, 588.	1.2	102
9	Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. <i>Nature Protocols</i> , 2009, 4, 44-57.	5.5	31,831
10	Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists. <i>Nucleic Acids Research</i> , 2009, 37, 1-13.	6.5	13,313
11	Extracting Biological Meaning from Large Gene Lists with DAVID. <i>Current Protocols in Bioinformatics</i> , 2009, 27, Unit 13.11.	25.8	375
12	DAVID gene ID conversion tool. <i>Bioinformatics</i> , 2008, 2, 428-430.	0.2	156
13	DAVID Bioinformatics Resources: expanded annotation database and novel algorithms to better extract biology from large gene lists. <i>Nucleic Acids Research</i> , 2007, 35, W169-W175.	6.5	1,934
14	The DAVID Gene Functional Classification Tool: a novel biological module-centric algorithm to functionally analyze large gene lists. <i>Genome Biology</i> , 2007, 8, R183.	13.9	2,105
15	DAVID Knowledgebase: a gene-centered database integrating heterogeneous gene annotation resources to facilitate high-throughput gene functional analysis. <i>BMC Bioinformatics</i> , 2007, 8, 426.	1.2	510
16	Identifying biological themes within lists of genes with EASE. <i>Genome Biology</i> , 2003, 4, R70.	3.8	1,664
17	DAVID: Database for Annotation, Visualization, and Integrated Discovery. <i>Genome Biology</i> , 2003, 4, 1.	3.8	7,168
18	DAVID: Database for Annotation, Visualization, and Integrated Discovery. <i>Genome Biology</i> , 2003, 4, P3.	3.8	4,682