

# Ben Busby

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/128025/publications.pdf>

Version: 2024-02-01

29  
papers

574  
citations

933447

10  
h-index

713466

21  
g-index

37  
all docs

37  
docs citations

37  
times ranked

1256  
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting drug-metagenome interactions: Variation in the microbial $\beta$ -glucuronidase level in the human gut metagenomes. PLoS ONE, 2021, 16, e0244876.	2.5	15
2	NCBI's Virus Discovery Codeathon: Building "The Federated Index of Viral Experiments API Index". Viruses, 2020, 12, 1424.	3.3	3
3	geneHummus: an R package to define gene families and their expression in legumes and beyond. BMC Genomics, 2019, 20, 591.	2.8	3
4	Magic-BLAST, an accurate RNA-seq aligner for long and short reads. BMC Bioinformatics, 2019, 20, 405.	2.6	216
5	Box, stalked, and upside-down? Draft genomes from diverse jellyfish (Cnidaria, Acraspeda) lineages: <i>Alatina alata</i> (Cubozoa), <i>Calvadosia cruxmelitensis</i> (Staurozoa), and <i>Cassiopea xamachana</i> (Scyphozoa). GigaScience, 2019, 8, .	6.4	53
6	NCBI's Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. Genes, 2019, 10, 714.	2.4	13
7	Reply to the paper: Misunderstood parameters of NCBI BLAST impacts the correctness of bioinformatics workflows. Bioinformatics, 2019, 35, 2699-2700.	4.1	17
8	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
9	Iron Hack - A symposium/hackathon focused on porphyrias, Friedreich's ataxia, and other rare iron-related diseases. F1000Research, 2019, 8, 1135.	1.6	11
10	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
11	NovoGraph: Human genome graph construction from multiple long-read de novo assemblies. F1000Research, 2018, 7, 1391.	1.6	5
12	Matchmaking in Bioinformatics. F1000Research, 2018, 7, 171.	1.6	2
13	NovoGraph: Genome graph construction from multiple long-read de novo assemblies. F1000Research, 2018, 7, 1391.	1.6	8
14	DangerTrack: A scoring system to detect difficult-to-assess regions. F1000Research, 2017, 6, 443.	1.6	10
15	PubRunner: A light-weight framework for updating text mining results. F1000Research, 2017, 6, 612.	1.6	5
16	Extending TCGA queries to automatically identify analogous genomic data from dbGaP. F1000Research, 2017, 6, 319.	1.6	0
17	Viewing RNA-seq data on the entire human genome. F1000Research, 2017, 6, 596.	1.6	2
18	PubRunner: A light-weight framework for updating text mining results. F1000Research, 2017, 6, 612.	1.6	4

#	ARTICLE	IF	CITATIONS
19	Mitogen-activated protein kinase signaling causes malignant melanoma cells to differentially alter extracellular matrix biosynthesis to promote cell survival. BMC Cancer, 2016, 16, 186.	2.6	13
20	MetaNetVar: Pipeline for applying network analysis tools for genomic variants analysis. F1000Research, 2016, 5, 674.	1.6	3
21	dbVar structural variant cluster set for data analysis and variant comparison. F1000Research, 2016, 5, 673.	1.6	18
22	dbVar structural variant cluster set for data analysis and variant comparison. F1000Research, 2016, 5, 673.	1.6	14
23	Closing gaps between open software and public data in a hackathon setting: User-centered software prototyping. F1000Research, 2016, 5, 672.	1.6	13
24	Closing gaps between open software and public data in a hackathon setting: User-centered software prototyping. F1000Research, 2016, 5, 672.	1.6	14
25	Effect of Domestication on the Spread of the [PIN+] Prion in <i>Saccharomyces cerevisiae</i> . Genetics, 2014, 197, 1007-1024.	2.9	11
26	Contribution of phage-derived genomic islands to the virulence of facultative bacterial pathogens. Environmental Microbiology, 2013, 15, 307-312.	3.8	79
27	A cloud-based learning environment for comparing RNA-seq aligners. F1000Research, 0, 5, 888.	1.6	0
28	NastyBugs: A simple method for extracting antimicrobial resistance information from metagenomes. F1000Research, 0, 6, 1971.	1.6	0
29	Lessons learned in virulence factor identification and data management from a hackathon on microbial virulence. F1000Research, 0, 11, 160.	1.6	1