

# Ben Busby

## List of Publications by Year in descending order

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docs citations

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1256  
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#	ARTICLE	IF	CITATIONS
1	Magic-BLAST, an accurate RNA-seq aligner for long and short reads. BMC Bioinformatics, 2019, 20, 405.	2.6	216
2	Contribution of phage-derived genomic islands to the virulence of facultative bacterial pathogens. Environmental Microbiology, 2013, 15, 307-312.	3.8	79
3	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
4	dbVar structural variant cluster set for data analysis and variant comparison. F1000Research, 2016, 5, 673.	1.6	18
5	Reply to the paper: Misunderstood parameters of NCBI BLAST impacts the correctness of bioinformatics workflows. Bioinformatics, 2019, 35, 2699-2700.	4.1	17
6	Predicting drug-metagenome interactions: Variation in the microbial $\beta$ -glucuronidase level in the human gut metagenomes. PLoS ONE, 2021, 16, e0244876.	2.5	15
7	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
8	dbVar structural variant cluster set for data analysis and variant comparison. F1000Research, 2016, 5, 673.	1.6	14
9	Closing gaps between open software and public data in a hackathon setting: User-centered software prototyping. F1000Research, 2016, 5, 672.	1.6	14
10	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
11	NCBI's Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. Genes, 2019, 10, 714.	2.4	13
12	Closing gaps between open software and public data in a hackathon setting: User-centered software prototyping. F1000Research, 2016, 5, 672.	1.6	13
13	Effect of Domestication on the Spread of the [PIN+] Prion in <i>Saccharomyces cerevisiae</i> . Genetics, 2014, 197, 1007-1024.	2.9	11
14	Iron Hack - A symposium/hackathon focused on porphyrias, Friedreich's ataxia, and other rare iron-related diseases. F1000Research, 2019, 8, 1135.	1.6	11
15	DangerTrack: A scoring system to detect difficult-to-assess regions. F1000Research, 2017, 6, 443.	1.6	10
16	NovoGraph: Genome graph construction from multiple long-read de novo assemblies. F1000Research, 2018, 7, 1391.	1.6	8
17	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
18	PubRunner: A light-weight framework for updating text mining results. F1000Research, 2017, 6, 612.	1.6	5

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19	NovoGraph: Human genome graph construction from multiple long-read de novo assemblies. F1000Research, 2018, 7, 1391.	1.6	5
20	PubRunner: A light-weight framework for updating text mining results. F1000Research, 2017, 6, 612.	1.6	4
21	geneHummus: an R package to define gene families and their expression in legumes and beyond. BMC Genomics, 2019, 20, 591.	2.8	3
22	NCBI's Virus Discovery Codeathon: Building "The Federated Index of Viral Experiments API Index. Viruses, 2020, 12, 1424.	3.3	3
23	MetaNetVar: Pipeline for applying network analysis tools for genomic variants analysis. F1000Research, 2016, 5, 674.	1.6	3
24	Viewing RNA-seq data on the entire human genome. F1000Research, 2017, 6, 596.	1.6	2
25	Matchmaking in Bioinformatics. F1000Research, 2018, 7, 171.	1.6	2
26	Lessons learned in virulence factor identification and data management from a hackathon on microbial virulence. F1000Research, 0, 11, 160.	1.6	1
27	A cloud-based learning environment for comparing RNA-seq aligners. F1000Research, 0, 5, 888.	1.6	0
28	Extending TCGA queries to automatically identify analogous genomic data from dbGaP. F1000Research, 2017, 6, 319.	1.6	0
29	NastyBugs: A simple method for extracting antimicrobial resistance information from metagenomes. F1000Research, 0, 6, 1971.	1.6	0