## Enis Afgan

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7623029/publications.pdf

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15 papers	5,511 citations	11 h-index	1125271 13 g-index
17	17	17	11821
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. Cell Genomics, 2022, 2, 100085.	3.0	59
2	GalaxyCloudRunner: enhancing scalable computing for Galaxy. Bioinformatics, 2021, 37, 1763-1765.	1.8	0
3	Cloud bursting galaxy: federated identity and access management. Bioinformatics, 2020, 36, 1-9.	1.8	11
4	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2020 update. Nucleic Acids Research, 2020, 48, W395-W402.	6.5	322
5	Jetstreamâ€"Early operations performance, adoption, and impacts. Concurrency Computation Practice and Experience, 2019, 31, e4683.	1.4	10
6	CloudLaunch: Discover and deploy cloud applications. Future Generation Computer Systems, 2019, 94, 802-810.	4.9	23
7	Federated Galaxy: Biomedical Computing at the Frontier. , 2018, 2018, .		9
8	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. Nucleic Acids Research, 2018, 46, W537-W544.	6.5	3,003
9	Bio-Docklets: virtualization containers for single-step execution of NGS pipelines. GigaScience, 2017, 6, 1-7.	3.3	12
10	CloudBridge., 2016, 2016, .		6
11	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. Nucleic Acids Research, 2016, 44, W3-W10.	6.5	1,751
12	Enabling cloud bursting for life sciences within Galaxy. Concurrency Computation Practice and Experience, 2015, 27, 4330-4343.	1.4	7
13	Genomics Virtual Laboratory: A Practical Bioinformatics Workbench for the Cloud. PLoS ONE, 2015, 10, e0140829.	1.1	119
14	BioBlend: automating pipeline analyses within Galaxy and CloudMan. Bioinformatics, 2013, 29, 1685-1686.	1.8	80
15	CloudMan as a platform for tool, data, and analysis distribution. BMC Bioinformatics, 2012, 13, 315.	1.2	43