



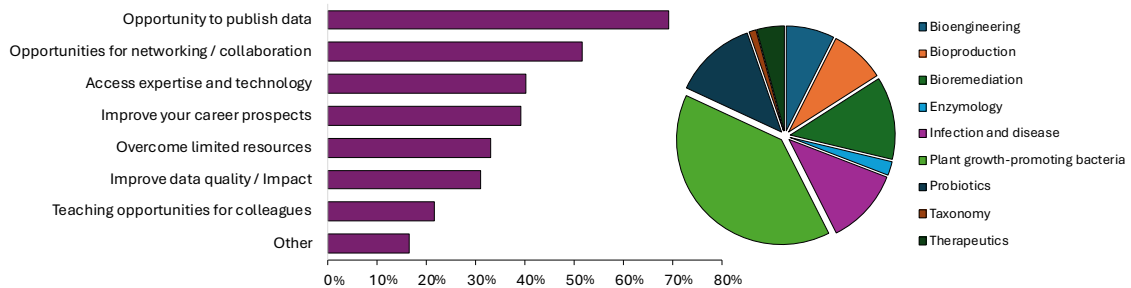
# GetGenome Newsletter

July 2024

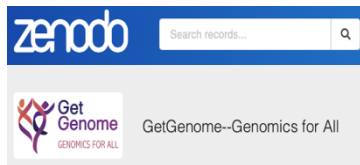
We are pleased to present the July 2024 edition of our monthly newsletter, providing a snapshot of GetGenome’s progress and key highlights. Remember, you can find all our monthly newsletters here- <https://getgenome.net/network>. The main highlights this month include:

## The GGMENA2024 CFP attracts 93 applicants from 6 countries!

The GetGenome CFP, #GGMENA2024 closed last month with a flurry of applications. Researchers from Morocco, Algeria, Tunisia and Egypt applied by the dozen with applications now in the hands of our experienced GGMENA2024 committee (<https://shorturl.at/8iFzv>) for assessment. The breadth of research represented within applications is remarkable, indicating our network is expanding and reaching new communities. Also notable is the applicants’ motivation to apply to GGMENA2024 with almost 70% stating that publishing data was a primary motivator.



## Open-science publishing – [Don't perish](#)



Speaking of publishing data, GetGenome will be running a WGS data sharing workshop on Friday 19<sup>th</sup> July on depositing data on NCBI and writing genome announcement articles. This workshop is primarily aimed at the GGPakistan2023 cohort but if you would like to join, please email us at [getgenome@tsl.ac.uk](mailto:getgenome@tsl.ac.uk) for the link.

## GGLatAm2024 participants joining GetGenome soon



Thanks to the wonderful efforts of our GGLatAm2024 committee (<https://shorturl.at/hjsC6>) applications have now undergone assessment. All applicants will be informed of the outcomes imminently and we look forward to welcoming selected applicants to GetGenome.

## GetGenome Impact

As GetGenome reaches new communities, we are excited to see the impact of our activities in regions where we have worked. If you would like to share any outputs such as talks, papers, posters etc. that GetGenome has supported you with, please do contact us at [getgenome@tsl.ac.uk](mailto:getgenome@tsl.ac.uk) to let us know.



81  
Early Career Researchers



334  
organisms studied



1,839,694,888  
bases sequenced



115  
BioSample accessions



23  
publications



1,000  
publication downloads