



Sample Eligibility Information

GGSouthAsia2024 is a competitive open call for projects eligible for researchers based in South Asian countries. The lead applicant must be based in one of these countries. Eligibility is informed according to the Word Bank and modified according to current FCDO advice.

If successful, deposited organisms will undergo illumina 250bp paired-end sequencing (NovaSeq 6000 (Illumina, San Diego, USA)), reads are adapter trimmed and *de novo* assembly is performed using SPAdes version 3.7. Contigs are annotated using Prokka 1.11. These data files are supplied without cost.

GetGenome will provide some training in basic genomics understanding and foundational techniques to enable you to identify your organism and build a phylogeny. We expect that data generated via GetGenome will be published on free-to-publish and free-to-access platforms such as NCBI / EBI, Zenodo etc (see below).

Strains

Importantly, this call is for non-pathogenic, culturable bacteria only. If your strain appears on the list accessible via the link provided, we cannot accept it for this call - <https://www.hse.gov.uk/pubns/misc208.pdf>

The list is not exhaustive. We cannot accept organisms with potential to cause harm to humans, plants or the environment. For this reason, we can only accept organisms that been adequately characterised (genotyped to species level) via a recognised molecular or biochemical method such as 16S, MALDI etc.

If you are successful, every organism will be assessed and we may reject some or all of your strains as they may present a hazard to health or the environment.

We ask that candidates only apply for up to 10 strains to be sequenced. Please do not apply for more strains than you have isolated and characterised at the time of

application. Typically, we will not accept strains that are characterised to genus-level only.

Applicants

Applications from Early Career Researchers are particularly welcomed (graduate student (BSc.), post-graduate student (MSc, MSci, PhD), post-doctoral scientists, assistants, associates and fellows in the early stage of their careers.

We are also happy to accept applications from more established researchers.

At GetGenome, we understand the challenges researchers, particularly across the global south experience to publish and access data. We overcome this challenge by advocating open science. We ask that data we generate for you is published and accessible for fellow researchers to access without barriers. Please take note of our open science expectations - https://getgenome.net/wp-content/uploads/2024/09/GetGenome-open-science-expectations_v01072024.pdf

If these expectations are not in line with yours, we kindly ask that you do not apply for our support.

Our MTA is available on our website - <https://getgenome.net/resource/mta>