

JGI to phase-out amplicon (iTag) sequencing

Dear Collaborator,

For the past several years, the DOE Joint Genome Institute has provided Illumina-based amplicon sequencing (iTag) services for targeted sequencing of the 16S and 18S ribosomal RNA genes, and internal transcribed spacer (ITS) regions for fungal species, directly from an environmental sample. This sequencing approach has become a mainstay in microbial ecology and is now readily accessible to researchers worldwide.

In April of 2017, the JGI's Prokaryotic Super Program Advisory Committee recommended that the JGI phase out iTag sequencing from our product portfolio considering the numerous commercial and academic sequencing centers that can now provide this service. This recommendation further rationalized that JGI should focus their community sequencing and analysis efforts on more complex products in line with our DOE mission mandate, such as shotgun metagenomics and metatranscriptomics. **Based on this high priority recommendation from our advisory committee and our internal analysis of resources and costs, the JGI has decided to phase out all amplicon sequencing services beginning September 2017 while increasing library, sequencing and analysis capacity for other products.** This decision opens opportunities for increased metagenome sequencing capacity, and developing and applying new approaches for community profiling through metagenomics.

For all outstanding commitments and calls in progress, including the large-scale CSP18 call, **the JGI will accept samples for iTag sequencing until March 1, 2018.** We encourage investigators who have iTag sequencing as part of their supported project to please contact your project manager to discuss sample availability and estimated shipping schedules as well as alternate products.

Investigators of prospective JGI proposals that would need an iTag component are encouraged to consider alternatives, or to seek amplicon sequencing and analysis services elsewhere. A short list of core facilities and contact information is included below. The full JGI amplicon library preparation, QC and sequencing protocols, along with detailed methods for peptide nucleic acid (PNA) blocks for mitochondrial and chloroplast DNA, are available [here](#).

As part of our ongoing commitment to support unique capabilities and services to the broader research community, the JGI is working towards implementing a robust database of ribosomal RNA gene sequences extracted from assembled shotgun metagenome data. Please stay tuned for updates regarding this new resource.

We thank you in advance for your support and understanding as we implement this change to our product portfolio. Please direct questions or comments to your project manager or to me.

Sincerely,

Emiley Eloë-Fadrosh
JGI Metagenome Program
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Core Facilities Offering Amplicon Sequencing Services

QB3 Vincent J. Coates Genomics Sequencing Laboratory

Contact: Shana McDevitt, shana.mcdevitt@berkeley.edu
<http://qb3.berkeley.edu/gsl>

Institute for Genome Sciences Microbiome Analysis Services

Contact: Mike Humphrys, MHumphrys@som.umaryland.edu
<http://www.igs.umaryland.edu/grc>

UNC Microbiome Core Facility

Contact: M. Andrea Azcarate-Peril, azcarate@med.unc.edu
<http://www.med.unc.edu/microbiome>

Environmental Sample Preparation and Sequencing Facility @ Argonne National Laboratory

Contact: Sarah Owens, Sarah.Owens@anl.gov
<http://www.bio.anl.gov/facilities/environmental-sample-preparation-sequencing-facility>