

## Metagenome Sequencing Program DNA Sample Submission Guidelines

The JGI has sequenced over 3000 prokaryotic, eukaryotic and metagenomic projects and finished over 300 genomes. DNA quality (molecular weight and purity) and quantity have always been the two critical factors in the success of the sequencing projects. If you cannot meet the JGI specifications for DNA submission have questions or concerns, contact your **Project Manager** ([pmo\\_jgi\\_project\\_management@lists.jgi-psf.org](mailto:pmo_jgi_project_management@lists.jgi-psf.org)) or Mansi Chovatia ([mrchovatia@lbl.gov](mailto:mrchovatia@lbl.gov)) regarding sample preparation and/or QC or Chew Yee Ngan ([cyngan@lbl.gov](mailto:cyngan@lbl.gov)) regarding library construction. **Samples not meeting minimum submission requirements with regard to quantity and quality will result in a delay to project initiation.**

Procedures for isolating DNA are available here: <http://my.jgi.doe.gov/index.html>

### **JGI Starting Material Specifications: Quality (purity)**

*All samples must meet the following criteria:*

1. Appropriate mass for project initiation as indicated by fluorometric measurement (PicoGreen – Life Technologies, Inc.).
2.  $A_{260/280}$  between 1.6 and 2.0 (spectrophotometer/NanoDrop)
3. We assess the mass of dsDNA in a sample using fluorometry (Qubit). NanoDrop measurements are generally only reliable indicators of DNA contamination with RNA, carbohydrate, organic solvents and other impurities that may interfere with sequencing. Obtaining DNA & RNA of suitable quantity and quality has been the rate-limiting step for many projects at the JGI. The quality of the starting material is one of the greatest predictors of a successful sequencing project. These documents (posted with permission) demonstrate the importance of utilizing this platform for nucleic acid quantification in our NextGen sequencing workflow:
  - [Importance of Sample QC.pdf](http://my.jgi.doe.gov/general/sampleprep/Importance-of-Sample-QC.pdf) : <http://my.jgi.doe.gov/general/sampleprep/Importance-of-Sample-QC.pdf>
  - [Sample Quality and Contamination.pdf](http://my.jgi.doe.gov/general/sampleprep/Sample-Quality-and-Contamination.pdf) : <http://my.jgi.doe.gov/general/sampleprep/Sample-Quality-and-Contamination.pdf>
4. Although the JGI does not require submission of a gel photo, investigators are **strongly advised** to assess the quality of materials to be submitted by gel electrophoresis. Heavily degraded samples cannot be used for construction of long mate pair libraries.

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5. RNA blobs and discrete bands require clean-up. Please refer to the recommended RNase I clean-up protocol:

<http://my.jgi.doe.gov/index.html>

6. In some cases, the presence of some impurities (polysaccharides or proteins) can be predicted by examining the way DNA fragments migrate (or do not migrate) in an agarose gel. If most of the DNA fragments form a streaky pattern or get stuck on top of the wells in the gel, the degree of impurity or contamination may cause problems in the shearing of the DNA. Also, if you notice your samples are too viscous (samples sticking to the outside of the pipette tips), which can lead to an incorrect quantitation of the samples, we request that you further purify your samples or dilute to the recommended concentration prior to shipping to the JGI.

7. For 16s tag sequencing, please make sure your samples are clean and amplifiable. We strongly recommend that you perform an amplification test of your samples following our "[iTag Sample Amplification QC](#)" procedure prior to shipment.

### **JGI Starting Material Specifications: Quality (molecular weight)**

Molecular weight of the DNA sample determines the insert size of the library we can construct. Most DNA preparation protocols should be able to generate DNA fragments of approximately 100kb in size, appropriate for Illumina and/or PacBio library construction. In general, we will not accept samples exhibiting a majority of DNA fragments smaller than 23Kb in size or heavily degraded DNA samples.

### **JGI Starting Material Specifications: Mass**

The table below should be used as a guide for preparation of DNA samples required to complete some of the common JGI product types:

	Metagenome 16s tag sequencing <i>*materials must be provided in 96-well plate format</i>	Metagenome Minimal Draft	Metagenome Standard Draft	Metagenome Improved Standard Draft
Volume per sample (or well)	25 uL	50-100 uL	50-100 uL	110-200 uL
Concentration	4-6 ng/uL *see note	5-10 ng/uL	5-10 ng/uL	110-200 ng/uL
Mass	100-150 ng	0.5 ug	0.5 ug	22 ug

\* if your sample dilution is different from what is indicated above but the samples can be amplified using the QC protocol referenced, then please work with your JGI Project Manager to properly submit the diluted samples to the JGI for processing.

Please consult with your project manager if you may not be able to provide adequate material. Projects will have the greatest odds of success with greater quantities of material. In some cases, JGI may be able to amplify the DNA. **The metagenome program does not recommend using MDA material for metagenome projects.**

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## **Shipping:**

Prior to shipping samples to the JGI, all sample metadata must be completed in its entirety using the JGI web interface. If you have questions about required information, consult with your Project Manager early in the submission process.

### **Preparation of DNA samples for shipping:**

1. DNA should be completely dissolved in  $1/_{10}$  TE DNA Suspension Buffer (10 mM Tris, pH 7.5-8.0, 0.1 mM EDTA) and shipped on dry ice.
2. Individual DNA samples should be shipped to the JGI in **one tube** (preps suitable for pooling should be pooled into a **single tube** for shipping to JGI). **You must ship all samples in the barcoded tubes (or plates) provided by the JGI.**

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