

**Metadata and Bioinformatics Accompaniment Form
(Required to be submitted as part of the proposal)**

Note: This form also drives the analysis for your project. Any changes or updates on analysis should be made through this form by updating, adding "rev#" to the filename, and re-submitting to inbre@ncgr.org.

1. Date

2. Submitted by

Institution

Email

Best Phone Number

3. Qualification

I am funded by NM-INBRE as an Investigator

IDeA-eligible institution (This requires co-funding support from applicant of approximately \$5k for basic project and depending on experimental design).

RAIN-eligible institution (ID, MT, NV, WY)

Yes I can co-fund award if my proposal is selected with approximately \$. (Required for proposal to be reviewed. This will also help us determine scope of your project).

4. Proposal Title

5. Species

6. Genome size

7. Sample Type

RNA

DNA

Data Files (FASTQ, etc.)

8. Sample Details

Number of Strains

Number of Conditions

Number of Time Points

Number of Replicates per Condition

Total number of samples (strains x conditions x time points x replicates)

9. From: Please specify the types of sequencing/bioinformatics tools or analysis you are requesting (check all that apply)

De novo Transcriptome Assembly

Differential Expression

Functional Annotation/Pathway Analysis

DNA-Seq Mutational Analysis

Genome Assembly

Metagenomics

Whole Genome

16S

18S

Metatranscriptomics

DNA Methylation (e.g. bisulfite-Seq, Pac Bio)

Small RNA-Seq (e.g., miRNAs)

ChIP-Seq

RIP-Seq

Genotyping by Sequencing

Custom bioinformatics/data analysis, please specify

Other, please specify

12. Genome/Transcriptome Reference Information and link.

13. For RNA-Seq Differential Expression Analysis

a. Please list (or attach spreadsheet) with sample names, sample descriptions, tissue, treatment, replicate, and other metadata.

b. Comparison Groups (e.g. treatment A vs. treatment B, control vs. all treatments, etc.)

14. Student Participation

15. Other Comments: