



Cram, Jacob <jcram@umces.edu>

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**FW: price for sequencing, samples are amplicons (~ 375 bp)**

1 message

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**Sairah Malkin** <smalkin@umces.edu>

Tue, Jun 4, 2019 at 10:52 AM

To: Jacob Cram <jcram@umces.edu>

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**From:** Sabeena Nazar [mailto:[sabeena@umces.edu](mailto:sabeena@umces.edu)]

**Sent:** Wednesday, December 5, 2018 3:13 PM

**To:** Sairah Malkin <[smalkin@umces.edu](mailto:smalkin@umces.edu)>

**Subject:** Re: price for sequencing, samples are amplicons (~ 375 bp)

Hi Sairah,

It was nice meeting you the other day. Please find attached protocol that I use for making 16S libraries. Here is the primer sequences for adding your specific gene of interest.

Forward overhang: 5' TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG-[locusspecific sequence]

Reverse overhang: 5' GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG-[locusspecific sequence]

Just to plan my runs, do you have any estimate time that you plan to send the amplicon libraries? Any plan in December?

Thanks,

Sabeena

Sabeena Nazar

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On 11/27/2018 3:37 PM, Sairah Malkin wrote:

Hi Sabeena,

We will prepare our amplifications and clean-up in our lab here at HPL.

Do you have a price per sample for sequencing if we provide amplicons (rather than DNA)? It would still need to be barcoded.

Many thanks,

Sairah

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*Sairah Malkin*

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**16s-metagenomic-library-prep-guide-15044223-b.pdf**

658K