Sample submission

Please submit your samples under the resource system (resource.cores.utah.edu). When you submit, you will need to have a fasta file for each plasmid ready. It does not need to contain the inserts, but will need to show the sequence of the backbone (vector). In the fasta file (open it in Notepad if on a Windows computer or TextEdit on a Mac) please make sure the comments section has no spaces or special characters other than underscore or hyphen (_ or -). The system will not allow you to submit if they are there. Simply remove them. If you need a space to make the name easier to read, use the underscore or hyphen.

NOTE: Snapgene addes the size of the plasmid in parenthesis and this messes up submission. Please correct it using the above guidelines.

Please provide 10uL of 50ng/uL in a 1.5mL snap top tube.

Please have the sample name on the side of the tube and the order number on a piece of tape on top of the tube(s) when you drop them off at one of our drop off locations.

Samples are currently run as they arrive. We need 20 samples to do a run, so if there are that many here, we will run quickly. If there are less, it may be a little bit before we can run our sample. As sample volumes pick up, we are perfectly happy to run multiple times per week.

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