```
/*Tricks to get proc mixed to work on a full scale model*/
    /*
        Assign unique integer value to each protein and for
        each peptide within a protein

        protein Peptide
            1       1
            1       2
            1       2
            2       1
            2       2
            2       3
            3       1
            3       1
            3       1
            3       2
            .........

        When starting SAS make sure you have enough temp work space (~2GB)
        as well as memory (~2GB) by using

        sas -work /workdirectroy -memsize 2000m

        where workdirectory is a pointer to a directroy with 2GB of space for
        reading and writing datasets

        Proc Mixed spends a lot of time and effort estimating the correct
        degrees of freedom for testing. This has NO effect on parameter
        estimates and since there is really no interest in testing at this
        point use the ddfm=bw (between-within) option since it uses the least
        amount of effort.

        lognote is a nice option since it sends notes to the log regarding
        where proc mixed is at in the fitting process. Its better than looking
        at a blank screen for 12 hours.

        outp creates the output dataset of the orginal data along with the
        residual or normalized abundance values

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        */




proc mixed data=four  noclprint lognote;
    class ms0343_run channel protein peptide;
    model abundance=ms0343_run|channel/ddfm=bw outp=normalized;
    random int peptide/subject=protein;
run;
```