

**Subject:** Re:**From:** Catherine <catherine.kirsanova@crg.eu>**Date:** 30/06/16 19:11**To:** Maria Lluch Senar <maria.lluch@crg.eu>**CC:** Samuel Miravet Verde <samuel.miravet@crg.eu>, Javier Delgado Blanco <javier.delgado@crg.eu>, Julia Ponomarenko <julia.ponomarenko@crg.eu>, "Luca Cozzuto" <luca.cozzuto@crg.es>

Guys,

Here are quick minutes after today meetings.

This wonderful Maria's plan was later commented by Luis Serrano as «what maria proposed does not make any sense». True.  
But I had no option to say the same that way directly:  
I used to get Maria's hysterical reaction: «you are not listening!»  
So I've tried my best to drive that dumb ideas the rational way.

1. MS data load from preprocessed file is declined.
2. Claimed that MS data are to be processed from raw files.
3. X!Tandem GPM tools was suggested (<https://www.biostars.org/p/66772/>) to attach it to our DB
4. Samuel claimed that their reference (list of species in particular and all necessary prerequisites) is easily configured to make X!Tandem GPM tools easily embedded into back-end and front-end to Mycoplasma database.
5. Samuel agreed to prepare all necessary information in «one week», i.e. all necessary file listed here:  
<http://thegpm.org/TANDEM/api/lpti.html>  
which also includes:  
«information about known single amino acid polymorphisms»  
«information about known potential modifications»  
«annotation spectrum library information»

6. Given that X!Tandem GPM tools can be configured for any external reference (putative ORFs too, this to be checked) p.2 is resolvable.  
I can only comment that the embedding of off-site stand-alone software (even when it's designed to be embedded to another automatic processing tool) is always time consuming task.

I think that there should more light and fine decision to secure p.2, like using frameworks/packages which are to be on the market for such tasks, and here is one:

<https://www.biostars.org/p/66772/>

— as an example

There are many: <http://strimmerlab.org/notes/mass-spectrometry.html>

I am sure Luca can comment all this better.

Have a nice night! —  
Catherine

On 29/06/16 17:32, Maria Lluch Senar wrote:

Hi all  
Is it ok for you to meet tomorrow at 15 to discuss about the Project? We have news about integration of proteomics data ]  
Thanks  
maria