Subject: RE: One question left
From: Maria Lluch Senar <maria.lluch@crg.eu>
Date: 17/11/16 17:25
To: Katerina Kirsanova <catherine.kirsanova@crg.eu>, Luis Serrano Pubul <luis.serrano@crg.eu>

It is true that the information of the first peptide is missing but if you detect the others of the long version you already know that it is the one that exist.
Also for having the short version you need to have the TSS.
In MS you can do de novo search. Thus, you can recover the sequence from the spectra and then you do blast and you could identify those cases (we did for the Proteomics paper).
I suggest you to read the MSB and Proteomics papers that we published.
Anyway, you made good points and questions J.
How is going the reporting and documentation of the webpage? It would be nice if Samuel or other person could continue the pipeline after you leave.
Thank you very much,

This started the next day she was set up (by Luis Serrano) as yet another my boss and she was putting this near in every 2nd her email to me

Cheers
Maria

From: Katerina Kirsanova
Sent: jueves, 17 de noviembre de 2016 16:43
To: Maria Lluch Senar <maria.lluch@crg.eu>; Luis Serrano Pubul <luis.serrano@crg.eu>
Subject: Re: One question left

El 11/17/16 a las 16:19, Catherine escribió:

> So if the 2nd guy does exist, but they look only for peps of the 1st guy, say, find only the last peps

El 11/17/16 a las 16:29, Maria Lluch Senar escribió:

> The peptide MALVSSPVLTNIV will could be still identified. If you do not identify the rest of the peptides it could be because the protein is shorter

Yes, last pep(s) is(are) always caught. But not the 1st one(s) in the given example.
Though if proteomic guys can process more exported data in the input files to prepare their pep refseqs,
i.e. including inner ORFs (at least with ATG as a start-codon) they are able to catch all peps from the shorter guys too, aren't they?