Data repository indication for MCP/2012/025023

Fast-sequencing (Fast-seq) dataset is accessible in

<http://proteomeview.hupo.org.cn/browseOneExperiment.jsp?experiment=Hela>

or  
<http://61.50.134.133/browseOneExperiment.jsp?experiment=Hela> (Figure 1)

Figure 1. Fast-sequencing (Fast-seq) dataset generated by QE MS platform in 12h mode.

A total of 7707 proteins were identified (Ion score >20, peptide length ≥7, Protein FDR <0.1%) by Q-Exactive in 12-hour mode. TotalSC stands for sum of spectra count (SPC) of the protein. #pep stands for number of identified peptides matched to the protein. The detailed protein identification information are available by clicking “gi|number” (Figure 2).

Figure 2. Comparison of protein identification in Fast-seq and Fast-quan dataset

Figure 2 shows the general view of protein identification in Fast-seq and Fast-quantification (Fast-quan) dataset.

Click “gi|number” in “Red box” of Figure 2 for the matched peptide information of Fast-seq dataset (Figure 3). Or click “gi|number” in “Green box” for the identification in Fast-quan dataset.

Figure 3 Detailed identification information of matched peptides in Fast-seq dataset

The basic information in Figure 3 includes peptide length, charge, modification, Mascot ion score, and so on.

Click “peptide sequence” for exact spectra (Figure 4).

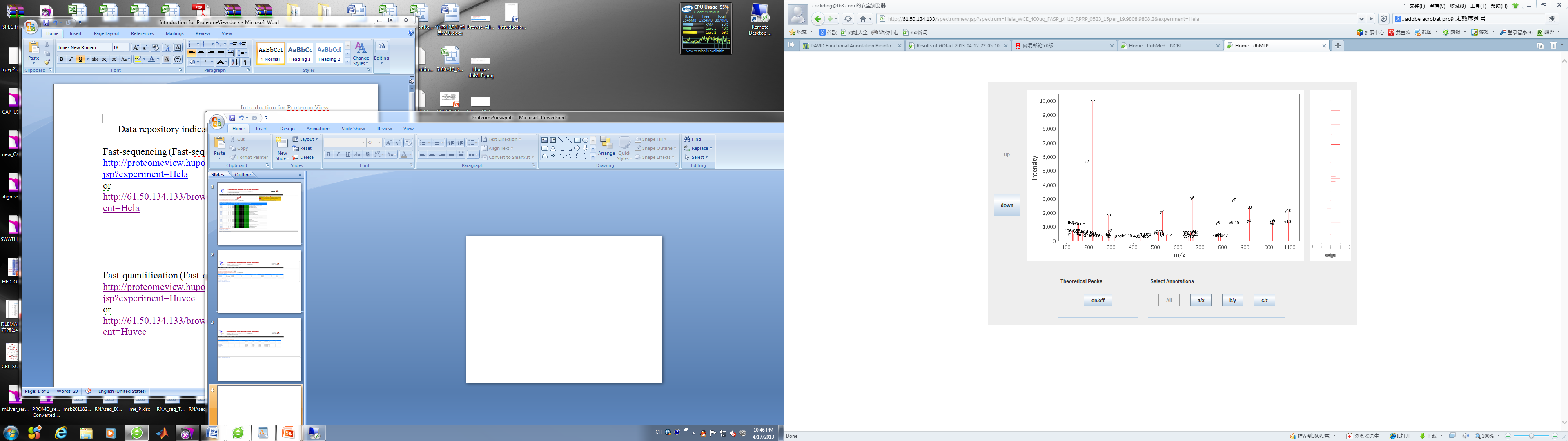


Figure 4. Peptide mass spectra. Experimental y/b ions were marked

Similarly, Fast-quantification (Fast-quan) dataset is accessible in

<http://proteomeview.hupo.org.cn/browseOneExperiment.jsp?experiment=HUVEC_DMSO_QE> (Figure 5)

Figure 5. Fast-quan dataset of 12h mode: Protein identifications in HUVEC cell treated by DMSO empty vehicle

and

<http://proteomeview.hupo.org.cn/browseOneExperiment.jsp?experiment=HUVEC_MLN_QE> (Figure 6)

Figure 6. Fast-quan dataset of 12h mode: Protein identifications in HUVEC cell treated by MLN empty vehicle

The following steps refer to indications for Fast-seq dataset.