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Dear Editor,

I would like to present a manuscript entitled “MGVB: a new proteomics toolset for fast and efficient proteomics data analysis” to be considered for publication in Nature Methods.

MGVB is a collection of tools for proteomics data analysis. It covers data processing from in silico digestion of protein sequences to comprehensive identification of posttranslational modifications and solving the protein inference problem. The toolset is developed with efficiency in mind. It enables analysis at a fraction of the resources cost typically required by existing commercial and free tools. MGVB, as it is a native application, is much faster than existing proteomics tools such as MaxQuant and MSFragger and, at the same time, finds very similar, in some cases even larger number of peptides at a chosen level of statistical significance.

In addition to its superior speed and lower resources requirements compared to existing tools, MGVB implements a novel combinatorial search strategy for finding post-translational modifications, which overcomes major limitations of the existing open database search algorithms.

MGVB is provided as free executable files at this stage but will be made open source in the future editions.

Data used to generate the reported results are available via ProteomeXchange with identifier PXD051331. The data can be accessed using the following reviewer’s credentials: **Username:**[reviewer\_pxd051331@ebi.ac.uk](mailto:reviewer_pxd051331@ebi.ac.uk); **Password:**EyGwUFfN.

I believe that the toolset will be useful for wide range of researchers dealing with large amount of LC-MS/MS data and hope it will be considered for peer review.

Yours sincerely



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