# Supporting information

## A Rapid and Simple Method for Identification of Metallothionein Isoforms in Cultured Human Prostate Cells by MALDI-TOF/TOF Mass Spectrometry

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**The supporting materials consist of two figures as following:**

**Figure S1. Trypsin digestion of the MT crude fractions prepared from RWPE assessed by SDS-PAGE**. The MT crude fractions were prepared by centrifugation of the cell lysates at 16 000 × g for 20 minutes. Ln 1 and Ln 2 show the MT crude fractions prior to and after trypsin treatment, respectively. As can be seen majority of the proteins were digested, leaving minimal amount of interfering proteins with MT samples. The protein samples were resolved by SDS-PAGE on a criterion gradient gel (8-16%) and subsequently stained with Coomassie blue.

**Figure S2. Mass distribution of the peptides produced by *in silico* trypsin digestion of human proteome in non-redundant Swiss-Prot protein database (Version 2007.01.09) with restriction that allows for one miss cleavage**. The *in silico* digestion was performed by using DB-STAT of ProteinProspector 4.0.8 (http://prospector.ucsf.edu/) with the parameters set as following: species, human; MW of proteins, 1000-300 000 Da; Protein pI from 3.0 to 10.0.

Fig. S1

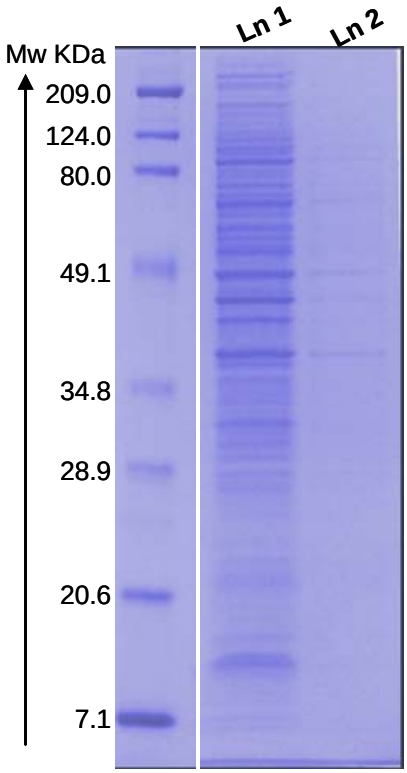
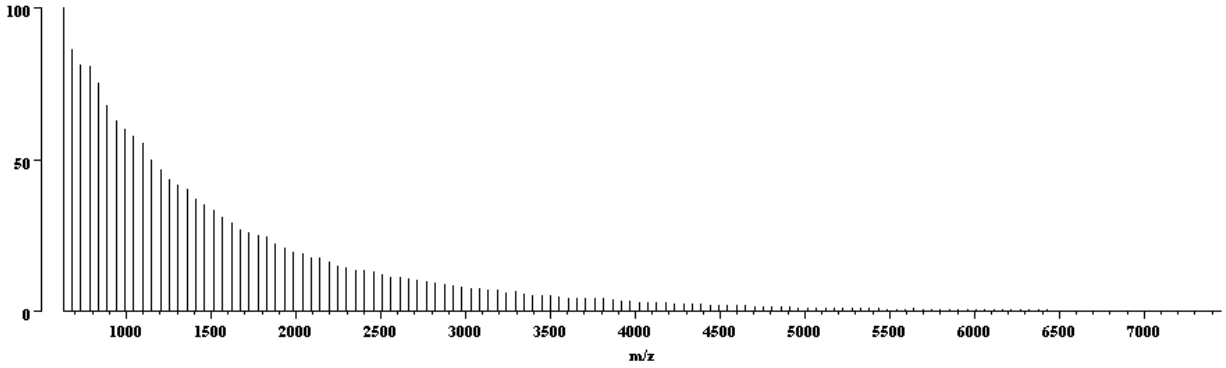


Fig. S2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