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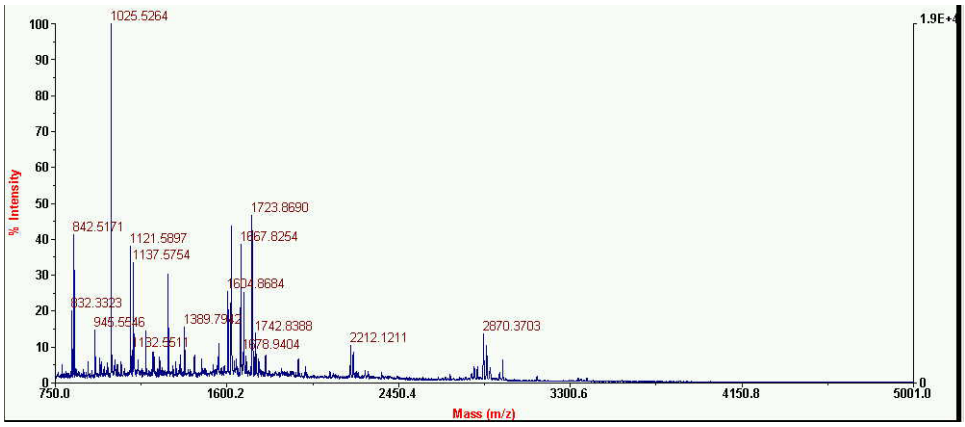

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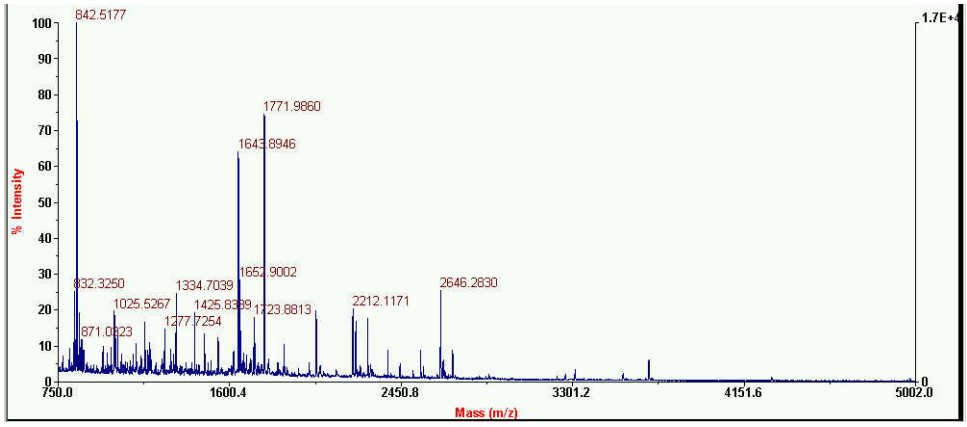

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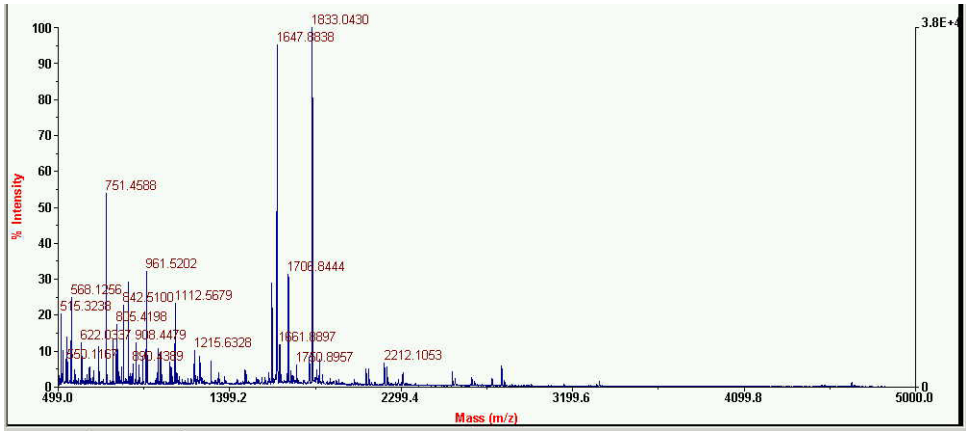

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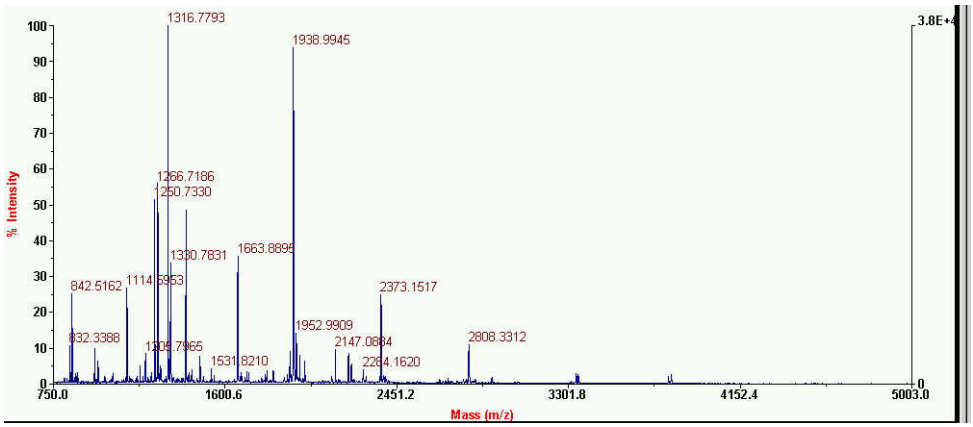

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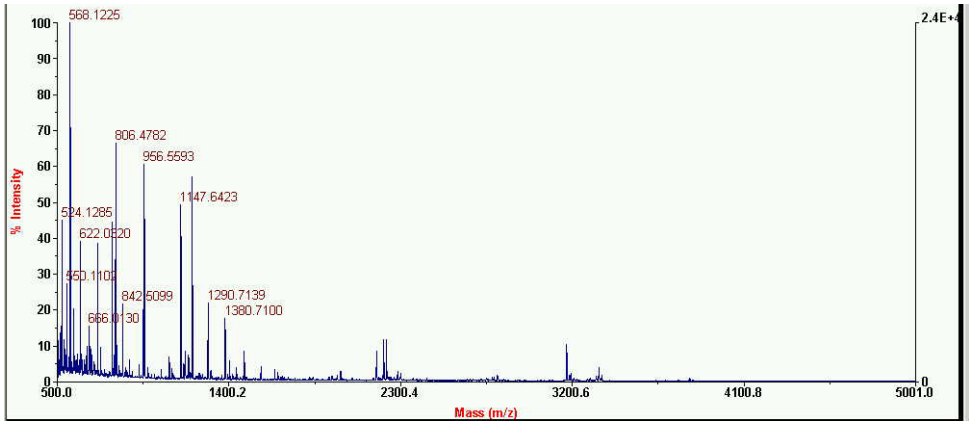

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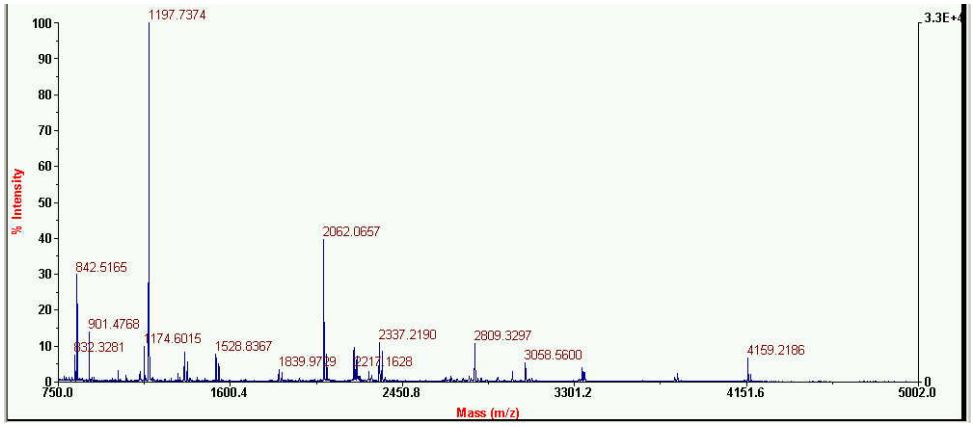

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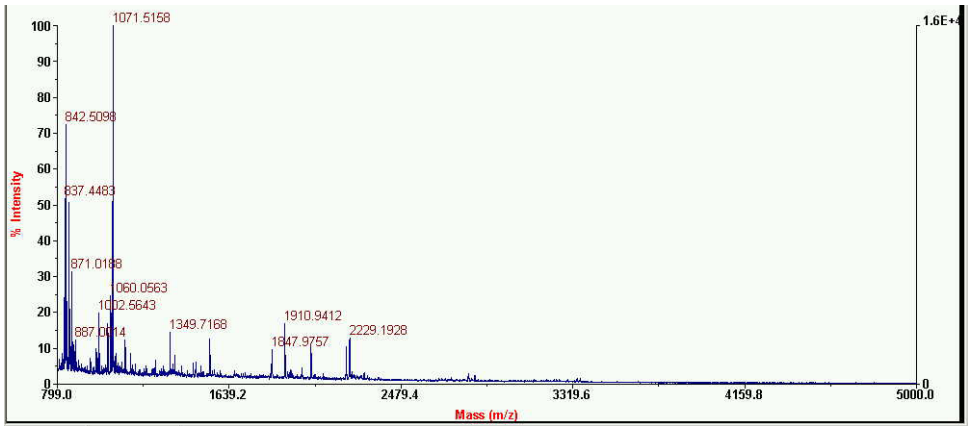

Figure S2 Annotated mass spectra used for identification of proteins in 2DGE experiments. Displayed are raw spectra. To obtain peptide mass fingerprint lists spectra were baseline corrected, noise removed, deisotoped and two point internally calibrated using trypsin peaks. Peak % intensity used for generating the final mass list ranged from a minimum of 4 to 12%.