

Supplementary table 1: Database search parameters used for peptides identifications

<i>Parameter</i>	<i>Value</i>
Enzyme :	Trypsin/P
Variable modifications :	Acetyl (Protein N-term), Carboxymethyl (C), Oxidation (M)
Mass values :	Monoisotopic
Protein Mass :	Unrestricted
Peptide Mass Tolerance :	± 5 ppm
Fragment Mass Tolerance:	± 0.8 Da
Max Missed Cleavages :	2
Instrument type :	ESI-TRAP