

Full Scan	
Resolution	70,000 (@ <i>m/z</i> 200)
AGC target value	3e6
Scan range	350-2000 <i>m/z</i>
Maximal injection time (ms)	100
Data-dependent MS/MS	
Resolution	17,500 (@ <i>m/z</i> 200)
AGC target value	2e5
Maximal injection time (ms)	50
Isolation window width (Da)	1.0 <i>m/z</i>
NCE (%)	31
First fixed mass	100.0 <i>m/z</i>
Data-dependent Settings	
Underfill ratio (%)	1
Charge exclusion	Charge states 1,5-8,>8
Peptide match	preferred
Exclusion isotopes	on
Dynamic exclusion (s)	30

DATABASE SEARCHING-- All MS/MS samples were analyzed using Mascot (Matrix Science, London, UK; version 2.4.1) and X! Tandem (The GPM, thegpm.org; version CYCLONE (2010.12.01.1)). Mascot was set up to search the UniProtSolan_20140120 database (109135 entries) assuming the digestion enzyme trypsin. X! Tandem was set up to search a subset of the UniProtSolan_20140120 database also assuming trypsin. Mascot and X! Tandem were searched with a fragment ion mass tolerance of 0.20 Da and a parent ion tolerance of 0.100 Da. Methylthio of cysteine and iTRAQ8plex of lysine and the n-terminus were specified in Mascot and X! Tandem as fixed modifications. Gln->pyro-Glu of the n-terminus, deamidated of asparagine and glutamine, oxidation of methionine and iTRAQ8plex of tyrosine were specified in Mascot as variable modifications. Glu->pyro-Glu of the n-terminus, ammonia-loss of the n-terminus, gln->pyro-Glu of the n-terminus, deamidated of asparagine and glutamine, oxidation of methionine and iTRAQ8plex of tyrosine were specified in X! Tandem as variable modifications.