Supplementary Material and Methods

4 µg protein of *Xpo*GH78 protein were reduced (2.5 mM DTT for 1 h at 60°C) and alkylated (10 mM iodacetamide for 30 min at 37°C). Proteolysis was performed overnight using trypsin (Promega, Madison, WI) with a ratio of 1:25 at 37°C. The digestion was stopped by adding acetic acid at the final concentration of 1%, followed by desalting and purification using ZipTip-µC18 tips (Millipore, Billerica, MA). 600 ng of proteolytically cleaved peptides were separated prior to mass spectrometric analyses by reverse phase on a 15 cm Acclaim PepMap100-column (Dionex, C18 3 µm, 100 Å) using an EASY-nLC Proxeon system (Thermo Scientific, Waltham, MA) at a constant flow rate of 300 nL/min. Separation was achieved using a non-linear gradient of 70 min with 0.1% acetic acid, 2% acetonitrile in water (solvent A) and 0.1% acetic acid in 100% acetonitrile (solvent B). Separated peptides were monitored using an LTQ-Orbitrap Velos mass spectrometer (Thermo Scientific) equipped with a nanoelectrospray ion source (PicoTip Emitter, New Objective, Woburn, MA). The MS-instrument was operated in data-dependent acquisition (DDA) mode. Survey full-scan MS spectra were acquired with resolution R = 30,000 at m/z 400. MS/MS scan events were repeated for top 12peaks using the higher energy dissociation mode (HCD) at normalized collision induced energy of 35%, activation time of 100 ms, minimum of ion signal threshold for MS/MS of 2,000 counts and a resolution of 7,500. Already targeted ions for MS/MS were dynamically excluded for 60 s.

Identification of proteins was performed using the Proteome Discoverer software (PD v1.3, Thermo Scientific). MS/MS data set was searched against the annotated *Xylaria polymorpha* GH78 peptide sequence using the SEQUEST algorithm embedded in the Proteome Discoverer software. Search parameters were as following: 10 ppm parent mass tolerance and 20 mmu for fragment ion mass tolerance. Up to two missed tryptic cleavages were allowed, carbamidomethylation of cysteines was specified as a fixed modification and methionine oxidation as a variable modification. Annotated peptide spectral matches were rescored by Percolator (Käll et al., 2007) and peptide identifications were considered significant with a q-value (FDR) <0.01 and X-correlation score >2. Proteins were considered as identified if at least two high-confident unique peptides were found.