Supporting Information 5. Overview of the "rescued" peptides. Presence of bio-active peptide hallmarks and other relevant characteristics is presented. The "rescue" operation itself becomes successful if several extra criteria are met: 1) a de novo derived tag coincides with the Mascot sequence, 2) the precursor protein comes with an above threshold score, 3) the Δmass between experimental and theoretical parent ion is within limits, 4) the error distributions of the Δmass between experimental and theoretical fragment ions are manually inspected, as is done for 5) the fragmentation patterns.

Protein/EST Id	Sequence	Ptm	Mascot ProtDB	Custom DB based on Maldi/Qtof MS	score	score threshold	delta mass	charge	basic cleavage motif	signal P	de novo tag	other peptides identified from same precursor	multiple spectra for this sequence	acceptable MS/MS spectrum (manual inspection)	acceptable error distribution of fragment ions (manual inspection)	Rescue
XP_001176287	A.EDGMELTHDEQPLNAMEI.R		√	√/-	26	37	0.3249	2	√	√	√	√	√		√	√
XP_785647	K.GFNTGAMEPLGSGFI.K		√	-/√	11	24	0.0157	2	√	√	√	√	√	√	√	√
XP_785647	K.DFNTGAMEPLGSGFI.K		√	-/√	11	22	0.0239	2	√	√	√	√	√	√	√	√
XP_799858	R.SLKNRQLFTQTRNKY.S		√	√/-	18	31	0.5412	4	√	√	√	√		√	√	√
XP_001199000	T.SIKADGEVTEDVDK.R		√	-/√	21	34	0.0383	2	√	√		√	√	√	√	√
XP_001199000	R.ANMFRSRLRGNG.K	Am	√	-/√	9	24	0.0445	2	√	√		√		√	√	√
XP_001199000	R.ANYFRGRGRKPG.K	Am	√	-/√	11	28	0.035	2	√	√		√		√	√	√
XP_001199000	R.ANMFRSRLRGKG.K	Am	√	√/√	18	25	0.0454	2	√	√		√		√	√	√
XP_001199000	R.DDPDAAEALVPGGDLSEE.K		√	√/√	19	33	0.0311	2	√	√	√	√		√	√	√
XP_001186882	R.PHGGSAFVFG.R	Am	√	-/-	25	42	0.1743	2	√	√		√		√	√	√
XP_001186882	R.DWAPREQDFANAAEESGPY.K		√	-/-	23	27	0.3151	2	√	√		√	√			√
CD294941	K.NFGGSMEPMQSGFY.K			√/-	18	32	0.2296	2	√	√	√	√	√			√
CD294941	R.FGSGLDSMQSGFY.K			-/√	21	25	0.0326	2	√	√	√	√	√	√	√	√
CD294941	R.FGSGSLEPMSSGFY.K			-/√	24	35	0.2291	2	√	√	√	√	√	√	√	√