Table 1. Calculated and measured masses of the peptides selected by the IMAC procedure

Peptide	Residues	Sequence	Calculated mass, Da	Measured mass, Da*	Measured mass, Da†
T_{31-32}	353–363	SQHSSIGDLKR	1227.6	1387.1	1227.4
T_{3-5}	14–22	RKNETSNSSPR	1275.6	1355.1	1275.4
T_{24}	255–269	SGSFSSQLGNFFSK	1639.8	1719.2/1799.4	1639.4
T_{13}	123–147	FGSLINDQGTAGLSSHGGSFAAQNR	2492.2	2572.3/2652.3/2732.1	2491.9
T_{12-13}	121–147	DRFGSLINDQGTAGLSSHGGSFAAQNR	2762.3	2843.6/2923.4/3003.7	2762.8
T_{11}	95–120	NQFSSSFLNANFAHTASFYGTSAQSR	2840.3	2921.4/3001.4/3080.8	2839.8
T_{30}	324–352	QPTGSYTDNFYGSPSSVHDHLPPSQSVPR	3157.5	3238.7/3318.4/3398.5	3156.9
T_{10}	63–94	ANVPVPGSVTTVTQIYSEEDSSSTAGSSLDDR	3269.5		3268.9

The peptide masses are given as monoisotopic values.

*The masses of phosphopeptides selected with the IMAC-beads before treatment with calf intestinal alkaline phosphatase were measured in the linear mode to avoid metastable decomposition of the phosphopeptides.

†Peptides after treatment with alkaline phosphatase were measured in reflector mode. Peptide numbering starts at the N-terminal methionine of NPR1.