Table S1. Identification of 10 *in vitro* phosphorylation sites of RUPO.

Peptide sequence[a]	Position	Prec MW[b]	ΔMass[c]	Confidence[d]	Score[e]
SGYTFS[Pho]STLGLGR	494 S	1424.6334	-0.0003	99	81
SGYTFSS[Pho]TLGLGR	495 S	1424.6387	0.0049	99	67
IQAAT[Pho]KNFE	512 T	1100.4880	-0.0022	99	33
IDDGT[Pho]KVAVKRGNPQSE	538 T	1892.9008	0.0016	99	71
DGPGMNQLHVS[Pho]TAVK	673 S	1632.7361	0.0029	99	76
DGPGMNQLHVST[Pho]AVK	674 T	1632.7354	0.0022	99	73
TLC[CAM]ARPPIDPQLPREQVS[Pho]LAE	726 S	2469.2075	-0.0009	99	80
LAGT[Pho]VNQESLNK	751 T	1352.6362	0.0025	99	88
LAGTVNQES[Pho]LNK	756 S	1352.6331	-0.0007	99	85
C[CAM]LAEFGS[Pho]DR	773 S	1133.4200	-0.0013	99	43

[a]The amino acid sequence of phosphorylated peptides, where Ser/Thr phosphorylation and carbamidomethyl modification are denoted by [Pho],[CAM] respectively. [b]The experimentally measured monoisotopic mass for the precursor ion fragmented. [c]The difference in mass between the precursor MW and the theoretical MW of the matching peptide sequence. [d]Peptide confidence given by ProteinPilot 4.5. [e]Mascot score. Individual ion score >34 (for trypsin) or score >29 (for Glu-C) means the probability of random match is less than 0.05. In total, the MS/MS data covered > 96.95% amino acid sequence of the intracellular domain, including all Ser/Thr/Tyr residues except for Tyr- 588.