

Supplementary Table S2.

Modified peptides identified from the mass spectrometry analysis of SFPQ from mammalian cells and *in vitro*. Modified amino acids are highlighted in bold. aDMA = asymmetric dimethylarginine, MMA= monomethylarginine. Heavy aDMA = asymmetric dimethylarginine (CD₃), Heavy MMA =monomethylarginine (CD₃).

Peptide	Modification	Position
Mammalian cells		
DRFRSRGGGGGGFHR.R	2 aDMA	7, 9
FRSRGGGGGGFHR	MMA,aDMA	7, 9
FRSRGGGGGGFHR	2 aDMA	7, 9
SRGGGGGGFHR	aDMA	9
RGGGGGRGGLHDFR	2 aDMA	19, 25
GMGPGTPAGYGRGR	MMA	693
GMGPGTPAGYGR	MMA	693
DRFRSRGGGGGGFHR	2 heavy aDMA	7, 9
FRSRGGGGGGFHR	2 heavy aDMA	7, 9
SRGGGGGGFHR	heavy aDMA	9
RGGGGGRGGLHDFR	2 heavy aDMA	19, 25
RGGGGGRGGLHDFRSPPPGMGLNQNR	2 heavy aDMA, MMA	19, 25, 32
GMGPGTPAGYGRGR	heavy MMA	693
PRMT1 in vitro		
SRGGGGGGFHR	MMA	9
SRGGGGGGFHR	aDMA	9
RGGGGGRGGLHDFR	aDMA, MMA	19, 25
GGGGGRGGLHDFR	aDMA	25
PADI4 in vitro		
SRGGGGGGFHR	Citrullination	9
RGGGGGRGGLHDFR	Citrullination	19
RGGGGGRGGLHDFR	2 Citrullination	19, 25
GGGGGRGGLHDFR	Citrullination	25
+PADI4/Ca² mammalian cells		
FRSRGGGGGGFHR	Citrullination, Dimethyl	7, 9
RGGGGGRGGLHDFR	2 Citrullination	19, 25
RGGGGGRGGLHDFR	Citrullination Dimethyl	19, 25,32
REEEMMIR	Citrullination	574
TERFGQGGAGPVGGQGP	Citrullination	666
GMGPGTPAGYGRGREEYEGPNK	2 Citrullination	693,695
GMGPGTPAGYGRGREEYEGPNKKPRF	2 Citrullination ,Methylation	693,695
GMGPGTPAGYGRGREEYEGPNKKPRF.	3 Citrullination Oxidation	693,695, 706
GMGPGTPAGYGRGREEYEGPNKKPRF	Dimethylation, 2 citrullination	693,695, 706
GMGPGTPAGYGRGREEYEGPNKKPRF	Monomethyl, 2 citrullination	693,695, 706