

P018 Identification of constitutive and induced SUMOylation and analysis of its function using the Ubc9 fusion-directed SUMOylation (UFDS) system

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Protein SUMOylation is involved in the regulation of different cellular processes. Its analysis is often hampered due to the low amount of the SUMOylated portion of a specific protein in cells. To circumvent this problem we developed the “Ubc9 fusion-directed SUMOylation” (UFDS) system that allows efficient SUMOylation of a protein at its specific SUMOylation site/s *in vivo*. Using UFDS we have analysed the function of the SUMOylation of STAT1. We discovered that the SUMOylation at lysine 703 inhibits the phosphorylation at tyrosine 701 and most likely inhibits the activation of STAT1. Then we used UFDS to identify new SUMOylation substrates. We found out that 14 of 37 analysed potential nuclear proteins became SUMOylated if they were fused to Ubc9. For eight of these 14 proteins we could subsequently verify SUMOylation of the native proteins in coexpression studies. Three of the eight proteins were constitutively SUMOylated, while the remaining five showed a stimulation dependent SUMOylation. This clearly demonstrates that the UFDS system is appropriate to study the function of SUMOylation and to identify constitutive and induced SUMOylation.