

P015 Structural characterisation of interactions between Ubc9 and the extended sumoylation consensus motif **Zoé Lens^{1,2}, Alexandre Wohlkonig¹, Frédérique Dewitte¹, Magalie Senechal¹, Yvan de Launoit¹, Andrew D. Sharrocks³, Carine Van Lint² and Vincent Villeret¹**

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Post-translational modification of proteins by SUMO has emerged as a central regulatory mechanism of protein function. Sumoylation has been linked to pathways as diverse as cell-cycle regulation, DNA repair and replication, intracellular trafficking and cell signalling. Sumo conjugation occurs in sequential steps analogous to ubiquitination requiring activities of ubiquitin-activating (E1) and -conjugating (E2) enzymes and could be assisted by a ligase (E3). This results in the covalent attachment of the 97 amino acid SUMO peptide to lysine residues within targeted proteins.

Ubiquitin-conjugating enzyme 9 (Ubc9) is known to have a key role in regulating sumoylation by directly recognizing the core consensus ψ KxE on substrates. Ubc9 presents a basic patch important for substrate binding and sumoylation. This patch was proposed to interact with a negatively charged amino acid-dependant sumoylation motif (NDSM) located downstream of the core motif. These two regions form an extended consensus motif. We plan to characterise the interactions of the conjugating enzyme Ubc9 with this extended consensus through crystallographic approaches. This study will give us insights on the molecular mechanisms governing target recognition by Ubc9.