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## Sumoylation and cell signaling

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1  
2  
3 Review

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5 **SUMOylation and cell signalling**

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23 **Keywords:** Post-translational modification / Signalling pathways / Stress /  
24  
25 SUMOylation

26  
27 **Abbreviations:** **DRP-1**, dynamin-related protein 1; **HSF1**, heat shock factor 1;

28  
29 **MAPL**, mitochondrial-anchored protein ligase; **PIAS**, protein inhibitors of activated  
30  
31 STAT; **PML**, promyelocytic leukaemia protein; **pRB**, retinoblastoma protein;

32  
33 **SENP**, sentrin-specific protease; **shRNA**, short hairpin RNA; **SUMO**, small ubiquitin-  
34  
35 related modifier; **Ubc9**, ubiquitin-like protein SUMO-1-conjugating enzyme 9

36  
37 SUMOylation is a highly transient post-translational protein modification. Attachment  
38  
39 of SUMO to target proteins occurs via a number of specific activating and ligating  
40  
41 enzymes that form the SUMO-substrate complex, and other SUMO-specific  
42  
43 proteases that cleave the covalent bond, thus leaving both SUMO and target protein  
44  
45 free for the next round of modification. SUMO modification has major effects on  
46  
47 numerous aspects of substrate function, including subcellular localisation, regulation  
48  
49 of their target genes, and interactions with other molecules. The modified SUMO-  
50  
51 protein complex is a very transient state, and it thus facilitates rapid response and  
52  
53 actions by the cell, when needed. Like phosphorylation, acetylation and  
54  
55 ubiquitination, SUMOylation has been associated with a number of cellular  
56  
57 processes. In addition to its nuclear role, important sides of mitochondrial activity,  
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2  
3 stress response signalling and the decision of cells to undergo senescence or  
4  
5 apoptosis, have now been shown to involve the SUMO pathway. With ever  
6  
7 increasing numbers of reports linking SUMO to human disease, like  
8  
9 neurodegeneration and cancer metastasis, it is highly likely that novel and equally  
10  
11 important functions of components of the SUMOylation process in cell signalling  
12  
13 pathways will be elucidated in the near future.  
14  
15  
16  
17

## 18 **1 Introduction**

22  
23 Transient post-translational modifications like acetylation, phosphorylation and  
24  
25 ubiquitination are a fast and very efficient way for the cell to respond to intra- and  
26  
27 extracellular stimuli, and are thus favoured in cell signalling cascades. A more  
28  
29 recently identified transient protein modification is the attachment of a SUMO  
30  
31 peptide, the process of which is often referred to as SUMOylation. This has also  
32  
33 been shown to occur in signalling pathways, initially within the nucleus and, more  
34  
35 recently, also in other parts of the cell. SUMO attachment has been implicated in a  
36  
37 number of cell processes, such as transcription, nuclear transport, DNA repair,  
38  
39 mitochondrial activity, plasma membrane ion channels, cell cycle and chromatin  
40  
41 structure. Although its function is as diverse as its substrates, one generalisation  
42  
43 could be that modification of a protein substrate by SUMO alters its interactions with  
44  
45 other protein and DNA molecules. At any given time, only a very small amount of  
46  
47 substrate is modified, usually around 1%. This may be one reason why SUMO and  
48  
49 the modified forms of substrate proteins were only discovered recently. Since its  
50  
51 identification, however, a great many proteins that are modified by SUMO species  
52  
53 and an equally great number of pathways in which SUMO partakes are now being  
54  
55 revealed, and the various effects of the modification are beginning to be elucidated.  
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## 2 The SUMO modification pathway

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5 Originally reported just over a decade ago as a protein related to Ubiquitin, the small  
6 ubiquitin-related modifier (SUMO) has been since shown to be present in all  
7 metazoans and take part in a number of diverse cellular functions, the number of  
8 which is still extending [1]. Although SUMO only shares 18% of overall sequence  
9 identity with ubiquitin, the general structure fold is conserved, where the C terminus  
10 of SUMO is almost super-imposable on the equivalent region of ubiquitin [2, 3].

11 SUMO proteins have a distinct overall surface charge distribution compared to  
12 ubiquitin, and the function of SUMO modification is completely different, and  
13 sometimes counteractive to the ubiquitin pathway. SUMO can occupy available  
14 lysine residues and inhibit ubiquitin attachment, thus protecting proteins from  
15 breakdown, or it can promote proteasome-mediated degradation, possibly by  
16 recruiting and/or regulating enzymes that control degradation.

17  
18 The SUMO protein sequence is around 100 amino acids, with a molecular mass of  
19 ~11 kDa; it is highly conserved in all eukaryotic cells, and is present in all tissues  
20 and developmental stages of higher organisms. It has been shown to be essential  
21 for cell viability both at the organism level and in cells in culture [4]. Different  
22 organisms contain different numbers of SUMO species, with a single SUMO present  
23 in yeast (*Smt3p*) [5], *Drosophila* (*SMT3*) [6], and *Caenorhabditis elegans* (*smo-1*)  
24 [7], and four SUMO peptides in mammals, termed SUMO-1, SUMO-2, SUMO-3 and  
25 SUMO-4 [8–11]. SUMO-4 is the most recently identified gene and has an 86%  
26 similarity to SUMO-2. Its mRNA transcripts are mainly present in kidney, lymph  
27 system and spleen, but show limited expression compared to the other SUMO  
28 species [8]. Since no native SUMO-4 protein has yet been detected in any tissue, it  
29 has been suggested that SUMO-4 might be an expressed pseudogene [12]. In  
30 addition, a proline in a position at its C terminus instead of a glutamine results in  
31 resistance of SUMO-4 to hydrolysis by SUMO-specific proteases and it can thus not  
32 be processed to a mature form capable for conjugation [13]. SUMO-1 shares 50%

1  
2  
3 sequence identity with SUMO-2 and -3, while SUMO-2/3 share a 95% identity. Also,  
4  
5 SUMO-2/3 possess consensus SUMOylation sites at their N-terminal tails that allow  
6  
7 formation of poly-SUMO chains, in contrast to SUMO-1, where these sites are  
8  
9 absent, along with the capacity for chain formation [14]. The differences between  
10  
11 the isoforms also translate to functional activity, as the function of SUMO-2/3 is  
12  
13 almost indistinct, whereas SUMO-1 has a dissimilar function. In the case of intrinsic  
14  
15 transcriptional repression ability, for example, SUMO-2 and -3 show stronger  
16  
17 inhibitory activity compared to SUMO-1, the activity of which appears weaker [15,  
18  
19 16]. Furthermore, while there are pools of free SUMO-2/3 available within cells,  
20  
21 SUMO-1 is rarely found unattached [17]. Certain proteins show a preference in  
22  
23 conjugation to either SUMO-1 or SUMO-2/3, but others can be modified equally well  
24  
25 by both SUMO species.  
26  
27

28 Attachment of SUMO to target proteins takes place using a similar mechanism to  
29  
30 ubiquitin attachment, where the enzymes that catalyse SUMO complex formation  
31  
32 are analogous to the ubiquitin pathway. SUMO modification enzymes are specific  
33  
34 for this peptide and not interchangeable with the equivalent for ubiquitination.  
35  
36 SUMOylation occurs via the formation of an isopeptide bond between the glycine  
37  
38 residue at the C-terminal end of SUMO to the  $\epsilon$ -amino group of an internal lysine  
39  
40 residue within the substrate [18]. The SUMO peptide is initially translated as a  
41  
42 precursor, with a short sequence extending past a conserved GG motif that defines  
43  
44 the carboxyl end of the mature protein. Proteolytic cleavage of this sequence  
45  
46 converts SUMO to its mature form. SUMO-specific peptidases, for example  
47  
48 members of the sentrin-specific protease (SENPs) family, catalyse this step. SUMO-  
49  
50 activating enzymes, also called E1, activate the mature SUMO in an ATP-  
51  
52 dependent reaction. Active SUMO is then transferred onto the E2 SUMO-  
53  
54 conjugating enzyme Ubc9 [19–21]. Conjugation of SUMO to target proteins occurs  
55  
56 through Ubc9 with the aid of an E3 ligase [22, 23] (Fig. 1). Substrate specificity for  
57  
58 SUMO is conferred by both Ubc9 and various E3 ligases, the former by forming the  
59  
60

1  
2  
3 covalent attachment of SUMO to its targets, while the latter probably interacts with  
4  
5 other areas of the substrate and provides more specificity [24].  
6

7 ((Fig. 1))  
8

9  
10 SUMO attachment is a reversible and highly transient modification. The same  
11  
12 enzymes that facilitate the initial maturation of SUMO molecules also catalyse the  
13  
14 cleavage from their substrates. Six human SENP family proteins, SENPs 1–3 and  
15  
16 5–7 have been shown to be SUMO-specific proteases [25]. Unlike the enzymes  
17  
18 catalysing SUMO attachment, SUMO proteases show little similarity to the  
19  
20 equivalent enzymes in the ubiquitin pathway, but appear closely related to viral  
21  
22 proteases [26]. The differential subcellular localisation of the SENP proteins, most  
23  
24 likely dictated by non-conserved N-terminal sequences, is thought to provide the  
25  
26 specificity for the SUMO-substrate complexes they regulate [27, 28]. SENP1 is  
27  
28 localised mainly in the nucleus with little, albeit persistent, cytoplasmic presence [29,  
29  
30 30]; SENP2 is associated with the nuclear pore [31]; SENP3 and SENP5 are  
31  
32 nucleolar [32], while separate reports place SENP6 in both the nucleoplasm and the  
33  
34 cytosol [33, 34]. Although the SUMO isoforms and the SUMOylation target proteins  
35  
36 described so far are predominantly nuclear, increasing numbers of enzymes of the  
37  
38 SUMO conjugation pathway as well as SUMO-target complexes are being identified  
39  
40 in other parts of the cell, like the cytosol, the plasma membrane and the  
41  
42 mitochondria [35–37]. Specificity in SUMO complex targeting may be achieved  
43  
44 through the subcellular location of each protease [38].  
45  
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47

48  
49 A short amino acid sequence motif within the target protein frequently serves as a  
50  
51 recognition site for SUMO attachment. This recognition site is conserved and  
52  
53 presents the consensus sequence  $\psi$ KXE/D [39, 40], where  $\psi$  is a large hydrophobic  
54  
55 amino acid, like leucine, isoleucine or valine; K is the lysine residue at which the  
56  
57 attachment takes place, and X is any amino acid followed by a glutamic (E) or  
58  
59 aspartic (D) acid. At the same time this sequence was identified as the SUMOylation  
60  
consensus, independent studies pinpointed it as a SUMOylation-dependent

1  
2  
3 transcriptional inhibitory motif in transcription factors [41, 42]. A number of  
4  
5 alternative SUMO modification sequences have also been described, in which for  
6  
7 example the amino acid before the lysine can be a different one from the three  
8  
9 consensus residues. Furthermore, SUMOylated proteins have been described that  
10  
11 either do not contain the consensus site, use a different motif for SUMO conjugation  
12  
13 [16], or maintain SUMOylation after the recognition site has been mutated. More  
14  
15 extensive SUMO conjugation motifs have also been described; it has been  
16  
17 suggested that acidic residues downstream of the core SUMOylation motif have a  
18  
19 role in enhancing specificity for substrates [43]. SUMO attachment sites are often  
20  
21 found in the vicinity of activation or repression domains of target proteins, as for  
22  
23 example in Msx1 [44].  
24  
25

26  
27 SUMOylation alters the relations of the modified target with other macromolecules,  
28  
29 through providing novel interaction surfaces. Thus, besides the sites for SUMO  
30  
31 conjugation, other sequences have been identified that mediate interactions  
32  
33 between SUMOylated complexes and their protein partners. A conserved SUMO-  
34  
35 interacting motif (SIM) has been found on proteins that associate with SUMO-  
36  
37 conjugated moieties, including the promyelocytic leukaemia protein (PML) and  
38  
39 members of the protein inhibitors of activated STAT (PIAS) family [16, 45]. Mutation  
40  
41 of these sites abolishes their interaction with the SUMO-target complex. In addition,  
42  
43 the surface of SUMO that the SIM of interacting proteins binds is an essential region  
44  
45 required for transcriptional repression when SUMO is recruited to promoter regions  
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47 [15, 46].  
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### 53 **3 Links with phosphorylation/acetylation/ubiquitination**

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58 Other post-translational protein modifications have been associated with the SUMO  
59  
60 pathway. The availability of certain proteins for SUMOylation has been shown to be  
dependent on their phosphorylation status, like for example GATA-1 (GATA-binding



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2  
3 protein 1, globin transcription factor 1), myocyte-specific enhancer factor 2A  
4  
5 (MEF2A), Smad nuclear interacting protein 1 (SNIP-1), and heat shock factors  
6  
7 HSF1 and HSF4b. The HSF1 factor, which is deficient in its phosphorylation  
8  
9 capacity, cannot become modified by SUMO, as this protein needs to undergo a  
10  
11 conformational change, mediated by phosphorylation of a serine residue, to allow  
12  
13 SUMO attachment [47]. Moreover, the phosphorylation of these heat shock factors  
14  
15 is heat inducible and may be directly associated with the inducible SUMOylation of  
16  
17 HSF1 [48]. A phosphorylation-dependent SUMOylation motif (PDSM), which greatly  
18  
19 resembles an extended consensus SUMO attachment site,  $\psi$ KxExxSP, has been  
20  
21 described for such proteins [49]. Furthermore, histone deacetylases, including  
22  
23 HDAC2 and HDAC6, have been shown to preferentially interact with SUMO-  
24  
25 modified substrates [50, 51]. It has been suggested that deacetylation of histones by  
26  
27 HDAC enzymes may make more lysine residues available for SUMOylation [52]. A  
28  
29 SUMOylation switch based on acetylation/deacetylation has been described in the  
30  
31 p53-HIC1-SIRT1 regulatory loop [53]. Hypermethylated in cancer 1 (HIC1), a protein  
32  
33 involved in the p53 tumour suppression pathway, has been shown to be both  
34  
35 SUMOylated and acetylated, possibly on the same lysine residue, as lysine mutants  
36  
37 that are SUMOylation deficient show much lower levels of acetylation compared to  
38  
39 the wild-type protein. Deacetylases with roles in the p53 pathway, sirtuin 1 (SIRT1),  
40  
41 a NAD-dependent deacetylase, and HDAC4, appear to promote deacetylation and  
42  
43 SUMOylation, respectively [53]. Increased SUMOylation of H4 correlates with  
44  
45 decreased acetylation of the gene when Ubc9 is targeted to the promoter region  
46  
47 [54]. An association between SUMOylation and the ubiquitin pathway is perhaps not  
48  
49 surprising due to the close relation between the two proteins. SUMO-1  
50  
51 overexpression results in reduced levels of p63 [55]. Since mutating the SUMO  
52  
53 acceptor sites of p63 appears not to have any effect on protein levels, this down-  
54  
55 regulation of the protein is not dependent on its own SUMOylation state and is more  
56  
57 likely to result from changes in the SUMOylation of other regulatory proteins [56]. In  
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3 the case of Smad4, when its SUMO attachment sites are mutated, the lysine mutant  
4 displays increased stability compared to wild-type protein due to reduced poly-  
5 ubiquitination [57]. Because SUMO peptides can use the same lysine residues as  
6 ubiquitin, SUMOylation of a substrate protein may lead to protection from  
7 degradation through the ubiquitin pathway. However, at the same time, if these sites  
8 are disrupted, ubiquitin attachment may also be hindered, and thus lead to  
9 increased stability. This effect is different to impaired SUMOylation due to increased  
10 activity of SENPs, where the lysine residues of the SUMO sites are still intact and  
11 available for interaction with ubiquitin. One of the rare cases where SUMOylation  
12 promotes protein catabolism involves the promyelocytic leukaemia gene product  
13 (PML) that concentrates in nuclear bodies, and the product of its fusion to the  
14 retinoic acid receptor  $\alpha$  (PML-RAR $\alpha$ ) that occurs after a chromosomal translocation  
15 in patients with acute promyelocytic leukaemia [58–61]. Induction of SUMO  
16 modification of PML and PML-RAR $\alpha$  upon arsenic treatment recruits a ubiquitin E3  
17 ligase (ring finger protein 4, RNF4) onto the nuclear bodies, where these proteins  
18 reside. RNF4, a small nuclear protein, contains a number of SUMO-interacting  
19 motifs in its sequence and preferentially interacts with PML and PML-RAR $\alpha$  proteins  
20 modified by poly-SUMO-2 chains. Along with RNF4, SUMO isoforms, ubiquitin, the  
21 20S proteasome and specific transcription factors are also recruited to PML nuclear  
22 bodies, and PML and PML-RAR $\alpha$  are degraded through SUMOylation-dependent  
23 ubiquitination [62, 63].  
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#### 51 **4 Involvement of SUMO in different cellular pathways**

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55 SUMO modification has been frequently associated with transcriptional regulation,  
56 mainly through promoting transcriptional repression, but also in some cases aiding  
57 activation, depending on the specific substrate and biochemical pathway [64]. In  
58 fact, the majority of SUMOylation targets reported to date have been sequence-  
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3 specific transcription factors and the essential role of the SUMO pathway has been  
4  
5 conclusively supported in all aspects of transcription regulation, from promoter  
6  
7 binding to recruitment of co-factors [18, 52, 65]. Nevertheless, it would be fair to say  
8  
9 that the function of SUMOylation extends a lot further than transcription control and  
10  
11 covers a great variety of cellular processes, including genome integrity, DNA repair,  
12  
13 protein trafficking, activity of voltage-gated ion channels and protein stability [4, 37].  
14  
15 In addition, since this review appears in this special issue of the Biotechnology  
16  
17 Journal, it seems important to mention the applications that SUMO has had in the  
18  
19 field of Biotechnology. N-terminal fusion of proteins, even ones that are difficult to  
20  
21 express, to native and truncated forms of SUMO results in greatly increased  
22  
23 expression levels and improved solubility, both in bacterial [66–69] and eukaryotic  
24  
25 expression systems [70–72]. The SUMO part of the fusion protein can be retained  
26  
27 and removed at will, through the use of appropriate SUMO proteases, thus making it  
28  
29 possible to closely regulate the activity of enzymes or toxic proteins.  
30  
31  
32  
33 Most recently, important roles for the SUMO pathway have been elucidated in areas  
34  
35 that may provide stronger links between SUMOylation and the process of aging,  
36  
37 including the activity of the mitochondria, the major tumour suppressor pathways  
38  
39 and signalling pathways leading to senescence. Further support to the significance  
40  
41 of this modification for maintaining normal cell and tissue homeostasis is provided  
42  
43 by the fact that defects in components of the SUMOylation pathway, either  
44  
45 individually or synergistically, have been linked to an increasing number of disease  
46  
47 phenotypes in humans [73–79]. Below, we present these areas in more detail.  
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### 53 **5 SUMO and mitochondrial activity**

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57 Mitochondria have been traditionally called the powerhouses of the cell as they  
58  
59 provide most of the energy (in the form of ATP) needed for cell metabolism. The  
60  
morphology of the mitochondria is crucial to their normal function and mutations that

1  
2  
3 affect the shape of these organelles have been linked to problematic cell  
4  
5 homeostasis and neurodegenerative conditions [80]. Normal mitochondrial  
6  
7 morphology is maintained through a balance between the processes of fusion and  
8  
9 fission, and these processes are essential for the maintenance of healthy cell  
10  
11 metabolism and homeostasis. Mitochondrial fusion forms a network of  
12  
13 interconnected organelles that maintains mitochondrial DNA and facilitates transfer  
14  
15 of electron potential between different areas of the cell [81]. Mitochondrial fission  
16  
17 ensures equal division of material between daughter cells after mitosis and provides  
18  
19 the cell with extra energy under specific circumstances, as for example during  
20  
21 spermatogenesis in *Drosophila* [82] and during the early stages of apoptosis [83].  
22  
23 The idea that mitochondrial activity and the regulation of the equilibrium between  
24  
25 fission and fusion in response to signalling cascades is maintained by dynamic post-  
26  
27 translational modifications has been positively regarded for a while, as transient  
28  
29 protein modifications present perhaps the easiest way to control systems that go  
30  
31 through rapidly changing states.  
32  
33  
34  
35 The first line of evidence that SUMOylation is involved in mitochondrial function  
36  
37 came 5 years ago, when mitochondrial dynamin-related protein 1 (DRP-1) was  
38  
39 reported to interact in a yeast two-hybrid screen with Ubc9 and SUMO-1 [84]. DRP-  
40  
41 1 is a large dynamin-like GTPase that is transported from the cytosol to the  
42  
43 mitochondrial membrane during the process of mitochondrial fission and functions to  
44  
45 facilitate the fragmentation of the mitochondria. Fluorescence immunostaining  
46  
47 experiments showed SUMO-1 signals to co-localise with DRP-1 at the site of  
48  
49 mitochondrial fission, while overexpression of SUMO-1 protects DRP-1 from  
50  
51 degradation (as does the presence of *N*-ethylmaleimide, a SUMO-1 hydrolase  
52  
53 inhibitor) and induces fragmentation of mitochondria, as shown by the specific  
54  
55 organelle morphology [84]. More recent studies have conclusively demonstrated the  
56  
57 modification of DRP-1 by SUMO-1 and identified the site of interaction at specific  
58  
59 residues [85]. Furthermore, high numbers of SUMO-1-conjugated proteins were  
60

1  
2  
3 identified in the mitochondrial part after cell fractionation, thereby suggesting that  
4  
5 SUMOylation is important in various aspects of mitochondrial activity.

6  
7  
8 In more recent years, the specific enzymes that catalyse the SUMO conjugation/ de-  
9  
10 conjugation cycle of DRP-1 have been identified. SENP5 has been shown to be  
11  
12 able to hydrolyse the SUMO-1/DRP-1 conjugate [86], while the mitochondrial-  
13  
14 anchored protein ligase (MAPL) has been identified as the complex-specific E3  
15  
16 ligase [35]. SENP5 has been shown to be essential for normal mitochondrial  
17  
18 morphology and function, as both overexpression and silencing of this protease  
19  
20 have profound mitochondrial phenotypes. Overexpression of SENP5 rescues the  
21  
22 mitochondrial fragmentation caused by SUMO-1 up-regulation, while blocking of  
23  
24 SENP5 by short hairpin RNA (shRNA) results in extensive mitochondrial  
25  
26 fragmentation and much lower rates of mitochondrial fusion compared to control  
27  
28 cells. In addition to problematic mitochondrial morphology, shRNA-SENP5 cells  
29  
30 show a significant rise in the production of reactive oxygen species (ROS), and it  
31  
32 has been suggested that this high concentration of free radicals may actually be the  
33  
34 cause of the decrease of mitochondrial fusion in these cells [86]. When DRP-1 is  
35  
36 down-regulated in these cells, ROS production returns to normal levels,  
37  
38 fragmentation is hindered and mitochondria appear fused into a network. Besides  
39  
40 DRP-1 regulation, SENP5 showed a broader specificity for a number of  
41  
42 mitochondrial SUMO-conjugated proteins, further supporting its importance in  
43  
44 mitochondrial function. The protective role of SENP5 in mitochondrial morphology  
45  
46 and metabolic status is specific, as another member of the SUMO protease family,  
47  
48 SENP2, has no effect on mitochondria morphology or substrates [86].  
49  
50  
51  
52  
53 MAPL has been identified as a protein ligase that contains a RING domain, is  
54  
55 anchored to the mitochondrial outer membrane and has a role in mitochondrial  
56  
57 fragmentation [87]. Recently, it has been shown that MAPL is a SUMO-specific E3  
58  
59 ligase and the first mitochondrial one [35]. Experiments with synthetic peptides as  
60  
well as native mitochondrial SUMO targets support this role. Down-regulation of

1  
2  
3 MAPL via shRNA leads to a significant decrease in SUMOylation, while there is  
4  
5 almost no effect on the ubiquitination state of the cells, unless enzyme  
6  
7 concentrations reached very high levels that are believed not to be biologically  
8  
9 relevant. Therefore, MAPL specifically and preferentially catalyses SUMO  
10  
11 conjugation and is not a ubiquitin ligase [35]. Furthermore, shRNA against MAPL  
12  
13 hinders global cell SUMOylation, but the mitochondrial fraction of the cells is the  
14  
15 mostly affected compared to the nuclear and cytosolic parts, suggesting that many  
16  
17 of the SUMO target proteins that MAPL specifically modifies may be present in  
18  
19 mitochondria. More data on the specific SUMOylated proteins that are affected by  
20  
21 such global down-regulation of the SUMO pathway through MAPL are needed to  
22  
23 further elucidate the function of SUMOylation in the mitochondria.  
24  
25  
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28

## 29 **6 SUMO and environmental stress**

30  
31  
32  
33 SUMO modification has been shown to be susceptible to environmental effects,  
34  
35 especially different types of cellular stress [88]. Such factors include oxidative  
36  
37 stress, osmotic stress, heat shock, exposure to ethanol and viral infection [17, 89–  
38  
39 92].  
40

41  
42 Initially SUMO-2 and -3 were mainly associated with cellular responses to stress,  
43  
44 with reports that showed altered substrate interactions after stress signals [93, 94]  
45  
46 and very recent experiments showing that they are essential for cell survival after  
47  
48 heat shock [95]. SUMO-1 has now also been demonstrated to play a role in stress  
49  
50 response as its expression increases during hypoxia [96]. Exposure of cells to  
51  
52 oxidative stress led to modification of the targeting patterns of the SUMO peptides,  
53  
54 which were de-conjugated from original complexes and re-distributed to new  
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56 substrates, including anti-oxidant proteins and proteins involved in signalling during  
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58 DNA damage. Reports on the response of the SUMO pathway to oxidative stress  
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60 have been contradictory, with some suggesting stress results in an increase in

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3 SUMO modification of target proteins, while others demonstrate a disappearance of  
4 SUMO-conjugated species under similar conditions [94, 97]. Experimental design  
5 may play a role in these results, but since SUMOylation has been associated with a  
6 variety of diverse cellular functions, it may also be that different mechanisms of  
7 conjugation and de-conjugation are in place for different signalling and transcription  
8 regulation pathways. For example, inducing oxidative stress by treating cells with  
9 hydrogen peroxide resulted in increased levels of SUMO-2/3-modified p53, while  
10 levels of p53/SUMO-1 conjugates appeared unaffected [98]. The observation that  
11 substrate proteins are not all affected at the same time or with the same speed may  
12 support this theory [88]. Mimicking oxidative stress conditions in cell-based assays  
13 with low, and thus perhaps more physiologically relevant, concentrations of reactive  
14 oxidative species inhibits the activity of SUMO-conjugating enzymes. This leads to a  
15 general decrease in SUMOylation of substrate proteins, including essential  
16 transcription factors [88]. This effect was shown to be specific to the SUMO  
17 modification process, since the ubiquitin pathway was not affected. Such stress can  
18 occur *in vivo* after exposure to UV, ionising radiation, chemotherapeutic agents and  
19 hyperthermia [99]. Cellular responses to elevated temperature have also been  
20 linked to SUMOylation through the modification by SUMO of HSF1, as mentioned  
21 before [47].

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44 Another likely influence on the SUMO process is viral infection [100, 101]. Gam-1, a  
45 viral protein from an avian adenovirus, can target E1 and E2 SUMO ligases for  
46 degradation and thus inhibits cellular levels of SUMO modification [100]. Down-  
47 regulation and loss of SUMOylated substrates leads to an up-regulation of cellular  
48 transcription and is thought to enhance viral replication. This association is made  
49 perhaps more interesting by the fact that, as mentioned earlier, the SUMO-specific  
50 hydrolases are much more closely related to viral proteases than to the  
51 corresponding enzymes in the ubiquitin pathway [102].  
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## 7 SUMO in cellular senescence and ageing

A number of senescence-associated proteins have been identified as targets for SUMO attachment and, more recently, SUMO peptides and enzymes that participate in the SUMO pathway have been linked with the process of senescence. The SUMO isoforms, a SUMO-specific E3 ligase and a SUMO hydrolase have been shown to have either positive or negative effects on the induction of cellular senescence (Fig. 2). In addition, elevated numbers of SUMOylated proteins have been shown to accumulate in senescent cells compared to normal replicating cells [103], while levels of SUMO isoforms and associated enzymes appear to decrease with age in a different tissue type [104].

((Fig. 2))

The different substrate specificity frequently observed for SUMO-1 and SUMO-2/3 species means they can take part in different cascades within the cell, even within the same greater pathway. Overexpression of SUMO-2/3 in cultured cells has been shown to induce premature senescence, observed by slow cell growth and early growth arrest of these cells [98], while SUMO-1 up-regulation does not appear to affect the process of cellular senescence [105]. This is perhaps not surprising, considering that SUMO-2/3 is thought to be the isoform(s) mainly and most frequently associated with the response to stress. However, it is interesting that under normal conditions SUMO-1 appears mainly conjugated to target proteins within the cells, while unconjugated pools of SUMO-2/3 species are abundant and available to be used as required.

When cells experience some form of stress, the p21/p53 and p16/retinoblastoma protein (pRB) response pathways are usually activated [106, 107]. Various genes that have been associated with the induction of senescence have been shown to be part of either the p53 or pRB pathways [108]. The major proteins in these signalling cascades, p53 and pRB, greatly influence the cell's response to the stress factor(s),



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3 *i.e.* if a cell will enter senescence or undergo apoptosis, as both mechanisms are  
4 used to manage unsolicited cell growth [109]. p53 and pRB can inhibit unsolicited  
5 cell growth through pathways regulated by post-translational modifications, including  
6 phosphorylation, acetylation, ubiquitination and SUMOylation, as both proteins are  
7 substrates for SUMO-1 and SUMO-2/3 modification [110–113]. SUMO-1 attachment  
8 promotes gene transactivation by p53, as shown by up-regulation of p21  
9 expression, a p53 target gene [98]. Moreover, components of the SUMO pathway  
10 control pRB repression of E2F-regulated target genes [114]. pRB is normally de-  
11 SUMOylated by E1A, a viral oncoprotein [111]; it has been suggested that this may  
12 be a strategy used by viruses to suppress cell senescence. Overexpression of  
13 SUMO-2/3 surpasses this de-SUMOylation, leaving pRB-SUMO-2/3 conjugates free  
14 to stimulate senescence [98].

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29 RNA interference on p53 and pRB cancels the senescence phenotype of SUMO-  
30 2/3-overexpressing cells, thus supporting the idea that the effect of SUMO-2/3  
31 modification on senescence occurs via p53- and pRB-mediated pathways [98]. p53-  
32 induced up-regulation of p21 is a known pathway for activation of senescence [115].  
33 During SUMO-2/3 overexpression, the transcriptional activity of p53 is significantly  
34 enhanced and p21 is clearly up-regulated; however, the levels of p53 protein remain  
35 unchanged. Since p21 is under the transcriptional control of p53, this increase in  
36 p21 protein levels may be due to the altered SUMOylation state of p53, modified by  
37 SUMO-2/3 [98].

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49 During replicative senescence the levels of endogenous PIASy, a member of the  
50 PIAS protein family of SUMO E3 ligases [116], are significantly increased compared  
51 to presenescent cells, as are levels of hyper-sumoylated proteins [114]. No other  
52 member of the PIAS protein family appears to have similar activity. High levels of  
53 PIASy can result in either cellular senescence or apoptosis, depending on the state  
54 of p53 and pRB within the cell. The E3 ligase activity of PIASy is essential for  
55 senescence stimulation and mutation of the ligase active site on the protein  
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3 abolishes the effect. The E6 oncoprotein inhibits the SUMO ligase activity of PIASy  
4 and blocks induction of senescence [114]. Interestingly, an extended lifespan is  
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6 observed in cells that overexpress mutant forms of PIASy with an inactive E3 ligase  
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8 site. Mouse embryo fibroblasts that are deficient in PIASy show a significant delay in  
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10 the onset of senescence after appropriate signalling. Even after induction of p53  
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12 expression by a pro-senescence signal, for example through oncogenic RAS, p53-  
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14 target genes p21 and murine double minute 2 (MDM2) are not up-regulated in the  
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16 absence of PIASy. In parallel, PIASy can induce p53-dependent apoptosis during  
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18 pRB deficiency; inactivation of pRB by hyper-phosphorylation is not enough to give  
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20 similar results and the effect of PIASy is not there when pRB is present, even in an  
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22 (as far as we know) inactive state [114]. The different cellular responses to PIASy,  
23  
24 depending on the pRB status, suggest a possible role for PIASy as one of the  
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26 factors influencing the cell's decision to undergo senescence or apoptosis. It might  
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28 be that PIASy is involved in altering the binding affinity between pRB and its co-  
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30 factors, through pRB SUMOylation. It has been suggested that hypophosphorylated  
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32 pRB enlists its co-repressors together with components of the SUMO pathway to the  
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34 site of genes promoting proliferation. A number of these co-factors could be  
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36 themselves targets of SUMOylation and these interactions could stabilise the pRB  
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38 repressor complex. Also, as it has been shown that SUMO attachment increases  
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40 affinity between protein partners [117], the presence of SUMO-modified pRB  
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42 repressor group on DNA could provide a high affinity site for the recruitment of  
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44 proteins involved in chromatin remodelling and reorganisation [103]. This process  
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46 could ultimately lead to the silencing of genes involved, also facilitated by the activity  
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48 of histones, which are substrates for SUMOylation and have major roles in  
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50 transcriptional repression in their modified state [54, 118].  
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52 Senescence may also be induced by down-regulation of a number of SUMO  
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54 proteases of the SENP family. SUMO proteases may thus be required for the  
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56 proliferation of normal human cells and have important roles in age-related  
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3 phenotypes. After many cell passages, when human fibroblasts undergo replicative  
4 senescence, SUMO-containing PML bodies accumulate in the nucleus; this effect is  
5 also seen when SUMO proteases Senp1, Senp2 and Senp7 are repressed.  
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9 Particularly Senp1 deficiency triggers premature senescence through the p53  
10 signalling pathway [119], as the p53 pathway needs to be intact for the full result of  
11 Senp down-regulation to be exerted. It is thus very likely that Senp1 has a role in  
12 maintaining the balance in the cell after exposure to stress and perhaps preventing  
13 premature senescence.  
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## 20 21 22 **8 SUMO in human disease**

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27 Disturbance of the SUMO modification pathway has recently been associated with a  
28 number of disease phenotypes in humans. Induction of SUMOylation has been  
29 shown for cerebral ischaemia and it has been suggested that this process may have  
30 a role in defining the outcome of neurons exposed to such conditions [120]. Other  
31 neurodegenerative diseases have been implicated in the SUMO pathway, including  
32 multiple system atrophy and Huntington's disease (HD), where SUMO peptides  
33 have been shown to localise within the protein aggregates characteristic for these  
34 conditions. In HD, SUMO modification of mutant huntingtin, which contains  
35 polyglutamine repeats, significantly inhibits its aggregation and promotes cell death  
36 [121]. This process is facilitated by Rhes (Ras homologue enriched in striatum), a  
37 small guanine-binding protein that shows E3 ligase activity and greatly enhances  
38 SUMOylation of mutant huntingtin and other proteins [121, 122]. Kennedy disease,  
39 or spinal and bulbar muscular atrophy, is also characterised by a polyglutamine  
40 expansion in the N terminus of the androgen receptor. Recent experiments have  
41 shown that SUMOylation hinders aggregation of these mutated protein forms, in a  
42 mechanism that is independent on androgen receptor transcription regulation [123].  
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The Parkin protein also appears to have a role in regulating the turnover of an E3

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3 SUMO ligase [124]. These findings strongly suggest that the SUMO pathway may  
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5 have a protective role against neurodegeneration. Furthermore, compromised  
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7 SUMOylation has been linked to some cancers, through regulation by SUMO of  
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9 nuclear receptor-mediated gene expression, for example the androgen and  
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11 estrogen receptors with roles in prostate and breast cancer, respectively [42, 125].  
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13 The regulation of a number of other genes with roles in cancer development has  
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15 been linked to SUMOylation [78], and a role for SUMO modification in cancer  
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17 metastasis has been suggested through association of the SUMO pathway with the  
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19 regulation of transcription of *KAI1*, a metastasis suppressor gene [126, 127].  
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21 Naturally occurring mutations in a number of genes have been associated with  
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23 defects in SUMOylation of the mutant proteins, like for example missense mutations  
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25 in the T-box transcription factor TBX22, present in patients with X-linked cleft palate  
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27 (CPX) [128], and missense and nonsense mutations in p63 that disrupt the  
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29 SUMOylation site(s) [55]. In the cases where mutation positions tested were distant  
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31 from the SUMO attachment site(s), it may be that conformational changes caused  
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33 by these single substitutions disrupt the availability of the SUMO attachment site or  
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35 cause mechanical problems that disturb the interactions with the SUMO peptide  
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37 and/or the SUMO-conjugating enzymes. Furthermore, other proteins with a direct  
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39 association to craniofacial defects have been shown to be SUMOylated, such as  
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41 MSX1 and special AT-rich sequence binding protein 2 (SATB2) [44, 55, 56, 129],  
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43 and SUMO modification has been shown to be necessary for their normal function.  
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45 In the case of SATB2, SUMO-1 attachment has been shown to directly regulate its  
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47 activation potential and its localisation into the nucleus [129], while mutations in the  
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49 SUMO acceptor sites of p63 result in a significant increase of the transactivation  
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51 potential of the protein and affect the transcription regulation of its target genes,  
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53 although they do not appear to disturb its nuclear localisation [56]. Mutation of  
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55 SUMO attachment sites for both TBX22 and SATB2 compromise their function,  
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60 while several other SUMOylated proteins have been shown to retain their

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3 transcriptional activity when their SUMOylation sites are disrupted, for example  
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5 LEF1, p53, Msx1 and STAT1 [113, 130–132]. In the case of Msx1, interaction of the  
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7 protein with PIAS1, an enzyme that acts as an E3 ligase in the SUMO modification  
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9 pathway, appears to modulate the function of Msx1 as a transcriptional repressor,  
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11 its ability to bind DNA elements in a target promoter sequence and inhibit terminal  
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13 myocyte differentiation, while no significant functional defects are observed with  
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15 mutations in SUMO attachment sites [133]. This supports the theory that SUMO  
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17 modification can affect target protein function through different mechanisms, and  
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19 hints to the fact that certain proteins that are involved in one signalling cascade may  
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21 share the same SUMO regulatory mechanism.  
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## 27 **9 Conclusions**

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31 For most of the SUMO target proteins described so far only a small fraction of the  
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33 total substrate protein present in cells appears to be SUMOylated, and very few  
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35 examples of substrates appear to be modified at a greater percentage; for example  
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37 50% of Ran GTPase-activating protein 1 (RanGAP1) is modified within the cell at  
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39 any given time [134]. The modified substrate may represent the functionally active  
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41 form, at least for a certain part of a biochemical pathway. It has been suggested that  
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43 SUMO modification is a very transient state, where target proteins get modified and  
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45 un-modified perhaps as part of a loop, rather than specific protein molecules staying  
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47 stably modified within a cell. Attachment of SUMO peptides to substrates may  
48  
49 facilitate a specific function (for example interaction with DNA, other proteins and  
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51 co-factors), and specific peptidases de-conjugate the SUMO molecules from  
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53 substrates when this function is complete, effectively freeing them up inside the cell  
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55 for the next round of modification [135]. In addition, it may also be possible that the  
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57 unmodified proteins have a different role within the cells, besides the one conferred  
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59 on them upon SUMOylation. It is becoming increasingly clear that the nature of such  
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3 protein modifications is essential for cells to maintain the balance between various  
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5 activities that need be completed, and be able to respond to internal and external  
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7 stimuli in rapidly and efficiently, when time is limited and of great importance. One  
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9 can also imagine that it must be much faster and more energy-efficient for the cell  
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11 when the same protein can fulfil different roles within one or more signalling  
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13 pathways, be ready for alternate protein-protein interactions and translocate to  
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15 various cell parts, only by going through rounds of such transient “on-off”  
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17 modification.

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20 Elucidating the relationship between environmental factors, the SUMO pathway and  
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22 the networks of proteins that are influenced by this post-transcriptional modification  
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24 may be crucial for our further understanding of the signalling cascades that underlie  
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26 complex cell and tissue states, like metabolism, cell death and ultimately, human  
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28 disease.  
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46 *The authors have declared no conflict of interest.*  
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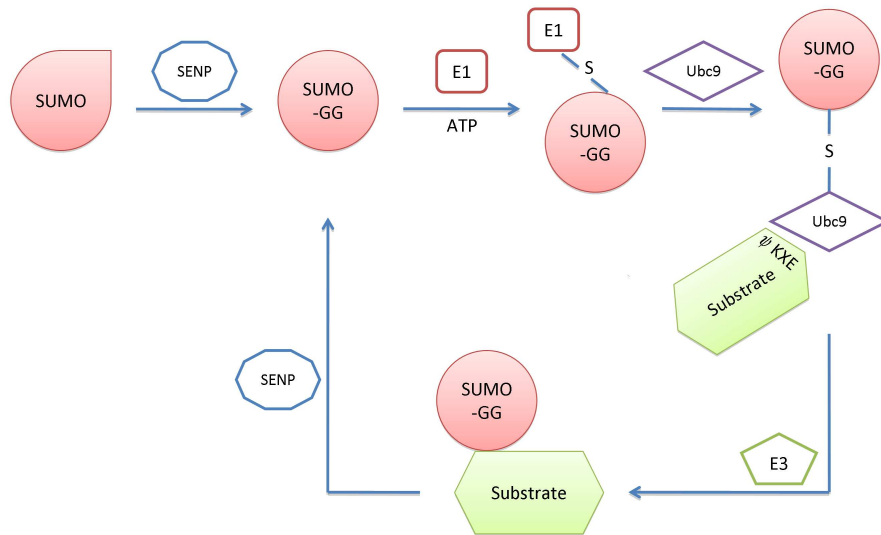
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18 **Figure 1.** Brief schematic representation of the SUMO pathway. SUMO is  
19 conjugated to and de-conjugation from target proteins in a series of steps that  
20 involve enzymes corresponding to those of the ubiquitin pathway. Mature SUMO is  
21 produced from the precursor protein, it is then activated by E1 enzyme, and passed  
22 on, through subsequent thioester bonds, from the E2-conjugating enzyme Ubc9  
23 onto the substrate protein. Release of SUMO from the complex is catalysed by a  
24 SUMO hydrolase of the SENP family.

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33 **Figure 2.** Components of SUMOylation in stress-response pathways leading to  
34 cellular senescence and ageing. Upon intra- or extracellular stress, the  
35 SUMOylation cycle of p53 is crucial to downstream signalling cascades that lead to  
36 senescence and ageing. Disturbances at both the SUMO conjugation and de-  
37 conjugation steps can impede the normal function of these pathways and block the  
38 onset of senescence. SUMOylation of pRB can influence the decision of the cell to  
39 undergo senescence or apoptosis. The SUMO E3 ligase PIASy and SUMO  
40 proteases of the SENP family also appear to have important roles in these  
41 pathways.

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Andreou &amp; Tavernarakis, Fig. 1

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