Targeting SUMO signaling to wrestle cancer

Kroonen, J.S.; Vertegaal, A.C.O.

CellPress
OPEN ACCESS

Trends in
Cancer

Review

Targeting SUMO Signaling to Wrestle Cancer

Jessie S. Kroonen [1] and Alfred C.O. Vertegaal [1,*]

The small ubiquitin-like modifier (SUMO) signaling cascade is critical for gene expression, genome integrity, and cell cycle progression. In this review, we discuss the important role SUMO may play in cancer and how to target SUMO signaling. Recently developed small molecule inhibitors enable therapeutic targeting of the SUMOylation pathway. Blocking SUMOylation not only leads to reduced cancer cell proliferation but also to an increased antitumor immune response by stimulating interferon (IFN) signaling, indicating that SUMOylation inhibitors have a dual mode of action that can be employed in the fight against cancer. The search for tumor types that can be treated with SUMOylation inhibitors is ongoing. Employing SUMO conjugation inhibitory drugs in the years to come has potential as a new therapeutic strategy.

Highlights

Cell cycle progression is mediated by small ubiquitin-like modifier (SUMO) ylation and blocking SUMOylation consequently inhibits cell cycle progression, particularly during mitosis.

SUMOylation has been identified as a 'master repressor' of gene expression in response to immune activating triggers, therefore inhibition of SUMOylation has the potential to activate the immune system to mount an antitumor response.

Specific small molecule inhibitors of the SUMO E1 enzyme have been generated recently that do not target related post-translational modification pathways like ubiquitylation and neddylation up to the micromolar range. These inhibitors can be used in the fight against cancer.

SUMOylation and Its Targets

Small ubiquitin-like modifiers (SUMOs) are post-translational modifications (PTMs) involved in various cellular processes, including cell cycle progression and the DNA damage response [1]. The conjugation of SUMO proteins to substrate proteins, called SUMOylation, occurs via an enzymatic cascade consisting of a dimeric SUMO-activating enzyme E1 [**SAE1/UBA2** (see Glossary)], a single E2 [**ubiquitin-conjugating enzyme 9 (UBC9)**], and a limited set of E3 ligases. Mammals have up to five SUMO family members. Mature SUMO2 and SUMO3 have 97% sequence similarity, whereas SUMO1 and SUMO2/3 have only 53% sequence similarity. SUMO2 and SUMO3 form chains in an efficient manner via an internal SUMO consensus site [2,3].

The reversible nature of SUMOylation is facilitated by SUMO-specific proteases (SENPs), which can deconjugate SUMOs from substrate proteins. SENPs are responsible for the deconjugation of mono-, di-, or poly-SUMO chains from target proteins. Additionally, the SENPs are crucial for maturation of precursor SUMO proteins by cleaving their carboxyl termini to expose their di-Gly motif required for conjugation.

The majority of SUMO targets are localized in the nucleus and are thought to undergo rapid cycles of SUMO conjugation and deconjugation, with a low overall stoichiometry of SUMOylation [4–7]. SUMO is thought to play important roles in different types of cancer due to the critical function of SUMOylation in cell cycle progression and genome integrity. Therefore, SUMOylation inhibitors have potential for anticancer therapy. In recent years, novel SUMO pathway inhibitors have been developed to target cancer and promising data on this topic have recently been published [8–11]. This review will focus on the role of SUMO in cancer progression and the use of SUMOylation inhibitors to halt cancer progression (Figure 1, Key Figure). In addition to the topics and targets discussed in this review, SUMOylation modulates many other proteins [12]. Furthermore, control of the DNA damage response and gene transcription by SUMOylation are important topics that have been discussed in more detail elsewhere [6,13–17].

SUMO Is Important for Cell Cycle Progression

The critical role of SUMOylation in cell cycle progression was uncovered by silencing several components of the SUMOylation cascade. Upon knockout or conditional knockdown of UBC9 in

[1]Department of Cell and Chemical Biology, Leiden University Medical Center, Albinusdreef 2, 2333, ZA, Leiden, The Netherlands

*Correspondence:
vertegaal@lumc.nl (A.C.O. Vertegaal).

Key Figure

Small Ubiquitin-like Modifier (SUMO)-Cycle Inhibitors Reduce Proliferation and Increase Antitumor Immune Responses

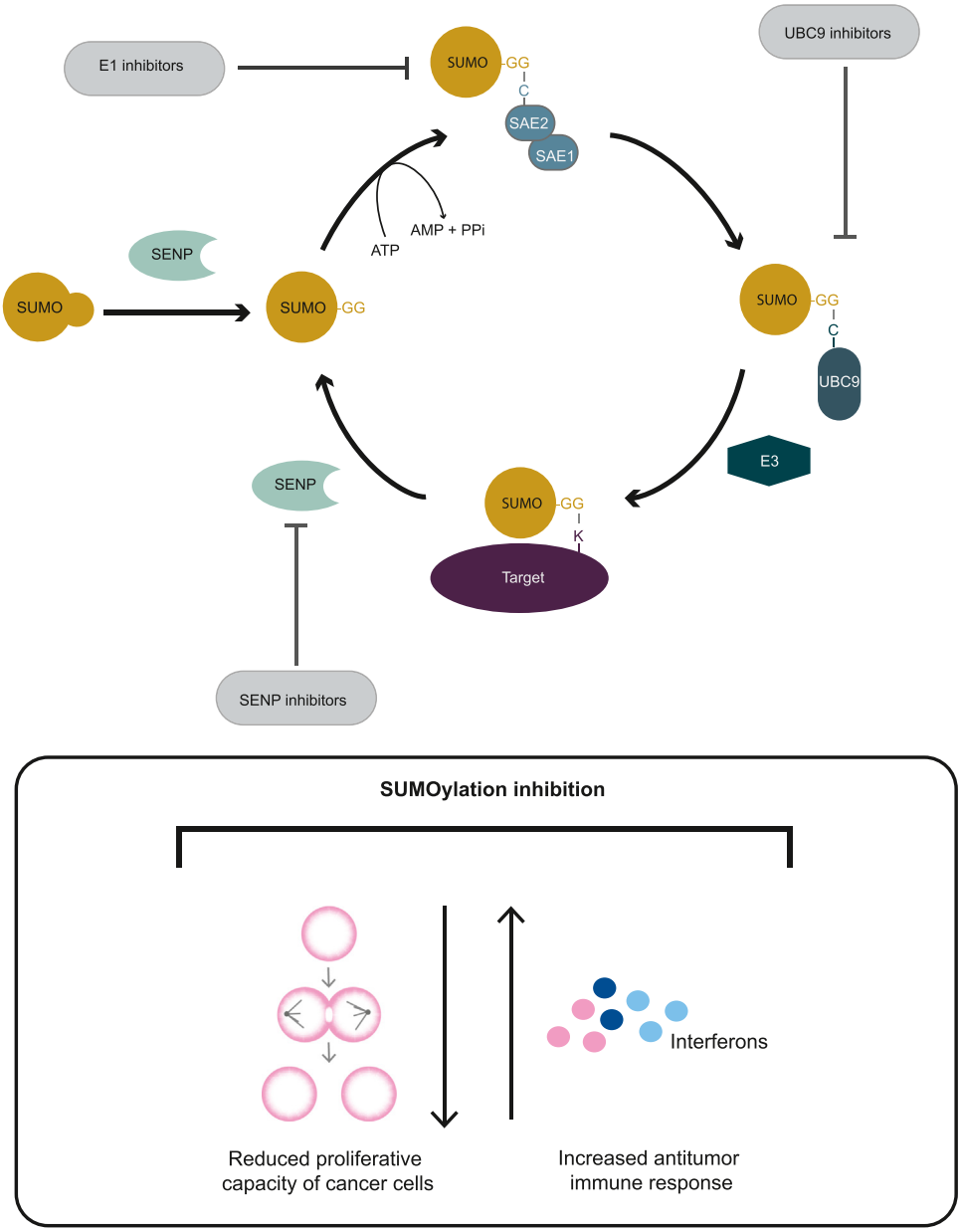

Figure 1. SUMO proteins mature via cleavage of their carboxyl termini, exposing their di-Gly motif needed for conjugation to target proteins. SUMO is conjugated to target proteins via its enzymatic cascade, including E1, E2, and E3-ligases. SUMO-specific proteases (SENPs) deconjugate SUMO proteins from their targets. Inhibitors of E1 and E2 can block the SUMOylation cascade and inhibitors of SENPs can block de-SUMOylation of subsets of targets and prevent maturation of

(Figure legend continued at the bottom of the next page.)

Glossary

Anaphase promoting complex/cyclosome (APC/C): a ubiquitin E3-ligase regulating the transition from metaphase to anaphase via ubiquitin-mediated degradation of, amongst others, Securin, releasing Separase to cleave cohesins, freeing sister chromatids.

Chromatin bridge formation: chromatin bridges are errors in chromosome segregation that are observed in cells entering mitosis with fused chromosomes. Chromosomes can remain fused at telomere ends, centromeres, or fragile sites, resulting in chromatin bridges connected to chromosomes traveling to opposite poles. Chromatin bridges most often occur in anaphase, therefore they are also called anaphase bridges. However, these bridges can persist, leaving two daughter cells connected by a stretch of chromatin.

c-Myc: the Myc family of proteins are transcription activators. The c-Myc gene is frequently involved in chromosomal translocations, leading to constitutive c-Myc expression. This induces the upregulation of a very extensive set of c-Myc target genes, leading to cell proliferation, contributing to the formation of cancer. Burkitt lymphoma is the classical example of a chromosomal translocation involving c-Myc.

Mitotic checkpoint complex (MCC): the MCC consists of MAD2, BubR1, Bub3, and CDC20. The MCC blocks APC/C activation via negatively regulating CDC20. When sister chromatids are properly linked to the bi-oriented mitotic spindle, the MCC is disassembled, releasing CDC20 to activate the APC/C.

p53: a transcription factor that, amongst others, regulates genes involved in inhibiting cell cycle progression and inducing apoptosis. p53 acts as a key tumor suppressor gene and mutations in the p53 pathway are found in the majority of cancers.

SAE1/UBA2: SUMO-activating enzyme 1/ubiquitin like modifier activating enzyme 2 is the dimeric single E1 in the SUMOylation cascade. The E1 activates SUMO in an ATP-dependent manner and transfers activated SUMO to the E2 UBC9.

Spindle assembly checkpoint (SAC): a feedback-control system to ensure correct chromosome segregation. The SAC delays anaphase

mammalian cell lines, severe nuclear defects were observed, including multinucleated cells, anaphase bridges, reduced chromatin condensation, and apoptosis [18,19]. UBC9 depletion blocks cell proliferation via chromatin and non-chromatin associated pathways [20]. Similar effects as seen for loss of UBC9 are also observed when knocking down the SAE1/2 enzyme, including strong reductions in cell proliferation [21–23]. Dynamic regulation of substrates by SUMOylation in all phases of the cell cycle has been identified via a proteomics approach [24]. SUMOylation thus appears crucial throughout the entire cell cycle, particularly in mitosis.

From the perspective of mammalian development, removal of several components of the SUMOylation cascade has extensive effects on their development. Mouse embryos deficient for UBC9 harbor severe mitotic defects, including anaphase bridges, an increased amount of polyploid cells, and hypo-condensation, resulting in embryonic lethality at the early postimplantation stage [18]. In particular, SUMO2-deficient mouse embryos do not develop past early stages of embryonic development [embryonic day (E)10.5], in contrast to SUMO1 or SUMO3 deficient mouse embryos, indicating the critical role of SUMO2 in development [25].

Phenotypical characteristics illustrating loss of SUMOylation in cells are aneuploidy (the presence of abnormal numbers of chromosomes per cell) [18] and **chromatin bridge formation** [23,26–28]. The remaining stretch of DNA between two daughter cells in the case of chromatin bridge formation prevents cells from properly dividing and starting their own independent cell cycle. To unravel the role of SUMO in the development of chromatin bridges and aneuploidy, it is important to understand the role of SUMOylation in chromosome segregation (Box 1).

If incorrectly attached chromosomes remain, the **spindle assembly checkpoint (SAC)** halts mitosis via inhibiting the **anaphase promoting complex/cyclosome (APC/C)**-CDC20. The SAC is an essential feedback-control system for proper chromosome segregation and is responsive to disruptions of microtubule–kinetochore attachment to prevent premature dissociation of sister chromatids [29,30]. Several proteins involved in the SAC are targets for SUMOylation. For example, a SUMO mutant of BubR1 cannot be removed from the kinetochores during metaphase, resulting in delayed mitosis and chromosomal mis-segregation [31]. BubR1, together with Bub3 and Mad2, bind CDC20 to form the **mitotic checkpoint complex (MCC)** in the presence of unattached kinetochores, which acts as an effector of the SAC and blocks mitosis via interfering with the formation of the APC/C-CDC20 [32]. The APC/C is a multisubunit ubiquitin E3-ligase that facilitates metaphase to anaphase transition. The APC/C amongst others ubiquitylates securin and cyclin B, resulting in their proteasomal degradation. Securin degradation leads to the activation of Separase, which cleaves cohesin, resulting in sister chromatid separation [29,32,33]. The APC4 subunit of the APC/C can be SUMOylated on two acceptor lysines, K772 and K798. SUMOylation of the APC4 subunit occurs preferentially in mitosis and is critical for timely metaphase to anaphase transition [34]. SUMOylation of the APC/C increases its ubiquitylation activity towards selected substrates [23], demonstrating the importance of SUMOylation for proper chromosome segregation.

Aberrant expression of SUMO proteases halts cell proliferation and results in defective nuclear morphology and binucleated cells [35]. During mitosis, SENP1 and SENP2 are localized at the kinetochore, while deregulating SENP1 and SENP2 leads to chromosomal segregation errors [36]. Phosphorylation of SENP3 inhibits its de-SUMOylating activity towards chromosome

until the sister chromatids are properly linked to the bi-oriented mitotic spindle to prevent premature dissociation of sister chromatids. When the SAC is active, mitosis is delayed via negative regulation of CDC20 by the MCC.

Ubiquitin-conjugating enzyme 9 (UBC9): the single SUMO E2 in the SUMOylation cascade. UBC9 accepts SUMO from SAE1/UBA2 and catalyzes SUMO attachment to substrates with help of an E3-ligase.

SUMOs. A block in the SUMOylation cascade leads to impaired cell proliferation and induces interferon production to stimulate antitumor immune responses, indicating its dual potential to target cancer cells. Abbreviations: SAE, SUMO-activating enzyme; UBC9, ubiquitin-conjugating enzyme 9.

Box 1. SUMO and Ultra-Fine Bridges (UFBs)

TOPIIα is crucial for decatenating chromosomes prior to chromosome segregation, to prevent impaired cell division. The SUMO E3-ligase RanBP2 is responsible for the SUMOylation of the C terminal part of TOPIIα in mammalian cells, which is required for proper localization of TOPIIα to inner centromeres [112,113]. Furthermore, SUMOylation reduces the activity of TOPIIα until anaphase, when decatenation of centromeric DNA is required [27]. Loss of TOPIIα SUMOylation will compromise the decatenation of DNA at the centromere and cause impaired cell division, via concatenated sister chromatids.

In anaphase a cell is presented with a 'final chance' to resolve concatenated sister chromatids. Sister chromatids in anaphase can still be connected via catenates, including centromeric catenates, which are also known as UFBs [114]. When UFBs remain unresolved, they can lead to chromatin bridges, which is the phenotype observed upon loss of SUMOylation, as mentioned earlier. UFBs are coated with, amongst others, the SUMO targets polo-like kinase 1-interacting checkpoint helicase (PICH) and the Bloom syndrome helicase (BLM). PICH was identified as an interaction partner of SUMOylated poly (ADP-ribose) polymerase 1 (PARP1) at the centromere [115]. The same study also identified the preferential binding of PICH to SUMOylated TOPIIα. Furthermore, PICH itself can also be SUMOylated, which reduces its affinity for DNA binding [115]. PICH comprises three SUMO-interacting motif (SIM) domains with distinct functions; two domains influence the enzymatic activity on the chromosomes, for example, via attenuating SUMOylated TOPIIα activity [116], whereas the most C terminally located SIM domain is crucial for centromeric localization of PICH [26]. PICH is known to recruit BLM and TOPIIα to UFBs; however, it remains unclear how these proteins act together in resolving UFBs [114,117,118] (Figure I).

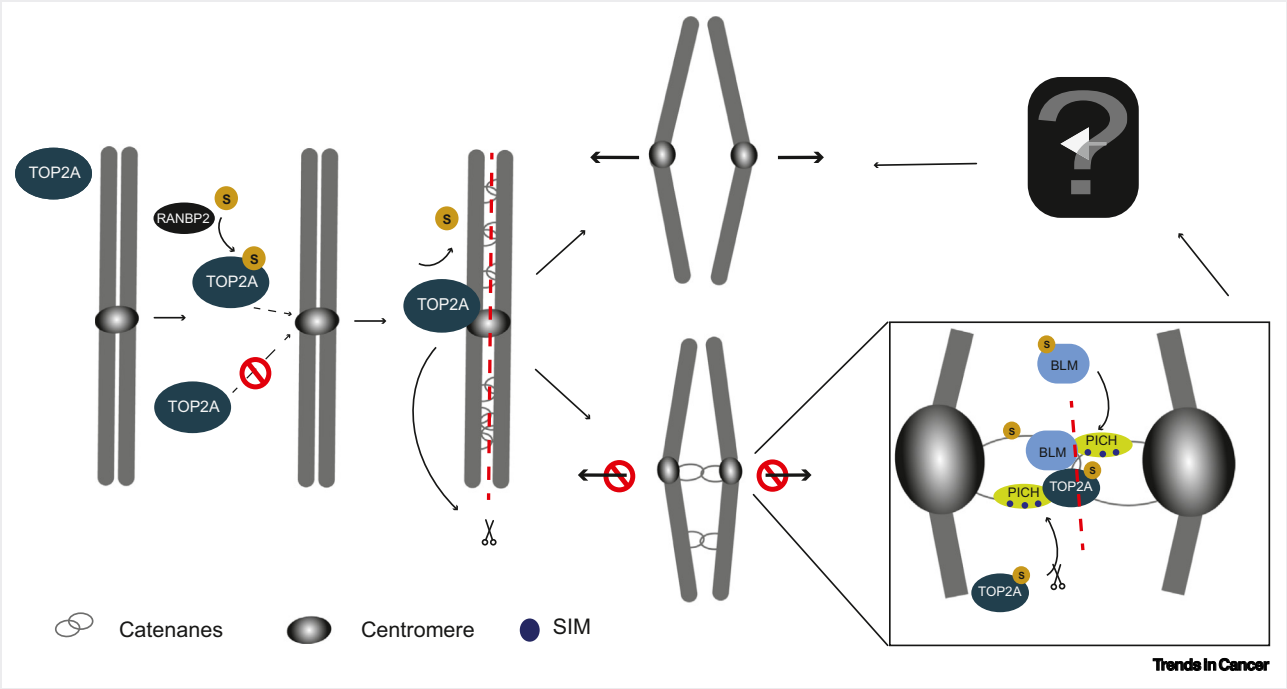

Figure I. Role of SUMOylation in Sister Chromatid Decatenation. TOPIIα is SUMOylated at its C terminal domain via the SUMO E3 RanBP2. SUMOylated TOPIIα localizes to the centromere. TOPIIα SUMOylation reduces its decatenating activity until anaphase onset, upon which TOPIIα is de-SUMOylated and decatenation can occur, leading to chromosome segregation. Impaired SUMOylation potentially reduces decatenation, resulting in ultra-fine bridges (UFBs). TOPIIα, Bloom syndrome helicase (BLM), and polo-like kinase 1-interacting checkpoint helicase (PICH) are recruited to and resolve the UFBs in a SUMO-dependent manner. The exact molecular mechanism to resolve these UFBs in a SUMO-dependent manner is still unclear. Abbreviations: S, SUMO; SIM, SUMO-interacting motif.

associated proteins, resulting in a mitotic arrest via upregulation of Mad2, a member of the MCC [28]. In addition, a knockdown of SENP7, which together with SENP6 is able to process SUMO chains, also delayed mitotic progression [37]. SENP7 depletion results in delocalization of HP1 from the pericentromeric heterochromatin, where it is important for centromeric cohesion [38,39]. SENP6 is crucial for the assembly of the inner kinetochore [40]. Depletion of SENP6 decreases the stability of the constitutive centromere-associated network [40,41].

SUMO Regulates p53 and c-Myc

One of the most well-known tumor suppressors is **p53**, a transcription factor that inhibits cell cycle progression or induces apoptosis upon genotoxic stress [42]. p53 is mainly SUMOylated

on lysine 386 by the PIAS-ligases and SUMOylation of p53 contributes to its activation [4,43]. The ubiquitin E3 ligase and oncoprotein MDM2 is the key p53 regulator that ubiquitylates p53, targeting it for proteasomal degradation [44]. More specifically, high levels of MDM2 are responsible for p53 degradation, whereas low levels of MDM2 cause mono-ubiquitylation and, consequently, nuclear export of p53 [45]. SUMOylation of MDM2 leads to p53 degradation via increasing MDM2 levels by decreasing its auto-ubiquitylating activity and, consequently, degradation [46]. SENPs can counteract MDM2 SUMOylation. UV radiation induces SUSP4, a mouse SUMO protease that removes SUMO from MDM2, leading to stabilization of p53 [47,48]. Lastly, RPL11 a regulator protein of the MDM2-p53 axis is also SUMOylated and potentially suppresses MDM2, via a currently unknown mechanism [49].

The protein product of the oncogene **c-Myc** is a transcription factor that has been linked to SUMOylation. c-Myc is a SUMO target that is specifically detected after heat shock or proteasome inhibition, implying that SUMOylation of c-Myc leads to its proteasomal degradation [50–52]. Interestingly, loss of SUMO via SAE1/2 knockdown is lethal for cells with high c-Myc expression, for example, in the classical c-Myc-driven Burkitt lymphoma [53,54]. Still, the precise mechanisms underlying the SUMOylation dependence of c-Myc-driven tumor development is not completely clear. So far, contradicting results regarding SUMOylation and c-Myc have been published. One study showed that SUMOylation of c-Myc via the SUMO E3 ligase PIAS1 leads to transcriptional repression and subsequent proteasomal degradation [55], whereas another study shows that PIAS1 positively regulates c-Myc transcriptional activity in B cell lymphomas [56]. Recently, it has been found that SENP1 is responsible for de-SUMOylating c-Myc, resulting in stabilization of c-Myc and, consequently, enhanced transcriptional activity [57,58], which supports the idea that SUMOylation suppresses c-Myc transcriptional activity. The inhibitory effect of SUMOylation on c-Myc transcriptional activity results in downstream repression of Pol I- and Pol II-dependent transcription activity [58,59]. The dependence of c-Myc-driven tumors on SUMOylation provides the opportunity to employ this weakness for therapeutic purposes [54,60].

Inhibiting the SUMOylation Cascade

Inhibiting proteins in the SUMOylation cascade could be beneficial for the treatment of malignancies. The expression of SUMOylation cascade proteins, SENPs, SAE1/2, UBC9, and E3-ligases, are upregulated in multiple cancers [7,61] and SUMOylation affects some proteins encoded by oncogenes and tumor suppressor genes. Combined, this paves the way for implementation of SUMOylation cascade inhibitors in the treatment of cancers. A considerable set of natural and synthetic compounds have been reported to inhibit the SUMOylation cascade (Table 1).

SAE1/UBA2

The SUMO E1 is a dimer consisting of the SAE1 and UBA2/SAE2 subunits. Knockdown of these subunits blocks the proliferative capacity of cancer cells, as shown in, for example, HCT116 colon cancer cells, U2OS osteosarcoma cells, Raji Burkitt lymphoma cells, Eμ-*Myc* lymphoma cells, and U87 and U251 human glioma cells *in vitro*. *In vivo* subcutaneous tumor models for glioma and Burkitt lymphoma and an orthotopic xenograft model for HCT116 showed a decrease in tumor growth upon short hairpin (sh)RNA-induced knockdown of SAE2 [22,53,54,62,63]. The first reported SAE1/2 inhibitors (Table 1) are natural compounds, including ginkgolic acid, its structural analog anacardic acid, and kerriamycin B [64,65]. Treatment with ginkgolic acid and anacardic acid decreased cancer cell growth of Eμ-Myc lymphoma cells and P493-6, BL70, Raji and Daudi Burkitt lymphoma cells *in vitro* [54]. These compounds inhibit formation of the SAE1/2-SUMO intermediate, consequently blocking the conjugation of SUMO to target proteins. Other natural compounds blocking SAE1/2 are Davidiin [66] and tannic acid [67] that employ a

Table 1. SUMOylation Cascade Inhibitors

Compound	Natural or synthetic	Type of molecule	Target	IC_{50} (inhibition of *in vitro* SUMOylation, μM)	Refs
Ginkgolic acid (15:1)	Natural product small molecule	Alkylphenol	E1	3.0	[64]
Anacardic acid	Natural product small molecule	Structural analog of ginkgolic acid (15:1)	E1	2.2	[64]
Kerriamycin B	Natural product small molecule	Antibiotic	E1	11.7	[65]
SUMO-AMSN SUMO-AVSN	Protein based	C-terminally modified SUMO proteins with 5′-sulfonyladenosine-based molecules	E1		[130]
Compound 21	Synthetic small molecule	Phenyl urea	E1	14.4	[70]
Davidiin	Natural product	Ellagitannin	E1	0.15	[66]
Tannic acid	Natural	Gallotannin	E1	12.8	[67]
Several compounds identified in a thiazole urea and pyrazole urea based screen	Synthetic small molecules	Thiazole urea and pyrazole urea	E1	30–100	[131]
ML-792	Synthetic small molecule	Pyrazole- carbonylpyrimidine	E1	0.003 (SUMO1) 0.011 (SUMO2)	[8]
COH-000	Synthetic small-molecule	Dimethyl 1-((R)-1-(phenylamino)-2-(p-tolyl) ethyl)-7-oxabicyclo [2.2.1] hepta-2,5-diene-2,3-dicarboxylate	E1	0.2	[11,71]
TAK-981	Synthetic small molecule	Pyrazole- carbonylpyrimidine	E1		[9]
ML-93	Synthetic		E1	0.037	[10]
GSK145A	Synthetic small molecule	Diamino-pyrimidine	E2	12.5	[75]
2-D08	Synthetic small molecule	Flavonoid	E2	6	[132]
Spectomycin B	Natural product small molecule	Antibiotic	E2	4.4	[78]
Compound 2	Synthetic small molecule	Pyridine	E2	75	[133]
SUBINs	Protein based	SUMO2 variants	E2	0.025	[76]
Compound 38	Synthetic small molecule	Benzodiazepine	SENP1	9.2	[134]
Triptolide	Natural product small molecule	Tripterygium wilfordii Hook F	SENP1	0.009754–0.0203 (*in vivo*)	[83]
Compound J5	Synthetic small molecule	2-(4-Chlorophenyl)-2-oxoethyl 4-benzamidobenzoate derivative	SENP1	2.385	[135]
GN6958	Synthetic small molecule	Phenyl urea	SENP1	29.6	[87]
Compound 69 and 117	Synthetic small molecules	Oxadiazoles	SENP2	5.9, 3.7	[136]
Compound 13m	Synthetic small molecule	Phenyl	SENP1	3.5	[85]
Momordin Ic (Mc)	Natural product small molecule	Pentacyclic triterpenoid	SENP1	15.37	[84]
Compound 3	Synthetic small molecule	Phenyl	SENP1/2	3.55, 2.98	[86]
Streptonigrin	Natural product small molecule	Antibiotic	SENP1	0.518	[137]
Ebselen	Synthetic small molecule	Organo-selenium	SENP2	2 (*in vivo*)	[89]
Compound 6, 7, and 10	Synthetic small molecules		SENP1	3.7, 0.99, 7.5	[88]

similar mechanism of action. Both compounds inhibit cancer cell growth, respectively, for NCI-H460 lung cancer cells, MKN-45 gastric cancer cells, DU-145 prostate cancer cells [66], and YD-38 cells, a gingival squamous cell carcinoma [68]. The limitations of these natural products are that they mostly function in the micromolar range and that they do not singly target SUMOylation. Ginkgolic acid is known to target proinflammatory molecules like prostaglandins and leukotrienes [69], and tannic acid can also induce cancer cell death via activation of apoptosis rather than via inhibition of cell cycle progression, as expected for a SUMOylation inhibitor [68].

The broad range of targets affected by these natural compounds complicates the mechanistic understanding of their anticancer effects.

Synthetic inhibitors of the SUMO E1, including compound-21 [70], ML-792 [8], its derivative TAK-981 (Takeda), and COH-000 [11] have been developed to tackle this problem. Compound-21 and COH-000 act similar to the natural compounds via interaction with the SAE1/2. Compound-21 specifically interacts with the ATP binding site in the SAE2 and COH-000 via binding to Cys30 in an allosteric site of the SAE2. ML-792, TAK-981, and ML-93 inhibit SAE1/2 activity by forming an adduct with SUMO in an ATP-dependent manner catalyzed by the enzyme itself [8–10] (Box 2). These single molecule compounds are highly specific and do not have side effects on, for example, ubiquitylation and neddylation up to the micromolar range [8,71]. For COH-000, ML-792, TAK-981, and ML-93 it was reported that they inhibit cancer growth *in vitro* in, for example, HCT116 and Colo-205 colon carcinoma cell lines, MDA-MB-231 and MDA-MB-249 breast cancer cell lines, and pancreatic ductal adenocarcinoma (PDAC). *In vivo*, the syngeneic immunocompetent BALB/c A20 lymphoma model treated with TAK981, and a HCT116 subcutaneous colon cancer xenograft treated with COH-000, exhibited reduced growth [8–10,71]. In the PDAC model it was observed that Myc hyperactivation sensitizes PDAC cell lines, including PSN1 and primary huPDAC cells towards SUMO inhibition via ML-93. Furthermore, a PaTu- 8988T xenograft model showed dose-dependent sensitivity towards SUMO E1 inhibition [10].

Interestingly, SUMOylation modulates type I interferon (IFN) signaling [72,73]. Consistently, the activity of TAK-981 against the murine A20 lymphoma is dependent on IFN alpha/beta receptor

Box 2. ML-792/TAK-981 SAE1/2 Inhibition

The selective SAE inhibitor ML-792 and its functional analog TAK-981 are structurally related to adenosine 5′-monophosphate (AMP) and are expected to bind in the nucleotide binding pocket of SAE. For the identification of selective SAE inhibitors, a pyrazole carbonylpyrimidine-based scaffold was used [8]. Inhibitory activity occurs via the formation of an adduct between ML-792 or TAK-981 and SUMO. The sulfamate ester in ML-792 forms a covalent irreversible adduct with the C terminus of SUMO, catalyzed by the SAE enzyme itself in an ATP-dependent manner. This ML-792-SUMO conjugate subsequently binds tightly to SAE2, also known as UBA2, the catalytic subunit of SAE, and inhibits its activity [8,119] (Figure I). Specificity was confirmed via screening ML-792 against a panel of ATP-dependent enzymes, which did not demonstrate any significant off-target effects. Furthermore, E1 activity of NAE, the E1 for Neddylation was only affected by ML-792 at very high doses [8]. UAE, the ubiquitin E1 was not inhibited by ML-792.

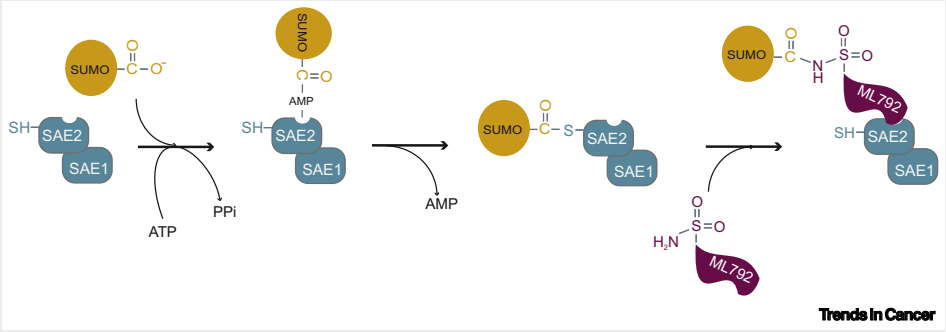

Figure I. Mechanism of SUMO-Activating Enzyme (SAE) Inhibition by ML-792. This graphical overview shows the enzymatic mechanism of SUMO-ML792 adduct formation in an ATP-dependent manner, via the SAE1/UBA2 enzyme. The SAE1/UBA2 enzyme catalyzes the formation of a SUMO-AMP intermediate, binding to the ATP-binding pocket in SAE2 and releasing inorganic pyrophosphate. Next, SUMO-AMP reacts with the active site cysteine to form a SAE2-SUMO thioester, releasing AMP. ML-792 binds the ATP binding-site in the SAE2-SUMO thioester complex and, subsequently, the sulfamate ester in ML-792 forms a covalent adduct with the C terminus of SUMO. The ML792-SUMO adduct occupies the SAE1/UBA2 enzyme and impairs its activity. This mechanism is analogous to the MLN4924-Nedd8 adduct formation inhibiting NAE, as described in Brownell et al. [138].

1 (IFNAR) activity, linking the activity of TAK-981 to IFN signaling *in vivo* [9]. Box 3 describes the interaction between SUMOylation and the IFN pathway. Furthermore, it is suggested that TAK-981 promotes antitumor immune responses via enhanced cross-presentation of exogenous antigens released by dying tumor cells, leading to cytotoxic T cell priming and activation in mice [74], implying a role for innate and adaptive immunity in TAK-981 antitumor activity. Notably, TAK-981 is currently in a Phase I clinical trial in patients with metastatic solid tumors or lymphomas (ClinicalTrials.gov Identifier: NCT03648372[i]) , focusing on safety, tolerability, and pharmacokinetics of the compound. Additionally, an early Phase I clinical trial with TAK-981 in combination with cetuximab or avelumab for intratumoral microdosing in patients with head and neck cancer has started (ClinicalTrials.gov Identifier: NCT04065555[ii]). This trial aims to study the biological effects of TAK-981 within the tumor microenvironment. Lastly, a Phase Ib/II interventional clinical trial with TAK-981 in combination with rituximab in patients with non-Hodgkin lymphoma (ClinicalTrials.gov Identifier: NCT04074330[iii]) focusing on safety of the drug, followed by an intervention study evaluating the efficacy of TAK-981 in combination with rituximab. All three clinical trials are currently recruiting patients and no results have been listed yet. Taken together, TAK-981 is the SUMOylation cascade inhibitor that is most advanced and up to now shows to be the most promising candidate for clinical purposes.

UBC9

UBC9 accepts SUMO proteins from the E1 and catalyzes their covalent attachment to target proteins. UBC9 is the sole E2-enzyme in the SUMOylation cascade and contributes to substrate specificity together with the E3-ligases. Knocking down UBC9 reduced the proliferative capacity of, for example, HCT116 colon cancer cells *in vitro* and *in vivo* in an orthotopic xenograft model [22]. Several UBC9 inhibitors (Table 1) have been identified through multicompound screening approaches, including GSK145A in a specific screen to detect inhibitors of TRPS1 SUMOylation [75] and SUBINs, which are SUMO-based UBC9 inhibitors that specifically inhibit SUMO-chain formation [76]. Spectomycin B1, a known antibiotic for Gram-positive bacteria [77], binds to UBC9 and inhibits its interaction with SUMO, which is possibly unrelated to its antibiotic activity. Estrogen-dependent proliferation of human breast cancer cells is inhibited by spectomycin B1 in a manner similar to UBC9 knockdown [78]. Lastly, 2′,3′,4′,-trihydroxyflavone (2-D08) is an inhibitor that specifically blocks the transfer of SUMO from UBC9 to substrates [79]. It reduces growth and induces apoptosis in non-acute promyelocytic leukemia (APL) acute myeloid leukemia (AML) cells and inhibits cell migration in K-Ras-mutated pancreatic cancer cells [80–82]. However, an *in vivo* effect of 2-D08 was only shown in a combination approach with all-trans retinoic acid (ATRA) in non-APL AML cells [82]. Thus, a variety of UBC9 inhibitors are able to block the SUMOylation cascade and have potential for being employed to target cancer cells.

To date, no small molecule inhibitors for SUMO E3-ligases have been identified. Future development of SUMO E3-ligase inhibitors will potentially add a level of specificity to inhibition of the SUMOylation cascade, since different E3-ligases are responsible for SUMOylation of subsets of target proteins.

SENPs

SENPs are responsible for the maturation of SUMO and for the deconjugation of SUMO from substrate proteins. The SENP family comprises six members, SENP1, SENP2, SENP3, SENP5, SENP6, and SENP7. Interestingly, SENP1 is upregulated in various cancers, and SENP2 and SENP3 to a lesser extent, as mentioned previously. Therefore, SENPs might represent targets for anticancer therapies. Several SENP inhibitors have been identified, targeting SENP1 or SENP2 (Table 1). SENP inhibitors derived from natural products include triptolide and Momordin Ic, both potential SENP1 inhibitors that were found to reduce LNCaP and PC3 prostate cancer

Box 3. SUMO and the Immune System

The SUMOylation cascade balances innate immune signaling via regulating type I interferon (IFN) responses and NF-kappa-B (NF-$_k$B) activity. As reviewed in [120], SUMOylation affects multiple regulators in type I IFN production to act in a stimulatory or inhibitory manner. SUMOylation of the IFN regulatory transcription factor IRF3 negatively regulates IFNß transcription. Consequently, de-SUMOylation of IRF3 by SENP2 induces IFNß transcription [121,122]. IFN transcription is regulated in a similar manner by IRF7 SUMOylation via the E3 ligase TRIM28 [123,124]. In addition, IRF8, a transcription factor activated by IFNs and interleukin-12, is regulated by SUMO in a similar manner as IRF3 and 7 [125] (Figure I).

Another effector of our innate immunity is the GMP-AMP synthase (cGAS), which senses viral DNA and consequently activates the stimulator of interferon genes (STING). Subsequently, STING stimulates type 1 IFNs. The E3 ligase TRIM38 SUMOylates cGAS and STING, resulting in their stabilization at early stages after infection. At late infective state, SENP2 de-SUMOylates cGAS and STING, which leads to their degradation and thus diminishes the immune response [126]. By contrast, it has also been found that SUMOylation suppresses cGAS DNA-sensing potential, which can be relieved by SENP7, showing a dampening effect of SUMOylation on immune activation [127]. The difference in SENP2 and SENP7 function can potentially be explained by the specificity of SENP7 for SUMO chains, whereas SENP2 can remove mono-SUMO conjugates and can also cleave poly-SUMOs [128]. Combined, this suggests a differential effect for mono- and poly-SUMOylation on the cGAS-STING pathway. Furthermore, the NF-$_k$B pathway can also be regulated by SUMOylation in an inhibitory and in a stimulatory manner [129].

Overall, it shows that SUMOylation is important for restraining the immune response by its predominant repressive effect on the pathways mentioned earlier. Loss of SUMOylation left mice susceptible to septic shock and increased protection against viral infection [72]. Thus, SUMOylation is a 'master repressor' of gene expression in response to immune-activating triggers. SUMO inhibition therefore has the potential to reactivate immune responses.

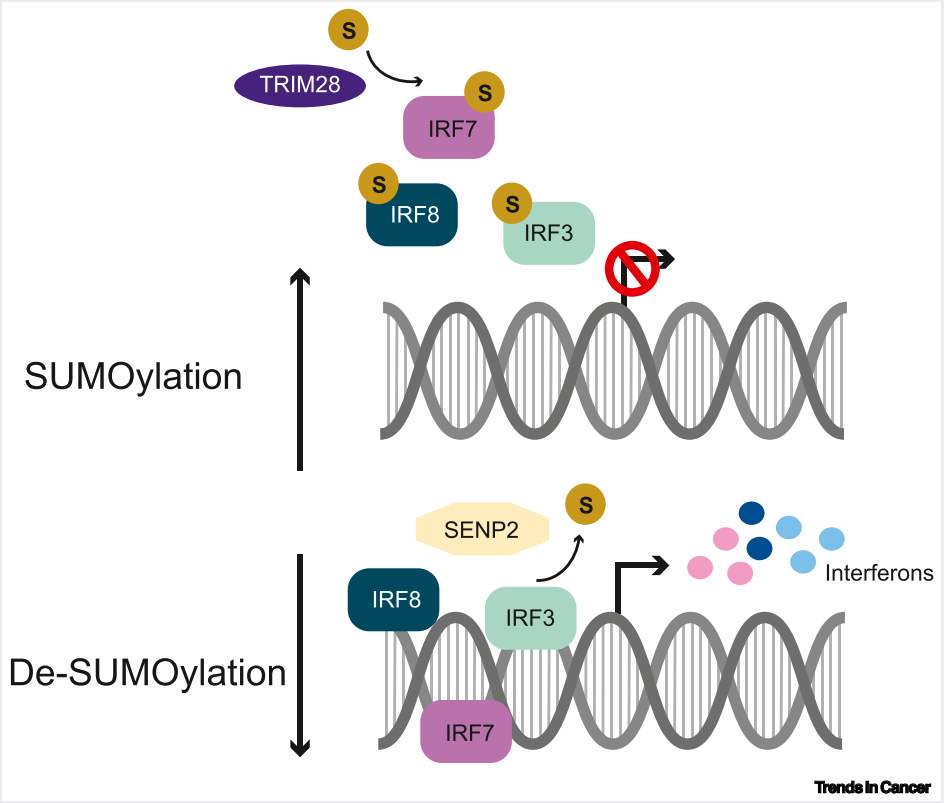

Figure I. The Role of SUMOylation in Interferon Production. Increased SUMOylation halts interferon production via SUMOylation of transcription factors IRF7, IRF8, and IRF3. De-SUMOylation of these proteins results in active transcription of interferons. Abbreviation: S, SUMO.

cell proliferation. PC3 cells express higher levels of SENP1 and, correspondingly, are more sensitive towards Momordin Ic treatment. PC3 xenograft models show sensitivity towards both Momordin Ic and triptolide [83,84]. More SENP1 inhibitors have been developed, including compound 13m through *in silico* screening [85], compound 3 in an effort to develop a highly reliable assay for SENP inhibitors [86], and GN6958 [87]. These inhibitors show proper SENP1 inhibitory potential *in vitro.* However, they have not been tested *in vivo* as has been done for the two natural SENP1 inhibitors. The development of SENP inhibitors is ongoing, with the latest result being identification of a novel class of noncompetitive SENP1 inhibitors [88]. As shown for the SENP2 inhibitor Ebselen, inhibition of SENPs will lead to an increase in overall SUMO conjugation in B35 cells and *in vivo* after injection in to mouse brains [89]. An increase in overall SUMOylation is proposed as a mechanism to protect the brain from ischemic damage [89]. Ebselen might therefore be suitable to prevent ischemic brain damage and may be useful in the clinic outside of the oncology field. These examples highlight the potential for SENP inhibitors as cancer therapy and potentially as treatment for other diseases.

Potential Toxicity and Risks of SUMO Inhibition

Potential toxicity and adverse effects need to be considered for SUMO cascade inhibitors. SUMOylation inhibition is probably not simply beneficial as a therapeutic approach in cancer therapy. Knockout of UBC9 in adult mice resulted in loss of intestinal epithelium stability and function, leading to diarrhea and death [90]. Embryonic lethality at the early postimplantation stage is the phenotype of a full UBC9 or SUMO2 knockout [18,25]. Interestingly, UBC9 haploinsufficiency promotes malignant phenotypes and cell growth in Lgr5+ CBC cells *in vitro* and as an intestinal cancer mouse model. This intestinal cancer model indicates a tumor suppressive role for fully functional UBC9, which seems in conflict with the established role of SUMO in cancer [91]. Extensive understanding of cell type-specific effects of SUMO inhibition is of major importance for therapeutic implementation.

Side effects of the selective SAE inhibitor ML-93 were irritation and ulceration at the injection site, observed in a PDAC xenograft model [10]. A counterindication for the use of SUMOylation inhibitors is the downregulation of SUMO proteins or SUMO conjugating enzymes or the upregulation of SUMO-deconjugating enzymes in some tumors [7,61]. Furthermore, combinations of SUMOylation inhibition with other drugs should be carefully analyzed for potential adverse effects. For example, proteasomal degradation of PML-RAR upon As_2O_3 treatment is dependent on its hyper-SUMOylation [92–94]. Naturally, inhibiting SUMOylation in combination with As_2O_3 to treat APL would thus be counterproductive. In addition, IRC117539 promotes SUMOylation and ubiquitylation of the androgen receptor (AR) as potential therapy for prostate cancers, reminiscent to As_2O_3 therapy in APL. IRC117539 reduced cell growth in AR-positive prostate cancer cells, whereas combining IRC117539 with ML-792 left the drug completely ineffective [95]. The above-mentioned considerations need to be considered for SUMO inhibition as tailored therapeutic options for a subset of malignancies.

Concluding Remarks

To implement SUMOylation inhibitors in clinical practice, a careful evaluation of cancers responsive to treatment must be made (see Outstanding Questions). TAK-981 is the only SUMOylation inhibitor that is currently evaluated in clinical trials for a broad range of cancers. To identify types of cancer that can be treated with TAK-981, research should focus on identifying biomarkers that sensitize cancer cells for SUMOylation inhibition. As mentioned earlier in this review and in other reviews, cancer cells overexpressing c-Myc are sensitive to SUMO inhibition and are thus potentially suitable for treatment with SUMO inhibitors [60]. Ultimately, SUMO inhibitors should be used as components of combination therapies. Deep biological insight in SUMO biology

Outstanding Questions

Which types of tumors are susceptible to SUMO E1 inhibitors, particularly considering SUMO conjugation levels and molecular characteristics of the tumors?

In addition to APL, which types of tumors should not be treated by SUMOylation inhibition because of counterproductive effects?

Which molecular mechanisms cause resistance or sensitivity towards SUMOylation inhibition and should be considered in the search for combination therapies?

Does inhibition of SUMOylation lead to toxicity for normal cells?

should enable the identification of potential combination therapies. Given the key role of SUMOylation in cell cycle progression, combination therapies with cell cycle inhibitors could be explored. For this purpose, inhibitors of CDK4/6, Wee1, and Aurora kinases could be considered [96]. Furthermore, it was recently reported that SUMO inhibition by TAK-981 activates the immune system to target tumors via the IFN pathway [9] (Box 3), indicating the opportunity of combination therapies with immune checkpoint inhibitors [97]. However, careful risk analysis is required to avoid combination therapies that induce adverse effects. Accurate predictions to identify responsive tumor types are challenging to make. A recent example is a prediction model for chemotherapy resistance in AML based on PTMs, including SUMO [98]. The authors identified a new class of biomarkers based on ubiquitin and SUMO conjugation, by comparing PTMs in extracts of chemosensitive and chemoresistant AML, and identified 122 proteins whose conjugation to SUMO or ubiquitin marks resistance. These biomarkers could potentially predict responses of AML patients to standard chemotherapies based on PTMs [98]. Extending this method could help to propose optimal therapeutic options, for example, novel PTM-based drugs, including SUMO inhibitors.

In addition to the emerging development of SUMOylation inhibitory drugs, mainly targeting SUMO E1, inhibitors of similar PTMs like ubiquitin and Nedd8 are also being developed for clinical purposes and being tested in clinical trials. The most well-known cancer therapeutics based on the ubiquitin system are proteasome inhibitors. These inhibitors were initially developed to prevent cancer-induced cachexia. Preclinical studies showed that in cultured cancer cells and murine cancer models, proteasome inhibitors induce apoptosis. In clinical trials, proteasome inhibitors emerged to enable the treatment of myelomas and lymphomas, establishing new standards of care [99]. More recent developments are focused on direct inhibition of ubiquitin conjugation and deconjugation. Inhibition of the ubiquitin activating enzyme (UAE) is one example and Pyr41 was the first UAE inhibitor established [100]. TAK-243 is a potent small-molecule inhibitor of UAE, which shows antitumoral activity via, amongst others, endoplasmic reticulum (ER) stress-induced apoptosis [101–103]. To date, two Phase I clinical trials have been listed for TAK-243. One study focusing on the dosage and side effects of TAK-243 for patients with AML or chronic myelomonocytic leukemia (CMML) unresponsive to conventional treatment has not yet started recruiting patients (ClinicalTrials.gov Identifier: NCT03816319[iv]). The second study listed for TAK-243 focusing on dosage and side effects in patients with advanced solid tumors listed several adverse effects and was terminated in 2019 (ClinicalTrials.gov Identifier: NCT02045095[v]). Future research has to demonstrate if TAK-243 or other new drugs targeting the ubiquitin system are suitable for treatment of cancers.

Epigenetic drugs focused on PTM modulation have large potential for the treatment of malignant diseases. For example, MLN4924 is a selective small-molecule inhibitor of the Nedd8 activating enzyme (NAE). The Neddylation pathway regulates, to a large extent, the turnover of a subset of proteins upstream of the proteasome via controlling the activity of the Cullin-RING ubiquitin ligases [104]. These ligases are known to play important roles in cellular processes associated with cancer growth and survival [105]. MLN4924 disrupts Cullin-RING ligase-related protein turnover, resulting in apoptosis in human cancer cells, via dysregulating S-phase DNA synthesis *in vitro*, leading to endoreplication. The use of MLN4924 in a xenograft model decreased the growth of the engrafted tumor [106–108]. This research suggests that Neddylation is a promising therapeutic target. Phase I clinical trial data demonstrate that MLN4924 is generally well tolerated and preliminary evidence suggests modest activity in refractory lymphoma [109–111]. Currently, MLN4924 is in Phase III clinical trials and is thus the most clinically advanced E1 drug. Both studies investigate the combination of MLN4924 with azacytidine. Enrolled patients will be randomly assigned to single treatment with azacytidine or to the combination therapy group. These studies

investigate improved event-free survival in AML, myelodysplastic syndromes, or CMML upon combination therapy (NCT03268954[vi]) and the efficacy of MLN4924 with azacytidine in patients with AML not eligible for standard chemotherapy (NCT04090736[vii]). For both studies, no results have been published.

For precision therapeutic purposes, it is important to understand the mechanisms driving malignant diseases to identify the most promising therapy for individual patients. Utilizing the potential of PTM drugs by identifying novel combination therapies will strengthen the outcome for patients. Commemorating the developments made in the past years, large advances have been made in the development of SUMO and other PTM inhibitory drugs. Developing and investigating SUMO conjugation inhibitory drugs in the coming years has the potential to lead to new therapeutic strategies.

Acknowledgments

The laboratory of A.C.O.V. is supported by the Netherlands Organization for Scientific Research (NWO) (724.016.003) and the Dutch Cancer Society (10835).

Disclaimer Statement

The authors have received ML-792 and TAK-981 from Millennium Pharmaceuticals, Inc., Takeda for preclinical research purposes.

Resources

[i]https://clinicaltrials.gov/ct2/show/NCT03648372

[ii]https://clinicaltrials.gov/ct2/show/NCT04065555

[iii]https://clinicaltrials.gov/ct2/show/NCT04074330

[iv]https://clinicaltrials.gov/ct2/show/NCT03816319

[v]https://clinicaltrials.gov/ct2/show/NCT02045095

[vi]https://clinicaltrials.gov/ct2/show/NCT03268954

[vii]https://clinicaltrials.gov/ct2/show/NCT04090736

References

1. Flotho, A. and Melchior, F. (2013) Sumoylation: a regulatory protein modification in health and disease. *Annu. Rev. Biochem.* 82, 357–385
2. Gareau, J.R. and Lima, C.D. (2010) The SUMO pathway: emerging mechanisms that shape specificity, conjugation and recognition. *Nat. Rev. Mol. Cell Biol.* 11, 861–871
3. Tatham, M.H. *et al.* (2001) Polymeric chains of SUMO-2 and SUMO-3 are conjugated to protein substrates by SAE1/SAE2 and Ubc9. *J. Biol. Chem.* 276, 35368–35374
4. Hay, R.T. (2005) SUMO: a history of modification. *Mol. Cell* 18, 1–12
5. Müller, S. *et al.* (2004) SUMO: a regulator of gene expression and genome integrity. *Oncogene* 23, 1998–2008
6. Jackson, S.P. and Durocher, D. (2013) Regulation of DNA damage responses by ubiquitin and SUMO. *Mol. Cell* 49, 795–807
7. Eifler, K. and Vertegaal, A.C.O. (2015) SUMOylation-mediated regulation of cell cycle progression and cancer. *Trends Biochem. Sci.* 40, 779–793
8. He, X. *et al.* (2017) Probing the roles of SUMOylation in cancer cell biology by using a selective SAE inhibitor. *Nat. Chem. Biol.* 13, 1164–1171
9. Berger, A.J. *et al.* (2019) Abstract 3079: pharmacodynamic evaluation of the novel SUMOylation inhibitor TAK-981 in a mouse tumor model. *Cancer Res.* 79, 3079
10. Biederstädt, A. *et al.* (2020) SUMO pathway inhibition targets an aggressive pancreatic cancer subtype. *Gut* 69, 1472–1482
11. Lv, Z. *et al.* (2018) Molecular mechanism of a covalent allosteric inhibitor of SUMO E1 activating enzyme. *Nat. Commun.* 9, 5145
12. Hendriks, I.A. and Vertegaal, A.C.O. (2016) A comprehensive compilation of SUMO proteomics. *Nat. Rev. Mol. Cell Biol.* 17, 581–595
13. Matt, S. and Hofmann, T.G. (2016) The DNA damage-induced cell death response: a roadmap to kill cancer cells. *Cell. Mol. Life Sci.* 73, 2829–2850
14. Rosonina, E. and A (2019) A conserved role for transcription factor sumoylation in binding-site selection Emanuel. *Curr. Genet.* 65, 1307–1312
15. Rosonina, E. *et al.* (2017) Regulation of transcription factors by sumoylation. *Transcription* 8, 220–231
16. Garvin, A.J. and Morris, J.R. (2017) SUMO, a small, but powerful, regulator of double-strand break repair. *Philos. Trans. R. Soc. Lond. Ser. B Biol. Sci.* 372
17. Schwertman, P. *et al.* (2016) Regulation of DNA double-strand break repair by ubiquitin and ubiquitin-like modifiers. *Nat. Rev. Mol. Cell Biol.* 17, 379–394
18. Nacerddine, K. *et al.* (2005) The SUMO pathway is essential for nuclear integrity and chromosome segregation in mice. *Dev. Cell* 9, 769–779
19. Hayashi, T. *et al.* (2002) Ubc9 is essential for viability of higher eukaryotic cells. *Exp. Cell Res.* 280, 212–221
20. Neyret-Kahn, H. *et al.* (2013) Sumoylation at chromatin governs coordinated repression of a transcriptional program essential for cell growth and proliferation. *Genome Res.* 23, 1563–1579
21. Tu, J. *et al.* (2015) Functional proteomics study reveals SUMOylation of TFII-I is involved in liver cancer cell proliferation. *J. Proteome Res.* 14, 2385–2397
22. He, X. *et al.* (2015) Characterization of the loss of SUMO pathway function on cancer cells and tumor proliferation. *PLoS One* 10, e0123882
23. Eifler, K. *et al.* (2018) SUMO targets the APC/C to regulate transition from metaphase to anaphase. *Nat. Commun.* 9, 1119

24. Schimmel, J. *et al.* (2014) Uncovering SUMOylation dynamics during cell-cycle progression reveals foxM1 as a key mitotic SUMO target protein. *Mol. Cell* 53, 1053–1066
25. Wang, L. *et al.* (2014) SUMO 2 is essential while SUMO 3 is dispensable for mouse embryonic development. *EMBO Rep.* 15, 878–885
26. Sridharan, V. and Azuma, Y. (2016) SUMO-interacting motifs (SIMs) in Polo-like kinase 1-interacting checkpoint helicase (PICH) ensure proper chromosome segregation during mitosis. *Cell Cycle* 15, 2135–2144
27. Ryu, H. *et al.* (2010) PIASy-dependent SUMOylation regulates DNA topoisomerase IIα activity. *J. Cell Biol.* 191, 783–784
28. Wei, B. *et al.* (2018) Mitotic phosphorylation of senp3 regulates desumoylation of chromosome-associated proteins and chromosome stability. *Cancer Res.* 78, 2171–2178
29. Musacchio, A. and Salmon, E.D. (2007) The spindle-assembly checkpoint in space and time. *Nat. Rev. Mol. Cell Biol.* 8, 379–393
30. Musacchio, A. (2015) The molecular biology of spindle assembly checkpoint signaling dynamics. *Curr. Biol.* 25, 1002–1018
31. Yang, F. *et al.* (2012) BubR1 is modified by sumoylation during mitotic progression. *J. Biol. Chem.* 287, 4875–4882
32. Pines, J. (2011) Cubism and the cell cycle: the many faces of the APC/C. *Nat. Rev. Mol. Cell Biol.* 12, 427–438
33. Alfieri, C. *et al.* (2016) Molecular basis of APC/C regulation by the spindle assembly checkpoint. *Nature* 536, 431–436
34. Lee, C.C. *et al.* (2018) Sumoylation promotes optimal APC/C activation and timely anaphase. *Elife* 7, e29539
35. Di Bacco, A. *et al.* (2006) The SUMO-specific protease SENP5 is required for cell division. *Mol. Cell. Biol.* 26, 4489–4498
36. Cubeñas-Potts, C. *et al.* (2013) SENP1 and SENP2 affect spatial and temporal control of sumoylation in mitosis. *Mol. Biol. Cell* 24, 3483–3495
37. Romeo, K. *et al.* (2015) The SENP7 SUMO-protease presents a module of two HP1 interaction motifs that locks HP1 protein at pericentric heterochromatin. *Cell Rep.* 10, 771–782
38. Maison, C. *et al.* (2012) The SUMO protease SENP7 is a critical component to ensure HP1 enrichment at pericentric heterochromatin. *Nat. Struct. Mol. Biol.* 19, 458–460
39. Yi, Q. *et al.* (2018) HP 1 links centromeric heterochromatin to centromere cohesion in mammals. *EMBO Rep.* 19, 1–13
40. Mukhopadhyay, D. *et al.* (2010) The SUMO protease SENP6 is essential for inner kinetochore assembly. *J. Cell Biol.* 188, 681–692
41. Liebelt, F. *et al.* (2019) The poly-SUMO2/3 protease SENP6 enables assembly of the constitutive centromere-associated network by group deSUMOylation. *Nat. Commun.* 10, 3987
42. Stehmeier, P. and Muller, S. (2009) Regulation of p53 family members by the ubiquitin-like SUMO system. *DNA Repair (Amst)* 8, 491–498
43. Bischof, O. *et al.* (2006) The E3 SUMO ligase PIASy is a regulator of cellular senescence and apoptosis. *Mol. Cell* 22, 783–794
44. Sane, S. and Rezvani, K. (2017) Essential roles of E3 ubiquitin ligases in p53 regulation. *Int. J. Mol. Sci.* 18, 442
45. Li, M. (2003) Mono- versus polyubiquitination: differential control of p53 fate by Mdm2. *Science* 302, 1972–1975
46. Ding, B. *et al.* (2012) Overexpression of SKI oncoprotein leads to p53 degradation through regulation of MDM2 protein sumoylation. *J. Biol. Chem.* 287, 14621–14630
47. Kim, D.-H. *et al.* (2017) Rescuing p53 from mdm2 by a pre-structured motif in intrinsically unfolded SUMO specific protease 4. *BMB Rep.* 50, 485–486
48. Kim, D.H. *et al.* (2017) The mechanism of p53 rescue by SUSP4. *Angew. Chem. Int. Ed.* 56, 1278–1282
49. Motiam, A. El *et al.* (2019) Interplay between SUMOylation and NEDDylation regulates RPL11 localization and function. *FASEB J.* 33, 643–651
50. Hendriks, I.A. *et al.* (2014) Uncovering global SUMOylation signaling networks in a site-specific manner. *Nat. Struct. Mol. Biol.* 21, 927–936
51. Kalkat, M. *et al.* (2014) Identification of c-MYC SUMOylation by mass spectrometry. *PLoS One* 9, e115337
52. Sabò, A. *et al.* (2014) SUMOylation of Myc-family proteins. *PLoS One* 9, e91072
53. Kessler, J.D. *et al.* (2012) A SUMOylation-dependent transcriptional subprogram is required for Myc-driven tumorigenesis. *Science* 335, 348–353
54. Hoellein, A. *et al.* (2014) Myc-induced SUMOylation is a therapeutic vulnerability for B-cell lymphoma. *Blood* 124, 2081–2090
55. González-Prieto, R. *et al.* (2015) c-Myc is targeted to the proteasome for degradation in a SUMOylation-dependent manner, regulated by PIAS1, SENP7 and RNF4. *Cell Cycle* 14, 1859–1872
56. Rabellino, A. *et al.* (2016) PIAS1 promotes lymphomagenesis through MYC upregulation. *Cell Rep.* 15, 2266–2278
57. Suna, X.X. *et al.* (2018) SUMO protease SENP1 deSUMOylates and stabilizes c-Myc. *Proc. Natl. Acad. Sci. U. S. A.* 115, 10983–10988
58. Peng, Y. *et al.* (2019) SUMOylation down-regulates rDNA transcription by repressing expression of upstream-binding factor and proto-oncogene c-Myc. *J. Biol. Chem.* 294, 19155–19166
59. Yu, F. *et al.* (2018) SUMO suppresses and MYC amplifies transcription globally by regulating CDK9 sumoylation. *Cell Res.* 28, 670–685
60. Boulanger, M. *et al.* (2019) The SUMO pathway in hematomalignancies and their response to therapies. *Int. J. Mol. Sci.* 20, 3895
61. Seeler, J.S. and Dejean, A. (2017) SUMO and the robustness of cancer. *Nat. Rev. Cancer* 17, 184–197
62. Liu, X. *et al.* (2015) Knockdown of SUMO-activating enzyme subunit 2 (SAE2) suppresses cancer malignancy and enhances chemotherapy sensitivity in small cell lung cancer. *J. Hematol. Oncol.* 8, 67
63. Yang, Y. *et al.* (2019) SAE1 promotes human glioma progression through activating AKT SUMOylation-mediated signaling pathways. *Cell Commun. Signal.* 17, 82
64. Fukuda, I. *et al.* (2009) Ginkgolic acid inhibits protein SUMOylation by blocking formation of the E1-SUMO intermediate. *Chem. Biol.* 16, 133–140
65. Fukuda, I. *et al.* (2009) Kerriamycin B inhibits protein SUMOylation. *J. Antibiot. (Tokyo)* 62, 221–224
66. Takemoto, M. *et al.* (2014) Inhibition of protein SUMOylation by davidiin, an ellagitannin from *Davidia involucrata*. *J. Antibiot. (Tokyo)* 67, 335–338
67. Suzawa, M. *et al.* (2015) A gene-expression screen identifies a non-toxic sumoylation inhibitor that mimics SUMO-less human LRH-1 in liver. *Elife* 4, e09003
68. Darvin, P. *et al.* (2015) Tannic acid inhibits the Jak2/STAT3 pathway and induces G1/S arrest and mitochondrial apoptosis in YD-38 gingival cancer cells. *Int. J. Oncol.* 47, 1111–1120
69. Gerstmeier, J. *et al.* (2019) Ginkgolic acid is a multi-target inhibitor of key enzymes in pro-inflammatory lipid mediator biosynthesis. *Front. Pharmacol.* 10, 797
70. Kumar, A. *et al.* (2013) Identification of sumoylation activating enzyme 1 inhibitors by structure-based virtual screening. *J. Chem. Inf. Model.* 53, 809–820
71. Li, Y.-J. *et al.* (2019) Allosteric inhibition of ubiquitin-like modifications by a class of inhibitor of SUMO-activating enzyme. *Cell Chem. Biol.* 26, 278–288
72. Decque, A. *et al.* (2016) Sumoylation coordinates the repression of inflammatory and anti-viral gene-expression programs during innate sensing. *Nat. Immunol.* 17, 140–149
73. Crowl, J.T. and Stetson, D.B. (2018) SUMO2 and SUMO3 redundantly prevent a noncanonical type I interferon response. *Proc. Natl. Acad. Sci. U. S. A.* 115, 6798–6803
74. Khattar, M. *et al.* (2019) Abstract 3252: TAK-981: a first in class SUMO inhibitor in Phase 1 trials that promotes dendritic cell activation, antigen-presentation, and T cell priming. *Cancer Res.* 79, 3252
75. Brandt, M. *et al.* (2013) Development of a high-throughput screen to detect inhibitors of TRPS1 sumoylation. *Assay Drug Dev. Technol.* 11, 308–325
76. Wiechmann, S. *et al.* (2017) Site-specific inhibition of the small ubiquitin-like modifier (SUMO)-conjugating enzyme Ubc9 selectively impairs SUMO chain formation. *J. Biol. Chem.* 292, 15340–15351
77. Staley, A.L. and Rinehart, K.L. (1994) Spectomycins, new antibacterial compounds produced by *Streptomyces spectabilis*:

isolation, structures, and biosynthesis. *J. Antibiot. (Tokyo)* 47, 1425–1433
78. Hirohama, M. *et al.* (2013) Spectomycin B1 as a novel sumoylation inhibitor that directly binds to SUMO E2. *ACS Chem. Biol.* 8, 2635–2642
79. Kim, Y.S. *et al.* (2014) Synthesis of 2′,3′,4′-trihydroxyflavone (2-D08), an inhibitor of protein sumoylation. *Bioorg. Med. Chem. Lett.* 24, 1094–1097
80. Zhou, P. *et al.* (2019) 2-D08 as a SUMOylation inhibitor induced ROS accumulation mediates apoptosis of acute myeloid leukemia cells possibly through the deSUMOylation of NOX2. *Biochem. Biophys. Res. Commun.* 513, 1063–1069
81. Choi, B.H. *et al.* (2018) K-Ras Lys-42 is crucial for its signaling, cell migration, and invasion. *J. Biol. Chem.* 293, 17574–17581
82. Baik, H. *et al.* (2018) Targeting the sumo pathway primes all-trans retinoic acid–induced differentiation of nonpromyelocytic acute myeloid leukemias. *Cancer Res.* 78, 2601–2613
83. Huang, W. *et al.* (2012) Triptolide inhibits the proliferation of prostate cancer cells and down-regulates SUMO-specific protease 1 expression. *PLoS One* 7, e37693
84. Wu, J. *et al.* (2016) Momordin Ic, a new natural SENP1 inhibitor, inhibits prostate cancer cell proliferation. *Oncotarget* 7, 58995–59005
85. Zhao, Y. *et al.* (2016) Identification of SENP1 inhibitors through in silico screening and rational drug design. *Eur. J. Med. Chem.* 122, 178–184
86. Xie, W. *et al.* (2016) Development and evaluation of a highly reliable assay for SUMO-specific protease inhibitors. *Bioorg. Med. Chem. Lett.* 26, 2124–2128
87. Uno, M. *et al.* (2012) Discovery of 1-[4-(N-benzylamino)phenyl]-3-phenylurea derivatives as non-peptidic selective SUMO-sentrin specific protease (SENP)1 inhibitors. *Bioorg. Med. Chem. Lett.* 22, 5169–5173
88. Lindenmann, U. *et al.* (2020) Discovery of a class of potent and selective non-competitive sentrin-specific protease 1 inhibitors. *ChemMedChem* 15, 675–679
89. Bernstock, J.D. *et al.* (2018) Quantitative high-throughput screening identifies cytoprotective molecules that enhance SUMO conjugation via the inhibition of SUMO-specific protease (SENP)2. *FASEB J.* 32, 1677–1691
90. Demarque, M.D. *et al.* (2011) Sumoylation by Ubc9 regulates the stem cell compartment and structure and function of the intestinal epithelium in mice. *Gastroenterology* 140, 286–296
91. López, I. *et al.* (2020) An unanticipated tumor-suppressive role of the SUMO pathway in the intestine unveiled by Ubc9 haploinsufficiency. *Oncogene* 39, 6692–6703
92. Lallemand-Breitenbach, V. *et al.* (2008) Arsenic degrades PML or PML-RARα through a SUMO-triggered RNF4/ ubiquitin-mediated pathway. *Nat. Cell Biol.* 10, 547–555
93. Tatham, M.H. *et al.* (2008) RNF4 is a poly-SUMO-specific E3 ubiquitin ligase required for arsenic-induced PML degradation. *Nat. Cell Biol.* 10, 538–546
94. Maroui, M.A. *et al.* (2012) Requirement of PML SUMO interacting motif for RNF4- or arsenic trioxide-induced degradation of nuclear PML isoforms. *PLoS One* 7, e44949
95. Auvin, S. *et al.* (2019) A molecule inducing androgen receptor degradation and selectively targeting prostate cancer cells. *Life Sci. Alliance* 2, e201800213
96. Mills, C.C. *et al.* (2018) Development of chemotherapy with cell-cycle inhibitors for adult and pediatric cancer therapy. *Cancer Res.* 78, 320–325
97. Havel, J. *et al.* (2019) The evolving landscape of biomarkers for checkpoint inhibitor immunotherapy. *Nat. Rev. Cancer* 19, 133–150
98. Gâtel, P. *et al.* (2020) Ubiquitin and SUMO conjugation as biomarkers of acute myeloid leukemias response to chemotherapies. *Life Sci. Alliance* 3, e201900577
99. Manasanch, E.E. and Orlowski, R.Z. (2017) Proteasome inhibitors in cancer therapy. *Nat. Rev. Clin. Oncol.* 14, 417–433
100. Yang, Y. *et al.* (2007) Inhibitors of ubiquitin-activating enzyme (E1), a new class of potential cancer therapeutics. *Cancer Res.* 67, 9472–9481
101. Best, S. *et al.* (2019) Targeting ubiquitin-activating enzyme induces ER stress-mediated apoptosis in B-cell lymphoma cells. *Blood Adv.* 3, 51–62
102. Hyer, M.L. *et al.* (2018) A small-molecule inhibitor of the ubiquitin activating enzyme for cancer treatment. *Nat. Med.* 24, 186–193
103. Barghout, S.H. *et al.* (2019) Preclinical evaluation of the selective small-molecule UBA1 inhibitor, TAK-243, in acute myeloid leukemia. *Leukemia* 33, 37–51
104. Brown, J.S. and Jackson, S.P. (2015) Ubiquitylation, neddylation and the DNA damage response. *Open Biol.* 5, 150018
105. Jang, S.M. *et al.* (2018) Chromatin-bound cullin-ring ligases: regulatory roles in DNA replication and potential targeting for cancer therapy. *Front. Mol. Biosci.* 5, 19
106. Soucy, T.A. *et al.* (2009) An inhibitor of NEDD8-activating enzyme as a new approach to treat cancer. *Nature* 458, 732–736
107. Soucy, T.A. *et al.* (2010) The NEDD8 conjugation pathway and its relevance in cancer biology and therapy. *Genes and Cancer* 1, 708–716
108. Wang, M. *et al.* (2011) Targeting protein neddylation: a novel therapeutic strategy for the treatment of cancer. *Expert Opin. Ther. Targets* 15, 253–264
109. Shah, J.J. *et al.* (2016) Phase I study of the novel investigational NEDD8-activating enzyme inhibitor pevonedistat (MLN4924) in patients with relapsed/refractory multiple myeloma or lymphoma. *Clin. Cancer Res.* 22, 34–43
110. Bhatia, S. *et al.* (2016) A phase I study of the investigational NEDD8-activating enzyme inhibitor pevonedistat (TAK-924/ MLN4924) in patients with metastatic melanoma. *Investig. New Drugs* 34, 439–449
111. Malhab, L.J.B. *et al.* (2016) The use of the NEDD8 inhibitor MLN4924 (pevonedistat) in a cyclotherapy approach to protect wild-type p53 cells from MLN4924 induced toxicity. *Sci. Rep.* 6, 37775
112. Yoshida, M.M. and Azuma, Y. (2016) Mechanisms behind topoisomerase II SUMOylation in chromosome segregation. *Cell Cycle* 15, 3151–3152
113. Antoniou-Kourounioti, M. *et al.* (2019) The impact of the C-terminal region on the interaction of topoisomerase II alpha with mitotic chromatin. *Int. J. Mol. Sci.* 20, 1238
114. Piskadlo, E. and Oliveira, R.A. (2017) A topology-centric view on mitotic chromosome architecture. *Int. J. Mol. Sci.* 18, 2751
115. Sridharan, V. *et al.* (2015) SUMOylation regulates polo-like kinase 1-interacting checkpoint helicase (PICH) during mitosis. *J. Biol. Chem.* 290, 3269–3276
116. Hassebroek, V.A. *et al.* (2020) PICH regulates the abundance and localization of SUMOylated proteins on mitotic chromosomes. *Mol. Biol. Cell* 31, 2537–2556
117. Chan, Y.W. *et al.* (2018) Unresolved recombination intermediates lead to ultra-fine anaphase bridges, chromosome breaks and aberrations. *Nat. Cell Biol.* 20, 92–103
118. Bisht, S. and Haering, C.H. (2019) Twist to disentangle. *Nat. Struct. Mol. Biol.* 26, 252–253
119. Schneekloth, J.S. (2017) Drug discovery: controlling protein SUMOylation. *Nat. Chem. Biol.* 13, 1141–1142
120. Hannoun, Z. *et al.* (2016) The implication of SUMO in intrinsic and innate immunity. *Cytokine Growth Factor Rev.* 29, 3–16
121. Ran, Y. *et al.* (2011) SENP2 negatively regulates cellular antiviral response by deSUMOylating IRF3 and conditioning it for ubiquitination and degradation. *J. Mol. Cell Biol.* 3, 283–292
122. Xia, P. *et al.* (2015) IRTKS negatively regulates antiviral immunity through PCBP2 sumoylation-mediated MAVS degradation. *Nat. Commun.* 6, 8132
123. Liang, Q. *et al.* (2011) Tripartite motif-containing protein 28 is a small ubiquitin-related modifier E3 ligase and negative regulator of IFN regulatory factor 7. *J. Immunol.* 187, 4754–4763
124. Liu, X. *et al.* (2013) Dynamic regulation of innate immunity by ubiquitin and ubiquitin-like proteins. *Cytokine Growth Factor Rev.* 24, 559–570
125. Chang, T.-H. *et al.* (2012) The small ubiquitin-like modifier-deconjugating enzyme sentrin-specific peptidase 1 switches IFN regulatory factor 8 from a repressor to an activator during macrophage activation. *J. Immunol.* 189, 3548–3556
126. Hu, M.-M. *et al.* (2016) Sumoylation promotes the stability of the DNA sensor cGAS and the adaptor STING to regulate the kinetics of response to DNA virus. *Immunity* 45, 555–569
127. Cui, Y. *et al.* (2017) SENP7 potentiates cGAS activation by relieving SUMO-mediated inhibition of cytosolic DNA sensing. *PLoS Pathog.* 13, e1006156

128. Lima, C.D. and Reverter, D. (2008) Structure of the human SENP7 catalytic domain and poly-SUMO deconjugation activities for SENP6 and SENP7. *J. Biol. Chem.* 283, 32045–32055
129. Adorisio, S. *et al.* (2017) SUMO proteins: guardians of immune system. *J. Autoimmun.* 84, 21–28
130. Lu, X. *et al.* (2010) Designed semisynthetic protein inhibitors of Ub/Ubl E1 activating enzymes. *J. Am. Chem. Soc.* 132, 1748–1749
131. Kumar, A. *et al.* (2016) Identification of new SUMO activating enzyme 1 inhibitors using virtual screening and scaffold hopping. *Bioorg. Med. Chem. Lett.* 26, 1218–1223
132. Kim, Y.S. *et al.* (2013) An electrophoretic mobility shift assay identifies a mechanistically unique inhibitor of protein sumoylation. *Chem. Biol.* 20, 604–613
133. Zlotkowski, K. *et al.* (2017) A small-molecule microarray approach for the identification of E2 enzyme inhibitors in ubiquitin-like conjugation pathways. *SLAS Discov.* 22, 760–766
134. Qiao, Z. *et al.* (2011) Design, synthesis, and biological evaluation of benzodiazepine-based SUMO-specific protease 1 inhibitors. *Bioorg. Med. Chem. Lett.* 21, 6389–6392
135. Chen, Y. *et al.* (2012) 2-(4-Chlorophenyl)-2-oxoethyl 4-benzamidobenzoate derivatives, a novel class of SENP1 inhibitors: virtual screening, synthesis and biological evaluation. *Bioorg. Med. Chem. Lett.* 22, 6867–6870
136. Kumar, A. *et al.* (2014) Identification of 1,2,5-oxadiazoles as a new class of SENP2 inhibitors using structure based virtual screening. *J. Chem. Inf. Model.* 54, 870–880
137. Ambaye, N. *et al.* (2018) Streptonigrin inhibits SENP1 and reduces the protein level of hypoxia-inducible factor 1α (HIF1α) in cells. *Biochemistry* 57, 1807–1813
138. Brownell, J.E. *et al.* (2010) Substrate-assisted inhibition of ubiquitin-like protein-activating enzymes: the NEDD8 E1 inhibitor MLN4924 forms a NEDD8-AMP mimetic in situ. *Mol. Cell.* 37, 102–111