



# Ubiquitin, SUMO, and NEDD8: Key Targets of Bacterial Pathogens

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# **Ubiquitin, SUMO, Nedd8 :**

## **privileged targets of bacterial pathogens**

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13

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15   **Abstract (100-120 words)**

16

17   Manipulation of host protein post-translational modifications is used by various pathogens to  
18   interfere with host cell functions. Among these modifications, Ubiquitin and Ubiquitin-like  
19   proteins constitute privileged targets as they represent regulators of pathways essential for the  
20   host cell. In particular, these post-translational modifiers control pathways that have been  
21   described as critical for infection such as pathogen entry, replication, propagation or detection  
22   by the host. Although bacterial pathogens lack Ubiquitin or Ubiquitin-like protein systems,  
23   many of them produce proteins that specifically interfere with these host post-translational  
24   modifications during infection. In this review, we will discuss the different mechanisms used  
25   by bacteria to interfere with host Ubiquitin and Ubiquitin-like proteins (UBLs), such as SUMO  
26   or NEDD8.

27 **Highlights :**

28

29 \* Ubiquitin and UBLs regulate essential pathways of the host cell involved in critical steps of  
30 bacterial infections. Not surprisingly, bacterial pathogens have evolved numerous strategies to  
31 interfere with these host post-translational modifications.

32

33 \* Besides Ubiquitin, Ubiquitin-like proteins such as SUMO and NEDD8 have recently emerged  
34 as privileged targets of bacterial pathogens.

35

36 \* Strategies used by bacteria to interfere with host Ubi/UBL encompass the targeting of  
37 Ubi/UBL conjugation machineries, the modulation of the Ubi/UBL conjugation level of  
38 specific host factors and the direct targeting of Ubi/UBL proteins.

39

40 \* Host proteins modified by Ubi/UBL and targeted by bacteria cluster into specific host cell  
41 functions such as gene regulation, cytoskeleton dynamics or cell-autonomous immunity.

42

43 \* Bacteria hijack the host Ubi/UBL systems to modify their own proteins allowing a regulation  
44 of their intracellular localization, stability or interaction abilities.

45

46 **Outstanding questions :**

47

48 \* Are the recently described non-canonical ubiquitination mechanisms (*i.e.* conjugation  
49 involving non-RING/non-HECT E3 ligases or E1/E2-independent ubiquitin conjugation)  
50 strictly restricted to bacteria? Or are there functional homologs of these bacterial enzymes  
51 encoded by human cells?

52

53 \* Recent improvements in proteomic analyses now allow to thoroughly monitor changes in the  
54 host ubiquitinome/"UBL-ome" in response to infection. These approaches usually generate lists  
55 of thousands of protein and/or sites modified during infection. Which strategies researchers  
56 should use to cope with this complex set of data and identify the key players affecting the  
57 outcome of infection ?

58

59 \* What are the mutations in the human population affecting the Ubi/UBL systems that may  
60 confer higher susceptibility to bacterial pathogens ?

61

62 \* Would drugs targeting bacteria-specific enzymes interfering with host Ubi/UBL conjugation  
63 be efficient to treat infectious diseases ?

64 **Ubiquitin and Ubiquitin-like proteins constitute essential modifiers of host proteins**

65

66 Post-translational modifications (PTM) of proteins encompass a wide range of chemical  
67 modifications. These PTMs include the cleavage of peptide bonds (proteolysis), the  
68 modification of specific amino acid side chains such as deamidation, eliminylation or the  
69 covalent addition of chemical moieties ranging from simple groups (such as phosphate, acetyl  
70 or methyl groups) to more complex groups such as sugar, lipids or even small polypeptides).

71 Ubiquitin is a small polypeptide of 76 amino acids that can be covalently linked, via its C-  
72 terminal glycine residue, to target proteins. Ubiquitination, *i.e.* the conjugation of Ubiquitin,  
73 usually occurs on lysine residues of target proteins although conjugation to other amino acids  
74 such as threonine, serine, tyrosine or cysteine may happen. Ubiquitin itself contains seven  
75 lysines (K6, K11, K27, K29, K33, K48 and K63) that can serve as sites for additional cycles of  
76 Ubiquitin attachment, resulting in the formation of Ubiquitin chains. The topology of these  
77 chains is very diverse, ranging from “homotypic” K48- or K63-linked chains, composed of only  
78 one type of Ubiquitin linkage, to “mixed” chains containing for example both K11 and K63  
79 linkages [1,2]. An additional type of chains, called “linear” chains, is generated when Ubiquitin  
80 is attached to the N-terminus of a second Ubiquitin [3]. Targeting of a given protein by  
81 Ubiquitin may thus result in mono-ubiquitination, multi-mono-ubiquitination (*i.e.* several  
82 mono-ubiquitination on different amino acids) or poly-ubiquitination. Ubiquitin is attached to  
83 substrates by a three-step enzymatic cascade involving E1 (Ubiquitin activating enzyme), E2  
84 (Ubiquitin-conjugating enzyme) and E3 (Ubiquitin ligase) enzymes [2]. Ubiquitin is first  
85 activated in an ATP-dependent manner by E1, which links the C-terminal glycine residue of  
86 Ubiquitin via a thioester bond to a cysteine residue within the E1 active site. This activated  
87 Ubiquitin is then transferred to the catalytic cysteine residue of an E2 enzyme. E3 ligases then  
88 finally mediate the transfer of ubiquitin from the E2 enzyme to specific substrates. There are

89 two major classes of E3s: the HECT (homologous to the E6-AP carboxyl terminus) type and  
90 the RING (really interesting new genes)/U-box type. HECT-type E3 Ubiquitin ligases form a  
91 reactive intermediate with ubiquitin before its transfer to the substrate protein whereas  
92 RING/U-box-type E3 ligases mediate transfer of ubiquitin from the E2 directly to the substrate  
93 protein, without formation of an E3-ubiquitin intermediate [4]. Conjugation of Ubiquitin is a  
94 reversible process as several cellular isopeptidases (called deubiquitinases or DUBs) can cleave  
95 the covalent bond between Ubiquitin and its targets and thereby remove ubiquitin [5].  
96 Besides Ubiquitin, other polypeptides such as SUMO (Small Ubiquitin-like MOdifier) [6],  
97 NEDD8 (neural precursor cell expressed developmentally downregulated protein 8) [7], ISG15  
98 (interferon-stimulated gene 15) [8] or FAT10 (HLA-F-adjacent transcript 10) [9] can be  
99 similarly conjugated to target proteins. These polypeptides are grouped in the so-called  
100 Ubiquitin-like proteins (UBL) family and share high structural homology with Ubiquitin [10].  
101 The mechanisms of UBL conjugation on target substrates are very similar to the ones observed  
102 for ubiquitination. The enzymes required for all these modifications (*i.e.* E1 UBL activating  
103 enzymes, E2 UBL conjugating enzymes and E3 UBL ligases) share highly conserved domain  
104 structures [10]. Of note, the number of UBL specific E1, E2 and E3 enzymes is usually smaller  
105 than for Ubiquitin. For example, SUMO conjugation to thousands of cellular targets seem to  
106 rely only on one single SUMO E1 enzyme (SAE1/UBA2), one single SUMO E2 enzyme  
107 (UBC9) and a dozen of SUMO E3 ligases [6]. As for Ubiquitin, the formation of UBL chains  
108 (where UBLs are conjugated to internal lysines of other UBLs) has been reported for SUMO  
109 and NEDD8 [6,7]. Finally, as for Ubiquitin, the host cell encodes several ULPs (UBL-specific  
110 proteases) that guarantee the reversibility of UBLs conjugation [6-9].  
111 The consequences of Ubi/UBL conjugation on the fate of the modified proteins are very diverse.  
112 Ubi/UBL can alter the half-life of the modified proteins, for example by targeting them to  
113 proteasome degradation. They can change the targets' structure thereby changing their catalytic

activity. They can add new surfaces of interactions or mask internal binding domains and change the targets' interactome. The cell encodes in particular many "receptors" containing Ubiquitin-binding domains (UBDs) or UBL binding domains (such as the SUMO interacting motifs [SIMs]), that interact with proteins once conjugated to Ubi/UBL and "decode" these modifications into biochemical cascades in the cell [6,11]. Besides the well-known example of K48-Ubiquitin chains conjugation that target modified proteins to proteasomal degradation, it is usually very difficult to anticipate the consequences of Ubiquitin or UBL conjugation of a given target.

Ubi/UBL are essential regulators of fundamental pathways in cell biology. Some of these pathways are critical for the outcome of infection by pathogens. For example, Ubiquitin is a major regulator of the NF- $\kappa$ B pathway, that triggers the expression of proinflammatory cytokines in response to pathogen detection [12]. SUMO is a central player in the regulation of type I interferon and in anti-viral gene expression programs [13]. ISG15 plays several independent roles in anti-viral defense and can restrict intracellular bacteria replication *in vitro* and *in vivo* [8,14,15]. FAT10 was reported to be involved in xenophagy and in antimicrobial defense [9,16]. It is thus not surprising that pathogens evolved strategies to target Ubi/UBL and interfere with these different cellular processes.

In this review, we will present how pathogens interfere with the host Ubi/UBL systems. Ubiquitin and UBL systems have been shown to be targeted by diverse pathogens such as viruses, bacteria or parasites, including *Plasmodium falciparum* or *Toxoplasma gondii* [17-24]. We will focus here on pathogenic bacteria as they display the widest variety of Ubi/UBL interfering strategies known to date. Although bacteria do not have their own Ubi/UBL systems, numerous species encode virulence factors that actually manipulate host Ubi/UBL systems. These factors can be toxins secreted in the extracellular space in the vicinity of the host cell, or effectors delivered directly into host cells via specialized secretion systems such as Type III

139 secretion systems (T3SS). We will discuss how bacterial pathogens (i) target Ubi/UBLs  
140 conjugation machineries, (ii) increase or decrease the Ubi/UBL conjugation on specific host  
141 factors, (iii) directly target Ubi/UBL polypeptides, or (iv) use host Ubi/UBL to modify their  
142 own proteins. We will enlighten how these mechanisms allow bacterial pathogens to manipulate  
143 specific host cellular pathways in order to promote infection.

144

#### 145 **Harnessing of host Ubiquitin and UBLs conjugation by bacterial pathogens**

146 *Targeting of host Ubiquitin and UBLs conjugation machinery enzymes*

147 Targeting of host E1 or E2 ubiquitin enzymes is a conserved strategy used by pathogens to  
148 dampen ubiquitination (Fig. 1, Key figure). This strategy is used for example by *Shigella*  
149 *flexneri*, the etiological agent of bacillary dysentery. This bacterium secretes through its T3SS,  
150 an effector, named OspI, that deamidates the human E2 Ubiquitin enzyme UBC13 [25]. This  
151 deamidation inactivates UBC13 Ubiquitin-conjugating activity, leading to the dampening of  
152 the Ubiquitin-dependent TRAF6-mediated signaling pathways and to the inhibition of host  
153 inflammatory responses during infection [25]. Extracellular pathogens such as  
154 enteropathogenic *Escherichia coli* (EPEC) also targets the host Ubiquitin conjugation  
155 machinery. Adhesion of these bacteria to human cells leads to the degradation of UBE1 and  
156 UBA6, the two E1 Ubiquitin enzymes, and to a global decrease of host protein ubiquitination  
157 [26]. The SUMO conjugation machinery constitutes another target for bacterial pathogens.  
158 *Listeria monocytogenes*, the bacterium responsible for human listeriosis, dampens  
159 SUMOylation of specific host factors by triggering the degradation of UBC9, the unique host  
160 E2 SUMO enzyme [27-29]. This degradation of UBC9 is triggered by the formation of pores  
161 into the host plasma membrane by the bacterial toxin Listeriolysin O (LLO) [27]. As LLO pores  
162 are not reported to affect the activity of host deSUMOylases, UBC9 degradation ultimately  
163 results in a shift in the SUMOylation/deSUMOylation equilibrium in the cell and to the

164 deSUMOylation of host proteins such as transcription factors [28]. The deSUMOylation events  
165 triggered by LLO were shown to promote *Listeria* infection [27]. Of note, other toxins of the  
166 same family as LLO, and secreted by extracellular pathogens, were shown to downregulate  
167 UBC9, indicating that interference with host SUMOylation is a strategy conserved between  
168 different classes of pathogenic bacteria [27]. Inhibition of the SUMOylation machinery is also  
169 observed during infection with *Salmonella* Typhimurium, a bacterium responsible for  
170 gastroenteritis in humans, and with *Shigella flexneri* but the underlying mechanisms involved  
171 here do not rely on the production of bacterial toxins. In the case of *Salmonella* Typhimurium,  
172 infection leads to the upregulation in the host cell of two small noncoding RNAs (miR30c and  
173 miR30e) that downregulate UBC9 level [30]. In the case of *Shigella flexneri*, infection is  
174 associated with an influx of calcium into the host cell. This ion flux activates the host proteases  
175 calpains, which cleave UBA2, one of the two components of the E1 SUMO enzyme [31]. The  
176 resulting inhibition of SUMOylation is associated with an increase in *Shigella* entry [31,32].  
177

#### 178 *Secretion of bacterial effectors mimicking host Ubiquitin and UBL enzymes*

179 Besides interfering with Ubiquitin or UBL-conjugation machineries, bacterial pathogens  
180 produce proteins that can replace or act as components of these machineries (Fig. 1). In  
181 particular, several bacterial effectors possess Ubiquitin E3-like activity. Some of these bacterial  
182 effectors share structural homologies with the two major types of eukaryotic E3 ligases, *i.e.* the  
183 HECT type and the RING/U-box type E3 ligases [20-22]. These effectors may have been  
184 acquired by bacteria via horizontal transfer from diverse eukaryotic sources [33]. In addition to  
185 these types, three other classes of bacterial effectors display structures completely distinct from  
186 eukaryotic E3 ligases: NELs (for Novel E3 ligase) [33], XL-box-containing E3 ligases [34] and  
187 SidC ligase [35]. These ligases may represent structures evolved by pathogens to mimic the  
188 functions of these essential host enzymes. These different classes of E3 ligases enable bacteria

189 to conjugate Ubiquitin on specific host factors, thereby altering their stability or function,  
190 subcellular localization or interaction with other cellular proteins. Bacterial E3 ligases may in  
191 particular conjugate K48-Ubiquitin chains to host proteins, thereby triggering their proteasome-  
192 dependent degradation. By re-routing host factors to one of the most efficient proteolytic system  
193 of the infected cell, bacteria manage to eliminate key host components that normally interfere  
194 with their replication and propagation. Finally, bacterial E3 ligases can also target other  
195 bacterial effectors, co-delivered during infection, allowing a tight restriction of their activity  
196 during a specific time frame[21,22,36] (see below).

197 In contrast to bacterial effectors mimicking host ubiquitin enzymes, a family of proteins  
198 secreted by the bacterial pathogen *Legionella pneumophila*, the causative agent of  
199 Legionnaires' disease, was recently shown to catalyze the ubiquitination of host proteins  
200 without the need for E1 and E2 Ubiquitin enzymes [37-39]. The *Legionella* SdeA effector  
201 belongs to this family of enzymes: it conjugates Ubiquitin on endoplasmic reticulum (ER)-  
202 associated Rab GTPases and participate to bacteria virulence [37]. By acting independently of  
203 E1- and E2-Ubiquitin enzymes, SdeA extends the repertoire of proteins potentially modified by  
204 Ubiquitin. Conjugation of Ubiquitin on host targets by SdeA does not rely on ATP and does  
205 not occur on lysines. Ubiquitin is instead phosphoribosylated by SdeA on a specific arginine  
206 residue, before being conjugated to a serine residue of its host target through a phosphodiester  
207 bond [38]. In addition to ER-associated Rab GTPases, the *Legionella* effector SdeA and other  
208 members of the Sde family ubiquitinate the host protein reticulon 4 (Rtn4), leading to ER  
209 reorganization and promoting *Legionella*-containing vacuoles formation [39]. Unconventional  
210 Ubiquitin conjugation by Sde effectors is reversible as *L. pneumophila* codes for a specific  
211 deubiquitinase, SidJ, that removes phosphoribosylated Ubiquitin from its substrate [40].  
212 Whether functional homologs of SdeA exist in eukaryotes and what roles they may play remain  
213 to be determined.

214

215 *Deconjugation of Ubiquitin and UBL proteins from host targets catalyzed by bacterial effectors*  
216 Another strategy used by bacteria to interfere with Ubiquitin or UBL conjugation consists in  
217 the secretion into host cells of effectors with isopeptidase activity, which remove Ubiquitin or  
218 UBL from their targets (Fig. 1). XopD, for example, is a T3SS effector secreted by the plant  
219 pathogen *Xanthomonas euvesicatoria*, which possesses a SUMO-specific isopeptidase activity  
220 [41]. Upon infection of tomato cells, it deconjugates SUMO from the SIERF4 transcription  
221 factor to suppress host ethylene production, which constitutes an important pathway of plants  
222 anti-bacterial immunity [42]. Many other bacterial proteases targeting Ubiquitin or UBLs have  
223 been identified in bacterial pathogens including *Salmonella*, *Shigella*, *Chlamydia*, and  
224 *Legionella*, some of them being specific for one UBL while others display cross-reactivity  
225 between different UBLs [43,44]. Interestingly, several bacterial effectors possessing a  
226 deubiquitinase activity display a strong preference for K63-linked chains over K48 or K11  
227 chains [44]. This may reveal a significant selection pressure for bacteria to interfere with this  
228 specific Ubiquitin-modification in order to promote infection.

229

230 *Direct targeting of Ubiquitin and UBL polypeptides*

231 Ubiquitin itself, as well as other UBLs, can be directly targeted and inactivated by bacterial  
232 effectors (Fig. 1). Phosphoribosylation of Ubiquitin for example, catalyzed by the *Legionella*  
233 SdeA effector, was reported to interfere with multiple steps of the ubiquitination cascade [38].  
234 The presence of phosphoribosylated Ubiquitin in chains further confers resistance to various  
235 deubiquitinases [45]. SdeA, by both triggering E1 and E2-independent ubiquitination of  
236 specific host targets and by inhibiting ubiquitination of others, thus efficiently controls the host  
237 ubiquitinome.

238 Ubiquitin and NEDD8 are also targeted by a family of bacterial T3SS effectors called Cifs (for  
239 cycle inhibiting factors), produced by diverse pathogenic bacteria such as some EPEC or  
240 *Burkholderia pseudomallei* [46]. Cifs directly target NEDD8 and Ubiquitin and catalyse the  
241 deamidation of the Gln<sup>40</sup> residue of these polypeptides [47]. Deamidation of Ubiquitin  
242 interferes with Ubiquitin chain formation, whereas deamidation of NEDD8 blocks the activity  
243 of neddylated Cullin-RING E3 Ubiquitin ligases (CRLs) and impairs ubiquitination of several  
244 CRL substrates in EPEC-infected cells [47,48]. Cifs interfere in particular with the  
245 ubiquitination of Perforin-2/MPEG1 (Macrophage-expressed gene 1), an anti-microbial host  
246 protein forming pores on bacteria cells, thereby blocking its intracellular trafficking and its  
247 bactericidal activity [49].

248

#### 249 **Main host pathways targeted by bacteria and regulated by Ubiquitin or UBLs**

250 During infection, bacterial pathogens alter the conjugation of Ubiquitin or UBLs on many  
251 different host proteins. These proteins belong to different pathways that are all essential for  
252 bacteria to efficiently enter into host cells and replicate therein, or to dampen host anti-bacterial  
253 responses. We will here detail some of the pathways tightly regulated by Ubi/UBL  
254 modifications and frequently targeted by bacterial pathogens.

255

#### 256 *The NF-κB pathway*

257 The NF-κB pathway is an essential pillar of innate immunity and inflammation. Activation of  
258 this pathway, for example after the detection of bacteria-derived molecules by host sensors,  
259 triggers the expression of a wide range of proinflammatory chemokines and cytokines. Not  
260 surprisingly, many bacterial effectors target the NF-κB pathway to dampen the host innate  
261 immune response. One given pathogen may in particular produce several independent effectors  
262 targeting this pathway [12]. This apparent redundancy of effectors, that all target the same

263 signaling cascade, reflects the diversity of danger signals sensed by the host and triggering this  
264 pathway.

265 One common strategy used by bacterial pathogens to dampen the NF- $\kappa$ B signaling cascade  
266 consists in conjugating K48-Ubiquitin chains to essential components of this pathway thereby  
267 triggering their proteasome-dependent degradation. *Shigella flexneri*, for example, uses at least  
268 five different effectors to inhibit essential branches of the NF- $\kappa$ B pathway: IpaH1.4 and IpaH2.5  
269 ubiquitinate LUBAC, a complex involved in the activation of the NF- $\kappa$ B pathway that  
270 conjugates linear Ubiquitin chains to the NF- $\kappa$ B modulator NEMO [50]; IpaH0722  
271 ubiquitinates TRAF2, a factor involved in the NF- $\kappa$ B pathway activation following the  
272 detection of intracytosolic bacteria [51]; IpaH9.8 ubiquitinates NEMO and thereby perturbs the  
273 NF- $\kappa$ B activation triggered by bacterial peptidoglycan detection [52].

274 Besides triggering proteasome-dependent degradation of components of the NF- $\kappa$ B pathway,  
275 bacterial pathogens also interfere with the endogenous Ubiquitination of critical NF- $\kappa$ B  
276 regulators: as mentioned above, the *Shigella* OspI effector inhibits the host E2 enzyme UBC13,  
277 thereby blocking TRAF6-mediated activation of the NF- $\kappa$ B pathway [25]; OspG, another  
278 *Shigella* effector, binds to and inhibits the host E2 Ubiquitin enzyme UBCH5, involved in IkBa  
279 ubiquitination [53]; the NleB effector, encoded by EPEC, blocks TRAF2 polyubiquitination,  
280 ultimately suppressing NF- $\kappa$ B activation [54] and NleE, another EPEC effector, inhibits IkBa  
281 phosphorylation, which is a prerequisite for its subsequent Ubiquitination and degradation [55].  
282 The NF- $\kappa$ B pathway thereby constitutes a nice example of the diverse mechanisms evolved by  
283 bacteria to promote or inhibit ubiquitination of a large number of components in a coordinated  
284 fashion, resulting in the dampening of an essential arm of the host anti-bacterial response. Of  
285 course, these interfering strategies are not restricted to the NF- $\kappa$ B pathway and other important  
286 signaling cascades of the innate immune response, such as the IFN response or the activation  
287 of inflammasome, can be similarly targeted [21,56].

288

289 *Host cytoskeleton*

290 Remodeling of the host cytoskeleton is frequently used by intracellular bacterial pathogens to  
291 enter into the targeted cells, create a niche where they can efficiently replicate, and disseminate  
292 to neighboring cells. Several components of the host cytoskeleton are regulated by Ubiquitin.  
293 RhoGTPases, for example, which control the actin cytoskeleton dynamics, are degraded by the  
294 proteasome following Ubiquitin conjugation [57]. Interestingly, the ubiquitination level of  
295 RhoGTPases can be modulated during *Salmonella* infection, suggesting that this bacterium may  
296 modulate RhoGTPases turn-over [58]. SUMO can be conjugated to different components of  
297 the host cytoskeleton as well, including actin itself and actin regulatory proteins, septins or  
298 intermediate filaments such as keratins and lamins [59,60]. The role of Ubiquitin and UBL  
299 modifications in the regulation of the cytoskeleton is only in its infancy but one can anticipate  
300 that it may represent an important target for bacterial pathogens to manipulate the cell  
301 architecture.

302

303 *Transcription factors*

304 In order to exploit host functions, bacterial pathogens remodel the proteome of infected cells.  
305 This remodeling may result from deregulation of gene transcription by injection of bacterial  
306 proteins such as nucleomodulins that act directly on host nucleus [61], or by interference with  
307 host transcription factors, some of them being regulated by Ubiquitin or UBLs. *Listeria*  
308 *monocytogenes*, for example, dampens the SUMOylation of numerous transcription factors  
309 during infection [28]. As SUMO conjugation either increases or decreases transcription factors  
310 activity, this decrease in SUMOylation may modulate the expression of specific subset of genes  
311 and lead to a reprogramming of host gene expression. As mentioned above, decreasing the  
312 SUMOylation of host transcription factors is a strategy also used by the plant pathogen

313 *Xanthomonas euvesicatoria* that specifically targets SUMO-SIERF4 to dampen the host  
314 ethylene-mediated antibacterial response [42]. Finally, the colibactin toxin, produced by some  
315 *Escherichia coli* strains in the intestine, induces a downregulation of the SUMO isopeptidase  
316 SENP1 and an increase in the SUMOylation of the transcription factor p53. This ultimately  
317 results in the emergence of senescent cells secreting growth factors that may promote colorectal  
318 carcinogenesis [62].

319

### 320 *PML Nuclear Bodies*

321 PML (Promyelocytic Luekemia Protein) is a protein that polymerizes in discrete nuclear  
322 assemblies known as PML nuclear bodies (NBs) and plays essential roles in many different  
323 cellular processes. Key to its function, PML can be post-translationally modified by SUMO. In  
324 addition to its role in anti-viral host defense [18], PML was recently identified as a sensor for  
325 bacteria producing pore-forming toxins [29]. Indeed, intoxication of human cells by the  
326 Listeriolysin O toxin, secreted by *L. monocytogenes*, triggers a massive deSUMOylation of  
327 PML. This deSUMOylation of PML, coupled to an oxidative stress-dependent multimerization  
328 of PML, initiates host cell anti-bacterial responses leading to a decrease in *Listeria* intracellular  
329 replication [29]. This example of PML highlights how SUMO alterations of some specific host  
330 proteins can constitute danger signals for the cells that triggers back adapted responses. The  
331 putative role of PML in other bacterial infections targeting host SUMOylation, such as *Shigella*  
332 or *Salmonella*, remains unknown but would deserves further investigation.

333

### 334 **Post-translational modifications of bacterial proteins during infection**

335 Besides interfering with host proteins post-translational modifications, bacteria can hijack host  
336 Ubiquitin or UBL-conjugation machineries to modify their own components (Fig. 1). As for  
337 eukaryotic proteins, conjugation of Ubiquitin or UBL have diverse effects on bacterial effectors

338 and may change their intracellular localization, their stability or their interaction with other  
339 bacterial or host factors. Post-translational modification of bacterial proteins couples their  
340 activity to their arrival into the host cell cytoplasm. Interestingly, post-translational  
341 modification of bacterial proteins can also be used by the host to tag exogenous proteins and  
342 target them for degradation.

343 Ubiquitination of *Salmonella* proteins constitutes a nice example illustrating the versatility of  
344 consequences of this post-translational modification on bacterial proteins activity. SopE and  
345 SptP are two *Salmonella* effectors that contribute to the transient remodeling of the host cell's  
346 cytoskeleton. These two effectors, which are delivered simultaneously by *Salmonella*, exhibit  
347 different half-lives. SopE, which is involved in actin cytoskeleton rearrangement, membrane  
348 ruffling and bacteria uptake, is rapidly polyubiquitinated and degraded by the host proteasome  
349 [63]. SptP, which displays an opposite activity to SopE, exhibits a much slower degradation  
350 kinetics, allowing recovery of the actin cytoskeleton's normal architecture a few hours after  
351 infection [63]. Conjugation of Ubiquitin to SopB, a phosphoinositide phosphatase secreted by  
352 *Salmonella* via T3SS, modifies its cellular localization [64]. Upon delivery, SopB associates  
353 with the host plasma membrane where it participates to actin-mediated bacterial entry. Later  
354 on, Ubiquitination of SopB by TRAF6 leads to its translocation to the *Salmonella*-containing  
355 vacuoles, where it modulates vesicle trafficking and interferes with the delivery of these  
356 vacuoles to lysosomes [64,65]. Mass spectrometry-based large-scale analysis of the  
357 Ubiquitinome of cells infected by *Salmonella* recently provided additional examples of  
358 bacterial proteins modified by Ubiquitin [58]. In addition to the previously reported SopE and  
359 SopB, several effectors were identified as being ubiquitinated during infection. Interestingly,  
360 integral outer membrane proteins were reported to be conjugated to Ubiquitin and may  
361 represent the targets forming the Ubiquitin coat surrounding cytosolic bacteria and involved in  
362 host anti-bacterial autophagy [58,66]. Indeed, autophagy of invasive bacteria serves as a cellular

363 autonomous immune mechanism. During this process, a dense coat of poly-Ubiquitin chains is  
364 formed around bacteria, which serves as pathogen recognition receptor and directs intracellular  
365 bacteria for autophagic degradation [66,67].

366 In contrast to Ubiquitination, only few bacterial proteins were reported so far to be modified by  
367 SUMO and the biological consequences of these modifications during infection often remains  
368 elusive. These SUMO-modified bacterial proteins include two effectors, TRP120 and AmpA,  
369 secreted by two intracellular pathogens, *Ehrlichia chaffeensis* and *Anaplasma phagocytophilum*  
370 respectively [68,69]. OspF, an effector secreted by *Shigella flexneri*, constitutes another  
371 example for which SUMO conjugation is required for the translocation of this effector into the  
372 host nucleus where it modulates the expression of proinflammatory cytokines [70].

373 One can anticipate that recently developed techniques for large scale proteomic studies of UBL  
374 conjugation will increase the list of bacterial proteins modified by SUMO or other UBLs, and  
375 provide new insights in the role of these modifications during infection.

376

### 377 **Concluding Remarks and Future Perspectives**

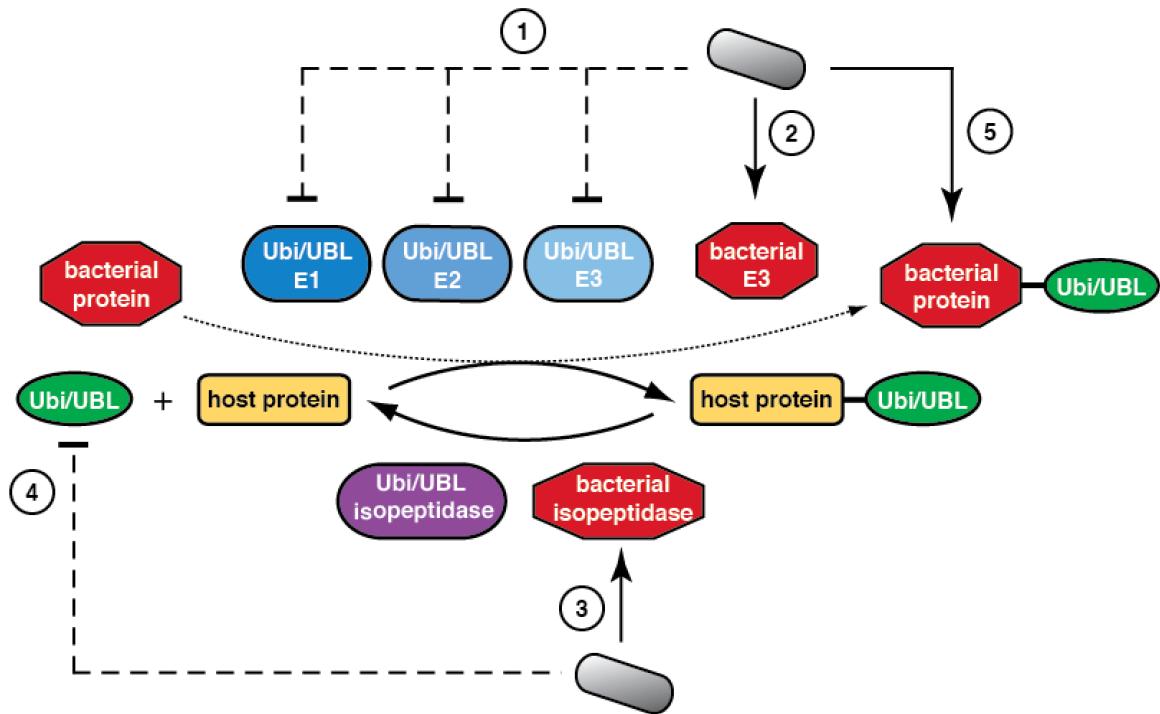
378 Ubiquitin and UBL are essential post-translational modifiers of eukaryotic cells. Thousands of  
379 Ubi/UBL targets have been identified during these last years, suggesting that most proteins will  
380 be modified by this type of PTMs at some point in their cellular lifetime. It is thus not surprising  
381 that pathogens evolved so many strategies to interfere with these particular PTMs in order to  
382 manipulate host cell physiology. Harnessing of host Ubi/UBL systems is in particular observed  
383 both for intracellular pathogens, that tightly interact with host cell cytoplasmic components to  
384 create for example a protective niche where they can acquire nutrients from the host, and for  
385 extracellular pathogens, that manipulate host cells to favor their maintenance at the surface of  
386 the cells or dampen host immune responses.

387 Thanks to the continuous improvement in proteomic analyses, the list of proteins known to be  
388 modified by Ubiquitin or UBLs has greatly expanded during these last years. It is in particular  
389 now feasible to compare the variations of the ubiquitinome (or other “UBL-ome”) of cells  
390 during infection by a pathogen or after exposure to a bacterial toxin [28,58]. Some of these  
391 techniques are furthermore compatible with *in vivo* analysis and the comparison of the content  
392 of proteins modified by Ubi/UBL in organs from infected or control animals is now possible  
393 [71,72]. Interestingly, current proteomic-based approaches not only reveal the identity of the  
394 proteins modified by Ubi/UBL but also the modifications sites. These data are critical for  
395 further analysis of the role of these PTM in the function of the identified protein and hence, to  
396 decipher the consequences of bacterial alteration of these PTMs. Several recent studies on  
397 ubiquitin conjugation revealed that ubiquitination establishes a much more complex code than  
398 originally thought. Indeed, in addition to “mixed” ubiquitin chains involving different types of  
399 linkages between Ubiquitin monomers, chains mixing ubiquitin and other UBLs such as SUMO  
400 have also been reported [1,2,73]. In addition, Ubiquitin has recently been found to be itself  
401 post-translationally modified by acetylation or phosphorylation, which further expands the  
402 repertoire of ubiquitination [1,2,73]. We are only beginning to understand the tremendous  
403 diversity of Ubiquitin modifications and their roles in cell biology but it is very likely that  
404 bacterial pathogens have long learned how to break this so-called “Ubiquitin code” and  
405 efficiently use it for their own profit (see Outstanding Questions).

406 Finally, while this review focused on pathogenic bacteria, some non pathogenic bacteria such  
407 as commensals of the intestinal microbiota were also reported to interfere with host Ubi/UBL  
408 systems [74]. For example, production of butyrate by commensal bacteria leads to the  
409 inactivation of the E2 NEDD8 enzyme in intestinal epithelial cells and was proposed to  
410 participate to the inflammatory tolerance of gut bacteria [75,76]. Some intestinal bacteria may  
411 even usurp host ubiquitin for their own purpose. Indeed, even though most bacteria lack

412 Ubiquitin or UBL genes, a Ubiquitin gene has been identified in the genome of some  
413 *Bacteroides fragilis* strains [77,78]. Interestingly, this eukaryotic-like Ubiquitin, which was  
414 probably acquired via horizontal gene transfer, does not seem to be involved in bacterial protein  
415 modification since it lacks the critical terminal glycine residue. This protein is instead secreted  
416 and acts as a bacterial toxin targeting and killing other intestinal bacteria [78]. Many other  
417 surprises like this one are probably still awaiting to be discovered and, even though the first  
418 report of a bacterium post-translationally modifying a host protein occurred almost 50 years  
419 ago [79], the field of pathogen and host post-translational modifications is, without a doubt, still  
420 very promising.

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425 **Figure 1 : Main strategies used by bacterial pathogens to interfere with host Ubiquitin or**  
426 **Ubiquitin-like protein modifications.**

427 During infection, bacteria may (1) inhibit Ubi/UBL conjugating enzymes, (2) secrete effectors  
428 possessing E3 ligase activity or (3) isopeptidase activity, or (4) directly inactivate Ubiquitin or  
429 UBLs. (5) Bacteria may also hijack the host Ubi/UBL systems to modify their own proteins  
430 during infection.

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**Table 1 : Examples of bacterial proteins interfering with Ubi/UBL conjugation to host proteins**

Ubi/UBL target	Bacteria	Extra/intracellular bacteria	Effector	Enzymatic activity	Effect	Refs
<b>Ubiquitin</b>	<i>Salmonella Typhimurium</i>	intracellular	SopA	E3 Ubi ligase (HECT)	Regulation of host inflammation	80
<b>Ubiquitin</b>	EPEC, EHEC	extracellular	NleL	E3 Ubi ligase (HECT)	Regulation of actin pedestal formation	81
<b>Ubiquitin</b>	EPEC, EHEC	extracellular	NleG	E3 Ubi ligase (RING)	?	82
<b>Ubiquitin</b>	<i>Pseudomonas syringae</i>	extracellular	AvrPtoB	E3 Ubi ligase (U-box)	Inhibition of plant pattern-triggered immunity	83,84
<b>Ubiquitin</b>	<i>Shigella flexneri</i>	Intracellular	OspI	Gln deamidase	Inactivation of UBE2N/UBC13 (E2 Ubi enzyme NF-κB pathway)	25
<b>Ubiquitin</b>	<i>Shigella flexneri</i>	intracellular	IpaH1.4	E3 Ubi ligase (NEL)	Ubiquitination of LUBAC (NF-κB pathway)	50
<b>Ubiquitin</b>	<i>Shigella flexneri</i>	intracellular	IpaH2.5	E3 Ubi ligase (NEL)	Ubiquitination of LUBAC (NF-κB pathway)	50
<b>Ubiquitin</b>	<i>Shigella flexneri</i>	intracellular	IpaH0722	E3 Ubi ligase (NEL)	Ubiquitination of TRAF2 (NF-κB pathway)	51
<b>Ubiquitin</b>	<i>Shigella flexneri</i>	intracellular	IpaH9.8	E3 Ubi ligase (NEL)	Ubiquitination of NEMO (NF-κB pathway)	52
<b>Ubiquitin</b>	<i>Legionella pneumophila</i>	intracellular	SdeA	non eukaryotic Ubi ligase	E1/E2-independent ubiquitination of Rab GTPases and RTN4	37-39
<b>Ubiquitin</b>	<i>Shigella flexneri</i>	intracellular	OspG	kinase	Inhibition of UBCH5 (E2 Ubi enzyme; NF-κB pathway)	53
<b>Ubiquitin</b>	EPEC, EHEC	extracellular	NleB	Glycosyltransferase	Inhibition of TRAF2 ubiquitination (NF-κB pathway)	54
<b>Ubiquitin</b>	EPEC	extracellular	?	?	Downregulation of UBE1 and UBA6 (E1 Ubi enzymes)	26
<b>Ubiquitin</b>	EPEC	extracellular	NleE	Cys methyltransferase	Inactivation of TAB2 and TAB3 (NF-κB pathway)	55, 85
<b>Ubiquitin</b>	<i>Legionella pneumophila</i>	intracellular	SidJ	deubiquitylase	?	40

<b>Ubiquitin</b>	<i>Shigella flexneri</i>	intracellular	ShiCE	deubiquitylase	?	44
<b>Ubiquitin</b>	<i>Chlamydia trachomatis</i>	intracellular	ChlaDUB1	deubiquitylase	Inhibition of NF-κB pathway activation	86, 87
<b>Ubiquitin</b>	<i>Burkholderia pseudomallei</i>	extracellular	CHBP	Gln deamidase	Deamidation of Ubiquitin	47
<b>SUMO</b>	<i>Listeria monocytogenes</i>	intracellular	LLO	Pore-forming toxin	Downregulation of UBE2I/UBC9 (E2 SUMO enzyme)	27
<b>SUMO</b>	<i>Clostridium perfringens</i>	extracellular	PFO	Pore-forming toxin	Downregulation of UBE2I/UBC9 (E2 SUMO enzyme)	27
<b>SUMO</b>	<i>Streptococcus pneumoniae</i>	extracellular	PLY	Pore-forming toxin	Downregulation of UBE2I/UBC9 (E2 SUMO enzyme)	27
<b>SUMO</b>	<i>Shigella flexneri</i>	intracellular	? / Ca <sup>2+</sup> influx	?	Proteolytic cleavage of UBA2/SAE2 (E1 SUMO enzyme)	31
<b>SUMO</b>	<i>Salmonella Typhimurium</i>	intracellular	? / miRNAs	?	Downregulation of UBE2I/UBC9 (E2 SUMO enzyme)	30
<b>SUMO</b>	<i>Xanthomonas euvesicatoria</i>	extracellular	XopD	deSUMOylase	DeSUMOylation of SIERF4 (plant immune response)	41,42
<b>NEDD8</b>	EPEC	extracellular	CIF	Gln deamidase	Deamidation of NEDD8	47,48
<b>NEDD8</b>	<i>Chlamydia trachomatis</i>	intracellular	ChlaDUB1	deNeddylase	Inhibition of NF-κB pathway activation	86, 87

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