

Table S1. YopJ-like proteins and genes (Family C55) in bacterial species.
(For details see the MEROPS database: <http://merops.sanger.ac.uk>)

Family C55: distribution among bacteria				
Organism	Counts of peptidase homologues	Acronym	Effect	Reference
Acidovorax avenae	2	HopZ2		
Aeromonas salmonicida	1	AopP	Inhibition of NF- κ B pathway downstream of I κ B kinase (IKK) activation. No effect on the MAPK signaling pathways.	Fehr et al., 2006
Bartonella quintana	1			
Bartonella tribocorum	2			
Erwinia amylovora	2			
Erwinia tasmaniensis	1			
Pseudomonas amygdali	2			
Pseudomonas savastanoi	1			
Pseudomonas syringae	7	HopZ2 (AvrPpiG1)		Hotson & Mudgett, 2004; Lewis et al., 2008
Ralstonia solanacearum	4	PopP1, PopP2, PopP3	Effectors controlling interaction between bacteria and their plant host (so called avirulence protein)	Lavie et al., 2002 Deslandes et al., 2003; Hotson & Mudgett, 2004
Rhizobium sp. NGR234	1	Y4IO		Hotson & Mudgett, 2004
Salmonella enterica	1	AvrA homologue		
Salmonella typhimurium	1	AvrA	Acetylates specific MAPKKs and potentially inhibits c-Jun N-terminal kinase (JNK and NF κ B signaling pathways. Alternatively, the inflammatory response is blocked by deubiquitination of I κ B α and β -catenin. In the effect the proapoptotic innate immune response to <i>Salmonella</i> is dampened and tight junction and function of intestinal	Liao et al., 2008; Jones et al., 2008; Ye et al., 2007; Collier-Hyams et al., 2002

			epithelial cells is preserved.	
Vibrio cholerae	1			
Vibrio parahaemolyticus	1	VopA	Inhibition of the MAPK signaling pathways but not NF-kB pathway.	Trosky et al., 2004
Xanthomonas campestris	2	AvrXv4, AvrBsT; AvrRxv, XopJ	Effectors controlling interaction between bacteria and their plant host (so called avirulence protein)	Roden et al., 2004; Hotson & Mudgett, 2004; Cunnac et al., 2007
Y. enterocolitica	2			
Y. pestis	1	YopJ		
Y. pseudotuberculosis	1	YopJ		

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- Ye Z, Petrof EO, Boone D, Claud EC, Sun J: Salmonella effector AvrA regulation of colonic epithelial cell inflammation by deubiquitination. *Am J Pathol* 2007;171:882-892.

Table S2: Bacterial species possessing functional genes encoding true SUMO isopeptidases.

Clan CE / Family C48: distribution among bacteria	
Organisms named in bold type are those for which the genomes have been completely sequenced.	
Organism	Counts of peptidase homologues
<u>Acidovorax avenae</u>	1
<u>Bradyrhizobium japonicum</u>	2
<u>Chlamydia muridarum</u>	2
<u>Chlamydia trachomatis</u>	4
<u>Chlamydophila abortus</u>	1
<u>Chlamydophila felis</u>	1
<u>Mesorhizobium loti</u>	2
<u>Pseudomonas syringae</u>	1
<u>Rhizobium leguminosarum</u>	1
<u>Xanthomonas campestris</u>	2

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Table S3: Distribution of genes encoding YopT-like proteases among bacteria

Family C58: distribution among bacteria	
Organism	Counts of peptidase homologues
<u><i>Acidovorax avenae</i></u>	1
<u><i>Bradyrhizobium japonicum</i></u>	2
<u><i>Haemophilus ducreyi</i></u>	2
<u><i>Haemophilus somnus</i></u>	1
<u><i>Hahella chejuensis</i></u>	1
<u><i>Pasteurella multocida</i></u>	2
<u><i>Photorhabdus luminescens</i></u>	3
<u><i>Pseudomonas syringae</i></u>	4
<u><i>Yersinia enterocolitica</i></u>	1
<u><i>Yersinia pestis</i></u>	1
<u><i>Yersinia pseudotuberculosis</i></u>	1

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