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Nota di contenuto	About the Special Issue Editor v -- Alexey S. Ladokhin Cellular Entry of Binary and Pore-Forming Bacterial Toxins doi: 10.3390 /toxins10010011 1 -- Masaya Takehara, Teruhisa Takagishi, Soshi Seike, Masataka Oda, Yoshihiko Sakaguchi, Junzo Hisatsune, Sadayuki Ochi, Keiko Kobayashi and Masahiro Nagahama Cellular Entry of Clostridium perfringens Iota-Toxin and Clostridium botulinum C2 Toxin doi: 10.3390/toxins9080247 3 -- Alfredo J. Guerra and Vern B. Carruthers Structural Features of Apicomplexan Pore-Forming Proteins and Their Roles in Parasite Cell Traversal and Egress doi: 10.3390 /toxins9090265 12 -- Sergey N. Savinov and Alejandro P. Heuck Interaction of Cholesterol with Perfringolysin O: What Have We Learned from Functional Analysis? doi: 10.3390/toxins9120381 27 -- Alexandra J. Machen, Narahari Akkaladevi, Caleb Trecazzi, Pierce T. ONeil, Srayanta Mukherjee, Yifei Qi, Rebecca Dillard, Wonpil Im, Edward P. Gogol, Tommi A. White and Mark T. Fisher Asymmetric Cryo-EM Structure of Anthrax Toxin Protective Antigen Pore with Lethal Factor N-Terminal Domain doi: 10.3390/toxins9100298 44 -- Alexey S. Ladokhin, Mauricio Vargas-Uribe, Mykola V. Rodnin, Chiranjib Ghatak and Onkar Sharma Cellular Entry of the Diphtheria Toxin Does Not Require the Formation of the Open-Channel State by Its Translocation Domain doi: 10.3390/toxins9100299 60 -- Primoz Knap, Toma Tebaldi, Francesca Di Leva, Marta Biagioli, Mauro Dalla Serra and Gabriella Viero The Unexpected Tuners: Are LncRNAs Regulating Host

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Sommario/riassunto

Bridging cellular membranes is a key step in the pathogenic action of both binary and pore-forming bacterial toxins. The former use their translocation domains, containing various structural motifs, to ensure efficient delivery of the toxic component into the host cell, while the latter act on the cellular membrane itself. In either case, the integrity of the membrane is compromised via targeted protein-lipid and protein-protein interactions triggered by specific signals, such as proteolytic cleavage or endosomal acidification. This Special Issue presents recent advances in characterizing functional, structural and thermodynamic aspects of the conformational switching and membrane interactions involved in the cellular entry of bacterial protein toxins. Deciphering the physicochemical principles underlying these processes is also a prerequisite for the use of protein engineering to develop toxin-based molecular vehicles capable of targeted delivery of therapeutic agents to tumors and other diseased tissues.
