cell growth was investigated by mitochondrial metabolic potential. Cellular uptake and ultrastructural changes of NPs was examined by transmission electron microscopy (TEM). Cell death was determined by flow cytometry. Protein level was detected by using Western Blot. The obtained results have demonstrated that exposure to ZnONPs significantly decrease viability of skin cells and inhibit cell proliferation, which haven't been observed for TiO₂NPs. Moreover, only ZnONPs lead to transformation of melanocytes to melanoma, induce inflammatory and mixed types of cell death. What is important, co-exposure both of types of NPs and UV radiation enhance toxic effect on melanocyte cells, which indicates high risk associated with the application of NPs in sunscreens. This work was supported by grant 2016/21/N/NZ3/03276 from the Polish National Science Center (NCN).

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High-throughput analysis of ubiquitination cascade by chloroplast E3 ligases in the reconstituted bacterial system

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Since the majority of the chloroplast proteome is nucleus-encoded, biogenesis and proper functioning of this organelle is highly dependent on its protein import capabilities. Translocon complexes localized at the outer envelope membrane (TOC) and the inner envelope membrane (TIC) transport pre-peptides across the respective membranes. A recently identified E3 RING-type ubiquitin ligase embedded in the OEM, called *suppressor of ppi1 locus1* (SP1) targets components of TOC and designates them for degradation by the ubiquitin-proteasome system (UPS). More recently, it has been shown that SP1 interacts with SP2 and CDC48, an Omp85-type β -barrel channel located in the OEM and a cytosolic AAA+ chaperone, respectively. Interestingly, SP1 is also present in the peroxisomal and mitochondrial outer membranes. The model plant *Arabidopsis thaliana* encodes two ubiquitin ligases homologous to SP1, the SP1-Like1 (SPL1) and the SP1-Like2 (SPL2) that share topological and significant sequence identity with SP1. Their subcellular localization is also alike, except that for SPL2 no peroxisomal association has been observed. Any further knowledge, especially about their ubiquitination substrates is lacking however. Our current aim is to elucidate the functions of SPL1 and SPL2. We employed several approaches based on co-immunoprecipitation (CoIP) and *in vitro* ubiquitination assays to identify SP1L substrates. We also adapted an *in vivo* ubiquitination system reconstituted in bacterial cells to identify E2-E3 pairs and putative substrates of these novel E3 ligases. We then further modified this system to determine the type of ubiquitin chain linkage that directs the modified proteins to different cellular fates. Obtained results provide an insight of the role fulfilled by SP1-Like ubiquitin ligases in a plant cell. This work was funded by National Science Centre, Poland (NCN) grant 2015/19/D/NZ1/02790 awarded to WB.

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A polyamorous repressor: deciphering the evolutionary strategy used by the phage-inducible chromosomal islands to spread in nature

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Staphylococcus aureus pathogenicity islands (SaPIs) are a family of related 15–17 kb mobile genetic elements that carry and disseminate superantigen and other virulence genes. SaPIs reside passively in the bacterial chromosome, repressed by a master repressor called StI, encoded by the own SaPI. The key feature of their mobility and spread is the induction by helper phages of their excision, replication, and efficient encapsidation into specific small-headed phage-like infectious particles. After infection or induction of a resident helper phage, SaPIs are de-repressed by the specific protein-protein interaction of phage proteins with StI. SaPIs have developed a fascinating mechanism to ensure their promiscuous transfer by targeting with the StI repressor structurally unrelated phage proteins performing the same conserved function. Combining structural biology approach and functional characterization *in-vivo* and *in-vitro* we decipher the molecular mechanism of this elegant strategy by which the SaPI hijacks the phage process to sense the starting of the lytic cycle. Our structural studies show that the StI of the island SaPI_{bov1} combines a canonic HTH N-terminal domain to bind DNA, and sequentially acquires new domains which act as recognizing modules for the different phage proteins (anti-repressors). Our *in-vivo* and *in-vitro* data deciphers the molecular mechanism that underlies the interaction between the StI repressor and different phage coded anti-repressors, showing how each StI module mimics the substrate for each anti-repressor type. The interaction of StI with different types of anti-repressor always disrupts the StI dimer, implying the DNA dissociation and SaPI derepression. Our results establish the molecular mechanism of the interaction event that denotes the intra- and inter- generic transference of the clinically relevant SaPIs. *The authors marked with an asterisk equally contributed to the work.

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hIL7-BAPmut fusion protein production and application for the specific scFv selection from combinatorial antibody library

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Human Interleukin-7 (hIL7) – cytokine which plays important role in the development and regulation of immune system (B and T cells proliferation). The results of modern studies testify about IL-7 antitumor effects in tumors such as glioma, melanoma, lymphoma, leukemia, prostate cancer, and glioblastoma. That why it's can be promising therapeutic candidate. Antibodies is one of the most widely used diagnostic tools for the biological molecules investigation. Single-chain antibodies (ScFv) compare to full-length antibodies have several advances: smaller sizes, animal-free antibody production, reproducibility, high-throughput, rapid and cost effective production, and can be genetically fused with marker protein. The aim of our investigation is the obtaining of bifunctional fusion protein hIL7-BAPmut for one-step selection