

NEWS:



How to get a large view on skin oxidation effects and protection.

Pollution, solar radiation, screen light and cigarette smoke generate free radicals in the skin which can be destructive with varying degrees of severity. Proteins (collagen, elastane), cellular membrane lipids and DNA can be damaged causing disorders that can range from premature ageing to cancer.

There were many studies that identify, through *in vitro* methodologies, the potential benefits of antioxidants for skin, however, there is little data reporting to its functions in experimental models contemplatives of methodologies *in vivo*. Most investigations are based on known biomarkers, but it does not give a complete view of the effects (1).

The new recent approaches allows to embrace a large view (2) of the induced effects through proteins or metaproteomics and bioinformatics, with a possible large view on skin oxidation (3)

(1)Arandas Monteiro e Silva S. and all. 2017. An overview about oxidation in clinical practice of skin aging An Bras Dermatol. 2017 May-Jun; 92(3): 367–374.
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5514578/>

(2)Ramallo Guevara C. and all.2016. Global Protein Oxidation Profiling Suggests Efficient Mitochondrial Proteome Homeostasis During Aging. Mol Cell Proteomics. 2016 May;15(5):1692-709
<https://www.ncbi.nlm.nih.gov/pubmed/26884511>

(3)Lee SH. and all. 2016. UV irradiation-induced methionine oxidation in human skin keratins: Mass spectrometry-based non-invasive proteomic analysis. J Proteomics. 2016 Feb 5;133:54-65.
<https://www.ncbi.nlm.nih.gov/pubmed/26655505>

With MS Phylogene, you can characterize and understand the effects of abiotic stress. Based on skin D-Squame or swabs sampling, the relative comparison of proteomes between Tested and Control provides a fold change between impacted proteins and oxidized sites. Then bioinformatics describes the “free of hypothesis” induced effects with CORAVALID workflow. An OxDeep ratio provides the deepness of oxidation on all proteins.

High-resolution nano LC-MS/MS quantitative proteomics with RedOxMics™ approach and OxDeep ratio and CORAVALID™ data processing.

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