TH047 Behavioral analysis and toxicoproteomics profiling of mianserin exposure of zebrafish K. Van Camp, Systemic Physiological and Ecotoxicological Research (SPHERE), University of Antwerp / Biology; G. Baggerman, Flemish Institute for Technological Research VITO / Department of Biology SPHERE; D. Valkenborg, R. Blust, University of Antwerp; S. Husson, University of Antwerp / Biology. Pharmaceuticals are widely used by humans, for food production or for veterinary purposes, but they may also enter the environment. Unfortunately, many pharmaceuticals have unknown mode of actions in the different environmental niches. Especially neuro-active drugs are of particular concern when acting on non-target species as the neural system is essential for the regulation of various physiological processes and behaviors. The occurrence of antidepressants in surface waters may lead to reduced anxiety of fish, which affects their abilities to deal with predators. In this research we will study effects of the pharmaceutical pollutant mianserin in aquatic environments, on different levels of complexity. In this respect, we will use the zebrafish (*Danio rerio*) which is known as a valid ecotoxicological model. We aim to study altered zebrafish behavior using 3D video tracking as a consequence of exposure to the psychoactive drug mianserin. Doing so, we found a significant effect of swimming angle, as well as the average swimming speed and the time that the fish spend in upper, middle and lower zone in the aquarium. Next, by adopting a differential proteomics approach, we aim to reveal mechanistic information of toxicity at the molecular level, or at least aim to provide a picture of (biochemical) pathways that are affected. While previous proteomics studies in ecotoxicology mainly employed labor-intensive gel-based methods, we explored the use of gel-free strategies. Neuroproteomes of individual brains of exposed zebrafish were compared with their non-exposed controls. Proteins from the entire brain region of the zebrafish were extracted using standard protocols and the resulting proteomes were treated with trypsin to yield thousands of small peptides. A tandem mass tag (TMT) labeling method was used to analyze and quantify six different samples (e.g. three control samples and three samples from exposed fishes) in one single nanoLC-MS experiment to obtain differential proteome maps. Finally, we aim to correlate obtained behavioral parameters with molecular fingerprints from differential proteomics datasets to obtain mechanistic and functional insights underlying aversive effects of exposures to mianserin.