

Construction of metabolic map in lead poisoning

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Since antiquity, lead was used by human beings as a tool for daily routine, due its unique properties, like malleability, ductility, corrosion resistance, low melting point and low electrical conductivity. Nowadays, lead is one of the most studied heavy metals worldwide due its relation with occupational exposure on industry workers or people who manipulate its compounds. Many effects of lead poisoning were already been reported on literature, showing a compromising of whole body health, with symptoms related to cardiovascular, immune, bone, reproductive, hematological, renal and gastrointestinal systems, even the most studied ones are related with neurological system. Although there is evidence of how it affects homeostasis at the cellular level, the description of metabolic pathways affected in lead poisoning is not fully established. To clarify the effects of lead poisoning, the aim of this study is to build a metabolic map of the cellular and biochemical pathways altered by the presence of lead, and to analyse which proteins and cellular components this heavy metal has the ability to bind and interfere with its normal function. For this purpose, we made a textmining search in literature in order to obtain information about lead interactions with biomolecules. On our preliminary results, we have already found a total of 22 proteins which can directly interact with lead, with many others proteins that can be indirectly affected by this metal. In order to validate our previous observations on literature, we analysed some data of lead intoxication of experimental models from public repositories. The metabolic map using the pathways affected by lead will then be built by the comparison of this two sources.