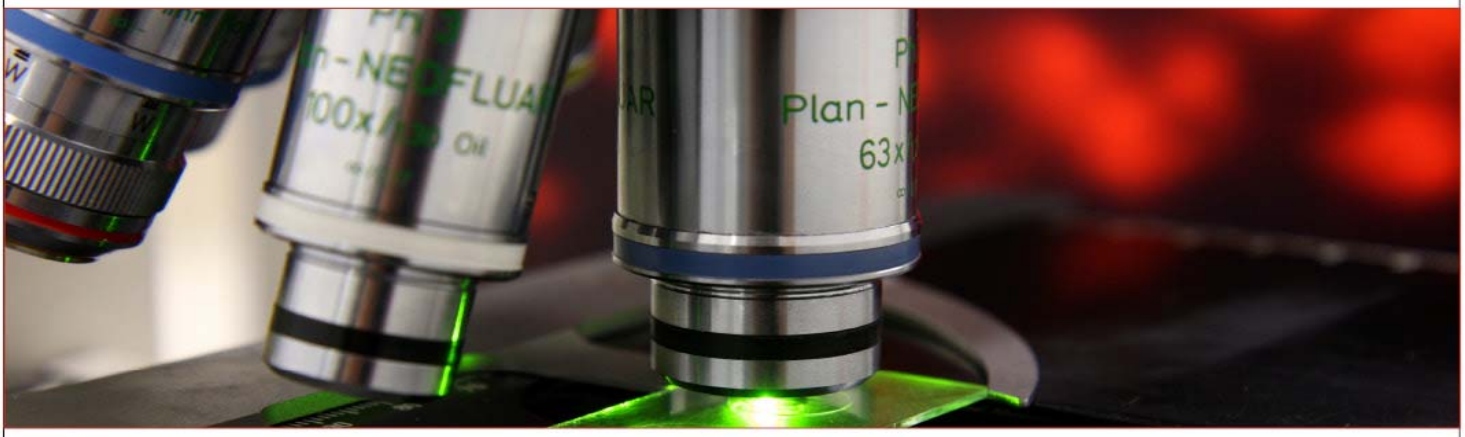
SÉMINAIRES ET CONFÉRENCES



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« Structural investigations into the mechanism of methylmercury degradation by enzymes of the bacterial mercury resistance system»

Mercury is introduced into the environment by both natural occurrences and through numerous different human activities. Once introduced into the environment, mercury can exist as elemental mercury (Hg0), ionic mercury (HgI and HgII) or as the organomercurial methylmercury (MeHg) and there is a constant flux between these three forms as part of the natural biogeochemical cycle. Of the various forms of natural mercury compounds, MeHg is the most toxic due to its hydrophobicity and its ability to bio-accumulate within the food chain. High levels of MeHg exists in sea life in many areas around the world, and high consumption of contaminated seafood represents a serious danger to human health. Bacteria isolated from mercury-contaminated environments have evolved a system that allows them to efficiently convert both ionic and organomercurial compounds to the less toxic elemental mercury. This resistance to mercury compounds is due to the acquisition of a transferable genetic element known as the mer operon. The mer operon encodes for several proteins including two enzymes, the organomercurial lyase MerB and the mercuric ion reductase MerA. Due to their unique ability to cleave MeHg (MerB) and reduce the resulting HgII product (MerA) to Hg0, MerB and MerA are viewed as ideal candidates for creating a “green chemistry” to help remediate mercury contaminated sites in the environment. In my talk, I will discuss our efforts to develop a mechanistic understanding of how MerB and MerA function together at the atomic level with the goal of using this information to better exploit these two unique enzymes in bioremediation efforts for mercury contamination.

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Le lundi, le 18 decembre 2017, 11:30

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