CELSA
Central Europe Leuven Strategic Alliance

CELSA - Collaborative research project - Application form - COVER PAGE

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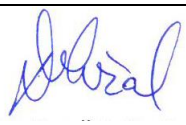
Signature[1]: 

3. Identification of third and fourth co-investigator(s) (if applicable) Expand table if more than four research units are involved.
Third co-investigator
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3. Non confidential and public friendly summary (max. 2000 characters)

Project title: Structure-based design of new antitubercular medicines.

Summary: Tuberculosis, an infectious disease that principally affects the lungs, is one of the top ten causes of death worldwide. Mycobacterium tuberculosis (MTB), the bacterium that causes the disease, is estimated to take more lives than both HIV and malaria each year. Such numbers have led the World Health Organisation to propose a global strategy, with the goal of reducing the yearly number of MTB caused deaths by 95 % between 2015 and 2035. While this disease can be readily treated with a six-month regime of antibiotics, the rapid spread of multi- and extensively drug-resistant strains of MTB is threatening to undermine this possibility, with the real risk of higher projected mortality rates in the future.

The goal of this collaborative proposal, involving research groups from KU Leuven, Belgium and Charles University in Prague, Czech Republic is to develop new antitubercular medicines, in the hope of improving treatment and helping combat the threat of drug resistance in MTB. Such drugs work by blocking essential processes in these bacterial cells that are necessary for life. One such process is called protein translation. Proteins can be considered as the workers of a cell, with a wide variety of jobs that include transport, construction and replication. As with humans, over time these workers need to be replaced. To do this the blueprint stored in the genetic code of DNA must be read and used to build a new protein. This step is called translation, and it not only requires many protein workers of its own, but also considerable amounts of raw materials. Our target is to prevent the production of such material and thus stop the assembly of new proteins, therefore killing the bacteria. We will do this by looking at the 3D-structure of one of these very small proteins, and use this information to design new drugs that bind to it and prevent it from doing its job.

4. List 5 key words

Antibiotics – tuberculosis – rational drug design – structure elucidation – mycobacteria