SCIENCES & BIOENGINEERING SCIENCES

The Research Group

Structural Biology Brussels

has the honor to invite you to the public defense of the PhD thesis of

Sander STROOBANTS

to obtain the degree of Doctor of Bio-Engineering Sciences

Title of the PhD thesis:

Crystallization and nucleation under constant shear conditions: A novel microfluidic approach

Promotor:

Prof. dr. Dominique Maes

The defense will take place on:

Wednesday, September 9 2020 at 17h

in Auditorium D.0.03 at the Campus Etterbeek of the Vrije Universiteit Brussel, Pleinlaan 2 - 1050 Elsene (limited capacity) and via livestream.
If you want to attend in person contact:
Sander.Stroobants@vub.be

Members of the jury

Prof. dr. ir. Eveline Peeters (VUB, voorzitter)
Prof. dr. ir. Gert Desmet (VUB, secretaris)
Prof. dr. Dominique Maes (VUB, promotor)
Prof. dr. ir. Wim De Malsche (VUB, co-promotor)
Prof. dr. ir. Johan Stiens (VUB, co-promotor)
Prof. dr. Nick Van Eijndhoven (VUB)
Prof. dr. Stephane Veesler (Université de Marseille, Frankrijk)
Dr. James Lutsko (ULB)

Curriculum vitae

Sander Stroobants (born on 04/01/1992) earned his master's degree in biomedical engineering at the Universiteit Gent in 2016. He performed his doctoral research at Structural Biology Brussels and the ▫Flow Group at the VUB under de supervision of Prof. Dr. Dominique Maes, Prof. Dr. Ir. Wim De Malsche and Prof. Dr. Ir. Johan Stiens. His research was funded by a grant from European Space Agency and focusses on protein crystal nucleation in constant shear conditions. His research resulted in 4 peer reviewed papers that were published in international journals. His results were also presented at various international conferences. He received the prestigious "IMT microfluidics on glass poster award" at the 23th international conference on miniaturized systems for chemistry and life sciences (μTAS 2019) in Basel.

Abstract of the PhD research

Protein crystallization is of major importance in several domains such as structural biology and pharmacy. Indeed, good quality protein crystals are a necessity for protein structure determination by X-ray crystallography. If proteins are administered as medication this is often in the form of crystal suspensions. Notwithstanding its importance, protein crystallization is still an elusive process. It consists of two steps: first a nucleus is formed, followed by growth of this nucleus into a crystal. Nucleation at the start of the crystallization process determines important characteristics of the resulting crystals like the number, size, morphology and polymorph. Nucleation also underlies aggregation processes observed in diseases such as Alzheimer and cataract.
However, predictions from classical theories do differ significantly from experimental results. Although it is known that different mass transport regimes will dramatically influence the crystallization process the exact mechanisms are still poorly understood. High mixed shear flows have been known to increase nucleation. To systematically investigate the influence of shear flow on protein crystallization, a novel microfluidic device was developed. We found that even low to moderate shear rates can dramatically increase the nucleation rate. We also tested the influence of shear on polymorphism during the nucleation of a pharmaceutical compound. In the conditions we tested, shear flow didn't affect the polymorph selection, suggesting that the kinetics and not the thermodynamics of the process were influenced. Additionally, the inherent stochastic nature of nucleation makes it difficult to predict when and where a critical nucleus will appear. Moreover, the small size of the nucleus prohibits direct observation. We used 3 new analytical techniques (THz waves, Brownian microscopy and confocal depolarized dynamic light scattering) and investigated their potential in detecting nucleation at an early stage. Finally, the structure from the peroxiredoxin protein from Sulfolobus islandicus was determined. The structure determination process of this protein consisted of different steps: first crystallization conditions were determined and optimized, in the next phase X-ray diffraction data were collected on these crystals and finally the structure was modelled using molecular replacement followed by refinement. The results were published and added to the "Protein Data Bank".