Notice of the Final Oral Examination
for the Degree of Master of Applied Science
of
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BSc (Ben-Gurion University, 2012)

“Characterization of Single Proteins Using Double Nanohole Optical Tweezers”

Department of Electrical and Computer Engineering

Thursday, May 10, 2018
10:00 A.M.
Engineering and Computer Science Building
Room 660

Supervisory Committee:
Dr. Reuven Gordon, Department of Electrical and Compute Engineering, University of Victoria (Supervisor)
Dr. Fayez Gebali, Department of Electrical and Computer Engineering, UVic (Member)

External Examiner:
Dr. Rustom Bhiladvala, Department of Mechanical Engineering, UVic

Chair of Oral Examination:
Dr. Trevor Lantz, School of Environmental Studies, UVic

Dr. Stephen Evans, Acting Dean, Faculty of Graduate Studies
Abstract

Proteomic studies at the single molecular level could provide better understanding of the protein’s behaviour and the affects of its interactions with other biomolecules. This could have an impact on drug development methods, disease diagnosis, and targeted therapy. Aperture assisted optical trapping is a proven technique for isolating single proteins in solution without the use of tethers or labels, and without denaturing them. Thus enabling studies of protein-protein interactions, protein-small molecule interactions, and protein-DNA interactions.

In this work, double nanohole (DNH) optical tweezers were used to analyze the protein composition of heterogeneous mixtures. The trapped proteins were grouped by molecular mass based on two metrics: standard deviation (SD) of the trapping laser intensity fluctuations, and the time constant ($\tau$) of the autocorrelation function of these fluctuations. The quantitative analysis is demonstrated first for two separate standard-size proteins, then to a mixed solution of both. Finally, the approach is applied to real unprocessed egg white solution. The results correspond well to the known protein composition of egg white found in the literature.

The DNH optical tweezers’ ability to distinguish proteins in unpurified heterogeneous mixtures, can progress this technique to the next level, allowing for single biomolecular studies of unprocessed physiological solutions like blood, urine, or saliva.