Experimental report

25/03/2026

Proposal: 8-03-1061 **Council:** 10/2022

Title: The role of red blood cells in Long Covid: a SANS and NSE study

Research area: Biology

This proposal is a new proposal

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Samples: human red blood cells
Human Hemoglobin
phosphate buffer
SARS-Cov-2 spike protein
heparin
Human red blood cell liposomes

Instrument	Requested days	Allocated days	From	To
D22	3	3	06/03/2023	08/03/2023
			29/05/2023	30/05/2023
D33	3	0		
IN15	3	3	31/05/2023	03/06/2023

Abstract:

A dramatic consequence of the Covid-19 pandemic is the emergence of Long Covid (LC). This syndrome includes, amongst other symptoms, shortness of breath, memory loss and, most prominently, a debilitating, chronic fatigue (CF). One important factor contributing to LC/CF appears to be the structure and dynamics of red blood cells (RBCs). Evidence suggests that the SARS-CoV-2 spike protein can induce the formation of RBC aggregates and increase the membrane stiffness of RBCs. This compromises the ability of RBCs to transport oxygen to vital organs, offering a potential explanation for some LC symptoms. However, a comprehensive, quantitative study of these effects is still missing and is therefore the topic of this proposal. We wish to investigate the effects of Spike on RBC structure and membrane dynamics using small-angle neutron scattering (SANS) and neutron spin-echo (NSE). In addition, the therapeutic influence of heparin on the effects that Spike has on RBC will be investigated. Since post-viral complications have also been demonstrated for infections with viruses other than SARS-CoV-2, this proposal is strong medical and societal interest, even beyond Long Covid.

Model for small-angle scattering analysis of membranes with protein-like inclusions

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Proteins are ubiquitous in biological membranes and have a significant impact on their scattering properties. In this contribution, we introduce a general mathematical construction to add proteins to any pre-existing membrane model and to calculate the resulting elastic and/or inelastic scattering cross section. The model is a low-resolution one, which describes the proteins as made up of regions of homogeneous scattering length density that extend through an arbitrary fraction of the membrane and possibly protrude out of it. In this construction, the protein characteristics that are relevant to scattering are their space and time correlation functions in the two-dimensional plane of the membrane. The results are particularized to a static bilayer model and to a Gaussian model of a fluctuating membrane. The models are then applied to the joint analysis of small-angle neutron and X-ray scattering of red blood cell membranes, of which transmembrane proteins constitute 25% of the volume, and to neutron spin–echo data measured on the same systems

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