



**NATIONAL INSTITUTE FOR
OCCUPATIONAL HEALTH**

Division of the National Health Laboratory Service



NIOH RESEARCH DAY - 2026

ABSTRACT SUBMISSION GUIDELINES

Please see the guidelines below

- Ensure that abstracts are prepared specifically in accordance with our submission requirements.
- Do not submit unformatted abstracts or abstracts which have been written for other publications or purposes, such as university academic days or conferences
- Abstracts that do not comply with these guidelines may be returned for revision before they can be considered.

Abstract Formatting Guidelines:

- Font Arial should be used.
- Single spacing
- Abstract is limited to **300 words** (this does not include the title, author's names, and institutions).
- Abstract title: Font size 14 pt, bold.
- Authors: Font size 12 pt, bold+italic. Please provide authors' full first and last names, and underline the presenting author.
- Affiliations: Font size 12 pt, italic, denoted by arabic numbers in superscript (^{1, 2, 3}) after each author's last name. Please indicate your Section at NIOH.
- Please provide the email address to which all the correspondence should be addressed.
- Abstract text: Font size 12 pt; should cover a brief introduction, main objectives, methods, results, and discussion.

E-mail your abstract to: Researchday@nioh.ac.za by 4 August 2026

- Indicate in your email whether you prefer an oral or a poster presentation.
- Poster presentations will be in electronic format and made available to delegates via an online platform.
- A short time will be allocated in the program for you to answer questions.

Feel free to use the example below (copy-paste your information):

Title: MD simulations of G6PD and potential risks using chloroquine/hydroxychloroquine based treatments

Natasha Sanabria¹, Özlem Tastan Bishop²

1. Department of Toxicology and Biochemistry, National Institute for Occupational Health, National Health Laboratory Service
2. Director of Research Unit in Bioinformatics (RUBi), Department of Biochemistry and Microbiology, Rhodes University

Correspondence: NatashaS@nioh.ac.za

Abstract:

Introduction

Human diseases associated with the Glucose-6-phosphate dehydrogenase (G6PD) enzyme coincide with certain geographical distributions that correlate with malaria areas. In most cases, the diseases are due to reduced enzyme activity. Since the enzyme has specific properties and functions, clinical pathology is manifested when this pivotal role is disrupted, e.g. G6PD deficiency. The enzyme deficiency is caused by changes in the protein, which originates from genetic mutations.

Methods

In this study, Molecular Dynamic (MD) simulations were used to investigate the effects of mutations on G6PD. In particular, the substrate and ligand interactions were analysed. Data was retrieved from the various databases for each genetic variant, i.e. Plymouth and Mahidol mutations. Thereafter, in silico predictions were performed to characterise and assess the substitutions.

Results and Discussion

The structure used herein contained the substrate, co-enzyme and structural NADP⁺, where previous studies have used one or the other. The communication between the residues within the structure of the protein was investigated via network analyses, e.g. MD-TASK, where the residue interaction network (RIN) was visualised by contact maps. All the resultant data were combined to identify which residues were most affected. This is important to assess potential clinical applications. Specifically, chloroquine/hydroxychloroquine have been proposed as potential treatments for coronavirus disease 2019 (COVID-19). However, G6PD deficiency occurs in 10-30% of Sub-Saharan Africans, with large allele frequency differences in sub-populations (e.g. Tsonga vs Xhosa).

Conclusion

These variants could be a significant factor in the interaction with clinical trials of chloroquine/hydroxychloroquine-based treatments for COVID-19 in Africans.