# USING IMMUNOPROTEOMICS TO CHARACTERISE THE HUMAN ANTIBODY RESPONSE DURING *MYCOBACTERIUM TUBERCULOSIS* INFECTION

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**Background**
Tuberculosis (TB) remains one of the three major killers among the world's infectious diseases. Despite major advances in vaccine research and our understanding of the human immune system, the rules of immune protection against TB remain unclear. Recently, the antibody response to *Mycobacterium tuberculosis* (Mtb) antigens during infection has been in the focus of studies. Most studies have used microarray technology to characterise the Mtb antigens recognised in different patients. However, this technology is cost and time intensive. Here, we report a novel and easy approach for assessing protein antigens of antibodies from TB patients using state-of-the-art immunoproteomics.

**Methods**
In a proof-of-concept study, the human antibody response to Mtb antigens was investigated in patients with latent TB infection and patients that have previously had active TB. Mtb antigens were isolated from H37Rv lysates using purified serum antibodies from both patient groups. The identities of isolated antigens were determined using a Q Exactive Orbitrap mass spectrometer. Also, different subcellular fractions from H37Rv were used in ELISA to characterise the reactivity of IgG and IgA antibodies in patients.

**Results**
Differential antibody responses were detected for different patient groups. The antibody response targeted differently localised antigens during different stages of infection. These findings were further validated by ELISA using different cellular fractions from H37Rv resulting in different antibody reactivity in patient groups.

**Conclusion**
Immunoproteomics might prove an important alternative to microarray technology to characterise the antibody response to Mtb antigens in patients. This will be especially helpful to understand the underlying mechanisms of immunity against infection with Mtb and might broaden available targets for vaccination in future.