

PE_PGRS33, an Important Virulence Factor of *Mycobacterium tuberculosis* and Potential Target of Host Humoral Immune Response

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Supplementary Material

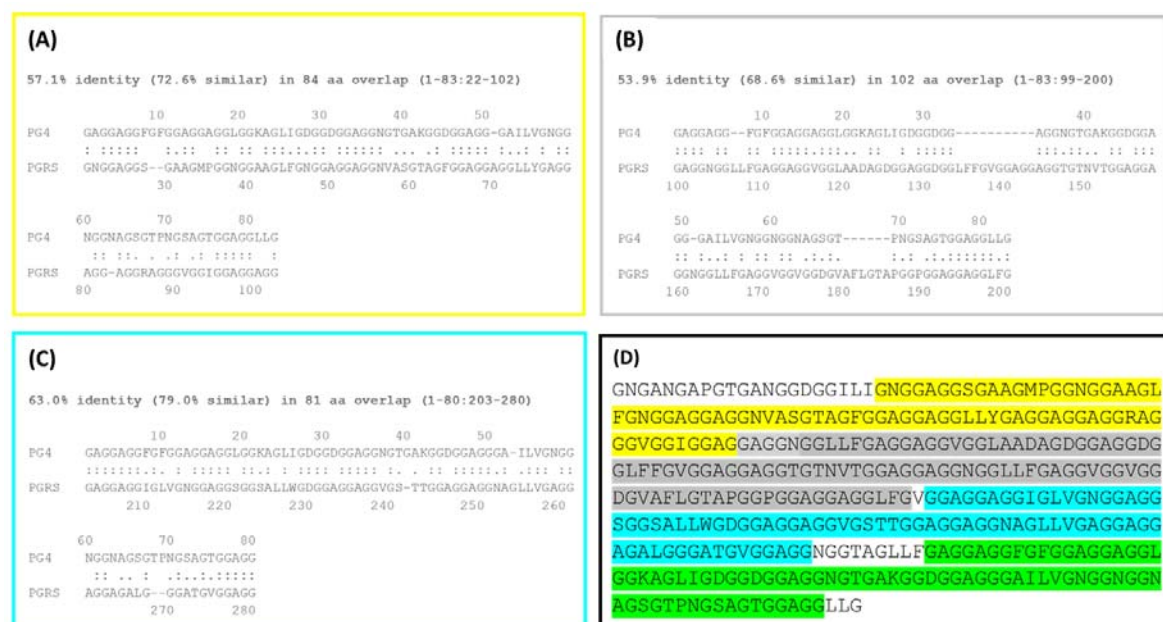


Figure S1. Alignment of the sequence of the C-terminal region of the PGRS domain of PE_PGRS33, PGII4, against the entire PGRS region, using the software LALIGN. Panels A, B, C show alignments of PGII4 with PGII1, PGII2 and PGII3, respectively. Sequence cover of the four domains is given in Panel D.