

Library Indian Institute of Science Education and Research Mohali



DSpace@IISERMohali (/jspui/)

- / Publications of IISER Mohali (/jspui/handle/123456789/4)
- / Research Articles (/jspui/handle/123456789/9)

Please use this identifier to cite or link to this item: http://hdl.handle.net/123456789/4796

Title: Trypanosoma evansi RoTat 1.2 variant surface antigen mimotopes selected by panning of the

random peptide phage-display library against monoclonal antibodies

Authors: Dubey, Abhishek (/jspui/browse?type=author&value=Dubey%2C+Abhishek)

Keywords: Trypanosoma evansi RoTat surface antigen mimotopes

monoclonal antibodies

Issue Date: 2022

Publisher: John Wiley & Sons, Inc

Citation:

Journal of Molecular Recognition, 35(11), 2984.

Abstract:

Mimotope peptides of native antigens are valuable for diverse applications such as diagnostics, therapeutics and modern vaccine design. Here, we report for the first time the selection and identification of peptide mimotopes of Trypanosoma evansi RoTat 1.2 variant surface glycoprotein (VSG) for their potential uses in surra diagnostics and multi-epitope vaccine research. First, we produced the mouse monoclonal antibodies (mAbs), designated as 2E11 (IgG1) and 1C2 (IgG1), against the antigens in T. evansi RoTat 1.2 lysates. We then used 2E11 mAb to immunoprecipitate the target antigen. The immunoprecipitated antigen was then identified to be the VSG by mass spectrometry. Both 2E11 and 1C2 mAbs reacted with the VSG in immunoblots. The surface plasmon resonance immunosensors developed with both the mAbs detected VSG in the parasite lysates as well as in the rodent sera. Further, the mAbs were biotinylated and used in three rounds of panning to select peptide mimotopes from the random peptide phage display library (PhD-12; New England Biolabs, USA). The phage clones selected against each mAb were amplified and tested by phage capture ELISA for specificity. The peptide coding regions of the selected phages were sequenced and the protein blast search of the deduced amino acid sequences was performed by accessing the non-redundant protein database at https://blast.ncbi.nlm.nih.gov/. The conformational B epitope prediction of the selected mimotope sequences was done by using 3D Pepitope algorithms accessed at: http://pepitope.tau.ac.il/. The potential applications of the selected mimotopes in surra diagnostics and research are being

Only IISERM authors are available in the record Description:

URI: https://doi.org/10.1002/jmr.2984 (https://doi.org/10.1002/jmr.2984)

http://hdl.handle.net/123456789/4796 (http://hdl.handle.net/123456789/4796)

Appears in

Collections:

Research Articles (/jspui/handle/123456789/9)

Files in This Item:

File Description Size **Format** Need To Add...Full Text PDF. 15.36 Unknown View/Open (/jspui/l (/jspui/bitstream/123456789/4796/2/Need%20To%20Add%e2%80%a6Full%20Text_PDF.) kΒ

Show full item record (/jspui/handle/123456789/4796?mode=full)

■ (/jspui/handle/123456789/4796/statistics)

Items in DSpace are protected by copyright, with all rights reserved, unless otherwise indicated.