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Exploring *Leishmania* Secretory Proteins to Design B and T Cell Multi-Epitope Subunit Vaccine using Immunoinformatics Approach

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Visceral leishmaniasis (VL) is a fatal form of leishmaniasis which affects 70 countries, worldwide. Increasing drug resistance, HIV co-infection, and poor health system require operative vaccination strategy to control the VL transmission dynamics. Therefore, a holistic approach is needed to generate T and B memory cells to mediate long-term immunity against VL infection. Consequently, immunoinformatics approach was applied to design the multi-epitope based subunit vaccine construct consisting of B and T cell epitopes. Further, the physiochemical characterization was performed to check the aliphatic index, theoretical PI, molecular weight, and thermostable nature of vaccine construct. The allergenicity and antigenicity were also predicted to ensure the safety and immunogenic behavior of final vaccine construct. Moreover, homology modeling, followed by molecular docking and molecular dynamics simulation study was also performed to evaluate the binding affinity and stability of receptor (TLR-4) and ligand (vaccine protein) complex. This study warrants the experimental validation to ensure the immunogenicity and safety profile of presented vaccine construct that may be helpful to control VL infection.