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Correlation between predicted immune epitopes and protein disorder: An immunoinformatic approach to find vaccine and diagnostic candidates

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Immunoinformatics is an innovative strategy for selection of targets for vaccine and diagnostics with reduced time and costs. Data mining of essential sequences for eliciting protective immune responses through immunoinformatics has been used for indicating good vaccine candidatesfor *Neisseria meningitides* and *Staphylococcus aureus* showing the efficacy of this approach. It was also shown that instrinsically disorded proteins play important role in trypanosomatids virulence. Our hypothesis is that protein disordered regions could be related to immunogenic epitopes facilitating their exposure to the immune system. In this work, we developed a computational approach that integrates: a) T and B cell epitope predictors, namely: NetCTL and NetMHC for T CD8+ epitope prediction; NetMHCII for T CD4+ epitope prediction; and BepiPred for B cell epitope prediction; and b) structural disorder predictors, namely: DisEMBL, IUPred, GlobPipe and VSL2B. In addition, data associated with subcellular location predictions performed by the algorithms WoLF PSORT (eukaryotic genomes), PSORTb (procariotic genomes), Sigcleave (signal peptides) and TMHMM (transmembrane domains) were integrated in a relational database. The workflow had been used for searching vaccine or diagnostic targets in prokaryotic and eukaryotic organisms, including *Leishmania infantum, Leishmania braziliensis, Schistosoma mansoni* and *Ehrlichia canis*. Experiments in wet lab are being performed in order to confirm the immunogenicity of the selected proteins from *Leishmania* and *S. mansoni*. The correlation between structural disorder and the epitope location will be presented together with the analytical approach developed.

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