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Prediction of B cell immunodominance for vaccine design using statistical feature discovery and protein language model

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Knowledge of B cell immunodominance is important for engineering immune response in vaccine design. However, few studies describe prevalence of B cell immunodominance thus far. In this work, we defined immunodominance score with novel data processing and discovered statistically significant characteristics of B cell immunodominance in residue and patch level. In particular, conservation and clustering pattern were found to be robust indicators which describe B cell immunodominance. From this observation, we developed BIDpred, a B cell ImmunoDominance predictor which learns newly discovered features using protein language model embeddings and graph attention network. BIDpred also showed comparable result to current state-of-the-art methods in B cell epitope prediction. To the extent of our knowledge, our work is the first to statistically analyze and predict B cell immunodominance using deep learning.