

# Bioinformatics for cancer immunotherapy target discovery

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## Abstract

The mechanisms of immune response to cancer have been studied extensively and great effort has been invested into harnessing the therapeutic potential of the immune system. Immunotherapies have seen significant advances in the past 20 years, but the full potential of protective and therapeutic cancer immunotherapies has yet to be fulfilled. The insufficient efficacy of existing treatments can be attributed to a number of biological and technical issues. In this review, we detail the current limitations of immunotherapy target selection and design, and review computational methods to streamline therapy target discovery in a bioinformatics analysis pipeline. We describe specialized bioinformatics tools and databases for three main bottlenecks in immunotherapy target discovery: the cataloging of potentially antigenic proteins, the identification of potential HLA binders, and the selection epitopes and co-targets for single-epitope and multi-epitope strategies. We provide examples of application to the well-known tumor antigen HER2 and suggest bioinformatics methods to ameliorate therapy resistance and ensure efficient and lasting control of tumors.

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