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Epitope Identification from Fixed-complexity Random-sequence Peptide Microarrays

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Abstract

Antibodies play an important role in modern science and medicine. They are essential in many biological assays and have emerged as an important class of therapeutics. Unfortunately, current methods for mapping antibody epitopes require costly synthesis or enrichment steps, and no low-cost universal platform exists. In order to address this, we tested a random-sequence peptide microarray consisting of over 330,000 unique peptide sequences sampling 83% of all possible tetramers and 27% of pentamers. It is a single, unbiased platform that can be used in many different types of tests, it does not rely on informatic selection of peptides for a particular proteome, and it does not require iterative rounds of selection.

In order to optimize the platform, we developed an algorithm that considers the significance of k-length peptide subsequences (k-mers) within selected peptides that come from the microarray. We tested eight monoclonal antibodies and seven infectious disease cohorts. The method correctly identified five of the eight monoclonal epitopes and identified both reported and unreported epitope candidates in the infectious disease cohorts. This algorithm could greatly enhance the utility of random-sequence peptide microarrays by enabling rapid epitope mapping and antigen identification.

Full text:

http://www.mcponline.org/content/14/1/136.abstract?maxtoshow=&HITS=10&hits=10&RESULTFORMAT=1&andorexacttitle=and&andorexacttitleabs=and&fulltext=innopsys&andorexactfulltext=and&searchid=1&FIRSTINDEX=0&sortspec=date&tdate=5/31/2015&resourcetype=HWCIT