

## Identification of B and T cell epitope peptide vaccines from IGF-1 Receptor in breast cancer

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### Abstract

**Introduction:** The insulin-like growth factor-1 receptor (IGF-1R) plays a key role in proliferation, growth, differentiation, and development of several human malignancies including breast and pancreatic adenocarcinoma. IGF-1R targeted immunotherapeutic approaches are particularly attractive, as they may potentially elicit even stronger antitumor responses than traditional targeted approaches. Cancer peptide vaccines can produce immunologic responses against cancer cells by triggering helper T cell (Th) or cytotoxic T cells (CTL) in association with Major Histocompatibility Complex (MHC) class I or II molecules on the cell surface of antigen presenting cells.

**Methods and Results:** In our previous study, we set a technique based on molecular docking in order to find the best MHC class I and II binder peptides using GOLD. In the present work, molecular docking analyses on a library consisting of 30 peptides mimicking discontinuous epitopes from IGF-1R extracellular domain identified peptides 249 and 86, as the best MHC binder peptides to both MHC class I and II molecules. The receptors most often targeted by peptide 249 are HLA-DR4, HLA-DR3 and HLA-DR2 and those most often targeted by peptide 86 are HLA-DR4, HLA-DP2, and HLA-DR3.

### Conclusions:

These findings, based on bioinformatics analyses, can be conducted in further experimental analyses in cancer therapy and vaccine design.

**Key words:** Docking, MHC, Bioinformatics, Peptide vaccine, IGF-1 receptor

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