2nd International Nastaran Cancer Symposium-2016

دومین سمپوزیوم بین المللی سرطان نستران-۱۳۹۵

Poster Presentation Certificate

Simulation And Stability Assessment Of Anti-EpCAM
Immunotoxin For Multiple Cancer Therapy

Seyyed Ali Hosseinian

Chairman, NCCP	Scientific Chair(Basic)	Scientific Chair(Clinical)
Dr. M. Taghi Mirahmadi	Dr. M. R. Abbaszadegan	Dr. A. Allahyari

Nastaran Symposium 2016

Simulation And Stability Assessment Of Anti-EpCAM Immunotoxin For Multiple Cancer Therapy

1. **Seyed-Ali Hosseinian** (Department Of Biology, Science And Research Branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran)
2. **Aliakbar Haddad-Mashadrizeh** (Cell And Molecular Biotechnology Research Group, Institute Of Biotechnology, And Department Of Biology, Faculty Of Science, Ferdowsi University Of Mashhad, Mashhad, Iran)
3. **Samaneh Dolatabadi** (Department Of Biology, Science And Research Branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran)

Abstract

Epithelial cell adhesion molecule (EpCAM) is a dominant antigen in human colon carcinoma tissue. Topology features of this antigen is different in normal and malignancies condition, so that in normal cells is predominantly located in intercellular spaces and is sequestered on normal epithelia and, therefore, much less accessible to antibodies than EpCAM in cancer tissue. Accordingly, EpCAM was considered as a suitable candidate for cancer target therapy via immunotoxins (ITs) development. In this regard, several ITs have been developed which could be provided context for ITs optimization. Bearing in mind, we have focused on the stability assessment of an anti-EpCAM-IT (anti-Ep-IT) for designing a novel IT. In this regard, 3D structure of EpCAM and toxin segments of anti-Ep-IT were retrieved from PDB, with the ID numbers 4MZV, 1IKQ, respectively. Discovery Studio3.0 was used for separation of the ligands and water molecules. Alignment of the antibody (Ab) fragment of anti-Ep-IT was performed through BLAST-p, and SWISS-MODEL database was used for Ab modeling. Moreover, IT modeling was accomplished through MODELLER9.15. GROMACS5.07, containing gromos96 43a1 force field were used for simulation 300°K, 100ps of the time for NVT and NPT steps and 20000ps(20ns) for MD step. RMSD and RMSF plots were drown by Excel. Finally, ERAAT database was used for quality assessment of the structure. In general, the both modeling results and quality evaluations of them were satisfactory for designing IT. Moreover, RMSD and RMSF plots reveal that IT stability has preserved during the simulation. On the whole, our findings led to designing a new anti-Ep-IT with more stability.

Corresponding Author: Aliakbar Haddad-Mashadrizeh (Cell and molecular biotechnology research group, institute of biotechnology, and Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran)