

## The 7th Conference on Bioinformatics, 3-5 January 2018



Faculty of Biological Sciences, Tarbiat Modares University, Tehran, Iran

## In silico study the natural APC3 inhibitor

M. marashian<sup>a</sup>, H. Rahimi<sup>a</sup>\* a, Molecular Medicine Department, biotechnology research center, Pasteur institute of Iran, Tehran-Iran \* rahimi.h1981@gmail.com

**Abstract:** The anaphase promoting complex/Cyclosome (APC/C) is the largest Cullin-RING E3 ligase. The function of APC/C was originally identified for controlling mitosis by ubiquitinating specific cell cycle regulatory proteins, such as cyclinB and Securin, Therefore, it triggers chromosome segregation[1] .Cdc20 and Cdh1 are activators of APC/C. studies are demonstrated that TAME have ability of mimiking IR tail of co-activators which is necessary for interaction with APC/C and it fills the IR tail binding domain of APC3B [2]. here docking approach applied by using the Smina which is a fork of AutoDock Vina to characterize the TAME binding pocket on APC3. The molecular docking result visualized in 2D and 3D representation via ligplot and pymol, respectively. The results of smina shown that TAME binds to TPR8 region of APC3B.

**Keywords:** Anaphase promoting complex; bioinformatics; TAME.

## References

- [1] N. B. Cronin, J. Yang, Z. Zhang, and K. Kulkarni, "Atomic-Resolution Structures of the APC / C Subunits Apc4 and the Apc5 N-Terminal Domain," *J. Mol. Biol.*, vol. 427, no. 20, pp. 3300–3315, 2015.
- [2] M. Yamaguchi *et al.*, "Structure of an APC3-APC16 complex: Insights into assembly of the anaphase-Promoting complex/cyclosome," *J. Mol. Biol.*, 2014.