



## Effect of *KLK2* nsSNPs on prostate related disease

F. Toghraei Semiromi, E. Moudi, A. Hosseinzadeh Colagar\*(10 regular) a Department of Molecular and Cell Biology, Faculty of Basic Sciences, University of Mazandaran, 47416-95447, Babolsar, Iran b Department of Urology, Babol University of Medical Sciences, Babol, 47745-47176, Iran \*ahcolagar@umz.ac.ir

**Abstract**:*Kallikrein2* codes serine protease enzyme that cleaves pro-PSA to active PSA which has an important role in liberation of sperm and fluidity of semen by shattering of Semenogelin and Fibronectin. Any polymorphism of this gene could effect on serine protease activity "[1]", which means they may associate with prostate cancer. In this study 7 nsSNPs were chosen which H65Y, and G214E are in active site; D207N, and S228A are in substrate binding site, and R250W that its GMAF is more than 1%, R24W in cleavage site and W38R. The influence of these substitutions on function and stability of protein and being deleterious were predicted by Polyphen2.0, Provean, Imutant3.0 and SIFT "[2-5]". All 7 nsSNPs were predicted as affected on protein functions. The *PolyPhen* 2.0 predicts that D207N and S228A are possibly damaging, G214E, R24W, W38R and H65Y are probably damaging and R250W is benign. Also D207N, G214E, R24W, W38R and H65Y are deleterious while S228A, and R250W are neutral. Unlike the other nsSNPs, the H65Y may increase the stability. Among intended nsSNPs, D207N has destructive effect on this enzyme, while R250W may has less destruction. Change of hK2 enzyme function by mentioned nsSNPs could associate with some prostate diseases. **Keywords:** Deleterious nsSNPs; KLK2; infertility; in-silico

## References:

- [1] Prassas, Ioannis, et al, "Unleashing the therapeutic potential of human kallikrein-related serine proteases." *Nature Reviews Drug Discovery.*, 14.3 (2015): 183-202.
- [2] P. Kumar, S. Henikoff, et al, "Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm". Nat Protoc., 4 (2009): 1073-81.
- [3] Y. Choi, AP. Chan, "PROVEAN web server: a tool to predict the functional effect of amino acid substitutions and indels." Bioinformatics., 31 (2015): 2745-7.
- [4] AI, Adzhubei, S. Schmidt, et al, "A method and server for predicting damaging missense mutations." Nat Methods., 7 (2010): 248-9.
- [5] ER. Capriotti, Calabrese, R. et al, "Predicting the insurgence of human genetic diseases associated to single point protein mutations with Support Vector Machines and evolutionary information." Bioinformatics., 22 (2006): 2729-34.