Structure Prediction and validation of mutant kir6.2 genes

Jaya Mary A[1], Rohini M[1] , Mumtaj P[1*]

[1] Post Graduate and Research Department of Biotechnology, Mohamed Sathak College of Arts and Science.

[*]Corresponding author e.mail: mumtajpeermohammed@yahoo.in

From National Conference on Interdisciplinary Research and Innovations in Biosciences, NATCON -2018. Post Graduate & Research Department of Biochemistry, Mohamed Sathak College of Arts & Science, Sholinganallur, Chennai-600119, India. 24th & 25th January 2018.

American J of Bio-pharm Biochem and Life Sci 2018 January, Vol. 4 (Suppl 1): **OP54**

ABSTRACT

Diabetes is one of the leading causes of morbidity and mortality, consuming a significant proportion of public health spending. Several receptors (insulin-like growth factor receptor, glucose transporter, and kir6.2 and their associated signaling pathways have been elucidated and are involved in glucose regulation and diabetes. Kir6.2, a major subunit of the ATP-sensitive K+ channel, an inward-rectifying potassium ion channel, is an integral membrane protein that allows K+ to flow from the outside of the cell to the inside, which is controlled by G-proteins associated with sulfonylurea receptor (SUR), to constitute the ATP-sensitive K+ channel.Ten possible mutations affecting the regular mechanism of kir6.2 have been identified as probable causes of type 1 diabetes. Due to the unavailability of the crystal structure of kir6.2 protein, an attempt was made here to predict both the secondary and tertiary structures using *in silico* approach.

Published: February 2018.