



International Conference & Exhibition on Vaccines & Vaccination

22-24 Nov 2011 Philadelphia Airport Marriott, USA

High throughput computational genome wide prediction and mapping of epitopes in severe acute respiratory syndrome coronavirus

Pallavi Somvanshi and B.N. Mishra

Department of Biotechnology, Institute of Engineering & Technology, Gautam Buddha Technical University, India

Severe acute respiratory syndrome (SARS) is a worldwide emerging infectious human disease caused by coronavirus. The genome size is approximately 31 kb of coronavirus. The epitopes were predicted from eleven putative proteins using immunoinformatics tools. Thirty two epitopes were predicted from MHC class I and thirty three epitopes from MHC class II molecules. In this study, the criteria for selecting epitopes were that the highest binding score at optimum threshold was chosen. Later on these may provide a suitable and safe antigen based designing of vaccine candidate for diagnosis, prevention and cure of SARS coronavirus.

Biography

Dr. Pallavi Somvanshi is currently a lecturer in Department of Biotechnology at Institute of Engineering & Technology, Lucknow (India). She obtained her PhD in 2009 in Bioinformatics from Uttar Pradesh Technical University, Lucknow (India). She pursued her career in bioinformatics with Senior Research Fellow and Research Associate from Bioinformatics Centre, Biotech Park, Lucknow (India). She has published more than 35 research articles, 4 review articles and book chapters. Additionally, she has contributed in public domains with submission of 252 three-dimensional protein structural models and more than 40 nucleotide sequence in NCBI Genbank. She is also supervising 20 post graduate students.