OMICS Group Conferences
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2ⁿᵈ International Conference and Exhibition on

Biometrics & Biostatistics

June 10-12, 2013   Hilton Chicago/Northbrook, USA

Searching for drug targets: The use of bioinformatics in protein sequencing and alignment of Hepatitis C core

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The Hepatitis C virus is the cause of an epidemic of liver cirrhosis and cancer for which there is currently no cure or vaccine for. One of the issues that arise when trying to develop a vaccine is the high mutation rate the virus undergoes. There are currently 6 different strains of the Hepatitis C virus, each having multiple subtypes. Vaccines in general work when an immune response is created after the immune system has been infiltrated by a foreign antigen. A new approach to vaccine design may be the solution needed for the ever changing Hepatitis C. Peptide vaccines involve the use of B-cell and T-cell epitopes of a target molecule creating an immunogenic universal vaccine. By using bioinformatics or various computational techniques, we hope to find and analyze protein sequences in the hepatitis C core that will lead to the development of a global drug.

Biography

Nicole S Williams is pursuing a B.S. in Biological Science from Atlanta Metropolitan State College. She has been actively involved in research since her freshman year, both at AMSC and the Morehouse School of Medicine.

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J Biomet Biostat 2013
ISSN: 2155-6180 JBMBS, an open access journal

Biometrics-2013
June 10-12, 2013

Volume 4 Issue 4

Page 88