

Prediction and Analysis of Human Transmembrane Transporter Proteins Based on SCM

Authors : Hui-Ling Huang, Tamara Vasylenko, Phasit Charoenkwan, Shih-Hsiang Chiu, Shinn-Ying Ho

Abstract : The knowledge of the human transporters is still limited due to technically demanding procedure of crystallization for the structural characterization of transporters by spectroscopic methods. It is desirable to develop bioinformatics tools for effective analysis of available sequences in order to identify human transmembrane transporter proteins (HMTPs). This study proposes a scoring card method (SCM) based method for predicting HMTPs. We estimated a set of propensity scores of dipeptides to be HMTPs using SCM from the training dataset (HTS732) consisting of 366 HMTPs and 366 non-HMTPs. SCM using the estimated propensity scores of 20 amino acids and 400 dipeptides -as HMTPs, has a training accuracy of 87.63% and a test accuracy of 66.46%. The five top-ranked dipeptides include LD, NV, LI, KY, and MN with scores 996, 992, 989, 987, and 985, respectively. Five amino acids with the highest propensity scores are Ile, Phe, Met, Gly, and Leu, that hydrophobic residues are mostly highly-scored. Furthermore, obtained propensity scores were used to analyze physicochemical properties of human transporters.

Keywords : dipeptide composition, physicochemical property, human transmembrane transporter proteins, human transmembrane transporters binding propensity, scoring card method

Conference Title : ICBBE 2015 : International Conference on Bioinformatics and Biomedical Engineering

Conference Location : Paris, France

Conference Dates : August 27-28, 2015