VIRTUAL TARGET SCREENING: VALIDATION USING KINASE INHIBITORS:

Wayne C. Guida, Daniel N. Santiago, Yuri Pevzner, Ashley A. Durand, MinhPhuong Tran, Rachel R. Scheerer, Kenyon Daniel, Shen-Shu Sung, H. Lee Woodcock and Wesley H. Brooks, Department of Chemistry, University of South Florida, Tampa, Florida 33620. Virtual screening could potentially be employed to discover new biomolecular targets for a molecule of interest (MOI). Existing scoring functions may not accurately differentiate proteins to which the MOI binds from a larger set of macromolecules in a structural database. In a method termed “Virtual Target Screening (VTS)”, a set of small drug-like molecules is docked against each structure in the protein library to produce benchmark statistics. This calibration provides a reference for each protein so that hits can be identified for an MOI. To validate our VTS method, twenty kinase inhibitors were docked to a collection of calibrated protein structures. VTS predicted protein kinases as hits in preference to other proteins in our database.