METHOD AND SYSTEM FOR FAST PROTEIN VISUALIZATION USING PRE-CALCULATED IMAGE SIMILARITY INDEX AND ATOM DEPTH

ABSTRACT

The present invention provides a method and system for rendering fast visualization of protein 3D structures. The method and system of the present invention improves the speed of visualization using pre-calculated image similarity index and atom depth. In one embodiment, the method comprises the steps of providing a file of the three dimension structure of a protein, calculating atom depth of each atom within the three dimension structure using a solvent accessible surface area, calculating image similarity indexes of images with different atom numbers in comparison with the original image, generating a rendering table that correlates the image similarity indexes with the atom depths, and displaying the three dimension structure with an accuracy that is input by a user. In one embodiment, the system comprises a computer readable medium; a computer program embedded within the computer readable medium, wherein the computer program enables fast visualization of protein three dimension structures; wherein the computer program comprises: means for providing a file of the three dimension structure of a protein; means for calculating atom depth of each atom within the three dimension structure using a solvent accessible surface area; means for calculating image similarity indexes of images with different atom numbers in comparison with the original image; and means generating a rendering table that correlates the image similarity indexes with the atom depths; and a display means for displaying the three dimension structure with an accuracy that is input by a user.

FIG 5