The analysis of CH-π interaction in protein–carbohydrate binding

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The molecular recognition of carbohydrates by proteins plays a key role in many biological processes including immune response, pathogen entry into a cell and cell-cell adhesion (e.g., in cancer metastasis). Carbohydrates interact with proteins mainly through hydrogen bonding, metal-ion-mediated interaction and non-polar dispersion interactions. The role of dispersion-driven CH-π interactions (stacking) in protein-carbohydrate recognition has been underestimated for a long time considering the polar interactions to be the main forces for saccharide interactions. However, over the last few years it turns out that non-polar interactions are equally important. Using the Protein Data Bank (PDB) structural data, we analyzed the CH-π interactions employing bioinformatics (data mining, structural analysis), several experimental (ITC, X-ray crystallography) and computational techniques [1]. Within 12 000 protein complexes with carbohydrates from PDB, the stacking interactions were found in about 39% of them. The calculations and the ITC measurement results suggest that the CH-π stacking contribution to the overall binding energy ranges from 4 kcal/mol up to 8 kcal/mol. All the results show that the stacking CH-π interactions in protein-carbohydrate complexes can be considered to be a driving force of the binding in such complexes.

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