SJSU | DEPARTMENT OF CHEMISTRY

CHEMISTRY Departmental Seminar

Spring 2022
CHEM 285/191 Schedule
Tuesday at 4:30-5:45PM
Duncan Hall 250
April 26th, 2022

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Characterization of Bridging Waters and the Role of Ions in a Diverse Set of Protein-RNA Complexes

Consideration of waters that bridge ribonucleotides and amino acids have been of interest because modeling energetics for such complexes are often not realistically scaled,[1] where the role of solvent remains undetermined, though the relative rankings by energy may still be appropriate. Early calculations involving a trinucleotide binding a tetrapeptide proposed additional stability from such a bridging water.[2] Here we explore the role of bridging waters in RNA-protein complexes. From an initial set of 43 high resolution X-ray crystal structures, 24 were identified where unbound chains with respect to the RNA-protein complex were found within 1 pH unit and their temperatures meeting one of two ranges (above or below freezing). Previously an earlier 28-set of data was not filtered as such, showing most interestingly that seventy percent with more hydrogen bonds in the interfacial regions for the bound complexes and their attendant exclusion of solvent. And interactions included two bridging waters per 125 Å^2 of BSA (buried surface area) associated with the complexes. More recently, the pH and temperature filtered 24-set and their constituent RNA and protein components showed nine complexes indicating more protein and RNA water hydrogen binding in their actual interfacial regions as opposed to those corresponding to the unbound components. All of these complexes indicate significant interfacial water hydrogen bonding and include waters that actually bridge amino acids and ribonucleotides. For the 24-set we characterized 3370 interfacial water hydrogen bonds. Of those interfacial water hydrogen bonds, 1285 have bridging waters, comparable to the earlier 28-set. Additionally, ion analysis was performed on the 24-set, where 19 complexes had ions in the chains of interest, where no significant differences due to ions have yet been noted. One issue of ongoing interest is the consideration of preserved waters where such an interfacial water is considered preserved if it makes an H-bond with the same donor or acceptor atoms of protein or RNA chains in both the bound and unbound structures.[3] Future studies also will need to address methods to better validate water positions, including an increase in the set of RNA-protein complexes.

1.Le, T., Computational Models Exploring the Role of Flexibility in Binding TAT Peptide to TAR RNA, M.S. Thesis, San Jose State University (2018).
2.Yoon, C. N. & Jhon, M. S. Conformational study of the trinucleotide CpGpCp-pentapeptide Gly5 complex: The important role of bridging water in the complex formation. *J. Comput. Chem.* **1986**, 7, 189-200.
3.Barik A. & Bahadur, R. P. Hydration of protein-RNA recognition sites. *Nucleic Acids Res.* **2014**, 42, 10148-60.

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