Geometries and Energetics of Valinomycin Alkali ion complexes

Dr. Vincent DeTuri, Semeret Munie, and Elvis Shehi
Department of Chemistry, Ithaca College, Ithaca, NY 14850

Valinomycin is an antibiotic which is a cyclic macro molecule made up of twelve alternating amino acids: D-Valine, L-Valine, D-Hydroxyisovaleric acid and L-Lactic acid. It is a transport protein that selectively binds to potassium ions and transports them across the cell membrane. In solution, valinomycin has a random floppy shape. But when it binds to potassium ion, it attains a donut shaped structure with the polar groups inside the "hole" and non polar groups on the outside. Despite the geometric similarities between the Na^+ and K^+ complexes of valinomycin, there is a 10^4-10^6 –fold preference for formation of a K^+- valinomycin complex over the corresponding Na^+ species.

We have used different ONIOM methods to optimize Na^+, K^+ and Li^+-valinomycin complexes, where the central parts of the complex involved in the interaction between the metal ion and valinomycin were optimized with higher level theories than the outer extensions of valinomycin like the methyl and propyl groups. This way of optimization allows us to save calculation time without losing accuracy on areas of importance. The geometry and binding strength of each valinomycin alkali ions are reported. Using the calculated binding strengths, we calculate the selectivity ratios of valinomycin to the alkali ion.

The computational calculations are supported by experimental analysis using a triple quadruple molecular mass analyzer with an atmospheric pressure electrospray ionizer source. We sample the alkali ion-valinomycin complexes in solution to investigate the equilibrium constants in mixed solvent systems.

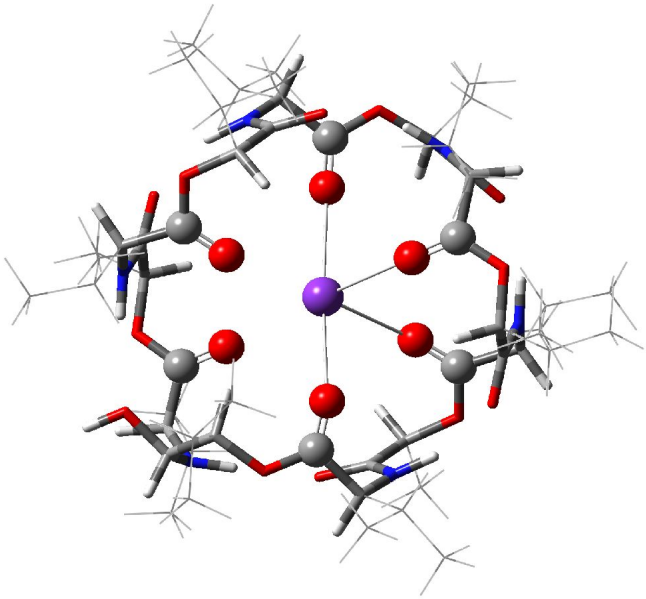

Figure 1: Optimized structure of K^+-valinomycin complex using ONIOM.