Conformational Analysis of Neutral and Ionic Forms of Lysine

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Lysine which contains a primary amine at its terminal group, is an essential amino acid. Under physiological conditions ε -amino group is positively charged. It is basic and prone to be out of hydrophobic surfaces of proteins. Because of this property, reactive group of lysine is essential for protein stability [1]. Ionization states of lysine side chain can regulate biological functions of membrane proteins like sodium channels, acetylcholine receptors, integrins, etc.[2].

In our study, conformational analysis of neutral and ionic lysine forms have been performed and isolelectronic forms were compared.



Conformational analysis has been carried out by using molecular mechanics methods for neutral and all possible charged states of lysine. All molecules have been fully optimized at B3LYP/cc-PVTZ and wB97XD/cc-PVTZ levels. Afterwards frequency analysis has been carried out at same levels for characterizing stationary points. Calculations have been carried out by using Spartan '08 [3] and Gaussian 09 program packages [4].

Lysine has 8 possible charged states. After conformational analysis; 369 structures for neutral lysine, 228 structures for anion, 26 structures for cation1, 60 structures for cation2, 39 structures for cation3, 44 structures for dication, 66 structures for zwitterion1, 35 structures for zwitterion2 have been determined. These numbers decreased after optimization and frequency analysis. Optimization of the conformers with different functionals has altered the stability order of the conformers.

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[2] N. J. Gleason, V. V. Vostrikov, D. V. Greathouse, R. E. Koeppe II, *Proc. Natl. Acad. Sci. USA*, 2012, *10*(5), 1692-1695.
[3] W. J. Hehre, *et. al.* Spartan 08 for Windows, Wavefunction, Inc., Irvine, CA, 2007.
[4] M. J. Frisch, *et al.* Gaussian 09 Revision C01, Gaussian Inc., Wallingford CT, 2011.