

Role of Hydrophobicity in Protein Evolution**Vitor Leite¹, Ricardo Silva¹, Michel Yamagishi², Jorge Chahine¹**¹Departamento de Física, IBILCE - Univ Estadual Paulista, Rua Cristovao Colombo, 2265, Sao Jose do Rio Preto, 15054-000, Brazil, ²Lab Bioinformatica Aplicada, Embrapa, Av. Andre Tosello, 209, Cidade Universitaria Zeferino Vaz, Campinas, 13083-970, Brazil

Effect of mutations on the stability of proteins is a crucial issue in protein evolution. Such effects depend strongly on the overall hydrophobic protein character. In a recent work we suggested two scenarios for folding with distinct protein evolution consequences [1]. Under low hydrophobic conditions, proteins collapse concomitantly with the formation of their native state, and are less robust to mutations. This feature implies higher homology among proteins of different species. On the other limit, at high hydrophobicity, proteins collapse before folding, and in this case they are more susceptible to mutations, suggesting lower homology among proteins of different species. In this work we investigate this conjecture studying the homology of four proteins for 41 different species, correlating it with their average hydrophobicity. The proteins studied were lysozyme, cytochrome-c, myoglobin and histone H3, and we used eighteen different hydrophobic scales. Along with the homology calculation, a comparison of structural similarity (rmsd) was also carried out. The results confirm the above suggestion, indicating that proteins at low hydrophobicity display low variations on sequences and conformations. On other hand, at high hydrophobicity, proteins exhibit high variability on sequences and conformations.

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[1] Oliveira LC, Silva RTH, Leite VBP, Chahine J, *J. Chem. Phys.*, **125**, 084904, (2006)