生物物理学报(2004) 20(4), 315-322

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压强温度耦合作用下小蛋白去折叠过程的分子动力学模拟

王吉华*[1]、张志勇[2,3]、刘海燕[2]、施蕴渝[2]
1 山东省德州学院生命科学研究所
2 中国科学技术大学生命科学学院
3 School of Health Information Sciences, University of Texas Health Science Center

在不同温度（280~540K）和压强（1×102~8×105 kPa）的耦合作用下，对GB1（the B1 domain of protein G）进行了56次独立分子动力学模拟，模拟时间达88.8 ns。在此基础上，研究了压强和温度对GB1去折叠过程的耦合效应。结果表明，压强对温度去折叠过程有明显影响，改变了蛋白质二级结构去折叠速度和蛋白质去折叠过程发生事件的先后次序。相同温度下，GB1的α-螺旋和β-折叠的稳定性随压强增大而提高；可及性表面积和其它结构特性参数随压强增大而减小。适度的压强（如2×105 kPa）会抑制温度导致的GB1二级结构去折叠速度，而更大的压强（如8×105 kPa）又加速了GB1的去折叠速度。在模拟的温度范围，当压强为100和 2×105 kPa时，GB1疏水核协同暴露于水，而5×105和8×105 kPa时没出现此现象，这与最近的高压变性实验结果一致。

STUDY ON UNFOLDING PROCESSES OF A SMALL PROTEIN BY MOLECULAR DYNAMICS SIMULATIONS UNDER THE COUPLING EFFECT BETWEEN PRESSURE AND TEMPERATURE

56 independent molecular dynamics (MD) simulations of the B1 domain of protein G (GB1) were performed to the amount of 88.8ns under fourteen temperatures (from 280 to 540 K) and four pressures (1×102, 2×105, 5×105 and 8×105 kPa). The coupling effect between temperature and pressure during GB1 unfolding processes was studied. The stability of α helix and the β strands increased with increasing pressure. The solvent accessible surface area (SASA) and the other structural parameters decreased with increasing pressure in general. The moderate pressures such as 2×105 and 5×105 kPa restrained the unfolding rate of secondary structure of the protein by slowing down the internal motion of GB1, while higher pressures such as 8×105 kPa accelerated its unfolding rate. The cooperative exposing of the hydrophobic core of GB1 to water occurred at 1×102 and 2×105 kPa among the simulations under different temperatures, but the same phenomena did not occur at 5×105 and 8×105 kPa. The results showed that the temperature-induced unfolding process was perturbed obviously by pressure. The simulation results agree with those obtained from recent experiments.

关键词