ZETA SIZE AND CHARGE EVALUATION OF COMPLEXES BASED ON PHOSPHORUS DENDRIMERS AND PLASMA REGULATORY PROTEINS

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Dendrimers, which are considered as one of the most promising tools in the field of nanobiotechnology due to their structural organization, showed a great potential in gene therapy, drug delivery, medical imaging, as antimicrobial and antiviral agents [1]. Considering numerous applications of dendrimers in the biomedical field, knowledge of their possible interactions with biological components at a molecular level is required.

This paper presents a study of the interaction of cationic phosphorus dendrimers, a class of dendrimers with potential medical relevance [2, 3], with regulatory plasma proteins: aspartate transaminase (AST), alkaline phosphatase (AP) and Lactic dehydrogenase (LDH) by dynamic and phase analysis light scattering.

The results show that water-soluble cationic phosphorus dendrimers of generation 3 and generation 4 interact with regulatory plasma proteins to form positively charged (+14 – +17 mV) dendrimer/protein complexes of different sizes (from 200 to 1800 nm) at a molar ratio of 10–15:1. This information could be useful in designing new drug delivery systems using dendrimers as potential carriers of biomolecules and in other fields of nanobiotechnology.

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CORRELATING ROSETTADOCK BINDING SCORE WITH PROTEIN-PROTEIN BINDING AFFINITY

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Many protein-protein docking algorithms are divided into two steps: the initial global search and subsequent steps of refinements to improve these initial predictions [1]. The global search is a full search of the orientations of the two proteins, typically keeping the larger protein (referred to as the receptor) fixed, while moving the smaller protein (the ligand). This is often a rigid-body search in six dimensions, utilizing a fast Fourier transform (FFT) for efficiency and softness for small overlaps [1]. Subsequently, one or more refinement and scoring steps of a set of preselected rigid docking solutions are added to achieve closer agreement with the native geometry and to recognize near-native docking solutions preferentially either as the best or among the best scoring complexes. The accuracy and speed of flexible refinement and rescoring of preselected docked protein structures are important for the success of the multistage docking protocol. Recently, it has been shown using Principal Component Analysis that the energy landscape of 42 interacting proteins, at least within the 10 Å IRMSD neighborhood of the native state, always includes a permissive subspace (‘tunnel’) along which the conformation of the complex can substantially change without crossing significant energy barriers and that the energy landscape is smooth funnel in a two dimensional permissive subspace [2]. This suggests that methods such as molecular dynamics (MD) or Monte Carlo (MC) simulations that start from productive encounter complexes should fairly quickly converge to native structure (or near-native one because of some inaccuracy of scoring functions) making these strategies as promising tools of the efficient refinement. The Monte Carlo approach is especially attractive as being much less computationally expensive as compared with MD. Several docking protocols including rigid-body