11:40 Oral

Homology modeling of G-protein coupled receptors

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The present presentation will give a short overview of G-protein coupled receptors (GPCRs). In mammalian species, there are three main families of GPCRs. Many drug targets belong to family A of GPCRs, which includes receptors for endogenous compounds including biogenic amines, lipid-like compounds, many neuropeptides, glycoprotein hormones, protease-activated receptors and receptors for exogenous compounds, opsins, odorants and some tastants (Kristiansen, 2004). Homology models of GPCRs were previously constructed by using bacteriorhodopsin x-ray structure (not a G-protein coupled receptor) or a template for family A receptor based on a cryo-microscopy microscopy and sequence analysis of family A receptors (Baldwin, 1997). Today, x-ray structures of several family A receptors have been reported, including bovine rhodopsin (Palczewski et al. 2000), beta1(Warne et al., 2008) and beta2 (Cherezov et al. 2007) adrenergic receptors and A2A adenosine receptor, which has given the opportunity to generate more accurate GPCR models. The x-ray structure of the aminoterminal extracellular domain of family C receptors has also been reported. However, all known x-ray structures of family A receptors represent the inactive state conformation. In the present presentation, a model of the human D2 dopamine receptor constructed by homology with bovine rhodopsin will be discussed. Several antipsychotic drugs were docked into the model by using automatic docking with the modeling software ICM.

Acknowledgements

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12:00 Oral

Polymer chains as molecular dispensers. Monte Carlo simulations of simple models

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A simple model of molecular dispenser consisting of protein-like copolymers was designed. A coarse-grained model of polymer chains was used for this purpose. In this model we replaced a real polymer chain with a sequence of statistical segments connected by united atoms while all the atomic details were suppressed. Such a chain was restricted to a lattice of a [310] type, which was frequently used in simulations of polymers and biopolymers. Different macromolecular architectures were studied: linear chains and star-branched chains. Two kinds of polymer segments were defined: hydrophilic and hydrophobic ones (the HP model). The force field used consisted of the long-range contact potential between polymer segments and the attractive potential between a large spherical particle and the polymer. The properties of the model system were determined using the Parallel Tempering (the Replica Exchange) Monte Carlo sampling scheme. The hompolymer chain was adsorbed on the large particle, then polymer segments in loops (non-adsorbed) were changed to hydrophilic ones (process of "colouring") and crosslinks between some hydrophobic segments were introduced. It was shown that a chain prepared in a such way is sensitive to the particle size. The introduction of branching led to the increase of the selectivity.

12:20 Oral

Keratin associated proteins (KAPs) as a new biomaterials for applications in medicine and cosmetology

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Micro- and nanobiotechnology are the most explored fields in contemporary life science. This stimulates development of new 3D structural synthetic and semisynthetic materials. Usually, application of proteins as structural biopolymers requires chemical modifications resulting in increased stability of their 3D structures. The biocompatibility of these materials is the most important problem. Our team developed new technology of producing keratin associated protein (KAP) scaffolds from hair, wool and bristle.

Hair keratin associated proteins (hKAP), as well as other biomaterials of this type, are essential for the formation of a rigid and resistant hair shaft. Rigid structures are obtained due to extensive disulfide bond cross-linking between abundant cysteine residues of hair kerat-