time scale to study kinetics of lumirhodopsin decay and the effect of membrane environment on the first equilibrium constant, K_1, and on the pK_a of the second equilibrium. Reconstituted membranes of rhodopsin with POPC, DOPC, or a mixture of DOPC and DOPE were studied at 30°C. We also extended previous 20°C studies of the pH dependence of the equilibria in the native disk membranes, to determine how increased temperature affects lumirhodopsin decay through the purely transient 380 nm absorbing species, Meta I_{380}, into the final equilibrium mixture. Meta I_{380} has recently attracted substantial interest, since time-resolved circular dichroism measurements on the microsecond timescale suggest the chromophore has a different conformation than in later 380-nm photointermediates. Our results suggest SB deprotonation precedes other activating changes in the protein. Significant details are now emerging that give new insights into rhodopsin activation and complement FTIR and spin-label approaches.

1509-Pos

Multi-Scale Dynamics of Rhodopsin Activation as a Paradigm for GPCR Function

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G-protein coupled receptors (GPCRs) are membrane proteins that act as signaling cascade initiators responsible for a myriad of cellular processes. Ligand binding causes GPCR conformational changes that allow the receptor to interact with its cognate G-protein. Several techniques have structurally characterized rhodopsin photointermediates, but none have directly revealed the protein dynamics.Here we report a model whereby ps-ns ligand dynamics are coupled to the μs-ms protein motions during activation. These protein motions represent activated conformational substates on a hierarchy of time scales. Previous models propose that rhodopsin activation is a simple switch whereby retinal isomerizes from an 11-*cis* to an *all-trans* conformer, transforming from an inverse agonist to an agonist. In contrast, our model is motivated by FTIR and UV-visible results showing thermodynamic coupling to several substates in rhodopsin activation (metaI, metaII$_a$, and metaII$_b$) [1]. Furthermore, new ^{2}H NMR data from selectively labeled retinal ligands bound to rhodopsin are able to show that each retinylidene methyl group, especially the C9-methyl, acts as a dynamical hotspot in the activation pathway [2]. Relaxation times are fitted to three-fold jump and continuous diffusion models and correlated to methyl rotation rates in the different rhodopsin activation states, revealing distinct site-specific characteristics for each photointermediate. Recent solid-state NMR [3] and EPR [4] studies showed appreciable protein movements in the photointermediate pathway, further supporting our data. An activation mechanism emerges whereby conformational substates depend on a multivariate energy landscape encompassing retinal and protein dynamics as well as lipid bilayer interactions. [1] M. Mahlingam *et al*. (2008) *PNAS***105**, 17795-17800. [2] M.F. Brown *et al.* (2009) *BBA*, in press. [3] S. Ahuja *et al*. (2009) *J. Biol. Chem.***284**, 10190-10201. [4] C. Altenbach *et al*. (2008) *PNAS***105**, 7439-7444.

1510-Pos

Consequences of Fast, Stochastic Rhodopsin Shutoff for a Model of Phototransduction in Rods

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Rod photoreceptors signal the number and timing of photon absorption, a property that requires that each single photon response be of similar amplitude from trial to trial. How such reproducibility is achieved has been the subject of much experimental and theoretical work, which has demonstrated the importance of multiple steps in rhodopsin deactivation and diffusion of second messengers (Mendez et al., 2000; Bisegna et al., 2008). So far, all previous models have assumed that rhodopsin lifetime is significantly longer than recent measurements indicate (Krispel et al., 2006; Burns and Pugh, 2009). Additionally, recent biochemical studies have provided new details about the dependence of rhodopsin deactivation on phosphorylation level (Vishnivetskiy et al., 2007) that should inform a complete model of light response kinetics and reproducibility. We have implemented a spatio-temporal model of phototransduction in which the rhodopsin deactivation scheme is a stochastic multi-step process lasting no more than 50 ms. The parameters of this model were constrained using an extensive data set obtained from a variety of transgenic mouse lines, each developed to perturb rhodopsin activity, PDE deactivation, or Ca^{2+} feedback. Our simulations demonstrate the relative contributions of stochastic rhodopsin deactivation, Ca^{2+} feedback to guanylate cyclase, and second messenger diffusion to single photon response variability under biologically relevant constraints.

1511-Pos

Functional Structures of Photo-Activated Rhodopsin Disk Membranes Using Single Particle Tracking

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Heterotrimeric G-proteins interact with their G-protein coupled receptors (GPCRs) via key binding elements comprising the receptor-specific C-terminal segment of the alpha-subunit and the lipid anchors at the alpha-subunit N-terminus and the gamma-subunit C-terminus. Direct information about diffusion and interaction of GPCRs and their G-proteins is mandatory for an understanding of the signal transduction mechanism. By using fluorescence microscopy and single particle tracking we showed that the encounters of the alpha-subunit C-terminus with the GPCR rhodopsin change after receptor activation revealing inhomogeneous and restricted diffusion of the receptor (1). To obtain further information about the underlying membrane structure in the signaling state of rhodopsin we now constructed high-resolution transducin visits maps on rhodopsin disk membranes using the inherent information from the single molecule traces.

(1) Kim, T.Y., Uji-i, H., Moeller, M., Muls, B., Hofkens, J. and Alexiev, U. *Biochemistry* 48, 3801-3803(2009)

1512-Pos

Molecular Dynamics Simulations of Active Receptor-G Protein Complex in a Lipid Bilayer

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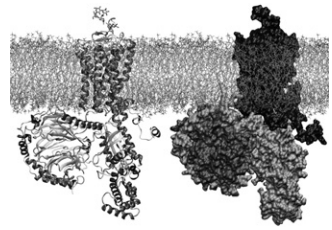

The crystal structure of opsin in its putative active state, the G-protein interacting conformation (Ops*-$G_t\alpha CT_{K341L}$), is arguably the most important breakthrough since the reports of structures for ground-state rhodopsin and the β_2-adrenergic receptor. We use this structure as a template and propose a structural model of the complex with full-length transducin (Ops*-$G_t\alpha\beta\gamma$) based on additional experimental structures including dark-state rhodopsin and holotransducin (Gt, $G_t\alpha\beta\gamma\bullet$GDP). We dock Gt with a reconstructed model of C-terminal α5 helix of $G_t\alpha$ to the open binding site in Ops*. Our model differs from others that propose a requirement for a 40°-tilt of $G_t\alpha\beta\gamma$ relative to the α5 helix in order to avoid steric clashes between $G_t\beta\gamma$ and the membrane. We further report a new method based on grid potentials to embed the complex into a POPC bilayer membrane. Compared with our previous molecular dynamics (MD) studies of the inactive states of rhodopsin[1] and β_2-adrenergic receptor,[2] these new simulations shed light on the role of the protonation state of the opsin residues K296(7.43) and E134(3.49) in stabilizing the receptor-G-protein complex. 1) T.Huber, et al. (2004) Biophys.J. 86:2078-2100. 2) T.Huber, et al. (2008) Biochemistry 47:11013-11023.

1513-Pos

Studying the Diffusion Characteristics of Different Activity States of the Human Adenosine-A3 Receptor Using Fluorescence Correlation Spectroscopy

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The adenosine-A_3 receptor is one of four known G-protein coupled receptors activated by the nucleoside adenosine. Here we use fluorescence correlation spectroscopy (FCS) in conjunction with pharmacological and molecular biology approaches to investigate the diffusion characteristics of different activity states of the human A_3-receptor. Initial FCS experiments using Chinese hamster ovary (CHO) cells expressing the wild type human A_3-receptor and the fluorescent adenosine receptor antagonist XAC-X-BY630 revealed both fast and slow moving complexes at the cell membrane, with average diffusion co-efficients of 1.58 ± 0.16 μm^2/s (τ_{D2}) and 0.081 ± 0.007 μm^2/s (τ_{D3}), respectively. At concentrations of XAC-BY630 ranging from 1-10 nM the amount of τ_{D3}, but not τ_{D2}, increased in a concentration-dependent manner. Pre-incubation of cells with the A_3-receptor specific antagonist MRS1220 at concentrations ranging from 0.3-300 nM significantly reduced the amount of slow moving (τ_{D3}) complexes in a concentration-dependent manner, indicating that they represent receptor bound ligand. Parallel experiments in which CHO cells were transfected with GFP tagged wild-type A_3-receptor (wt), a G-protein uncoupled mutant (W243A, W243F), or a constitutively active

mutant (R108A) were performed to investigate the diffusion characteristics of these 'inactive' and 'active' states of the A_3-receptor. One slow moving complex was identified at the cell membrane of wild-type A_3-GFP transfected cells, with a diffusion co-efficent (0.087 $\mu m^2/s$) similar to that of τ_{D3} for the XAC-X-BY630; similar complexes were identified in the mutant A_3-receptor cell lines.We have subsequently used FCS in conjunction with fluorescent agonist and antagonist A_3-receptor ligands to compare the ligand binding and diffusion properties of these different activity states of the receptor at the subcellular level.

1514-Pos

Computational Insight into the Ligand-Induced Conformational Specificity of G-Protein Coupled Receptors

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Several observations in the G-protein coupled receptor (GPCR) literature support the existence of ligand-specific intermediate conformational states that are likely to be involved in differential activation of signaling pathways. Fluorescence spectroscopy studies provide direct evidence for ligand-specific receptor conformations of the β2-adrenergic receptor, making this system an attractive target to test the ability of computational methodologies to predict different activated states of GPCRs. To this end, we designed a computational strategy that combines adiabatic biased molecular dynamics (ABMD) and metadynamics simulations. Firstly, ABMD is used to generate transition paths between the experimental inactive crystal structure of the β2-adrenergic receptor and a conformation containing established features of activated states of GPCRs (modeled using the opsin crystal structures). Secondly, metadynamics is applied to study how ligands with different efficacies affect the free-energy of different metastable states identified along these putative activation pathways. The calculated free-energy profiles of the different ligand-β2 adrenoceptor complexes help rationalize the published experimental results, including the different kinetics of catecholaminergic agonists such as epinephrine, norepinephrine, dopamine, and isoproterenol. Representative structures of the identified energy basins suggest specific residues and contacts that may help stabilize different activated states of the receptor. This information holds promise for the crystallization of different GPCR conformations.

1515-Pos

Structural and Kinetic Modeling of an Activating Helix Switch in the Rhodopsin-Transducin Interface

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Extracellular signals prompt G protein-coupled receptors (GPCRs) to adopt an active conformation (R*) and to catalyze GDP/GTP exchange in the α-subunit of intracellular G proteins ($G\alpha\beta\gamma$). Kinetic analysis of transducin ($G_t\alpha\beta\gamma$) activation shows that an intermediary $R^*G_t\alpha\beta\gamma GDP$ complex is formed which precedes GDP release and formation of the nucleotide-free R*G protein complex. Based on this reaction sequence we explore the dynamic interface between the proteins during formation of these complexes. We start from the R* conformation stabilized by a $G_t\alpha$ C-terminal peptide (GαCT) obtained from crystal structures of the GPCR opsin. Molecular modeling allows reconstruction of the fully elongated C-terminal α-helix of $G_t\alpha$ (α5) and shows how α5 can be docked to the open binding site of R*. Two modes of interaction are found. One of them - termed stable or S-interaction - matches the position of the GαCT peptide in the crystal structure and reproduces the hydrogen bridge networks between the C-terminal reverse turn of GαCT and conserved E(D)RY and $NPxxY(x)_{5,6}F$ regions of the GPCR. The alternative fit - termed intermediary or I-interaction - is distinguished by a tilt (42°) and rotation (90°) of α5 relative to the S-interaction. It shows different α5 contacts with the $NPxxY(x)_{5,6}F$ region and the second cytoplasmic loop of R*. From the two α5 interactions, we derive a 'helix switch' mechanism for the transition of $R^*G_t\alpha\beta\gamma GDP$ to the nucleotide-free R*G protein complex. It illustrates how α5 might act as a transmission rod to propagate the conformational change from the receptor-G protein interface to the nucleotide binding site.

1516-Pos

Agonist-Specific Effects of TM V Serine Mutations on Dopamine D2S Receptor Voltage-Sensitivity

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Voltage-sensitivity has recently been demonstrated for agonist potency and affinity at certain G protein-coupled receptors. Using an electrophysiology assay in Xenopus oocytes, we have previously shown that the potency of dopamine in activating G protein-coupled potassium channels (GIRK) via the dopamine D2S receptor is reduced by depolarization from −80 to 0 mV. We recently investigated the voltage-sensitivities of a range of structurally related dopaminergic agonists at the D2S receptor.

The findings of this study led us to propose that a conformationally constrained interaction of the agonist with transmembrane segment (TM) VI of D2 is required for voltage-sensitivity. The hypothesis assumes that for the flexible phenethylamines, two hydroxyls (such as in dopamine) interacting with the conserved serines in TM V are necessary for voltage-sensitivity. Conversely, N,N-dipropyl-2-aminotetralin (DPAT) agonists do not require hydroxyls for voltage-sensitivity due to their inherently more rigid structure. To test this hypothesis, we mutated three conserved serines in TM V (S193A, S194A, and S197A) which have been shown to mediate binding to agonist hydroxyls. The voltage-sensitivity of non-hydroxylated DPAT was similar to that observed with the wild-type receptor at all of the three mutants, suggesting that the mutations did not allosterically alter the voltage-sensing properties of the receptor.

The S193A mutation drastically diminished voltage-sensitivity of dopamine, concomitantly with a marked reduction in potency. However, the S194A mutation which slightly decreased potency, did not appreciably affect the voltage-sensitivity of dopamine. At the S197A mutant, dopamine efficacy was decreased to such a degree that voltage-sensitivity could not be assessed.

In the literature, S193 has consistently been assigned a major role in dopamine binding. Our results suggest that this residue might also be important for voltage-sensitive interactions between dopamine and the D2S receptor.

1517-Pos

Influence of Membrane Composition on Function of Human Peripheral Cannabinoid Receptor CB2

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The human peripheral cannabinoid receptor CB2 is abundant in tissues of immune and hematopoietic systems. CB2 belongs to the class of heptahelical G-protein coupled receptors and regulates a wide range of physiological functions through binding of endogenous and exogenous cannabinoid ligands. We studied the influence of electrical surface potential of membranes and of hydrocarbon-chain order on rates of G-protein activation by CB2. The membrane surface potential was determined by a measurement of the electrophoretic mobility of proteoliposomes, while lipid hydrocarbon-chain order was quantified by a measurement of the order parameters using ^2H NMR. The receptor, expressed in *E. coli*, was purified and functionally reconstituted into lipid bilayers composed of phosphatidylcholine (PC), phosphatidylserine (PS), and cholesteryl hemisuccinate (CHS). CB2 was fully activated with the synthetic agonist CP-55,940. The rate of G-protein activation by the receptor increased about two-fold with increasing CHS content in the lipid matrix from 25 to 41 mol%. Similar effect was observed with increasing PS content. The increased activation rate correlated with a larger negative ζ-potential caused by the negatively charged headgroups. The increased order of lipid acyl chains due to interactions with the cholesteryl backbone of CHS had no significant effect on G-protein activation rates, as confirmed by addition of cholesterol instead of CHS. The results indicate the importance of anionic lipids for efficient coupling between the CB2 receptor and G-proteins.

1518-Pos

A Polybasic Region in the C-terminus of M3 Muscarinic Acetylcholine Receptors Mediates an Interaction with Gq Heterotrimers

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G protein-coupled receptors (GPCRs) form stable complexes with heterotrimeric G proteins when the former are activated and when the latter are not bound to guanine nucleotides. In addition to these active-state ternary (ligand-receptor-G protein) complexes some GPCRs have been suggested to form preassembled or precoupled complexes with G proteins prior to activation. We have previously reported that immobile M3 muscarinic receptors (M3Rs) decrease the mobility of heterotrimers that contain Gαq, consistent with an M3R-Gq complex. This interaction is unaffected by receptor ligands in intact cells, and is specific for M3Rs and Gq, as immobile M4Rs do not decrease the mobility of Gq heterotrimers, and immobile M3Rs do not decrease the mobility of GoA heterotrimers. In order to determine the structural basis of this interaction, we constructed a series of CFP-labeled M3R/M4R chimeras and tested their ability to decrease the mobility of venus-labeled Gq (Gq-V) using fluorescence recovery after photobleaching (FRAP). A chimera consisting of the M3R with the c-terminus of the M4R (M3M4ct) did not decrease Gq-V mobility. A polybasic region