

## Article

# Explicit Spatiotemporal Simulation of Receptor-G Protein Coupling in Rod Cell Disk Membranes

Johannes Schöneberg,<sup>1</sup> Martin Heck,<sup>2,\*</sup> Klaus Peter Hofmann,<sup>2</sup> and Frank Noé<sup>1,\*</sup>

<sup>1</sup>Department of Mathematics, Computer Science and Bioinformatics, Freie Universität Berlin, Berlin, Germany; and <sup>2</sup>Institut für Medizinische Physik und Biophysik, Charité, Universitätsmedizin Berlin, Berlin, Germany

**ABSTRACT** Dim-light vision is mediated by retinal rod cells. Rhodopsin (R), a G-protein-coupled receptor, switches to its active form (R<sup>\*</sup>) in response to absorbing a single photon and activates multiple copies of the G-protein transducin (G) that trigger further downstream reactions of the phototransduction cascade. The classical assumption is that R and G are uniformly distributed and freely diffusing on disk membranes. Recent experimental findings have challenged this view by showing specific R architectures, including RG precomplexes, nonuniform R density, specific R arrangements, and immobile fractions of R. Here, we derive a physical model that describes the first steps of the photoactivation cascade in spatiotemporal detail and single-molecule resolution. The model was implemented in the ReaDDy software for particle-based reaction-diffusion simulations. Detailed kinetic *in vitro* experiments are used to parametrize the reaction rates and diffusion constants of R and G. Particle diffusion and G activation are then studied under different conditions of R-R interaction. It is found that the classical free-diffusion model is consistent with the available kinetic data. The existence of precomplexes between inactive R and G is only consistent with the data if these precomplexes are weak, with much larger dissociation rates than suggested elsewhere. Microarchitectures of R, such as dimer racks, would effectively immobilize R but have little impact on the diffusivity of G and on the overall amplification of the cascade at the level of the G protein.

## INTRODUCTION

In retinal rod cells, absorption of a photon by the visual G-protein-coupled receptor rhodopsin (R) initiates a cascade of biochemical reactions that eventually generates an electrical signal. A first stage of signal transduction and amplification is provided by the receptor-catalyzed nucleotide exchange in the rod G protein, transducin (G). R and G are located in disk membranes that fill the rod outer segment. Although R and G display fundamental similarities to other receptors and heterotrimeric G<sub>αβγ</sub> proteins (1), the single-quantum detective function of the rod cell requires that both proteins have specific properties, including a very low basal activity to ensure low noise and a rapid and efficient sequential activation of multiple copies of the G protein by single activated molecules of the receptor. In the dark, the catalytic activity of rhodopsin is efficiently blocked by the covalently bound inverse agonist 11-*cis*-retinal. Light-induced *cis/trans* retinal isomerization triggers conformational changes in the receptor protein that culminate in an equilibrium between inactive Meta I (M1) and active Meta II (R<sup>\*</sup>) intermediates (2,3). The G holoprotein is peripherally bound to the disk membrane by weak hydrophobic and ionic interactions. After the exchange of GDP for GTP in the R<sup>\*</sup>-G<sub>αβγ</sub> complex, the G protein dissociates and active G<sub>α</sub>-GTP (G<sup>\*</sup>) binds to a cGMP phosphodi-

esterase in a noncatalytic, stoichiometric interaction. The active G<sup>\*</sup>-phosphodiesterase complex rapidly hydrolyzes cGMP, leading to the closure of cGMP-dependent ion channels in the plasma membrane of the rod outer segment. Ca<sup>2+</sup>-dependent feedback leads to a delayed recovery of the dark concentration of cGMP. At the receptor level, deactivating proteins, namely, a receptor kinase and arrestin, bind to R<sup>\*</sup> to mediate its phosphorylation and to cap it against further interaction with G. Deactivation by arrestin takes 0.2–0.3 s, thereby enabling sufficient G-protein activation. The whole system forms a closed signal-transduction module that transforms the input-signal photon into a transient receptor current that provides the electrical signal for the synapse of the rod (4).

Mathematical descriptions of the photocurrent response of retinal rod cells by a system of ordinary differential equations (ODEs) date back to the early seventies (5). Once the visual cascade was understood as a G-protein-coupled system, known partial steps were increasingly incorporated into schemes of differential equations describing signal transduction (6), eventually including downstream reactions (7,8) and leading to a full simulation of the electrical response.

In the dim-light working range of the rod, each disk membrane receives only one or a few photon hits, triggering the whole cascade. To study these single-photon responses, the stochastic spatiotemporal nature of the system had to be incorporated into the simulations. The

Submitted February 24, 2014, and accepted for publication May 19, 2014.

\*Correspondence: frank.noé@fu-berlin.de or martin.heck@charite.de

Editor: Reinhard Lipowsky.

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0006-3495/14/09/1042/12 \$2.00

<http://dx.doi.org/10.1016/j.bpj.2014.05.050>



well-mixed assumption of ODE methods (i.e., ODEs have no concept of location, such as the position of the single activated rhodopsin) rendered these approaches not useful for our application. As a result, grid-based spatiotemporal chemical master equations (ST-CMEs) were used (9,10), allowing for discrete particle numbers rather than concentrations and a higher spatial resolution of the disk membrane. However, this method relies on the well-mixed assumption being true for small subspaces (i.e., lattice boxes), in which the system is discretized. In a different approach, partial differential equations (PDEs) were used on the photoactivation cascade to achieve the same goal of a higher spatial resolution (11–13). The PDE approach is also useful for deriving general theoretical results, such as first passage times in specific geometries (14–17). However, PDEs use concentrations of molecules and are therefore impractical when small particle numbers are important.

Recent experimental findings oppose the scenario of a well-mixed, free-diffusion, uniformly distributed disk membrane by reporting large rhodopsin clusters (18), immobile fractions of R (19), and special paracrystalline rhodopsin structures called racks of dimers (20).

The specific inhomogeneous architecture of these structures on all levels of detail together with the importance of individual molecules (a single  $R^*$  triggers the cascade) goes beyond the limits of ST-CME and PDE methods. Individual molecules, arranged in their specific architectures, have been used in a Monte Carlo simulation to characterize the influence of such structures on the diffusion properties on the disk membrane (21). That study revealed a high impact of these structures on the diffusion but did not investigate their impact on reactions.

Such methods, which also treat reactions, are usually referred to as particle-based reaction-diffusion simulations (PBRD). Here, every molecule is represented individually in continuous space and time and its diffusion and reaction dynamics is simulated on a microscopic level. Individual molecules can be modeled as freely diffusing, as immobile obstacles, or in some trap potential. At the same time, reactions between particles can occur only upon physical encounter of reactive particles. In this way, complex interactions between particle mobility and reaction rates, such as inhibition of reactions due to spatial occlusion, can be investigated.

Covering all scenarios of rhodopsin architecture on a disk membrane requires single-particle resolution, particle diffusion, a simulation geometry, particle-particle interaction potentials, and reactions between particles. Other available tools (22–35) covered some but not all of these requirements. For this reason, the new PBRD package ReaDDy was developed (36). Using ReaDDy, we are able to test the effect of different supramolecular arrangements of R on molecule diffusivity and outcome of signal transduction at the same time.

We chose three representative cases to compare, namely, 1), the classic case, in which all particle species diffuse freely and are uniformly distributed; 2), the precomplex case, which is the same as case 1 but with an additional precomplex interaction between the inactive receptor and G (37); and 3), the rack case, where G diffuses freely and is uniformly distributed, but a large fraction of R is arranged in racks of dimers (20) and thereby rendered immobile (19).

For our model, a to our knowledge new set of kinetic rates of the G activation step was derived based on near-infrared light-scattering experiments using native disk membranes, as in a previous study (38). These rates give new insight into G-protein activation kinetics, revealing that the conformational changes leading from a receptor-G-protein encounter complex to an active complex and the GDP release are most probably the rate-limiting steps.

In using this set of kinetic rates in the particle-based simulation and combining it with the experimentally known kinetics of G-protein activation (38), we can assess the consistency of different R-architectures with experimental kinetics and give parameter ranges in which this consistency is provided.

The salient result of our study is that the supramolecular architecture has a surprisingly modest impact on the overall amplification of the cascade at the level of the G protein. It turns out that the diffusivity of the G-protein can override the influence of receptor architecture. An important exception is the case of precomplexes between R and G, which are only possible if they are formed very transiently. Considering the uniformity of the simulated signals, signal variability is moderate if there is only one fraction of receptor mobility present. Signal variability is increased by different fractions, i.e., mobile and immobile fractions of R, occurring at the same time (19).

Our derived model, at present containing the first steps of the photoactivation cascade including diffusion, crowding, molecular architecture, and detailed kinetics, can now serve as a building block for larger-scale physical simulations, e.g., of the entire signal cascade in a rod cell.

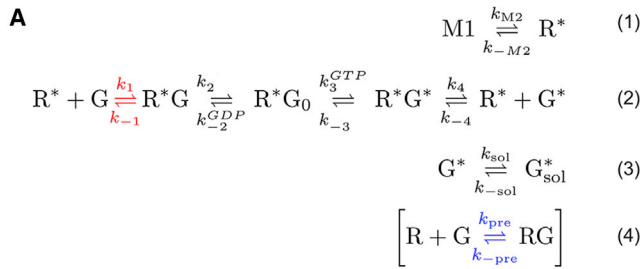
## MATERIALS AND METHODS

### Kinetic parameter derivation and ODE modeling

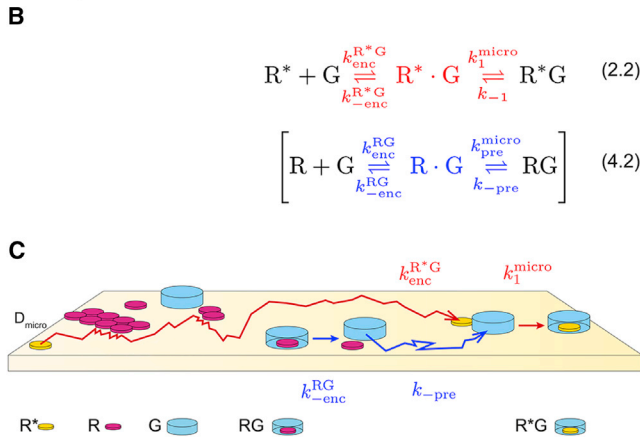
Based on the reaction scheme in Fig. 1 (Eqs. 1–4) and the scenario (with or without precomplexes), the kinetic reaction rates are estimated from enzymatic parameters obtained in a previous study (38). These experiments were conducted at 22°C with purified disk membranes. Rhodopsin concentrations were  $[R] = 25,000 \mu\text{M}^{-2}$  and  $[R^*] = 5.7 \mu\text{M}^{-2}$ . G-protein activation ligand concentration was set to yield maximal  $G^*$  production rates:  $[\text{GDP}]^0 = 0 \mu\text{M}^{-2}$  and  $[\text{GTP}]^0 = 3000 \mu\text{M}^{-2}$ .

Reaction rates were then determined by fitting the ODE model (Fig. 1 A) to experimental traces of  $G_{\text{tot}}^*$  production over time (Fig. 2 A). To verify the results, another series of dissociation signals measured in the presence of 200  $\mu\text{M}$  GTP (0  $\mu\text{M}$  GDP, data taken from (38)) were simulated with both sets of rate constants. As seen in Fig. 2 B, the resulting traces are in

## ODE Model



## ReaDDy Model

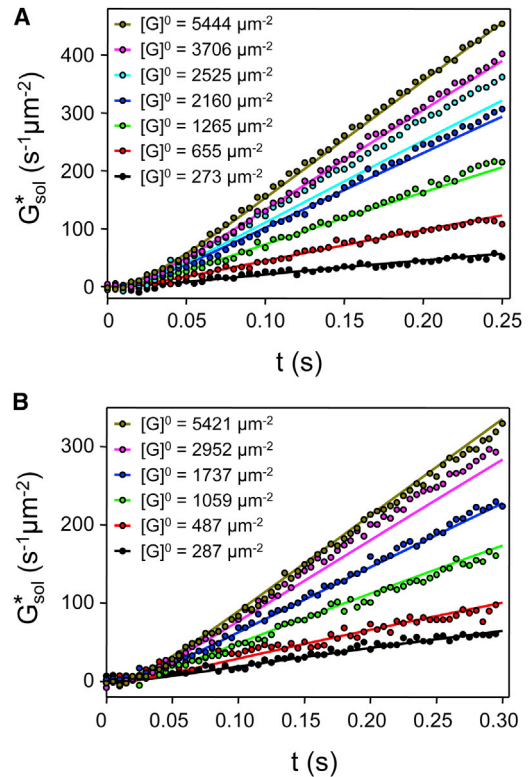


**FIGURE 1** Reaction kinetics at two levels of modeling detail. (A) The first steps of the photoactivation cascade consist of the following activation reactions: M1/R<sup>\*</sup> equilibrium (1); G-activation reactions, comprising formation of R<sup>\*</sup>G complex, subsequent nucleotide exchange in G, and R<sup>\*</sup>G<sup>\*</sup>-complex dissociation (2); and dissociation of G<sup>\*</sup> from the membrane (3). A nonproductive RG-complex formation (4) is added for the precomplex case. These reactions are used for the ODE model of the cascade. (B) Using particle-based reaction-diffusion (ReaDDy), bimolecular association reactions have to be split into the explicitly simulated diffusional encounter and the first-order transition from encounter complex to stable complex. This affects the R<sup>\*</sup>G- and RG complex formation in (2.2) and (4.2) (red and blue). (C) Graphical representation of the microscopic diffusion and reaction components, illustrating space exclusions, molecular shape, and crowding. To see this figure in color, go online.

good agreement with the experimental data (see Table 1 for the derived reaction rates and the Supporting Material for the details of rate derivation).

## ReaDDy Model

The detailed spatiotemporal model was set up and simulated with the particle-based reaction-diffusion simulation software ReaDDy, version 1.1 (36). All molecules are modeled as spherical particles. These particles collide with each other if they get closer than the sum of their collision radii ( $r_c$ ). These radii come in two types,  $r_{c,mb}$ , for membrane internal collisions, and  $r_{c,sol}$ , for the collisions of soluble parts of the molecules. A collision results in particle-particle repulsion, governed by a harmonic potential. If particles collide, such that the distance between them is smaller than the sum of their reaction radii ( $r_r$ ), a reaction can be triggered. All radii are taken from crystal structures (39–42) (see Fig. 3 A). Due to the properties of the reference experiment (38), particle diffusion is confined to a spherical surface by applying a harmonic potential along the surface normal. The surface size (radius,  $r = 120$  nm, and surface area,  $A = 0.18 \mu m^2$ ) was chosen such that it would host on average 1 R<sup>\*</sup>, 4499 R, and 450 G (see Fig. 3 B). The Brownian dynamics are integrated with a time step of  $\Delta t = 20$  ns. Typi-



**FIGURE 2** ODE fit and modeling. (A) ODE fits (solid lines) to representative dissociation signals (circles; measuring conditions and rate constants as in Tables 1, S1, and S2). (B) ODE modeling (solid lines) of representative dissociation signals (200  $\mu M$  GTP, 0  $\mu M$  GDP; values taken from Heck and Hofmann (38)), with rate constants as in Table 1. Note that the two sets of rate constants (sets A and B in Table S4) yield essentially identical traces. To see this figure in color, go online.

cally, the total simulation time is 200 ms, corresponding to  $10^7$  time steps; on a standard CPU (Intel Xeon E5345@2.33 GHz), this would take  $\sim 400$  h. See the Supporting Material for a more detailed description of the ReaDDy model.

## Microscopic modeling of diffusion and crowding

The simulation resolves all major disc membrane proteins explicitly and therefore, the diffusion constants used are those for a protein diffusing in a pure lipid membrane,  $D_0$ . Collisions between particles lead to crowding effects: Depending on particle density, mobility, and size (43–46), either normal diffusion but with a decreased diffusion constant,  $D$ , or anomalous diffusion with a time-dependent diffusion constant,  $D(t)$ , is observed on long timescales (47,48). Published values for rhodopsin and G protein correspond to such observed diffusion constants (19,49–54).  $D_0$  is first parametrized in the free-diffusion case by sampling and theoretical calculations (see Fig. S3 in the Supporting Material). The effect of rhodopsin architecture is investigated by comparing  $D_0$  and  $D$ .

## Microscopic reaction modeling

In mass-action kinetics, bimolecular association rates,  $k_{on}^{macro}$ , incorporate both encounter complex formation due to diffusion (with rate  $k_{enc}$ ) and actual complex formation (with rate  $k^{micro}$ ). Since the diffusion is simulated explicitly in the ReaDDy simulation,  $k^{micro}$  has to be derived from  $k_{on}^{macro}$ . This is necessary for R<sup>\*</sup>G- and RG-complex formation reactions, resulting in Eqs. 2.2 and 4.2 in Fig. 1. (The other two bimolecular reactions involve the small, cytosolic molecules GDP and GTP that diffuse orders of



**TABLE 1** Experimental parameters and derived reaction rates

Parameter	Value	Description
$T^a$	22°C	Temperature of the experiment
$[R]^a$	25,000 $\mu\text{m}^{-2}$	Rhodopsin density on disk vesicles
$[R^*], [M1]^{a,c}$	5.7 $\mu\text{m}^{-2}$	Activated Rhodopsin density on disk vesicles
$[G]_1^{0,a,e}$	273 $\mu\text{m}^{-2}$	Initial G density in first experiment
$[G]_2^{0,a,e}$	1265 $\mu\text{m}^{-2}$	Initial G density in second experiment
$[G]_3^{0,a,e}$	2525 $\mu\text{m}^{-2}$	Initial G density in third experiment
$[G]_4^{0,a,e}$	5444 $\mu\text{m}^{-2}$	Initial G density in fourth experiment
$[GDP]^{0a}$	0 $\mu\text{m}^{-2}$	Initial GDP concentration in experiment
$[GTP]^{0a}$	3000 $\mu\text{m}^{-2}$	Initial GTP concentration in experiment
$k_{M2}^b$	35.4 $\text{s}^{-1}$	Rate of M1 to R* conversion of rhodopsin
$k_{-M2}^b$	14.4 $\text{s}^{-1}$	Rate of R*-to-M1 conversion of rhodopsin
$k_1^b$	0.36 $\mu\text{m}^2 \text{s}^{-1}$	Rate of R*G-complex formation
$k_1^{\text{micro}d}$	5000 $\text{s}^{-1}$	Microscopic rate of R*G-complex formation
$k_{-1}^b$	200 $\text{s}^{-1}$	Rate of R*G-complex dissociation
$k_2^b$	600 $\text{s}^{-1}$	Rate of GDP release from R*G complex
$k_{-2}^{\text{GDP}} = k_{-2}$	2.2 $\text{s}^{-1} \mu\text{M}^{-1}$	Rate of GDP uptake by R*G complex
$[GDP]^b$	[GDP]	
$k_3^{\text{GTP}} = k_3$	2.6 $\text{s}^{-1} \mu\text{M}^{-1}$	Rate of GTP uptake by R*G complex
$[GTP]^b$	[GTP]	
$k_{-3}^b$	600 $\text{s}^{-1}$	Rate of GTP release by R*G* complex
$k_4^b$	60,000 $\text{s}^{-1}$	Rate of R*G* complex dissociation
$k_{-4}^b$	0 $\text{s}^{-1}$	Rate of R*G* complex formation
$k_{\text{sol}}^b$	10,000 $\text{s}^{-1}$	Rate of G* membrane dissociation
$k_{-\text{sol}}^b$	0 $\text{s}^{-1}$	Rate of G* membrane binding
$k_{\text{pre}}^b$	1.67 $\mu\text{m}^2 \text{s}^{-1}$	Rate of RG-complex formation
$k_{\text{pre}}^{\text{micro}d}$	10 <sup>8</sup> $\text{s}^{-1}$	Microscopic rate of R*G-complex formation
$k_{-\text{pre}}^b$	11,200 $\text{s}^{-1}$	Rate of RG-complex formation

<sup>a</sup>Experimental conditions in (38).

<sup>b</sup>Rates were obtained via an ODE fitting procedure of experimental data (see methods and SI for details).

<sup>c</sup>ODE simulations start with  $[M1] = 5.7 \mu\text{m}^{-2}$ , ReaDDy simulations start with  $[R^*] = 5.7 \mu\text{m}^{-2}$ .

<sup>d</sup>Rate required for ReaDDy simulations only. Rate applies for the complexation reaction, once the particles are closer than their reaction radii.

<sup>e</sup>Concentrations used for both ReaDDy and ODE simulations. The ODE fit contained three additional experiments (see Table S2).

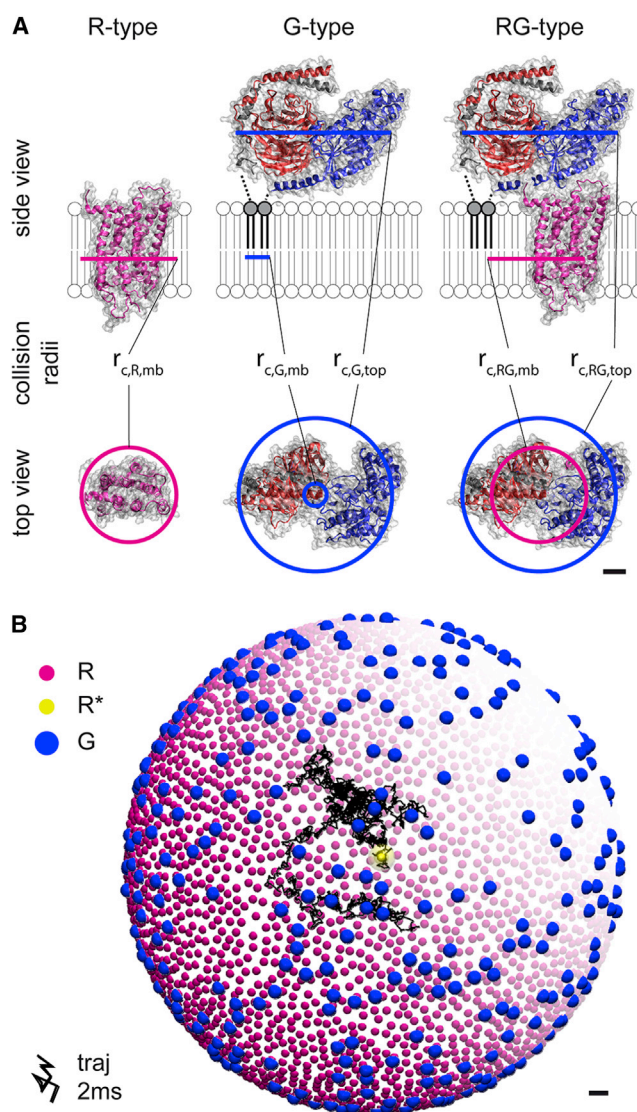
magnitude faster than do membrane-bound proteins and are therefore considered unimolecular on our timescales). See the [Supporting Material](#) for derivation of the microscopic reaction rates and [Table 2](#) for the resulting parameters.

## RESULTS AND DISCUSSION

### Free-diffusion model

We first derive a model assuming that both R and G are uniformly distributed and freely diffusing. This is the simplest assumption for the experimental preparation described in Heck and Hofmann (38), which used R and G on purified membranes.

First, the diffusion constants of R and G are parametrized. As shown in the work of Saxton (43), no percolation threshold exists if obstacles and tracers (both being rhodopsin in this case) diffuse at the same rate. In such cases, the mean-squared displacement of particles,  $\langle r^2 \rangle$ , will start as  $\langle r^2 \rangle \propto D_0$ , will show anomalous diffusion for a short period of time, and will finally display normal diffu-



**FIGURE 3** ReaDDy model. (A) Collision radii of R-type, G-type, and RG-type particles were chosen based on crystal structures (R and R\*, bovine 1U19 and 3PQR (40); G, bovine 1GOT (41); RG, 3SN6 (42)). Due to the different molecular shapes within and on the surface of the membrane, there are two types of collision radii:  $r_{c,mb}$  for collisions within the membrane and  $r_{c,sol}$  for collisions on the membrane surface (see [Table 2](#) for radius parameters). (B) Disk-vesicle geometry with 4499 R (purple), 450 G (blue), and 1 R\* (yellow) on a 0.18  $\mu\text{m}^2$  surface. The diffusion trajectory (black line; and see inset) of R\* is drawn for 2 ms. To see this figure in color, go online.

sion with  $\langle r^2 \rangle \propto D$  (43,44,48,56–59) (see Klafter and Sokolov (60) for an introduction to anomalous diffusion). In our case, we operate at an occupied area fraction of  $c = 0.35$ , given a rhodopsin density of 25,000  $\mu\text{m}^{-2}$ . For this scenario, a crowding factor  $D_{free}^* = D/D_0 = 0.5$  was calculated (43,61). Our model reproduces these calculations, resulting in the diffusion parameters presented in [Table 2](#).

Reactions in the model include the Meta1-R\* equilibrium of light-activated receptor (Eq. 1), G activation reactions

**TABLE 2** Parameters of the ReaDDy model.

Parameter	Value	Description
$r_{\text{vesicle}}$	120 nm	Radius of the simulated vesicle
$A_{\text{vesicle}}$	$0.18 \mu\text{m}^2$	Surface area of the simulated vesicle
$n_{\text{R}}^{\text{a,b}}$	4499	Number of rhodopsin particles on a vesicle
$n_{\text{R}}^{\text{a,b}}$	1	Number of activated rhodopsins on a vesicle
$n_{\text{G},1}^{\text{a}}$	49	Initial number of Gs for first experiment simulation
$n_{\text{G},2}^{\text{a}}$	228	Initial number of Gs for second experiment simulation
$n_{\text{G},3}^{\text{a,b}}$	454	Initial number of Gs for third experiment simulation
$n_{\text{G},4}^{\text{a}}$	980	Initial number of Gs for fourth experiment simulation
$r_{\text{c,R,mb}}^{\text{c}}$	2.1 nm	Collision radius of R-type particles within the membrane
$r_{\text{r,R}}^{\text{c}}$	2.1 nm	Reaction radius of R-type particles
$r_{\text{c,G,mb}}^{\text{d}}$	0.6 nm	Collision radius of G-type particles within the membrane
$r_{\text{c,G,sol}}^{\text{d}}$	3.4 nm	Collision radius of G-type particles on top of the membrane
$r_{\text{r,G}}^{\text{d}}$	3.0 nm	Reaction radius of G-type particles
$r_{\text{c,RG,mb}}$	2.1 nm	Collision radius of RG-type particles within the membrane
$r_{\text{c,RG,sol}}$	3.4 nm	Collision radius of RG-type particles on top of the membrane
$k_{\text{pot}}^{\text{c}}$	$10 \text{ kJ/mol/nm}^2$	Force constant of the repulsive particle-particle potential, Eq S8.
$\Delta t$	20 ns	Integration timestep
$D_0^{\text{Rf}}$	$1.4 \mu\text{m}^2/\text{s}$	Diffusion constant of R in free lipid.
$D_0^{\text{Gf}}$	$2.0 \mu\text{m}^2/\text{s}$	Diffusion constant of G in free lipid.
$D_{\text{free}}^{\text{f}}$	0.5	Crowding factor in free diffusion at density [R].
$D_{\text{free}}^{\text{Rf}}$	$0.7 \mu\text{m}^2/\text{s}$	Apparent diffusion constant of R in the free scenario.
$D_{\text{free}}^{\text{Gf}}$	$1.2 \mu\text{m}^2/\text{s}$	Apparent diffusion constant of G in the free scenario
$D_{\text{racks}}^{\text{Rf}}$	0.26	Crowding factor in racks model at density [R].
$D_{\text{racks}}^{\text{Rf}}$	$0.4 \mu\text{m}^2/\text{s}$	Apparent diffusion constant of R in the racks scenario.
$D_{\text{racks}}^{\text{Gf}}$	$0.8 \mu\text{m}^2/\text{s}$	Apparent diffusion constant of G in the racks scenario

<sup>a</sup>Experimental conditions (38).<sup>b</sup>Conditions referred to as native.<sup>c</sup>Based on crystal structure 2I36 (55), see SI for detailed derivation.<sup>d</sup>Based on crystal structure 1GOT, see SI for detailed derivation.<sup>e</sup>See Supporting Information and Ref (36), for potential parametrization.<sup>f</sup>Diffusion constants are based on values in (49), calculations in this work and (43,45), see SI for details.

(Eq. 2) and  $G^*$  membrane dissociation (Eq. 3). In this model, no precomplex reaction is included (Eq. 4). To get a comprehensive set of reaction rates, a set of experimental  $G^*$  traces of different G concentrations (Table S2) was fitted simultaneously to an ODE model of the reaction scheme (Fig. 2). Two sets of reaction rates were obtained, and both fit the data (Table S4). The two sets are similar as to the rates of the initial  $R^*G$  complex formation and dissociation ( $k_1$ ,  $k_{-1}$ ) and the final  $G^*$  membrane dissociation ( $k_{\text{sol}}$ ). Once the  $R^*G$  complex is formed, the rate-limiting step in  $G^*$  production remains ambiguous. Placing the kinetic barrier on

GDP release or the final  $R^*G^*$ -complex dissociation, both fit the experiments equally well (compare rate sets A and B in Table S4). It is widely accepted that GDP release is generally rate-limiting in G-protein-coupled receptor systems for nucleotide exchange reactions (see review by Johnston and Siderovsky (62)). We therefore select rate set A and use it for all further investigations and microscopic simulations.

The association of G and  $R^*$  (by  $k_1$ ) is the only bimolecular reaction in our model that describes protein-protein interactions. Having parametrized all other reaction rates and model parameters, we can perform simulations with different values of  $k_1^{\text{micro}}$ , measure the resulting  $G_{\text{sol}}^*$  production, and choose the  $k_1^{\text{micro}}$  value that reproduces the experimental  $G_{\text{sol}}^*$  production rate (see the Supporting Material, especially Fig. S6, for the  $k_{\text{micro}}$  sampling setup). We observe that  $k_1^{\text{micro}} = 5000 \text{ s}^{-1}$  matches experimental observations of  $285 G_{\text{sol}}^*/R^*/\text{s}$  (for a setup of  $[G] = 2525 \mu\text{m}^{-2}$ ), leading to a reaction probability of  $10^{-4}$  upon collision, given our chosen time discretization (see Eq. S12). The sampling reveals that the reaction does not operate at its diffusion limit, which is reached for  $k_1^{\text{micro}} > 10^6 \text{ s}^{-1}$ . In the limit, a production of  $583 \pm 86 G_{\text{sol}}^*/R^*/\text{s}$  is reached (see Fig. S2). At this point, GDP release is likely to become rate-limiting.

The microscopic model is now fully parametrized (see Tables 1 and 2). Simulation results are validated by comparing the kinetics of activated G-protein production ( $G_{\text{sol}}^*$ ) with both the ODE model and experiments. We observe that within statistical error, the model is consistent with experimental data for all concentrations (Fig. 4 A). The initial delay of the signals, observed in experiments, can be fully attributed to the Meta1-Meta2 equilibrium. The variability of the individual simulation trajectories is quite low, considering that they are consecutive single-molecule events of one  $R^*$  activating multiple G. On the investigated timescale of 200 ms, the free-diffusion model does not exhibit significant spatial effects such as local G depletion around the location of  $R^*$ . There is sufficient time for the system to equilibrate locally during G activation while the single active  $R^*$  is in complex with G.

We find a mean time of  $3.11 \pm 2.09 \text{ ms}$  for the overall G activation at physiological  $[G] = 2525 \mu\text{m}^{-2}$  (Fig. 4 A). Note that this time does not include the Meta1-Meta2 equilibrium. Decomposing the mean cycle time into individual steps, we find that the first encounter between  $R^*$  and G occurs very rapidly ( $0.03 \pm 0.03 \text{ ms}$ ). The bottlenecks for G activation are the next two steps: the conformational change required to form the reactive  $R^*G$  complex ( $1.31 \pm 1.06 \text{ ms}$ ) and the subsequent GDP release ( $1.61 \pm 1.82 \text{ ms}$ ). We can identify the complex formation as a bottleneck with high confidence, since the uncertainty of  $k_1$  is small (see Estimation of reaction rates in the Supporting Material). These two steps combined account for 94% of the average activation time. In the presence of

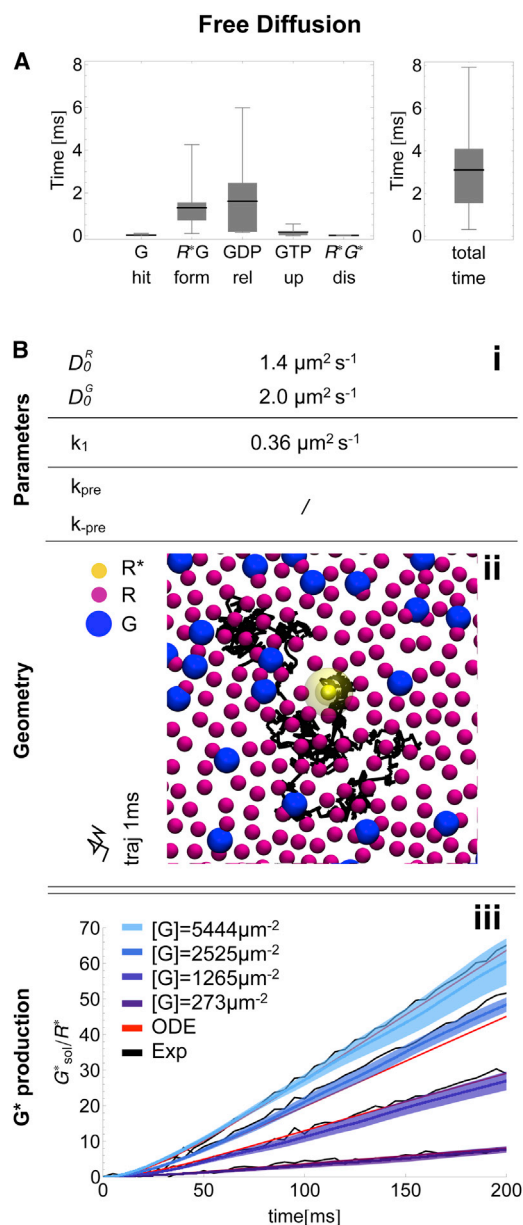


FIGURE 4 Microscopic ReaDDy simulation of the free-diffusion scenario. (A) Box-whisker plot of mean times required for individual reaction steps in the G activation:  $R^*$  hits the first free G (*G hit*), formation of the first  $R^*G$  complex ( *$R^*G$  form*), first GDP release (*GDP rel*), first GTP uptake (*GTP up*) and first  $G^*$  dissociation ( *$R^*G^*$  dis*). The cumulative time of all individual steps is depicted on the righthand side. Shown are data from 12 simulations that ran for 10 ms. (B) Microscopic model. (i) Model parameters. (ii) Snapshot of the simulated geometry, containing R (purple),  $R^*$  (yellow), and G (blue). Diffusion of  $R^*$  is depicted for 1 ms. Note that all particles are freely diffusing, similar to the trajectory of  $R^*$ . (iii)  $G^*$  activation over time. Compared are averages of 10 ReaDDy simulations (blue, standard error in light blue) with the ODE model (red) and the experimental data (black). To see this figure in color, go online.

millimolar GTP, the following GTP uptake and complex dissociation reactions occur on microsecond timescales ( $0.14 \pm 0.11$  ms and  $0.02 \pm 0.01$  ms).

Let us compare our results with the free-diffusion limit. To probe this limit, all forward reaction rates were set to infinity and all backward reaction rates to zero (i.e., a collision event between  $R^*$  and G immediately leads to  $R^*$  and  $G_{\text{sol}}^*$ ). Under such conditions, we observe the initial  $G_{\text{sol}}^*$  production of  $10,047 \pm 331 G_{\text{sol}}^*/R^*/\text{s}$  (see [Movie S1](#)). This value is close to previous estimates ( $9590 G_{\text{sol}}^*/R^*/\text{s}$  after 10 ms of the flash, calculated from Lamb and Pugh (63)). In comparison, the measured activation rate is  $\sim 300 G_{\text{sol}}^*/R^*/\text{s}$  (38). This emphasizes that in the free-diffusion setup, the output of the system is entirely determined by the series of chemical reactions or conformational transitions that take place during catalysis within the  $R^*G$  complex.

### Existence of RG precomplexes

We next considered that inactive R and G could form a nonproductive precomplex (see Eq. 4 in the reaction model (Fig. 1)). Evidence for the existence of such precomplexes has been reported in several studies (21,37,64–69), and it has been hypothesized that they are beneficial for G activation (37). Analogous to the formation of the reactive complex  $R^* + G \rightleftharpoons R^*G$  (Eqs. 2 and 2.2), formation of the inactive precomplex is a bimolecular reaction that needs to be separated into its contributions of diffusional encounter and microscopic reaction (Eq. 4.2).

In the presence of inactive precomplexes, both  $k_1^{\text{micro}}$  and  $k_{\text{pre}}^{\text{micro}}$  must be parametrized. Generation of an ensemble of ReaDDy simulations to parametrize the two rates independently is computationally prohibitive. Therefore, we restrict ourselves to a limit analysis by setting both parameters to their diffusion limit,  $k_1^{\text{micro}} = k_{\text{pre}}^{\text{micro}} = \infty$ . This limit is equivalent to setting the macroscopic association rates in the ODE model to their Smoluchowski rate:  $k_1 = k_{\text{pre}} = 1.67 \mu\text{m}^2/\text{s}$  (see the [Supporting Material](#) for derivation). In the ReaDDy model,  $k_1^{\text{micro}} = k_{\text{pre}}^{\text{micro}} = \infty$  translates to a rate of  $10^8 \text{s}^{-1}$  due to time discretization. Apart from including the precomplex reaction, the model setup is identical to the free-diffusion setup.

The only remaining undetermined parameter is the precomplex dissociation rate,  $k_{-\text{pre}}$ , which together with the association rate determines the precomplex binding constant. We first consider using  $k_{-\text{pre}} = 0.148/\text{s}$ , which was estimated from recent surface plasmon resonance measurements (37). Using this rate, the  $G^*$  production is virtually zero and the kinetic model is thus inconsistent with the kinetic experimental data shown in Fig. 4. This is clear from the fact that  $k_{-\text{pre}} = 0.148/\text{s}$  corresponds to precomplexes with a mean lifetime of 6.76 s—a factor of 3000 longer than the entire catalytic G activation found above. The situation is similar when the activated rhodopsin is precomplexed with G. Here, the first G gets activated faster, but owing to the fact that there is less G than R available, the system then becomes stuck while  $R^*$  is waiting for a second free G. The time to reach a target ( $R^*$ ) when multiple trap



sites are around (R, to form a precomplex) has been studied by Saxton (70), who showed that traps always increase the mean time to reach the target, indicating that precomplexes cannot increase the  $G^*$  production rate.

Precomplexes can only be consistent with measured kinetics if the precomplex is not too stable. ODE fitting reveals that the experimental  $G^*$  production could only be reproduced with precomplex dissociation rates of at least  $k_{\text{pre}} > 11,200/\text{s}$  (Fig. 5 A and Supporting Material). This setting leads to a ratio of 20% free G to 80% RG precomplexes. Note that  $k_{\text{pre}} = 11,200/\text{s}$  is a lower bound to the dissociation rate; when the association rates  $k_1$  and  $k_{\text{pre}}$  are smaller than their diffusion limits, the precomplex dissociation rate must be even larger to keep the overall  $G^*$  production consistent with measured kinetics.

### Existence of racks of rhodopsin dimers

Using the microscopic model, we test the molecular mobility and  $G^*$  production when R is arranged in rows of dimers. For the construction of a putative R arrangement, we combine experimental observations from Fotiadis et al. (20) (racks of rhodopsin dimers) and Govardovski et al. (19) (immobile rhodopsin fractions). Both observations are consistent, because supramolecular R structures would be expected to diffuse much more slowly than single free R molecules. In our model, 80% of the R molecules are immobilized and assigned to racks of different sizes (i.e., governed by a distribution derived from Fotiadis et al. (20) (see the Supporting Material), whereas individual rhodopsins and all G proteins are freely diffusing. Note, that diffusion of G through the racks is not possible in our simulation setup.

In this geometry, a photon could activate an immobilized R that is part of a rack or an R that is freely diffusing. Position and mobility of the single  $R^*$  in the simulation is consequently modeled for these two cases (see Fig. 6 A and Fig. S8 C).

The effects of immobile clustered obstacles on diffusion have been investigated in several theoretical studies (44,57,58,71). It was shown by Saxton (43) that a percolation threshold,  $c_p$ , exists when the occupied area fraction of obstacles,  $c$ , exceeds 0.332. If  $c > c_p$ , the obstacles separate the diffusion-accessible space into smaller subspaces. In such a scenario, the observed diffusion coefficient,  $D$ , is distance-dependent and anomalous. In our model, the immobile obstacles occupy an area fraction of  $c_{\text{im}} = 0.277$  and the diffusion-accessible space is fully connected. The behavior of  $\langle r^2 \rangle$  for this mixture of mobile and immobile obstacles was found to be similar to that in the free-diffusion case described above, leading to a crowding factor of  $D_{\text{racks}}^* = 0.26$  (45). We reproduce these findings in our model and obtain  $D_{\text{racks}}^R = 0.42 \mu\text{m}^2 \text{s}^{-1}$  and  $D_{\text{racks}}^G = 0.77 \mu\text{m}^2 \text{s}^{-1}$ . Note that a higher R density (e.g., the local density of  $50,000 \mu\text{m}^{-2}$  reported in Fotiadis et al. (20)) would result

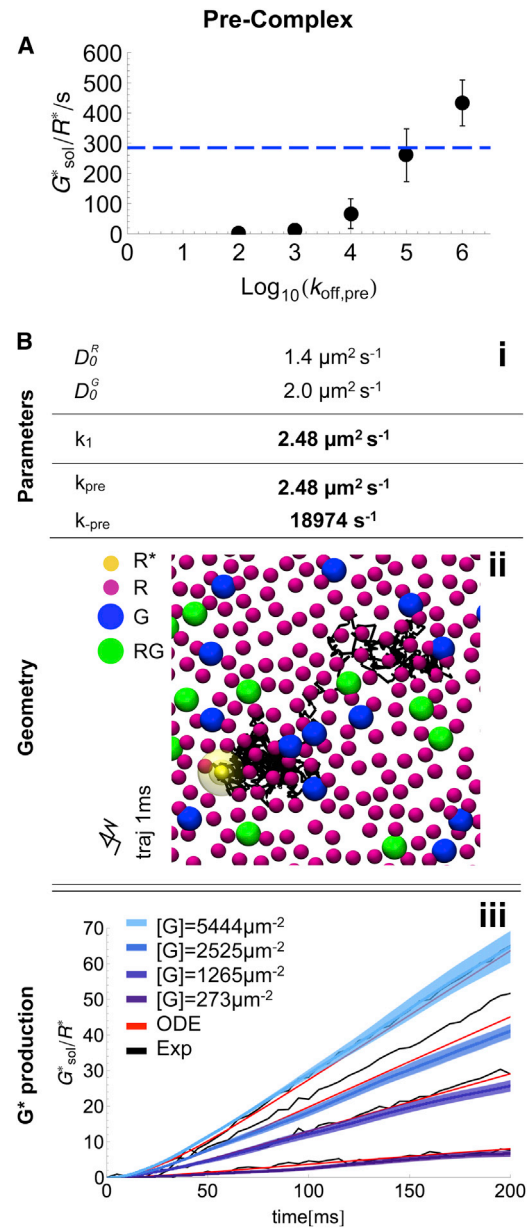
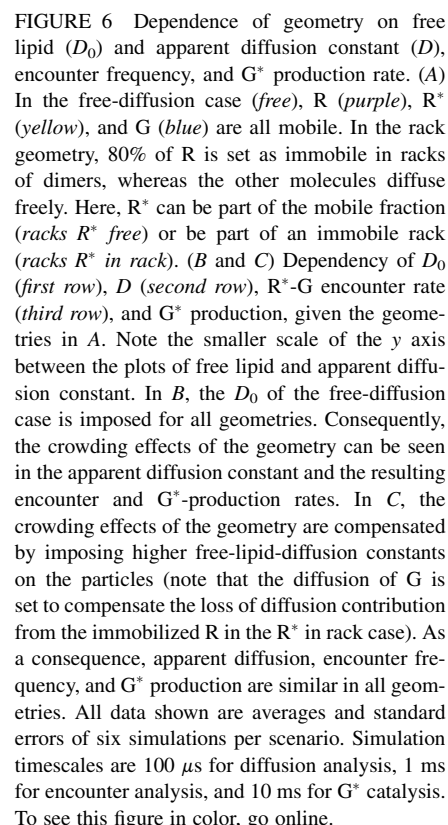


FIGURE 5 Microscopic ReaDDy simulation of the pre-complex scenario. (A) Dependence of the  $G^*$  production rate on the pre-complex off rate, given that the on rate is in the diffusion limit (simulations ran for 10 ms, depicted are mean and standard error). The dashed blue line indicates the experimentally found  $G^*$  production rate. (B) Microscopic model: (i) model parameters, (bold) parameters different to the free diffusion scenario. (ii) Snapshot of the simulated geometry, containing R (purple),  $R^*$  (yellow), G (blue) and RG-precomplex (green) particles. The diffusion of  $R^*$  is depicted for 1ms. Note that all particles are freely diffusing similar to the trajectory of  $R^*$ . (iii) G activation over time. Averages of 10 ReaDDy simulations (blue, with standard error (light blue)) are compared with the ODE model (red) and the experimental data (black). To see this figure in color, go online.

in the system crossing the percolation threshold and likely showing anomalous diffusion.

It has been shown that obstacles can increase educt encounter rates (71). In our case, the  $R^*G$  encounter rate



The effects are different when  $R^*$  is part of an immobile rack (Fig. 6 B, third column). Now,  $R^*$  is only accessible from one side and the  $R^*G$  encounter rate is solely due to the mobility of  $G$ , leading consequently to an approximately fivefold decrease in encounters compared to the number observed in free diffusion. This results in an approximately threefold decrease in  $G^*$  production. In effect, the racks geometry led to a slight increase in  $G^*$  catalysis when  $R^*$

In summary, racks of rhodopsin dimers are also consistent with available kinetic data when the free lipid diffusion



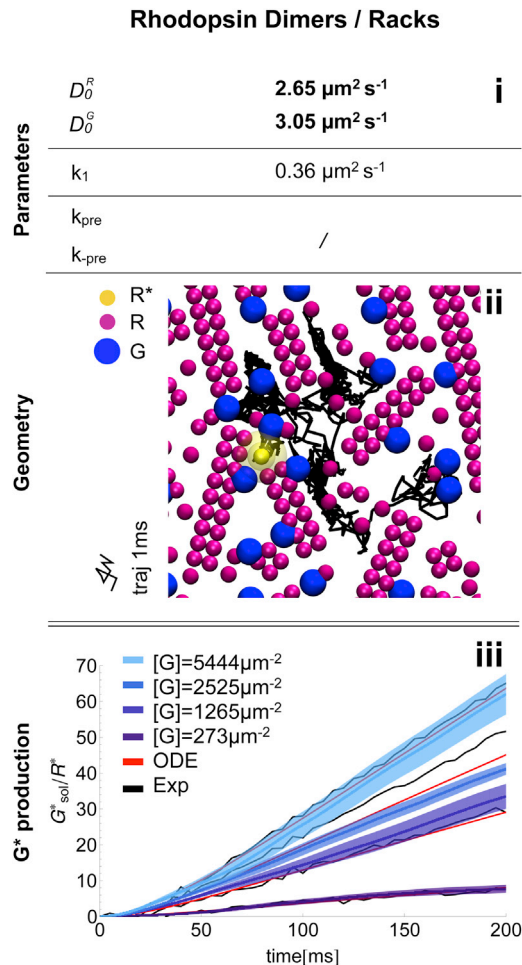


FIGURE 7 Microscopic ReaDDy simulation of the racks of rhodopsin dimers scenario. (i) Model parameters, highlighting (**bold**) parameters different from the free-diffusion scenario. (ii) Snapshot of the simulated geometry, containing R (purple), R\* (yellow), and G (blue). Note that only G, monomeric R, and R\* particles are freely diffusing. R oligomers are considered immobile. (iii) G activation over time. Averages of 10 ReaDDy simulations (blue, with standard error in light blue) are compared with the ODE model (red) and the experimental data (black). To see this figure in color, go online.

constants are chosen to be slightly higher than the respective values predicted by theory. The confinement conditions of racks slightly increases  $G^*$  production on short timescales if the activated receptor is mobile. If R\* is part of a rack (i.e., it is immobile), the rack geometry decreases  $G^*$  catalysis substantially, a reduction that can only be compensated by high G-diffusion constants. Although both cases, i.e., R\* mobile and R\* immobile, could be made consistent with kinetic data individually, the occurrence of both scenarios on the same disk membrane would pose a challenge. Given these results, fractions of mobile and immobile rhodopsin on the same disk simultaneously would lead to a higher variance of the  $G^*$  output rate, compared to the case of a homogeneous geometry.

## CONCLUSION

We have presented a particle-based reaction-diffusion model for light-induced, rhodopsin-mediated activation of G-proteins. Although we have chosen rod cell phototransduction as an example, for which there is a large body of experimental data, the results should be applicable to G-protein activation in general. The kinetic parameters of the model were parametrized to fit observed effective diffusion constants (see Pugh and Lamb (49)) and the extensive G-activation kinetics measurements of Heck and Hofmann (38) via an ODE model. The model was implemented in and simulated with the particle-based reaction-diffusion software ReaDDy (36). The free-diffusion parametrization could quantitatively reproduce  $G^*$  production during the first 200 ms after photoactivation of R\* for a set of different initial G concentrations. The main observations for this model are as follows. 1), Diffusional G-R\* encounter is fast, consistent with previous predictions that the typical  $G^*$  production rates (on the order of several hundred per second) are well below the diffusion limit (which would be on the order of 10,000/s). 2), Due to the high protein density in the disk membrane, the mobility of R and G is reduced compared to diffusion in a pure lipid membrane (to 0.5  $D_0$ ). 3), The conformational change required to form an active R\*G complex after R\* and G encounter is a bottleneck, requiring a lower millisecond timescale. 4), It is likely that GDP release from the R\*G complex is the second bottleneck of the overall catalysis. Findings 3 and 4 define interesting targets for future investigations: With the advent of high-throughput computing technologies, such as special-purpose hardware (72), massive distribution computing (73–75), and Markov state models (76–79), molecular dynamics simulations are now able to describe processes on the millisecond timescale in full atomistic detail. Investigation of the detailed mechanisms of the  $R^* + G \rightleftharpoons R^*G$  conformational change and the GDP release in  $R^*G \rightarrow R^*G + \text{GDP}$  would shed light on two steps that are important for the kinetics of phototransduction.

We have considered the existence of a nonproductive RG precomplex formation:  $R + G \rightleftharpoons RG$ . The existence of such precomplexes has been suggested by others (21,37,64–69). Here, we found that the existence of precomplexes is consistent with our kinetic data if they are sufficiently transient. In particular, the precomplex dissociation rate needs to be on the order of  $10,000 \text{ s}^{-1}$  or larger. This bound arises from the fact that longer-lived precomplexes would arrest the system in an inactive state dominated by the waiting time of R\* for G proteins stuck at inactive rhodopsins and would consequently reduce  $G^*$  production to values incompatible with the present kinetic experimental data, a case referred to as inhibition by substrate depletion in enzyme kinetics. The existence of transient RG precomplexes must be compensated by increasing the rates in the rate-limiting steps described above. In particular, the conformational change

$R^* + G \rightarrow R^*G$  could proceed somewhat faster, e.g., on the 100  $\mu$ s timescale.

Please note that under no circumstances can the existence of precomplexes increase the production rate of  $G^*$ , independent of whether the activated  $R^*$  is initially precomplexed with a G or not (see Saxton (70) for a theoretical study on the effect of traps on the way to a target). If precomplexes exist, they may be due to side effects (since  $R^*G$  has interactions that form a stable complex, it is reasonable that some of these interactions are also present in RG, forming transient complexes), but precomplexes may also play a role in the regulation of signal transduction, e.g., by limiting the  $G^*$  output.

We have also considered the situation that rhodopsin forms rows of dimers (racks), as observed by Fotiadis et al. (20). One rhodopsin fraction (20%) consists of individual freely diffusing particles, and the other fraction (80%) is fixed in racks of dimers. In this model, each row of dimers is densely packed such that G cannot diffuse through it. This setup reduces the diffusional mobility of R and G by a factor of 2 more strongly than in the free-diffusion case (to  $0.26D_0$ ), a behavior that has already been suggested in theoretical studies (61). If the single  $R^*$  is considered to be not part of a rack, the encounter rate between  $R^*$  and G is increased due to confinement compared to the free-diffusion case (also compare to Soula et al. (71)). This increase is compensated by the decreased long-range diffusion through racks. If  $R^*$  is considered to be part of a rack, the lower accessibility of  $R^*$ , its immobility, and the decrease in long-range diffusion together drastically decrease the  $R^*$ -G encounter frequency, as well as  $G^*$  formation. Note that our tested scenarios have an R density of 25,000  $\mu\text{m}^{-2}$  and are therefore below the percolation threshold (i.e., the free diffusion space is fully connected). Higher R densities would likely partition the disc membrane and lead to anomalous diffusion (56,59). In summary, as has been shown in experiments (80), the diffusion conditions and the microscopic environment on the disk membrane have a strong effect on the  $R^*$ -G encounter frequency and therefore on the output of the cascade.

We find that all these effects can be compensated for if the free lipid diffusion constants ( $D_0$ ) are adapted to the geometry so as to reproduce published (49) apparent diffusion constants. Compensation is possible even if  $R^*$  is immobilized completely. In this case, G-protein diffusion can make up for the encounter events alone if it is given a high free lipid diffusion constant ( $2.3D_0^G$ ). Such values might be possible (81), especially given that the slow membrane diffusion is likely only affecting the relatively small anchor of G-proteins.

Compensation is only possible for uniform conditions on the disk membrane. In a setup in which both scenarios coexist, i.e., fractions of free and immobile R on the disk membrane, it is difficult to compensate for the effects of both conditions at the same time. Such a situation could

be experimentally detected by different  $G^*$  formation rates for different individual photon events, depending on whether  $R^*$  is freely diffusing or immobile.

## SUPPORTING MATERIAL

Five tables, eight figures, one movie and Supporting Methods are available at [http://www.biophysj.org/biophysj/supplemental/S0006-3495\(14\)00690-0](http://www.biophysj.org/biophysj/supplemental/S0006-3495(14)00690-0).

This work was funded by Deutsche Forschungsgemeinschaft through SFB 740 to F.N., M.H., and K.P.H., a European Research Council starting grant (pcCell) to F.N., and a European Research Council advanced grant (TUDOR) to K.P.H.

## SUPPORTING CITATIONS

References (82–89) appear in the Supporting Material.

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