Sodium Ion Binding Pocket Mutations and Adenosine A2A Receptor Function

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ABSTRACT

Recently we identified a sodium ion binding pocket in a high-resolution structure of the human adenosine A2A receptor. In the present study we explored this binding site through site-directed mutagenesis and molecular dynamics simulations. Amino acids in the pocket were mutated to alanine, and their influence on agonist binding was explored. Mutations of the polar residues in the Na+ pocket were shown to either abrogate (D52A2.50 and N284A7.49) or reduce (S91A3.39, W246A6.48, and N280A7.45) the negative allosteric effect of sodium ions on agonist binding. Mutations D52A2.50 and N284A7.49 completely abolished receptor signaling, whereas mutations S91A3.39, W246A6.48, and N280A7.45 elevated basal activity and mutations S91A3.39, W246A6.48, and N280A7.45 decreased agonist-stimulated receptor signaling. In molecular dynamics simulations D52A2.50 directly affected the mobility of sodium ions, which readily migrated to another pocket formed by Glu131.39 and His2787.43. The D52A2.50 mutation also decreased the potency of amiloride with respect to ligand displacement but did not change orthosteric ligand affinity. In contrast, W246A6.48 increased some of the allosteric effects of sodium ions and amiloride, whereas orthosteric ligand binding was decreased. These new findings suggest that the sodium ion in the allosteric binding pocket not only impacts ligand affinity but also plays a vital role in receptor signaling. Because the sodium ion binding pocket is highly conserved in other class A G protein-coupled receptors, our findings may have a general relevance for these receptors and may guide the design of novel synthetic allosteric modulators or bitopic ligands.

INTRODUCTION

G protein-coupled receptors (GPCRs) are seven transmembrane helical proteins, which regulate a multitude of physiologic processes and therefore are targeted by 30–40% of the drugs currently on the market (Rask-Andersen et al., 2011). GPCR crystal structures are becoming increasingly available, which considerably contributes to our understanding of both drug-receptor interactions and receptor activation mechanisms (Katritch et al., 2013). Still, much remains to be discovered, and therefore the new crystal structure repertoire of GPCRs is continuously analyzed by biochemical, computational, and pharmacological studies.

One of the most widely explored GPCRs is the human adenosine A2A receptor (hA2AAR), a drug target related to Parkinson’s disease, cardiovascular diseases, and inflammatory disorders (Chen et al., 2013). Recently, a high-resolution crystal structure of the inactive hA2AAR in complex with antagonist 4-(2-[7-amino-2-(2-furyl)-1,2,4-triazolo[1,5-a][1,3,5]triazin-5-yl-amino]ethyl)phenol (ZM241385) (Liu et al., 2012) identified the precise location of a sodium ion in the region around the conserved Asp522.50, as previously hypothesized for other GPCRs (Parker et al., 2008; Selent et al., 2010) [numbering in superscript according to Ballesteros and Weinstein (1995)]. Residues Ser913.39, Trp2466.48, Asn2807.45, and Asn2847.49, together with a network of structural water molecules, completed the coordination of the ion in the hA2AAR. The fact that this site changes dramatically its conformation between inactive and active-like structures of the hA2AAR (Xu et al., 2011; Liu et al., 2012) inspired us to further explore the nature of this allosteric binding site.

In a recent report we used a combination of computational molecular dynamics (MD) simulations and biophysical and biochemical experiments (Gutiérrez-de-Terán et al., 2013b) to conclude that sodium ions selectively stabilize the inactive conformation of the wild-type receptor and that a physiologic concentration of NaCl was sufficient to achieve this effect. This mechanism
was further corroborated with radioligand binding data, indicative of a competitive interaction between the sodium ion in this allosteric pocket and an agonist in the orthosteric pocket. Furthermore, we proposed that the diuretic drug amiloride and analogs compete for the same site and exert an allosteric control on the hA2A AR quite similar to that of sodium ions, albeit with pharmacological differences in modulation of orthosteric ligand binding (Gutiérrez-de-Terán et al., 2013b).

In the present study we mutated the residues in the first and second coordination shell around the sodium ion to define the role of individual amino acids in the modulation by sodium ions, amiloride, and its derivative 5-(N,N-hexamethylene)amiloride (HMA). In this way we were able to analyze the effects of these manipulations on orthosteric ligand binding and receptor activation, employing a combination of biochemical and computational techniques.

Materials and Methods

Cell Growth and Transfection. HER293 cells were grown in culture medium consisting of Dulbecco’s modified Eagle’s medium supplemented with 10% newborn calf serum, 50 μg/ml streptomycin, and 50 IU/ml penicillin at 37°C and 7% CO₂. Cells were cultured twice a week at a ratio of 1:20 on 10 cm diameter plates. Single point mutations were introduced in the wild-type hA2A AR-plasmid DNA (FLAG-tag at N-terminus, in pcDNA3.1) by BaseClear (Leiden, The Netherlands). Cells were transfected with the indicated plasmids (1 μg each) using the calcium phosphate precipitation method (Sambrook et al., 1989). All experiments were performed 48 hours after transfection. HER293 cells stably expressing the wild-type receptor were grown in the same medium as the other HEK293 cells but with the addition of G-418 (200 μg/ml).

Enzyme-Linked Immunosorbent Assay. Twenty-four hours after transfection, cells were brought into 96-well poly-D-lysine-coated plates at a density of 10⁶ cells per well. After an additional 24 hours, the monolayers were washed with phosphate-buffered saline (PBS) and fixed for 10 minutes with 3.7% formaldehyde. Subsequently, cells were washed twice with PBS, and cell-surface receptors were labeled with mouse anti-FLAG (M2) primary antibody (Sigma-Aldrich, Zwijndrecht, The Netherlands; 1:1000) in culture medium for 30 minutes at 37°C. The cells were then washed once with Dulbecco’s modified Eagle’s medium supplemented with 25 mM HEPES and then incubated for two times with Dulbecco’s modified Eagle’s medium supplemented with 10% newborn calf serum, 50 μg/ml streptomycin, and 50 IU/ml penicillin at 37°C. The reaction was stopped with 8 ml of Tris buffer, and the homogenization and centrifugation step was repeated. Assay buffer (4 ml) was used to resuspend the pellet and adenosine deaminase was added (0.8 IU/ml) to break down endogenous adenosine. Membranes were stored in 250-μl aliquots at −80°C. Membrane protein concentrations were measured using the bicinchoninic acid method (Smith et al., 1985).

For competition binding experiments with [3H]ZM241385 membranes with transiently expressed A2A AR-wild type (WT; 7 μg of total protein), A2A AR-D52A,2.50 (5 μg), A2A AR-S91A,1.39 (1 μg), A2A AR-W246A,4.85 (2 μg), A2A AR-N280A,4.45 (1.5 μg), A2A AR-N284A,4.49 (1 μg) were used; we added different protein amounts to ensure that total binding to the membrane preparations was less than 10% of the total radioactivity added to prevent radioligand depletion. For [3H]HECA competition binding experiments, 30, 15, 10, 45, 50, and 10 μg of expressed A2A AR-WT, D52A,5.0, S91A,3.39, W246A,6.45, N280A,4.45, and N284A,4.49 receptors were used, respectively. Membrane aliquots were incubated in a total volume of 100 μl of assay buffer at 25°C for 2 hours. For homologous competition curves, radioligand displacement experiments were performed in the presence of nine concentrations of NECA (0.1 nM–100 μM) and ZM241385 (0.01 nM–10 μM). For concentration-effect curves, radioligand displacement experiments were performed in the presence of six concentrations of NaCl (10 μM–1 M) and five concentrations of amiloride (100 nM–1 mM) and HMA (10 nM–1 mM). [3H]ZM241385 and [3H]HECA were used at concentrations of 2.5 nM and 20 nM, respectively. Nonspecific binding was determined in the presence of 10 μM ZM241385 ([3H]HECA) or 100 μM NECA ([3H]ZM241385) and represented less than 10% of the total binding. Incubations were terminated by rapid vacuum filtration to separate the bound from free radioligand through 96-well GF/B filter plates using a Filtermate-harvester (PerkinElmer Life Sciences). Filters were subsequently washed three times with ice-cold assay buffer. The filter-bound radioactivity was determined by scintillation spectrometry using a PE 1450 Microbeta Wallac Trilux scintillation counter (PerkinElmer Life Sciences).

Functional cAMP Assays. HER293 cells were grown and transfected as described above. Experiments were performed 48 hours after transfection. The amount of cAMP produced was determined with the LANCE cAMP 384 kit (PerkinElmer). In short, 5000 cells per well were preincubated for 30 minutes at 37°C and subsequently at room temperature for 1 hour with a range of CGS21680 concentrations (0.1 nM–10 μM), one concentration of ZM241385 (10 μM), or without addition of ligand. cAMP generation was performed in the medium containing cistostamide (50 μM), rolipram (50 μM), and adenosine deaminase (0.8 IU·ml⁻¹). The incubation was stopped by adding detection mix and antibody solution, according to the instructions of the manufacturer. The generated fluorescence intensity was quantified on an EnVision Multilabel Reader (PerkinElmer). cAMP production by 10 μM CGS21680 on the parental HEK293 cell line represented less than 5% of cAMP production generated in cells expressing the hA2A AR receptor.

Molecular Dynamics Simulations. Molecular dynamics (MD) simulations of wild-type (WT) and mutant forms of the hA2A AR were performed following the computational protocol published recently (Gutiérrez-de-Terán et al., 2013b). Briefly, the inactive structure of the hA2A AR in complex with ZM241385 and a sodium ion [PDB code 4EY (Liu et al., 2012)] was used as a basis for our simulations, after a refinement process that consisted in modeling the missing ICL3 segment and proton addition, assessing the protonation state of titratable residues (i.e., all charged and histidine residues, which were protonated on Nδ, except for His155ECL2 and His264ECL3, respectively). The sodium ion and coordinating water molecules were explicitly considered except in the simulations with amiloride or HMA, which occupied the allosteric sodium ion site (Data Supplements 1–3). Further details are summarized in our recent publication (Gutiérrez-de-Terán et al., 2013b). Building mutant2
variants of the A2A receptor explored in this work was achieved by means of the “protein mutation tool” in Maestro (version 9.3; Schrödinger, New York, NY).

MD simulations were performed with the GROMACS software (Hess et al., 2008), using our original protocol for the MD simulations of GPCRs (Rodríguez et al., 2011). Our PyMemDyn program was used for membrane insertion, soaking with bulk water and inserting the resulting system, consisting of approximately 50,000 atoms (~74% belong to solvent molecules, ~15% to lipids and ~11% to protein and ligand atoms), into a hexagonal prism-shaped box, which was then energy-minimized and carefully equilibrated in the framework of periodic boundary conditions for 5 nanoseconds. (Gutiérrez-de-Terán et al., 2013a). Three replicate production simulations (i.e., changing the initial velocities of the system) were followed for 100-nanosecond simulation time each, thus accounting for a total of 300 nanoseconds MD sampling of each system. The OPLSAA force field was adopted throughout the simulations (Kaminski et al., 2001), with ligand parameters obtained from Macromodel (Macromodel, version 9.7; Schrödinger, New York, NY) and lipid parameters adapted from Berger (Berger et al., 1997) together with the use of the half-e double-pairlist method (Chakrabarti et al., 2010) and the SPC water model (Berendsen et al., 1981). A Nose-Hoover thermostat (Nose and Klein, 1983) with a target temperature of 310 K was used. Electrostatic interactions beyond a cutoff of 12 Å were estimated with the particle mesh Ewald method.

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Displacement curves of [3H]ZM241385 and [3H]NECA binding were recorded with different concentrations of NaCl, amiloride, and its more lipophilic derivative HMA for the wild-type and mutant receptors (Fig. 3). Whenever possible, IC50 values were derived for the inhibitory modulation of agonist [3H]NECA and antagonist [3H]ZM241385 binding by NaCl, amiloride, and HMA (Tables 2 and 3). NaCl inhibited

Cell Surface Receptor Expression of Mutated Receptors. Enzyme-linked immunosorbent assay was performed on HEK293 cells transiently expressing FLAG-tagged wild-type and mutant hA2AAR (Fig. 2). Wild-type and mutant receptors were expressed efficiently at similar levels.

Homologous Competition Assays. First we analyzed the effect of mutation of these residues on the affinity of radioligands [3H]NECA (agonist) and [3H]ZM241385 (antagonist) in the absence of NaCl (Table 1). The affinity of [3H]NECA and [3H]ZM241385 for the wild-type hA2AAR was 81 and 4.6 nM, respectively. D52A2.50 showed the same affinity as the wild-type receptor for both radioligands (77 and 3.5 nM, respectively). The other mutations caused some decrease in affinity for both radioligands, with a more pronounced effect on the agonist. An approximately 3-fold decrease of [3H]NECA affinity was observed for receptors with mutations S91A3.39 and N284A7.49, whereas [3H]ZM241385 affinity did not change significantly by these mutations. Radioligand agonist affinity decreased approximately 9-fold on N280A7.45 whereas a 1.8-fold decrease was observed for the antagonist. The W246A6.48 mutation affected affinities most, i.e., a 24-fold decrease in [3H]NECA affinity and a 5-fold decrease in [3H]ZM241385 affinity.

Concentration-Effect Curves in Radioligand Displacement Studies. Displacement curves of [3H]ZM241385 and [3H]NECA binding were recorded with different concentrations of NaCl, amiloride, and its more lipophilic derivative HMA for the wild-type and mutant receptors (Fig. 3). Whenever possible, IC50 values were derived for the inhibitory modulation of agonist [3H]NECA and antagonist [3H]ZM241385 binding by NaCl, amiloride, and HMA (Tables 2 and 3). NaCl inhibited

Results

Design of Mutations in the Sodium Ion Binding Pocket. We mutated the residues important for the sodium ion coordination (Fig. 1) to alanine, i.e., D52A2.50, S91A3.39, W246A6.48, N280A7.45, and N284A7.49. This approach thus yielded a total of five mutant receptors, which were studied further and compared with wild-type receptor with respect to their expression levels and pharmacology.

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![Fig. 1. Residues in or close to the sodium ion binding site that we subjected to an alanine scan in the hA2AAR and mapped on the crystal structure of the hA2AAR in the inactive ZM241385 and sodium ion bound conformation (PDB code 4EIY (Liu et al., 2012)). Residues Asp522.50, Ser913.39, Trp2466.48, Asn2807.45, and Asn2847.49 (represented by sticks, of which red and blue sticks are oxygen and nitrogen atoms, respectively) coordinate the sodium ion (purple sphere). Numbering of the residues follows Ballesteros-Weinstein system for comparison of positions between GPCRs (Ballesteros and Weinstein, 1995). Water molecules interacting with the sodium ion are represented by red spheres; hydrogen bonds are represented by black dotted lines; receptor backbone is represented by ribbons. Purple stick structure on top represents (part of) cocrystallized ZM241385.](image1)

![Fig. 2. Receptor expression levels on the cell surface of HEK293 cells transiently transfected with wild-type hA2AAR and single point mutations D52A2.50, S91A3.39, W246A6.48, N280A7.45, and N284A7.49, represented as fold-over-mock transfected human embryonic kidney cells (HEK293T) cells. The figure represents data combined from at least two separate experiments performed in quadruplicate.](image2)
respectively (Fig. 3A). [3H]NECA binding was not inhibited by NaCl on mutant N284A7.49 (Fig. 3A). Increasing concentrations of NaCl showed a tendency to enhance [3H]ZM241385 binding to the wild-type receptor as well as to the mutants tested, with W246A6.48 showing the biggest enhancement (Fig. 3B). At the highest concentration tested (1 M) NaCl exerted allosteric effects that are different from the specific effect of the sodium ion binding at Asp522.50.

Amiloride and HMA were capable of displacing [3H]NECA and [3H]ZM241385 binding on the point mutant receptors (Fig. 3, C–F), although with different IC50 values with respect to the wild-type receptor (Tables 2 and 3). D52A2.50 was particularly insensitive to amilorides: the inhibitory potency of amiloride increased significantly only in case of [3H]ZM241385 displacement. Mutant S91A3.39 exhibited similar potencies as the wild-type receptor for displacement of both radioligands by amiloride and HMA (Tables 2 and 3). These observations suggest that although polar interactions of the wild-type receptor and the receptors with mutated Ala522.50 to a vestibular pocket formed by residues Glu131.39 and His2787.43, where the sodium ion remained stable for the remaining 90 nanoseconds of the simulation (Fig. 5). In contrast, the wild-type receptor and mutated receptors D52A2.50 and W246A6.48 were simulated with ZM241385 in the orthosteric pocket and amiloride or HMA in the sodium ion binding site. Analysis of the root mean squared fluctuation confirmed no major conformational changes in the receptor due to any of the mutations. The effect of each single point mutation on the sodium ion mobility and coordination was assessed (Table 5). During the simulation in the WT model, the sodium ion alternated between two resonance positions, in which the sodium ion had a direct interaction with either Ser91.39 (22% occurrence of direct interaction during the simulations) or Asn2807.45 (29%), while maintaining a continuous direct interaction with Asp522.50 (90%) (Gutiérrez-de-Terán et al., 2013b). In mutation D52A2.50, however, sodium ion mobility increased by 5-fold and almost no direct interactions with residues Ser91.39 (1%) and Asn2807.45 (0%) occurred. In the first 10 nanoseconds of the simulation with the D52A2.50 mutant receptor, the sodium ion migrated from its starting position in the sodium ion binding site near Ala522.50 to a vestibular pocket formed by residues Gln131.39 and His2787.43, where the sodium ion remained stable for the remaining 90 nanoseconds of the simulation (Fig. 5). In contrast, mutants S91A3.39, W246A6.48, N280A7.45, and N284A7.49 did not show major deviations as compared with the wild-type situation with regards to either the ion mobility or the average number of oxygen atoms coordinating it (Supplemental Table 2; Harding

### Table 1

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<th>[3H]NECA</th>
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<td><strong>nM</strong></td>
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<tr>
<td><strong>Change</strong></td>
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<tr>
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<tr>
<td>D52A2.50</td>
<td>81 ± 5</td>
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<tr>
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<td>3.2</td>
</tr>
<tr>
<td>W246A6.48</td>
<td>1942 ± 124***</td>
<td>24</td>
</tr>
<tr>
<td>N280A7.45</td>
<td>752 ± 147***</td>
<td>9.3</td>
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<tr>
<td>N284A7.49</td>
<td>237 ± 27***</td>
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*Change in fold over wild type.

Significantly different from wild type with *P < 0.05 or ***P < 0.001 [one-way analysis of variance with Dunnett’s post-test performed on corresponding pKd values].

### Concentration-Effect Curves for cAMP Production

Functional assays were performed to further characterize the effect of the single point mutations on hA2A AR signaling. As an agonist CGS21680 was used to activate the receptor, yielding an increase in cAMP production through Gs protein activation (Fig. 4; Table 4). The use of the selective agonist CGS21680 for the hA2A AR rather than the nonselective NECA ensured that no endogenously expressed hA2B AR was activated in the HEK293 cells. The absence of activation by 10 μM CGS21680 in the untransfected parental cell line confirmed that indeed no endogenously expressed receptor was activated in this experimental setup. Mutations of the residues involved in the sodium ion binding site affected basal activity and efficacy of cAMP signaling by the hA2A AR. D52A2.50 and N284A7.49 mutants showed neither basal activity nor any activation by CGS21680. In all other cases, the mutant receptor showed a dramatically decreased receptor signaling response to CGS21680 binding (E<sub>max</sub>−E<sub>basal</sub>), ranging from only 27 to 46% of the wild-type response. The basal activity significantly increased over wild type in mutation S91A3.39. The N280A7.45 mutant also showed a tendency to increased basal activity, but this was not significantly different from wild type. This constitutive activity was inhibited by addition of 10 μM ZM241385, confirming that the elevated basal cAMP production in the transiently transfected cells was caused by these mutant receptors (Supplemental Fig. 1). CGS21680 activated both the wild-type and mutant N280A7.45 hA2A AR with an EC<sub>50</sub> value of 17 nM. The potency of CGS21680 was somewhat decreased on mutant W246A6.48 (approximately 5-fold). In the case of S91A3.39 the difference between basal and maximum activity was judged too small to derive an accurate EC<sub>50</sub> value.

### Molecular Dynamics Simulations

The dynamic behaviors of the wild-type receptor and the receptors with mutated residues important for sodium ion coordination D52A2.50, S91A3.39, W246A6.48, N280A7.45, and N284A7.49 were simulated with either only antagonist ZM241385 present or with both ZM241385 in the orthosteric pocket and the sodium ion in its allosteric binding site (Supplemental Table 1). In addition, the wild-type receptor and mutated receptors D52A2.50 and W246A6.48 were simulated with ZM241385 in the orthosteric pocket and amiloride or HMA in the sodium ion binding site. Analysis of the root mean squared deviation revealed equilibrated trajectories typically after 20–30 nanoseconds, with an average value of 1.8 Å in all simulations, and analysis of the root mean squared fluctuation confirmed no major conformational changes in the receptor due to any of the mutations.
(2006]) due to the replacement of the mutated side chain by an additional water molecule. However, the occurrence of direct interactions with the three coordinating residues appeared lowered to some extent, indicative of a nonoptimal ion coordination for these mutants. This was true in particular for the interaction with Asp522.50 (51–76%; see Table 5).

Mobility and interactions with the receptor of amiloride and HMA, as docked in the sodium ion binding site, were assessed in simulations of the wild-type receptor and mutant receptors D52A2.50 and W246A6.48 (Fig. 6). In these relatively short MD runs amiloride was equally stable in the proposed binding site upon both mutations, with a root mean square fluctuation value of \( \sim 2 \) Å. The mobility of the amiloride derivative HMA was increased 3-fold by mutation D52A2.50, and in one out of three simulations it left the putative binding pocket following the same pathway as depicted in Fig. 5B. Mutation W246A6.48, on the contrary, did not affect HMA stability in the same way. However, it is worth noting that specific contacts changed for the two ligands with both mutants. In the wild-type receptor, both ligands achieved an average number of four simultaneous hydrogen bonds, mainly with residues Asp522.50 and Trp2466.48 [Supplemental Fig. 2; Gutiérrez-de-Terán et al. (2013b)]. For amiloride, the number of hydrogen bonds dropped to approximately two in the two mutants examined, as well as for HMA with mutant W246A6.48, whereas mutation D52A2.50 had a more dramatic effect on HMA with only one hydrogen bond left on average (Supplemental Fig. 2). Note that in this analysis, interactions between amino (amilorides) and carbonyl (Asp522.50) groups were approximated as hydrogen bonds, instead of the stronger salt bridge interactions that occur in reality, the loss of which is expected to have a large effect on the affinities of amilorides. This analysis did not reveal stable hydrogen bonds of amilorides with either of the asparagines close by (Asn2807.45 and Asn2847.49).

![Fig. 3.](https://molpharm.aspetjournals.org/)

Displacement/enhancement of specific \[^{3}H\]NECA (A, C, and E) and \[^{3}H\]ZM241385 (B, D, and F) binding by NaCl (A and B), amiloride (C and D), and HMA (E and F) on wild-type human A2AAR and point mutants D52A2.50, S91A3.39, W246A6.48, N280A7.45, and N284A7.49 transiently expressed on HEK293T cell membranes. Representative graphs from one experiment performed in duplicate are shown.
in the hA2AAR sodium ion binding site in more detail, through properties to coordinate a sodium ion. May differ, but collectively they apparently maintain the properties of variance with Dunnett posttest performed on corresponding pIC50 values). These observations made us examine the residues involved in the hA2AAR sodium ion binding site in more detail, through a combined approach of mutational and computational studies. Most importantly, we learned that all mutations in the sodium ion binding pocket impact hA2AAR signaling significantly, including both constitutive and agonist-stimulated activity. Although all mutant data in the present study are novel, we have shown a number of similar findings on the wild-type receptor before (Lane et al., 2012; Gutiérrez-de-Terán et al., 2013b). Mutation of Asp2.50 is known to silence signaling in many GPCRs (Parker et al., 2008). The migration of the sodium ion to Glu131.39 and His2787.43 agrees with their involvement in sodium ion allosterism observed previously by Gao et al. (2000). From a reversed perspective, this simulation could envisage a pathway for the entrance of the sodium ion, which should occur from the extracellular side according to the physiologic gradient (Selent et al., 2010; Shang et al., 2014), and where residue Glu131.39, conserved in all adenosine receptors, could stabilize such a pathway. The enhancement of agonist binding to the D52A2.50 mutant receptor (Tables 2 and 3), strongly suggests that binding of the ion to alternative sites may produce further allosteric effects, different from the effects on wild-type Asp522.50. The affinities of amiloride and HMA were 10- to 20-fold decreased on the D2.50N (Schetz and Sibley, 2001). In the adenosine A3 and A2A receptors, affinities of amiloride and HMA from wild-type human A2AAR and point mutants D52A2.50, S91A3.39, W246A6.48, N280A7.45, N284A7.49 transiently expressed on HEK293 cell membranes Values are means ± S.E.M. of at least three separate assays performed in triplicate.

**Discussion**

The sodium ion binding site appears conserved among class A GPCRs (Katritch et al., 2014). Subsequent to the hA2AAR, the crystal structures of the human protease-activated receptor 1 (Zhang et al., 2012), the β1-adrenergic receptor (Christopher et al., 2013; Miller-Gallacher et al., 2014), and the human δ-opioid receptor (Fenalti et al., 2014) further confirmed the common role of this site in the inactive conformation of GPCRs. A sequence comparison of the sodium ion binding site between more distant class A GPCRs shows that individual amino acids may differ, but collectively they apparently maintain the properties to coordinate a sodium ion. These observations made us examine the residues involved in the hA2AAR sodium ion binding site in more detail, through a combined approach of mutational and computational studies. Most importantly, we learned that all mutations in the sodium ion binding pocket impact hA2AAR signaling significantly, including both constitutive and agonist-stimulated activity. Although all mutant data in the present study are novel, we have shown a number of similar findings on the wild-type receptor before (Lane et al., 2012; Gutiérrez-de-Terán et al., 2013b), indicative of the robustness of the assay system. We will discuss our findings in the light of available mutation data in literature by examining the mutated amino acids individually. For the search we made use of data available in the GPCRDB (Isberg et al., 2014).

**Asp2.50**. The pronounced effects of mutation of the conserved Asp2.50 are in agreement with previous studies. Mutation of Asp2.50 abolished the effect of NaCl on agonist binding in studies on a multitude of GPCRs, for example in the α2-adrenergic receptor (Horstman et al., 1990), dopamine D2 (Neve et al., 1991), adenosine A1 (Barbhaiya et al., 1996), adenosine A3 (Gao et al., 2003), and δ-opioid receptors (Fenalti et al., 2014). In MD simulations of the wild-type hA2AAR, Asp522.50 dominated coordination of the sodium ion (Gutiérrez-de-Terán et al., 2013b). Mutation of Asp2.50 is known to silence signaling in many GPCRs (Parker et al., 2008). The migration of the sodium ion to Glu131.39 and His2787.43 agrees with their involvement in sodium ion allosterism observed previously by Gao et al. (2000). From a reversed perspective, this simulation could envisage a pathway for the entrance of the sodium ion, which should occur from the extracellular side according to the physiologic gradient (Selent et al., 2010; Shang et al., 2014), and where residue Glu131.39, conserved in all adenosine receptors, could stabilize such a pathway. The enhancement of agonist binding to the D52A2.50 mutant receptor (Tables 2 and 3), strongly suggesting that the positively charged guanidinium moiety of the compounds interacts with the negatively charged aspartic acid. A more modest 4-fold decrease in affinity for an amiloride derivative was reported for the D4 dopamine receptor with D2.50N (Schetz and Sibley, 2001). In the adenosine A3 and α2-adrenergic receptors, affinities of amiloride and its derivatives were largely undisturbed by mutation D2.50N (Horstman et al., 1990; Gao et al., 2003), suggesting that the more drastic mutation to Ala in the current study more precisely revealed the importance of this residue for amiloride binding.

**Trp4.49**. It appeared that sodium ions and agonist NECA can bind simultaneously to the W246A6.48 receptor (Fig. 3A), in contrast with the wild-type receptor where NECA and...
sodium ion binding are mutually exclusive (Gutiérrez-de-Terán et al., 2013b). Conversely, mutant W246A\textsuperscript{6.48} augmented the positive effect of sodium ions on antagonist ZM241385 binding (Fig. 3B). It seems that Trp246\textsuperscript{6.48} may clash with both agonists and antagonists in the orthosteric pocket, because the absence of this residue has a positive effect on binding of both agonists and antagonists in presence of the sodium ion. Trp\textsuperscript{6.48} conserved in many GPCRs, has long been suggested to act as a ”toggle switch” in receptor activation (Nygård et al., 2009) but has never been studied in the context of allosteric modulation by sodium ions. It has been mutated to both Phe and Ala in the human adenosine A\textsubscript{3} receptor, being the closest homolog to the A\textsubscript{2A} receptor (Gao et al., 2002, 2003). Interestingly, agonist binding was hardly affected by these mutations, whereas antagonists showed a modest decrease in affinity. Receptor activation, however, was largely impeded, seemingly more than our current findings on the A\textsubscript{2A} receptor (e.g., see Fig. 4). Remarkably, the affinities for amiloride and HMA were strongly increased on this mutant (Tables 2 and 3), suggesting that the wild-type tryptophan creates a substantial steric strain for the binding of amilorides. In the adenosine A\textsubscript{3} receptor the W\textsuperscript{6.48}A mutation increased HMA potency on agonist binding as well (Gao et al., 2003). The mobility of sodium ions alternates direct interactions with Ser91\textsuperscript{3.39} and His278\textsuperscript{7.43} (Fig. 5). The bulkier hexamethyl group of HMA collides with Ser91\textsuperscript{3.39}, Asn7\textsuperscript{7.45}, and Asn7\textsuperscript{7.49}. The sodium ion in root mean squared fluctuation (RMSF) in wild-type and mutant receptor and the occurrence in percent of direct interactions with the different residues coordinating the ion in the crystal structure along the simulation time.

### Table 5

<table>
<thead>
<tr>
<th>Na\textsuperscript{+} Mobility</th>
<th>Na\textsuperscript{+} Interactions</th>
</tr>
</thead>
<tbody>
<tr>
<td>RMSF in Å</td>
<td>% Occurrence with Indicated Residues</td>
</tr>
<tr>
<td></td>
<td>Asp22\textsuperscript{2.50}</td>
</tr>
<tr>
<td>Wild type</td>
<td>2.5 ± 0.3</td>
</tr>
<tr>
<td>D52A\textsuperscript{2.50}</td>
<td>11.2 ± 3.8</td>
</tr>
<tr>
<td>S91A\textsuperscript{3.39}</td>
<td>1.8 ± 0.2</td>
</tr>
<tr>
<td>W246A\textsuperscript{6.48}</td>
<td>2.5 ± 0.3</td>
</tr>
<tr>
<td>N280A\textsuperscript{7.45}</td>
<td>2.6 ± 0.2</td>
</tr>
<tr>
<td>N284A\textsuperscript{7.49}</td>
<td>2.6 ± 0.1</td>
</tr>
</tbody>
</table>

Significantly different from control with *P < 0.05 (Student’s t test).
while maintaining contact with Asp522.50. This is in agreement with the observation that sodium ion modulation of agonist binding is not completely abolished in mutant receptors S91A3.39 and N280A7.45 (Fig. 3A) and that the two remaining residues in mutants S91A3.39 and N280A7.45 (Asp522.50 and Asn2807.45, respectively) still interact directly with the sodium ion, although less than in the wild-type receptor (Table 5). Jiang et al. (1996) found that the same S91A mutation did not affect orthosteric ligand binding very much, even less so than the slight decrease in affinity in our experiments (Table 1). In the adenosine A1 receptor, however, orthosteric ligand binding could not be detected for this mutation, maybe due to lack of expression (Barbhaiya et al., 1996).

In mutant N284A7.49, sodium ion modulation of agonist binding was completely abolished (Fig. 3A). In the antagonist-bound inactive conformation of the receptor, Asn284 7.49 might improve sodium ion coordination through stabilization of the side chain of Asp522.50, explaining the disruption of sodium ion binding by mutation N284A7.49. The same role of Asn 7.49 in stabilization of Asp522.50 was proposed previously in, e.g., the guanidinium group of both amilorides coordinated by Asp522.50, yet they only make sporadic H-bond contacts (Supplemental Fig. 2). Thus alanine substitutions might indeed facilitate binding of amilorides by avoiding unfavorable polar interactions (Asn2807.45) or by allowing more conformational freedom to Asp522.50 (Asn2847.49), accommodating in particular the bulky HMA and enhancing its binding.

The MD simulations showed only minor effects on the capacity of mutants S91A3.39, W246A6.48, N280A7.45, and N284A7.49 to bind the sodium ion in the inactive conformation of the receptor. This seems in contrast to the greatly reduced sensitivity of these mutants to physiologic concentrations of NaCl (Fig. 3A). In addition to the explanations discussed above, an alternative explanation arises from the observation that each of these four side chain annihilations creates additional room for an extra water molecule, thus fulfilling the coordination number of the ion (Supplemental Table 2). This might allow that, in contrast to the wild-type receptor, the mutants also bind the sodium ion in an active receptor conformation, resulting in the observed loss of modulatory effect on agonist binding.

In conclusion, our results show the importance of the sodium ion binding site in orthosteric ligand binding and receptor activity. Mutation D522A2.50 caused an immediate displacement of the sodium ion to a distant pocket in MD simulations, in agreement with the loss of the modulatory effect in our molecular pharmacology experiments. The effects of the other mutations were varied, but they significantly affected sodium ion modulation of agonist binding and modulation by amilorides of both agonist and antagonist binding. In addition, all mutations influenced receptor activation, particularly by affecting the levels of constitutive and agonist-stimulated activity, emphasizing the importance of the sodium ion binding pocket for the receptor’s active conformation(s). These findings imply that because of allosteryism by sodium ions and amilorides, the sodium ion binding pocket is a prominent player in receptor functionality and ligand affinity. Our study also opens the door to the design of novel synthetic allosteric modulators or bitopic ligands connecting the sodium ion binding site and the orthosteric binding pocket.

Authorship Contributions

Participated in research design: Massink, Gutiérrez-de-Terán, Lenselink, Heitman, Katritch, Stevens, IJzerman.
Conducted experiments: Massink, Gutiérrez-de-Terán, Lenselink, Ortiz Zacarías, Xia.
Performed data analysis: Massink, Gutiérrez-de-Terán, Lenselink, Ortiz Zacarías, Xia.
Wrote or contributed to the writing of the manuscript: Massink, Gutiérrez-de-Terán, Lenselink, Katritch, Stevens, IJzerman.

References

Supplemental Data

*Molecular Pharmacology*

Sodium ion binding pocket mutations and adenosine $A_2A$ receptor function

Arnault Massink, Hugo Gutiérrez-de-Terán, Eelke B. Lenselink, Natalia V. Ortiz Zacarias, Lizi Xia, Laura H. Heitman, Vsevolod Katritch, Raymond C. Stevens, and Adriaan P. IJzerman

**Figure S1.** Inhibition by 10 µM ZM241385 of basal cAMP production in HEK293T cells, transiently expressing S91A$^{3.39}$, W246A$^{6.48}$, or N280A$^{7.45}$ hA$_{2A}$AR, or in untransfected parental HEK293T cells. Statistically significant differences in the inhibitory effect of ZM241385 for each mutant were analyzed by a paired Student’s t-test and are indicated with ** $p < 0.01$ or *** $p < 0.001$. The figure represents all data combined (± S.E.M.) from at least three separate experiments performed in triplicate.
Figure S2. Average number of hydrogen bonds (Y-axis) as a function of time (X-axis) between the protein and either HMA or amiloride in wild-type receptor, D52A\textsuperscript{2.50}, and W246A\textsuperscript{6.48} mutant receptors. Salt bridge interactions between the amino group of the amilorides and the carbonyl group of Asp52\textsuperscript{2.50} were approximated as hydrogen bonds. The data plotted is the mean from three independent 100 ns simulations.
Table S1. Overview of molecular dynamics simulation runs. Simulations account for a total of 5.4 μs. In all simulations antagonist ZM241385 was present in the orthosteric binding site of the receptor.

<table>
<thead>
<tr>
<th>Receptor</th>
<th>-</th>
<th>Sodium ion</th>
<th>Amiloride</th>
<th>HMA</th>
</tr>
</thead>
<tbody>
<tr>
<td>WT</td>
<td>3*100 ns$^a$</td>
<td>3*100 ns$^a$</td>
<td>3*100 ns$^a$</td>
<td>3*100 ns$^a$</td>
</tr>
<tr>
<td>D52A$^{2.50}$</td>
<td>3*100 ns</td>
<td>3*100 ns</td>
<td>3*100 ns</td>
<td>3*100 ns</td>
</tr>
<tr>
<td>S91A$^{3.39}$</td>
<td>3*100 ns</td>
<td>3*100 ns</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>W246A$^{6.48}$</td>
<td>3*100 ns</td>
<td>3*100 ns</td>
<td>3*100 ns</td>
<td>3*100 ns</td>
</tr>
<tr>
<td>N280A$^{7.45}$</td>
<td>3*100 ns</td>
<td>3*100 ns</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>N284A$^{7.49}$</td>
<td>3*100 ns</td>
<td>3*100 ns</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

$^a$ Extracted from Gutiérrez-de-Terán, Structure (Gutiérrez-de-Terán et al., 2013), see also Data Supplements 1-3.

$^b$ An alternative setup with His278$^{7.43}$ positively charged was evaluated (3*100 ns).

Table S2. Average number of oxygen atoms in the first coordination shell of the sodium ion, as averaged from the three independent MD simulations in each case. Numbers in parentheses indicate the average number of interacting water molecules.

<table>
<thead>
<tr>
<th>Receptor</th>
<th>Na$^+-$O$^a$</th>
</tr>
</thead>
<tbody>
<tr>
<td>WT</td>
<td>4.4 (2.6)</td>
</tr>
<tr>
<td>D52A$^{2.50}$</td>
<td>4.0 (2.7)</td>
</tr>
<tr>
<td>S91A$^{3.39}$</td>
<td>4.5 (2.9)</td>
</tr>
<tr>
<td>W246A$^{6.48}$</td>
<td>4.5 (3.0)</td>
</tr>
<tr>
<td>N280A$^{7.45}$</td>
<td>4.5 (2.9)</td>
</tr>
<tr>
<td>N284A$^{7.49}$</td>
<td>4.6 (2.7)</td>
</tr>
</tbody>
</table>

* The coordination numbers were calculated at every snapshot using a maximum Na$^+$—O cutoff distance of 2.6 Å, as indicated by the calculated radial distribution function for the Na$^+$—O pairs (Gutiérrez-de-Terán et al., 2013).