

To bind or not to bind, that is an important question! : Development of covalent probes for adenosine receptors Yang, X.

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Chapter 4

Development of Covalent Ligands for G Protein-Coupled Receptors: A Case for the Human Adenosine A₃ Receptor

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Abstract

The development of covalent ligands for G protein-coupled receptors (GPCRs) is not a trivial process. Here, we report a streamlined workflow thereto from synthesis to validation, exemplified by the discovery of a covalent antagonist for the human adenosine A₃ receptor (hA₃AR). Based on the 1*H*,3*H*-pyrido[2,1-*f*]purine-2,4-dione scaffold, a series of ligands bearing a fluorosulfonyl warhead and varying linker was synthesized. This series was subjected to an affinity screen, revealing compound 17b as the most potent antagonist. In addition, a nonreactive methylsulfonyl derivative 19 was developed as a reversible control compound. A series of assays, comprising time-dependent affinity determination, washout experiments and [35S]GTPγS binding assays, then validated 17b as covalent antagonist. A combined in silico hA₃AR-homology model- and site-directed mutagenesis study was performed to demonstrate that amino acid residue Y265^{7,36} was the unique anchor point of the covalent interaction. This workflow might be applied to other GPCRs to guide the discovery of covalent ligands.

1. Introduction

The adenosine A₃ receptor (A₃AR) is one of four G protein-coupled receptor subtypes stimulated by adenosine [1]. Different from the other subtypes (A₁, A_{2A} and A_{2B}) A₃AR was identified by molecular biology studies prior to its pharmacological characterization [2]. The initial studies indicated its important role in both physiological and pathophysiological conditions, such as cell proliferation, cell differentiation, neuroprotection, cardioprotection and apoptosis [3]. Nevertheless, the medical relevance of the human adenosine A₃ receptor (hA₃AR) is enigmatic due to its dichotomy in different therapeutic applications [3]. In this regard, there is a continuing interest in the development of the selective ligands of the hA₃AR to investigate its pharmacological effects. For instance, selective A₃AR antagonists have been applied for the treatment of glaucoma [4] and respiratory tract inflammation such as asthma [5]. In particular, a tricyclic xanthine derivative, 1-benzyl-8-methoxy-3-propyl-1*H*,3*H*-pyrido[2,1-*f*]purine-2,4-dione (compound 1, Figure 1a), has been reported to exert high affinity for the hA₃AR [6-8].

Figure 1. (A) Reference antagonist (1) for hA_3AR . (B) DU172 (2), a covalent antagonist for hA_1AR .

Initial efforts to study the structural biology of GPCRs suffered from numerous limitations, such as low expression, dynamic conformational states, and inherent instability. Covalent ligands, i.e., compounds that irreversibly bind to the receptor and possess a reactive moiety to target specific amino acid residues, helped to solve some of these obstacles [9]. This is also the case for adenosine receptors. For example, the structure of the human adenosine A₁ receptor, having the highest similarity to hA₃AR among all adenosine receptors subtypes (61% of sequence homology) [10], has been elucidated by X-ray crystallography with a covalent antagonist DU172 (2) (Figure 1b) [11]. However, the application of covalent ligands in hA₃AR studies has been limited to the characterization of the receptor type [12-14], far from providing a comprehensive study of receptor structure elucidation, pharmacological characteristics and ligand-receptor binding description.

To this end, we devoted our efforts to the discovery of a well-defined covalent antagonist based on xanthine analogue 1 mentioned above. Inspired by the resemblance in chemical structure between the potent hA₃AR antagonist 1 and irreversible adenosine A₁ receptor antagonist 2, we incorporated the reactive moiety, a fluorosulfonyl benzoyl group, connected to a spacer, at the N¹ position of the scaffold. Using a structured approach to bring the reactive fluorosulfonyl group in close proximity to a nucleophilic amino acid residue, we diversied the type of linker, linker length and position of the fluorosulfonyl substituent on the phenyl group, resulting in a series of analogues with a wide range of affinities. Our efforts led to the discovery of a best-in-class antagonist, 17b, which bound to hA₃AR with an apparent affinity in the nanomolar range. To keep the chemical structure similarity, we replaced the warhead with a methylsulfonyl moiety to obtain a non-reactive derivative 19 as a reversible control compound. 17b was then validated to covalently bind and inactivate the hA₃AR in an insurmountable manner. Molecular modelling suggested the fluorosulfonyl functionality of 17b in close proximity to Y265^{7,36}, which was identified as the unique anchor point of the covalent interaction in a subsequent mutagenesis study. The confirmed binding mode between this novel covalent antagonist and hA₃AR opens the door for exploring other ligand binding motifs and will benefit receptor stabilization and further structure elucidation of the hA₃AR.

2. Results and Discussion

2.1. Design of Covalent hA₃AR Antagonists

In previous studies, our research group disclosed several series of hA₃AR antagonists based on the pyrido[2,1-f]purine-2,4-dione scaffold [6-8]. Using compound 1, a nanomolar probe from the previous series, as the starting point, we further designed and synthesized compounds based on a previously suggested binding mode of the pyrido[2,1-f]purine-2,4-dione scaffold [7]. When examining the suggested binding mode of this scaffold, we noted that this scaffold inserted into the binding pocket with a receptor interaction between TM3, TM6 and EL2. Two key H-bonds include the carbonyl-oxygen at the C⁴-position with residue N250^{6.55} and the methoxy substituent at the C⁸-position bonding to Q167^{EL2}. Taking this into account, we reasoned the only available space to incorporate the reactive warhead is limited to C¹-position substituents.

To explore the chemical space required to optimally position the warhead in close proximity to a nucleophilic amino acid residue, we examined various linker systems, connecting the warhead and the pyrido[2,1-f]purine-2,4-dione scaffold. First, variation in the length of the spacer, between two and four carbon atoms, may offer more steric freedom allowing the

fluorosulfonyl group to orient toward an adjacent nucleophilic residue in the receptor binding site [15, 16]. Additionally, the type of chemical bond connecting the warhead to the spacer was varied between the slightly differently oriented ester or amide bond. Finally, since the exact position of an appropriate nucleophilic residue is unknown, the sulfonyl fluoride moiety was positioned at either the 3- or 4-position of the phenyl ring. To this end, four series of compounds 13a-c, 14a-c, 17a-c and 18a-c, bearing three different spacer lengths, ester or amide linkage and 3- or 4-fluorosulfonylphenyl warhead were targeted for synthesis.

2.2. Synthesis.

Scaffold. The scaffold, 8-methoxy-3-propyl-1*H*,3*H*-pyrido-[2, 1-*f*]purine-2, 4-dione (1), was synthesized according to the previously published procedure [6-8]. Starting from the commercially available benzylurea (3), the fused tricyclic intermediate (6) was generated by excess NBS bromination and 4-methoxypyridine cyclization (Scheme 1). Then alkylation at the N³-nitrogen by 1-bromopropane in dry DMF, using dry potassium carbonate as a weak base, afforded the reference compound (1) in 73% yield. Removing the benzyl protecting group by palladium hydroxide afforded the fused xanthine core (7).

Scheme 1. Synthetic route towards scaffold 7

Reagents and conditions: (a) i) Ac_2O , 80 °C, 2 h; ii) Et_2O , rt, 1 h; iii) 3M NaOH, 85 °C, 1 h; iv) HCl (37%), 25%; (b) i) NBS, MeCN, 80 °C; ii) 4-methoxypyridine, 80 °C, 64%; (c) 1-bromopropane, DBU, MeCN, 70 °C, 73%; (d) Pd(OH)₂/C, HCOONH₄, EtOH, reflux, 40%.

Ester Linker The fluorosulfonyl warhead is notorious for its reactivity resulting in undesired side reactions or hydrolysis under several harsh reactions [17]. So we adopted a convergent synthetic strategy in which the fluorosulfonyl phenyl linker unit was prepared separately and attached directly to scaffold 7 at the N³ position. This approach offers the flexibility to accommodate a variety of different linker lengths. The warhead was synthesized from commercially available chlorosulfonylbenzoic acids (8a and 8b) (Scheme 2), followed by a 2 M solution of potassium bifluoride treatment to afford fluorosulfonylbenzoic acids (9a and 9b) in good yields. [18] The next step converted the carboxylic acids to acid chlorides (10a and 10b) by excess thionyl chloride treatment. These acyl chlorides are prone to hydrolysis and

Scheme 2. Synthetic route towards the bromoalkyl fluorosulfonylbenzoates 13a-c and 14a-c

Reagents and conditions: (a) 2M KHF₂ solution, dioxane, rt, 1h, 87%-90%; (b) SOCl₂ reflux; (c) corresponding bromoalkylalcohol, anhydrous dioxane, 100 °C, 18h, 55%-83%, (d) **11a-c** or **12a-c**, K₂CO₃, anhydrous DMF, 50 °C, 5%-57%.

were thus used in the next step reaction without further purification. To incorporate the acyl chlorides with the corresponding bromoalkylalcohols, compounds 10a and 10b were heated to 100 °C with the addition of bromoalkylalcohols to afford the desired bromoalkyl fluorosulfonylbenzoates (11a-c and 12a-c) in decent yields. The final step was to couple the core to the corresponding bromoalkyl fluorosulfonylbenzoates. In order to preserve the functional fluorosulfonyl group, the reactions were carried out under mild conditions at low temperature. Additionally, excess DMF was removed by multiple washing steps, instead of vacuum removal at high temperature. Six final products (13a-c and 14a-c) were obtained in acceptable yields.

Amide Linker A similar synthetic approach was initially pursued to prepare analogues with an amide linker. However, the basicity and instability of bromoalkylamine caused complex side reactions with itself and with the warhead, ending up with an unacceptably low yield of amide-linked building blocks. An alternative synthetic route was devised, where 1-phthalimidopropyl bromide was attached directly to the N³ position of scaffold 6, to afford the substituted intermediates 15a-c (Scheme 3). Liberation of the amine took place by treatment with hydrazine monohydrate in methanol to obtain compound 16a-c in moderate yield. Then 16b and 16c were acylated with acyl chlorides 10a and 10b, respectively, to obtain 17c and 18b. However, impurities brought by the acylation reaction were not easily removed by column chromatography or preparative TLC.

Scheme 3. Synthetic route towards the amide-linker antagonists 17a-c, 18a-c and 19

Reagents and conditions: (a) N-(bromoalkyl)phthalimide, K_2CO_3 , DMF, 100 °C, 5-96%; (b) $N_2H_4\cdot H_2O$, MeOH reflux, 86-90%; (c) EDC, corresponding acid (**9a-b**), CHCl₃ or CH₂Cl₂, rt; (d) SOCl₂, K_2CO_3 , dry DMF, 40 °C, 3-78%

To overcome this, we used peptide coupling conditions with the corresponding benzoic acids (9a and 9b) to convert the free amine to the target compounds (17a-b, 18a and 18c) in good yields (Scheme 4). A similar synthetic strategy was adapted to obtain reversible ligand 19 as a control compound.

2.3. Pharmacological Evaluation.

Determination of the apparent affinity (Ki) of synthetized ligands. To determine the binding affinity for the hA₃AR receptor, all compounds were tested in a radioligand displacement binding assay in the presence of 10 nM [3H]PSB-11 at 25 °C according to previously reported procedures [7, 19]. All compounds were able to concentration-dependently inhibit specific [3H]PSB-11 binding to the hA₃AR. As detailed in Table 1, all putative covalent compounds, except the two carbon linker compounds (13a, 14a, 17a and 18a), displayed high affinities for the hA₃AR (K_i < 100 nM). It should be mentioned that the putative covalent nature of the interaction between hA₃AR and ligands precludes the determination of equilibrium binding parameters. Therefore, we expressed the ligands' affinity for the hA₃AR as "apparent K_i ". Of note, 17b, bearing three carbon atoms with amide linkage and positioning the sulfonyl fluoride at the 4-position of phenyl ring, interacted with hA₃AR with comparable affinity (10 nM) as the parent compound 1. High affinity is desirable for covalent ligand design, as it allows sufficient receptor occupancy with the electrophilic warhead in proximity to a nucleophilic residue in the binding site over time concomitant with putatively negligible or less interaction with off-targets. Thus, we chose compound 17b for further studies. However, featuring an electrophilic fluorosulfonyl functionality, 17b was no longer a close analogue of compound 1, while a non-reactive control compound, chemically similar to the designed

Table 1. Apparent Affinities of Pyrido[2,1-f]purine-2,4-dione Derivatives 13-19.

Compound	n	X	\mathbb{R}^1	pK _i \pm SEM ^a or disp. at 10 μ M (%)	
13a	1	O	$4-SO_2F$	6.7 ± 0.1	
13b	2	О	4-SO ₂ F	7.7 ± 0.1	
13c	3	О	4-SO ₂ F	7.5 ± 0.1	
14a	1	О	3-SO ₂ F	6.4 ± 0.1	
14b	2	О	$3-SO_2F$	7.0 ± 0.05	
14c	3	О	3-SO ₂ F	7.1 ± 0.05	
17a	1	NH	4-SO ₂ F	27%	
17b (LUF7602)	2	NH	4-SO ₂ F	8.0 ± 0.05	
17c	3	NH	$4-SO_2F$	7.5 ± 0.05	
18a	1	NH	$3-SO_2F$	18%	
18b	2	NH	3-SO ₂ F	7.5 ± 0.01	
18c	3	NH	3-SO ₂ F	6.8 ± 0.1	
19 (LUF7714)	2	NH	4-SO ₂ Me	6.3 ± 0.03	

^a Data are expressed as means ± SEM of three separate experiments each performed in duplicate. Apparent affinity determined from displacement of specific [³H]PSB-11 binding from the hA₃AR stably expressed on CHO cell membranes at 25 °C during 2 h incubation.

covalent ligand, is needed for the further pharmacological characterization. A non-substituted phenyl to replace the warhead might impose different steric and electronic characteristics of the ligand. To avoid this, we performed a conservative structural modification to replace the reactive warhead with an electron-withdrawing methylsulfonyl group, yielding derivative 19 as a nonreactive control compound.

Table 2. (Apparent) Affinities of **17b** and **19** for all adenosine receptor subtypes, hA₃AR-WT and hA₃AR-Y265F^{7,36}

	hA_1AR^a	$hA_{2A}AR^b$	$hA_{2B}AR^c$	h <i>A</i>	A ₃ AR	hA ₃ AR- WT ^f	hA ₃ AR- Y265F ^{7.36g}
cpd	$pK_i\pm$	SEM	Displ. (%) at 1 μM	pK _i ^d (pre-0 h)	pK _i ^e (pre-4 h)	pIC ₅₀ ±	: SEM ^e
17b ^h	6.1 ± 0.03	5.9 ± 0.09	0% (7, -7)	6.9 ± 0.06	8.0 ± 0.01**	7.6 ± 0.05	$6.0 \pm 0.3^*$
19	4.8 ± 0.20	5.2 ± 0.20	0% (-10, -13)	6.2 ± 0.03	$6.1\pm0.06^{\rm NS}$	5.9 ± 0.02	$6.1\pm0.1^{\text{NS}}$

Values represent mean \pm SEM of three separate experiments each performed in duplicate or percent age displacement at 1 μ M of two separate experiments each performed in duplicate.

^aAffinity determined from displacement of specific [³H]DPCPX binding on CHO cell membranes stably expressing human adenosine A₁ receptors at 25 °C during 2 h incubation;

^bAffinity determined from displacement of specific [³H]ZM241385 binding on HEK293 cell membranes stably expressing human adenosine A_{2A} receptors at 25 °C during 2 h incubation; ^c% displacement at 1 μM concentration of specific [³H]PSB-603 binding on CHO cell membranes stably expressing human adenosine A_{2B} receptors at 25 °C during 2 h incubation.

^dDisplacement of specific [³H]PSB-11 binding on CHO cell membranes stably expressing hA₃AR at 25 °C during 0.5 h incubation.

°Displacement of specific [³H]PSB-11 binding from CHO cell membranes stably expressing hA_3AR preincubated with antagonist for 4 h at 25 °C, followed by a 0.5 h co-incubation with [³H]PSB-11. P < 0.01^{**} compared with the pK_i values in displacement experiments during 0.5 h incubation time; NS: no significant difference compared with the pK_i values in displacement experiments during 0.5 h incubation time; Student's test.

^fDisplacement of specific [³H]PSB-11 binding from CHO-K1 cell membranes transiently transfected with hA₃AR-WT at 25 °C during 2 h incubation

^gDisplacement of specific [³H]PSB-11 binding from CHO-K1 cell membranes transiently transfected with $hA_3AR-Y265F^{7.36}$ at 25 °C during 2 h incubation. $P < 0.01^*$ compared with the pIC₅₀ values in displacement experiments on hA_3AR-WT . NS: no significant difference compared with the pIC₅₀ values in displacement experiments on hA_3AR-WT membranes; Student's test.

^hFor 17b, pKi values are apparent affinity values as no dynamic equilibrium can be obtained.

To better understand the time-dependent binding characteristics of these compounds, we carried out radioligand displacement assays under two different protocols. In detail, the CHO cell membranes overexpressing hA₃AR were either pre-incubated with the indicated compound for 4 h, followed by a 0.5 h co-incubation or only co-incubated for 0.5 h with the radioligand [3 H]PSB-11. As detailed in Table 2, both compounds had comparable binding affinity in the low micromolar range (pK_i= 6.9 ± 0.06 for 17b and pK_i= 6.2 ± 0.03 for 19) at 0.5 h incubation time. However, compound 17b showed a significantly increased affinity (pK_i = 8.0 ± 0.01) when it was pre-incubated with hA₃AR, while the affinity of compound 19 did not change (pK_i= 6.1 ± 0.06).

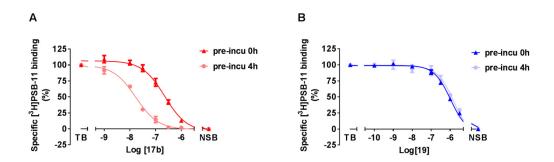


Figure 2. (A) Displacement of [3 H]PSB-11 binding from hA₃AR at 25°C by **17b** with and without a pre-incubation of 4 h. (B) Displacement of [3 H]PSB-11 binding from hA₃AR at 25°C by **19** with and without a pre-incubation of 4 h. Data represent the mean \pm SEM of three individual experiments performed in duplicate.

The effect of pre-incubation on the affinity of 17b and 19 is illustrated in Figure 2, i.e. the [3 H]PSB-11 displacement curve was shifted to the left with an increased incubation time for compound 17b (Figure 2A), while no difference was observed for compound 19 (Figure 2B). Presumably this time-dependent binding affinity of compound 17b (i.e. resulting from an increased receptor occupancy over time) is a result of an increasing level of covalent binding. Similar results on other GPCRs, such as β_2 adrenergic receptor [20] and A_{2A} adenosine receptor [21], showed that covalent bond formation generates an increased affinity over time. Meanwhile, control compound 19 showed no substantial pK_i shift in affinity at the two incubation times, indicating that a dynamic equilibrium was achieved at both incubation times. We can thus speculate that the possible covalent interaction between compound 17b and the receptor may be attributed to the presence of a reactive warhead. Finally, we tested 17b and 19 for their affinity on the other adenosine receptor subtypes, and learned that the two compounds were at least modestly selective for the hA₃AR (Table 2). Finally, we tested 17b and 19 for their affinity on the other adenosine receptor subtypes, and learned that the two compounds were at least modestly selective for the hA₃AR (Table 2).

Kinetic characterization of the covalent ligand. Subsequently, the significant shift in "apparent K_i " drove us to explore the binding kinetic profile of 17b at the hA₃AR, and specifically its dissociation rate and residence time (RT). Previously, the k_{on} (k_1 = 0.281 ± 0.04 ×10⁸ M⁻¹·min⁻¹) and k_{off} (k_2 = 0.3992 ± 0.02 min⁻¹) values of [³H]PSB-11 at 25 °C had been determined in our laboratory by traditional association and dissociation assays. Here we performed a competition association assay to characterize the binding kinetics of 17b and 19 following previously reported procedures from our research group [7]. Using the on- and off-rate constants from [³H]PSB, the k_{on} (k_3) and k_{off} (k_4) values for 17b were determined using the equations from the (equilibrium) Motulsky and Mahan model [22]. 17b had a much

slower association rate ($k_{on} = 3.48 \pm 0.22 \text{ x} 10^5 \text{ M}^{-1} \text{ min}^{-1}$) than the radioligand and a negligible dissociation rate ($k_{off} = 1.38 \pm 0.22 \text{ x} 10^{-12} \text{ min}^{-1}$), yielding an almost infinite residence time (RT = $7.63 \pm 1.19 \times 10^{11} \text{ min}$), indicative of irreversible receptor binding by **17b**. The inadequacy of the Motulsky-Mahan equations to fit this data is further evidence for the non-equilibrium features of the binding of **17b** to the receptor. Compound **19** showed fast association and dissociation rate constants (Figure 3). Unfortunately, the data did not converge in the fitting procedure, possibly due to the low binding affinity of compound **19** ($K_i = 525 \text{ nM}$).

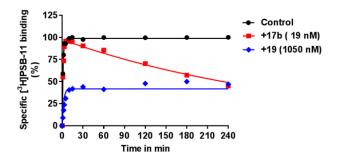


Figure 3. Competition association assay of [³H]PSB-11 in the absence (control) or presence of **17b** and **19** at the indicated concentration. Association and dissociation rate constants for the unlabeled ligands were calculated by fitting the data to the equations described in the experimental section ("data analysis"). Representative graphs are from one experiment performed in duplicate.

As detailed in Figure 3, the control curve represented the association curve of radioligand [³H]PSB-11 alone, approaching equilibrium over time. Compound **19** equally associated to and dissociated from the receptor and reached equilibrium within 30 min, evidenced by the same curve shape as the control curve. Of note, **17b**'s behavior caused an initial 'overshoot' of the competition association curve, followed by a linear decline over time indicating that no equilibrium was reached. The shape of **17b**'s kinetic curve is a quintessential example for the irreversible interaction, similar to the reported covalent ligands' behavior for the adenosine A_{2A} receptor [21] and mGlu2 receptor [23].

Wash-resistant interaction between 17b and hA_3AR . Inspired by the negligible dissociation of compound 17b from the hA₃AR, we performed a "washout" experiment to ascertain the irreversible binding between the ligand and receptor. A protocol previously reported by our laboratory [21] was adapted. We first exposed hA₃AR cell membranes to 17b or 19 both at

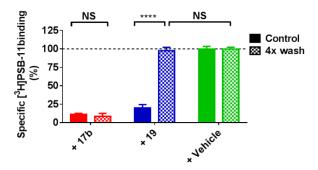


Figure 4. hA₃AR membranes pre-incubated with buffer (vehicle) or a $10 \times K_i$ concentration of indicated ligand, followed by no washing (Control) or four-cycle washing treatment (4x wash) before being exposed to [3 H]PSB-11. Data represent the mean \pm SEM of three individual experiments performed in duplicate, normalized to the vehicle (set at 100%). Statistics were determined using unpaired Student's t test. NS: no significant difference, **** P < 0.0001, significant difference between indicated groups.

10-fold K_i for 2 h, and without washing the samples were supplemented with [3 H]PSB-11 to assess the competitive binding capacity of the receptor ('Control group' in Figure 4). For washed samples, hA₃AR cell membranes were subjected to four-cycle washing steps to remove unbound ligand following the pre-incubation ('4x wash group' in Figure 4), after which the membranes were exposed to [3H]PSB-11 to determine the remaining binding capacity. In the absence of ligand (labeled '+ vehicle' in Figure 4), we normalized membranes' binding ability to 100%. Following preincubation with 17b, membranes containing the hA₃AR lost most of the ability to bind to the radioligand (11.3 \pm 1.2% binding remaining). Furthermore, after the pre-incubation, membranes were washed by cycles of centrifugation in an attempt to regenerate binding capacity. However, washing steps failed to restore hA₃AR binding of [3 H]PSB-11 (8.7 \pm 3.8%). This was in contrast to preincubation of the hA₃ARexpressing membranes with ligand 19, in which binding function was completely restored from $19.8 \pm 4.7\%$ to $97.6 \pm 4.5\%$ following four washing steps. This result indicates 19 is a reversible ligand which can be rapidly washed off the membranes, while 17b forms a washresistant bond between the ligand and the receptor. Similar experiments on other GPCRs, such as adenosine A₁ [24, 25] and A_{2A} [21] receptors and the metabotropic glutamate receptor 2 (mGluR2) [23], demonstrated that the covalent interaction between the ligand and the receptor resulted in a wash-resistant bond formation.

Insurmountable antagonism caused by covalent interaction. To further evaluate the effect of irreversible inhibition by covalent ligand 17b on receptor function, we performed a membrane functional assay using [35 S]GTP γ S, which is a typical readout for activation of receptor-coupled $G_{i/o}$ proteins [26].

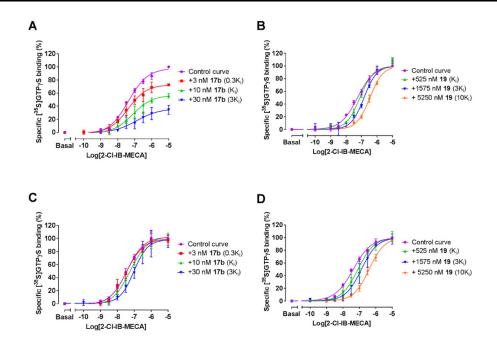


Figure 5. Effects of **17b** and **19** on hA₃AR activation as measured by [35 S]GTPγS binding. (A, B) Compound **17b** (A) or **19** (B) were pre-incubated with hA₃AR stably expressed on CHO cell membranes (25 °C) for 60 min prior to the addition of 2-Cl-IB-MECA at a concentration ranging from 0.1 nM to 10 μM for 30 min. (C, D) Compound **17b** (C) or **19** (D) were co-incubated with 2-Cl-IB-MECA, at a concentration ranging from 0.1 nM to 10 μM, for 30 min. The agonist curves were generated in the presence of increasing concentrations of antagonists, namely 0.3-, 1-, 3-, 10-fold their respective K_i values. Data are from three independent experiments performed in duplicate, normalized according to the maximal response (100%) produced by 10 μM 2-Cl-IB-MECA alone. The shift in agonist EC₅₀ values was determined to perform Schild analyses.

Pretreatment of hA₃AR with increasing concentrations of ligand 17b, prior to the stimulation with hA₃AR agonist 1-[2-chloro-6-[[(3-iodophenyl)methyl]amino]-9*H*-purin-9-yl]-1-deoxy-N-methyl- β -D-ribofuranuronamide (2-Cl-IB-MECA), produced rightward shifts of agonist concentration-response curves with a concomitant decline in maximal stimulation (Figure 5a). Therefore, the covalent ligand 17b generated insurmountable antagonism in the pre-incubation experiment. In contrast, pretreatment of hA₃AR with 19, followed by 2-Cl-IB-MECA agonist exposure resulted in surmountable antagonism (Figure 5b), i.e. shifting dose-response curves to the right with no alteration of its maximum effect. The extent of the shifts was used to construct a Schild plot as previously described [7], which would have a slope of unity if the interaction is competitive and the pA₂-value corresponds to the pK_i of the antagonist. The slope for 19 was found to be 1.1 \pm 0.1 and the compound's pA₂ value was 5.9 \pm 0.1, comparable with its pK_i value (6.3 \pm 0.03), suggesting that 19 competed with 2-Cl-IB-MECA for the same receptor binding site.

Table 3. Functional Analysis of hA₃AR Antagonism from [³⁵S]GTPγS Binding Assays

	Pre-incubation		Co-incubation		1 0	
compound	pA_2	Schild slope	pA_2	Schild slope	mode of antagonism	
17b	N.A.	N.A.	7.4 ± 0.1	1.1 ± 0.1	Competitive Insurmountable	
19	5.9 ± 0.1	1.1 ± 0.1	6.2 ± 0.1	1.0 ± 0.1	Competitive Surmountable	

Values represent mean \pm SEM of three separate experiments each performed in duplicate.

To unravel the molecular mechanism responsible for the insurmountable antagonism of 17b, we also co-incubated either 17b or 19 with hA₃AR in the presence of 2-Cl-IB-MECA. Both ligands produced a rightward shift of the agonist's concentration–response curve (Figure 5c and 5d) with no suppression of maximal response, indicative of surmountable antagonism. The Schild plot showed that both antagonists inhibited receptor activation in a competitive manner, with their Schild-slopes close to unity $(1.1 \pm 0.1 \text{ for } 17b, 1.0 \pm 0.1 \text{ for } 19$, Table 3). In addition, 19's pA₂ value was in agreement with that from the pre-incubation experiments $(6.2 \pm 0.1, \text{ Table } 3)$, and the pA₂ value of 17b was also comparable with its pK_i value $(7.4 \pm 0.1 \text{ vs } 8.0 \pm 0.05)$. Taken together, both ligands fully competed with 2-Cl-IB-MECA bound to hA₃AR. Notably, it is likely that the insurmountable behavior relates to covalent binding of 17b due to an irreversible blockade that reduces the total receptor population available.

Binding model for 17b in the hA_3AR receptor-binding pocket. To examine the interaction between receptor residues possibly involved in covalent binding, we docked 17b into a ligand optimized homology model on the basis of the A_{2A} receptor crystal structure (PDB: 4EIY [27]), as described previously [7]. As detailed in Figure 6, the core structure of compound 17b interacted with the TM3, TM6 and EL2 regions. Additionally, the carbonyl-oxygen at the C^4 -position participated in H-bond formation with residue $N250^{6.55}$ and the methoxyl moiety at the C^8 -position functioned as H-bond acceptor with $Q167^{EL2}$. Interestingly, the latter is a unique residue in hA_3AR , as it is not conserved in other subtypes of adenosine receptors. Due to the flexibility of the three-carbon linker, the tyrosine residue $Y265^{7.36}$ is in close proximity of the ligand, and could therefore interact with the 4-fluorosulfonylbenzoic warhead to form a covalent sulfonyl amide. Similarly, the same residue $Y271^{7.36}$ located within the human adenosine A_1 receptor has also been reported to covalently interact with the fluorosulfonyl warhead of compound 2 [11]. Comparison of the binding modes of compound 2 and ligand 17b in an A_1/A_3 receptor overlay showed that key interactions between ligands and binding sites are preserved, such as a hydrogen bond with $N^{6.55}$ (Figure S1).

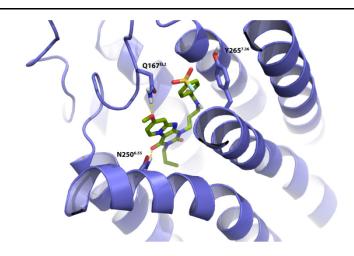


Figure 6. Proposed binding mode of compound **17b** (green carbon sticks) in a homology model (violet ribbons) of hA_3AR . The hA_3AR homology model was based on the high-resolution antagonist-bound crystal structure of the adenosine A_{2A} receptor (PDB: 4EIY [27]). Atoms color code: red = oxygen, blue = nitrogen, white = hydrogen, yellow = sulfur, cyan = fluorine. Hydrogen bonds between ligand and receptor are indicated by yellow dashed lines. Residue Y265^{7.36} is in the proximity of the fluorosulfonyl warhead.

Y265^{7.36} as an anchor point for the covalent bond. Based on the docking study, we postulated that Y265^{7.36} is the anchor point for covalent bond formation. To investigate our hypothesis this tyrosine was mutated to phenylalanine (hA₃AR-Y265F^{7.36}), to remove the nucleophilic reactivity of the phenolic hydroxyl group. First we performed standard [3H]PSB-11 displacement assays to investigate the binding affinity of 17b and 19 using CHO-K1 cell membranes transiently transfected with either wild type (hA₃AR-WT) or mutant receptors (hA₃AR-Y265F^{7.36}). As shown in Table 2 and Figure 7, the affinity of control compound 19 on hA₃AR-Y265F^{7.36} (pIC₅₀ = 6.09 ± 0.11) was similar to the affinity to hA₃AR-WT (pIC₅₀ = 5.95 ± 0.03), indicating that the mutation has no impact on the binding affinity of the reversible ligand. In marked contrast, 17b's affinity was decreased nearly 43-fold relative to WT, from an IC₅₀ value of 27 nM to 1072 nM, indicative of the loss of irreversible interaction. Moreover, there were no marked affinity differences on hA₃AR-Y265F^{7.36} between **17b** and 19. This suggests that the chemically dissimilar ligands 17b (reactive) and 19 (nonreactive) exhibit a similar binding interaction with hA₃AR-Y265F^{7.36}. We thus speculate the amino acid in position 7.36 plays a prominent role in the covalent bond formation between the fluorosulfonyl warhead and receptor. To support this idea, we repeated the "washout" assay on hA₃AR-Y265F^{7.36}. Membranes treated with **17b** at 10-fold IC₅₀ inhibited the specific [3 H]PSB-11 binding to 7.2 \pm 0.6%. After extensive washing, hA₃AR-Y265F^{7.36} showed a complete recovery of [3 H]PSB-11 binding to 91 \pm 2% (Figure 7c). This full recovery for mutant hA₃AR-Y265F^{7.36} is in sharp contrast to the findings in the wild type washout assay (Figure 4), indicating Y265F^{7.36} completely prevented the wash-resistant bond formation. In

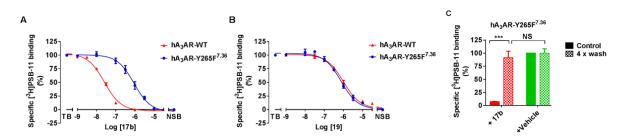


Figure 7. (A, B) Displacement of specific [3 H]PSB-11 binding from transiently transfected hA₃AR-WT and hA₃AR-Y265F^{7.36} at 25°C by compound **17b** (A) and **19** (B) during an incubation of 2 h. (C) hA₃AR-Y265F^{7.36} cell membranes were pretreated with buffer (vehicle) or $10 \times IC_{50}$ of compound **17b** for 2 h followed by no washing (Control) or four-cycle washing treatment (4x wash) before exposed to [3 H]PSB-11. Data represent the mean \pm SEM of three individual experiments performed in duplicate, normalized to the vehicle (set at 100%). NS: no significant difference between groups; ***Significant difference between groups (P<0.001); Student's *t*-test

other words Y265^{7.36} is the unique amino acid residue involved in the covalent attachment of 17b's fluorosulfonyl group within the hA₃AR binding pocket. A similar approach was also adopted to pinpoint the anchor point between covalent probes and other subtypes of GPCRs, such as the adenosine A2A receptor [21] mGlu2 receptor [23] and cannabinoid CB1 receptor [28]. 17b can be a useful structural biology tool as it would be expected to stabilize the 7TM domain in its inactive state, thereby potentially facilitating crystallization of receptor material. This could be highly valuable for the structure elucidation of hA₃AR which up to now remains unreported. Furthermore, understanding the precise molecular interactions between ligand and receptor may stimulate the more rational design of novel ligands. Such ligands may have improved receptor subtype selectivity, fewer undesirable side effects, and enhanced potency and efficacy, leading to potentially attractive therapeutic agents that produce their effects by modulating the functionality of the adenosine system. Given that GPCR-targeted covalent drugs went through clinical success across various indications,[29] our covalent compound 17b may serve as a probe to explore the problematic translation of hA₃AR ligands into clinical utility in certain disease states such as eye disorder glaucoma, in which an increased A₃ adenosine receptor mRNA and protein level have been detected.

3. Conclusions

By introducing a reactive sulfonyl fluoride warhead onto the 1-benzyl-3-propyl-1*H*,3*H*-pyrido [2,1-*f*]purine-2,4-dione scaffold, we designed and synthesized a series of novel covalent hA₃AR antagonists. Compound **17b** acted as the most potent antagonist, with a time dependent apparent affinity in the low nanomolar range. Meanwhile, we removed the warhead and inserted a methylsulfonyl moiety into the scaffold, to obtain ligand **19** as a reversible control compound. Ligand **17b** was then validated as covalent antagonist through its wash-

resistant nature and insurmountable antagonism in [35S]GTPyS binding assays. *In silico* homology-docking suggested that Y265^{7,36} is responsible for the covalent interaction. Site-directed mutagenesis showed that removal of the nucleophilic tyrosine phenolic hydroxyl group resulted in the complete loss of covalent binding, validating that Y265^{7,36} is the only anchor point of reactive covalent ligand **17b**. The results contribute to a better understanding of pharmacological behaviors caused by covalent interaction with GPCRs. In the end, we developed a structured approach to quickly obtain a well-defined covalent ligand. Besides, we envisioned that a methylsulfonyl replacement would be suitable for providing a non-reactive sulfonyl-bearing control compound. The rational design of covalent probes may have further value in receptor structure elucidation or in new technologies such as affinity-based protein profiling [15, 30] with the perspective of imaging or structurally probing GPCRs.

4. Experimental Section

4.1. Chemistry All solvents and reagents were purchased from commercial sources and were of analytical grade. Demineralized water is simply referred to as H₂O, and was used in all cases unless stated otherwise (i.e. brine). ¹H were recorded on a Bruker AV 400 liquid spectrometer (¹H NMR, 400 MHz) at ambient temperature and ¹³C NMR spectra was performed on a Bruker AV 600 liquid spectrometer (13C NMR, 125 MHz) at indicated temperature. Chemical shifts are reported in parts per million (ppm), using residual solvent as the internal reference in all cases. The values are given in δ scale. Coupling-constants are reported in Hz and are designated as J. Analytical purity of the final compounds was determined by high performance liquid chromatography (HPLC) with a Phenomenex Gemini 3μ m C18 110Å column (50 × 4.6 mm, 3 μm), measuring UV absorbance at 254 nm. Sample preparation and HPLC method was as follows: 0.3-1.0 mg of compound was dissolved in 1 mL of a 1:1:1 mixture of MeCN/H₂O/tBuOH and eluted from the column within 15 minutes at a flow rate of 1.3 mL/min with a three component system of H₂O/MeCN/1% TFA in H₂O. The elution method was set up as follows: 1-4 min isocratic system of H₂O/MeCN/1% TFA in H₂O, 80:10:10, from the 4th min, a gradient was applied from 80:10:10 to 0:90:10 within 9 min, followed by 1 min of equilibration at 0:90:10 and 1 min at 80:10:10. All final compounds showed a single peak at the designated retention time and are at least 95% pure. Liquid chromatography—mass spectrometry (LC-MS) analyses were performed using Thermo Finnigan Surveyor - LCQ Advantage Max LC-MS system and a Gemini C18 Phenomenex column (50 × 4.6 mm, 3 µm). High resolution mass spectrometry (HRMS) analyses were performed using a Thermo ScientificTM LTQ Orbitrap XLTM Hybrid Ion Trap-Orbitrap Mass Spectrometer. The sample preparation was the same as for HPLC and HRMS analysis. The compounds were eluted from the column within 15 minutes after injection, with a three component system of H₂O/MeCN/0.2% TFA in H₂O, decreasing polarity of the solvent mixture in time from 80:10:10 to 0:90:10. Thin-layer chromatography (TLC) was routinely consulted to monitor the progress of reactions, using aluminum coated Merck silica gel F254 plates. Purification by column chromatography was achieved by use of Grace Davison Davisil silica column material (LC60A 30-200 micron). Solutions were concentrated using a Heidolph Laborota W8 2000 efficient rotary evaporation apparatus. All reactions in the synthetic routes were performed under nitrogen atmosphere unless stated otherwise. The procedure for a series of similar compounds is given as a general procedure for all within that series, annotated by the numbers of the compounds.

1-benzyl-8-methoxy-3-propyl-1*H*,3*H*-pyrido[2,1-*f*]purine-2,4-dione (1) [7, 8]. To a stirred suspension of **6** (6.0 g, 19 mmol, 1.0 equiv) in MeCN (120 mL) were added 1-bromopropane (5.6 mL, 57mmol, 3.0 equiv) and DBU (50 mL, 57 mmol, 3.0 equiv). This mixture was stirred at 70 °C overnight. Conversion of starting material was confirmed by TLC (2% MeOH in CH₂Cl₂) and the solvent was removed under vacuum. The residue was suspended in CH₂Cl₂ (200 mL) and the organic phase was washed with 1M HCl (200 mL), H₂O (200 mL), brine (200 mL) and dried over MgSO₄, filtered and concentrated *in vacuo*. The crude was purified by column chromatography (0.5% MeOH in CH₂Cl₂) to obtain **1** as a white solid (5.0 g, 14 mmol, 73%). ¹H NMR (400 MHz, CDCl₃): δ 8.82 (d, J = 7.6 Hz, 1H), 7.58 – 7.51 (m, 2H), 7.34 – 7.22 (m, 3H), 6.98 (d, J = 2.0 Hz, 1H), 6.74 (dd, J = 7.4, 2.2 Hz, 1H), 5.36 (s, 2H), 4.04 – 3.97 (m, 2H), 3.92 (s, 3H), 1.76 – 1.65 (m, 2H), 0.97 (t, J = 7.4 Hz, 3H)

6-amino-1-benzyl-1,3-dihydropyrimidine-2,4-dione (5)[7, **8**]. The synthesis of the compounds adapted from the procedure reported before [7, 8]. Benzylurea **(3)** (25 g, 167 mmol, 1.0 equiv) and **4** (16 g, 191 mmol, 1.1 equiv) were dissolved in acetic anhydride (100 mL). This mixture was stirred at 80 °C for 2 h. After the mixture was cooled to room temperature, diethyl ether (150 mL) was added followed by 1 hour of stirring at room temperature. The precipitate was filtered off and suspended in a mixture of EtOH (75 mL) and H₂O (150 mL). This mixture was heated to 85 °C and 3 M NaOH (aq.) (50 mL) was added dropwise. After 1 h, the mixture was concentrated and neutralized dropwise with HCl (37 %). The precipitate was filtered off and washed with acetone, obtaining **5** as a white solid (9.0 g, 42 mmol, 25%). ¹H NMR (400 MHz, DMSO-*d*₆): δ 10.42 (brs, 1H), 7.48 – 7.08 (m, 5H), 6.85 (brs, 2H), 5.03 (s, 2H), 4.60 (s, 1H)

1-benzyl-8-methoxy-1*H*,3*H*-pyrido[2,1-*f*]purine-2,4-dione (6) [7, 8]. To the intermediate (5) (9.0 g, 42 mmol, 1.0 equiv) and NBS (15 g, 83 mmol, 2.0 equiv) was added MeCN (100 mL). This mixture was stirred at 80 °C. After 1.5 h conversion of starting material was confirmed by TLC (10% MeOH in CH₂Cl₂), 4-methoxypyridine (13 g, 125 mmol, 3.0 equiv) was added and the reaction mixture was stirred at 80 °C for 4.5 h. After cooling to room temperature, the precipitate was filtered off and washed with diethyl ether and MeOH, yielding product **6** as a white solid (8.5 g, 26 mmol, 64%). ¹H NMR (400 MHz, DMSO- d_6): δ 11.31 (br s, 1H), 8.70 (d, J = 7.2 Hz, 1H), 7.38 – 7.16 (m, 6H), 6.90 (dd, J = 7.4, 2.2 Hz, 1H), 5.18 (s, 2H), 3.89 (s, 3H)

8-methoxy-3-propyl-*1H*,3*H*-**pyrido**[2,1-*f*]**purine-2**,4-**dione** (7) [7, 8]. To a mixture of the intermediate 1 (1.1 g, 3.0 mmol, 1.0 equiv), Pd(OH)₂/C (2.0 g, 14 mmol, 1.0 equiv) and ammonium formate (0.20 g, 3.0 mmol, 1.0 equiv) was added EtOH (250 mL). During the reaction, five portions of ammonium formate (0.20 g, 3.0 mmol, 1.0 equiv) was added, after which completion of the reaction was observed on TLC (5% MeOH in CH₂Cl₂). The reaction was filtered over Celite and the residue was extracted with hot DMF. Purification of the crude product by column chromatography using 2-10% MeOH in CH₂Cl₂ to obtained **5** as a white solid (0.30 g, 1.2 mmol, 40%). ¹H NMR (400 MHz, DMSO- d_6): δ 12.05 (s, 1H), 8.73 (d, J = 7.2 Hz, 1H), 7.12 (d, J = 2.0 Hz, 1H), 6.89 (dd, J = 7.4, 2.6 Hz, 1H), 3.90 (s, 3H), 3.85 – 3.78 (m, 2H), 1.64 – 1.52 (m, 2H), 0.88 (t, J = 7.4 Hz, 3H)

General procedure for the synthesis of fluorosulfonylbenzoic acids (9a–b). To a solution of chlorosulfonylbenzoic acid (8a-b) (2.2 g, 10 mmol, 1.0 equiv) in dioxane (25 mL) was added a solution of HF:KF (15 mL, 2.0 M, 3.0 equiv). The mixture was stirred at room temperature. After 1 h, the reaction mixture was dilute with EtOAc (80 mL). The organic phase was washed with H₂O (50 mL), dried over MgSO₄, filtered and concentrated *in vacuo*.

3-(fluorosulfonyl)benzoic acid (9a). White solid (1.9 g, 8.7 mmol, 87%). ¹H NMR (400MHz, DMSO- d_6): δ 8.47-8.44 (m, 2H), 8.4 (d, J = 8.0 Hz, 1H), 7.94 (t, J = 7.6 Hz, 1H).

4-(fluorosulfonyl)benzoic acid (9b). White solid (2.0 g, 9.0 mmol, 90%). ¹H NMR (400 MHz, DMSO- d_6): δ 13.86 (s, 1H), 8.28 (s, 4H)

General procedure for the synthesis of bromoalkyl (fluorosulfonyl)benzoates (11a-c and 12a-c) A mixture of thionyl chloride (8 mL) and fluorosulfonylbenzoic acid (9a-b) (1 equiv) was refluxed at 75 °C for 3 h. The solvent was removed under vacuum. And the product was used in the next step without further analysis. Dry dioxane (6 mL) was added to the (fluorosulfonyl)benzoyl chloride (10a-b). To this solution the corresponding bromoalkylalcohol (0.85 equiv) was added and the mixture was refluxed overnight. After

completion was observed on TLC (CH₂Cl₂) the volatiles were removed *in vacuo* and the crude product was purified by column chromatography using CH₂Cl₂ as an eluent to afford the products.

2-bromoethyl-4-(fluorosulfonyl)benzoate (11a) Colorless oil (0.088 g, 0.28 mmol, 23%) 1 H NMR (400 MHz, DMSO- d_6): δ 8.31 (d, J = 8.2 Hz, 2H), 8.11 (d, J = 8.5 Hz, 2H), 4.69 (t, J = 5.9 Hz, 2H), 3.67 (t, J = 5.9 Hz, 2H).

3-bromopropyl-4-(fluorosulfonyl)benzoate (11b) White solid (2.0 g, 6.2 mmol, 50%) 1 H NMR (400 MHz, CDCl₃): δ 8.27 (d, J = 8.4 Hz, 2H), 8.09 (d, J = 8.4 Hz, 2H), 4.54 (t, J = 6.0 Hz, 2H), 3.54(d, J = 6.4 Hz, 2H), 2.35 (m, 2H).

4-bromobutyl-4-(fluorosulfonyl)benzoate (11c) White solid (0.30 g, 0.89 mmol, 45%) Compound was used without further purification.

2-bromoethyl-3-(fluorosulfonyl)benzoate (12a). Colorless Oil (0.51 g, 1.7 mmol, 55%) 1 H NMR (400 MHz, CDCl₃): δ 8.69 (s, 1H), 8.47 (d, J = 7.6 Hz, 1H), 8.25 – 8.20 (m, 1H), 7.78 (t, J = 8.0 Hz, 1H), 4.71 (t, J = 6.0 Hz, 2H), 3.68 (t, J = 6.0 Hz, 2H).

3-bromopropyl-3-(fluorosulfonyl)benzoate (12b).Colorless oil (0.12 g, 0.38 mmol, 23%) 1 H NMR (400 MHz, CDCl₃) δ 8.65 (t, J = 1.6 Hz, 1H), 8.44 (d, J = 7.8 Hz, 1H), 8.21 (d, J = 8.0 Hz, 1H), 7.76 (t, J = 7.9 Hz, 1H), 4.55 (t, J = 6.1 Hz, 1H), 3.55 (t, J = 6.4 Hz, 1H), 2.37 (p, J = 6.3 Hz, 1H).

4-bromobutyl-3-(fluorosulfonyl)benzoate (12c). Colorless Oil (0.84 g, 2.5 mmol, 83%,) 1 H NMR (400 MHz, CDCl₃): δ 8.65 (s, 1H), 8.45 (d, J = 8.0 Hz, 1H), 8.21 (d, J = 8.0 Hz, 1H), 7.78 (t, J = 7.6 Hz, 1H), 4.44 (t, J = 6.0 Hz, 2H), 3.50 (t, J = 6.4 Hz, 2H), 2.11 – 1.85 (m, 4H).

General procedure for the synthesis of 13a-c and 14a-c

The synthesis of these compounds were adapted from the conditions previously described by Priego et al [6]. The scaffold, 8-methoxy-3-propyl-1H,3H-pyrido[2,1-f]purine-2,4-dione 7 (1.0 equiv), and K₂CO₃ (1.6 equiv) were suspended in anhydrous DMF. The mixture was added dropwise to stirred solution of the corresponding bromoalkyl a (fluorosulfonyl)benzoate (11a-c or 12a-c) (1.0 equiv) in anhydrous DMF (4 mL). The reaction was stirred at 50 °C overnight. After conversion on TLC was observed, excess amount of CH₂Cl₂ was added. Then the mixture was washed with 1M HCl (aq.), water and brine. The organic layer was dried over MgSO₄, filtered and concentrated in vacuo. The crude product was purified by column chromatography, followed to a prep TLC was used to further purify the compound if necessary.

2-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purine-1(2H)-yl)ethyl 4-(fluorosulfonyl)benzoate (13a) Prepared from 11a and purified by column chromatography

(1% CH₃OH in CH₂Cl₂) to give the desired product as white solid (0.038 g, 0.07 mmol, 52%). ¹H NMR (400 MHz, CDCl₃): δ 8.80 (d, J = 8.0 Hz, 1H), 8.17 (d, J = 8.0 Hz, 2H), 7.98 (d, J = 8.4 Hz, 2H), 6.76-6.73 (m, 2H), 4.78 (t, J = 4.8 Hz, 2H), 4.64 (t, J = 5.2 Hz, 2H), 4.00 (t, J = 7.6 Hz, 2H), 3.89 (s, 3H), 1.73-1.62 (m, 2H), 0.95 (t, J = 7.2 Hz, 3H). MS: [ESI+H]⁺: 505.1. HPLC: 9.99 min

- **3-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-***f***]purine-1(2***H***)-yl)propyl 4-(fluorosulfonyl)benzoate (13b)** Prepared from **11b** and purified by column chromatography (1% CH₃OH in CH₂Cl₂) to give the desired product as white solid (0.096 g, 0.19 mmol, 76%). ¹H NMR (400 MHz, CDCl₃): δ 8.76 (d, J = 7.2 Hz, 1H), 8.23 (d, J = 8.0 Hz, 2H), 8.06 (d, J = 8.4 Hz, 2H), 6.77 (d, J = 2.4 Hz, 1H), 6.73 (dd, J = 7.2, 2.4 Hz, 1H), 4.50 (t, J = 6.0 Hz, 2H), 4.41 (t, J = 6.8 Hz, 2H), 4.00 (t, J = 7.2 Hz, 2H), 3.90 (s, 3H), 2.38 (pentet, J = 6.0 Hz, 2H), 1.71 (sextet, J = 7.2 Hz, 2H), 0.99 (t, J = 7.6 Hz, 3H). MS: [ESI+H]⁺: 519.1. HPLC: 10.18 min
- **4-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purine-1(2H)-yl)butyl 4-(fluorosulfonyl)benzoate(13c)** Prepared from **11c** and purified by column chromatography (2% CH₃OH in CH₂Cl₂) to give the desired product as white solid (0.010 g, 0.019 mmol, 5.2%.) ¹H NMR (400 MHz, CDCl₃): δ 8.83 (dd, J = 7.6, 0.8 Hz, 1H), 8.27 (d, J = 8.0 Hz, 2H), 8.07 (d, J = 8.8 Hz, 2H), 6.93 (d, J = 2.4 Hz, 1H), 6.76 (dd, J = 7.6, 2.4 Hz, 1H), 4.46 (t, J = 6.4 Hz, 2H), 4.28 (t, J = 6.8 Hz, 2H), 4.02 (t, J = 7.2 Hz, 2H), 3.93 (s, 3H), 2.05 1.90 (m, 4H), 1.77 1.68 (m, 2H), 0.99 (t, J = 7.2 Hz, 3H). MS: [ESI+H]⁺: 533.1. HPLC: 9.40 min
- **2-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purine-1(2H)-yl)ethyl 3-** (fluorosulfonyl)benzoate (14a) Prepared from 12a and without purification to give the desired product as white solid (0.19 g, 0.36 mmol, 57%). ¹H NMR (400 MHz, CDCl₃)): δ 8.80 (d, J = 7.2 Hz, 1H), 8.51 (s, 1H), 8.36 (d, J = 7.6 Hz, 1H), 8.14 8.09 (m, 1H), 7.66 (t, J = 7.8 Hz, 1H), 6.84 (d, J = 2.4 Hz, 1H), 6.74 (dd, J = 7.6, 2.6 Hz, 1H), 4.78 (t, J = 4.8 Hz, 2H), 4.65 (t, J = 4.8 Hz, 2H), 4.04 3.97 (m, 2H), 3.90 (s, 3H), 1.68 (sextet, J = 7.6 Hz, 2H), 0.96 (t, J = 7.4 Hz, 3H). MS: [ESI+H]⁺: 505.1. HPLC: 8.47 min
- **3-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purine-1(2H)-yl)propyl 3-(fluorosulfonyl)benzoate (14b)** Prepared from **12b** and purified by column chromatography (1% CH₃OH in CH₂Cl₂) to give the desired product as white solid (0.035 g, 0.068 mmol, 34%). ¹H NMR (400 MHz, CDCl₃): δ 8.74 (d, J = 7.6 Hz, 1H), 8.65 (s, 1H), 8.36 (d, J = 8.0 Hz, 1H), 8.18 (d, J = 8.0 Hz, 1H), 7.73 (t, J = 8.0 Hz, 1H), 6.86 (d, J = 2.0 Hz, 1H), 6.72 (dd, J = 7.2, 2.4 Hz, 1H), 4.51 (t, J = 6.0 Hz, 2H), 4.41 (t, J = 6.0 Hz, 2H), 3.99 (t, J = 7.6 Hz, 2H),

3.91 (s, 3H), 2.39 (pentet, J = 6.0 Hz, 2H), 1.70 (sextet, J = 7.6 Hz, 2H), 0.98 (t, J = 7.6 Hz, 3H). MS: $[ESI+H]^+$: 519.1. HPLC: 8.84 min

4-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purine-1(2H)-yl)butyl **3-(fluorosulfonyl)benzoate**(14c) Prepared from 12c and purified by column chromatography (first 30% DCM in EtOAc). Further purification by another column (4:1= MTBE: PET) gives the desired product as white solid (0.20g, 0.37 mmol, 38%). ¹H NMR (400 MHz, CDCl₃): δ 8.85 (d, J = 7.2 Hz, 1H), 8.67 (s, 1H), 8.45 (d, J = 8.0 Hz, 1H), 8.21 (d, J = 8.0 Hz, 1H), 7.75 (t, J = 8.0 Hz, 1H), 6.97 (d, J = 2.4 Hz, 1H), 6.77 (dd, J = 7.2, 2.4 Hz, 1H), 4.49 (t, J = 6.4 Hz, 2H), 4.30 (t, J = 7.2 Hz, 2H), 4.08 – 4.01 (m, 2H), 3.95 (s, 3H), 2.10 – 2.00 (m, 2H), 2.00 – 1.89 (m, 2H), 1.81 – 1.69 (m, 2H), 1.01 (t, J = 7.2 Hz, 3H). MS: [ESI+H]⁺: 533.1. HPLC: 9.14 min

General procedure for the synthesis 1-(2-(1,3-dioxoisoindolin-2-yl)alkyl)-8-methoxy-3-propyl-1*H*,3*H*-pyrido-[2,1-*f*]purine-2,4-dione (15a-c). To a mixture of the core (7) (0.8 mmol, 1 equiv), *N*-(bromoalkyl)phthalimide (1.2 mmol, 1.5 equiv) and K₂CO₃ (1.2 mmol, 1.5 equiv) was added anhydrous DMF (8 mL). The mixture was refluxed at 100 °C. After completion of the reaction, monitored by TLC (1% MeOH in CH₂Cl₂), the mixture was concentrated *in vacuo* and diluted with EtOAc (30 mL). The organic layer was washed with H₂O (3 × 30 mL), brine (15 mL) and dried over MgSO₄. The solvent was evaporated under reduced pressure, and the residue was purified by column chromatography using 1% MeOH as an eluent to give **15a–c** as solids.

1-(2-(1,3-dioxoisoindolin-2-yl)ethyl)-8-methoxy-3-propyl-1*H***,3***H***-pyrido-[2,1-***f*]**purine-2,4-dione (15a)** Prepared from *N*-(2-bromoethyl)phthalimide and purified by column chromatography to give the desired product as white solid (0.20 g, 0.44 mmol, 5%). ¹H NMR (CDCl₃): δ 8.77 (d, J = 6.8 Hz, 1H), 7.73 (s, 2H), 7.64 (s, 2H), 6.69 (d, J = 14.0 Hz, 2H), 4.53 (s, 2H), 4.17 (s, 2H), 3.89 (d, J = 6.2 Hz, 2H), 3.85 (s, 3H), 1.58 – 1.45 (m, 3H), 0.86 (t, J = 7.2 Hz, 3H).

1-(2-(1,3-dioxoisoindolin-2-yl)propyl)-8-methoxy-3-propyl-1*H*,3*H*-pyrido-[2,1-*f*]purine-**2,4-dione** (**15b**) Prepared from *N*-(3-bromoethyl)phthalimide and purified by column chromatography to give the desired product as yellow solid (0.31 g, 0.66 mmol, 66%). ¹H NMR (400 MHz, CDCl₃): δ 8.81 – 8.75 (m, 1H), 7.86 – 7.76 (m, 2H), 7.73 – 7.61 (m, 2H), 6.80 (s, 1H), 6.72 (dd, J = 7.2, 2.4 Hz, 1H), 4.29 (t, J = 6.8 Hz, 2H), 4.04 – 3.93 (m, 2H), 3.90 (s, 3H), 3.86 – 3.78 (m, 2H), 2.35 – 2.20 (m, 2H), 1.78 – 1.60 (m, 2H), 1.06 – 0.87 (m, 3H). **1-(2-(1,3-dioxoisoindolin-2-yl)butyl)-8-methoxy-3-propyl-1***H*,3*H*-pyrido-[2,1-*f*]purine-**2,4-dione** (**15c**) Prepared from *N*-(4-bromoethyl)phthalimide and purified by column

chromatography to give the desired product as white solid (0.37 g, 0.76 mmol, 96%). 1 H NMR (400 MHz, CDCl₃): δ 8.82 (d, J = 7.2 Hz, 1H), 7.82 (dd, J = 5.2, 2.8 Hz, 2H), 7.70 (dd, J = 5.2, 2.8 Hz, 2H), 6.93 (d, J = 2.4 Hz, 1H), 6.74 (dd, J = 7.2, 2.4 Hz, 1H), 4.22 (d, J = 7.2 Hz, 2H), 4.04 – 3.96 (m, 2H), 3.92 (s, 3H), 3.75 (d, J = 7.2 Hz, 2H), 1.95 – 1.85 (m, 2H), 1.85 – 1.77 (m, 2H), 1.74 – 1.65 (m, 3H), 0.97 (d, J = 7.6 Hz, 3H).

General procedure for the synthesis 1-(2-aminoalkyl)-8-methoxy-3-propyl-1*H*,3*H*-pyrido-[2,1-*f*]purine-2,4-dione (16a-c). To a stirred suspension of 15a-c (0.66 mmol, 1 equiv) in MeOH (8 mL) was added excess hydrazine monohydrate (4.8 mL, 99 mmol). The mixture was stirred for 2–4 h at reflux. After conversion of the starting material, the mixture was cooled to room temperature. The solvents were removed under vacuum and the residue was dissolved in 2 M NaOH (aq.) (25 mL). This aques phase was extracted three times with CH₂Cl₂ (25 mL). The organic layers were combined, dried over MgSO₄ and concentrated *in vacuo* to obtain 16a-c.

1-(2-aminoethyl)-8-methoxy-3-propyl-1*H*,3*H*-pyrido-[2,1-*f*]purine-2,4-dione (16a).

Prepared from **15a** and purified by column chromatography to give the desired product as white solid (0.13 g, 0.39 mmol, 90%). ¹H NMR (400 MHz, CDCl₃): δ 8.84 (d, J = 7.6 Hz, 1H), 6.95 (d, J = 2.4 Hz, 1H), 6.75 (dd, J = 7.2, 2.4 Hz, 1H), 4.27 (t, J = 6.4 Hz, 2H), 4.05 – 3.99 (m, 2H), 3.93 (s, 3H), 3.15 (t, J = 6.4 Hz, 2H), 1.78 – 1.67 (m, 2H), 0.99 (d, J = 7.6 Hz, 3H).

1-(3-aminopropyl)-8-methoxy-3-propyl-1*H*,3*H*-pyrido-[2,1-*f*]purine-2,4-dione (16b).

Prepared from **15b** and purified by column chromatography to give the desired product as white solid (0.25 g, 0.75 mmol, 97%). ¹H NMR (400 MHz, CDCl₃): δ 8.82 (d, J = 7.2 Hz, 1H), 6.95 (d, J = 2.4 Hz, 1H), 6.75 (dd, J = 7.6, 2.4 Hz, 1H), 4.29 (t, J = 6.8 Hz, 2H), 4.07 – 3.98 (m, 2H), 3.93 (s, 3H), 2.75 (t, J = 6.6 Hz, 2H), 1.98 (p, J = 6.6 Hz, 2H), 1.78 – 1.65 (m, 2H), 0.99 (t, J = 7.4 Hz, 3H).

1-(4-aminobutyl)- 8-methoxy-3-propyl-1H,3H-pyrido-[2,1-f]purine-2,4-dione (16c).

Prepared from **15c** and purified by column chromatography to give the desired product as white solid (0.23 g, 0.66 mmol, 86%). ¹H NMR (400 MHz, CDCl₃): δ 8.84 (d, J = 7.6 Hz, 1H), 6.97 (d, J = 2.4 Hz, 1H), 6.75 (dd, J = 7.2, 2.4 Hz, 1H), 4.20 (t, J = 7.2 Hz, 2H), 4.06 – 3.98 (m, 2H), 3.92 (s, 3H), 2.77 (d, J = 6.8 Hz, 2H), 1.92 – 1.82 (m, 2H), 1.78 – 1.66 (m, 2H), 1.63 – 1.53 (m, 2H), 0.99 (t, J = 7.2 Hz, 3H).

4-((2-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purin-1(2H)-

yl)ethyl)carbamoyl)benzenesulfonyl fluoride (17a) EDC (0.12 g, 0.60 mmol, 1.2 equiv) was dissolved in CHCl₃ (4 mL). To this stirring solution was added the acid (9a) (0.11g, 0.55 mmol, 1.1 equiv). The amine (16a) (0.16 g, 0.50 mmol, 1.0 equiv) was suspended in CHCl₃ (6

mL), then was added dropwise via an automatic syringe at a rate of 0.2 mL/min. The reaction was stirred for 1.5 h at room temperature and monitored by TLC (CH₂Cl₂: acetone = 3:2). After completion the solvent was removed under vacuum and the residue was redissolved in CHCl₃ (40 mL). The organic layer was washed with 1 M HCl (40 mL), H₂O (2 × 40 mL), dried over MgSO₄ and concentrated *in vacuo* to obtain **17a** as white solid (0.20 g, 0.39 mmol, 78%). ¹H NMR (400 MHz, CDCl₃): δ 8.83 (d, J = 7.2 Hz, 1H), 8.07 – 8.00 (m, 5H), 6.91 (d, J = 2.4 Hz, 1H), 6.80 (dd, J = 7.2, 2.0 Hz, 1H), 4.62 – 4.55 (m, 2H), 4.03 (t, J = 7.6 Hz, 2H), 3.95 (s, 3H), 3.94 – 3.89 (m, 2H), 1.68 (sextet, J = 7.6 Hz, 2H), 0.97 (t, J = 7.2 Hz, 3H). MS: [ESI+H]⁺: 504.1. HPLC: 7.93 min.

4-((3(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purin-

1(2H)yl)propyl)carbamoyl)benzenesulfonyl fluoride (17b). To a suspension of EDC (0.22 g, 0.80 mmol, 1.5 equiv) and 9a (0.16 g, 0.80 mmol 1.05 equiv) was dissolved in CH₂Cl₂ (4 mL). To this stirring solution was added the amine (16b) (0.25 g, 0.76 mmol, 1.0 equiv) at room temperature. The reaction was stirred for 2 h and monitored by TLC (3% MeOH in CH₂Cl₂). After completion, the solvent was removed in vacuo and the residue was dissolved in CHCl₃ (40 mL). The organic layer was washed with 1 M HCl (40 mL), twice with H₂O (2 × 40 mL), dried over MgSO₄ and concentrated *in vacuo*. The product was purified by column chromatography using 2% MeOH in CH₂Cl₂ to afford the title compound as white solid (0.26 g, 0.50 mmol, 66%). ¹H NMR (400MHz, CDCl₃) δ : 8.86 (d, J = 7.2 Hz, 1H), 8.38 (t, J = 5.6Hz, 1H), 8.25 (d, J = 8.4 Hz, 2H), 8.16 (d, J = 8.4 Hz, 2H), 6.85 (d, J = 2.4 Hz, 1H), 6.81 (dd, J = 7.2, 2.4 Hz, 1H), 4.35 (t, J = 6.0 Hz, 2H), 4.05 (t, J = 7.6 Hz, 2H), 3.92 (s, 3H), 3.47 (q, J= 6.4 Hz, 2H), 2.19–2.13 (m, 2H), 1.73 (sextet, J = 7.6 Hz, 2H), 1.00 (t, J = 7.6 Hz, 3H). ¹³C NMR (600 MHz, DMSO-d₆, 348K) δ 164.0, 160.9, 153.4, 150.6, 150.5, 149.1, 141.3, 133.3 (d, J = 96 Hz), 128.5, 127.9, 127.3, 107.0, 99.8, 95.4, 55.7, 41.5, 40.6, 36.8, 27.1, 20.5, 10.6.MS: [ESI+H]⁺: 518.1. HRMS-ESI⁺: [M + H] ⁺ calcd: 518.1510 found: 518.1540, C23H25O6N5FS. HPLC: 8.27 min.

4-((4-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purin-1(2H)-

yl)butyl)carbamoyl)benzenesulfonyl fluoride (17c) The acid 9a (0.11 g, 0.53 mmol, 1.5 equiv) was dissolved in an excess of thionyl chloride (20 mL) at 75 °C under nitrogen for 3 h. After removal of solvent and other volatiles in vacuum, 10a was obtained as colorless oil. Subsequently the amine 16c (0.12 g, 0.35 mmol, 1.0 equiv), K₂CO₃ (0.073 g, 0.53 mmol, 1.5 equiv)) and dry DMF were added and the reaction as stirred at 40 °C overnight. After completion of the reaction, 1M HCl (200 mL) was added and extracted with CH₂Cl₂ (150 mL). The organic layer was washed with water (100 mL) and brine (100 mL). The organic layer

was dried, filtered and concentrated *in vacuo*. The residue was purified by column chromatography using CH₂Cl₂ with 1% methanol as eluent to give **17c** as white solid (5.0 mg, 0.0094 mmol, 4%). ¹H NMR (400 MHz, CDCl₃): δ 8.87 (d, J = 7.6 Hz, 1H), 8.17 (d, J = 8.4 Hz, 2H), 8.09 (d, J = 8.4 Hz, 2H), 7.54 (brs, 1H), 6.85 (s, 1H), 6.80 (dd, J = 7.2, 2.4 Hz, 1H), 4.29 (t, J = 7.6 Hz, 2H), 4.06 (t, J = 7.6 Hz, 2H), 3.92 (s, 3H), 3.68 (q, J = 6.0 Hz, 2H), 2.01 (pent, J = 6.8 Hz, 2H), 1.84-1.70 (m, 4H), 1.02 (t, J = 7.6 Hz, 3H). MS: [ESI+H]⁺: 532.3 . HPLC: 8.28 min.

3-((2-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purin-1(2H)-

yl)ethyl)carbamoyl)benzenesulfonyl fluoride (18a) EDC (0.12 g, 0.60 mmol, 1.2 equiv) was dissolved in CHCl₃ (4 mL). To this stirring solution was added the acid 9b (0.11 g, 0.55 mmol, 1.1 equiv). The amine 16a (0.16 g, 0.50 mmol, 1.0 equiv) was suspended in CHCl₃ (6 mL), then was added dropwise via an automatic syringe at a rate of 0.2 mL/min. The reaction was stirred for 3 h at room temperature and monitored by TLC (CH₂Cl₂: Acetone = 3:2). After completion, the solvent was removed *in vacuo* and the residue was resolubilized in CHCl₃ (40 mL). The organic layer was washed with 1 M HCl (40 mL), twice with H₂O (2 × 40 mL), dried over MgSO₄ and concentrated *in vacuo* to give 18a as white solid (0.17g, 0.35 mmol, 70%). ¹H NMR (400 MHz, CDCl₃): δ 8.81 (d, J = 7.6 Hz, 1H), 8.37 (s, 1H), 8.29 (d, J = 8.0 Hz, 1H), 8.11 (d, J = 7.6 Hz, 1H), 8.04 (br s, 1H), 7.71 (t, J = 8.0 Hz, 1H), 7.02 (d, J = 2.4 Hz, 1H), 6.77 (dd, J = 7.6, 2.4 Hz, 1H), 4.61 – 4.54 (m, 2H), 4.03 (t, J = 7.6 Hz, 2H), 3.96 (s, 3H), 3.94 – 3.89 (m, 2H), 1.76 – 1.63 (m, 2H), 0.97 (t, J = 7.6 Hz, 3H). MS: [ESI+H]⁺: 504.1. HPLC: 7.67 min.

3-((3-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purin-1(2H)-

yl)propyl)carbamoyl) benzenesulfonyl fluoride (18b) The acid 9b (0.42 g, 2.0 mmol, 3.0 equiv) was dissolved in thionylchloride (20 mL) and stirred for 3 h at 75 °C. The thionylchloride was evaporated and the residue was co-evapped twice with toluene. Then the amine 14b (0.23 mg, 0.7 mmol, 1.00 equiv), K_2CO_3 (0.073 g, 0.53 mmol, 1.5 equiv) and dry DMF were added and the reaction as stirred at 40 °C overnight. 1M HCl (200 mL) was added and extracted with CH₂Cl₂ (150 mL). The organic layer was washed with water (100 mL) and brine (100 mL). The organic layer was dried, filtered and concentrated *in vacuo*. The residue was purified by column chromatography using CH₂Cl₂ with 1% methanol as eluent to give 18b as white solid (0.0050g, 0.01 mmol, 2.7%). ¹H NMR (400MHz, CDCl₃) δ: 8.88 (d, J = 7.2 Hz, 1H), 8.68 (s, 1H), 8.55-8.50 (m, 2H), 8.20 (d, J = 8.0 Hz, 1H), 7.82 (t, J = 8 Hz, 2H), 7.00 (d, J = 2.4 Hz, 1H), 6.80 (dd, J = 7.2, 2.4 Hz, 1H), 4.33 (t, J = 6.0 Hz, 2H), 4.05 (t, J = 8.0 Hz)

7.6 Hz, 2H), 3.94 (s, 3H), 3.47 (q, J = 6.0 Hz, 2H), 2.17-2.12 (m, 2H), 1.74 (sextet, J = 7.6 Hz, 2H), 1.00 (t, J = 7.6 Hz, 3H). MS: ESI [M+H]⁺: 518.1 HPLC: 8.28 min.

3-((4-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purin-1(2H)-

yl)butyl)carbamoyl)benzenesulfonyl fluoride (18c) EDC (0.13 g, 0.69 mmol, 1.2 equiv) was dissolved in CH₂Cl₂ (3 mL). The acid 9b (0.13 g, 0.63 mmol, 1.1 equiv) was added to this solution and the mixture was stirred. The amine 16c (0.20 g, 0.57 mmol, 1 equiv) was dissolved in CHCl₃ (8 mL) and added dropwise via an automatic syringe at a rate of 0.2 mL/min to the stirring solution. After 3 h at room temperature the reaction was completed and the mixture was concentrated *in vacuo*. The residue was dissolved in CH₂Cl₂ (40 mL) and washed with 1 M HCl (40 mL) and twice with H₂O (2 × 40 mL). The organic layer was dried over MgSO₄ and concentrated *in vacuo*. Purification by column chromatography (CH₂Cl₂: acetone = 3:2) gave the 18c as a white solid(0.14 g, 0.26 mmol, 47%). ¹H NMR (400 MHz, CDCl₃): δ 8.84 (d, J = 7.2 Hz, 1H), 8.54 (s, 1H), 8.36 (d, J = 7.6 Hz, 1H), 8.12 (d, J = 7.6 Hz, 1H), 7.72 (t, J = 7.6 Hz, 1H), 7.62 (br s, 1H), 6.84 (s, 1H), 6.80 – 6.70 (m, 1H), 4.27 (t, J = 7.2 Hz, 2H), 4.04 (t, J = 8.0 Hz, 2H), 3.89 (s, 3H), 3.74 – 3.60 (m, 2H), 2.07 – 1.92 (m, 2H), 1.85 – 1.64 (m, 4H), 0.98 (t, J = 7.2 Hz, 3H). MS: [ESI+H] +: 532.3. HPLC: 8.21 min.

N-(3-(8-methoxy-2,4-dioxo-3-propyl-3,4-dihydropyrido[2,1-f]purin-1(2H)-yl)propyl)-4-(methylsulfonyl)benzamide (19). To a solution of EDC (0.061 g, 0.32 mmol, 1.2 equiv) in CHCl₃ (5 mL) was added 4-(methylsulfonyl)benzoic acid (0.060 g, 0.30 mmol, 1.1 equiv). The amine 16b (0.090 g, 0.27 mmol, 1 equiv) was taken up in CHCl₃ (5 mL) and was subsequently added dropwise via an automatic syringe at a rate of 0.15 mL/min. The reaction was stirred at room temperature and monitored by TLC (4% MeOH in CH2Cl2). After 3 h the reaction was completed and CHCl₃ (50 mL) was added. The organic layer was washed with 1 M HCl (60 mL), H₂O (60 mL), brine (60 mL), dried over MgSO₄ and concentrated under vacuum. The product was purified by column chromatography using 2% MeOH in CH₂Cl₂ to afford the title compound (0.075 g, 0.14 mmol, 54%). ¹H NMR (400 MHz, CDCl₃): δ 8.86 (d, J = 7.2 Hz, 1H), 8.36 (t, J = 5.6 Hz, 1H), 8.19 (d, J = 8.4 Hz, 2H), 8.09 (d, J = 8.4 Hz, 2H), 6.90 - 6.71 (m, 2H), 4.45 - 4.28 (m, 2H), 4.13 - 3.99 (m, 2H), 3.91 (s, 3H), 3.55 - 3.41 (m, 2H), 3.11 (s, 3H), 2.27 – 2.09 (m, 2H), 1.83 – 1.61 (m, 2H), 1.00 (t, J = 7.4 Hz, 3H). ¹³C NMR (600 MHz, DMSO-d₆, 318K): δ 164.7, 161.1, 153.5, 150.7, 150.6, 149.3, 142.8, 138.9, 127.9, 127.5, 126.7, 107.4, 99.9, 95.4, 56.0, 43.2, 41.6, 40.8, 36.8, 27.4, 20.7, 10.9. MS: [ESI+H]⁺: 514.2. HRMS-ESI⁺: [M + H]⁺ calcd: 518.1760 found: 518.1791, C₂₄H₂₈O₆N₅S. HPLC: 6.89 min.

4.2. Computational studies

All calculations were performed using the Schrodinger Suite [31]. Since compound 17b shares a high similarity with the ligands on which we previously published [7], the same homology model based on the high resolution antagonist-bound crystal structure of the adenosine A_{2A} receptor (PDB: 4EIY [27]) was used for the docking studies performed here. Based on those proposed docking poses, we used induced fit docking [32] with core constraints on the pyridopurinedione to dock the different ligands.

4.3. Biology

[³H]8-Ethyl-4-methyl-2-phenyl-(8R)-4,5,7,8-tetrahydro-1*H*-imidazo[2,1-*i*]-purin-5-one ([³H]PSB-11, specific activity 56 Ci·mmol⁻¹) was a gift from Prof. C.E. Müller (University of Bonn, Germany). Unlabeled PSB-11, 1-deoxy-1-[6-[((3- and 2-chloro-N6-(3-iodobenzyl)-adenosine-5'-N-methyluronamide (2-Cl-IB-MECA) were purchased from Tocris Ltd. (Abingdon, UK). 5'-N-ethylcarboxamidoadenosine (NECA) was purchased from Sigma-Aldrich (Steinheim, Germany). Adenosine deaminase (ADA) was purchased from Boehringer Mannheim (Mannheim, Germany). Bicinchoninic acid (BCA) and BCA protein assay reagents were purchased from Pierce Chemical Company (Rockford, IL, USA). Chinese hamster ovary (CHO) cells stably expressing the human A₃ adenosine receptor (CHOhA₃) were a gift from Dr. K-N Klotz (University of Würzburg, Germany). All other chemicals were obtained from standard commercial sources and were of analytical grade.

Cell Culture and Membrane Preparation. Chinese Hamster Ovary (CHO) cells, stably expressing the human A₃ adenosine receptor (CHOhA₃), were cultured and membranes were prepared and stored as previously reported [7, 33]. Protein determination was performed based on the bicinchoninic acid (BCA) method [34].

Y265F^{7.36} Site-Directed Mutagenesis. The single tyrosine mutation introduced in TM7 of the hA₃AR was performed with the QuickChange II Site Directed Mutagenesis system (Stratagene, Huizen, The Netherlands). The wild type pcDNA_{3.1}(+)-A₃AR plasmid DNA with N-terminal 3 x HA-tag was used as a template for polymerase chain reaction (PCR) mutagenesis. Mutant primers for directional PCR product cloning were designed using the online Quickchange primer design program (Agilent Technologies, Santa Clara, CA), and obtained from Eurogentec (Maastricht, The Netherlands). Forward primer used for this procedure was 5'-cacagcttgtgctgttcatgggcatcctgct-3' and the reverse primer was 5'-agcaggatgcccatgaacagcacaagctgtg-3'. All DNA sequences were verified by Sanger sequencing at LGTC (Leiden, The Netherlands).

Transient Expression of Wild Type (WT) and Mutant Receptors in CHO-K1 Cells. CHO-K1 cells were seeded into 150-mm culture dishes to achieve 60% confluence in the presence of 20 ml culture medium consisting of DMEM/F12 (1:1) supplemented with 10% (v/v) newborn calf serum, streptomycin (50 μg/mL) and penicillin (50 IU/mL). Cells were transfected approximately 24 h later with plasmid DNA (20 μg of DNA/dish) by the PEI method [35] (PEI:DNA = 3:1) and left for 24 h. Subsequently medium was removed and fresh medium containing 5 mM sodium butyrate was added (to enhance the receptor expression level [36]), and cells were grown for an additional 24 h at 37 °C and 5% CO₂. Membrane preparation followed the procedure described above for the CHO cell membranes stably expressing hA₃AR. [7, 33]

Radioligand Displacement Assay. Radioligand displacement experiments were performed as in previously published methods [7]. Membrane aliquots containing 15 μg of protein were incubated in a total volume of 100 μL assay buffer (50 mM Tris-HCl, 5 mM MgCl₂, supplemented with 0.01% CHAPS and 1 mM EDTA, pH 7.4) at 25 °C for 120 min. Displacement experiments were performed using six concentrations of competing antagonist in the presence of ~10 nM [³H]PSB-11. Nonspecific binding (NSB) was determined in the presence of 100 μM NECA and represented less than 10% of total binding. Incubation was terminated by rapid filtration performed on 96-well GF/B filter plates (Perkin Elmer, Groningen, the Netherlands) in a PerkinElmer Filtermate-harvester (Perkin Elmer, Groningen, the Netherlands). After the filter plate was dried at 55 °C for 30 min, the filter-bound radioactivity was determined by scintillation spectrometry using a 2450 MicroBeta² Plate Counter (Perkin Elmer, Boston, MA).

Radioligand Competition Association Assay. The competition association assay was performed by incubation of ~10 nM [³H]PSB-11 in the absence or presence of competing hA₃AR antagonist at its IC₅₀ concentration with membrane aliquots. The amount of receptor-bound radioligand was determined at different time points up to 240 min. Incubations were terminated and samples were obtained as described under Radioligand Displacement Assay.

 $[^{35}S]$ GTPγS Binding Assay. The assays were started by adding 15 µg of homogenized CHOhA3 membranes in an ice-cold assay buffer to a total volume of 80 µL containing 50 mM Tris-HCl buffer, 5 mM MgCl₂, 1 mM EDTA, 0.05% BSA and 1 mM DTT, 100 mM NaCl, pH 7.4, supplemented with 1 µM GDP and 5 µg saponin. The assays were performed in a 96-well plate format, where stock solutions of the compounds were added to a total volume

of 100 μ L using an HP D300 Digital Dispenser (Tecan, Männedorf, Switserland). The final concentration of DMSO per assay point was \leq 0.1%. The basal level of [35 S] GTP γ S binding was determined in the absence of ligand, whereas the maximal level of [35 S] GTP γ S binding was determined in the presence of 10 μ M 2-Cl-IBMECA. For the insurmountability experiments, membrane preparations were pre-incubated with or without antagonists (1-, 3-, 10-fold K_i values) for 60 min at 25 °C, prior to the addition of 2-Cl-IBMECA (10 μ M to 0.1 nM) and 20 μ l [35 S] GTP γ S (final concentration \sim 0.3 nM), after which incubation continued for another 30 min at 25 °C. For the surmountability (control) experiments, antagonists (1-, 3-, 10-fold K_i values) and 2-Cl-IBMECA (10 μ M to 0.1 nM) were co-incubated with [35 S] GTP γ S for 30 min at 25 °C. For all experiments, incubations were terminated and samples were obtained as described under *Radioligand Displacement Assay*, by using GF/B filters (Whatman International, Maidstone, UK).

Data Analysis. All experimental data were analyzed using the nonlinear regression curve fitting program GraphPad Prism 7.0 (GraphPad Software, Inc., San Diego, CA). Data from the radioligand displacement assays were fit into one-site binding mode, and the obtained IC50 values were converted into K_i values using the Cheng-Prusoff equation to determine the affinity of the ligands [37]. The observed association rate constants (k_{obs}) derived from both assays were obtained by fitting association data using one phase exponential association. The dissociation rate constants were obtained by fitting dissociation data to a one phase exponential decay model. The k_{obs} values were converted into association rate constants (k_{on}) using the equation $k_{on} = (k_{obs} - k_{off})/[L]$, where [L] is the amount of radioligand used for the association experiments. Association and dissociation rate constants for unlabeled compounds were calculated by fitting the data into the competition association model using "kinetics of competitive binding" [22].

$$K_{A} = k_{1}[L] \cdot 10^{-9} + k_{2}$$

$$K_{B} = k_{3}[I] \cdot 10^{-9} + k_{4}$$

$$S = \sqrt{(K_{A} - K_{B})^{2} + 4 \cdot k_{1} \cdot k_{3} \cdot L \cdot I \cdot 10^{-18}}$$

$$K_{F} = 0.5(K_{A} + K_{B} + S)$$

$$K_{S} = 0.5(K_{A} + K_{B} - S)$$

$$Q = \frac{B_{\text{max}} \cdot k_{1} \cdot L \cdot 10^{-9}}{K_{F} - K_{S}}$$

$$Y = Q \cdot (\frac{k_{4} \cdot (K_{F} - K_{S})}{K_{F} \cdot K_{S}} + \frac{k_{4} - K_{F}}{K_{F}} e^{(-K_{F} \cdot X)} - \frac{k_{4} - K_{S}}{K_{S}} e^{(-K_{S} \cdot X)})$$

Where X is the time (min), Y is the specific [3 H]PSB-11 binding (DPM), k_1 and k_2 are the k_{on} (nM $^{-1}$ min $^{-1}$) and k_{off} (min $^{-1}$) of [3 H]PSB-11, B_{max} is the total binding (DPM), L is the radioligand concentration (nM), I is the concentration of the unlabeled competitor (nM). Association and dissociation rate constants for [3 H]PSB-11 ($k_1 = 0.281 \pm 0.04 \times 10^8$ M $^{-1}$ ·min $^{-1}$ and $k_2 = 0.3992 \pm 0.02$ min $^{-1}$) were obtained from Xia *et al* [7]. With that the k_3 , k_4 and B_{max} were calculated, where k_3 represents the k_{on} (nM $^{-1}$ min $^{-1}$) of the unlabeled ligand, k_4 stands for the k_{off} (min $^{-1}$) of the unlabeled ligand and B_{max} equals the total binding (DPM). All competition association data were globally fitted. The residence time (RT, in min) was calculated using the equation RT = $1/k_{off}$, as k_{off} values are expressed in min $^{-1}$. [35 S] GTP γ S binding curves were analyzed by nonlinear regression using "log (agonist) vs response-variable slope" to obtain potency, inhibitory potency or efficacy values of agonists and antagonists (EC50 and E_{max} , respectively). In the (in)surmountability assays, Schild EC50 shift equations were used to obtain Schild-slopes and pA2 values. All experimental values obtained are means of three independent experiments performed in duplicate.

Supporting Information

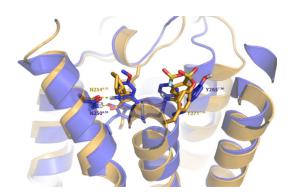


Figure S1. Overlay of a view from crystal structure of compound 2 (mustard carbon sticks) bound to human adenosine A_1 receptor (mustard; PDB: 5UEN)[11] and the hA_3AR (violet) homology model docking with 17b (violet carbon sticks). Atoms color code: red = oxygen, blue = nitrogen, white = hydrogen, yellow = sulfur, cyan = fluorine. Hydrogen bonds between ligands and relevant amino acid residues are indicated by dashed lines.

Abbreviations used

ADA, adenosine deaminase. BCA, bicinchoninic acid. CHAPS, 3-[(3-Cholamidopropyl) dimethylammonio]-1-propanesulfonate. CHO, Chinese hamster ovary. CHO-K1, a subclone from the parental CHO cell line. 2-Cl-IB-MECA, 1-[2-chloro-6-[[(3-iodophenyl) methyl] amino]-9*H*-purin-9-yl]-1-deoxy-*N*-methyl-β-D-ribofuranuronamide. DBU, 1,8-diazabicyclo [5.4.0] undec-7-ene. EDC, 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide. E_{max}, maximum response elicited by an unlabeled ligand in a functional assay (relatively to 2-Cl-IB-MECA) at

membranes of CHO cells stably expressing the A₃ adenosine receptor. EtOAc, ethylacetate. FBS, fetal bovine serum. G418, geneticin. GTPγS, guanosine 5'-*O*-[γ-thio] triphosphate. hA₁AR, human A₁ Adenosine Receptor. hA₃AR, human A₃ Adenosine Receptor. MeCN, acetonitrile. NECA, 5'-(*N*-ethylcarboxamide) adenosine . PSB-11, 8-Ethyl-4-methyl-2-phenyl-(8*R*)-4,5,7,8-tetrahydro-1*H*- imidazo[2,1-*i*]-purin-5-one. PET, petroleum ether

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