[1,2,4]Triazolo[1,5-c]pyrimidines as Adenosine Receptor Antagonists: Modifications at the 8 Position to Reach Selectivity towards A₃ Adenosine Receptor Subtype

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Abbreviations: AR, adenosine receptor; cAMP, cyclic adenosine monophosphate; CCPA, 2-chloro-N6-cyclopentyladenosine; CHO, chinese hamster ovary; Cl-IB-MECA, 2-cChloro-N6-(3-iodobenzyl)-adenosine-5'-N-methyluronamide; DBU, 1,8-diazabicyclo[5.4.0]undec-7-ene; HEMADO, 2-(1-hHexynyl)-N6-methyladenosine; HMDS, hexamethyldisiloxane; IB-MECA, N6-(3-iHodobenzyl)adenosine-5'-N-methyluronamide; MAPK, mitogen-activated protein kinase; NECA, 5'-N-ethylcarboxamidoadenosine; PLC, phospholipase C; R-PIA, R-(-)-N6-(2-phenylpropyl)adenosine; TP, [1,2,4]triazolo[1,5-c]pyrimidine.

Keywords: G protein-coupled receptor; adenosine receptor; A₃ antagonist; [1,2,4]triazolo[1,5-c]pyrimidine; molecular modeling; docking.

Abstract

[1,2,4]Triazolo[1,5-c]pyrimidine is a promising platform to develop adenosine receptor antagonists. Here, we tried to investigate the effect of the substituent at the 8 position of [1,2,4]triazolo[1,5-c]pyrimidine derivatives on affinity and selectivity at the human A₃ adenosine receptor subtype. In particular we have introduced both esters and amides, principally with a benzylic nature. In addition, a small series of 5-substituted [1,2,4]triazolo[1,5-c]pyrimidines was designed in order to complete the structure-activity relationship analysis. Several of this these new compounds showed affinity towards $\frac{hA_3}{ARhuman}$ $\frac{A_3}{A}$ adenosine receptor in the low nanomolare range, with the most potent derivative of the series bringing a 4-ethylbenzylester at the 8 position (compound 18, $\frac{hA_3}{ARhA_3AR}$ $\frac{A_3}{AR}$ $\frac{A_3}{AR}$

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Introduction

Adenosine is an endogenous autacoid which carries out its actions by interacting with specific G protein-coupled receptors named adenosine receptors (ARs).[1] Adenosine possesses a double face in pathological conditions: in some cases it can help to resolve or to limit the disease process; while in others, it has a detrimental effect on the pathological event. It is exactly in this second situation that antagonists towards the adenosine receptors could be useful therapeutic agents.[2] Adenosine receptors are divided in four different subtypes: A₁, A_{2A}, A_{2B} and A₃ARs.[3] A_{2A} and A_{2B} ARs are mainly coupled to G_s proteins; on the contrary, A₁ and A₃ ARs are generally coupled to G_i proteins, thus leading to an enhancement or decrease of intracellular cAMP levels, respectively.-[1] Additionally, the various AR subtypes are able to activate other pathways, such as PLC (A₁, A_{2B} and A₃ ARs; A_{2B} and A₃ via G_q coupling) and MAPK (all ARs) pathways.[4] A₁-AR was found also to activate potassium channels and to inactivate calcium (N, P and Q type) channels.[1] AR subtypes showed different organ and tissue distribution in the human body, which confers to them diverse physio-pathological implications. In particular, antagonists for human A₁ AR (hA, AR) were studied for the treatment of heart and renal failure, [5] [6] while Parkinson's disease is the main therapeutic application for hA_{2A} -AR antagonists, +7 even if a possible use was suggested also for other neurodegenerative diseases such as Alzheimer's disease and depression, [87] and in addiction problems. [8] Concerning hA_{2B}—AR antagonists there is high interest for their potential as drugs in inflammatory conditions such as asthma [9] but also in hypoxic conditions like sickle cell disease.[10] Finally, antagonists towards hA3-AR were principally proposed for the treatment of glaucoma, but a beneficial effect was suggested also for some kind of cancer and inflammation.[11] For the hA3-AR subtype, opposite or contradictory results were found in various pathophysiological conditions (i.e. inflammation and cancer), also depending on the species involved.[12] Maybe for these reasons, even though a lot of many ligands targeting hA₃-AR are available, only few of them reached the clinical or preclinical phases of experimentation (Figure 1). In particular, the agonist IB-MECA is advancing in phase II and II/III

for conditions like psoriasis, rheumatoid arthritis and dry eye disease[13] while Cl-IB-MECA is under phase II clinical trial for the treatment of hepatocellular carcinoma, and phase I/II for chronic hepatitis genotype 1.[14] Instead, as antagonists, Palobiofarma compound PBF-677 (structure not disclosed) has recently positively completed a "first in human" phase Ia study to assess safety and tolerability in healthy volunteers.[15]

$\label{eq:hambeca} \begin{aligned} \textbf{IB-MECA, I} \\ \text{hA}_1 \text{AR } \text{K}_i &= 51 \text{nM} \\ \text{hA}_{2\text{A}} \text{AR } \text{K}_i &= 2,900 \text{ nM} \\ \text{hA}_{2\text{B}} \text{AR } \text{K}_i &= 11,000 \text{ nM} \\ \text{hA}_3 \text{AR } \text{K}_i &= 1.8 \text{ nM} \end{aligned}$

HN N CI

CI-IB-MECA, II $hA_1AR K_i= 220 \text{ nM}$ $hA_{2A}AR K_i= 5,360 \text{ nM}$ $hA_{2B}AR K_i> 10,000 \text{ nM}$ $hA_3AR K_i= 1.4 \text{ nM}$

Figure 1. hA₃-AR ligands in clinical phases: agonists IB-MECA (I) and Cl-IB-MECA (II).

In a previous work, we have reported a series of [1,2,4]triazolo[1,5-c]pyrimidines (TP) as adenosine receptor antagonists.[16] Concerning the <u>h</u>A₃AR subtype, two compounds emerged from the series: compound **1** and **2** (Figure 2). These compounds bear a methylamino (compound **1**) and ethylamino (compound **2**) <u>moiety moieties</u> at the 5 position of the [1,2,4]triazolo[1,5-c]pyrimidine scaffold, respectively. Both of them showed an affinity value towards the <u>h</u>A₃-adenosine receptor <u>AR</u> in the nanomolar range (**1**, hA₃AR K_i = 4.14 <u>nM</u>; **2**, hA₃AR K_i = 3.30 <u>nM</u>), with compound **1** displaying a better selectivity profile against the other AR subtypes (**1**, hA₁/hA₃ = 236; hA_{2A}/hA₃ = 25 ν s **2**, hA₁/hA₃ = 49; hA_{2A}/hA₃ = 15).

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Figure 2. Reference [1,2,4]triazolo[1,5-c]pyrimidine compounds 1-2.[16]

The aim of this work was to enhance affinity, but especially, selectivity towards the $\underline{h}A_3AR$, maintaining the methylamino moiety at the 5 position of TP and exploring the 8 position through substitution of the ethyl ester moiety with other alkyl or aralkylesters and amides. In addition, a further investigation on the 5 position of TP was performed. In particular, different moieties which share the presence of a second functional group (i.e. amino or ester moieties) where introduced in order to explore their ability to gain new key interactions within the binding site of $\underline{h}A_3$ -AR.

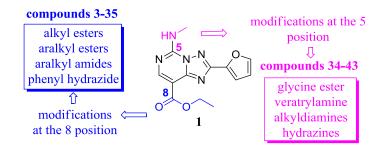


Figure 3. Modifications carried out at the 5 (pink) and 8 (blue) positions of reference compound 1 which led to newly synthesized compounds **3-43**.

Results and Discussion

Chemistry

Designed compounds **3-43** were synthesized as depicted in schemes 1-3, following procedures already reported in literature.[16][17] The synthesis started with the—the pyrimidine nucleus (**44**) by reacting S-methylisothioureahemisulfate salt with diethyl ethoxymethylenmalonate in basic conditions. The resulting 5-methylthio-pyrimidine derivative **44** was in turn chlorinated

with phosphorous oxychloride and then reacted with the 2-furoylhydrazide to afford the 4-hydrazinyl-pyrimidine_derivative **45**. The last underwent cyclization under dehydrative conditions (hexamethyldisiloxane and phosphorous anhydride in dry xylene) to the TP **46**. At this point, substitution at the 5 position was carried out using methylamine in ethanol and heating to 90-110°C in a sealed tube, yielding compound **1**. Finally, in order to obtain different substitutions at the 8 position, the ethyl ester was hydrolyzed with lithium hydroxide to the corresponding carboxylic acid (**47**), which was in turn reacted with the corresponding alcohol or amine in the presence of phosphorous oxychloride and pyridine affording the desired esters (**3-19**) and amides (**20-32**), respectively (Scheme 1).

Scheme 1. Synthetic pathway for compounds **3-33**. Reagents and conditions. *a*: NaOH, water,_EtOH,_rt, 24h; *b*: 1. POCl₃, reflux, 3h, 2. 2-furoylhydrazide, DBU, THF, rt, 16h; *c*: P₂O₅, <u>HMDS</u>, xylene, <u>90°C</u>, <u>2h</u>, reflux, <u>2448</u>h; *d*: NH₂CH₃ 33 wt.% in EtOH, EtOH, 120°C in a sealed tube, 3h; *e*: LiOH'H₂O, water, EtOH, reflux,

3h;– f: NH₂NHPh, EDCI, HOBT, EtOH, rt, 16h; g: ROH or NH₂R, POCl₃, pyr, reflux rt, 16h. For R specification of compounds **3-32** see table 1.

The only exception is represented by compound 33 which was obtained by a coupling reaction between acid derivative 47 and phenylhydrazine in the presence of EDCI and HOBT. The same strategy reported in scheme_Scheme_1 was applied also to obtain compound 34: TP 46 was reacted with veratrylamine in ethanol under heating to afford compound 48, which was hydrolyzed and the obtained acid (49) was finally reacted with benzhydryl amine (Scheme 2).

Scheme 2. Synthetic pathway for compound **34**. *a*: NH₂CH₂Ph-3,4(OCH₃)₃, EtOH, 120°C in a sealed tube, 3h; *b*: LiOH·H₂O, water, EtOH, reflux, 3h; *c*: NH₂CH(Ph)₂, POCl₃, PCl₅₃ pyr, refluxrt, 16h.

Furthermore, in order to obtain the desired compounds 3536-39, the same strategy used for compound 1 was applied, that is a nucleophilic substitution on derivative 46 with the corresponding amines in ethanol at 90-11120°C. On the other hand, the same reaction using glycine ethyl ester as amine gave both the substitution at the 5 position and the amidation at the 8 position, affording compound 35. Deprotection with hydrochloric acid in ethyl acetate of Boc-protected derivatives 37-39 afforded then diamino derivatives 40-42 (Scheme 3). Instead, carboxylic acid derivative 43 was obtained from compound 37 analogously to compounds 47,49. Finally, compound 50 is a

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secondary product isolated from reactions of derivatives 3538- and 39 in ethanol, which was also characterized and assayed at adenosine receptor subtypes. In fact, the yields for these reactions were low (e.g. 38 = 45%; 39 = 15%), indicating a poor reactivity of the amines used which allowed to ethanol (solvent) to play as reagent for the substitution at the 5 position.

Scheme 3. Synthetic pathway for compounds **35-43**._*a*: appropriate amine (NH₂CH₂COOEtHCl for **35**, NH₂NHPh for **36**, NH₂CH₂CH₂NHBoc for **37**, N-Boc-Pyperazine for **38**, NH₂NHBoc for **39**), EtOH, 120°C in a sealed tube, 3h; *b*: TFAHCl/DCM 1:1EtOAc, rt, 2h, *c*: LiOH-H₂O, H₂O, EtOH, reflux, 3h-; *d*: Ethyl 5-ethoxy-2-(furan-2-yl)-[1,2,4]triazolo[1,5-*c*]pyrimidine-8-carboxylate (**50**) was obtained as byproduct.

Pharmacology

All the synthesized compounds 3-43,50 were tested at the four adenosine receptor subtypes.

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In particular, radioligand binding assays were applied to hA_1 , hA_{2A} and hA_3 ARs expressed in CHO cells which afforded affinity values, expressed as K_i for the tested compounds. [3H]CCPA (1 nM), [3H]NECA (10 nM) and [3H]HEMADO (1 nM) were used as radioligands for hA_1 , hA_{2A} and hA_3 ARs binding assays, respectively.

Instead, for hA_{2B} -AR, potency of newly synthesized compounds was determined using a functional assay, which consists in measurement of the inhibition of NECA-stimulated adenylyl cyclase activity on membranes of CHO cells expressing hA_{2B} -AR. In this case, potency of inhibitors was expressed as IC_{50} -

Structure-activity relationship

As previously described, the first aim of this work was to explore the 8 position of the [1,2,4]triazolo[1,5-c]pyrimidine scaffold by introducing various esters and amides of different nature (e.g. alkyl and aralkyl), while maintaining the methylamino group at the 5 position and the fur-2-yl ring at the 2 position such as in compound 1, which showed the best affinity/selectivity profile in the previous series.-[16] Pharmacological results about synthesized esters and amides 3-34 33 are reported in table 1. In order to better exploit the chemical space around 5 and 8 positions and to explore the effect on selectivity among ARs, compound 34, bearing big substituents at both positions, was synthesized. In particular, the already reported compound 48, which bears a veratrylamino group at the 5 position and displayed good affinity and poor selectivity towards hA₃AR was selected as starting point and modified by introduction of the big benzhydrylamido moiety at the 8 position. [16]

Table 1. Binding affinity (hA_1 , hA_{2A} , hA_3) and potency (hA_{2B}) of compounds <u>31-34-35</u> and <u>50-48</u> at the four human adenosine receptor subtypes and selectivity towards hA_3AR .

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NH N-N-N O-R 3-33

Cm R hA₁AR hA_{2A}AR hA_{2B}-AR hA₃AR $hA_{1/}$ hA_{2A} pd $(K_i nM)$ $(K_i nM)$ $(K_i nM)$ $(K_i nM)$ hA_3 hA_3 4.14 $\mathbf{1}^{\underline{a}}$ **OEt** 978 104 2,450 236 25 (716-1,340)(89.2-122) (1,770-3,370) (3.53-4.86)3,060 OEt 50.3 3.30 49 162 15 (157-167)(48.8-51.9)(2,230-4,200)(2.85-3.83)3 $OCH(CH_3)_2$ 744 86.5 > 3,000 2.75 270 32 (577-959)(63.9-117)(2.43-3.12)OCH₂Ph > 3,000 16 4 277 114 7.21 38 (220-350)(80.3-161)(4.22-12.3)99 5 OCHPh₂ 48.3 197 > 10,000 1.99 24 (118-329)(43.0-54.2)(1.6-2.47)6 OCH₂Ph-2-CH₃ 93.9 37.2 > 10,000 30.6 3 1 (29.2-47.4) (73.0-121)(19.0-49.1)7 OCH₂Ph-3-CH₃ 79.7 21.0 > 10,00010.8 7 2 (17.2-25.6) (47.8-133) (6.92-16.8)8 OCH₂Ph-4-CH₃ 190 62.2 > 10,000 3.72 51 17 (180-201)(36.8-105)(3.07-4.50)9 OCH₂Ph-2-OCH₃ 55.2 13.2 > 10,000 1.71 32 8 (42.0-72.4)(8.03-21.8)(1.14-2.57)14.9 ≈1,000 5 2 10 OCH₂Ph-3-OCH₃ 34.3 7.42 (28.6-41.0)(10.5-21.0)(5.51-9.99)194 > 10,000 35 11 OCH₂Ph-4-OCH₃ 102 5.62 18 (79.9-131)(111-337)(4.73-6.67)OCH₂Ph-2-Cl 6.05 12 348 32.0 > 10,000 58 5 (249-485)(23.8-43.2)(4.61-7.95)6.73 26.4 4 2 13 OCH₂Ph-3-Cl 15.7 ≈10,000 (15.1-46.2)(13.5-18.4)(4.06-11.2)15 14 OCH₂Ph-4-Cl 216 71.9 > 10,000 4.88 44 (195-238)(61.1-84.5)(3.03-7.86)2 15 OCH₂Ph-2-Br 313 24.3 > 10,00014.3 22 (231-423)(21.1-27.9)(6.56-31.2)39 10 16 OCH₂Ph-3-F 130 32.5 > 10,0003.37 (26.5-39.9) (93.5-181)(1.99-5.73)17 71.5 14 OCH₂Ph-4-F 556 > 10,000 5.21 107 (316-980)(58.2 - 87.8)(4.30-6.32)98 17 18 OCH₂Ph-4-CH₂CH₃ 119 21.0 > 10,000 1.21 (0.907-1.62)(79.1-178)(17.2-25.6)19 OCH(CH₃)Ph 51.0 11.0 3,720 3.19 16 3 (35.3-73.8)(6.83-17.6)(1,980-6,990)(2.06-4.93)5 20 NHCH₂Ph 23.4 18.6 > 10,000 3.73 6 (19.0-28.9)(10.8-32.1)(3.00-4.65)

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34,48

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21	$NHCHPh_2$	28.3 (20.5-39.1)	61.6 (52.3-72.5)	≈10,000	5.08 (4.53-5.70)	6	12
22	NHCH ₂ Ph-4-CH ₃	46.6 (41.5-52.4)	100 (75.6-132)	> 10,000	5.02 (3.9-6.46)	9	20
23	NHCH ₂ Ph-4-OCH ₃	41.0 (29.3-57.3)	81.3 (60.3-110)	> 10,000	12.5 (9.9-15.8)	3	7
24	NHCH ₂ Ph-4-CF ₃	3,850 (2,430-6,090)	2,950 (1,930-4,500)	> 10,000	15.3 (11.6-20.1)	252	193
25	NHCH ₂ Ph-4-Cl	137 (110-169)	59.4 (50.8-69.4)	> 10,000	10.0 (9.58-10.5)	14	6
26	NHCH ₂ Ph-4-F	250 (228-274)	47.6 (39.8-56.8)	> 10,000	7.23 (5.96-8.77)	35	7
27	NHCH ₂ Ph-4-Ph	> 100,000	9,390 (8,600-10,300)	> 10,000	521 (341-797)	>191	18
28	$NHCH_2Ph-3,4(OCH_3)_2$	246 (166-365)	141 (106-187)	> 10,000	102 (90.2-115)	2	1
29	$NH(CH_2)_2Ph$	73.1 (47.8-112)	29.7 (27.1-32.6)	> 10,000	6.82 (5.10-9.12)	11	4
30	NH(CH ₂) ₂ Ph-3,4(OCH ₃) ₂	177 (121-259)	169 (105-271)	> 10,000	107 (91.4-124)	2	2
31	NHC(CH ₃) ₂ CH ₂ Ph	38.0 (30.0-48.0)	6.12 (5.92-6.33)	> 3,000	6.52 (4.40-9.66)	6	1
32	NH(CH ₂) ₂ OPh	172 (165-180)	38.2 (28.0-52.2)	> 10,000	16.4 (10.5-25.7)	10	2
33	NH-NH-Ph	58.7 (54.2-63.6)	342 (286-408)	> 10,000	15.1 (13.3-17.2)	4	23
34	NHCHPh ₂ -	122 (77.0-193)	137 (115-163)	> 30,000	69.9 (46.8-105)	2	2
<u>35</u>	=	<u>21,900</u>	<u>1,540</u>	<u>> 10,000</u>	<u>646</u>	<u>34</u>	<u>2.4</u>
		(21,500-22,300)			<u>(524-797)</u>		
50 4	OEt	4,100 <u>315</u>	1,86016	1012 00020	10838.7 (04.428.2	3 8	17 3
o a		(2 ,790 03- 6,020 489)	(1,451 44.3, 2,387 305)	1013,000 <u>30</u>	(94.428.2- 12453.1)		
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^a data from reference 16.

All the derivatives (3-354) displayed good affinities at the hA₃AR with different degrees of selectivity *versus* the other receptor subtypes, while they were inactive, in the nanomolar range, towards the hA_{2B}AR receptor (K_i > 3,000 nM for all compounds except for compound 10). Instead, at the hA₁ and hA_{2A} AR subtypes, substitution at the 8 position on the TP nucleus was able to modulate affinity and consequently also selectivity against hA₃-AR.

In the ester <u>series</u> an improvement of affinity towards the hA₁-AR was observed with the increase of the size of the ester substituent. The affinity order <u>iwas</u>: benzhydryl (5) $\geq \alpha$ -

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methylbenzyl (19) \gg benzyl (4) \gg isopropyl (3) \approx ethyl (1). In particular, benzhydryl (5) and α methylbenzyl (19) derivatives showed affinity values of 48.3 and 51.0 nM, respectively. Introduction of a methyl (but also ethyl such as for compound 18) or methoxy substituent on the phenyl ring of benzyl ester derivative 4 improved the affinity at the hA₁AR (compounds 6-11). In detail, substitution at the *meta* position gave the best results (7, hA_{1} -AR K_{i} = 79.7 nM; 10, hA_{1} AR $K_i=34.3$ nM), followed by substitutions at the ortho (6, hA_1AR $K_i=93.9$ nM; 9, hA_1AR $K_i=55.2$ nM) and para positions (8, hA₁AR K_i= 190 nM; 11, hA₁AR K_i= 102 nM). A different behaviour was observed when a halogen atom was introduced in the benzyl ester group (compounds 12-17). In fact, the substitution with halogens did not necessarily lead to an improvement of affinity at the hA₁ AR. For example, *ortho* chlorine (12, $hA_1AR_K = 348_nM$) and bromine (15, $hA_1AR_K = 313_nM$) derivatives displayed a worse affinity than unsubstituted derivative 4 (hA₁AR K_i= 277_nM). Compound 13 (meta-chlorine) is the most potent benzyl ester compound at the hA₁-AR with a K_i of about 26.4 nM. Regarding the amide series (20-34), it could be observed that while the benzylester (4) was poorly active at the hA₁AR, the benzylamide derivative (20) displayed a K₁ of 23.4 nM at the hA1 ARsame receptor (about ten-fold more potent). This affinity value was comparable to that showed by the benzhydrylamide derivative 21 (hA₁AR K_i =_28.3 nM). Also the α -dimethylphenylethylamide (31, hA₁AR K_i=38 nM) gave good results in terms of affinity at the hA₁AR, while the corresponding not branched phenylethylamide (29) and the longer phenoxyethylamide (32) derivatives had a detrimental effect (29, hA_1AR K_i = 73.1 nM and 32, hA_1AR K_i = 172 nM). Regarding substitutions on the benzyl group of derivative 20, only the para position was investigated (compounds 22-27). The introduction of a moiety at this position led to a decrease of affinity at the hA₁-AR, especially when halogen atoms were present (24-26). The same behaviour was observed in the veratrylamido derivative 28 (hA₁AR K_i= 246 nM). Finally, also the replacement of methylene in the benzyl derivative 20 with an amino group as in the phenylhydrazide derivative 33 was detrimental in terms of affinity towards the hA₁AR (20, hA₁AR K_i= 23.4 nM versus 33, hA₁ K_i= 58.7 nM). In conclusion, it is interesting to note that compound 50,

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which bears an ethoxy group at the 5 position of TP instead of an ethylamino group of reference compound 2, showed a complete loss of affinity against hA_{\perp} -AR (hA_{\perp} -K_i= 4,100 nM), suggesting that the amino group at the 5 position is involved in crucial interactions inside the hA_{\perp} -AR binding pocket.

In general, in the ester series (3-19) affinities were better towards the hA_{2A}AR than towards hA₁AR and the affinity trend was not related to the size of ester substituent. In fact, the order of affinity values <u>i</u>was: α -methylbenzyl (19) >> isopropyl (3) >ethyl (1) > benzyl (4) >>benzhydryl (5). Substitution on the phenyl ring of the benzylester 4 led to an improvement of affinity at the hA_{2A}-AR (compounds 6-18), excepted for the *para*-methoxy derivative 11 (4, hA_{2A}AR K_i= 114 nM *versus* 11, hA_{2A}AR K_i= 194 nM). *Meta* and *ortho* susbtitutions were preferred to *para* substitution (i.e. 6, hA_{2A}AR K_i= 37.2 nM and 7, hA_{2A}AR K_i= 21 nM *versus* 8, hA_{2A}AR K_i= 62.2 nM). Similarly, regarding amide series (20-34), unsubstituted benzylamide group (20, hA_{2A}AR K_i= 18.6 nM) was preferred over substituted benzylamido moieties as present in compounds 22-28 (i.e. 22, hA_{2A}AR K_i= 100 nM). The introduction of a phenylethyl (29), phenoxyethyl (32) or benzhydryl (21) amido group at the 8 position of TP led to a slight decrease of affinity at the hA_{2A}-AR compared to the benzylamido group (i.e. 32, hA_{2A}AR K_i= 1838.6-2 nM *versus* 20, hA_{2A}AR K_i= 3818.2-6 nM). On the contrary, α -dimethyl-phenylethylamido derivative 31 showed the best affinity value towards A_{2A}AR, with a K_i value of 6.12 nM.

Concerning the hA₃AR subtype, which is the target of this work, most of the synthesized derivatives displayed affinity values below 30 nM. The isopropyl derivative **3** exhibited a slightly better affinity and selectivity against hA₃AR than the corresponding ethyl ester **1** (**3**, hA₃AR K_i=2.75 nM *versus* **1**, hA₃AR K_i=4.14 nM). Among arylalkyl esters, benzylester (**4**) led to a decrease of affinity toward hA₃-AR (**4**, hA₃AR K_i=7.21 nM) which was gained again with bulkier esters such as α-methyl-benzyl (**19**, hA₃AR_K=3.19 nM) and benzhydryl esters (**5**, hA₃AR K_i=1.99 nM). In general, the substitution on the phenyl ring of the benzyl group of compound **4** conferred an improvement in affinity towards the hA₃AR. A particular relationship between affinity

and the position of the substituent on the phenyl ring was not observed. The only observation that could be made is that para-substitutions (8,11,14,17,18) led to an increase of affinity at the hA₃-AR compared to the unsubstituted derivative 4 (i.e. 18, hA₃AR K_i= 1.21 nM versus 4, hA₃AR K_i= 7.21 nM), independent of the nature of the substituent. Also, sSelectivity against the other adenosine receptor subtypes was better in the para-substituted benzyl ester derivatives (8,11,14,17,18) than in the other benzyl-susbtituted compounds (8, $hA_1/hA_3 = 51$, $hA_2/hA_3 = 17$, versus 7, $hA_1/hA_3 = 7$, hA_{2A}/hA₃=2) as well. Instead, in the amide series (20-34), the benzylamido group (compound 20) gave an affinity at the hA₃AR of 3.73 nM and substitutions on the phenyl ring led to a detrimental effect in terms of affinity at the hA₃AR (22-28), especially when a big moiety such as another phenyl ring was introduced at the para position (27, hA₃AR_K_i= 521 nM). Interestingly, when a para-trifluoromethyl-benzylamido group was introduced at the 8 position of TP (24), the affinity at hA_3 -AR was 15.3 nM, thus was less potent than reference compound 1 (hA_3 AR_ K_i = 4.14 nM), but selectivity against both hA₁ and hA_{2A} ARs was good. In fact, compound 24 was 252- and 193- fold selective for hA_3 -AR ver<u>s</u>us hA_1 and hA_{2A} ARs, respectively. Also In addition, elongation of the amide chain such as for compounds 29-32 did not improve affinity at the hA₃-AR. Surprisingly, the phenylhydrazide moiety was well tolerated at this receptor subtype. In fact, derivative 33 showed an affinity of 15 nM at the hA₃-AR, which was four-fold less potent than benzylamido compound 20, but more than four-fold selective against hA_{2A}-AR (33, hA₃AR K_i= 15.1 nM, hA₁/hA₃= 4, $hA_{2A}/hA_{3}=23$ versus **20**, $hA_{3}AR$ $K_{i}=3.73$ nM, $hA_{1}/hA_{3}=6$, $hA_{2A}/hA_{3}=5$). Both affinity and selectivity were completely lost when a bigger moiety than a methylamino group was introduced at the_5 position of compound 521, such as in compound 34 (hA₃AR K_i= 69.9 nM, hA₁/hA₃= 2, $hA_{2A}/hA_{3}=2$). Comparing compound 34 to its parent compound 48 it is possible to observe that substitution of the ethyl ester with a big amido moiety does not enhance selectivity versus hA₃AR. In fact, compound 34 is actually two fold less potent at this receptor subtype than derivative 48. A

worst behaviour in terms of affinity was observed when the less bulky ethyl glycine ester was

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introduced at the 5 position and on the carboxylic acid at the 8 position in compound 35 (hA₃AR

 $K_i = 646 \text{ nM}$).

Most importantly, the introduction of both, different esters and amides at the 8 position of the TP compared to that present in the reference compound 1, led in general to a decrease of selectivity against hA_1 and hA_{2A} ARs. An exception, as described before, was represented by isopropyl ester derivative 3 which displayed a slight improvement in both affinity and selectivity for the hA_3 -AR (hA_3 AR K_i = 2.75 nM, hA_1/hA_3 = 270, hA_{2A}/hA_3 = 32), but selectivity against hA_{2A} -AR remained poor. Unfortunately, if an improvement of both, affinity at the hA_3 -AR and selectivity against hA_{2A} AR was obtained, a detrimental effect was observed regarding selectivity against hA_1 AR, such as for compound 5, which bears the benzhydryl ester group at the 8 position of TP (5, hA_3 AR K_i = 1.99 nM, hA_1/hA_3 = 24, hA_{2A}/hA_3 = 99).

In order to better define the structure-activity relationship of TP at the hARs, also additional substitutions at the 5 position of the TP scaffold (compounds 3536-43) were investigated which were not considered in the previous work.[16] In particular, moieties containing an additional functional group such as another amino group or a carboxylic group were introduced to explore the opportunity to gain other key electrostatic interactions inside the hA₃-AR binding cleft which could confer an enhancement of both, affinity and selectivity for the targeted AR subtype. In addition, these substituents could be considered as spacers containing a site of linkage for other possible functionalizing moieties, such as fluorophores, that can be useful in the study of the physiopathological role of hA₃-AR.[18][19] Pharmacological results about compounds 3536-43 were reported in table 2.

Table 2. Binding affinity (hA_1 , hA_{2A} , hA_3) and potency (hA_{2B}) of compounds <u>1-2, 3536-43, 50</u> at the four human adenosine receptor subtypes and selectivity towards hA_3AR .

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Cmpd	R	hA ₁ AR	hA _{2A} AR	hA _{2B} AR	hA ₃ AR	hA _{1/}	hA _{2A/}
		(Ki nM)	(Ki nM)	(Ki nM)	(Ki nM)	hA_3	hA ₃
1 <u>a</u>	CH_3	978	104	2,450	4.14	236	25
		(716-1,340)	(89.2-122)	(1,770-3,370)	(3.53-4.86)		
2 <u>a</u>	CH_2CH_3	162	50.3	3,060	3.30	49	15
		(157-167)	(48.8-51.9)	(2,230-4,200)	(2.85 - 3.83)		
35	CH₂CO₂Et	21,900	1,540	> 10,000	646	34	2.4
		(21,500 22,300)	(1,090 2,170)	Ź	(524-797)		
36	NHPh	1,360	41.8	6,060	339	4	0.1
		(1,060-1,740)	(35.9-48.8)	(4,140-8,910)	(235-488)		
37	CH ₂ CH ₂ NHCO ₂ C(CH ₃) ₃	> 100,000	376	> 30,000	129	>775	2.9
			(337-420)		(124-133)		
38	$CO_2C(CH_3)$	> 100,000	> 100,000	> 10,000	> 30,000	-	-
39	$NHCO_2C(CH_3)_3$	12,100	827	> 10,000	89	136	9.3
		(11,800-12,300)	(674-1,010)		(63.5-125)		
40	$CH_2CH_2NH_2$	2,340	829	> 30,000	2,000	1.2	0.4
		(1,880-2,900)	(772-890)		(1,620-2,480)		
41	Н	> 100,000	> 30,000	> 10,000	28,600	>3.5	>1
					(9,710-84,300))	
42	NH_2	2,080	63.1	> 10,000	159	13	0.40
		(1,360 3,190)	(49.3 80.7)		(128-199)		
43	-	> 100,000	22,600	> 30,000	7,750	>13	2.9
			(17,800-28,800)	1	(7,580-7,910)		
<u>50</u>	Ξ	<u>4,100</u>	<u>1,860</u>	> 10,000	<u>108</u>	<u>38</u>	<u>17</u>
		(2,790-6,020)	(1,451-2,387)		(94.4-124)		

^a data from reference 16.

As could be seen, not only aminoester (35) and diamino (36,40-42) compounds, but also the mono-Boc protected diamino derivatives (38,39,43) were tested for their affinity against the ARs. All derivatives showed a loss of affinity against the hA₃-AR subtype. A free amino group at the 5 position was not tolerated (40,41) for substituents bigger than hydrazine (42). In fact, hydrazine derivative 42 was the only derivative with a free amino group which exhibited an affinity value in

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Tabella formattata

the sub-micromolar range ($hA_3AR_k_i$ = 159 nM). The presence of a Boc moiety on the second amino group led to a more potent and selective compound towards hA_3 -AR (**39**, $hA_3AR_k_i$ = 89 nM), while a phenyl group was less well tolerated (**36**, $hA_3AR_k_i$ = 339 nM). Also, the Bocethylendiamino chain gave some affinity at the hA_3 -AR (**37**, $hA_3AR_k_i$ = 129 nM), but the corresponding acid derivative **43** was 60-fold less potent (**43**, $hA_3AR_k_i$ = 7,750 nM), confirming that an ester (or amido) moiety was essential at the 8 position of TP in order to obtain affinity in the nanomolar range against this AR subtype.

Finally, compound **50**, which bears an ethoxy group at the 5 position of TP instead of an ethylamino group of reference compound **2**, showed a loss of affinity against all ARs, suggesting that the amino group at the 5 position is involved in crucial interactions inside the binding pocket.

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Molecular modeling

Molecular docking simulations were performed with the aim to rationalize binding at a molecular level. The compounds were docked to the hA_1 , hA_{2A} and hA_3 adenosine receptor subtypes, while disregarding the hA_{2B} receptor, since none of the compounds showed significant interaction with this receptor (Ki-> 3000 nM). As reported in the methods section, a crystallographic structure was retrieved from the Protein Data Bank for hA_1 (PDB ID: 5UEN [20]) and hA_{2A} (PDB ID: 3PWH [21]) subtypes, while a homology model constructed on the 3PWH $hA_{2A}AR$ structure was employed for the hA_3 receptor. 3PWH structure was chosen because the ionic interaction between E169 and H264 is lacking, leaving more space for the placement of the compounds (especially for the substituted amine at position 5). Poses with positive electrostatic potentials and highly positive van der Waals interactions (higher than 50 kcal/mol) were rejected; in the case of some non-binders or low affinity binders it was not possible to satisfy this condition (compounds 8 on hA_1 , 27 and 50 on hA_{2A} , 38 on hA_3), but the pose with the lowest energy contribution was retained also for these compounds for completeness. In the other cases, a single pose was chosen for each ligand by visual inspection, in a way to optimize the ligand-protein interaction network.

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According to the selected poses, the ligands bind to the three AR subtypes in a similar fashion, comparable with the typical crystallographic binding mode of the inverse agonist ZM-241385, as summarized in Videos S1-2-3. Electrostatic and hydrophobic interactions were computed for each compound and each receptor at a per residue level; the results, plotted in the form of heat maps called Interaction Energy Fingerprints (Figures 4-5-6, panels A and B), highlight conserved hot spots in the three receptor subtypes. These zones are focused on the upper portion of transmembrane helices TM2, TM3, TM6 and TM7, and on extracellular loop EL2. In particular, significant hydrophobic interactions are common to two apolar residues at positions 2.64 and 3.32, leucine 3.33, a phenylalanine in EL2, tryptophan 6.48, leucine 6.51, isoleucine 7.39; while a strong electrostatic interaction is found at level of asparagine 6.55.

The main interactions of conserved and non-conserved residues are reported by the histograms in panels C of Figures 4-5-6: the strength of the interactions at equivalent positions of the three AR subtypes is shown to highlight how single point differences among the receptors could affect binding. Data are reported for compounds 5, 9 and 18, the ligands with highest affinity for hA₃AR; and, in addition, for compound 21, the amide homolog of compound 5. As an example, the binding mode of compounds 5 and 21 is described representing the ester and amide substitutions at position 8 of the [1,2,4]triazolo[1,5-c]pyrimidine scaffold.

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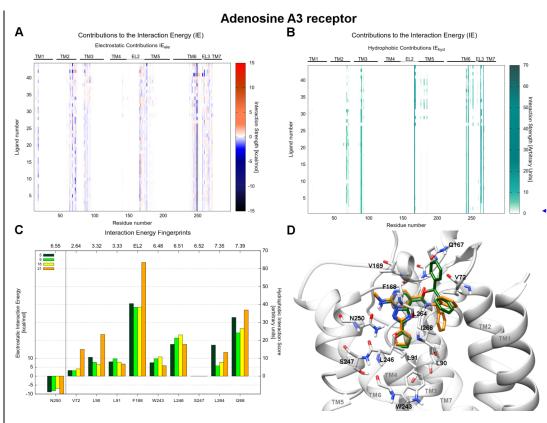


Figure 4. Panel A. Electrostatic Interaction Energy Fingerprints (IEFele) shown as heat map reporting the electrostatic interaction between each compound (y-axis) and each residue (x-axis) of hA₃AR. The strength of the interaction is rendered by a colorimetric scale going from blue to red for negative to positive values. Panel B. Hydrophobic Interaction Energy Fingerprints (IEFhyd) shown as heat map representing the hydrophobic interaction between each compound (y-axis) and each residue (x-axis) of hA₃AR. The strength of the interaction is rendered by a colorimetric scale going from white to dark green for low to high values. Panel C. Histograms representing electrostatic and hydrophobic interactions of few selected hA₃AR residues with compounds **5** (dark green), **9** (light green), **18** (yellow) and **21** (orange). Panel D. Representation of the predicted structure of the complex between hA₃AR (grey) and compounds **5** (green) and **21** (orange).

Concerning the hA₃-AR, the selected poses of compounds **5** and **21** point the furan substituent at position 2 towards the bottom of the binding pocket, the methylamino group at position 5 towards TM6 and the benzhydrylester or benzhydrylamido substituent at position 8 towards TM2 and TM7 (Figure 4, panel D). The triazolopyrimidine TP scaffold is stabilized by a π - π stacking interaction

with F168 (EL2), and by hydrophobic interactions with L264 (7.35) and I268 (7.39). Residues L90 (3.32), L91 (3.33), W243 (6.48) and L246 (6.51) define a hydrophobic region that accommodates the furan substituent, while V72 (2.64) contributes to the stabilization of the benzhydryl substituent by hydrophobic effect. The compounds are engaged in a double hydrogen bond with N250 (6.55), where the methylamino group at position 5 behaves as donor and the endocyclic nitrogen at position 3 as acceptor. The presence of the double hydrogen bond with an asparagine at position 6.55 is observed also in the other AR subtypes, and explains the loss of affinity of compounds which do not present a hydrogen bond donor at position 5 of the triazolopyrimidine-TP scaffold (compounds 50, 38, 41).

With regard to the hA_{2A}-AR (Figure 5, panel D), the ligands are involved in the already described double hydrogen bond with N253 (6.55), the triazolopyrimidine-TP scaffold is engaged in a π - π stacking interaction with F168 (EL2) and in a hydrophobic interaction with I274 (7.39), while the interaction with the residue at position 7.35, here M270, is feeble. The furan substituent is positioned in a hydrophobic cleft defined by V84 (3.32), L85 (3.33), W246 (6.48), L249 (6.51), H250 (6.52), while I66 (2.64) is involved in interactions with the benzhydryl group.

A similar binding mode was predicted on hA₁AR (Figure 6, panel D), where the ligands interact through a double hydrogen bond with N254 (6.55) and through a π - π stacking interaction with F168 (EL2). An hydrophobic environment is created also in this case by residues V87 (3.32), L88 (3.33), W247 (6.48), L250 (6.51), close to the furan moiety, and by residues I274 (7.39) and I69 (2.64), surrounding the benzhydryl group. The presence of T270 at position 7.35, which substitutes the L264 encountered in the hA₃ receptor, reduces the hydrophobic interactions between the ligands and the receptor in comparison with hA₃ subtype.

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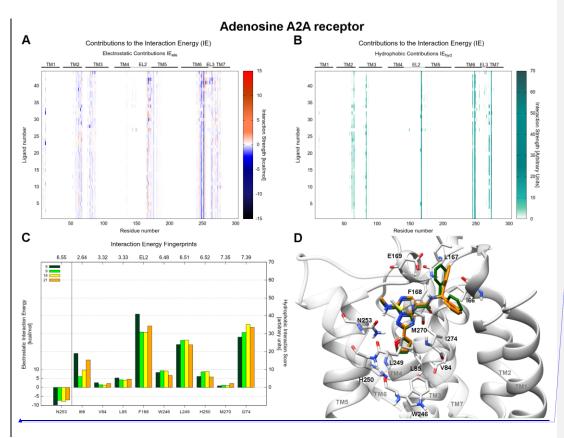


Figure 5. Panel A. Electrostatic Interaction Energy Fingerprints (IEFele) shown as heat map reporting the electrostatic interaction between each compound (y-axis) and each residue (x-axis) of hA_{2A}-AR. The strength of the interaction is rendered by a colorimetric scale going from blue to red for negative to positive values. Panel B. Hydrophobic Interaction Energy Fingerprints (IEFhyd) shown as heat map representing the hydrophobic interaction between each compound (y-axis) and each residue (x-axis) of hA_{2A}-AR. The strength of the interaction is rendered by a colorimetric scale going from white to dark green for low to high values. Panel C. Histograms representing electrostatic and hydrophobic interactions of few selected Ha_{2A} hA_{2A}AR residues with compounds 5 (dark green), 9 (light green), 18 (yellow) and 21 (orange). Panel D. Representation of the predicted structure of the complex between hA_{2A}-AR (grey) and compounds 5 (green) and 21 (orange).

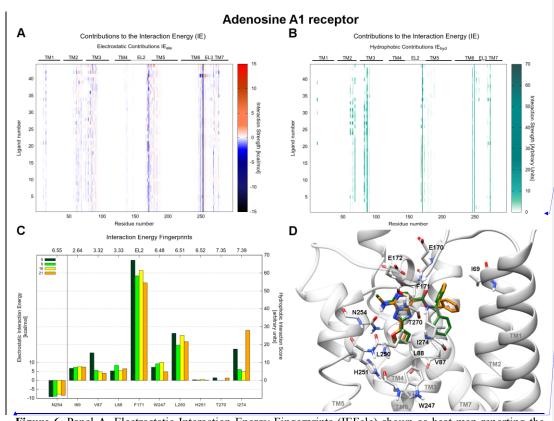


Figure 6. Panel A. Electrostatic Interaction Energy Fingerprints (IEFele) shown as heat map reporting the

electrostatic interaction between each compound (y-axis) and each residue (x-axis) of hA₁-AR. The strength of the interaction is rendered by a colorimetric scale going from blue to red for negative to positive values. Panel B. Hydrophobic Interaction Energy Fingerprints (IEFhyd) shown as heat map representing the hydrophobic interaction between each compound (y-axis) and each residue (x-axis) of hA₁-AR. The strength of the interaction is rendered by a colorimetric scale going from white to dark green for low to high values. Panel C. Histograms representing electrostatic and hydrophobic interactions of few selected hA₁-AR residues with compounds 5 (dark green), 9 (light green), 18 (yellow) and 21 (orange). Panel D. Representation of the predicted structure of the complex between hA₁-AR (grey) and compounds 5 (green) and 21 (orange).

In general, the compounds under investigation present a slight selectivity towards hA₃ receptor, which is difficult to be rationalized by molecular docking results, in which a hypothesis on just the static and final situation of the complex binding process is proposed. Considering the dynamic behavior behaviour of the receptor, a relevance can be attributed to two residues of EL2 that

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differentiates the hA₃ from the other subtype, but which are not directly involved in interactions in the docked poses. The position that in hA₁AR and hA_{2A}AR is occupied by a glutamate (E172 and E169, respectively), in hA₃AR is substituted by V169 (EL2), which can better stabilize the methylamino group in 5. Moreover, E170 of hA₁ and L167 of hA_{2A} are replaced by Q167 on hA₃ receptor, which can play a role in the stabilization of both the ester and amide moiety at position 8, acting as hydrogen bond donor as well as acceptor.

Conclusions

A novel series of [1,2,4]triazolo[1,5-c]pyrimidines variously substituted at the 8 and 5 position (3-43) were synthesized as A_3 adenosine receptor antagonists and pharmacologically characterized at the four adenosine receptor subtypes. In all cases, substitution at the 5 position had a detrimental effect in terms of affinity towards $\underline{h}A_3$ -AR. Instead, substitution at the 8 position of TP with various esters and amides generally led to $\underline{h}A_3$ -AR antagonists with affinity in the nanomolar range. Unfortunately, selectivity against the other adenosine receptor subtypes was not improved; in fact, obtained compounds displayed similar or worse selectivity profile than reference compound 1. The only exception was the 4-trifluoromethylbenzylamido derivative 24, which showed a quite good affinity at the hA_3 -AR (K_i = 15.3 nM) accompanied to an optimal selectivity against hA_1 , hA_{2A} and hA_{2B} ARs. This behaviour is difficult to be rationalized by molecular docking studies, in fact, the ligands bind the three AR subtypes in a similar fashion. In conclusion, despite the goal to obtain potent $\underline{h}A_3$ -AR antagonists with a [1,2,4]triazolo[1,5-c]pyrimidine scaffold was achieved, selectivity against other AR subtypes remains unmet. Future perspectives will be the exploration of the 2 position of the TP scaffold, in order to assess its role in regulation of affinity/selectivity at the four ARs.

Experimental part

Chemistry

General: Reactions were routinely monitored by thin-layer chromatography (TLC) on silica gel (precoated F254 Macherey-Nagel aluminium sheets). Flash chromatography was performed using

Macherey-Nagel 230-400 mesh silica gel. Light petroleum ether refers to the fractions boiling at 40-60 °C. Melting points were determined on a Büchi-Tottoli instrument and are uncorrected. ¹H-NMR were determined in CDCl₃, DMSO-d₆, or D₂O solutions with a Varian Gemini 200 spectrometer , peaks positions are given in parts per million (δ downfield relative to the central peak of the solvent, and J values are given in Hz). The following abbreviations were used: s, singlet; bs, broad singlet; d, doublet; dd, double doublet; t, triplet; q, quartet; m, multiplet. Electrospray mass spectra were recorded on an ES_Bruker 4000 Esquire spectrometer, accurate mass spectra were recorded on micrOTOF-Q---Bruker and compounds were dissolved in methanol.

Procedures for the obtainment of compounds 1,44-49 were previously reported.[16]

General procedure for the synthesis of ester and amide derivatives 3-3332

To 2.45 mmol of carboxylic acid derivatives (47) dissolved in 0.7 mL of dry pyridine were added 0.1 mL of phosphorous oxychloride. The mixture was led to -10°C and then was added 39.2 mmol of the appropriate amine or alcohol. The reaction was stirred at room temperature for 16 hours, then was added water and the product extracted with ethylacetate. The organic layer was washed with a NaHCO₃ solution, dried and concentrated. The residue was purified by flash chromatography (Ethyl acetate 9: Light Petroleum 1).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid isopropyl ester (3): yield 12%; pale yellow solid; mp 161°C; 1 H-NMR (200 MHz, CDCl₃) δ 1.41 (6H, d, J=6,2 Hz), 3.30 (3H, d, J=5,1 Hz), 5.32 (1H, m), 6.58-6.65 (2H, m), 7.38 (1H, d, J=4,1 Hz), 7.61 (1H, d, J=2,3 Hz), 8.69 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for C₁₄H₁₆N₅O₃ 302.1253; Found 302.1254 (Δ =0.0001); [M+Na]⁺ Calcd for C₁₄H₁₅N₅NaO₃ 324.1073, Found 324.1067 (Δ =0.0006). 2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid benzyl ester (4): yield 31%; brown solid; mp 130°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.31 (3H, d, J=4,1 Hz), 5.47 (2H, s), 6.60-6.76 (2H, m), 7.33-7.40 (5H, m), 7.56-7.63 (2H, m), 8.76 (1H, s). ES-MS m/z: [M+H]⁺ 350.1, [M+Na]⁺ 372.1.

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2-Furan-2-yl-5-methylamino-[1,2,4] triazolo[1,5-c] pyrimidine-8-carboxylic acid benzhydryl ester (5): yield 23%; white solid; mp 117°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.31 (3H, d, J=5,4 Hz), 6.61-6.75 (2H, m), 7.16 (1H, s), 7.29-7.40 (8H, m), 7.59-7.63 (4H, m), 8.81 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H] $^{+}$ Calcd for C₂₄H₂₀N₅O₃ 426.1566; Found 426.1565 (Δ =0.0001); [M+Na] $^{+}$ Calcd for C₂₄H₁₉N₅NaO₃ 448.1386, Found 448.1384 (Δ =0.0002).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 2-methyl-benzyl ester (**6**): yield 16%; white solid; mp 170°C; 1 H-NMR (200 MHz, CDCl₃) δ 2.48 (3H, s), 3.30 (3H, d, J=5,4 Hz), 5.47 (2H, s), 6.60 (1H, dd, J=2,1 Hz, J=4,2 Hz), 6.47 (1H, bs), 7.22-7.28 (3H, m), 7.39 (1H, d, J=4,2 Hz), 7.62-7.67 (2H, m), 8.74 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for C₁₉H₁₈N₅O₃ 364.1410; Found 364.1415 (Δ =0.0005); [M+Na]⁺ Calcd for C₁₉H₁₇N₅NaO₃ 386.1229, Found 386.1229 (Δ =0).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 3-methyl-benzyl ester (7): yield 13%; white solid; mp 170°C; 1 H-NMR (200 MHz, CDCl₃) δ 2.38 (3H, s), 3.30 (3H, d, J=5.4 Hz), 5.43 (2H, s), 6.59 (1H, dd, J=2.1 Hz, J=4.2 Hz), 6.67 (1H, bs), 7.13-7.17 (1H, m), 7.24-7.38 (5H, m), 7.61 (1H, d, J=2.1 Hz), 8.75 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for C₁₉H₁₈N₅O₃ 364.1410; Found 364.1411 ($\Delta=0.0001$); [M+Na]⁺ Calcd for C₁₉H₁₇N₅NaO₃ 386.1229, Found 386.1229 ($\Delta=0$).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 4-methyl-benzyl ester (8): yield 23%; white solid; mp 202°C; 1 H-NMR (200 MHz, CDCl₃) δ 2.36 (3H, s), 3.29 (3H, d, J=5.4 Hz), 5.42 (2H, s), 6.59-6.64 (2H, m), 7.20 (2H, d, J=8.3 Hz), 7.37 (1H, d, J=4.1 Hz), 7.45 (2H, d, J=8.3 Hz), 7.62 (1H, d, J=2.1 Hz), 8.73 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H] $^{+}$ Calcd for C₁₉H₁₈N₅O₃ 364.1410; Found 364.1403 (Δ =0.0007); [M+Na] $^{+}$ Calcd for C₁₉H₁₇N₅NaO₃ 386.1229, Found 386.1221 (Δ =0.0008).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 2-methoxy-benzyl ester (9): yield 19%; white solid; mp 181°C; ¹H-NMR (200 MHz, CDCl₃) δ 3.30 (3H, d, *J*=5.4 Hz), 3.87 (3H, s), 5.51 (2H, s), 6.58-6.63 (2H, m), 6.89-7.06 (2H, m), 7.37 (1H, d, *J*=4.1 Hz), 7.62 (1H,

d, J=2.3 Hz), 7.76 (1H, d, J=8.3 Hz), 8.76 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for $C_{19}H_{18}N_5O_4$ 380.1359; Found 380.1355 ($\Delta=0.0004$); [M+Na]⁺ Calcd for $C_{19}H_{17}N_5NaO_4$ 402.1178, Found 402.1174 ($\Delta=0.0004$).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 3-methoxy-benzyl ester (**10**): yield 13%; white solid; mp 156°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.30 (3H, d, J=5,4 Hz), 3.83 (3H, s), 5.45 (2H, s), 6.59 (1H, dd, J=2,1 Hz, J=4,3 Hz), 6.70 (1H, bs), 6.87 (1H, dd, J=1,6 Hz, J=8,3 Hz), 7.11-7.14 (1H, m), 7.20 (1H, m), 7.31-7.35 (1H, m), 7.41 (1H, d, J=4,3 Hz), 7.61 (1H, d, J=2,1 Hz), 8.76 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for C₁₉H₁₈N₅O₄ 380.1359; Found 380.1354 (Δ =0.0005); [M+Na]⁺ Calcd for C₁₉H₁₇N₅NaO₄ 402.1178, Found 402.1171 (Δ =0.0007).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 4-methoxy-benzyl ester (11): yield 23%; white solid; mp 189°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.29 (3H, d, J=5,4 Hz), 3.81 (3H, s), 5.40 (2H, s), 6.60 (1H, dd, J=2,1 Hz, J=4,3 Hz), 6.70 (1H, bs), 6.91 (2H, dd, J=2,1 Hz, J=7,2 Hz), 7.36 (1H, d, J=4,3 Hz) 7.47 (2H, dd, J=2,1 Hz, J=7,2 Hz), 7.61 (1H, d, J=2),1 Hz, 8.72 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H] $^+$ Calcd for C₁₉H₁₈N₅O₄ 380.1359; Found 380.1364 (Δ =0.0005); [M+Na] $^+$ Calcd for C₁₉H₁₇N₅NaO₄ 402.1178, Found 402.1182 (Δ =0.0004). 2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 2-chloro-benzyl ester (12): yield 29%; white solid; mp 205°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.29 (3H, d, J=5,4 Hz), 5.56 (2H, s), 6.60 (1H, dd, J=2,1 Hz, J=4,3 Hz), 6.69 (1H, d, J=5,4 Hz), 7.28-7.52 (4H, m), 7.62 (1H, d, J=2,1 Hz), 7.90 (1H, dd, J=2,1 Hz, J=7,3 Hz), 8.78 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H] $^+$ Calcd for C₁₈H₁₅ClN₅O₃ 384.0863 and 386.0834; Found 384.0871 (Δ =0.0008) and 386.0850 (Δ =0.0016); [M+Na] $^+$ Calcd for C₁₈H₁₄ClN₅NaO₃ 406.0683 and 406408.0653, Found 406.0688 (Δ =0.0005) and 408.0668 (Δ =0.0015).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 3-chloro-benzyl ester (13): yield 32%; white solid; mp 195°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.31 (3H, d, J=5<u>.4</u> Hz), 5.44 (2H, s), 6.60 (1H, dd, J=2<u>.1 Hz</u>, J=4<u>.3 Hz</u>), 6.70 (1H, d, J=5<u>.4 Hz</u>), 7.30-7.33 (2H, m),

7.41-7.42 (2H, m), 7.63 (1H, d, J=1.2 Hz), 7.68 (1H, d, J=2.1 Hz), 8.77 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for C₁₈H₁₅ClN₅O₃ 384.0863 and 386.0834; Found 384.0867 ($\Delta=0.0004$) and 386.0857 ($\Delta=0.0023$); [M+Na]⁺ Calcd for C₁₈H₁₄ClN₅NaO₃ 406.0683 and 406.0683, Found 406.0680 ($\Delta=0.0003$) and 408.0672 ($\Delta=0.0019$).

2-Furan-2-yl-5-methylamino-[1,2,4] triazolo[1,5-c] pyrimidine-8-carboxylic acid 4-chloro-benzyl ester (14): yield 32%; white solid; mp 205°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.30 (3H, d, J=5,4 Hz), 5.43 (2H, s), 6.62 (1H, dd, J=2,1 Hz, J=4,3 Hz), 6.69 (1H, d, J=5,4 Hz), 7.32-7.40 (3H, m), 7.53 (2H, d, J=8,3 Hz), 7.62 (1H, d, J=2,1 Hz), 8.75 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for C₁₈H₁₅ClN₅O₃ 384.0863 and 386.0834; Found 384.0869 (Δ =0.0006) and 386.0850 (Δ =0.0016); [M+Na]⁺ Calcd for C₁₈H₁₄ClN₅NaO₃ 406.0683 and 406408.0653, Found 406.0685 (Δ =0.0002) and 408.0658 (Δ =0.0005).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 2-bromo-benzyl ester (15): yield 17%; white solid; mp 223°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.31 (3H, d, J=5,4 Hz), 5.53 (2H, s), 6.60 (1H, dd, J=2,1 Hz, J=4,3 Hz), 6.68 (1H, bs), 7.19 (1H, d, J=6,2 Hz), 7.35-7.42 (2H, m), 7.58-7.63 (2H, m), 7.91 (1H, d, J=8,3 Hz), 8.80 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H] $^{+}$ Calcd for C₁₈H₁₅BrN₅O₃ 428.0358 and 430.0338; Found 428.0368 (Δ =0.000*\(\delta\$00010\)) and 430.0344 -0345 (Δ =0.00060007); [M+Na] $^{+}$ Calcd for C₁₈H₁₄BrN₅NaO₃ 450.0178 and 452.0157, Found 450.0174-0175 (Δ =0.00040003) and 452.0166-0164 (Δ =0.00090007).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 3-fluoro-benzyl ester (**16**): yield 4.4%; white solid; mp 193°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.30 (3H, d, J=5<u>.4</u> Hz), 5.46 (2H, s), 6.61 (1H, dd, J=2<u>.1 Hz</u>, J=4<u>.3 Hz</u>), 6.70 (1H, d, J=5<u>.4 Hz</u>), 6.99-7.07 (1H, m), 7.31-7.41 (3H, m), 7.53 (1H, d, J=10<u>.6 Hz</u>), 7.63 (1H, d, J=2<u>.1 Hz</u>), 8.77 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+Na]⁺ Calcd for C₁₈H₁₄FN₅NaO₃ 390.0978 and 391.1012, Found 390.0983 (Δ =0.0005) and 391.1013 (Δ =0.0001).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 4-fluoro-benzyl ester (17): yield 16%; white solid; mp 181°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.30 (3H, d, J=5.4

Hz), 5.43 (2H, s), 6.61 (1H, dd, J=2,.1 Hz J=4.3 Hz), 6.68 (1H, bs), 7.03-7.12 (2H, m), 7.34 (1H, d, J=4.3 Hz), 7.53-7.63 (3H, m), 8.74 (1H, s). HRMS (ESI/Q-TOF) m/z: $[M+Na]^+$ Calcd for $C_{18}H_{14}FN_5NaO_3$ 390.0978 and 391.1012, Found 390.0985 (Δ =0.0007) and 391.1013 (Δ =0.0001). 2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 4-ethyl-benzyl ester (18): yield 16%; white solid; mp 175°C; ¹H-NMR (200 MHz, CDCl₃) δ 1.24 (3H, t, *J*=8.2 Hz), 2.66 (2H, q, J=8.2 Hz), 3.29 (3H, d, J=5.4 Hz), 5.43 (2H, s), 6.59-6.65 (2H, m), 7.20-7.24 (2H, m), 7.36 (1H, d, *J*=4<u>.3 Hz</u>), 7.47 (2H, d, *J*=8<u>.2 Hz</u>), 7.62 (1H, d, *J*=2<u>.1 Hz</u>), 8.74 (1H, bs). ¹³C NMR (101 MHz, CDCl₃) δ 163.31, 158.03, 152.22, 151.86, 148.64, 145.71, 144.80, 144.41, 133.46, 128.35, 128.15, 113.91, 112.17, 104.74, 66.71, 28.78, 28.11, 15.76. HRMS (ESI/Q-TOF) m/z: $[M+H]^+$ Calcd for $C_{20}H_{20}N_5O_3$ 378.1566; Found 378.1574 (Δ =0.0008); $[M+Na]^+$ Calcd for $C_{20}H_{19}N_5NaO_3$ 400.1386, Found 400.1389 (Δ =0.0003). 2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic 1-methyl-2acid phenyl-ethyl ester (19): yield 18%; brown sticky foam; ¹H-NMR (200 MHz, CDCl₃) δ 1.39 (3H, d, J=6.3 Hz), 2.97-3.15 (2H, m), 3.28 (3H, s), 5.42-5.48 (1H, m), 6.58 (1H, dd, J=2.1 Hz, J=4.3 Hz), 6.76 (1H, bs), 7.19-7.39 (6H, m), 7.61 (1H, d, J=2.1 Hz), 8.65 (1H, s). ES-MS m/z: $[M+H]^+$ 400.1. 2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid benzylamide (20): yield 16%; white solid; mp 246°C; ¹H-NMR (200 MHz, CDCl₃) δ 3.30 (3H, d, *J*=5.4 Hz), 4.77 (2H, d, J=6.2 Hz), 6.49 (1H, bs), 6.59 (1H, dd, J=2.1 Hz, J=4.3 Hz), 7.16 (1H, d, J=4.3 Hz), 7.32-7.46 (5H, m), 7.62 (1H, d, J=2.1 Hz), 8.86 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+Na]⁺ Calcd for $C_{18}H_{16}N_6NaO_2$ 371.1232, Found 371.1236 (Δ =0.0004). 2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid benzhydryl-amide (21): yield 42%; pale yellow solid solid; mp 199°C; ¹H-NMR (200 MHz, CDCl₃) δ 3.32 (3H, d, *J*=5<u>.4 Hz</u>), 6.50-6.53 (2H, m), 6.63 (1H, dd, *J*=2<u>.1 Hz</u>, *J*=4<u>.3 Hz</u>), 7.15 (1H, d, *J*=4<u>.3 Hz</u>),7.21-7.46 (10H, m), 7.66 (1H, d, *J*=2<u>.1 Hz</u>), 8.85 (1H, s), 9.72 (1H, d, *J*=8<u>.2 Hz</u>). HRMS (ESI/Q-TOF) m/z: $[M+H]^+$ Calcd for $C_{24}H_{21}N_6O_2$ 425.1726, Found 425.1722 (Δ =0.0004); $[M+Na]^+$ Calcd for

 $C_{24}H_{20}N_6NaO_2$ 447.1545, Found 447.1541 (Δ =0.0004).

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2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 4-methyl-benzylamide (22): yield 11%; white solid; mp 236°C; 1 H-NMR (200 MHz, CDCl₃) δ 2.35 (3H, s), 3.30 (3H, d, J=5.4 Hz), 4.72 (2H, d, J=5.4 Hz), 6.43 (1H, bs), 6.59 (1H, dd, J=2.1 Hz, J=4.3 Hz), 7.16-7.35 (5H, m), 7.62 (1H, d, J=2.1 Hz), 8.66 (1H, s), 9.03 (1H, bs). HRMS (ESI/Q-TOF) m/z: [M+H] $^+$ Calcd for C₁₉H₁₉N₆O₂ 363.1569, Found 363.1564 (Δ =0.0005); [M+Na] $^+$ Calcd for C₁₉H₁₈N₆NaO₂ 385.1389, Found 385.1382 (Δ =0.0007).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 4-methoxy-benzylamide (23): yield 20%; pale yellow solid; mp 232°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.29 (3H, d, J=5,4 Hz), 3.80 (3H, s), 4.69 (2H, d, J=5,4 Hz), 6.48 (1H, bs), 6.58 (1H, dd, J=2,1 Hz, J=4,3 Hz), 6.90 (2H, dd, J=2,1 Hz, J=7,2 Hz), 7.15 (1H, d, J=4,3 Hz), 7.37 (2H, dd, J=2,1 Hz, J=7,2 Hz), 7.62 (1H, d, J=2,1 Hz), 8.85 (1H, s), 8.99 (1H, bs). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for C₁₉H₁₉N₆O₃ 379.1519, Found 379.1522 (Δ =0.0003); [M+Na]⁺ Calcd for C₁₉H₁₈N₆NaO₃ 401.1338, Found 401.1341 (Δ =0.0003).

2-Furan-2-yl-5-methylamino-[1,2,4] triazolo[1,5-c] pyrimidine-8-carboxylic acid 4-trifluoromethyl-benzylamide (24): yield 18%; orange solid; mp 249°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.31 (3H, d, J=5.4 Hz), 4.82 (2H, d, J=5.4 Hz), 6.52 (1H, bs), 6.60 (1H, dd, J=2.1 Hz, J=4.3 Hz), 7.17 (1H, d, J=4.3 Hz), 7.52-7.64 (5H, m), 8.86 (1H, s), 9.13 (1H, bs). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for C₁₉H₁₆F₃N₆O₂ 417.1287, Found 417.1315 ($\Delta=0.0028$).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 4-chloro-benzylamide (25): yield 13%; pale brown solid; mp 225°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.30 (3H, d, J=5,4 Hz), 4.72 (2H, d, J=5,4 Hz), 6.52 (1H, bs), 6.60 (1H, dd, J=2,1 Hz, J=4,3 Hz), 7.17 (1H, d, J=4,3 Hz), 7.29-7.35 (4H, m), 7.63 (1H, d, J=2,1 Hz), 8.85 (1H, s), 9.06 (1H, bs). HRMS (ESI/Q-TOF) m/z: [M+Na]⁺ Calcd for C₁₈H₁₅ClN₆NaO₂ 405.0843 and 407.0813, Found 405.0847 (Δ =0.0004) and 407.0820 (Δ =0.0007).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid 4-fluoro-benzylamide (**26**): yield 26%; white solid; mp 225°C; ¹H-NMR (200 MHz, CDCl₃) δ 3.30 (3H, d,

J=5,4 Hz), 4.72 (2H, d, J=5,4 Hz), 6.51 (1H, bs), 6.59 (1H, dd, J=2,1 Hz, J=4,3 Hz), 7.00-7.09 (2H, m), 7.15 (1H, d, J=4,3 Hz), 7.36-7.43 (2H, m), 7.63 (1H, d, J=2,1 Hz), 8.85 (1H, s), 9.05 (1H, bs). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for $C_{18}H_{16}FN_6O_2$ 367.1319, Found 367.1310 ($\Delta=0.0001,0009$); [M+Na]⁺ Calcd for $C_{18}H_{15}FN_6NaO_2$ 389.1138, Found 389.1131 ($\Delta=0.0007$). 2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid (biphenyl-4-ylmethyl)-amide (27): yield 5.5%; pale yellow solid; mp>250°C; ¹H-NMR (200 MHz, DMSO-d₆) δ 3.01 (3H, d, J=5,4 Hz), 4.70 (2H, d, J=5,4 Hz), 6.75 (1H, dd, J=2,1 Hz, J=4,3 Hz), 7.32 (1H, d, J=4,3 Hz), 7.38-7.50 (5H, m), 6.66 (4H, d, J=8,2 Hz), 7.98 (1H, d, J=2,1 Hz), 8.58 (1H, s), 8.92 (1H, bs), 9.10 (1H, bs). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for $C_{24}H_{21}N_6O_2$ 425.1726, Found 425.1726 ($\Delta=0$); [M+Na]⁺ Calcd for $C_{24}H_{20}N_6NaO_2$ 447.1545, Found 447.1546 ($\Delta=0.0001$).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid [2-(3,4-dimethoxy-phenyl)-ethyl]-amide (**30**): yield 25%; pale yellow solid solid; mp 211°C; ¹H-NMR (200 MHz, CDCl₃) δ 2.94 (2H, t, *J*=7.2 Hz), 3.29 (3H, d, *J*=5.4 Hz), 3.74-3.86 (8H, m), 6.50 (1H, bs), 6.60 (1H, dd, *J*=2.1 Hz, *J*=4.3 Hz), 6.83-6.88 (3H, m), 7.07 (1H, d, *J*=4.3 Hz), 7.64 (1H, d, *J*=2.1 Hz),

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8.70 (1H, bs), 8.83 (1H, s). HRMS (ESI/Q-TOF) m/z: $[M+H]^+$ Calcd for $C_{21}H_{23}N_6O_4$ 423.1781; Found 423.1782 (Δ =0.0001); $[M+Na]^+$ Calcd for $C_{21}H_{22}N_6NaO_4$ 445.1600, Found 445.1605 (Δ =0.0005).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid (1,1-dimethyl-2-phenyl-ethyl)-amide (31): yield 40%; white solid solid; mp 172°C; 1 H-NMR (200 MHz, CDCl₃) δ 1.52 (6H, s), 3.23 (2H, s), 3.29 (3H, d, J=5.4 Hz), 6.44 (1H, bs), 6.57 (1H, dd, J=2.1 Hz, J=4.3 Hz), 7.12 (1H, d, J=4.3 Hz), 7.18-7.27 (5H, m), 7.62 (1H, d, J=2.1 Hz), 8.58 (1H, bs), 8.82 (1H, s). 13 C NMR (101 MHz, CDCl₃) δ 161.87, 156.32, 151.60, 150.22, 147.82, 145.38, 145.00, 138.14, 130.82, 128.00, 126.34, 113.45, 112.11, 107.27, 54.85, 46.10, 28.11, 27.20. HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for $C_{21}H_{23}N_6O_2$ 391.1883; Found 391.1886 (Δ=0.0003); [M+Na]⁺ Calcd for $C_{21}H_{22}N_6NaO_2$ 413.1702, Found 413.1703 (Δ=0.0001).

2-Furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid (2-phenoxy-ethyl)-amide (32): yield 34%; white solid solid; mp 198°C; 1 H-NMR (200 MHz, CDCl₃) δ 3.29 (3H, d, J=5.4 Hz), 3.96 (2H, q, J=5.2 Hz), 4.23 (2H, q, J=5.2 Hz) 6.50 (1H, d, J=5.4 Hz), 6.58 (1H, dd, J=2.1 Hz, J=4.3 Hz), 6.70-7.03 (3H, m), 7.15 (1H, d, J=4.3 Hz), 7.30-7.34 (2H, m), 7.63 (1H, d, J=2.1 Hz), 8.83 (1H, bs), 9.13 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for C₁₉H₁₉N₆O₃ 379.1519; Found 379.1530 ($\Delta=0.0011$); [M+Na]⁺ Calcd for C₁₉H₁₈N₆NaO₃ 401.1338, Found 401.1347 ($\Delta=0.0009$).

Procedure for the synthesis of 2-furan-2-yl-5-methylamino-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid N'-phenyl-hydrazide (33).

150 mg of compound 47 (0.58 mmol) were dissolved in 10 mL of ethanol, then 333 mg of N-(3-dimethylaminopropyl)-N'-ethylcarbodiimide hydrochloride (1.74 mmol), 235 mg of 1-hydroxybenzotriazole hydrate (1.74 mmol) and 68 μ L of phenylhydrazine (0.70 mmol) were added. The mixture was stirred at room temperature overnight. Then, ethanol was removed under reduced pressure and 30 mL of water were added to the residue. The product was extracted three times with

10 mL of ethylacetate. The organic layers were combined, dried over anhydrous sodium sulfate and concentrated. The residue was purified by flash chromatography (from Light Petroleum 7: Ethyl acetate 3 to Light Petroleum 3: Ethyl acetate 7) to afford 79 mg of a pale yellow solid (yield 39%). Mp>220°C; ¹H-NMR (200 MHz, CDCl₃) δ 3.30 (3H, d, *J*=5.4 Hz), 6.60-6.63 (2H, m), 6.91-7.00 (3H, m), 7.21-7.29 (4H, m), 7.65 (1H, d, *J*=2.1 Hz), 8.82 (1H, s), 10.03 (1H, bs). ES-MS m/z: [M+H]⁺ 350.2, [M+Na]⁺ 372.2, [M+K]⁺ 388.1.

Synthesis of 5-(3,4-Dimethoxy-benzylamino)-2-furan-2-yl-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid benzhydryl-amide (34).

For the synthesis of compound **34** was applied the same procedure reported for derivatives **3-33-32** but using derivative **49** as carboxylic acid derivative and benzhydrylamine as amine. Yield 63%; pale brown solid; mp 170°C; ¹H-NMR (200 MHz, CDCl₃) δ 3.85 (6H, s), 4.82 (2H, d, *J*=6.2 Hz), 6.48 (1H, d, *J*=6.2 Hz), 6.60 (1H, dd, *J*=2.1 Hz, *J*=4.3 Hz), 6.74 (1H, bs), 6.82-6.98 (3H, m), 7.14 (1H, d, J=4.3 Hz), 7.32-7.46 (10H, m), 7.62 (1H, d, *J*=2.1 Hz), 8.88 (1H, s), 9.68 (1H, d, *J*=6.4 Hz). ES-MS (negative mode) m/z: [M-H]⁻ 559.2.

General procedure for nucleophilic substitution with amino compounds (compounds 35-39)

To 100 mg (0.33 mmol) of compound **46** dissolved in ethanol was added the appropriate amine (0.99 mmol to 1.98 mmol). The mixture was heated in a sealed tube at 120°C for three hours. The solvent was then removed and the residue was purified by flash chromatography (from Light petroleum 7: Ethyl acetate 3 to Ethyl acetate). Sometimes ethyl 5 ethoxy 2 (furan 2 yl) [1,2,4]triazolo[1,5 c]pyrimidine 8 carboxylate (50) was obtained as by product. Derivative 50 was isolated and characterized (see below for chemical characterization).

ethyl 2-(5-((2-ethoxy-2-oxoethyl)amino)-2-(furan-2-yl)-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxamido)acetate (35): reaction was performed using 138 mg of glycine ethyl ester hydrochloride (0.990 mmol) and 138 μL of TEA (0.99 mmol) leading to concomitant substitution at the 5 position and amidation at the 8 position of [1,2,4]triazolo[1,5-c]pyrimidine; yield 55%; pale

yellow solid; mp 182°C; ¹H-NMR (200 MHz, CDCl₃) δ 1.28 (3H, t, J=7.2 Hz), 1.44 (3H, t, J=7.2 Hz), 4.12 (2H, d, J=5.4 Hz), 4.22 (2H, q, J=7.2 Hz), 4.47 (4H, m), 6.59 (1H, dd, J=2.1 Hz, J=4.3 Hz), 6.76 (1H, bs), 7.35 (2H, m), 7.62 (1H, d, J=2.1 Hz), 8.65 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for $C_{18}H_{21}N_6O_6$ 417.1523; Found 417.1521 ($\Delta=0.0002$); [M+Na]⁺ Calcd for $C_{18}H_{20}N_6NaO_6$ 439.1342, Found 439.1341 ($\Delta=0.0001$).

Ethyl 2-(furan-2-yl)-5-(2-phenylhydrazinyl)-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylate (36): reaction was performed using 97 μL of phenylhydrazine (1.32 mmol); yield 71%; brown solid; mp 141-155 °C; 1 H-NMR (200 MHz, CDCl₃) δ 1.42 (3H, t, J=7.2 Hz), 4.46 (2H, q, J=7.2 Hz), 6.62 (1H, dd, J=2.1 Hz, J=4.3 Hz), 6.95-6.99 (3H, m), 7.22-7.28 (4H, m), 7.43 (1H, d, J=3.2 Hz), 7.65 (1H, d, J=2.1 Hz), 8.66 (1H, s). ES-MS m/z: [M+H]⁺ 365.1, [M+Na]⁺ 387.1.

5-(2-tert-Butoxycarbonylamino-ethylamino)-2-furan-2-yl-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid ethyl ester (37): reaction was performed using 159 mg of mono-Bocethylendiamine (0.99 mmol); yield 45%; pale yellow solid; mp 170°C; ¹H-NMR (200 MHz, CDCl₃) δ 1.43-1.53 (12H, m), 3.52 (2H, bs), 3.83 (2H, bs), 4.47 (2H, q, *J*=7.2 Hz), 4.92 (1H, bs), 6.59 (1H, dd, *J*=2.1 Hz, *J*=4.3 Hz), 7.14 (1H, bs), 7.37 (1H, d, *J*=4.3 Hz), 7.62 (1H, d, *J*=2.1 Hz), 8.68 (1H, s). ES-MS m/z: [M+Na]⁺ 439.2.

[M+H]⁺ Calcd for $C_{14}H_{15}N_4O_4$ 303.1093; Found 303.1097 (Δ =0.0004); [M+Na]⁺ Calcd for $C_{14}H_{14}N_4NaO_4$ 325.0913, Found 325.0911 (Δ =0.0002).

Ethyl 5-(2-(tert-butoxycarbonyl)hydrazinyl)-2-(furan-2-yl)-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylate (39): reaction was performed using 260 mg of tert-butyl hydrazinecarboxylate (1.98 mmol); yield 15%; white solid; mp 159°C; 1 H-NMR (200 MHz, CDCl₃) δ 1.41-1.49 (12H, m), 4.49 (2H, q, J=7.2 Hz), 6.58-6.60 (1H, m), 7.40 (1H, d, J=4.3 Hz), 7.63 (1H, s), 7.94 (1H, bs), 8.71 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for C₁₇H₂₁N₆O₅ 389.1573; Found 389.1584 (Δ =0.0011); [M+Na]⁺ Calcd for C₁₇H₂₀N₆NaO₅ 411.1393, Found 411.1393 (Δ =0). This reaction afforded also ethyl 5-ethoxy-2-(furan-2-yl)-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylate (50): see compound 38 synthesis for its charachterization.

Ethyl 5 ethoxy 2 (furan 2 yl) [1,2,4]triazolo[1,5 e]pyrimidine 8 earboxylate (50): white solid; mp 126°C; ¹H NMR (200 MHz, CDCl₃) δ 1.46 (3H, t, *J*=7.2 Hz), 1.61 (3H, t, *J*=7.2 Hz), 4.50 (2H, q, *J*=7.2 Hz), 4.87 (2H, q, *J*=7.2 Hz), 6.59 (1H, dd, <u>J</u>=2.1, Hz *J*=4.3 Hz, J=2), 7.39 (1H, d, *J*=4.3 Hz), 7.63 (1H, d, *J*=2.1 Hz), 8.68 (1H, s). HRMS (ESI/Q TOF) m/z: [M+H][±] Calcd for C₁₄H₁₅N₄O₄ 303.1093; Found 303.1097 (Δ=0.0004); [M+Na][±] Calcd for C₁₄H₁₄N₄NaO₄ 325.0913, Found 325.0911 (Δ=0.0002).

General procedure for the removal of tert-butyloxy carbonyl protecting group (compounds 40-42) 0.05 mmol of derivatives 37-39 (21 mg of 37, 22 mg of 38 and 19 mg of 39) were dissolved in 5 mL of a saturated solution of hydrochloric acid in ethyl acetate. Reaction was stirred at room temperature for 2 hours. Solvent was then removed under reduced pressure and the solid was filtered off to give the desired compounds 40-42.

2-(8-Ethoxycarbonyl-2-furan-2-yl-[1,2,4]triazolo[1,5-c]pyrimidin-5-ylamino)-ethyl-amine hydrochloride (40): yield 75%; white solid; mp 250°C; ¹H-NMR (200 MHz, d₆-DMSO) δ 1.35 (3H, t, *J*=7.2 Hz), 3.14 (2H, bs), 3.93 (2H, bs), 4.34 (2H, q, *J*=7.2 Hz), 6.55 (1H, dd, *J*=2.1 Hz, *J*=4.3

<u>Hz</u>), 7.21 (1H, d, J=4.3 Hz), 7.61 (1H, d, J=2.1 Hz), 8.30 (3H, bs), 8.53 (1H, s). ES-MS m/z: $[M+H]^+$ 317.1.

2-(furan-2-yl)-5-(piperazin-1-yl)-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylate hydrochloride (41): yield quantitative; white solid; mp 270°C; 1 H-NMR (200 MHz, D₂O) δ 1.39 (3H, t, J=7.2 Hz), 3.50 (4H, bs), 4.36-4.47 (4H, m), 4.79 (2H, under solvent signal), 6.69 (1H, m), 7.28 (1H, d, J=3.2 Hz), 7.75 (1H, s), 8.62 (1H, s). HRMS (ESI/Q-TOF) m/z: [M+H]⁺ Calcd for C₁₆H₁₉N₆O₃ 343.1519; Found 343.1519 (Δ =0); [M+Na]⁺ Calcd for C₁₆H₁₈N₆NaO₃ 365.1338, Found 365.1338 (Δ =0.0008).

Ethyl 2-(furan-2-yl)-5-hydrazinyl-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylate hydrochloride (42): yield quantitative; brown solid; mp 146-154°C; 1 H-NMR (200 MHz, D₂O) δ 1.39 (3H, t, J=7.2 Hz), 4.40 (2H, q, J=7.2 Hz), 6.67 (1H, s), 7.26 (1H, s), 7.73 (1H, s), 8.63 (1H, s). ES-MS m/z: [M+H] $^{+}$ 289.1, [M+Na] $^{+}$ 311.1.

Synthesis of 5-(2-tert-Butoxycarbonylamino-ethylamino)-2-furan-2-yl-[1,2,4]triazolo[1,5-c]pyrimidine-8-carboxylic acid (43)

To 0.167 mmol of ethyl ester compound **37** dissolved in ethanol was added 1.67 mmol of LiOH $_{12}$ O and 1.5 mmol of water. The mixture was refluxed and stirred for three hours. Then, a little amount of water was added and HCl was added since pH 3. The carboxylic acid derivative precipitated and the solid was filtered off. Yield 78%; pale yellow solid; mp 150°C; 1 H-NMR (400 MHz, $_{12}$ H-DMSO) $_{13}$ O (9H, s), 3.22 (2H, m), 3.68 (2H, m), 6.75 (1H, dd, $_{12}$ Hz, $_{13}$ Hz, $_{14}$ Hz, $_{15}$ Hz,

Biology

Binding at the human A_1 , A_{2A} and A_3 ARs

All pharmacological methods followed the procedures as described earlier.[22] Briefly, membranes for radioligand binding were prepared from CHO cells stably transfected with human AR subtypes

in a two-step procedure. In a first low-speed step (1,000 x g), cell fragments and nuclei were removed, thenthe crude membrane fraction was sedimented from the supernatant at 100,000 x g. The membrane pellet was resuspended in the buffer used for the respective binding experiments (50 mMTris/HCl buffer pH 7.4 for hA₁ and hA_{2A} AR; 50 mMTris/HCl,10 mM MgCl₂, 1 mM EDTA, pH 8.25 for hA₃-AR), frozen in liquid nitrogen and stored at -80 °C. For radioligand binding at the hA₁ AR 1 nM [³H]CCPA was used, whereas 10 nM [³H]NECA and 1 nM [³H]HEMADO were used for hA_{2A} and hA₃ ARs, respectively. Non specific binding of [³H]CCPA was determined in the presence of 1 mM theophylline, in the case of [³H]NECA and [³H]HEMADO, 100 μM R-PIA was used.[22][23][24]K_i-values from competition experimentswere calculated with the program SCTFIT. [25]

Adenylyl cyclase activity

The potency of antagonists at the hA_{2B} -AR was determined in adenylyl cyclase experiments. The procedure was carried out as described previously with minor modifications. [22][26] In this case only one high speed centrifugation of the homogenate of CHO cells stably transfected with human A_{2B} -AR subtypes was used. The resulting crude membrane pellet was resuspended in 50 mMTris/HCl, pH 7.4 and immediately used for the cyclase assay. Therefore, inhibition of NECA-stimulated adenylyl cyclase activity (stimulation with 5 μ M of NECA) was determined as a measurement of affinity of compounds. Membranes were incubated with about 150,000 cpm of [α - 32 P]ATP for 20 min in the incubation mixture as described without EGTA and NaCl. [26] IC₅₀ values were calculated with the Hill equation. Hill coefficients in all experiments were near unity.

Molecular modelling

Software overview

Molecular modeling studies were performed on a 8 CPU (Intel® Xeon® CPU E5-1620 3.50GHz) linux workstation. General molecular modeling operations were executed using the MOE suite (Molecular Operating Environment, version 2018.01) [27].

GOLD (Genetic Optimization for Ligand Docking, version 5.4.1) [28] suite was used as docking program, and the collected poses were analyzed (energy computation and visual inspection) through MOE.

Three-dimensional structures of Adenosine Receptors

A crystallographic structure was retrieved from the Protein Data Bank for hA_{2A} and hA_1 adenosine receptors, resulting in structure 3PWH [21] and 5UEN [20], respectively. Among the various crystallographic structures available for hA_{2A} -AR, one complex with the inverse agonist ZM-241385 was chosen, because of the chemical similarity of its 7-amino[1,2,4]triazolo[1,5,a][1,3,5]triazine scaffold with the 5-amino[1,2,4]triazolo[1,5-c]pyrimidine moiety of the compounds under investigation.

Given the lack of any crystallographic structures for hA₃-AR, a homology model was retrieved from the *Adenosiland* web-platform [29][30] previously developed by our research group. The model was constructed using 3PWH as a template, considering the presence of ZM-241385 as environment for induced fit.

The residues of ARs are identified according the generic Ballesteros Weinstein numbering system [31] throughout this work.

Molecular docking

Three dimensional structures of the ligands were built by the MOE-builder tool. Ionization states were predicted using the MOE-protonate 3D tool [32]. Tautomers and atom hybridation were checked, and structures were minimized by the MMFF94x until the root mean square (RMS) gradient fell below 0.1 kcal mol⁻¹ A⁻¹. GOLD docking tool was selected as a conformational search program and Goldscore as scoring function, referring to a previous docking benchmark study performed by our team [33] [34]. For each ligand, 20 docking simulation runs were performed on each receptor subtype, searching on a sphere of 20 Å radius, centered on the lateral chain nitrogen of the conserved N6.55.

Docking Analysis

Ligand and protein partial charges were calculated using the PM3 [35] method and AMBER12EHT force field respectively. Then, electrostatic and Van der Waals energy contributions to the binding energy were calculated by MOE, together with per residue electrostatic and hydrophobic interactions. Per residue information were reported in the so-called "Interaction Energy Fingerprints" (IEF) [33]: they consists in heat maps reporting the strength of the interaction of each residue (x-axis) and each ligand (y-axis) according to a colorimetric scale going from blue to red for negative to positive values in the case of electrostatic contributions (IEFele), and from white to dark green for low to high values for hydrophobic contributions (IEFhyd). The interactions of most relevant residues were also reported in histograms, whose height is proportional to the strength of the interaction. All the plots were produced using GNUPLOT 4.6 [36].

MMSDocking Video Maker

The in-house MMsDocking video maker tool was exploited to produce videos showing the docking poses, per residue IEFhyd and IEFele data for selected residues, experimental binding data and scoring values. Representations of docking poses were produced using CHIMERA52 [37], two-dimensional depictions were constructed through the cheminformatics toolkit RDKit [38], the heat maps were obtained through GNUPLOT 4.6 [36]; in the end, videos were mounted using MEncoder [39].

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References

- [1] B.B. Fredholm, A.P. IJzerman, K.A. Jacobson, K.-N. Klotz, J. Linden, International Uunion of pPharmacology . XXV . Nomenclature and cClassification of aAdenosine receptors, Pharmacol. Rev. 53 (2001) 527–552.
- [2] B.B. Fredholm, Adenosine a physiological or pathophysiological agent?, <u>J. Mol. Med. 92</u>

Formattato: Giustificato

- (20132014) 201-6. doi:10.1007/s00109-013-1101-6.
- [3] B.B. Fredholm, A.P. IJzerman, K.A. Jacobson, J. Linden, C.E. Mu, International <u>u</u>Union of <u>b</u>Basic and <u>c</u>Clinical <u>p</u>Pharmacology . LXXXI . Nomenclature and <u>c</u>Classification of <u>a</u>Adenosine <u>r</u>Receptors An <u>u</u>Update, <u>Pharmacol. Rev.</u> 63 (2011) 1–34. doi:10.1124/pr.110.003285.1.
- [4] K.A. Jacobson, Z. Gao, Adenosine receptors as therapeutic targets, Nat. Rev. Drug Discov. 5 (2006) 247–264. doi:10.1038/nrd1983.
- [5] V. Mitrovic, P. Seferovic, S. Dodic, M. Krotin, A. Neskovic, K. Dickstein, H. De Voogd, C. Böcker, D. Ziegler, M. Godes, R. Nakov, H. Essers, C. Verboom, B. Hocher, Cardio-renal effects of the A₁ adenosine receptor antagonist SLV320 in patients with heart failure, Circ. Hear. Fail. 2 (2009) 523–531. doi:10.1161/CIRCHEARTFAILURE.108.798389.
- [6] S.C. Yap, H.T. Lee, Adenosine and protection from acute kidney injury, Curr. Opin. Nephrol. Hypertens. 21 (2012) 24–32. doi:10.1097/MNH.0b013e32834d2ec9. Adenosine.
- [7] P.A. Borea, K. Varani, F. Vincenzi, P.G. Baraldi, M.A. Tabrizi, S. Merighi, S. Gessi, The A3 Adenosine Receptor: History and Perspectives, Pharmacol. Rev. 67 (2014) 74–102. doi:10.1124/pr.113.008540.
- [7] D. Preti, P.G. Baraldi, A.R. Moorman, P.A. Borea, K. Varani, History and perspectives of A_{2A} adenosine receptor antagonists as potential therapeutic agents., Med. Res. Rev. 35 (2015) 790–848. doi:10.1002/med.21344.
- [8] R.M. Brown, J.L. Short, Adenosine A_{2A} receptors and their role in drug addiction, J. Pharm. Pharmacol. 60 (2008) 1409–1430. doi:10.1211/jpp/60.11.0001.
- [9] B. Cacciari, G. Pastorin, C. Bolcato, G. Spalluto, M. Bacilieri, S. Moro, A_{-2B} adenosine receptor antagonists: recent developments, Mini-Reviews Med. Chem. 5 (2005) 1053–1060.
- [10] K. Sun, Y. Xia, New insights into sickle cell disease: a disease of hypoxia., Curr. Opin. Hematol. 20 (2013) 215–21. doi:10.1097/MOH.0b013e32835f55f9.
- [11] S.L. Cheong, S. Federico, G. Venkatesan, A.L. Mandel, Y. Shao, S. Moro, G. Spalluto, G.

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Pastorin, The A-3 Adenosine adenosine rReceptor as mMultifaceted tTherapeutic_tTarget:

Ppharmacology, mMedicinal cChemistry, and iIn sSilico aApproaches, Med. Res. Rev. 31

(2011). doi:10.1002/med.20254.

[12] K.A. Jacobson, A.M. Klutz, D.K. Tosh, A.A. Ivanov, D. Preti, Medicinal <u>c</u>Chemistry of the A₃ Aadenosine <u>r</u>Receptor: <u>a</u>Agonists, <u>a</u>Antagonists, and <u>r</u>Receptor <u>e</u>Engineering, <u>Handb.</u>

<u>Exp. Pharmacol.</u> 193 (2009) 123—159. doi:10.1007/978-3-540-89615-9.

- [13] CF101 clinical trials, https://clinicaltrials.gov/ct2/results?term=CF101&Search=Search.
- [14] CF102 clinical trials, https://clinicaltrials.gov/ct2/results?term=CF102&Search=Search.
- [15] Palobiofarma SL, "First-in-human" <u>s</u>Study <u>t</u>To <u>a</u>Assess the <u>s</u>Safety and <u>t</u>Tolerability of PBF-677 in <u>h</u>Healthy <u>v</u>Volunteers, (2016).

 https://clinicaltrials.gov/ct2/show/NCT02639975?term=A3+antagonist&rank=1.
- [16] S. Federico, A. Ciancetta, N. Porta, S. Redenti, G. Pastorin, B. Cacciari, K.-N. Klotz, S. Moro, G. Spalluto, Scaffold decoration at positions 5 and 8 of 1,2,4-triazolo[1,5- c] pyrimidines to explore the antagonist profiling on adenosine receptors: A preliminary structure-activity relationship study, J. Med. Chem. 57 (2014) 6210–6225. doi:10.1021/jm500752h.
- [17] H. Tsumuki, J. Shimada, H. Imma, A. Nakamura, H. Nonaka, S. Shiozaki, S. Ichikawa, T. Kanda, Y. Kuwana, M. Ichimura, F. Suzuki, [1,2,4]triazolo[1,5-c]pyrimidine derivatives, EP0976753A1, 2000.
- [18] S. Federico, A. Ciancetta, D. Sabbadin, S. Paoletta, G. Pastorin, B. Cacciari, K.-N. Klotz, S.-Moro, G. Spalluto, Exploring the dDirectionality of 5-sSubstitutions in a nNew sSeries of 5-aAlkylaminopyrazolo[4,3-e-]1,2,4-triazolo[1,5-c-]pyrimidine as a Sstrategy tTo Ddesign Nnovel hHuman A. Adenosine adenosine Receptor receptor Antagonists antagonists., J. Med. Chem. 55 (2012) 9654—9668. doi:10.1021/jm300899q.
- [19] E. Kozma, T.S. Kumar, S. Federico, K. Phan, R. Balasubramanian, Z.-G. Gao, S. Paoletta, S. Moro, G. Spalluto, K.A. Jacobson, Novel fluorescent antagonist as a molecular probe in A.

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Formattato: Giustificato

Formattato: Tipo di carattere: Corsivo

Formattato: Tipo di carattere: Corsivo

Formattato: Pedice

cinfc3 //infc adenosine receptor binding assays using flow cytometry, Biochem. Pharmacol. 83 (2012) 1552–61. doi:10.1016/j.bcp.2012.02.019.

[20] A. Glukhova, D.M. Thal, A.T. Nguyen, E.A. Vecchio, M. Jörg, P.J. Scammells, L.T. May, P.M. Sexton, A. Christopoulos, Structure of the <u>a</u>Adenosine A_J <u>Receptor receptor reveals the</u> basis for subtype selectivity, cell. 168 (2017) 867–877.e13. doi:10.1016/j.cell.2017.01.042.

[21] A.S. Doré, N. Robertson, J.C. Errey, I. Ng, K. Hollenstein, B. Tehan, E. Hurrell, K. Bennett, M. Congreve, F. Magnani, C.G. Tate, M. Weir, F.H. Marshall, Structure of the adenosine A receptor in complex with ZM241385 and the xanthines XAC and caffeine, Structure- 19 (2011) 1283–1293. doi:10.1016/j.str.2011.06.014.

[22] K.-N. Klotz, J. Hessling, J. Hegler, C. Owman, B. Kull, B.B. Fredholm, M.J. Lohse, Comparative pharmacology of human adenosine receptor subtypes -- characterization of stably transfected receptors in CHO cells, Naunyn. Schmiedebergs. Arch. Pharmacol. 357 (1998) 1–9. doi:10.1007/PL00005131.

[23] K.-N. Klotz, E. Camaioni, R. Volpini, S. Kachler, S. Vittori, G. Cristalli, 2-Substituted N - ethylcarboxamidoadenosine derivatives as high-affinity agonists at human A_{x-3} adenosine receptors, Naunyn. Schmiedebergs. Arch. Pharmacol. 360 (1999) 103–108. doi:10.1007/s002109900044.

[24] K.-N. Klotz, N. Falgner, S. Kachler, C. Lambertucci, S. Vittori, R. Volpini, G. Cristalli, [³H]HEMADO- a novel tritiated agonist selective for the human adenosine A₃ receptor, Eur. J. Pharmacol. 556 (2007) 14–18. doi:10.1016/j.ejphar.2006.10.048.

[25] A. De Lean, A.A. Hancock, R.J. Lefkowitz, Validation and statistical analysis of a computer modeling method for quantitative analysis of radioligand binding data for mixtures of pharmacological receptor subtypes, Mol. Pharmacol. 21 (1982) 5–16.

[26] K.-N. Klotz, G. Cristalli, M. Grifantini, Photoaffinity labeling of A₁-adenosine receptors, J. Biol. Chem. 260 (1985) 14659–14664.

[27] Chemical Computing Group ULC, MOE, Mol. Oper. Environ. Available from:

Formattato: Pedice

Formattato: Giustificato

Formattato: Pedice

Formattato: Pedice

Formattato: Apice
Formattato: Pedice

- http://www.chemcomp.com
- [28] The Cambridge Crystallographic Data Centre (CCDC), Genetic Optimization for Ligand Docking (GOLD),. Available from: https://www.ccdc.cam.ac.uk/solutions/csd-discovery/components/gold/
- [29] M. Floris, D. Sabbadin, R. Medda, A. Bulfone, S. Moro, European Journal of Medicinal Chemistry—Adenosiland: Walking through adenosine receptors landscape, Eur. J. Med. Chem. 58 (2012) 248–257. doi:10.1016/j.ejmech.2012.10.022.
- [30] M. Floris, D. Sabbadin, A. Ciancetta, R. Medda, A. Cuzzolin, S. Moro, Implementing the "Best Template Searching" tool into Adenosiland platform-, Silico Pharmacol. 1 (2013) 25. doi:10.1186/2193-9616-1-25.
- [31] J.A. Ballesteros, H. Weinstein, Integrated methods for the construction of three-dimensional models and computational probing of structure-function relations in G protein-coupled receptors, Methods Neurosci. 25 (1995) 366–428. doi:10.1016/S1043-9471(05)80049-7.
- [32] P. Labute, Protonate3D: Assignment of ionization states and hydrogen coordinates to macromolecular structures, Proteins Struct. Funct. Bioinforma. 75 (2009) 187–205. doi:10.1002/prot.22234.
- [33] A. Ciancetta, A. Cuzzolin, S. Moro, Alternative quality assessment strategy to compare performances of GPCR-ligand docking protocols: The human adenosine A_{2A} receptor as a case study, J. Chem. Inf. Model. 54 (2014) 2243–2254. doi:10.1021/ci5002857.
- [34] A. Cuzzolin, M. Sturlese, I. Malvacio, A. Ciancetta, S. Moro, DockBench: An integrated informatic platform bridging the gap between the robust validation of docking protocols and virtual screening simulations, Molecules. 20 (2015) 9977–9993. doi:10.3390/molecules20069977.
- [35] J.J.P. Stewart, Optimization of parameters for semiempirical methods V: Modification of NDDO approximations and application to 70 elements, J. Mol. Model. 13 (2007) 1173—1213. doi:10.1007/s00894-007-0233-4.

- [36] Gnuplot. Available from: http://www.gnuplot.info/index.html
- [37] E.F. Pettersen, T.D. Goddard, C.C. Huang, G.S. Couch, D.M. Greenblatt, E.C. Meng, T.E. Ferrin, UCSF Chimera A visualization system for exploratory research and analysis, J. Comput. Chem. 25 (2004) 1605—1612. doi:10.1002/jcc.20084.
- [38] RDKit: Cheminformatics and Machine Learning Software. Available from: http://www.rdkit.org
- [39] MEncoder. Available from: http://www.mplayerhq.hu/design7/projects.html

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