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Discovery of novel quinolinone adenosine A_{2B} antagonists

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ABSTRACT

A novel series of quinolinone-based adenosine A_{2B} receptor antagonists was identified via high throughput screening of an encoded combinatorial compound collection. Synthesis and assay of a series of analogs highlighted essential structural features of the initial hit. Optimization resulted in an A_{2B} antagonist (2i) which exhibited potent activity in a cAMP accumulation assay (5.1 nM) and an IL-8 release assay (0.4 nM).

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Extracellular adenosine provides regulatory signals through interaction with a family of G-protein coupled adenosine receptors (subtypes A_1 , A_{2A} , A_{2B} , and A_3). In lung tissue, for example, interaction of extracellular adenosine with the A_{2B} receptor has been shown to cause the release of pro-inflammatory cytokines. Hence, antagonism of the A_{2B} adenosine receptor subtype has been proposed as a treatment for respiratory disease. A_{2B} antagonists have also been suggested as treatments for diabetes, diabetic retinopathy, colitis, and cancer. Efforts to develop selective, small molecule A_{2B} antagonists have originally stemmed from xanthine-based lead structures such as MRS-1754. Optimization of this lead led to CVT-6883, a selective A_{2B} antagonist which entered human clinical trials. Non-xanthine-based A_{2B} antagonists have also been discovered including 2-aminopyrimidines, A_{2B} A_{2B} A_{2B} antagonists have also been discovered including 2-aminopyrimidines, and aminothiazoles.

We have previously described the discovery of various A_{2A} receptor antagonists via the high throughput screening of a large, encoded combinatorial compound collection. Herein, we detail the optimization of a novel series of A_{2B} antagonists based on quinolinone hits also discovered from this encoded combinatorial collection. The series of A_{2B} antagonists based on quinolinone hits also discovered from this encoded combinatorial collection.

Two hit molecules, ${\bf 1a}$ and ${\bf 1b}$, were initially identified as A_{2B} antagonists. While both were active in a hA_{2B} cAMP accumulation assay (Table 1), neither was stable in a human liver microsome assay (0% remaining after 0.5 h treatment with human liver microsomes). In addition, while these hits proved highly selective against the A_{2A} receptor subtype, they exhibited only minimal A_1 receptor selectivity. Hence, a series of analogs aimed at increasing both human liver microsome (HLM) stability and A_1 receptor selectivity were synthesized.

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Table 1 SAR of quinolinone analogs

Compd	R ¹	R ²	R ³	CHO-hA _{2B} cAMP K _i (nM)	Human A _{2B} binding av K _i (nM)	Human A _{2A} binding av K _i (nM)	A1 binding av K_i (nM)	HLM stability (% remaining-0.5 h) ¹³
1a	CI NH O	Н	O=\sqrt{0}=0	315 ± 102	211 ± 36	>10,000	811 ± 6	0
1b	0 N N O S	Me	F	633 ± 83	677 ± 44	>10,000	3623 ± 1536	0
1c	0 N N O N	Н	F	>5000	>10,000	>10,000	6050 ± 3175	ND
1d	CI	Me	O=0=0	>5000	>7000	ND	>10,000	ND
1e	0 N N O S	Н	O=S=O	>5000	ND	>10,000	10,443 ± 5032	ND
1f	NH O	Н	O=\$=O	352 ± 227	70 ± 19	>10,000	159 ± 34	0
1g	N O O	Me	F	>5000	3655 ± 1332	>10,000	7027 ± 616	ND
1h	MeO−{}	Н	0 	3474 ± 739	11,310 ± 470	>10,000	>10,000	28
1i	O S	Н	O=S=O	1675 ± 671	>10,000	>10,000	1334 ± 309	67
1j	N O S	Н	O S= O	>5000	>10,000	ND	>10,000	ND
1k	CI	Н	O=S=O	1017 ± 37	710 ± 44	>10,000	602 ± 25	0

The synthetic route used to generate the majority of the analogs in this study is outlined in Scheme 1. The hydroxyl moiety of 4-aminophenol was protected as the *t*-butyldimethylsilyl ether followed by protection of the amino group as the *t*-butoxycarbamate. The dianion of this protected intermediate was reacted with tributyltin chloride to generate stannane **4** which was employed in a Stille coupling with the appropriate acid chloride to yield ketone **5**. Deprotection of the phenol and alkylation with methyl bromoacetate produced **6** which was further deprotected by TFA treatment to yield aniline **7**.

Various methods were employed at this stage to generate the quinolinone ring (8) depending on the targeted R^3 group. For the methanesulfonyl and 2,4-difluorophenyl R^3 analogs, a two step procedure of amide formation followed by base-mediated cyclization was required. For the 2-thiazolyl R^3 analogs, however, cyclization

tion occurred spontaneously with warming during the EDC-mediated amide formation conditions. The required 2-thiazolylacetic acid was prepared by the homologation route described in Scheme 2. Although phosphorus oxychloride (employed for the synthesis of analogs **2n–2q**) was also effective in producing a cyclized structure, the 2-chloroquinoline was isolated. Subsequent treatment with acetic acid under microwave heating was employed to produce the desired quinolinone **8**.

If desired, methylation of the R² position was completed at this stage (**8**) via methyl iodide treatment in the presence of potassium carbonate. Ultimately, base-mediated deprotection of the methyl ester followed by amide bond formation yielded the completed analogs

A similar route was followed to generate the aminomethyl quinolinones **2d–2f** (Scheme 3). **4-**Chloroaniline was Boc-protected and

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