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Drug-like antagonists of P2Y receptors - from lead identification to drug development

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Abstract

P2Y receptors are expressed in virtually all cells and tissue types and mediate an astonishing array of biological functions including platelet aggregation, smooth muscle cell proliferation and immune regulation. The P2Y receptors belong to the GPCR superfamily and are composed of eight members encoded by distinct genes that can be subdivided into two groups based on their coupling to specific G-proteins. Extensive research has been undertaken to find modulators of P2Y receptors, although to date there have only been a limited number of small molecule P2Y receptor antagonists that have been approved by drug/medicines agencies. This Perspective reviews the known P2Y receptor antagonists, highlighting oral drug-like receptor antagonists, and considers future opportunities for the development of small molecules for clinical evaluation.

Introduction

Although nucleotides, such as adenosine-5'-triphosphate (ATP) and uridine triphosphate (UTP) are important intracellular molecules, they are also released into extracellular fluids by various mechanisms. The receptors for these extracellular nucleotides have been progressively characterized and classified as purinergic receptors.¹ The subdivision of these purinergic receptors into P1 (adenosine) and P2 (ATP, ADP) was originally proposed by Burnstock in 1978² and further subdivision of the P2 receptors between P2X and P2Y was made in 1985.³ It is now well established that signalling by extracellular nucleotides is mediated by two families of receptors, where P2Y receptors are metabotropic G protein-

coupled receptors (GPCRs) and P2X receptors are trimeric ion channels.⁴ The P2Y receptors belong to the GPCR superfamily and possess the characteristic molecular topology of an extracellular *N*-terminus, an intracellular *C*-terminus and seven transmembrane spanning loops.⁵ However, in comparison to other GPCR families, P2Y receptors show limited sequence homology; possibly explaining the differences in ligand selectivity and specificity for the relevant G-protein they signal through. In addition, P2Y receptors are found to be expressed in virtually all cells, in all tissue types and mediate an astounding array of biological functions including platelet aggregation, smooth muscle cell proliferation and immune regulation. The discovery of oral, drug-like⁶⁻⁷ compounds with favourable ADME (absorption, distribution, metabolism, and excretion) properties⁸ for these receptors, specifically antagonists of the P2Y₁₂ receptor that have proven therapeutic benefit in various disease states, could address many unmet areas of clinical need.⁹

The P2Y family is composed of eight members encoded by distinct genes that can be subdivided into two groups based on their primary signalling through specific coupled G-proteins. From a phylogenetic and structural (i.e. protein sequence) perspective, two distinct P2Y receptor sub-groups have been characterized by the relatively high level of sequence divergence. The first sub-group includes the P2Y_{1,2,4,6,11} receptors and the second sub-group encompasses the P2Y_{12,13,14} receptor subtypes. In addition, the various P2Y receptors differ by their selectivity for distinct nucleotides (Table 1). P2Y₁₁ is an ATP receptor, whereas P2Y₁, P2Y₁₂, and P2Y₁₃ are ADP receptors. P2Y₄ and P2Y₆ are pyrimidine nucleotide receptors activated by UTP and UDP respectively. P2Y₂ is a dual ATP and UTP receptor. P2Y₁₄ is a receptor for UDP-glucose and other nucleotide sugars as well as for UDP itself.

 Table 1: Properties of human P2Y receptors.

Receptor	Tissue distribution	Agonist	G
			Protein
P2Y ₁	wide, including platelets, CNS, heart, skeletal	ADP	Gq

muscle, GI tract		
wide, including lung, heart, skeletal muscle,	ATP=UTP	Gq
kidney, brain		
placenta, lung, vascular smooth muscle	UTP	Gq
wide, including brain, lung, heart, placenta, spleen,	UDP	Gq
intestine		
spleen, intestine, dendritic cells	ATP	G_q + G_s
platelets, brain	ADP	Gi
brain, spleen	ADP	Gi
wide including brain, heart, adipose tissue,	UDP-	Gi
placenta, intestine and hematopoietic cells	glucose/UDP	
	muscle, GI tract wide, including lung, heart, skeletal muscle, kidney, brain placenta, lung, vascular smooth muscle wide, including brain, lung, heart, placenta, spleen, intestine spleen, intestine, dendritic cells platelets, brain brain, spleen wide including brain, heart, adipose tissue, placenta, intestine and hematopoietic cells	muscle, GI tract wide, including lung, heart, skeletal muscle, ATP=UTP kidney, brain placenta, lung, vascular smooth muscle UTP wide, including brain, lung, heart, placenta, spleen, UDP intestine spleen, intestine, dendritic cells ATP platelets, brain ADP brain, spleen ADP wide including brain, heart, adipose tissue, UDP- placenta, intestine and hematopoietic cells glucose/UDP

For further information relating to the specificity of P2YRs see Alexander et al¹⁰

This perspective aims to examine the various approaches used to discover drug-like antagonists of P2Y receptors and builds on recent reviews in the area concentrating on P2Y receptor agonists and the early nucleotide containing modulators.¹¹ Recently, X-ray crystal structures of ligand-bound P2Y₁¹² and P2Y₁₂¹³⁻¹⁴ receptors have been published. It is hoped that structural information resulting from these disclosures can assist in the design of new modulators for P2Y receptor subtypes, as many of the reported modulators still lack the potency and selectivity for viable chemical drug-like leads. Oral drug design has been hampered by the importance of retaining the negatively charged phosphates of nucleotides for their interaction with the P2Y receptors. This presents huge issues for drug development because of their metabolic instability, low bioavailability, nonspecific binding to biological membranes, and chemically due to their demanding purification. To date, the only clinically proven role for P2Y receptor antagonists lays in the antithrombotic area, where extracellular nucleotide signalling has been shown to be involved in platelet aggregation. Extracellular ADP has a crucial role in platelet activation through activation of cell surface P2Y₁ and P2Y₁₂ receptors. In so

doing, platelets secrete several factors that initiate clot formation and recruit other platelets to the point of injury. Based on this, several antagonists for each of these receptors show anti-thrombotic activities. However, to date only P2Y₁₂ receptor antagonists have been successfully developed for clinical use.

The development of clinically relevant $P2Y_{12}$ receptor antagonists and further case histories for the discovery of other P2Y receptor subtype antagonists will be presented in this perspective. Each sub-section, containing a brief introduction to the underlying pharmacology and potential clinical benefit for the P2Y receptor antagonist, is followed by a detailed study of the search for effective orally bioavailable, drug-like molecules.

Drug-like antagonists of the P2Y₁ receptor (P2Y₁R)

Advances in platelet biology¹⁵ revealed that ADP played a crucial role in platelet function. Therefore, receptor antagonists of the two ADP receptors, P2Y₁ and P2Y₁₂, may provide antithrombotic efficacy¹⁶ with reduced bleeding liabilities. Through a G₁-dependent pathway, P2Y₁₂R activation is responsible for mediating the inhibition of adenylyl cyclase, which sustains platelet aggregation. Through a G_q-dependent pathway, P2Y₁R activation is responsible for calcium mobilisation, which causes platelet shape change and initiates reversible aggregation.¹⁷ It has been demonstrated in pre-clinical studies using P2Y₁-deficient (P2Y₁^{-/-}) mice, and by using selective nucleotide-derived P2Y₁R antagonists such as **1** (MRS2179)¹⁸ (Figure 1), that a complete blockade of ADP-induced platelet aggregation occurs leading to an effective reduction of arterial thrombosis with a moderate prolongation of the bleeding time.^{19-20,21,22} Inhibition of the P2Y₁R is therefore a promising approach for the discovery of new antithrombotic drugs.²³⁻²⁴

In the search for selective antagonists of the P2Y₁R, structural modifications were made on the natural agonist **2** (adenosine diphosphate, ADP). In the first reported work in this field, building on the observation that **3** was a weak partial agonist,²⁵ **4** was shown to be an antagonist of the P2Y₁R.²⁵ Substitution of the ribose with an acyclic group afforded **5**, a

potent bisphosphate antagonist (Figure 1).²⁶ These compounds proved useful tools for interrogating the scope of modulating the P2Y₁R. However, their pharmacokinetic properties may not make them ideal oral, drug-like candidates. A series of adenosine derivatives **5a-b** were shown to have weak antagonist activity when linked to aspartic acid through a carbamate.²⁷ Further studies in these areas delivered **6** (MRS2279) and **7** (MRS2500)²⁸ as useful tool compounds to probe the mechanism and highlight the potential clinical significance of P2Y₁R antagonism.²⁹



Figure 1: The natural agonist **2** (ADP) and a selection of nucleoside-based $P2Y_1R$ antagonists.

The following section focuses on the study of P2Y₁R antagonists specifically aimed at the identification and development of oral drugs.

Scientists at Bristol-Myers Squibb (BMS) have reported the discovery and development of a series of potent, selective and bioavailable diarylurea P2Y₁R antagonists. In their discovery program a high throughput screening (HTS) effort, using >1 million compounds against the human P2Y₁R, revealed that diarylurea $\mathbf{8}^{30}$ had good affinity and binding selectivity toward the P2Y₁R versus P2Y₁₂R (P2Y₁ K_i = 75 nM, P2Y₁₂ K_i > 70 µM).



In light of its profile, compound **8** was chosen as the starting point for further modification. The hit series was amenable to rapid exploration by parallel synthesis, initially through substitution of the phenyl ring attached to the urea group. In this synthetic strategy, isocyanate **9** was reacted with a diverse array of 96 amines to afford a series of urea derivatives (such as **10a-i**) that rapidly generated a structure-activity relationship (SAR). To explore substitution of the phenyl ether group, the 2,4-difluorophenyl urea was kept constant and a range of substituted 3-aminopyridines **11a-i** were condensed with 2,4-difluorophenyl isocyanate, key results from these arrays are summarized in Table 2.





-		(nM) ^a			(nM) ^a
10a	Ph	171	12a	3-CF ₃	75
10b	2-F-Ph	47	12b	Н	2000
10c	2-CI-Ph	>5000	12c	2- <i>t</i> -Bu	18
10d	3-F-Ph	607	12d	3- <i>t</i> -Bu	33
10e	4-CI-Ph	69	12e	2- <i>i</i> -Pr	28
10f	4-MePh	48	12f	2-Et	77
10g	4-OCF ₃ -Ph	313	12g	2-CF ₃	172
10h	CH_2Ph	>5000	12h	4-CF ₃	>5000
10i	CH_2CH_2Ph	>5000	12i	4-Me	>5000

^aMeasured by displacement of [β^{-33} P]-2-MeS-ADP binding to cloned *h*P2Y₁ receptors

From this work, it was demonstrated that mono-substitution was preferred for activity at the distal aromatic group (R_1) and that aliphatic substituents were not tolerated in this position. Data also supported the concept that lipophilicity at the *ortho*-position of the phenyl ether (R_2) was required for affinity. The importance of the ether link between the phenyl and pyridyl rings was also explored by replacing it with either a thio-ether or amino variants. Whilst substitution with sulphur afforded a 3-fold drop in affinity, replacement with nitrogen resulted in a 20-fold loss, and *N*-methylation resulted in a more significant loss (Figure 2).



Figure 2: Structure activity relationship for the replacement of the oxygen atom with sulfur or nitrogen.

A follow-on array was then synthesized using a combination of eight preferred substituents from the phenyl ether group and the aromatic ring attached to the urea group. Using a human platelet rich plasma assay (*h*PRP), these compounds demonstrated a clear trend that combination of a lipophile at the *ortho*-position alongside substitution of the phenyl urea at the *para*-position gave receptor antagonists, with several compounds displaying micro-molar activity. In order to ensure that the anti-platelet activity was due exclusively to P2Y₁R antagonism, all compounds were tested for antagonism at other P2Y receptors such as P2Y₂, P2Y₆, P2Y₁₁, P2Y₁₂ and P2Y₁₄. Compounds with good *in vitro* P2Y₁R binding affinity and functional activity were evaluated to determine their metabolic stability. From these studies, compound **13** (BPTU) showed reasonable metabolic stability in rats and was progressed to an *in vivo* rat pharmacokinetic (PK) study. This compound showed modest bioavailability (F = 18%) when dosed at 30 mg/kg and the compound was subsequently progressed to a rat antithrombotic assay (Figure 3).



Figure 3: Rat *in vivo* PK study on compound **13.** V_{ss} is the volume of distribution at steadystate.

Compound **13** clearly improved blood flow and reduced thrombus weight in a dose dependent manner showing a maximum of $68 \pm 7\%$ thrombus weight reduction compared to vehicle using a 10 mg/kg bolus followed by 10 mg/kg/h infusion. *Ex vivo* platelet aggregation responses to ADP were also significantly inhibited at all antithrombotic doses.

Diarylurea-containing compounds of the type shown (Figures 2-3) are generally associated with poor solubility at physiological pH. BMS scientists addressed this issue by addition of amine-containing, water-solubilizing groups (R_3) onto the distal phenyl ring (Figure 4).³¹



Figure 4: Incorporation of an amine as a water-solubilizing group to improve physicochemical properties of the urea derivatives.

This afforded a series of compounds, as illustrated by **14** and **15**, with comparable binding affinities when compared to the parent **13**. Compound **14** was chosen as the new lead compound as it possessed similar levels of activity in the platelet aggregation assay (IC₅₀ 2.9 μ M at 25 μ M ADP) but had significantly higher solubility. However, further profiling of **14** showed it was metabolically unstable in rat and human liver microsomes and displayed high inhibition against several GPCR targets [ca. 90% inhibition (at 10 μ M) 5-HT2A, 5-HTT, α -2A adrenoreceptor and α -1D adrenoreceptor]. Further investigation revealed **15** as a more metabolically-stable compound with enhanced rat bioavailability (F = 40%), due in part to the increase in aqueous solubility. Unfortunately, **15** also had similar off-target activity, as well as showing activity against the *h*ERG potassium ion channel.

In order to address the poor physico-chemical properties of their lead compounds, scientists at BMS looked into bioisostere replacements of the core urea moiety. In a series of papers they explored replacement of the urea with amino thiadiazole³² **16** and 2-aminothiazole³³ **17** mimetics (Figure 5).



Figure 5: Bioisosteric replacement of the urea group: a) 2-amino-3,4-thiadiazole replacement and b) 2-aminothiazole replacement

High P2Y₁R antagonism was demonstrated for a range of azole bioisosteric replacements (*e.g.* **16**). Several five-membered heterocycles were used as replacement for the urea moiety, with comparable levels of P2Y₁R antagonism and ADP-induced aggregation activity. These receptor antagonists suffered from the same poor physico-chemical properties as the previous lead series (high lipophilicity including poor aqueous solubility <1 μ g/mL at pH 6.5) and were not pursued further. In the case of the 2-aminothiazole bioisosteric replacements, a series of new analogues were discovered with excellent P2Y₁R binding affinity. Several of the analogues demonstrated moderate inhibition of platelet aggregation, with compound **17** showing a reasonable rat PK profile (CL 6.7 mL/min/kg; T_{1/2} 2.1 h, F 27%). However, poor solubility and high plasma protein binding (99.9% bound) may have contributed to the modest activity seen in the human serum platelet aggregation assay (IC₅₀ 17 μ M) and this series was not pursued.

In another approach to address the poor physico-chemical properties inherent in the biaryl urea lead compounds, incorporation of an amine containing, water-solubilizing group into the phenyl ether portion of the core structure was explored (Figure 6).



Figure 6: Changes to the phenyl ether portion of 13 to increase water solubility

Compounds (**18-20**) displayed similar $hP2Y_1R$ antagonism to that of **13**, however improved physico-chemical properties resulted in good functional activities as well as improved aqueous solubility. From this set of compounds, piperidine **20** showed the best overall profile and favourable PK parameters (Table 3).³⁴

Compound	<i>h</i> P2Y ₁ K _i	PA ^a IC ₅₀	Solubility	CL	V_{ss}	T _{1/2}	F	PPB ^b
	(nM)	(μM)	(µg/mL)	(mL/min/kg)	(L/kg)	(h)	(%)	(% bound)
18 ^c	11	2.5	3	48	22	14	16	100
19 °	57	1.2	270	84	10	1.7	13	99.7
20 ^d	16	2.4	105	18	14	11	89	99.9

Table 3: In vitro data and rat PK profile for the diarylureas 18-20.

^aPlatelet aggregation (PA) was tested with 2.5 μM of ADP. ^bPlasma protein binding (PPB). ^c Cassette dosed 0.5 mg/kg (i.v./p.o.) ^d2 mg/kg (i.v.), 5 mg/kg (p.o.)

In a continuing theme, a range of conformationally-constrained, anilino-substituted diarylureas were synthesized to generate a new series of potent and selective $P2Y_1R$ antagonists. These compounds possessed an oral antithrombotic effect with mild bleeding liability in rat thrombosis and homeostasis models (Figure 7).³⁵



Figure 7: Evolution of new conformational constrained, ortho-anilino diarylurea 23.

In the evolution of compound **23**, compounds **21-22** demonstrated good P2Y₁R antagonism (**21** *h*P2Y₁ K_i = 8.7 nM, **22** *h*P2Y₁ K_i = 20.3 nM). It is interesting to note that among these ring-constrained analogues, the aryl compound **21** had slightly enhanced activity at the P2Y₁R and this seemed to be a general trend observed within this series of compounds. After further optimization, **23** was identified, with an excellent overall profile (**23**, *h*P2Y₁ K_i = 4.3 nM, *h*P2Y₁; PA = 4.9 μ M (at 10 μ M ADP); solubility 4 μ g/mL; rat PK: CL 9.1 mL/min/kg; T_{1/2} 7.5 h; F 32%). Compound **23** inhibited arterial thrombus formations and improved blood flow in a dose-dependent manner when administered by either *IV* or *PO* routes. Maximum thrombus weight reductions of 66% and 64% were observed in comparison to vehicle at doses of 0.6 mg/kg + 2.25 mg/kg/h (*IV*) and 10 mg/kg (*PO*), respectively. In these same rat models, a 20 mg/kg oral dose of clopidogrel reduced carotid artery thrombus weight by 67% and prolonged mesenteric bleeding time by 8.2-fold. These results suggested that inhibition of P2Y₁ by **23** compared favourably to the antithrombotic and haemostatic effects of clopidogrel - a clinically established P2Y₁₂R antagonist.

In a further disclosure, potency in the spiropiperidine indoline-substituted diarylureas was enhanced through the introduction of a 7-hydroxyl substitution on the spiropiperidinyl indoline chemotype. Further SAR studies were conducted to improve pharmacokinetics and potency, resulting in the identification of **24** (P2Y₁ calcium mobilization assay = 0.12 nM; PA = 0.13 μ M (at 10 μ M ADP); solubility 680 μ g/mL; CL 7.3 mL/min/kg; T_{1/2} 8.4 h; F 23%), a compound that demonstrated a robust antithrombotic effect *in vivo* and improved bleeding

risk profile compared to the P2Y₁₂R antagonist clopidogrel in a rat bleeding model.³⁶ This exciting improvement in activity led to investigation of a series of urea bioisosteres of the diarylurea lead **24**, culminating in the discovery of a series of 2-amino-1,3,4-thiadiazoles, such as compound **25** (P2Y₁ K_i 16 nM; PA 0.45 μ M (at 10 μ M ADP); rat PK: CL 4.0 mL/min/kg; T_{1/2} 24 h; F 22% (cassette dosed 0.5 mg/kg (p.o.)), as potent P2Y₁R antagonists; the first series of non-urea containing P2Y₁R antagonists.³⁷



Several analogs of **25** were shown to have more favourable PK profiles, such as higher maximal trough concentration (C_{trough}), lower CL, smaller V_{ss}, and similar bioavailability compared with **25**.

Further optimization of **25**, by introducing 4-aryl groups at the hydroxylindoline in two neutral and basic sub-series, have been described.³⁸⁻³⁹ In the neutral series, **26** had excellent potency and a highly desirable PK profile. Meanwhile, in the basic series, **27** (BMS-884775) had an improved PK profile (Figure 8).





Figure 8: Discovery of **27** – a potent and orally bioavailable P2Y₁R antagonist (n.b. no dose given for the PK studies).

Scientists at Pfizer have reported a series of potent and orally bioavailable diarylurea P2Y₁R antagonists⁴⁰ resulting from an HTS campaign. The HTS hits (**28** and **29**) were further explored to deliver aryloxypyrazole **30** as a suitable template for further elaboration (Figure 9).



Figure 9: Discovery of the aryloxypyrazole template (such as 30) for further elaboration

During their optimization project, attention was paid to the A- and B-rings of the template. Interestingly, substitution in the *ortho*-position of the A-ring increased binding affinity and was preferred over *meta-* and *para*-substitution, with either small lipophilic or halogen substituents being optimal. Limited examination of the B-ring was undertaken at this time. However, it was noted that larger lipophilic substituents in the pyrazole 3-position led to inactivity, thus the 3-methyl substitution was preferred. Subsequent optimization then focussed on the D-ring while maintaining the optimal substitution on the A- and B-rings (Figure 10).



Figure 10: Lead optimization of the aryloxypyrazole template

Compound **31** had good *in vitro* metabolic stability and was further evaluated for its rat PK where it demonstrated a very favourable profile (CL 81 mL/min/kg; V_{ds} 15.7 (L/kg); T_{1/2} 2.8 h; F 59%). This compound was progressed to a rat arterial injury model where it resulted in a dose-dependent decrease in both the incidence of occlusive thrombus formation and the average time to occlusion. It is interesting to note that high affinity was achieved when lipophilic groups were incorporated at the *para*-position of the D-ring (**32**, *h*P2Y₁ K_i = 0.03 μ M), whereas a more polar substituent (**33**, *h*P2Y₁ K_i > 10 μ M) led to a substantial loss in activity. When heterocyclic replacements were made in the C-ring, it was discovered that substitution with a pyridyl group afforded compounds (e.g. **34**) with reasonable activity.

A series of HTS-derived diarylurea $P2Y_1R$ antagonists were reported by scientists at GlaxoSmithKline (GSK).⁴⁰ In their work, they described the discovery of a hit (**35**) which was optimized to give a series of benzofuran-substituted urea derivatives *e.g.* **36** (Figure 11).





35 HTS Lead *h*P2Y₁ FLIPR IC₅₀ = 0.79 μM



Figure 11: A series of HTS-derived diarylurea P2Y₁R antagonists

Scientists at GSK also reported on a non-urea containing series of receptor antagonists, once more obtained as a result of HTS.⁴¹ A high throughput calcium mobilization assay employing a fluorescent imaging plate reader (FLIPR) identified tetrahydro-4-quinolinamine **37** as an antagonist of *h*P2Y₁R. Exploration of this screening hit led to the identification of urea **38** where the importance of the absolute stereochemistry was highlighted through the separation of the enantiomers through chiral HPLC and it was discovered that all P2Y₁R antagonism was derived from a single enantiomer (Figure 12).



37 HTS Lead38 $hP2Y_1$ FLIPR IC50 = 1.6 μ M $hP2Y_1$ FLIPR IC50 = 0.6 μ M $hP2Y_1$ Ki = 0.5 μ M $hP2Y_1$ Ki = 0.07 μ M

Figure 12: Evolution of the HTS-derived lead to the active single enantiomer 38

Compound **38** was progressed to a platelet aggregation assay and was shown to inhibit ADP-induced aggregation with an $IC_{50} = 504$ nM.

In a seminal paper, researchers have established the X-ray co-crystallised structure of inhibitors bound into the $hP2Y_1R$.¹² Structures of the $hP2Y_1R$ in complex with either a nucleotide antagonist **1** (2.7Å resolution) or a non-nucleotide antagonist **13** (2.2Å resolution) reveals two distinct ligand-binding sites. Interestingly **13** was originally identified by a radio-ligand binding assay and described as a competitive antagonist. Antagonist **1** occupies a binding site within the seven transmembrane bundles of the P2Y₁R, and **13** binds to an allosteric pocket on the external receptor interface with the lipid bilayer (Figure 13).



Figure 13: Compounds **7** and **13** co-crystallised into the *h*P2Y₁R showing the two distinct binding sites. An overlay of structures pdb codes 4XNV and 4XNW visualised with PyMOL Molecular Graphics System, Version 1.3. Schrödinger, LLC.

Perspective comment

The story of the discovery of **27**, covered over several papers, illustrates a classical medicinal chemistry project where core pharmacological optimisation (P2Y₁R antagonism) was run in multi-parameter optimisation to improve physico-chemical properties (such as solubility and pharmacokinetics) of the lead compounds. It is also important to note that during this optimisation phase, consideration of all parts of the structure was examined including the utilisation of bioisosteric replacements (Figure 14).



Figure 14: Summary of the discovery of 27. cLogD is the calculated distribution coefficient.

While this optimisation process led to a dramatic increase in biological activity and improvement in solubility, increases in the core physical properties, such as MWt and lipophilicity, would lead to future issues in the development of a pre-clinical candidate.⁴² Hopefully, elucidation of the co-crystal structure of the P2Y₁R antagonist ligands will enable structure-based drug design of future P2Y₁R antagonists, facilitating discovery of compounds with physical properties for improved oral absorption.

Drug-like antagonists of the P2Y₂ receptor (P2Y₂R)

The P2Y₂R is activated by endogenous agonists UTP ($hP2Y_2$, EC₅₀ = 140 nM) and ATP ($hP2Y_2$, EC₅₀ = 230 nM) with almost equipotent activity in a transfected 1321N1 human

astrocytoma cell line.⁴³ The P2Y₂R is predominately G_q -coupled and receptor agonism leads to activation of phospholipase C (PLC), IP₃ release and elevation of intracellular Ca²⁺ concentration, as well as the activation of protein kinase C (PKC) and activation of the mitogen activated protein kinase (MAPK) cascade.⁴⁴



P2Y₂R agonism has shown potential as a treatment for cystic fibrosis (CF), as defective chloride secretion in the respiratory epithelium of CF patients can be compensated by activation of chloride secretion channels. Through a knockout study,⁴⁵ comparison of P2Y₂R^(+/+) with P2Y₂R^(-/-) mice revealed that the P2Y₂R mediated 85-95% of nucleotide-stimulated chloride secretion in the trachea, and agonist **39** (INS37217, *h*P2Y₂, EC₅₀ = 220 nM) was shown to increase chloride and water secretion, as well as an increased mucin release of tracheal tissue in an *ex vivo* model.⁴⁶ It has also been shown that receptor agonism of the P2Y₂R leads to keratinocyte proliferation⁴⁷ and neutrophil migration,⁴⁸ suggesting that receptor antagonists could show promise in treating psoriasis. Offermanns *et al*⁴⁹ reported that ATP released from tumor cell-activated platelets and induced the opening of the endothelial barrier, leading to migration of tumor cells and hence cancer-proliferation. More importantly they identified P2Y₂R sa the primary mediator of this effect; demonstrating a strong reduction of tumor cell metastasis in P2Y₂R deficient mice and showing the therapeutic potential of P2Y₂R antagonists as anti-metastatic agents.

The only reported development of P2Y₂R antagonists from an industrial research group are compounds patented by scientists at AstraZeneca in the late 1990s (formerly Fison's and Astra Pharmaceuticals). Unfortunately, no absolute potency values for the compounds were

reported and so a detailed SAR cannot be given here. However, looking chronologically at the patents, it is possible to see the sequential development of several structurally distinct classes of receptor antagonists, culminating in compounds which could be classed as druglike.



Figure 15: $P2Y_2R$ antagonists patented by AstraZeneca. All exemplified compounds were reported as being $P2Y_2R$ antagonists with a $pA_2 > 4.0$ in $hP2Y_2R$ transfected Jurkat cells. cLogP was calculated using instant J Chem.⁵⁰

Within the first patent, a series of triphosphate receptor antagonists were reported (Figure 15).⁵¹ It was shown, in an analogous series of P2Y₂R agonists, that taking UTP as the starting point and replacing the βγ-oxygen with a dichloromethylene group, along with conversion to a 4-thiouridine, induced enhanced metabolic stability as well as maintaining full agonist activity.⁵² Conversion to a P2Y₂R antagonism profile was achieved through the introduction of a large, lipophilic group at the C-5 position of the uridine. This key substitution was extensively exemplified with a biphenyl and dibenzo-suberenyl substituent **40** and **41** respectively; however further substituents are reported throughout the patent.⁵¹ The *in vivo* use of these triphosphate analogues would probably be limited to *intravenous* and topical administration. With the scope of developing oral, drug-like compounds, there is a desire to move away from excessively high molecular weight and highly-charged triphosphate

moieties. To this extent, a subsequent patent⁵³ was published detailing acidic, non-phosphate P2Y₂R antagonists, exemplified by **42** and **43** (Figure 16).



Figure 16: P2Y₂R antagonist patented by AstraZeneca. All exemplified compounds were reported as being P2Y₂R antagonists with a $pA_2 > 4.0$ in *h*P2Y₂R transfected Jurkat cells.

Within this second series of acidic receptor antagonists, it is possible to see distinct structural changes. Across the majority of the exemplified compounds, the core 4-thiouridine was maintained along with the dibenzo-suberenyl substituent, now further substituted with two additional methyl groups. Presumably these features were required to maintain or enhance the activity seen in the first series of compounds.

In this series, the ribose group was replaced with a simpler 5-membered heterocycle, in most cases a substituted furan ring. In addition to this modification, a further notable structural change was replacement of the triphosphate with an acidic phosphate mimetic. This modification was reported as *L*-aspartic acid derivative **42** and the acyltetrazole analogue **43** (AR-C118925XX), along with other bioisosteric replacements. However, in achieving this structural change, a substantial increase in the overall lipophilicity was observed that would compromise their physico-chemical properties.



Figure 17: P2Y₂R antagonists patented by AstraZeneca including acidic (such as **44**) and neutral receptor antagonists (such as **45-46**).

A series of less lipophilic receptor antagonists were reported in the final patent and a selection of these compounds is shown (Figure 17).⁵⁴ The key strategy appeared to be replacement of one of the phenyl rings in the dibenzo-suberenyl substituent with a 5-membered heterocyclic ring. This can be shown through considering **44** (cLogP = 3.3) which is appreciably less lipophilic than **43** (cLogP = 5.3) whilst remaining structurally similarity. More importantly, this change allowed for generation of a neutral receptor antagonist series as exemplified by **45** and **46**. Although there have been no further reports on the activity of these compounds, structurally they appear to be more drug-like than the compounds in the previous patent applications.

Since disclosure of these P2Y₂R antagonists from AstraZeneca, several studies using **43** with success in both *in vivo* and *ex vivo* models have been reported; further validating the therapeutic benefit of P2Y₂R antagonists. In 2004, scientists at Novartis⁵⁵ showed that **43** was inactive at 10 μ M concentrations against a panel of 37 receptors (except for *h*P2Y₂). In an *ex vivo* model **43** concentration-dependently antagonized ATPγS-induced mucin secretion in human bronchial epithelial cells (IC₅₀ ~ 1 μ M). In 2015, Ceruti *et al*⁵⁶ showed that in an *in vivo* model, **43** completely inhibited satellite glial cell activation and cross talk

with trigeminal neurons, exerting a potent anti-allodynia effect. This suggests P2Y₂R antagonists also have therapeutic potential for management of trigeminal neuralgia.

It has been reported⁵⁷ that several members of the flavonoid family displayed P2Y₂R antagonism (*m*P2Y₂R, IC₅₀ \approx 10-50 µM). When screening a series of 40 flavonoids (Figure 18), **48** (Tangeretin, *m*P2Y₂R, IC₅₀ = 12 µM) reduced the amplitude of the P2Y₂R response to UTP but not the EC₅₀ value, indicating it could be acting as an allosteric P2Y₂R antagonist.



Figure 18: A series of 40 flavonoids 47 (generic structure) and 48

More recently it has been suggested⁵⁸ that amphiphilic phytochemicals, similar to these flavonoids, appear to function indirectly through disruption of cell membranes in which the transmembrane proteins reside. This might explain the non-competitive antagonism observed for **48** and the difficultly encountered in extracting meaningful SAR from the compound series. However more importantly, the promiscuity in developing polyphenolic compounds is well known and is generally avoided when selecting lead-like compounds.

From the unselective, broad-spectrum P2YR antagonist **49** (Reactive Blue-2, *h*P2Y₂R, IC₅₀ = 1.85 μ M), a series of receptor antagonists were reported (Figure 19).⁵⁹ The most potent (**50** *h*P2Y₂R, IC₅₀ = 9.82 μ M), although unpublished, 'appeared to be selective versus other P2Y subtypes as well as nucleotide-metabolizing enzymes'.



Figure 19: Evolution of 50 (PSB-716) and 51 (PSB-416) from 49

To develop a greater understanding for the binding of these P2Y₂R antagonists, work was reported⁶⁰ on site-directed mutagenesis studies, to understand the binding modes of UTP, **49** and **50** (*h*P2Y₂R, IC₅₀ = 11.5 μ M). It is worth highlighting several of these point mutations as they provide insight into ligand binding within the P2Y₂R.

Mutant	UTP	49	51
	EC ₅₀ /µM	IC₅₀/µM	IC₅₀/µM
wt4	0.0590	1.85	21.7
Y114A	0.0372	>>100	24.6
R272A	20.60	nd	nd
C278S	2.09	1.05	3.44
wt3	0.0804	1.62	21.9
Y198A	0.108	9.30	21.1
S296A	>>300	nd	nd

Table 4: Mutagenesis data for selected P2Y₂R antagonists

With respect to the receptor expression, mutants Y114A, R272A and C278S can be compared to wt4; mutants Y198A and S296A can be compared to wt3.

Mutation Y114A on the TM3 domain and Y198A on the TM5 domain did not significantly affect the UTP response, but did affect the antagonistic response of **49** but not **51**. Mutation S296A on the TM7 domain significantly affected the agonistic response to UTP and similarly mutation R272A on the extracellular loop 3 (EL3) in close proximity to the TM6 domain, resulted in a significant loss of agonist response to UTP. The mutation C278S significantly affected agonist response to UTP. It was proposed that this mutation inhibited formation of a key Cys²⁵-Cys²⁷⁸ disulfide bridge, which is thought to be important for the increase in receptor antagonism observed for **49** and **51**.

From this mutagenesis data, a bovine rhodopsin-based P2Y₂R homology model was developed. It was hypothesized that Arg²⁷² has a 'gatekeeper' role, helping to 'guide' the phosphates of the agonists into the receptor. Ser²⁹⁶ is located at the bottom of the binding pocket where it forms key hydrogen bonding networks with the nucleobase of UTP and ATP. A docked antagonist-binding pose of **50** was reported. However, even with the publication of this homology model in 2009 no further development of these compounds has been reported.

Recent crystal structures of $P2Y_{12}R^{10}$ show significant difference in antagonist and agonist bound conformations. In the absence of an X-ray crystal structure for the $P2Y_2R$, further work into developing $P2Y_2R$ homology models, focusing on antagonist receptor binding could prove invaluable for future development of drug-like $P2Y_2R$ antagonists.

Antagonists of the P2Y₄ receptor (P2Y₄R)

The *h*P2Y₄R is fully activated by the endogenous agonist UTP (*h*P2Y₄, EC₅₀ = 550 nM, *r*P2Y₄, EC₅₀ = 200 nM) in transfected 1321N1 cells and is considerably more potent than ADP and UDP. ADP was shown to be a weak, partial agonist (*h*P2Y₄, 15% max at 100 μ M, *r*P2Y₄, 34% max at 100 μ M) and the weak agonist activity, sometimes observed for UDP, can be attributed to contaminating UTP. Interestingly, there are disparate differences when comparing the pharmacological properties of ATP on human and rat P2Y₄Rs. In human, ATP acts as a competitive antagonist ($hP2Y_4$, $pA_2 = 6.2$) whereas in rat, ATP acts as a full agonist ($rP2Y_4$, $EC_{50} = 1.17 \mu$ M).⁶¹ Mutagenesis work has shown that residues on the second extracellular loop (EL2) of the P2Y₄R were responsible for ATP's ability to act as an agonist in rat and an antagonist in human. In the triple $hP2Y_4R$ mutant (S177N, V183I, R190L), ATP was an equipotent agonist compared to UTP.⁶²

The first selective P2Y₄R agonist **52** (*h*P2Y₄, EC₅₀ = 23 nM) was reported in 2011 and showed a 28-fold and 32-fold selectivity versus the P2Y₂R and P2Y₆R respectively (*h*P2Y₂, EC₅₀ = 640 nM; *h*P2Y₆, EC₅₀ = 740 nM). Through development of CXCR4-derived P2Y₄R homology models, the selectivity gain was thought to be due to unconserved residues in the EL2 domain.⁶³



In a similar manner to the P2Y₂R, activation of the G_q-coupled dependent pathways of P2Y₄R leads to stimulation of chloride secretion channels and water secretion. Work with P2Y₄-deficient mice showed P2Y₄R expression in liver, stomach and intestine.⁶⁴ It was shown that the P2Y₄R was the primary mediator of UTP-stimulated chloride secretion in both small and large intestines, suggesting the potential use for the development of P2Y₄R antagonists as anti-diarrheal agents.⁶⁵

Unlike most P2Y receptors, the P2Y₄R does not show the same susceptibility to broadspectrum P2YR antagonists and is only antagonized by **49**. Using *h*P2Y₄R stably transfected into 1321NI cells, **53** (suramin) gave no antagonistic response and **54** (pyridoxal phosphate-6-azo(benzene-2,4-disulfonic acid) tetrasodium salt hydrate (PPADS)) was shown to be relatively ineffective.⁶⁶ Compound **49** was demonstrated to be a competitive P2Y₄R antagonist in rat transfected *Xenopus* oocytes (*r*P2Y₄, pA₂ = 6.43).⁶⁷ It is thought that the P2Y₄R may play a causative role in hypoglycemic cell death and, using **49**, it was shown that P2Y₄R antagonism increased cell survival in both cerebellar granule neurons and HEK-293 cells under hyperglycemic conditions.⁶⁸ This gives scope for future P2Y₄R antagonists to be used as neuroprotective agents in diabetes. As with P2Y₂, there is scope to use **49** as a starting point for the development of selective anthraquinone-based P2Y₄R antagonists.



However, there has been no further published work on any P2Y₄R antagonists. Hence, there remains a large scope and unmet need for the development of lead- and drug-like P2Y₄R antagonists.

Antagonists of the P2Y₆ receptor (P2Y₆R)

The P2Y₆R receptor is activated by UDP (EC₅₀ = 0.30 μ M). Its transcript has been detected in numerous organs, including spleen, thymus, intestine, blood leukocytes and the aorta. The majority of research has been performed on agonists of this receptor as typified by **55** (PSB0474)⁶⁹ and **56** (MRS2957).



From these studies, it was shown that activation of the P2Y₆R amplifies mucosal ATP release underlying bladder over-activity in patients with benign prostatic hyperplasia. Therefore, a potential use of a selective P2Y₆R antagonist could be as a novel strategy to control persistent storage symptoms in obstructed patients.⁷⁰ In a recent article, Hirota *et al* suggested that a P2Y₆R antagonist could have benefit in *Clostridium difficile* toxin-induced CXCL8/IL-8 production and intestinal epithelial barrier dysfunction and may therefore provide a new therapeutic target for the treatment of *C. difficile* infections.⁷¹ In a further recent study, it was shown that endothelium-dependent relaxation of the aorta by UDP was abolished in P2Y₆ KO mice with the authors postulating that these observations might be relevant to several physio-pathological conditions, such as atherosclerosis or hypertension.⁷² Inhibition of P2Y₆R has also been suggested as a potential therapeutic target for monosodium urate (MSU)-associated inflammatory diseases, such as tophaceous gout.⁷³ With these and other⁵ recent observations, inhibition of the P2Y₆R could prove a viable therapeutic mechanism in many potential disease areas. Unfortunately, there are only a few known non drug-like inhibitors of the P2Y₆R (**57-58**) available.^{74,75,76}

Fischer *et al.* recently described the SAR of uracil nucleotide derivatives and found that uridyl phosphosulfate (**59**) was a weak P2Y₆R antagonist (Figure 20).⁷⁵



Figure 20: Known P2Y₆R antagonists; 57 (MRS2578), 58 (MRS2567) and 59

Even though these compounds have been used to study the potential therapeutic role of $P2Y_6R$ antagonism, the combination of their chemical functionality and bulk physical properties make them less than optimal starting points for oral drug discovery programs.⁷⁷

Antagonists of the P2Y₁₁ receptor (P2Y₁₁R)

The P2Y₁₁R was cloned from human placenta and genomic DNA libraries.⁷⁸ It is coupled to both G_q and G_s with its activation leading to increases in cAMP and IP₃ levels. The rank order of potency of a series of nucleotides for the P2Y₁₁R, transfected into two cell lines, 1321N1 astrocytoma cells and CHO-K1 cells, is: ATP γ S ~ BzATP>dATP>ADP_βS>2MeSATP.⁷⁹ P2Y₁₁ mRNA has been found to be highly expressed in macrophages, platelets, lymphocytes, neutrophils, megakaryocytic cells and has also been detected in neuronal-derived and glial-derived cell lines.⁸⁰

The P2Y₁₁R is expressed on some leukocyte types including monocytes,⁸¹ neutrophils,⁸² lymphocytes and monocyte-derived dendritic cells.⁸³ It has been found to mediate ATP-induced maturation and regulate trafficking of specific dendritic cell types,^{84–86} regulate macrophage activation⁸⁷ and regulate release of cytokines such as IL-6,^{88,89} IL-8 and the production of IL-12.⁹⁰ It has also been shown that inhibition of neutrophil apoptosis by ATP is mediated by the P2Y₁₁R.⁹¹

The SAR of a series of suramin-derived $P2Y_{11}R$ antagonists have been investigated.⁹² In this study, the methyl groups of (**53**) were replaced by a range of substituents (Table 5).



Table 5: Structure activity relationship of suramin analogues

CH ₃ (53)	54.5	50.5	6.52
C_2H_5	48.7	48.8	6.00
CH(CH ₃) ₂	45.0	31.1	6.35
Ph	75.1	73.2	6.52
F (60 , NF157)	63.3	42.8	7.35
CI	40.6	55.2	6.97
OMe	23.2	44.9	7.12
CH ₂ OCH ₃	47.5	44.3	5.62

*Percentage inhibition by a single dose (100 μ M) of agonist-induced calcium mobilization of native P2Y₁R and P2Y₂R in HEK293 cells and at P2Y₁₁R recombinantly-expressed in 1321N1 astrocytoma cells). **The pK_i values for P2Y₁₁R on 1321N1 astrocytoma cells are shown.

Interestingly, the same changes to structurally simpler compounds (**61a-h**) gave compounds with little or no antagonism at $P2Y_{11}$ (Figure 21).



Figure 21: Synthetic changes to 61a-h gave compounds with little or no activity at P2Y11

A wide range of substituents were tolerated with the difluoro-substituted analogue, with compound **60** being the most potent (P2Y₁₁, $pK_i = 7.35$). This analogue, as well as having significant selectivity over P2Y₁R and P2Y₂R (> 650-fold), has 3- to > 67-fold selectivity over P2X_{2,3,4,7}.

A systematic screening of a library of naphthalene phosphonic acid and sulfonic acid compounds led to the identification of **62** (P2Y₁₁, $pK_i = 7.8$). This compound was 2.6-fold more potent than **60** and almost 1000-fold more potent than its very close structural analogue **61b**. At concentrations up to 100 µM there were no observed effects at the P2Y₁R, P2Y₂R and P2Y₆R (expressed in 1321N1 astrocytoma cells).



A rat formalin-induced inflammatory pain model, using the selective $P2Y_{11}R$ antagonist **62** (NF340) and agonist **63** (NF546), suggested that activation of the receptor, along with activation of the $P2Y_1R$ and $P2Y_6R$, lead to nociception.⁹²⁻⁹³

A computational model using the β_1 -bovine rhodopsin crystallographic structure as a template in combination with site-directed mutagenesis was used to deduce the key ATP-binding site interactions. ATP was 10-fold less potent at the E186A mutant P2Y₁₁R and 1000-fold less potent at the R268A mutant, whilst being functionally inactive at the R106A and R307A mutants. It is proposed that Arg¹⁰⁶, Arg²⁶⁸, Arg³⁰⁷ and Glu¹⁸⁶ are involved in ionic interactions with the tri-phosphate chain. Arg³⁰⁷ may also be H-bonded to the adenine N⁶. Computational modelling also suggests Ser²⁰⁶ is involved in an interaction with the γ -phosphate of ATP and Met³¹⁰ interacts with the adenine ring.⁹⁴⁻⁹⁵

Drug-like antagonists of the P2Y₁₂ receptor (P2Y₁₂R)

The P2Y₁₂R is found on many cell types including megakaryocytes and platelets. The endogenous agonist is ADP and, following a thrombotic event, activation of the P2Y₁₂R amplifies platelet activation and aggregation, leading to thrombus formation.⁹⁶ Although the involvement of ADP in platelet aggregation was first discovered in the 1960s,⁹⁶⁻⁹⁷ it was not

until 2001 that the P2Y₁₂R was structurally characterized.⁹⁸⁻⁹⁹ Activation of both P2Y₁R and P2Y₁₂R are important for platelet activation and thrombus formation. However, the wide distribution of the P2Y₁R amongst different cell types compared with the P2Y₁₂R have made P2Y₁R antagonists a less desirable target in drug discovery for treatment and prevention of thrombosis.

The thienopyridine class of irreversible binders for the P2Y₁₂R was discovered in the 1970s by researchers at Sanofi, whilst screening compounds with structural similarity to the nonsteroidal anti-inflammatory drug tinoridine; although it is interesting to note that the actual drug target was not known at this time.¹⁰⁰⁻¹⁰¹ It was shown that some of these compounds did not exhibit anti-inflammatory properties but did have an anti-thrombotic effect after oral dosing in a rat model. One of the most effective compounds **64 (**ticlodipine) was chosen for development and was launched in 1978 as an anti-thrombotic agent for a range of high risk patients. Unfortunately, (**64**) was found to suffer from a poor benefit/risk ratio and a backup program resulted in the launch of **65** (clopidogrel) in 1998, which had a much improved safety profile. Interestingly, **65** was initially tested as a racemate, but it was eventually found that the anti-thrombotic activity resided with the S-enantiomer.¹⁰¹

This class of inhibitor required activation through conversion to the active metabolite **66**, which binds irreversibly to the receptor. Binding to the P2Y₁₂R was confirmed in 2001¹⁰² and site-directed mutagenesis identified two extracellular cysteine residues, Cys¹⁷ and Cys²⁷⁰ as candidates for disulfide bond formation with this active metabolite¹⁰³ which was later confirmed when the X-ray crystal structure was published in 2014.¹³

In 2009, another irreversible inhibitor within this class **67** (prasugrel - a racemate) was launched.¹⁰⁴



AstraZeneca scientists took the weak P2Y₁₂R antagonist ATP as the starting point for their discovery project. Replacement of the $\beta\gamma$ -oxygen with a dihalomethylene group and installation of substituents on the adenine ring gave a series of high affinity reversible antagonists.¹⁰⁵ One of these, **68** (cangrelor, P2Y₁₂ IC₅₀ = 0.4 nM), was approved in 2015 for use as a quick onset/quickly reversed intravenous antiplatelet drug, over twenty years from its discovery.



The next objective was to develop a drug suitable for oral administration. This required a move away from compounds containing highly acidic groups.¹⁰¹ As ADP is an agonist for the P2Y₁₂R and ATP an antagonist, it was hypothesized that the terminal phosphate was important for receptor antagonism. Effort was therefore directed at finding alternative acidic groups to the triphosphate chain, in particular the terminal phosphate. This work led to the aspartic acid-derived analogues **69-71**. Within this series, conversion of the purine ring to a triazolopyrimidine **70** gave a > 100-fold increase in binding affinity over the purine analogue. Replacement of the ribose with a cyclopentyl ring gave a series of compounds, such as **71**, with similar activity and increased metabolic stability (Figure 22).



69 X = C, Y = O $hP2Y_{12} = pIC_{50} 7.0$ **70** X = N, Y = O $hP2Y_{12} = pIC_{50} 9.5$ **71** $X = N, Y = CH_2$ $hP2Y_{12} = pIC_{50} 9.3$

Figure 22: Key SAR of glycoside analogues showing the evolution to the potent cyclopentyl analogue **71**. Affinity pIC_{50} values were derived from an ADP-induced aggregation assay using washed platelets.

The physical properties of these molecules (MW>500, >5 H-bond donor groups and the dicarboxylic acid moiety) were not conducive to good oral absorption. Replacement of the butylamine group on the triazolopyrimidine ring with a 1*R*,2*S*-*trans*-phenylcyclopropylamine gave an increase in potency across a number of analogs. Further modifications aimed at finding a suitable replacement for the dicarboxylic acid led, with fluorine fine tuning, to **72** (ticagrelor),¹⁰⁶ an orally active reversible P2Y₁₂R antagonist, which was launched in Europe in 2010 (*h*P2Y₁₂ pK_i 8.7; rat PK CL 21 mL/min/kg; Vss 3.8 L/kg; T_{1/2} 2.6 h, F 24%).



Outside of the work patented by AstraZeneca other companies have developed other nucleotide-based P2Y₁₂R antagonists. Inspire Pharmaceuticals reported the monophosphate, **73** (INS50589, IC₅₀ 16 nM) that showed inhibition of platelet aggregation in a washed human platelet assay. Unfortunately, this compound proved unsuccessful in clinical trials as an intravenously-delivered drug.¹⁰⁷ Further carboxylic acid replacements for

the phosphate groups were investigated with the 2-carboxybenzyl analogue **74** ($hP2Y_{12}$, IC₅₀ = 40 nM) being the most potent of this series.



A series of analogues of **72**, primarily focussed on replacing the hydroxyethoxy substituent with a heterocycle, was reported by researchers at Johnson & Johnson. Compounds containing the 1*H*-tetrazol-5-yl group were the most potent (e.g. **75**, $hP2Y_{12}$, K_i = 2 nM). No *in vivo* data was reported.¹⁰⁸

A number of ester and carbonic ester derivatives (**76a-d**) of **72** and **77** (a major metabolite of **72** with similar binding affinity) have a comparable effect to **72** and **77** on platelet aggregation after oral dosing (5 mg/kg) to rats. No *in vitro* data was given and the activity is assumed to be due to hydrolysis (presumably metabolic) to **72** and **77** (Figure 23).¹⁰⁹



Figure 23: Derivatives of 72, 76a-d and 77 - the active metabolite of 72.
More recently,¹¹⁰ researchers at Shanghai Hengrui Pharmaceutical Co Ltd. described their SAR exploration of the cyclopentyl ring and cyclopropylamino groups of **72**. Compound **78**, a fluorinated analogue of **77**, was more potent than **72** *in vitro* and *in vivo*, with a satisfactory PK profile and a shorter bleeding time observed.

With the scope of developing non-nucleotide antagonists, high throughput screening of the AstraZeneca compound bank identified piperazinyl-pyridine, **79** as a hit ($hP2Y_{12} IC_{50} = 330$ nM). SAR investigations were amenable to parallel synthesis and this eventually led to acyl sulfonamide **80** (AZD1283, $hP2Y_{12} IC_{50} = 11$ nM), a compound with a PK profile suitable for progression into human clinical trials.^{111–113} It is interesting to note that an acyl sulphonamide group is also present in **81** (elinogrel), a P2Y₁₂R antagonist which progressed into clinical trials supported by Portola Pharmaceuticals,¹¹⁴ then by Novartis. However, development of this compound was terminated in 2012.





With the use of fusion protein, the crystal bound structures of the P2Y₁₂R with full agonist 2methylthio-adenosine-5'-diphosphate (2-MeSADP), 2-methylthio-adenosine-5'-triphosphate (2-MeSATP) and **80** have been published.¹³⁻¹⁴ Both 2-MeSADP and **80** bind in the same pocket with the adenine group of 2-MeSADP and the nicotinate group of **80** forming similar π - π interactions with Tyr¹⁰⁵. However, the pocket shape in these structures is different and 2-MeSADP and **80** display only a partial overlap. It is interesting to note the movement in TM7 observed for binding of **80** in the antagonist-bound P2Y₁₂R state compared to that of the agonist-bound P2Y₁₂R state (Figure 24).



Figure 24: a) Overlay of agonist (cyan) and antagonist (brown) bound P2Y₁₂Rs with **80** and 2MeSADP. b) Crystal structure of **80** in an antagonist-bound state P2Y₁₂R c) Methylthioadenosine-5'-diphosphate (2-MeSADP) in the agonist-bound state P2Y₁₂R. An overlay of structures pdb codes 4PXZ (brown) and 4NTJ (cyan) visualised with PyMOL Molecular Graphics System, Version 1.3. Schrödinger, LLC.

The 2-thioether group occupies a lipophilic pocket formed by Phe¹⁰⁶, Lys¹⁵⁵, Ser¹⁵⁶ and Asn¹⁵⁹, providing an explanation for the affinity enhancing effect of the alkylthio group. The 2-MeSATP structure has a similar conformation to 2-MeSADP. Furthermore, **82**, **83** and **68**, with the modified triphosphate chain and larger 2-alkylthio substituent, can be docked in a similar way to 2-MeSADP within the binding cavity of P2Y₁₂R-2-MeSADP, suggesting the reason for receptor agonism and antagonism is unclear. The docking of **72**, with the large N^6 substituent, requires conformational change of the receptor in order to be accommodated.



Berlex Biosciences reported ¹¹⁵ that the piperazinyl-glutamate **84** (BX-667, $hP2Y_{12}$ IC₅₀ 129.9 nM) and its active metabolite **85** (BX-048, IC₅₀ 8.3 nM), are reversible antagonists for the P2Y₁₂R in an *in vitro* ADP-induced washed platelet aggregation assay.¹¹⁶ The compounds were shown to inhibit platelet aggregation and thrombus formation *in vivo* in both rat and dog models.¹¹⁷



Taking **84** as a starting point, scientists at Pfizer used parallel synthesis to find a replacement for the quinoline ring (Figure 25).^{118,119,120}



Figure 25: Chemical expansion of 84 illustrating the range of compounds prepared

A large number of substituted heterocycles were evaluated (group R_3 in Figure 25) and it was found that a nitrogen atom in the ring *ortho*- to the amide was preferred along with a phenyl ring *ortho*- to the same nitrogen (Figure 26).



Figure 26: A series of substituted heterocyclic P2Y₁₂R antagonists

Optimization showed that R₄ could be a wide variety of substituents and did not need to contain an acidic group. Compound **86** ($hP2Y_{12}$, K_i = 15 nM), which contains only one carboxylic acid group, was found to have the best overall profile, with a PK and safety profile suitable for pre-clinical evaluation. Further refinement¹²¹ gave the closely related compounds **87-88**, with activity (**87** $hP2Y_{12}$ K_i 2.1 nM, **88** hK_i 2.8 nM) and PK profiles suitable for clinical backups.



Actelion¹²² reported the development of P2Y₁₂R antagonists using **85** as the starting point, leading to **89**, which is structurally similar to **86-88**. This compound has very good activity (*h*P2Y₁₂R IC₅₀ = 4.8 nM) and a PK profile suitable for further evaluation. In a later paper¹²³ replacement of the carboxylic acid was investigated. A number of acidic carboxylic acid bioisosteres, including acyl sulphonamides, tetrazole and 3-hydroxyisoxazole exhibited similar potencies to the parent compound, with the phosphonic acid derivative, **90** (ACT246475) chosen as the pre-clinical candidate. Unfortunately, the bioavailability was found to be low in both rat and dog. This led to the development of the *bis*((isopropoxycarbonyl)oxy)methyl ester pro-drug **91** (ACT281959).



Sanofi-Aventis¹²⁴ found the 1-phenylpyrazolone scaffold **92** (*h*P2Y12 K_i = 139 nM) as a suitable replacement for the quinoline ring of **84**. A comparison of **92** and **84** docked into a

P2Y₁₂ homology model showed the 1-phenylpyrazolone moiety of **92** occupies the same hydrophobic pocket as the quinoline group of **84**. The 5-substituent of the 1-phenylpyrazolone, which did not overlay with the 4-substituent of quinoline of **84**, was selected for systematic change; followed by variations to the piperazine ethyl carbamate and the central amino acid group. Optimization led to the neutral antagonist **93** (*h*P2Y₁₂ K_i = 7.7 nM). Removal of the acidic moiety led to a substantial reduction of PPB to give high activity in the human platelet rich plasma assay (*h*PRP IC₅₀ = 30 nM). Compound **93** showed antiaggregator activity in an *ex-vivo* dog model (10 mg/kg, *p.o.*), showing the potential for preclinical development.



Pfizer reported thienopyrimidine-based P2Y₁₂R antagonists¹²⁵ with the most potent examples being **94** (*h*P2Y₁₂ K_i = 4 nM) and **95** (*h*P2Y₁₂ K_i = 3 nM). However, a significant drop in activity was observed in the *h*PRP assay (3 and 5 μ M respectively), which was attributed to the highly hydrophobic biphenyl group.



Taking the HTS hit **96** (P2Y₁₂ IC₅₀ = 1.5 μ M) as a starting point, Sanofi-Aventis developed **97** (SAR216471) as a pre-clinical candidate.¹²⁶ With high binding affinity (IC₅₀ = 17 nM), the compound exhibited a small activity drop-off in the *h*PRP assay (IC₅₀ = 100 nM) resulting in good activity in the *ex-vivo* rat platelet aggregation model (ED₅₀ = 2.75 mg/kg *p.o.*). A number of anthraquinone derivatives have been found to be selective, high affinity P2Y₁₂R antagonists, the most potent of which are **98** (*h*P2Y₁₂ K_i = 25 nM) and **99** (*h*P2Y₁₂ K_i = 21 nM).^{127,128} Compound **100** (*h*P2Y₁₂ IC₅₀ = 170 nM) was found after screening the COR compound library.¹²⁹ Limited investigation of the SAR through simultaneous changing of the ethoxy groups failed to find more potent analogues (Figure 27).





99 100 Figure 27: A selection of $P2Y_{12}R$ antagonists from Sanofi-Aventis and **100** (CT50547) discovered through screening the COR screening collection.

Perspective comment

The important role the P2Y₁₂R plays in thrombus formation and the huge commercial success of clopidrogrel, has meant that a number of pharma companies have invested significantly in P2Y₁₂R antagonist programmes.

The thienopyridine class of irreversible binders was discovered incidentally in rat and mouse *in vivo* and *ex-vivo* anti-inflammatory screens. The requirement for metabolic transformation to an active species for P2Y₁₂R activity means that compounds, within this series, would be inactive in either a cellular or membrane-based HTS assay. Furthermore, the active metabolite **66** is chemically unstable and would not therefore be present in a compound screening library.

The risks involved in developing an irreversible antagonist and its potential for deleterious binding to proteins could be seen as being prohibitive to most pharmaceutical groups. As a consequence, P2Y₁₂R antagonist programmes have focussed on finding reversible receptor antagonists. The first of these company programs, Fison's Pharmaceuticals, before the advent of high throughput screening, used ATP as a starting point. It is commendable that these investigators were able to develop an oral drug, ticagrelor, from such a non-lead-like chemical starting point.

Antagonists of the P2Y₁₃ receptor (P2Y₁₃R)

The P2Y₁₃R was first identified at the turn of this century,^{130,131} with its primary sequence demonstrating a 48% amino acid homology with the P2Y₁₂R. Coupled to G_i, it is activated by a range of diphosphate adenine nucleotides (ADP, 2MeSADP, ADP β S). A more thorough evaluation of the receptor revealed a number of key similarities and differences between the P2Y₁₃ form of the receptor and its closely related P2Y₁₂ subtype.¹³² P2Y₁₃ is less sensitive to activation *via* triphosphate nucleotides, 2MeSADP displays a superior or equal potency to that of ADP depending upon the endpoint measurement and the receptor is only weakly antagonized by **83**.¹⁰⁵ In addition, the P2Y₁₃R is not antagonized by the active metabolite of **66** at concentrations up to 2 μ M.¹³² Meanwhile, the similarities between the two receptor subtypes were also revealing; both subtypes, for example, are antagonized by 2MeSAMP, diadenosine tetraphosphate (Ap₄A) and most interestingly **68**, with the latter behaving in a non-competitive manner with respect to the P2Y₁₃R. It was further noted that ADP activation of the P2Y₁₃R could be antagonized by **49** (IC₅₀ = 1.9 μ M), **53** (IC₅₀ = 2.3 μ M) and **54** (IC₅₀ = 11.6 μ M). The P2Y₁₃R is expressed in the brain, spleen lymph nodes and bone marrow where it is also expressed on hemopoietic cells.¹³³

To date, there remains a paucity of $P2Y_{13}$ selective antagonists, with the main structural contribution arising from derivatives of **54**.¹³⁴ Recognizing that the pyridine derivative **54** had been previously identified as a low potency antagonist of the $P2Y_{13}R$,¹³² Kim *et al* embarked

upon the design and synthesis of a range of new derivatives, assessing their pharmacology through attenuation of ADP-induced PLC activity in human astrocytoma 1321NI-G α_{16} cells stably transfected with human P2Y₁₃Rs (*h*P2Y₁₃-1321N1- G α_{16}).



The most potent compounds generated from this synthesis campaign were **101** (MRS2211 $hP2Y_{13}$ pIC₅₀ = 5.97) and **102** (MRS2603 $hP2Y_{13}$ pIC₅₀ = 6.18). **102** demonstrated a competitive antagonism ($hP2Y_{13}$ pA₂ = 6.3) alongside a >20-fold selectivity towards the P2Y₁₃R when compared to P2Y₁ and P2Y₁₂. Its subsequent commercial availability has made it the molecular probe of choice for further investigation of P2Y₁₃R subtype pharmacology.^{135–144}

Drug-like antagonists of the P2Y₁₄ receptor (P2Y₁₄R)

The P2Y₁₄R was, at its time of identification, the eighth member of the P2Y receptor family.¹⁴⁵ It is a G_i-coupled receptor, which is activated by at least four naturally occurring UDP-sugars. These include UDP-galactose, UDP-glucuronic acid, UDP-Nacetylglucosamine and UDP-glucose (UDP-Glc), with the latter acting as the most potent agonist. P2Y₁₄ mRNA has been detected in a range of human tissues including the stomach, intestine, adipose, brain, lung, spleen, heart and placenta.¹³³ Additionally, this receptor has been found in neutrophils.¹⁴⁶ Since UDP-Glc promoted signalling in multiple types of immune cells has been described; the P2Y₁₄R may possess a role in regulation of immune system homeostasis.¹⁴⁷ More recently, experiments with P2Y₁₄ knockout mice have highlighted the potential of P2Y₁₄R antagonism in the treatment of diabetes.¹⁴⁸

Using a yeast model system, it was demonstrated that UDP antagonized the UDP-Glc promoted P2Y₁₄R activation in a concentration-dependent manner.¹⁴⁹ Cognisant of this report, Harden *et al* undertook a more detailed study to ascertain that UDP acted as a competitive antagonist at the human P2Y₁₄R ($pK_B = 7.8$).¹⁵⁰ A similar level of receptor antagonism was observed using uridine 5'-*O*-thiodiphosphate whereas ADP, CDP and GDP produced no antagonist activity. An interesting observation from this study identified a striking ortholog variance, whereby UDP was demonstrated to act as a potent agonist (*r*P2Y₁₄R EC₅₀ = 0.35 µM) highlighting a polarized pharmacological difference in ligand behaviour. The authors then reassessed the action of UDP in three different cell lines; human embryonic kidney (HEK) 293, C6 glioma, and Chinese hamster ovary (CHO) cells, all stably expressing the human form of the P2Y₁₄R.¹⁵¹ This series of experiments ultimately concluded that UDP was in fact acting as an agonist with EC₅₀ values of 74, 29 and 33 nM respectively in the previously highlighted cell lines.

The first non-nucleotide based antagonists for the P2Y₁₄R were originally reported by Merck and comprised a series of compounds based around a tetrahydropyrido[4,3-*d*]pyrimidine scaffold.¹⁵² The initial hit **103** was identified *via* an high-throughput calcium²⁺ mobilization assay screen of the Merck sample collection. Whilst displaying only modest potency (*m*P2Y₁₄ IC₅₀ = 4.9 μ M), the scaffold was seen as attractive to pursue a hit-to-lead optimization programme; comparing activity at both the mouse and chimpanzee orthologs of the P2Y₁₄R. The authors comment that the selection of chimpanzee P2Y₁₄ (99% sequence homology to human) for screening was driven by the larger window (signal/background noise) with this receptor over the human P2Y₁₄, while the mouse receptor (83% identical to human) was used to enable future evaluation of the compounds in mouse models of disease. Systematic modification of the substitution pattern on the phenyl urea moiety eventually revealed that a 3,4- or 3,5-disubstitution pattern afforded the most potent antagonists as long as the 3-position substituent was an ethyl group, *e.g.* **104** (Figure 28).



Figure 28: The first non-nucleotide based antagonists for the P2Y₁₄R.

Turning their attention to the *o*-tolyl group at the 4-position of the heterocylic core generated a series of analogs highlighting that either *ortho*-positions could be substituted by either a methyl or chloro group, maintaining very good activity at both receptors, *e.g.* **105**. The final series of analogs retained the 3-ethylphenyl urea and the *o*-tolyl moieties and then altered the 3-pyridyl group to produce nineteen new compounds of which five are highlighted (Table 6).

Table 6: Antagonist potency of 2-aryl substituted tetrahydropyrido[4,3-*d*]pyrimidines on the mouse and chimpanzee P2Y₁₄Rs.¹⁵²



Compound	Ar	Mouse P2Y ₁₄ IC ₅₀	Chimpanzee P2Y ₁₄ IC ₅₀ (µM)
		(µM)	
106	3,4-(OCH ₂ O)-Ph	0.010	0.081
107	4-(CN)-3-Pyr	0.003	0.004
108	5-pyrimidyl	0.012	0.008
109	2-(CN)-5-pyrimidyl	0.001	0.001
110	Me ₂ -4-isoxazolyl	0.004	0.002

Compounds **107** and **109** were not progressed due to potent *h*ERG potassium ion channel binding (<200 nM), whereas compounds **106**, **108** and **110** displayed reduced *h*ERG binding (>5 μ M). Preliminary *in vivo* analysis of these compounds when dosed as suspensions (50 mg/kg p.o. or *iv* at 5 mg/kg *i.v.*) in C57B6 mice revealed compounds with high volumes of distribution and extended half-lives. Compound **106** gave the best overall PK parameters and was considered suitable for further *in vivo* experiments to interrogate the pharmacological role of P2Y₁₄. Further characterization of **106** revealed that its antagonistic activity was mediated through a non-competitive manner with respect to UDP-mediated receptor activation.

The Merck group followed this report with a back-to-back manuscript highlighting a different scaffold, a 4,7-disubstituted naphthoic acid **111**, which had been identified as displaying antagonism of UDP-Glc activation ($IC_{50} = 3.5 \mu M$) of both the mouse and chimpanzee P2Y₁₄R variants using the same assay methodology.¹⁵³⁻¹⁵⁴ Unlike **106**, this compound exhibited competitive antagonism of ³H-UDP in a recombinant simian P2Y₁₄ binding assay (K_i 0.16 μ M). A comprehensive SAR study focused upon substituents in the 3-, 4- and 7- positions of the naphthoic acid scaffold and revealed **112** as the most potent compound whilst confirming the essential role of aryl substituents at the 4- and 7-positions.



Early PK assessment of **112** was undertaken through oral dosing of C57BL/6 mice at 50 mg/kg and *i.v.* administration at 2 mg/kg. (F = 12%, $T_{1/2}$ = 2.7 h). Further studies identified that **112** was extensively metabolized *via* phase II metabolism (>99%) to the glucuronide and excreted *via* the bile.

A second round of synthetic variants were synthesized in an attempt to attenuate this level of

glucuronidation through decreasing the electron density of the carboxylic acid moiety. This ultimately led to identification of **113** as the best molecule in terms of its potency and PK profile ($K_i = 4 \text{ nM}$, F = 67% (mouse) CL = 1.6 ml/min/kg, $T_{\frac{1}{2}} = 3.0 \text{ h}$, $C_{max} = 113 \mu M$).



However, it was identified that **113** displayed high affinity for plasma proteins, being >99% bound in the presence of 4.5% human serum albumin (HSA).¹⁵⁵ Further synthetic efforts identified zwitterion **114** as a compound which retained its pharmacological potency ($K_i = 1.9$ nM in the chimpanzee P2Y₁₄ binding assay) as well as displaying acceptable levels of HSA binding. The latter assay was determined by using a binding assay incorporating 2% HSA for antagonist measurements. Harden *et al* subsequently reported a more thorough evaluation of the pharmacology of **114**.¹⁵⁶ They successfully demonstrated that in C6 glioma cells stably expressing the P2Y₁₄R, the concentration-effect curve of UDP-Glc for promoting inhibition of adenylyl cyclase was right-shifted in a concentration-dependent manner by **114**. In addition, at a concentration of 1 μ M **114** exhibited no agonist or antagonist effect at the P2Y₁, P2Y₂, P2Y₄, P2Y₆, P2Y₁₁, P2Y₁₂ or P2Y₁₃Rs.

The zwitterionic nature of **114** imbued detrimental effects upon its oral bioavailability (F = 5%, $C_{24h} = 0.68 \mu$ M). Therefore a series of ester derivatives were synthesized to investigate whether a pro-drug strategy would be beneficial. Of the ten esters described, four displayed good lability to afford high conversion rates to the parent drug **114** in the presence of whole blood. However of these, only **115** and **116** were able to replicate this in an *in vivo* setting with **116** being identified as the most promising candidate.



Compound **116**, when orally dosed in mice at 50 mg/kg, delivered plasma levels of **114** ($F_{virtual} = 67\%$, $C_{24h} = 2.28 \mu$ M, AUC = 54 μ M h and CL = 1.6 mL/min/kg) which were significantly higher than when **114** was administered as the free zwitterion (F = 5%, $C_{24h} = 0.68 \mu$ M, AUC = 23 μ M h).

As a pharmacological tool, **114** was also identified as a potential congener for the development of a fluorescent tool for receptor interrogation.¹⁵⁷ Molecular modelling studies of **114** bound to a homology model of the P2Y₁₄R were undertaken, the model being constructed on the basis of X-ray crystal structures of the P2Y₁₂R.¹³⁻¹⁴ Modelling established that the piperidyl nitrogen was suggested to be pointing towards the extracellular opening of the ligand binding pocket such that the charged piperidine nitrogen is solvent exposed and therefore a potential tether point on which to build a linker moiety. To this end an alkyl acetylene linker was appended to the piperidyl nitrogen to afford a congener primed for conjugation with an azide modified fluorophore *via* a copper-catalyzed [2+3] cycloaddition, ultimately affording Alexafluor488 **117** and a BODIPY 630/650-X **118** fluorescent conjugates.



117 exhibited exceptionally high affinity towards the P2Y₁₄R (K_i = 80 pM) whereas **118** displayed a much weaker interaction (K_i >100 nM) illustrating the critical influence of both the linker and the fluorophore on the final pharmacology of the conjugate.¹⁵⁸ Fluorescent conjugate **117** was employed in flow cytometry studies to quantify specific binding to the P2Y₁₄R and further utilized to confirm the binding selectivity's and affinities of established P2Y receptor ligands.

Conclusion

Within the past 2 decades, numerous P2Y receptor antagonists have been reported in both peer-reviewed and patent literature. The therapeutic relevance and efficacy of some of these antagonists has been proven *in vitro*, *ex vivo and in vivo*. The most clinically relevant and successful antagonists to-date have centered on new anti-thrombotics targeting the P2Y₁₂R. The serendipitous discovery of the thienopyridine class of irreversible P2Y₁₂R binders led to the development and commercial success of clopidogrel (launched in 1998),¹⁰¹ followed by prasugrel (2009).¹⁰⁴ Their successes encouraged numerous pharma-companies to invest into P2Y₁₂R antagonist programs. It is commendable that taking ATP as a starting point, scientists at AstraZeneca developed the oral drug ticagrelor (2011);¹⁰⁶ a program which has also led to the approval of cangrelor (2015).¹⁰⁵ P2Y₁R antagonists have also showed promise as anti-thrombotics and substantial research into developing suitable clinical candidates has been reported by scientists at BMS, Pfizer and GSK. To-date, it remains that no compounds have progressed to FDA approval. Notwithstanding this fact, drug-like

compounds (e.g. **27** and **31**) are available to further optimize, however the core physico chemical properties of these P2Y₁R antagonists have no doubt hindered their clinical development. Outside of anti-thrombotics, antagonists of the other P2Y receptors show promise for the treatment of a variety of diseases. P2Y₁₄R antagonists show potential as preventative agents for type-2 diabetes, with Merck reporting both potent competitive and non-competitive antagonists, with the pro-drug **116** being the most advanced and promising clinical candidate.¹⁵⁵ Antagonists of the P2Y₂R look to be therapeutically viable in a variety of conditions, with a growing body of evidence to support their use as anti-metastatic agents.⁴⁹ Several patents published by AstraZeneca reported the most relevant P2Y₂R antagonists; with **43** being used by many research groups in *in vivo* and *ex vivo* studies.^{55,56} There is a need to develop drug-like P2Y₂R antagonists which would further validate the therapeutic potential of P2Y₂R antagonism in many disease states.

In our opinion there are at present no drug-like P2Y₄R, P2Y₆R, P2Y₁₁R and P2Y₁₃R antagonists in the published or patent literature. The structural class of the majority of these antagonists can, with exceptions, be derived from the broad-spectrum P2 receptor antagonists: **49**, **53** and **54**. Although some of these have shown potency and selectivity, their overall physico chemical properties are not commensurate with good oral absorption and metabolic stability. With growing evidence for these receptors having a fundamental role in a variety of disease states, the identification of new lead-like compounds, will hopefully afford new P2YR clinical candidates.

Throughout the identification and optimization of P2Y₁, P2Y₁₂ and P2Y₁₄R antagonists, radioligand binding and Ca²⁺ mobilization (FLIPR-based) HTS assays have been reported, that helped identify new lead-like receptor antagonists. Importantly, several fluorescent ligands have recently been reported for the P2Y₂, P2Y₄, P2Y₆ and P2Y₁₄ receptors.^{157,159,160} We feel that these, and future fluorescent ligands, could underpin fragment-based approaches to identify new lead-like antagonists of the P2Y receptors. These fluorescent ligands will also be of huge importance in interrogating the pharmacology of these receptors in healthy and diseased cell lines. The most significant recent development towards understanding the binding of agonists and antagonists to P2YRs, has been the publication of ligand-bound $P2Y_1R^{12}$ and $P2Y_{12}R^{13,14}$ X-ray crystal structures. The homology models that have been reported for P2Y receptors have predominately focused on agonist-nucleotide binding. With this new structural information, and *in-lieu* of structural information for all P2Y receptors, there is now scope to develop antagonist-focused homology models across the two subsets of P2Y₁-like and P2Y₁₂-like receptors. This is something which will undoubtedly aid identification and optimization of new lead-like antagonists of P2Y receptors.

Biographies

Sean Conroy received his Master's in Chemistry (MChem) from The University of Southampton (U.K.) in 2013. During which, he also worked in industry on the development of oral small molecule plasma kallikrein inhibitors. Currently he is a doctoral student within the Division of Medicinal Chemistry and Structural Biology at the University of Nottingham (U.K.), under the supervision of Dr. Michael Stocks, Prof. Barrie Kellam and Prof. Stephen Hill with his research focusing on the development of P2Y receptor antagonists.

Nicholas Kindon received his degree in Natural Sciences from Cambridge University in 1984 and stayed on to do a PhD in Organic Chemistry under the supervision of Dr. Ian Fleming, completing in 1987. He then undertook 2 years of post-doctoral research with Professor Steven D. Burke at the University of Wisconsin. Upon his return to the UK he started his industrial career at Fison's Pharmaceuticals, later to become Astra then AstraZeneca where he remained for over 20 years. He is currently a research fellow in the Centre for Biomolecular Sciences at the University of Nottingham.

Barrie Kellam is Professor of Medicinal Chemistry in the School of Pharmacy and his research is focused on the synthesis of novel molecular entities and their application to a wide arena of biological and pharmacological problems. Most recently his research has centred on the medicinal chemistry of G- Protein Coupled Receptors (GPCRs) and current work is focused on the beta-adrenoceptor, adenosine, cannabinoid, orexin, P2Y and

histamine families. His research also involves the area of fluorescent ligand design. This work has produced numerous papers and patents and also resulted in the successful formation of the University of Nottingham spinout company CellAura Technologies Ltd.

Michael Stocks was appointed as an Associate Professor in Medicinal Chemistry in 2012 within the School of Pharmacy at The University of Nottingham. He has over 20 years of industrial experience in drug discovery within AstraZeneca and during his industrial career; he was both the lead scientist and project leader on multiple pre-clinical research projects as well as being the synthetic medicinal chemistry lead of the AstraZeneca compound enhancement initiative. Since joining the School of Pharmacy in 2012, he has grown his research group and his research has focused on the medicinal chemistry design of compounds to study and modulate the function of biological targets.

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Abbreviations Used: ADME absorption, distribution, metabolism, and excretion; Ap₄A diadenosine tetraphosphate; ATP adenosine-5'-diphosphate; CF cystic fibrosis; CHO Chinese Hamster Ovary; CL clearance; FLIPR fluorescent imaging plate reader; F bioavailability; GPCR G protein-coupled receptor; HEK human embryonic kidney; *h*ERG human ether-à-go-go-related gene; *h*PRP human platelet rich plasma; HTS high throughput screening; PA platelet aggregation; PK pharmacokinetics; PPB plasma protein binding; SAR structure activity relationship; T_{1/2} terminal half-life; UTP uridine triphosphate; V_{ss} volume of distribution.

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