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A quest for connections : ligands for the HCA2, adenosine A3 and GPR88 receptors

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Chapter 1



General introduction

G protein-coupled receptors in health and disease

G protein-coupled receptors (GPCRs), alternatively called 7-TM receptors (for 7 transmembrane domains), comprise a large family of eukaryotic membrane proteins. When a GPCR is activated, for example by a hormone or a neurotransmitter, it transfers the message to intracellular signaling cascades. The most well-known of these cascades involve G protein activation, but recently it has become clear that other possible signaling mechanisms exist. In the end, these GPCR signals mediate vital functions of the human body, such as perception of the world around us, communication between the brain and other parts of the body, energy storage or mobilization, movement and fertility.

Table 1. Examples of drugs acting on GPCRs. Adapted from [5].

GPCR	Drug	Indication
β_2 adrenergic	albuterol	asthma
angiotensin AT ₁	losartan	hypertension
calcitonin	calcitonin	osteoporosis
dopamine D ₂	haloperidol	schizophrenia
gonadotropin-releasing factor	goserelin	cancer
histamine H ₂	ranitidine	ulcer
serotonin 1D	sumatriptan	migraine
leukotriene	pranlukast	allergy, asthma
μ opioid	morphine	pain

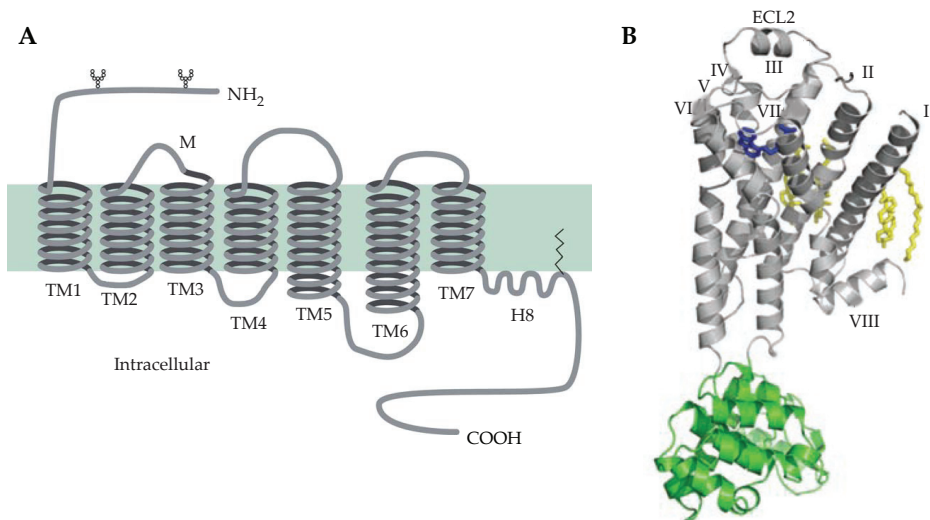


Figure 1. Common secondary structure of GPCRs. **A:** Schematic representation of a GPCR, indicating transmembrane domains 1-7 (TM1-7), the α -helical domain termed helix 8 (H8), a palmitoylation site next to it (zigzag line) and two potential glycosylation sites in the N-terminal tail (Y shapes). From [6]. **B:** High-resolution crystal structure of the β_2 adrenoceptor bound to carazolol (blue) together with the stabilizing T4 lysozyme protein (green) in place of the third intracellular loop. The helices that are shown next to each other in A form a barrel-like arrangement here, which is probably the form of the protein in vivo. The helices are indicated in roman numerals, including helix VIII in the C-terminal region. A small helix in extracellular loop 2 (ECL2), which may be typical for this receptor subtype, is also clearly visible. From [7].

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A total of 799 verified human GPCRs are known, thus representing about 3% of all genes in our genome [1]. These receptors bind to a large variety of ligands including small organic compounds, lipids, peptides, proteins and even photons. Approximately 50% of the GPCR repertoire is dedicated to olfaction.

From a pharmacological point of view, GPCRs are interesting drug targets because they are implicated in many different pathophysiological processes. Furthermore, it is relatively straightforward to design molecules that interact with GPCRs and this type of drugs are successfully used in the clinic [2]. An estimated 30 to 40% of all available drugs target GPCRs, with annual sales of over 65 billion dollars [3]. Some examples are given in table 1. The variety of indications, for which these drugs are used, illustrates the omnipresence of GPCRs in the human body.

On a molecular level, all GPCRs have a common secondary structure. Their most striking features are the seven hydrophobic membrane-spanning alpha-helices (TM1-7) [4]. Extracellular and intracellular loops (EL and IL) connect the helices, and an extracellular N-terminal domain and intracellular C-terminus complete the protein (see figure 1A). The TM helices have been shown to form a barrel-like tertiary structure in the membrane, with TM1 and TM7 in close proximity (figure 1B).

GPCR classification

Several classifications have been proposed for the GPCR superfamily on the basis of primary structure, endogenous ligand specificity and species source. In a classical system by Kolakowski, the GPCRs are segregated into seven families or classes (A-F and O) [8]. A modern version of this system is used in the GPCRDB database www.gpcr.org [9], distinguishing the following classes: A: rhodopsin-like, B: secretin-like, C: metabotropic glutamate-like, D: pheromone receptors, E: cAMP receptors and F: frizzled/smoothened. After the human genome sequence became available, a slightly different system called GRAFS was proposed [10-12]. In this system, the classes are named Glutamate, Rhodopsin, Adhesion, Frizzled and Secretin, plus a recent addition, Taste2. Thus, class B from the A-F system is divided in the Adhesion and Secretin classes, which reflects the inherent differences between these receptor clusters. Classes A (Rhodopsin), B (Secretin&Adhesion) and C (Glutamate) are most important in mammalian physiology. Of these, class A is by far the largest and most diverse. It contains 672 receptors, which includes 388 olfactory receptors [13]. The GPCRs that will be discussed in this thesis all belong to the class A, rhodopsin-like, GPCR family.

Properties of Rhodopsin-like GPCRs

Although the class A receptors are highly diverse in sequence and ligand binding properties, certain residues in the TM regions are conserved (see figure 2). Most striking are the microdomains D/ERY (TM3), CWxP (TM6) and NPxxY (TM7). Furthermore, two conserved cysteine residues are present in the extracellular domain, at the end of TM3 and in extracellular loop 2. They are thought to form a disulfide bridge in most class A GPCRs, which may be crucial to structural integrity and receptor function (see for example [14]).

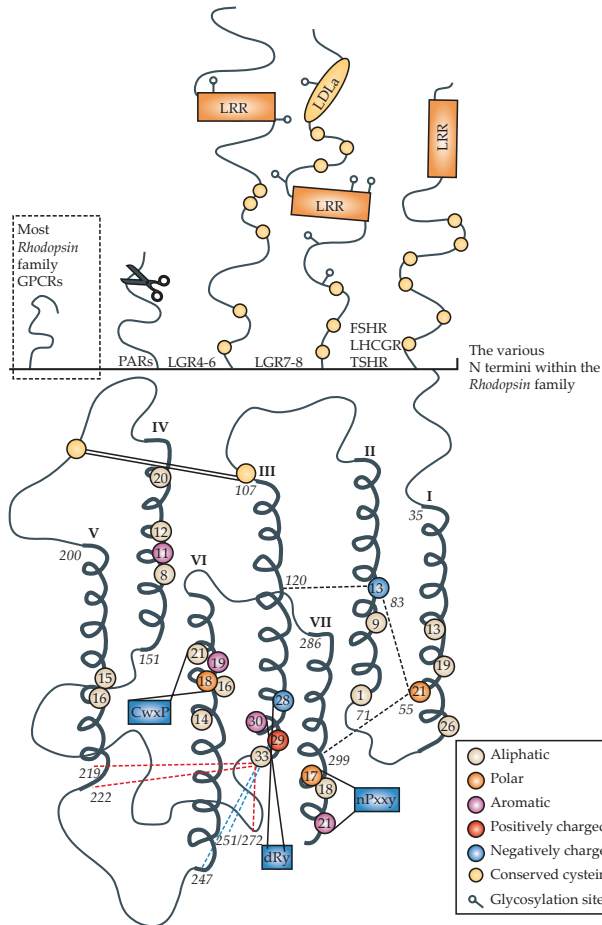


Figure 2. Conserved features and structural motifs within the Class A, rhodopsin-like, GPCRs. The lower part of the figure shows the conserved residues from eight diverse class A GPCRs. Conserved residues are shown as circles colour-coded for amino acid properties. In the blue boxes conserved class A motifs are indicated with uppercase letters for completely conserved positions, lowercase letters for well-conserved positions (>50%) and x for variable positions. Conserved cysteine residues are shown in yellow and the disulphide bridge between EL1 and EL2, which is conserved in most GPCRs, is indicated as two lines. Dashed black lines show hydrogen bonds within bovine rhodopsin whereas dashed blue lines (from DRY to 247 and 251) show the postulated ionic lock, which is thought to keep the receptor in the inactive state. Dashed red lines display Van der Waals interactions within the β_2 -adrenoceptor model. In the upper part of the figure different N-termini of class A GPCRs are shown. The scissors indicate the cleavage site for the protease-activated receptors (PARs). From [13].

The position of the ligand binding site varies among class A receptors. Small ligands (such as biogenic amines, nucleosides, eicosanoids, lysophosphatidic acid and sphingosine-1-phosphate) bind in a so-called TM cavity, formed by the seven TM alpha helices ([15] and references therein). The ligands for the hydroxy-carboxylic acid receptors and the adenosine receptors, which are described in the present work, fall in this category. Larger ligands, such as peptides and glycoprotein hormones, interact with the N-terminus and/or the extracellular loops, and in some cases also with the outer portions of the transmembrane helices. Examples are oxytocin, vasopressin, opioids, thyroid-stimulating hormone (TSH) and follicle-stimulating hormone (FSH) [16].

High-resolution GPCR structures

Recently, some of the most important advances in the field have been made using X-ray crystallography. Structural analysis of GPCR molecules is very challenging and until recently, only the structure of rhodopsin was known [17-19]. In the last four years crystallization efforts finally paid off with the elucidation of high resolution crystal structures of squid rhodopsin, the β_2 adrenergic receptor (β_2 AR), the β_1 AR, the A_{2A} adenosine receptor (for a review see [20], see also figure 1), and most recently, the CXCR4 receptor [21], the dopamine D_3 receptor [22] and the histamine H_1 receptor [23]. These receptors were all stabilized in the inactive state, since this facilitates crystallization. For (rhod)opsin, the active apoprotein was also crystallized [24-25]. In 2011, active, transmitter-bound GPCRs have finally been crystallized, namely rhodopsin [26-27], the human β_2 AR [28] and the adenosine A_{2A} receptor [29-30]. The newest structure of activated β_2 AR is even complexed with a G_s protein [31]. This new (relative) wealth of structural information has increased our understanding of the structure of the specific GPCRs, the position of the ligand binding pockets and the orientation of the ligands in those pockets. The structures of the different receptors are remarkably similar, confirming that the secondary and tertiary structure of GPCRs is highly conserved, although there are, of course, subtle differences. For example, the binding pocket of the antagonist ZM241385 in the A_{2A} receptor was not as was anticipated on the basis of the β_2 adrenergic crystal structure with its antagonist carazolol. Therefore, care should be taken when homology models are used to predict the structure of a receptor that has not been crystallized yet. Comparison of active and inactive structures suggests that binding of an agonist results in conserved rearrangements near the binding site, which then propagate through the transmembrane domains to yield an active state. Binding of a G protein or substitute seems necessary to stabilize a fully active state [32].

Receptor activation leads to G protein signaling

GPCRs form an important connection between the outside and the inside of the mammalian cell. When an endogenous agonist like a hormone or a neurotransmitter binds to a GPCR, a conformational change occurs in the receptor protein, which commonly leads to the activation of a G protein (guanine nucleotide-binding protein) [33]. The G protein α subunit will release GDP from its GTPase catalytic site and bind GTP. This causes the G protein to dissociate from the GPCR, and divide into the α subunit and the $\beta\gamma$ complex. Both parts of the G protein can activate downstream effectors. The main $G\alpha$ families are $G\alpha_s$, $G\alpha_{i/0}$ and $G\alpha_q$. $G\alpha_s$ stimulates adenylate cyclase, thus stimulating cAMP production, whereas $G\alpha_{i/0}$ has the opposite effect, inhibiting adenylyl cyclase. $G\alpha_q$ can stimulate phospholipase C, which causes an increase in cytoplasmic calcium concentrations. $G\beta\gamma$ dimers can activate phosphoinositide 3-kinases, which in turn activate other proteins, including MAP-kinases. Interestingly, these mitogen-activated protein kinases can also be activated by GPCRs via other, G protein-independent pathways [34]. When activated, they can influence gene expression. Other effects can also occur; the skin flushing side effect of drugs acting on the hydroxy-carboxylic acid receptor 2 (HCA₂) is possibly mediated by this pathway (see

chapter 2 and 3). The $G\alpha$ subunit is deactivated when it converts GTP into GDP in its intrinsic GTPase domain. $G\beta\gamma$ dimers are deactivated when they bind a $G\alpha$ subunit again.

The next step: internalization and arrestins

After a receptor has been activated, it is in many cases removed from the cell membrane. This internalization process is often (but not always) mediated by arrestins, which act as scaffold proteins that assemble a protein complex at the intracellular face of the receptor. Once inside the cell, the receptor protein can be broken down or recycled to the membrane after removal of the bound agonist [35-36]. Recruitment of arrestins to a receptor protein can also result in arrestin-mediated signaling, leading for example to the MAP-kinase activation mentioned above [37-38].

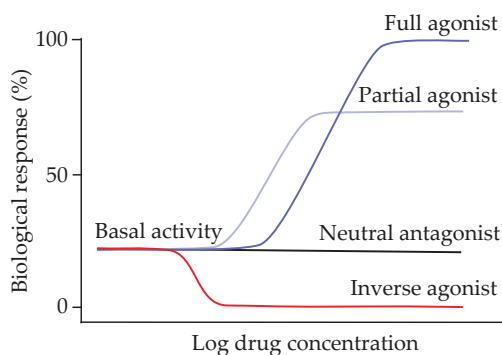


Figure 3. Dose-response curves of ligands with different efficacy. Many GPCRs also display some basal activity in absence of a ligand. From: [20].

Different ligands have different effects

Next to agonists, GPCR ligands exist that de-activate the receptor (inverse agonists), as well as ligands that block the binding site but do not change the receptor activation state (neutral antagonists) (figure 3). We can also distinguish full agonists, which fully activate the receptor, and partial agonists, which cannot cause full activation even at concentrations that fully occupy the receptor. This last type of ligands for the HCA_2 receptor is investigated in chapter 3. The existence of partial agonists suggests that GPCRs are not simply on-off switches. Rather, the receptor protein is now thought to exist in a range of conformational states. A bound ligand stabilizes a particular subset of states, and this determines which of all possible signaling pathways will be influenced, and also with which efficacy. In this more complex view of the receptor protein, a ligand is not simply an agonist, antagonist or inverse agonist, but can be, for example, an inverse agonist for the G_s pathway, and at the same time an agonist for the arrestin pathway [38-39]. In fact, this extreme example of ‘biased signaling’ has been demonstrated for the β_2 -adrenoceptor, where propranolol functioned as an inverse agonist on the G_s protein and its downstream pathways, but as a partial agonist on (most likely arrestin-mediated) activation of extracellular signal-regulated kinase (ERK)1/2 [40]. Thus, one ligand binding to one receptor can have a whole spectrum of effects. A slightly different ligand may prompt the downstream cascades of

the same receptor in a different manner. These phenomena, termed ligand texture and ligand-directed signaling, have only recently been recognized [39]. Ligand bias on the HCA₂ receptor is discussed in chapters 2 and 3 of this thesis.

Manipulating downstream signaling

Understanding of the intracellular signaling cascades and how GPCRs stimulate them made it possible to bend these pathways to suit research purposes. For example, in immortalized cell lines expressing high levels of the chimeric G protein G_{qi5}, all GPCRs that normally interact with G_i proteins are forced to signal through the G_q pathway, leading to an easily detectable increase in intracellular calcium concentration [41-42]. G_{qi5} is identical to the G_q protein, except for five C-terminal residues which are exchanged for their G_i counterparts. These five amino acids determine the interaction with the receptor. Many variations of this strategy exist and are employed in the search for new GPCR ligands, often in a high-throughput screening setup where thousands of compounds can be tested per day. One example of such a screen is reported in chapter 7 of this work.

Allosteric modulators

A special class of GPCR ligands is formed by allosteric modulators. These compounds bind to the receptor at a site distinct from the so-called orthosteric binding site, where the endogenous ligand binds. Binding of the modulator can influence the conformation of the receptor and modify the affinity and/or efficacy of orthosteric ligands. Some allosteric modulators also have intrinsic efficacy themselves and can activate the receptor without binding of an orthosteric agonist. Allosteric modulators can be promising drug candidates since they may be more specific and have less side effects. Allosteric binding sites of synthetic ligands are, in principle, not evolutionarily conserved, which makes it less likely for an allosteric modulator to have affinity for related GPCRs [43]. Furthermore, an allosteric enhancer that makes the endogenous agonist more potent could boost the natural signal without constantly activating the receptor. This can be an important therapeutic advantage because it improves the timing and localization of receptor activation. Two allosteric GPCR modulators are currently on the market: the calcimimetic cinacalcet, which is a positive allosteric enhancer of Ca²⁺-sensing receptors, and the anti-HIV drug maraviroc, an allosteric inhibitor of chemokine receptor CCR₅ [44]. In chapter 5 of this thesis a number of new allosteric modulators for the HCA₂ receptor are presented.

Orphan receptors and the quest for ligands

As mentioned above, a total of 799 human GPCRs have been identified, of which 369 are presumably non-sensory GPCRs (not involved in taste, vision or smell). Approximately 100 to 140 of these potential drug targets are still 'orphans', with no known endogenous ligand and in most cases no known function [1, 45].

Classic and reverse pharmacology

The first GPCRs that were purified and cloned in the 1980s, were receptors for known signaling molecules (adrenalin and noradrenalin) that had been studied for decades (for

a review see [46]). This approach, where receptors are identified to match the known signaling molecules, has later been termed the classic pharmacology approach (see figure 4, left scheme). After the first expression cloning of the β_2 -adrenoceptor in 1986 [47], and the finding that this receptor probably shared the 7 transmembrane domain topology of rhodopsin, pioneers of GPCR research soon suspected that this feature was common to many receptors signaling through G proteins. The rapid homology cloning of many other GPCRs, including those for acetylcholine, serotonin and the neuropeptide substance K, confirmed their hypothesis [48-49]. Some of the receptors that were cloned did not have a known ligand, but in many cases they were readily paired to one of the many 'orphan' signaling molecules. However, in the 1990s the number of cloned receptors had vastly increased due to the advent of PCR techniques, and the number of known signaling molecules that were not yet coupled to a receptor was dwindling. This imbalance reversed the roles of transmitter and receptor in research: known orphan receptors were used to fish for novel signaling molecules, instead of the other way around. The term reverse pharmacology is used for this approach. In this thesis, it was applied on the orphan receptor GPR88 (chapter 7).

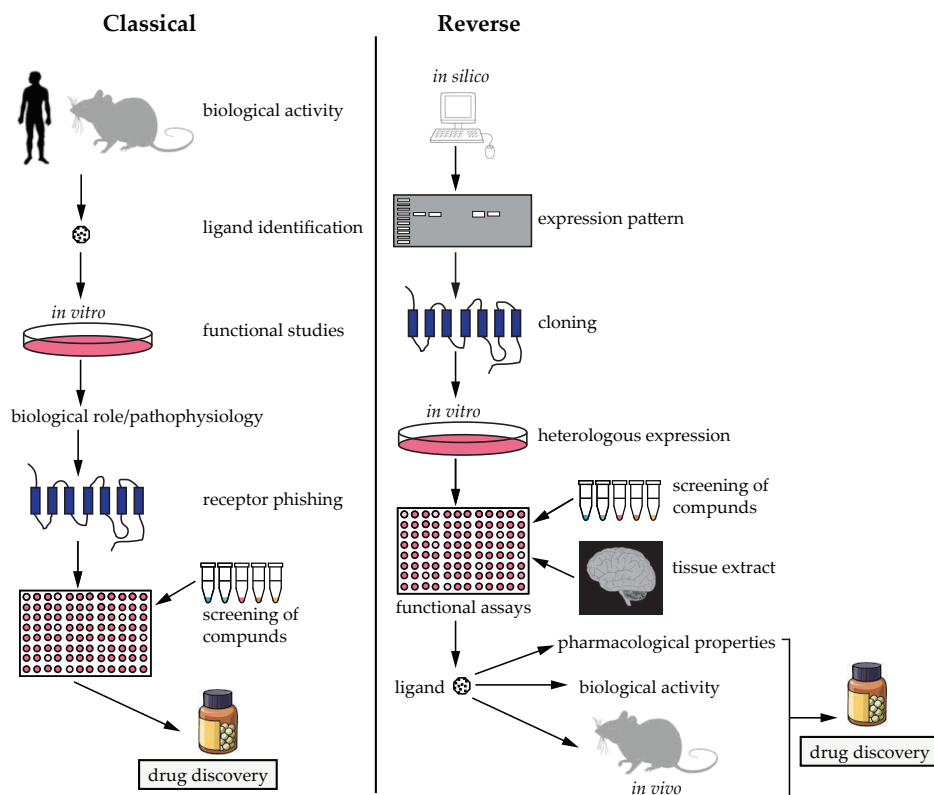


Figure 4. Flow charts of the classical pharmacology approach and the reverse pharmacology approach that arose in the 1990s, mostly due to advances in homology cloning. Adapted from [5, 50].

The differences between the classical approach and the reverse pharmacology approach are illustrated in figure 4. In reverse pharmacology, an orphan GPCR is first identified

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by homology cloning using molecular biology techniques, or, since the sequence of the human genome is known, *in silico*. The GPCR of interest is then expressed in a heterologous cell system, followed by screening against a compound collection or purified tissue extracts for receptor activation. The use of tissue extracts increases the chances of finding the endogenous ligand. However, important technical difficulties are associated with the latter strategy, including low signal-to-noise ratio and failure to isolate the ligand from an active extract. Therefore, synthetic compound collections are often used instead. The first receptors that were deorphanized by reverse pharmacology were the 5-HT_{1A} serotonin receptor and the dopamine D₂ receptor [51-52]. In total, the application of the reverse pharmacology approach led to the 'deorphanization' of more than 150 GPCRs, coupling them to approximately 75 endogenous ligands. Many of these ligands were novel

Table 2. GPCRs listed as orphan receptors by IUPHAR with (putative) ligands identified from the literature.

Name	Pseudonyms	Ligand(s)	References
CCRL2	CRAM	CCL5 (RANTES), CCL19, chemerin	[53-56]
CMKRLL1	ChemR23	chemerin, resolvin E1 (RvE1), SIV/HIV-1 coreceptor	[57-60]
CMKOR1	CXCR7, RDC1	CXCL12/SDF-1 α	[61-62]
GPR1		chemerin; glucose/sucrose (<i>S. cerevisiae</i>), HIV/SIV coreceptor	[63-65]
GPR3		sphingosine 1-phosphate (S1P)	[66]
GPR4		protons, lysolipids (?)	[67-69]
GPR6		S1P (?)	[66, 70]
GPR12		tyrosol, S1P, sphingosylphosphorylcholine (SPC)	[66, 71-72]
GPR17		nucleotides, cysteinyl leukotriene (CysLT)	[73]
GPR18		N-arachidonoylglycine, Δ (9)-tetrahydrocannabinol	[70, 74-75]
GPR23	P2Y9, LPA4	lysophosphatidic acid (LPA)	[76]
GPR32		resolvin D1 (RvD1)	[77]
GPR34		lysophosphatidyl-L-serine	[78]
GPR35		kynurenic acid, 2-acyl lysophosphatidic acids	[79-80]
GPR37	PAEL	neuropeptide head activator	[81]
GPR39		Zn ²⁺	[82-83]
GPR55		lysophosphatidylinositol, cannabinoids	[84-85]
GPR63		S1P (?), dioleoylphosphatidic acid	[70, 86]
GPR65	TDAG8	protons, psychosine (?)	[87-88]
GPR68	OGR1	protons, sphingosylphosphorylcholine (?)	[68, 89-90]
GPR75		CCL5 (RANTES)	[91]
GPR84		medium-chain free fatty acids (FFA)	[92]
GPR92	GPR93, LPA5	LPA, farnesyl pyrophosphate, geranyl geranyl diphosphate	[93-96]
GPR119		oleoyl-lysophosphatidylcholine (OLPC), oleoylethanolamide (OEA), N-oleoyldopamine (OLDA)	[97-99]
GPR120		FFA	[100]
GPR132	G2A	protons, lysolipids (?), oxydized FFA (9-HODE, 11-HETE)	[101-103]
MAS1	Mas	Angiotensin 1-7, neuropeptide FF	[104-105]
MRGPRD		β -alanine	[106]
MrgprX1	MrgX1, SNSR4	BAM8-22, BAM22 (1-22) and related peptides	[107]
MrgprX2	MrgX2	corticostatin-14	[108]
OPN5	GPR99	photoreceptor (birds)	[109]
OXGR1	GPR99	α -ketoglutarate (2-oxoglutarate)	[110]
SUCNR1	GPR91	succinate	[110]

and unexpected signaling molecules, including calcium ions, trace amines, bile acids, kynurenic acid, protons, oleoylethanolamide, lysophosphatidylinositol, lysophosphatidic acid and a plethora of new neuropeptides.

Ligands recently proposed for class A orphans

In the receptor database of the International Union of Basic and Clinical Pharmacology (IUPHAR-db), 97 rhodopsin-like (class A) orphans are listed. However, a search of the recent literature yielded putative endogenous ligands for 33 of these receptors (see table 2). In some cases further studies may be needed, but we can assume that many of these receptors are now truly deorphanized. This shows that the deorphanization efforts still yield results. All but four of the new receptor-ligand pairs belong in 6 subgroups: proton/lysolipid (GPR4, GPR65, GPR68, G2A), chemokine (CCRL2, CMKRL1, CMKOR1, GPR1, GPR75), lipid mediators (GPR3, GPR6, GPR12, GPR23, GPR32, GPR34, GPR63, GPR92, GPR119), cannabinoid (GPR18, GPR55), Mas related (Mas, MRGPRD, MrgprX1, MrgprX2), and metabolic intermediates (GPR84, OXGR1, SUCNR1, GPR120). A number of these receptors seem to have more than one endogenous ligand. One could state that these receptors were not truly deorphanized when only one of the ligands was identified. Of course, it is impossible to prove that no additional ligands remain to be discovered for any given receptor. In chapter 6 of the current work, a new, possibly endogenous, ligand for the adenosine A₃ receptor is reported.

Deorphanized receptors and the regulation of food intake

Clearly, deorphanization of GPCRs has had a profound influence on our understanding of mammalian physiology. For example, particularly large advances have been made in our understanding of the regulation of food intake. Several novel neuropeptides have been discovered as ligands for orphan GPCRs, including leptin, ghrelin and orexin [for a review see 45]. Furthermore, several GPCRs have been shown to react to nutrients and metabolic intermediates. These receptors seem to function as sensors for food and metabolic status, which is an unexpected new role for GPCRs. Nutrient sensing receptors include the calcium sensing receptor, GPRC6A and the dimeric taste receptor complex T1R1/T1R3, which are promiscuous receptors for several L- α -amino acids and divalent cations, as well as the T1R2/T1R3 dimer, which responds to sugars and D-amino acids [111]. These receptors are expressed in taste tissue, the gastrointestinal tract, endocrine glands, adipose tissue, and/or kidney, where they regulate the release of hormones important for metabolism and the regulation of food intake. They can also influence gene expression, for example yielding an increase in the expression of nutrient transporters. Next to these class C receptors, several class A receptors are also involved in nutrient sensing. GPR92/93 expressed in the small intestine is activated by proteolytic degradation products and by lysophosphatidic acid [93-96]. Medium- and long-chain free fatty acids, from the hydrolysis of ingested fat and oil, activate the free fatty acid receptor 1 (FFA1) as well as GPR84 and GPR120 [92, 100, 112-114]. FFA1 is expressed in the islets of Langerhans in the pancreas and the gut, whereas GPR120 is expressed in the gut, in adipose tissue and in the lung. FFA1 activation stimulates the release of the hormone GLP-1 from the gut, a role which may be shared

by GPR120. Activated FFA1 also potentiates glucose-stimulated insulin release from the pancreas, and it might be involved in the toxic effect of chronic high circulating free fatty acid levels on pancreatic β cells [115]. GPR84 is expressed in immune cells and its role in physiology has not yet been elucidated. Short-chain free fatty acids, which are mainly fermentation products of carbohydrate fibers, are ligands of the FFA2 and FFA3 receptors [116-117]. FFA2 is primarily expressed in immune cells, and has been shown to play an important role in neutrophil recruitment during intestinal inflammation [118], and it is thought to be involved in leukocyte chemotaxis by sensing the presence of bacterial fermentation products. Additionally, it appears to be involved in energy homeostasis and appetite regulation [119], including the mediation of the anti-lipolytic effect of acetate and propionate [120]. FFA3 is more widely expressed than FFA2, with the highest expression in adipose tissue, and more moderate levels in immune cells and tissues. It has been suggested that FFA3 mediates the effect of propionate on leptin release [121]. Next to nutrients, intermediates in (energy) metabolism have also been identified as GPCR ligands, some of which were mentioned above (see table 2). More specifically, succinate and α -ketoglutarate (2-oxoglutarate), two intermediates from the citric acid cycle, are the endogenous ligands of GPR91 and GPR99, respectively, and the receptors are now named SUCNR1 and OXGR1 [110]. These receptors are predominantly expressed in the kidney. Succinate stimulates renin release via GPR91, which causes an increase in blood pressure. Intermediates of the β -oxidation process, which is upstream of the citric acid cycle, activate HCA₃ (GPR109B) [122]. The main ligand seems to be 3-hydroxy-octanoic acid. The same receptor has also been reported as a receptor for aromatic D-amino acids [123]. Two related receptors, HCA₂ (GPR109A) and HCA₁ (GPR81), are activated by the ketone body 3-hydroxybutyrate and by lactate, respectively [124-126]. Butyrate, a short-chain free fatty acid, may be an additional ligand for HCA₂ in the gut [127]. All three hydroxy-carboxylic acid receptors have an anti-lipolytic effect when activated. HCA₂ and HCA₃ are part of a negative feedback loop which keeps the release of fat stores in check under starvation conditions, whereas HCA₁ plays a role in the antilipolytic effect of insulin [review 128]. This family of hydroxy-carboxylic acid receptors is discussed in detail in chapter 2, and HCA₂ is the focus of chapters 3, 4 and 5.

Current challenges in deorphanization

After a peak in 2003 the deorphanization rate seems to be declining (see figure 5) [129]. This may be partly due to a shift in focus in the pharmaceutical industry. Many companies are currently faced with expiring patents of major blockbusters and increasing rules and regulations regarding safety, resulting in increased numbers of leads that fail to reach the market. The cost of compound screens for deorphanization is high and success not assured. Even if a ligand can be linked to an orphan receptor many years of additional R&D are needed to put a drug on the market. Less costly R&D programs could target the approximately 175 non-orphan GPCRs that are not currently targeted by drugs. Novel ligands, including allosteric modulators, or optimized versions of known ligands, can also be developed for the ~50 current GPCR drug targets. In the present climate pharmaceutical companies may more likely choose these R&D strategies.

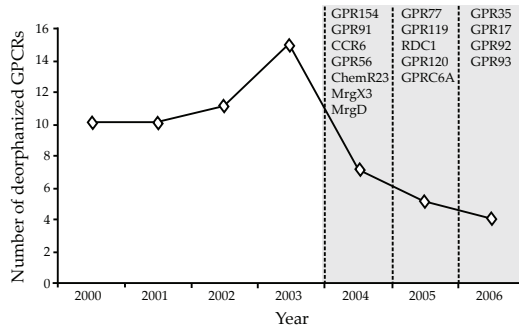


Figure 5. Declining rate of deorphanization since 2004. Adapted from [129].

Furthermore, a number of challenges complicate the identification of ligands for the remaining orphan GPCRs. Many of the remaining orphan GPCRs do not show high sequence homology to a cluster of GPCRs with similar ligands. When orphans are phylogenetically localized between two receptor subfamilies it may mean they bind ligands that share properties of both ligand families. Some other orphans, such as GPR88, do not show any significant homology to a known receptor subfamily. Purification of a known ligand type from tissue extracts is already a highly challenging task, and if the ligand properties are totally unknown another degree of complexity is added.

Why did traditional screening methods fail to bring to light the ligands for the remaining orphan GPCRs? It is possible that some of these orphans display non-traditional signaling, for example through G protein-independent signaling cascades. Traditional assays are

Table 3. Ligand-independent functions of orphan GPCRs. Adapted from [130].

GPCR	Orphan 7TM protein	Effect on function
GABA _{B1}	GABA _{B2}	Export to the cell surface and G protein coupling
DOR22a	DOR83b	Export and improvement of functionality
DOR43a	DOR83b	Export and improvement of functionality
T1R1	T1R3	Effect on receptor functionality and pharmacology
T1R2	T1R3	Effect on receptor functionality and pharmacology
MrgD	MrgE	Decrease of internalization; increase of ERK phosphorylation and intracellular [Ca ²⁺]
MT ₁	GPR50	Loss of ligand binding and function
	ORF74	Constitutive activity responsible for oncogenic action of Herpesvirus 8
	UL33	Constitutive activity responsible for HCMV-related pathologies
	EBI2	Constitutive activity in Epstein-Barr virus-infected cells

DOR: *Drosophila* odorant receptors; EBI2: Epstein-Barr virus-induced receptor 2; ERK: extracellular signal-regulated kinase; HCMV: human cytomegalovirus; Mrg: Mas related gene; MT₁: melatonin receptor 1; Smo: Smoothened; T1R: taste receptor.

not equipped to identify this activation. The orphans may also need unknown interacting partners in order to function, for example another GPCR to form a functional heterodimer. In heterologous cell systems correct expression of functional GPCRs cannot always be obtained due to the absence of necessary protein partners.

Finally, some of the orphans may be 'real' orphans with no physiological ligand at all,

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Table 4. Remaining class A orphan GPCRs from IUPHAR-db excluding the putatively liganded GPCRs shown in table 2. The receptors are classified according to a phylogenetic analysis by Joost and Methner [143]. The receptors at the bottom of the table were not included in this analysis.

Group	Orphan	Pseudonyms	Remarks
A03	GPR15 GPR25	GPRF	
A06	GPR22	GPRM	constitutive activity [144]
A08	MAS1L MRGPRE MRGPRF MRGPRG MRGPRX3 MRGPRX4	GPR169 SNSR1/2	
A09	GPR19 GPR50	GPRJ	
A10	LGR4 LGR5 LGR6	GPR48 GPR49, GPR67	
A11	GPR31 GPR42 GPR82	GPRV	
A12	GPR34 GPR87	GPRy	
A15	EBI2 P2RY5 P2RY8 P2RY10 GPR21	GPR183 GPRL	constitutive activity [140]
A18	GPR27 GPR45 GPR52 GPR61 GPR62 GPR78 GPR85 GPR88 GPR101 GPR173	SREB1 SREB2 SREB3	constitutive activity [145] constitutive activity [146]
	GPR20 GPR26 GPR33 GPR37L1 GPR79 GPR83 GPR135 GPR139 GPR1 GPR142 GPR146 GPR148 GPR149 GPR150 GPR151 GPR152 GPR153 GPR160 GPR161 GPR162 GPR171 GPR174 GPR182 OPN3 TAAR2 TAAR3 TAAR4 TAAR5 TAAR6 TAAR8 TAAR9	GalR4, GalRL GPR58	constitutive activity [147] constitutive activity [146] pseudogene in most individuals [148] probable pseudogene [149] probable pseudogene in primates [150] probable pseudogene in primates [150]

that exert their function(s) through ligand-independent mechanisms. Some examples of orphan GPCRs with known ligand-independent activity are summarized in table 3 [130]. The top four 'orphan 7TM proteins' (indeed, they may not be receptors, nor G protein-coupled) in the table interact with the listed non-orphan GPCR to help it reach the cell surface (GABA, DOR) [131-133], change its functionality and/or signalling (DOR, T1R, Mrg) [131-132, 134-137], or inhibit its function (MT₁/GPR50) [138]. The bottom three orphans, all virus-encoded, do not need a ligand to function because they are active in the absence of a ligand [139-142]. Evolutionary analysis showing the presence or absence of evolutionary pressure on the protein as a whole, or on the predicted binding site, can be used to determine whether the protein is likely to be functional and whether it is likely to interact with a ligand in order to function.

Inventarisation of Class A orphan GPCRs

In table 4, all remaining class A (Rhodopsin-like) orphan receptors are shown, taken from the IUPHAR-db but not including the receptors listed in table 2. Some of the receptors display constitutive activity, which may indicate that these proteins do not need ligands to function. Others are likely to be pseudogenes in some or all individuals. Phylogenetic analysis showing sequence similarities between orphan and liganded receptors can give valuable clues where to start the quest for a ligand. In table 4 the orphan GPCRs are classified according to an analysis by Joost and Methner [143]. Another useful method to classify orphan receptors is using phylogenetic analysis of the residues predicted to line the ligand binding cavity, as was done by Surgand and colleagues [15]. This method yielded surprising results in the case of GPR88, which belongs to the Rhodopsin-like receptors on the basis of its full sequence, but was classified with the Glutamate-like receptors (class C) in this analysis.

Deorphanization of the 65 orphan GPCRs in table 4, and/or elucidation of their biological functions, could have a great impact on our understanding of mammalian physiology. Furthermore, keeping in mind that drugs on the market today target only ~50 GPCRs, understanding of these orphans may give rise to a whole range of new medicines.

Objectives and overview of this thesis

In the current work deorphanization and receptor-ligand pairing are a leading theme. I will describe studies on three GPCRs: the hydroxy-carboxylic acid receptor 2 (HCA₂), the orphan receptor GPR88 and the adenosine A₃ receptor (A₃R).

HCA₂ is a recently deorphanized GPCR that is of great interest as a drug target. In fact, one of its ligands, nicotinic acid, has been used as an anti-dyslipidemia drug for over 50 years. As described above, the endogenous ligand of HCA₂ is 3-hydroxybutyrate, which acts as a negative feedback signal to preserve fat tissue during times of starvation. The biological and pharmacological roles of the HCA₂ receptor and its two close family members HCA₁ and HCA₃ are reviewed in chapter 2. In my research, I explored the signaling cascades that are influenced upon HCA₂ activation by synthetic and endogenous agonists (chapter 3). In the same chapter I describe the in vivo effects of two partial agonists for HCA₂.

Furthermore, I investigated the binding of synthetic compounds to HCA₂ both in an orthosteric and in an allosteric manner (chapter 4 and 5).

As I have mentioned above, a receptor does not necessarily have only one unique ligand. For the adenosine A₃ receptor, there are indications that it binds an additional ligand next to its canonical agonist adenosine. This ligand could be involved in the resistance of muscle tissue to tumor metastases. I attempted to identify this elusive ligand, and identified the antiproliferative compound N⁶-isopentenyl adenosine as an A₃R ligand that may or may not be endogenous (chapter 6).

GPR88 is an orphan GPCR expressed predominantly in two brain regions: the striatum and the central extended amygdala. GPR88 could be of major interest therapeutically, and I set out to identify a synthetic, if not endogenous, agonist for this receptor, screening a large number of compounds in a functional assay (chapter 7).

In this thesis, a recently discovered and deorphanized receptor is further investigated, expanding the ligand repertoire for two binding sites on the receptor; a new ligand is proposed for a GPCR long since paired to its ligand; and a ligand screen on an orphan GPCR is described, clearly identifying the challenges of such an operation. This research into the 'simple' interaction between small molecules and membrane proteins gives insights into human physiology and the mechanism of action of (future) drugs, and opens new horizons for pharmacotherapy.

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