

Optical functionalization of human Class A Orphan G-Protein Coupled Receptors

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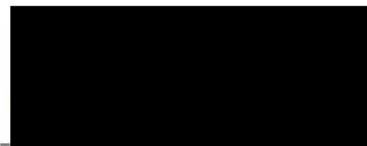
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July, 2016

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1-Introduction

1.1 Definition of G-Protein coupled receptor

Membrane receptors share the property of being able to respond to an extracellular stimulus(i) and translate it in a large variety of intracellular signaling cascades that modify cell behavior. Membrane receptors can be divided in three principal groups:

- Ion channels that allow flow of ions across the cell membrane in order to maintain or alter the membrane potential.
- Enzyme-coupled receptors that act as enzyme themselves or coupled to intracellular enzymes.
- G-Protein coupled receptors that couple to membrane bound heterotrimeric GTP binding G-proteins (G-Proteins) regulating a series of heterogeneous intracellular signals.

Among membrane receptors, G-Protein coupled receptors (GPCRs) form the largest protein family in the mammalian genome. However, an exact size of this protein family has yet to be determined¹.

According to the classical definition of GPCRs, a membrane protein to be classified as GPCR has to show the following two characteristics²:

- Seven domains in the amino acid sequences formed each by 25 to 35 consecutive residues with high hydrophobicity.
- The ability to couple to one or several G-Proteins

The presence of the seven consecutive highly hydrophobic stretches of amino acid residues leads to the formation in the tertiary protein structure of a strongly preserved topology. Seven α -helices cross the cell membrane in an anti-

clockwise manner leading to the N-terminus being exposed to the extracellular side and the C-terminus exposed to the cell intracellular environment. Three extracellular and three intracellular loops connect the transmembrane domains. The overall structure can vary in length among the wide group of GPCRs, with the shorter receptors being around 300 amino acids long and the longest ones around ~1000 amino acids in length³.

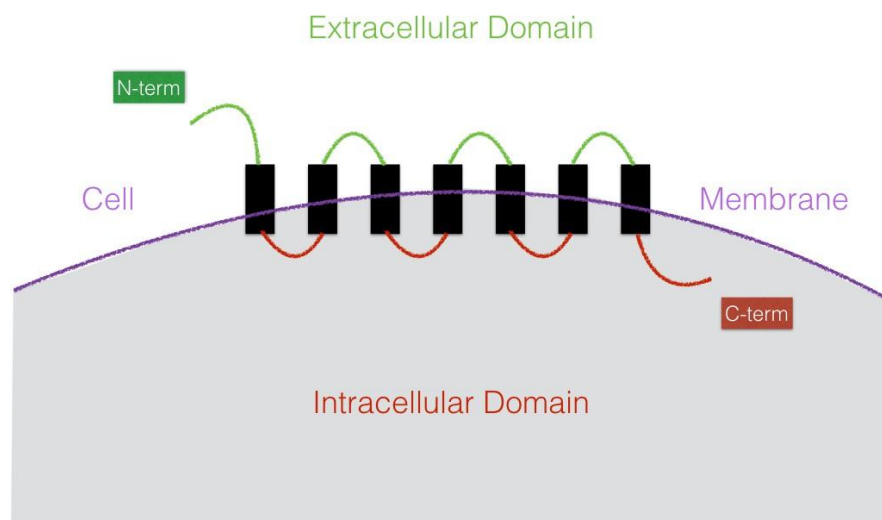


Figure 1.1 Topology of GPCRs: the seven transmembrane α -helices (black) connected by three intracellular loops (red, plus C-terminus) and three extracellular loops (green, plus N-terminus).

The GPCRs main function is to translate extracellular stimuli presented in form of a large variety of ligands into activation of intracellular signaling cascades. In the canonical description of these receptors the translation is achieved by activation of the heterotrimeric G-Proteins, but also a large variety of other proteins such as β - arrestins and neurochondrin.

The activation of the G-Proteins has not yet been shown for most of GPCRs, especially for the ones recently discovered or predicted by genome analysis. This is the reason why it has been suggested to define GPCRs as seven transmembrane domain receptors⁴, considering that the presence of the seven α -helices is always conserved, but the term GPCRs is nowadays still more widely established.

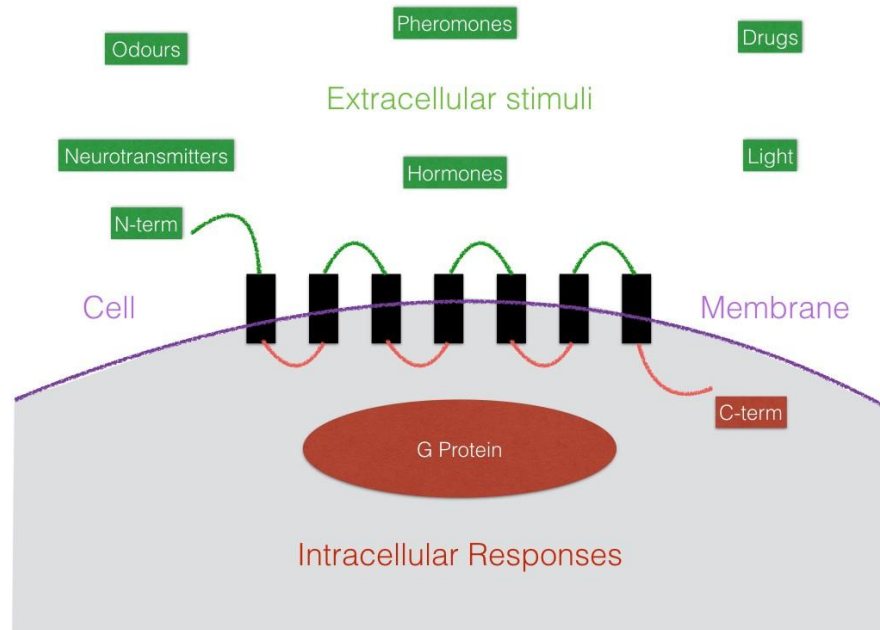


Figure 1.2 Different possible ligands that can interact with GPCRs and drive intracellular responses through activation of G-Proteins.

1.2 GPCRs classification

The ability of GPCRs to sense a wide range of extracellular inputs and drive different intracellular signal cascades is reflected in their heterogeneous sequences. Sequence similarity can however still be used as criteria to classify this large number of receptors in different subfamilies. Two classifications are currently used:

- The first classification divides GPCRs in different classes (from A to F) and clans (identified by a roman numeration) and it was proposed and introduced by both Atwood and Findlay⁵, in separate work by Kolakowsky⁶ in 1994 and refined by Bockaert and Pin⁷ in 1999. This classification system spans all GPCRs in vertebrates and invertebrates, and it is based on the development of sequence-based fingerprints in the seven hydrophobic transmembrane domains common among GPCRs.
- A more complete view of the human repertoire of GPCRs was achieved in 2001 when the sequencing of the entire human genome was completed. This led in the following years to the development of an alternative

classification system⁸. This classification system called GRAFS has been proposed by Fredriksson⁹ and divides the GPCRs expressed in the human genome in five main families: glutamate, rhodopsin, adhesion, frizzled/taste2 and secreting. The GRAFS system also provided a classification for the large family of rhodopsin like GPCRs.

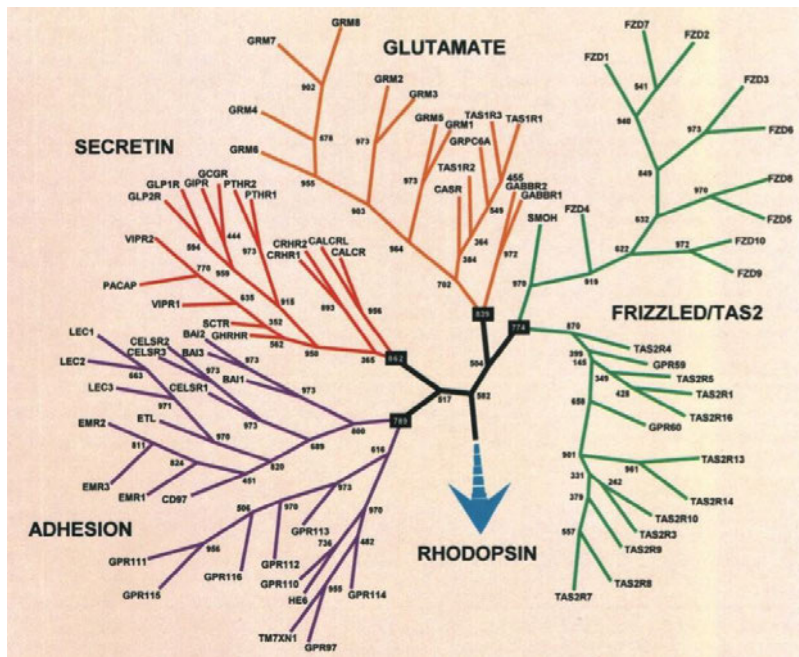


Figure 1.3 GRAFS classification of human GPCR genes based on their sequence homology according to Fredriksson *et al.*⁹

The main difference between the GRAFS classification systems and the formerly proposed system is the further division of the Class B GPCRs into secretin-like and adhesion GPCRs.

1.2.1 Class A (rhodopsin-like)

Class A GPCRs are the biggest and the most studied subfamily. The receptors belonging to this subfamily are also identified as rhodopsin-like receptors. All Class A GPCRs shared highly conserved common motifs with the amino acid

sequence of rhodopsin, although the overall homology across the entire subfamily can be low¹⁰. The common amino acid motifs are located in the transmembrane domains and in the first and second intracellular loops.

According to the different mechanism they used for the ligand binding process, Class A GPCRs can be divided in three different subgroups¹¹:

- **A- α** that includes rhodopsin, adrenergic and dopamine receptors. The ligand binding mechanism in this receptor group is mainly based on a core structure formed by the transmembrane domains.
- **A- β** , in which the ligand binding process is mostly carried out by the N-terminus plus extracellular loops as well as the transmembrane domains (ligands for this group are usually small peptides). Chemokines, opioids and somatostatin receptors belong to this subgroup.
- **A- γ** , in which the ligand binding process is mostly carried out by the N-terminus of the receptor that in this group is longer in comparison with the previous two. Glycoprotein hormones such as luteinizing hormone belong to this subgroup.
- **A- δ** , in which the ligand binding process is mostly carried out by the N-terminus. Belongs to this group purinoreceptors 2 (P2RYs), glycolipid-binding receptors, protease-activated receptors (PARs) and olfactory receptors.

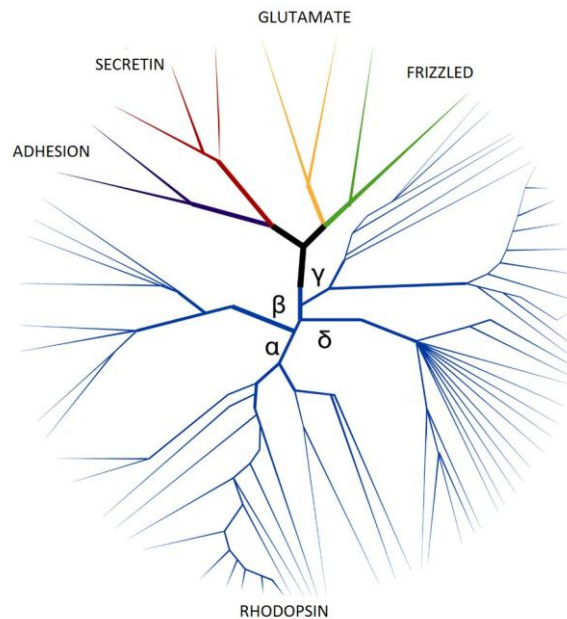


Figure 1.4 Classification of human Class A (rhodopsin-like) GPCR genes according to their different ligand-binding processes (adapted from Cardoso *et al.*¹²)

1.2.2 Class B (secretin-like)

Class B GPCRs do not share most of the common motifs of the Class A GPCRs and additionally harbor a large extracellular domain that is involved mainly in the ligand binding process. The receptors that belong to this family are also known as secretin-like receptors. They are regulated by peptides belonging to the glucagon hormone family, involved in regulating important endocrine and neuroendocrine functions.

1.2.3 Class C (glutamate receptor-like)

Class C GPCRs, or the metabotropic glutamate/pheromone-like receptors, are characterized by an extremely long N-terminus (about 500 to 600 amino acids) and share a large hydrophilic extracellular agonist-binding pocket. These residues form a disulphide bond (the crystal structure for this ligand binding domain have been solved for metabolic glutamate receptors). This GPCR subfamily includes mostly glutamate receptors, as well as calcium and GABA receptors.

1.2.4 Adhesion GPCRs

Adhesion GPCRs, partially belonging to the class B GPCRs, are a set of ~30 receptors that present a hybrid structure. The peculiarity of their protein structure is an extremely long extracellular domain that includes different subdomains¹³, responsible for facilitating and integrating the interaction between two different cells and between the cell and its surrounding matrix. The huge extracellular domain is connected to the seven-transmembrane domain in the cell membrane by a GAIN domain (GPCR-Autoproteolysis Inducing), responsible for the expression of the receptor at the cell membrane. Despite the main propose function for this receptor is probably to regulate cell position in space, it has been proposed an active role also for cell-cell communication¹⁴ and cell migration¹⁵, as well as in formation and development of cancer metastasis¹⁶.

1.2.5 Other GPCRs classes

The remaining classes are formed by genes encoding for fungi GPCRs (**class D**) pheromones receptors (**Class E**), frizzled/smoothened receptors (**class F**) and a group of cAMP-receptors found in Dictyostelium discoideum (**class G**). Frizzled receptors present a common long N-terminus that is supposed to interact actively in the ligand binding process by exposing the binding pocket in the extracellular domain of the receptor normally masked. These receptors have a predominant role in embryonic development and present similarity with the class B GPCRs.

1.3 G-Protein classification

1.3.1 Common G-Protein activation mechanism

Once activated, GPCRs undergo conformational changes that trigger the activation of internal signaling cascades¹⁷. These internal signaling cascades are mediated by the interaction of GPCRs with the G- Protein gene ensemble. G-Proteins can be classified according to the secondary messenger they activate; however, a common activation mechanism for these proteins can be identified. Every G-protein should is composed by three different subunits, which

are defined as the α , β and γ subunit. In the inactive state the α and the β subunits are anchored to the plasma membrane by short lipid tails while the β subunit is placed in between the α and the γ subunits, forming a tight complex¹⁸. The G-protein α subunit contains a binding site for the guanosine 5' diphosphate (GDP) that makes the G-protein idle in the inactive state. The activation of a GPCR act as guanine nucleotide exchange factor: the affinity of the α subunit for the GDP is reduced, leading to the release of the GDP from its binding site and causing its replacement by guanine 5' triphosphate (GTP) that is present in a higher concentration in the intracellular cell matrix. The dissociation of GDP from the α subunit causes the dissociation of the G-protein into two separate complexes: one of which is made by the α subunit and one formed by the β and γ subunit tighten together. In this state, both the α and the β - γ subunits are able to trigger different intracellular signaling pathways, translating the activation of the GPCR into a cellular response.

G-proteins can come back to their inactive state by its intrinsic GTPase activity that hydrolases the terminal GTP-phosphate. This brings back the α subunit to its inactive state in which it is bound to GDP and promotes the binding between the α subunit and the β - γ complex.

The GTP-GDP exchange completed by the GTPase activity of the α subunit is not the only mechanism that revert to its inactive state the G-protein. Concurrent mechanisms have been proposed that involve regulators of G- protein signaling, or RGS proteins^{19,20} (GTPase activating proteins). The RGS proteins have been proved to interact with the α subunit-GTP complex and promote the hydrolysis of the GTP in a shorter time scale in comparison with the one associated to the intrinsic α subunit GTPase activity.

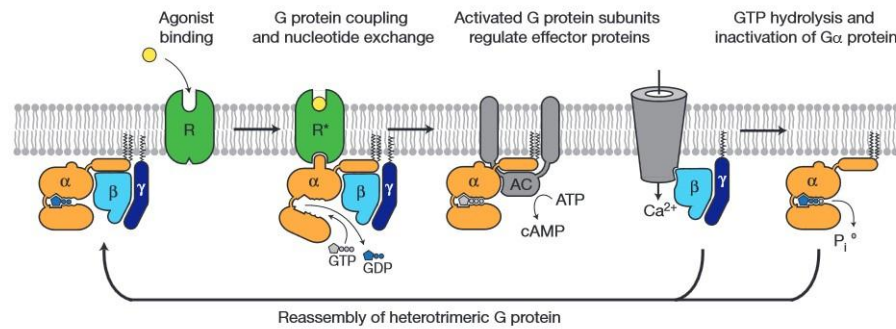


Figure 1.5 G-Protein activation cycle upon agonist binding: once the agonist binds to a GPCR, the GTP-GDP exchange enables morphological change and dissociation of the α and $\beta\gamma$ subunits and the initiation of the signaling cascade (in the case in figure, cAMP production). GTP hydrolysis brings back the heterotrimeric G-protein to the initial inactive condition²¹

The previously described mechanisms control the length of activation for a G-proteins, depending on the action of the intrinsic GTPase activity of the α subunit and the RGS activity. In some specific cases the activated signaling cascade has an intrinsic GTPase activity, like phospholipase C- β in its C-terminus^{22,23}.

1.3.2 G-Protein subunits and their signaling functions

Sixteen different genes are currently identified for coding for 28 different G-Protein α subunits. These 28 different α subunits can be grouped into four families according to the second messenger they activate:

- **G α -s** subunits activate production of cyclic AMP (cAMP) through adenylyl cyclase. It has been shown that G α -s subunits can interact with potassium channels, Src tyrosine kinases and tubulin GTPase^{24,26}. In the G α -s family we list the G α -s (S), the G α -s (L) and the G α -s (XL), s p l i c e d products of the same gene (*GNAS*). A fourth G α -s subunit is expressed mainly in olfactory and some CNS ganglia and called G α -s-olf (*GNAL*).
- **G α -i/o** subunits inhibit the production of cAMP by adenylyl cyclase and can be seen as having an inverse G α -s physiological function. They can also activate potassium channels, inhibit calcium channels, activate RAP1GAPII-dependent ERK/MAP kinase and activate Src tyrosine kinases. There are five different versions of G α -i/o:

- $G\alpha$ -o1 (*GNAO1*) $G\alpha$ -o2 (*GNAO2*), specifically expressed in neurons and neuroendocrine cells^{27,28}.
 - $G\alpha$ -i1-3 (*GNAI1*, *GNAI3*), ubiquitously express although it has been found preferential expression in neuronal system^{29,30}.
 - $G\alpha$ -z (*GNAZ*), found predominantly in neuronal tissues, which has functional roles remained largely undefined³¹.
 - $G\alpha$ -t1/2 (*GNAT1*, *GNAT2*) stimulate cGMP phosphodiesterases and have a highly specific expression in the visual system (retinal rod and cone outer segments) although expression has been reported also in taste buds^{32,33}.
 - $G\alpha$ -gust (*GNAT3*) has a specific taste function and it has been reported express in the taste buds involved in the sweet and bitter taste and also in chemoreceptors in the airways³⁴.
- **$G\alpha$ -q/11** subunits have all the common function of activating phospholipase C β (PLC β) isoforms. PLC β in the active form hydrolyse the phospholipid phosphatidylinositol 4,5 biphosphate to 1,2 diacylglycerol (DAG) and inositol 1,4,5 triphosphate (IP3). IP3 interact with specific IP3 channel that are expressed in the smooth endoplasmatic reticulum (SER)³⁵. The release of calcium from IP3 channels establishes a positive feedback that drives the release of more calcium from other IP3 channels. Ryanodine receptors can also be activated by this positive feedback system, increasing the release of calcium. The initial concentration of calcium in the intracellular matrix is restored by the activation of calcium ATPases on the plasma membrane and endoplasmatic reticulum and by calcium and sodium channels. Five different α subunits belong to the $G\alpha$ -q/11 family: $G\alpha$ -q (*GNAQ*), $G\alpha$ -11 (*GNA11*), $G\alpha$ -14 (*GNA14*), $G\alpha$ -15 (*GNA15*) and $G\alpha$ -16 (*GNA16*). $G\alpha$ -q

and G α -11 are widely expressed, while the rest of the members of the family are specifically expressed in hematopoietic cells. Also, one striking difference is that G α -11, G α -14, G α -15 and G α -16 are known to be promiscuous G α subunits involved in the coupling of G α -s and G α -i/o coupled GPCRs with the IP3 pathway³⁶⁻³⁸.

- **G α -12/13** (*GNA12*, *GNA13*) are widely expressed and are associated with responses linked to monomeric GTP-binding G-Proteins such as RAS. When RAS is bound to GTP and activated, it starts a phosphorylation cascade that end with the activation of mitogen- activated protein kinases MAPK. The activation of MAPK leads to the phosphorylation of various effector proteins that effect gene transcription and influence cell behaviors such as cell proliferation, differentiation and morphology^{39,40}.

1.4 GPCRs structure

1.4.1 Data gathering for GPCR crystal structures

Only 148 GPCRs solved crystal structures belonging to 23 different GPCRs are currently published.

Receptor name	Receptor ID	PDB ref. num.	GPCR class
Muscarinic Receptor 2 ^{41,42}	CHRM2	4MQT, 4MQS, 3UON	Rhodopsin- α
Muscarinic Receptor 3 ^{43,44}	CHRM3	4DAJ, 4U14,4U15, 4U16	Rhodopsin- α
Dopamine Receptor 3 ⁴⁵	DRD3	3PBL	Rhodopsin- α
Serotonin 5-HT1b Receptor ⁴⁶	HTR1B	4IAQ, 4IAR	Rhodopsin- α
Serotonin 5-HT2b Receptor ^{47, 48}	HTR2B	41B4, 4NC3	Rhodopsin- α
β 2 Adrenergic Receptor ²¹	ADRB2	4QKX, 4LDE, 4LDL, 4LDO, 4GBR, 3SN6, 3P0G, 3PDS, 3NY8, 3NY9, 3NYA, 3KJ6, 3D4S, 2R4R, 2R4S, 2RH1	Rhodopsin- α
β 1 Adrenergic Receptor ⁴⁹	ADRB1	1DEP, 2VT4, 2Y00, 2Y02, 2Y03, 2Y04, 2Y01, 2YCW, 2YCX, 2YCZ, 2YCY, 4AMI, 4AMJ, 4GPO, 3ZPQ, 3ZPR, 2LSQ, 4BVN, 5A8E, 5F8U	Rhodopsin- α
Rhodopsin ⁵⁰	RHO	4ZWJ, 4WW3, 4BEY, 4BEZ, 4A4M, 3AYM, 3AYN, 2X72, 3PQR, 3PXO, 3OAX, 3C9L,	Rhodopsin- α

		3C9M, 3CAP, 2Z73, 2Z1Y, 2PED, 2J4Y, 2J28, 2I35, 2I36, 2I37, 2G87, 2HPY, 1U19, 1GZM, 1LN6, 1L9H, 1JFP, 1HZX, 1F88	
Histamine 1 Receptor ⁵¹	HRH1	3RZE	Rhodopsin- α
A2A Adenosine Receptor ^{52,53}	ADORA2A	4UG2, 4UHR, 3UZA, 3UZC, 3VG9, 3VGA, 3PWH, 3REY, 3RFM, 2YDO, 2YDV, 3QAK, 3EML	Rhodopsin- α
Purinergic P2Y12 ^{54,55}	P2Y12	4PXZ, 4PYO, 4NTJ	Rhodopsin- δ
Protease-activated Receptor ⁵⁶	PAR1	3VW7	Rhodopsin- δ
Neurotensin Receptor 1 ⁵⁷	NTSR1	3ZEV, 4BUO, 4BV0, 4BWB, 4XEE, 4XES, 4GRV	Adhesion
Corticotropin releasing factor 1 Receptor ⁵⁸	CRHR1	3EHT, 3EHU, 2L27, 4K5Y	Secretin
Glucagon Receptor ⁵⁹	GCGR	2A83, 3CZF, 4ERS, 4L6R, 4LF3, 4L6R	Secretin
Smoothed Receptor ⁶⁰	SMOH	4N4W, 4JKV, 4N4W	Glutamate
Glutamate mGluR1 Receptor ⁶¹	GRM1	1EWK, 1EWT, 1EWV, 1ISR, 1ISS, 3KS9, 4OR2	Glutamate
CXCR4 Chemokine Receptor ⁶²	CXCR4	4RWS, 3ODU, 3OE0, 3OE6, 3OE8, 3OE9, 2K01, 2K03, 2K04, 2K05, 1VMC, 2SDF, 1SDF	Rhodopsin- γ
C_C Chemokine Receptor 5 ⁶³	CCR5	4S2S, 4MBS, 2QAD	Rhodopsin- γ
Nociceptin Receptor ⁶⁴	ORL1	5DHG, 5DHH, 4EA3	Rhodopsin- γ
Kappa-Opioid Receptor ⁶⁵	OPRK1	4DJH	Rhodopsin- γ
Opioid Receptor, Mu 1 ⁶⁶	OPRM1	4DKL, 5C1M	Rhodopsin- γ
Opioid Receptor delta 1 ⁶⁷	OPRD1	4EJ4, 4N6H, 4RWA, 4RWD	Rhodopsin- γ

Table 1.1 List of available 3D GPCR crystal structures solved by X-Ray diffraction and laser-based imaging techniques with relative PDB reference numbers

In most cases the GPCR is crystalized together with an agonist or antagonist that has the function to stabilize the protein crystal, making the structure acquisition easier. Only in two cases was it possible to acquire a diffraction pattern from a GPCRs bound to the related G- Protein complex^{21,68}.

The surprisingly low amount of crystal structures can be explained by taking in account that the protein crystallization process is not trivial, especially in the case of proteins like GPCRs. The presence of loops on the intracellular and the extracellular side and the elasticity suggested by morphological changes upon activation makes even more difficult to obtain a sufficiently resolved diffraction spectra that allow to identify a crystal structure^{69,70}.

The use of Synchrotron Radiation sources as well as improved crystallization protocols might increase the limited number of solved 3D GPCR crystal structures⁷¹. However, taking in account the topological resemblance between GPCRs, it is possible to use solved crystal structures to model mechanism of ligand binding, signal transduction and morphology changes as well as other common protein mechanisms.

1.4.2 Current GPCR model based on crystal structures

The crystal structure of bovine rhodopsin is considered as a good model for describing GPCRs. Indeed, the majority of the GPCRs are identified as belonging to the Class A subfamily. Second, the intermediate amino acid sequence length of rhodopsin among the GPCRs suggests that the functionally important sequences are included in the rhodopsin sequence, while the poorly conserved sequences are most likely located at protein sites responsible for the interaction with the G-protein (i.e. the intracellular loops or at the N-terminus level).

The first crystal structure of the inactive state of bovine rhodopsin was the first GPCRs crystal structure solved by Palczewski *et al.*⁵⁰ in 2000. Upon the absorption of a photon, the 11-cis retinal linked to the Lys296 of the rhodopsin sequences undergoes an isomerization in all-trans state, leading to a conformational change of the protein structure. Hydrolyzation of the all-trans retinal leads to retinal dissociation from rhodopsin that can be regenerated by new 11-cis retinal produced by retinoid isomerohydrolase (RPE65) in retinal epithelial cells. The conformational changes upon light activation can be performed by rhodopsin thanks to the flexibility of its transmembrane domains (between 19 and 34 amino acids long and able to be tilted and kinked).

Different features of the rhodopsin crystal structure are found to be conserved in many other GPCRs, not exclusively belonging to the Class A. An Asp/Glu-Arg-Tyr (D/ERY) motif is found at the end of the TM3 and well conserved among

most Class A GPCRs. It is involved in receptor stabilization in the inactive state and in the activation process itself. In the TM7, a highly conserved NPXXY motif is present in order to give to the receptor structure stability by interaction with the adjacent TM6. The extracellular loops contain two cysteine residues highly conserved among all GPCR families. These residues are supposed to increase the receptor structure stability by forming a disulphide bond.

One attribute of the rhodopsin structure is the presence of the ionic lock, a salt bridge between the Arg residue in the (D/ERY) motif in the TM3 and a Glu residue in the TMVI⁷². The same Arg residue forms another salt bridge with the adjacent Asp residue that is found to be present in all other class A GPCRs in their inactive state.

The presence of the salt bridge between the Arg and the Glu in TM3 and TM6 is the reason why rhodopsin has no basal activity and a stable ON state: upon interaction with a photon, the isomerization of the 11-cis retinal and consequent structural changes allows the break of the salt bridge that is not present in any active state of rhodopsin⁷³.

The break of the ionic lock allows the interaction of the TM3 and TM6 with the G-Protein in the receptor active state. Mutations in the amino acid residues involved in the formation of the ionic lock lead to modifications in the constitutive and agonist-binding activity.

In 2011, Standfuss *et al.*⁷⁴ solved the crystal structure of a mutated-constitutively active form of bovine rhodopsin, together with a peptide derived from the C-Terminus of the α -subunit of the $G\alpha$ -t1/2. This crystal structure suggests that the rotation of the TM6 is critical in the conformational changes involved in rhodopsin activation, and also how the rearrangement of hydrogen bonds between the retinal-binding pocket and the previously cited common GPCRs motif can be proposed as common mechanism of agonist-related GPCRs activation. In 2011 the crystal structure of the complex between the β 2- adrenergic receptor (B2AR) and the $G\alpha$ -s subunit was solved by Rasmussen *et*

*al.*²¹ This was the first crystal structure ever showing a high-resolution view of transmembrane signaling by GPCRs.

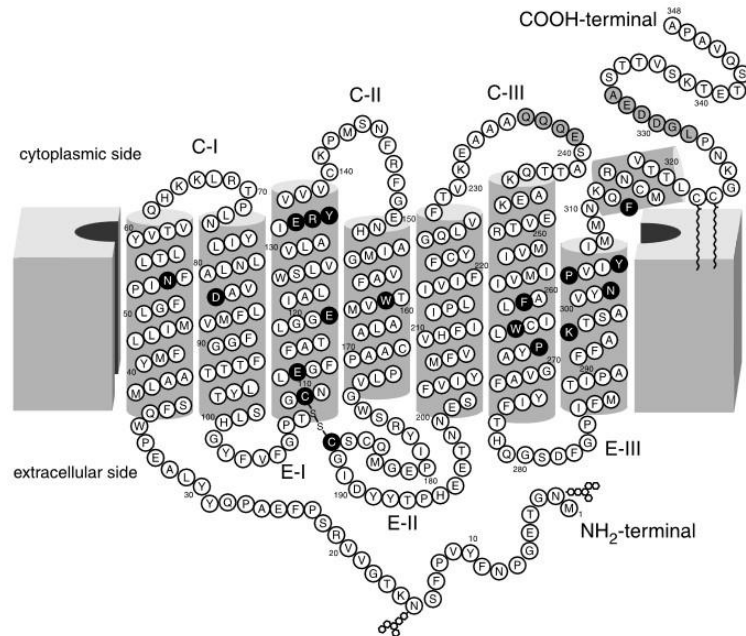


Figure 1.6 Rhodopsin amino acid sequence represented in a structure-based model (from top to bottom: intracellular loops [C-I, C-II, C-III and COOH-terminal], transmembrane domains and extracellular loops [E-I, E-II, E-III and NH₂-terminal] sequences)⁵⁰

The additional information brought by this crystal structure describe the interaction between the B2AR and the G α -s protein as mainly focused on the C-terminal α helices of the G α -s protein and the nucleotide-binding pocket. Also, in the active state the B2AR shown a displacement of the TM6 of ~ 14 Å caused by the interaction with the G α -s protein.

1.5 Mechanisms of GPCR activation

1.5.1 A two states model of GPCR activity

In a simple description, a GPCR can occupy two different energetically stable states: a ground state (or inactive state) and an “excited” state (or active state), in which receptor activation and corresponding intracellular signal transduction are started by the ligand-receptor interaction⁷⁵. This description is missing

important aspect of GPCRs activity such as constitutive activity⁷⁶ and intermediate states of activation, but it gives a general idea of the different mechanism of interaction between a GPCR and its ligands⁷⁷.

Rhodopsin and the β 2-adrenergic receptor with their corresponding crystal structures can be considered as standard reference model to explain ligand-binding mechanism for GPCRs^{78,79}. Also, mutagenesis studies in biogenic amine receptors such as the α 1 and β 2 adrenergic receptors, the H2 histamine receptor and the muscarinic acetylcholine receptor family show peculiar binding sites and morphological changes in the ligand binding process.

In rhodopsin, 11-cis retinal acts as an inverse agonist, keeping the receptor inactivated in the dark. The 11-cis retinal is covalently bonded to Lys296 in the TM7. The exposures to light cause the isomerization of the 11-cis retinal in all-trans retinal that has an agonist function in rhodopsin activation.

In the cases of ligand-activated GPCRs, such as the biogenic amine receptors (Class A GPCRs), the ligand-binding pocket is formed by different transmembrane domains, where the main interaction happens at TM3, TM5 and TM6. It has been shown by using mutagenesis approaches that the interaction between the positively charged amine and the receptor is mainly controlled by a highly conserved aspartic acid residue in the TM3.

This mechanism of activation that involves the interaction between the ligand and the transmembrane domains of GPCRs shown in rhodopsin and biogenic amine receptors is actually not common in all Class A GPCRs^{80,81}.

In the case of peptide-activated GPCRs (Class A), such as angiotensin and chemokine receptors, the mechanism of ligand binding involves also the N-terminus and the first and second extracellular loops. The transmembrane domains are also involved, in particular the TM6 and TM7⁸².

For receptors such as adenosine receptors (Class A) the ligand binding process more closely resembles the rhodopsin- β 2-adrenergic model, with an important role of the transmembrane domains together with the second extracellular loop.

Among Class A GPCRs, protease-activated receptors present a unique mechanism of activation. They have on the N-terminus a site for cleavage by protease such as thrombin. Once the receptor's N-terminus is cleaved, this act as agonist by interacting with its own extracellular loops, in a way comparable to the peptide activated GPCRs⁸³⁻⁸⁵.

For the other GPCRs classes previously described, there is a prominent role of the N-terminus in comparison with the Class A GPCRs. In the case of Class C metabotropic glutamate receptors, the complete ligand-binding site is made by the receptor N-terminus⁸⁶. As shown in the metabotropic receptor 1 (mGluR1, Class C GPCRs) crystal structure, the formation of a disulphide-linked dimer allows an open-close formation in response to ligand binding⁸⁷.

The two state model is actually a very good approximation in the case of rhodopsin, in which the presence of the 11-cis retinal as inverse agonist brings close to zero the probability of receptor activation in the dark. Retinal isomerization (and consequently the presence of light) is necessary condition to allow the conformational changes necessary to induce signal transduction by rhodopsin. For all other GPCRs, including genes belonging to the Class A rhodopsin-like, it has been recorded widely spontaneous activation in the absence of any agonist, and this phenomenon is defined as constitutive activity.

1.5.2 Beyond the two state model

The two state model is consistent with GPCRs activation curves obtained from radio ligand-binding assay and it is able to explain a variety of effects, such as basal activity and ligand potency of adrenergic and muscarinic receptors. Also, constitutive activity can be explained using this model with statistical arguments: without the presence of activating molecules, a GPCR population would be mostly found in its ground or inactive state (G1). If the difference in energy between the ground state and the excited (activated, E1) state is low enough, it will be possible to observe spontaneous transitions

between the G1 and E1, also without the presence of an agonist. In this way the constitute activity of GPCRs can be described as a product of statistical oscillations in the receptor population, depending on the difference in energy levels between the ground and active states at equilibrium. The presence of an agonist modifies this equilibrium, moving the GPCR statistical distribution towards a majority of receptor being in the E1 state instead of the G1.

Experiments such as fluorescence quenching studies on amine receptors suggest the presence of different agonist induced receptors conformation rather than an agonist dependent action in modulating the equilibrium between a single inactive and active state⁸⁸. The activity of GPCRs might be determined by a series of structural switches upon activation and different agonist might have different abilities to modulate the activity of these switches.

These recent results made necessary to modify also the simple model based on agonist-antagonist effects when talking about GPCR-ligand interactions. The classical definition of agonist has to be updated: a molecule can be defined as a full agonist when the interaction between the molecule and the GPCRs produces a maximal effect (i.e. signal intensity) in a specific assay. A partial agonist is a molecule that produces a signal detectable, submaximal and bigger than the constitute activity one. GPCRs antagonist can be defined as molecules that block the interaction between the agonist and the GPCRs, but also as compounds that blocks the receptor state at the ground state G1, removing constitutive activity. The efficiency of this blocking action makes possible to distinguishes between molecules that are full antagonists and partial antagonists.

In the case of rhodopsin, the active state E1 is attained through the formation of multiple intermediate states. The G1 state (or dark state) is maintained by the action of the 11-cis retinal. Without the 11-cis retinal rhodopsin shows a basal activity a million time smaller than the one registered in the fully activated E1 state. The spectral property of the 11-cis retinal allow to monitor the multiple intermediate states that can be trapped at low temperature and can be detected at physiological temperatures in two-dimensional crystals⁸⁹.

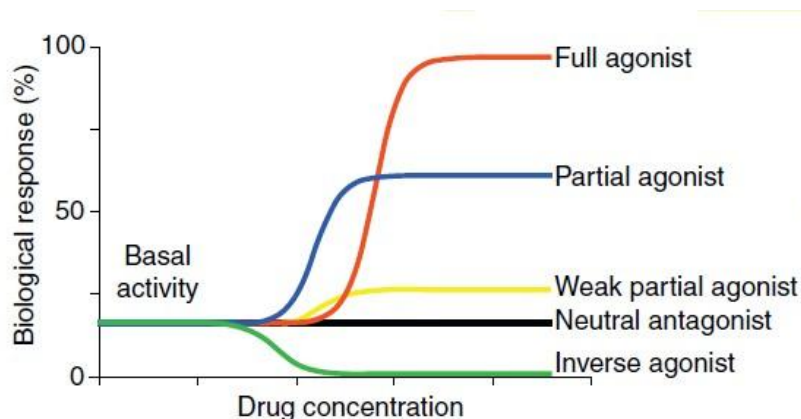


Figure 1.7 Different pharmacological roles of GPCR ligands represented as potency of activating or inhibiting biological responses.

The structures of the dark ground state of rhodopsin show high similarity with respect to the transmembrane domains, while they differ the most at the level of the cytoplasmic loops⁹⁰ (due also to the flexibility of the loops themselves).

For three of the inactive intermediate states of rhodopsin crystal structures are also available. Bathorhodopsin and lumirhodopsin are basically isomorphous of the dark state receptor structure. Although the isomerization process that lead to the conformational change of retinal from 11-cis to all trans is completed by the stage of the lumirhodopsin, this results only in minor local changes in the structure of the receptor.

It has been observed that GPCRs can couple to different G-Proteins according to the full or partial agonist that activates them. Different agonists can promote distinct conformational states that dictate the class of G-protein to couple or if a G-Protein independent pathway will be activated.

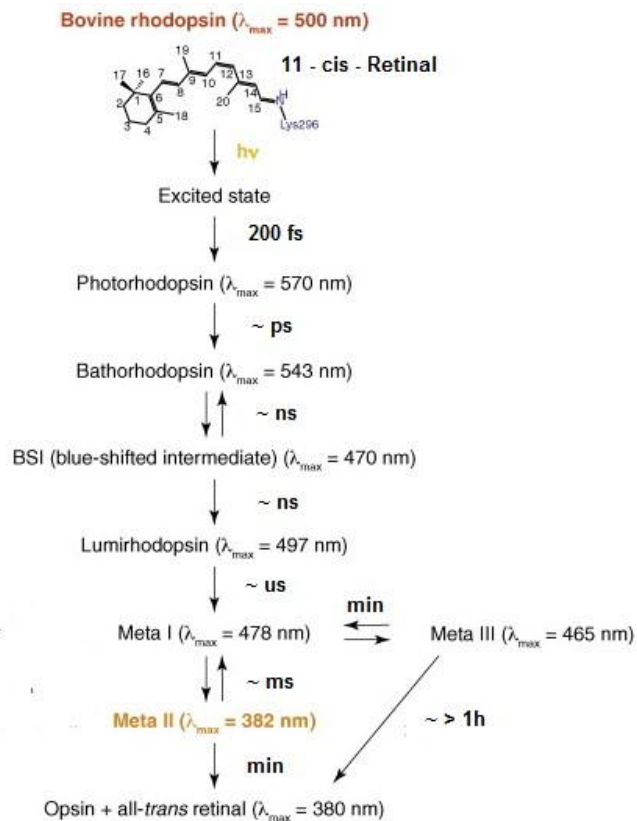


Figure 1.8 Rhodopsin activation mechanism through different intermediated meta-states with relative absorption spectra maxima and estimated life-times

Most of the available information about GPCR structures comes from X-ray spectroscopy techniques. One of the limit of this approach is that it gives access to structural information only of GPCR states that are stable enough to be crystalized with sufficient purity to get a readable diffraction spectrum. This limit makes not accessible to X-ray spectroscopy many other less stable states that could have however important functional roles

This notion that different active conformational states give GPCRs the ability to stimulate a diverse array of signaling pathways is defined as ligand bias or functional selectivity⁹¹. Actually, ligand bias and functional selectivity for GPCR are two slightly different concepts⁹²:

- Ligand bias is a system-independent concept. It reflects how different ligands might thermodynamically control through energy exchange stabilization of distinct conformations of the ligand-bound receptor, exposing different receptor coupling mechanisms. This implies that although in vivo signaling assays might be influenced by presence and distribution of receptor coupling properties, in vitro assays can identify intrinsic bias associated with specific ligand-receptor states.
- Functional selectivity is general concept that describes differential pharmacological effects of ligands on specific GPCRs including pharmacokinetics, target receptor conformation and activation of different molecular targets. Unlike ligand bias, functional selectivity is system dependent and it is indeed the most appropriate term to use when speaking about in vivo pharmacology tested on different assays in different systems.

The main consequences of GPCRs functional selectivity is that the pharmacological properties and classification of ligands (full or partial agonist, antagonist etc.) will depend upon their efficacy, target and biochemical pathways investigated^{93,94}.

The search for ligands having the properties of modulating different responses of a specific target receptor has pushed the development of techniques for large compound screening. While such techniques are currently available for screening G-protein mediated pathways, in the last years a significant number of techniques have been developed to screen for β -arrestins activation for GPCRs. One of the earliest techniques to monitor β -arrestins-GPCR interaction was based on the use of a fluorescent-tagged β -arrestin and the study of its relocalization upon GPCR activation (transfluor approach). A more recent approach is based on bioluminescent energy transfer (BRET): both β -arrestins and the target GPCR are tagged with a fluorescent protein and Renilla luciferase (the GPCR is tagged on its C-terminus). When the two proteins get close enough, the bioluminescence emitted from the Renilla luciferase is enough to excite the fluorescent tag that will then emit a detectable signal at higher wavelength.

A similar approach, also based on proximity between GPCRs and β -arrestins, is the so-called TANGO approach^{95, 96}. The target GPCR gets tagged at the C-terminus with a transcription factor (Gal4) using a protease cleavage site.

The β -arrestin is tethered with a Tobacco Etch Virus nuclear-inclusion-antipeptidase (TEV). When the two proteins are close enough, the protease on the β -arrestin cleaves the linker site on the GPCR C-terminus, with consequent release of the transcription factor. The screening system expresses a β -lactamase reporter gene, which is activated by the Gal4 transcription factor.

The previously described techniques were used to detect ligand bias properties for different GPCRs. Probably the most studied GPCR for ligand bias is the angiotensin II type 1 receptor⁹⁷ (AT1R). Ligands that stimulate β -arrestin mediated pathways through AT1R are proved to have anti-apoptotic and cardio protective functions. Other GPCRs for which ligand bias (in vitro) and functional selectivity (in vivo) has been proved are H-HT4 and H-HT7 serotonin receptors^{98,99}, β 1 and α 2 adrenergic receptors^{100,101}, dopamine 2 receptor¹⁰², histamine 2 and histamine 4 receptors¹⁰³⁻¹⁰⁵, EDG1 receptor¹⁰⁶ and the glucagon-like peptide-1 receptor¹⁰⁷.

1.6 Orphan G-Protein coupled receptors (oGPCRs)

In the human genome around 350 genes encode for not-olfactory GPCRs, and for about 200 of them a candidate agonist has been determined. For the remaining genes, any agonists have no yet been discovered, making them orphan G-Protein coupled receptors¹⁰⁸ (oGPCRs). As for the other GPCRs, also the oGPCRs can be divided by sequence homology in different families, placing most of them in the Class A rhodopsin- like family. Considering the importance of GPCRs in drug development, different approaches have been used in order to identify possible agonists¹⁰⁹.

The first approach to be used was the “reverse pharmacology”: enormous libraries of different exogenous compounds were screened by monitoring the change in level of intracellular second messengers. Later on the reverse pharmacology approach was enhanced in the so called “orphan receptor strategy”, in order to increase the rate of deorphanization of oGPCRs¹¹⁰.

The orphan receptor strategy’s aim is to reduce the amount of compounds included in the screening process by using only extract from tissue in which the oGPCR was found mostly expressed. The candidate (ant)agonist in this technique is isolated by further titration of the tissue extract and finally identified using mass spectroscopy techniques¹¹¹.

These two process focus on measuring the change in the intracellular level of second messenger upon interaction of the receptor with a possible agonist. Always looking at the intracellular environment, it is possible to detect oGPCR activation by monitoring the level of protein connected to the internalization of the receptor such as β -arrestin2 (in a modified GFP tagged version). This approach, called “transfluor technology”, quantify the modification in distribution of β -arrestin2 from broadly in the cell cytosol to a localized distribution as a consequence of ligand-dependent internalization¹¹². oGPCRs can also be extracellular-tagged using a pH sensitive fluorescence antibody such as CypHer5. Cypher5 is a cyanine pH-sensitive dye not fluorescent at pH7.4 and brightly fluorescent at lower pH. Due to the acidic nature of the endosomal recycling compartments, the use of the cyanine dye Cypher5 permits to identify ligand-dependent internalization by measuring an intense intracellular fluorescence.

Despite the availability of different approaches, the rate of deorphanization of oGPCRs in the last ten years has decreased in a sensitive manner¹¹³. This might have different explanations. For example, oGPCRs might have a not G- Protein mediated signaling function not possible to detect with the current screening methods, or the lack of accessory proteins such as β -arrestins in the screening essay might as well interfere with the expression, the ligand and signaling coupling properties of the oGPCRs¹¹⁴.

1.6.1 Class A oGPCRs

oGPCRs are distributed among the different GPCRs subfamilies according to their sequence similarity with not-orphan GPCRs belonging to the same subfamily. In human, most oGPCRs belong to the Class A rhodopsin-like family. In April 2011 the IUPHAR (International Union of Basic and Clinical Pharmacology) database listed 94 genes supposed to be human Class A oGPCRs.

The composition of this family is heterogeneous, and it is possible to identify different subfamilies among the family of human Class A oGPCRs¹¹⁵.

- **65** genes are considered as human Class A oGPCRs, but due to their lack of similarity with other GPCRs subfamilies they are currently identified with a GPRXX (where xx is a number) nomenclature.
- **Eight** genes are identified as MAS related GPCRs (MRGPRD, MRGPRE, MRGPRF, MRGPRG, MRGPRX1-X2-X3-X4).
- **Seven** genes are identified as trace amine associated receptor (TAAR2-3-4-5-6-8-9).
- **Three** genes are classified as leucine-rich repeat containing G-protein-coupled receptor (LGR4, LGR5, LGR6).
- **Two** genes are identified as proto-oncogenes (MAS1, MAS1L).
- **Two** genes are identified as opsins (OPN3, OPN5).
- **One** gene is identified as a lysophosphatidic acid receptor 6 (LPR6).
- **One** gene is identified as an oxoglutamate receptor (OXGR1).
- **One** gene is identified as a purinergic receptor (P2RY8).
- **One** gene is identified as a succinate receptor (SUCNR1).

Human Class A oGPCR present a wide range of expression^{116,117}. Most of them are expressed ubiquitously in human tissues, while a considerable number of

oGPCR genes is found expressed in the brain and in the central nervous system (suggesting that these receptors might have a physiological relevance in neurological functions). Several other oGPCR genes are expressed in organs involved in the immune response such as bone marrow, thymus, spleen and lungs.

Another hint suggesting that human Class A oGPCRs might have relevant physiological roles is coming from observed phenotypes in case of knockout and overexpression in murine models of these receptor¹¹⁸.

For class A oGPCR genes there are no or few information about possible candidate agonists and relative G-Protein mediated signaling pathways that they might activate. This lack of information has driven in the past years the rise of alternative-signaling hypothesis for oGPCRs.

1.6.2 Class C oGPCRs

Six oGPCRs have been group in the Class C GPCR subfamily. GPR5CA-B-C-D all shares a similar N-terminus structure, short and containing two conserved cysteine residues. These four oGPCRs can be divided into two clusters based on sequence analogy (limited to the transmembrane domains): one formed by GPRC5B and 5C that are 50% identical, and one formed by GPRC5A and 5D that are 52% identical. The sequence identity between these two clusters can be measured around 40%. Both clusters contain typical conserved motifs of Class C GPCRs (such as the W in the TM6 and the P in the PKXY motif in the TM7) that are involved in the activation machinery and G-Protein signaling. Two other orphans were identified as belonging to Class C GPCRs, GPR158 and GPR158L that don't show any conserved domain in their respective N termini. Only recently, GABABRL (a new proposed member of the GABABR group) was proposed to be added to the list of Class C oGPCRs. GABABRL shows a sequence similarity with GABABR1 and GABABR2 of ~30%, but cells that express GABABRL alone or co-localized with GABABR1 or GABABR2 were not able to respond to GABA, suggesting that GABABRL might be a GABABR-like orphan with the ligand still awaiting identification.

1.6.3 Adhesion oGPCRs

Most of adhesion GPCRs are considered as orphans, including LEC receptors and EGF-TM7-lathophilin related protein^{119,120} (ETL/ELTD1). While the endogenous ligand for LEC receptors is still unknown, α -latrotoxin (a molecule present in the venom of the black widow spider) can bind the extracellular adhesion part and the first transmembrane domain with consequent activation of the LEC1 receptor.

Three cadherin EGF LAG seven-pass-G-Type-receptors (CELSR1-2-3) are contained in the human genome. Mutations in the last cadherin domain of mouse CELSR1 gave rise to the spin cycle mutant, inducing a phenotype with abnormal head-shaking behavior and neural tube defect.

GPR64, GPR97, GPR111 till 116, GPR123, GPR 126, GPR128, GPR133, GPR144, three brain angiogenesis inhibitor (BAI) and MASS1 are all considered as adhesion oGPCRs. In rat, GPR116 has been shown to exist as a homodimer that is linked by disulphide bonds and it has been shown that can undergo endoproteolytic cleavage.

The MASS1 can be expressed as three different isoforms with its longest isoform being composed of ~6000 amino acids. Mutations in the gene are associated with audiogenic seizures in mice.

1.7 Physiological relevance of oGPCRs in human diseases

Information about oGPCR role in physiology can currently only be obtained in case of constitutive activity and by knockout studies. Also, high expression of an oGPCRs in a specific tissue and/or specific environmental conditions (i.e. cancer, inflammation, etc.) can be interpreted as a role that oGPCR in that specific physiological context.

1.7.1 Tumorigenesis and metastatic formation

Orphan GPCRs are physiologically relevant in different kind of cancer, such as triple negative breast cancer¹²¹, skin and lung cancer. In last years, attention

was focused on GPR161¹²², which is expressed in the triple negative breast cancer. This cancer is known to be connected with a poor diagnosis, decreasing the possibility of success of the usual treatment approaches. The overexpression of GPR161 in this cancer increases cell proliferation and migration enhancing cancer metastatic activity^{123,124}. In contrast, the knockout of the GPR161 gene impairs the proliferation of human breast cancer cell lines, making GPR161 a good candidate target for new therapeutic approaches. GPR19^{125,126} is as well considered a possible target to treat small-cell lung cancers (SCLC or oat cell cancer, about 10% to 15% of all lung cancers), due to its overexpression in tissue sample of lung cancer patients. GPCR5a^{127,128} in breast cancer and GPR34^{129,130} in lymphoma are supposed play a relevant role in the metabolism and growth of the relevant cancer cells types.

1.7.2 Neurological and psychiatric disorders

Most of the human oGPCRs are expressed in different parts of the nervous system, especially in the brain. Several studies proposed that oGPCRs might have a physiological relevant role in neurodegenerative and psychiatric diseases, as well as high-order functional brain activities. Among all, GPR37 and GPR37L1 have attracted attention in the last years^{131,132} because they are expressed exclusively in the brain (both in neurons and glia) and they are both associated with juvenile Parkinson's disease. Knockout of GPR37 in murine models leads to an underdevelopment of the dopaminergic tone in the brain and the arising of perturbation of dopaminergic signals.

GPR6^{133,134}, GPR52^{135,136} and GPR88^{137,138,139} are in various forms connected to major mental illness by altering the dopaminergic system in the striatum. The knockout of GPR6 leads to reduction of production of cAMP in the striatopallidal neurons and consequent alteration of the striatal dopaminergic system. GPR6 knockdown mice show reduced abnormal involuntary movements. In mice missing GPR52 a psychosis-related behavior was recorded, while GPR52 transgenic mice show an opposite antipsychotic behavior. GPR88 is highly expressed in Dopamine1 (D1R)-Dopamine2 (D2R) containing medium spiny

neurons (MSN) in the striatum of rodents. The co-localization of GPR88 with DR1 and DR2 dopamine receptors suggest a role of GPR88 in schizophrenia.

1.7.3 Metabolic disorders

For many oGPCRs a role in metabolic disorders has been proposed. GPR21^{140, 141}, GPR26^{142, 143}, GPR27^{144, 145}, GPR50^{146, 147} and GPR82^{148, 149} have shown to be involved in diverse ways in the reduction of body weight, food intake and increase in insulin sensitivity and glucose tolerance in mouse models. GPR26 has been proposed as a strong regulator of energy homeostasis through the control of hypothalamic AMP activated protein kinase (AMPK); GPR27 modulates pancreatic β -cell function, its knockdown in these cells is responsible for the reduction of insulin promoter activity and glucose stimulated insulin secretion, a phenotype similar to the one of the GPRC5B knockout.

On the other hand, the hyper activation of GPRC5B impairs the insulin production in pancreatic β -cells, resulting in a phenotype comparable to Type 2 diabetes. GPRC5B is therefore considered a possible target for diabetes therapy in order to restore a normal insulin secretory function in patients affected by Type 2 diabetes.

1.8 Ligand-independent functions of oGPCRs

The examples of the previous section on the physiological relevant roles of oGPCRs are mostly obtained by studying the effect of knockdown, knockout and overexpression of those receptors in murine models. For other GPCRs for which it is not possible to identify a physiological function by these genetic methods, hypothesis about their physiological roles are more difficult.

This is why it has been theorized that some or more oGPCRs might have a ligand-independent function, or might be not functional at all^{150, 151}.

1.8.1 Constitutive activity of oGPCRs

In some specific cases it is possible to identify signaling properties and physiological importance of oGPCRs by high levels of constitute activity.

Constitutive activity for GPCRs is common and is due to specific sequences in the receptor structure that stabilize the active form, permitting the interaction with. Examples of oGPCRs constitutive activity are GPR3^{152,153}, GPR6¹³⁴ and GPR12¹⁵⁴. These oGPCRs all couple to G α -s subunit, increasing the amount of cAMP in the intracellular matrix. These receptors are also an example of the large amount of information that the constitutive activity bring with it: all three oGPCRs are shown to mediate different neurological functions, like promoting neuronal survival by inhibiting apoptosis in various physiological conditions, enhance neurite outgrow and increasing cAMP levels during neurite elongations. These receptors have a function in memory and learning (GPR6 knockout mice shown locomotion and memory problems), as well as a role in regulating pain and analgesia induced by morphine and cocaine. GPR3 has been identified as a molecular target for neuropathic pain therapy and as part of the pro-opioid receptor system.

The degree of constitutive activity of GPCRs and oGPCRs depends also on the tissue specific levels of G-Proteins and β -arrestin2, and on the level of proteins such as G-Protein coupled receptor kinase 2 involved in GPCRs internalization and recycling.

Taking in account the importance of the constitutive activity for deciphering signaling coupling and physiological relevance of oGPCRs, a more precise description of the mechanism has been proposed in order to predict constitutive activity also for other oGPCRs.

The study of GPR61¹⁵⁵ has demonstrated that removing the N-terminus from this oGPCR reduce in a sensitive way the magnitude of the signal supposed to be related to constitutive activity. This lead to the hypothesis of the existence of an N-terminus tethered ligand that might regulate receptor activation.

The high constitute activity for the previously mentioned oGPCRs can be triggered by structural properties of the receptor, stabilized in its active form, or by the presence in the native tissue of an endogenous ligand no yet detected with any of the currently available approaches. This was the case for two oGPCRs, the GPR40 and the GPR174^{156,157,158}. The GPR40¹⁵⁹ is now known

as FFAR1, or free- fatty acid receptor 1, because it was discovered that its constitutive activity was actually triggered by the permanent occupation of its ligand-binding pocket by the endogenous free fatty acid 1.

1.8.2 Orphan GPCRs acting as co-receptors

The struggle to identify oGPCRs ligands might also reflect that some oGPCRs might have a truly ligand-independent mechanism of activation of their signal transduction. One possible function without the need of agonists is if they act as co-receptors, forming heterodimeric (or higher order) complexes with other oGPCRs, GPCRs or other proteins. The properties of GPCRs to heterodimerize and form functional complex has been shown mostly for receptors belonging to the Class C.

One example of this kind of interaction is the heterodimer between GABAB1 and GABAB2^{160,161}: GABAB1 is responsible for ligand binding, while GABAB2 is then activating the G-Protein mediated signal cascade. In this case, the GABAB2 receptor can be seen as the oGPCRs that use the ligand binding process and the related conformational change of his heterodimer partner to enhance signal transduction through G-protein.

A similar process has been recently observed for GPR179 in the retina¹⁶², which can heterodimerize with the glutamate receptor mGluR6¹⁶³. The functional heterodimer is involved in the signal transmission from photoreceptors in the retina to ON bipolar cells in case of dim light conditions.

In some cases, the presence of an oGPCRs can interfere positively or negatively with the function and activity of an independent ligand-activated GPCRs: this is the case of the dimer complex between GPR50 and the melatonin receptor MT^{164,165}, where the role of GPR50 after formation of the dimers is to negatively interfere with the melatonin-depended signal by interaction with its long C-terminal tail. In a similar case, the β -alanine binding mas-related receptor MRGD signal gets potentiated and its internalization inhibited by interacting with its orphan homolog MRGE¹⁶⁶.

It has been shown also that oGPCRs can form heteromeric complexes also with proteins other than GPCRs. GPR37 can associate with the dopamine transporter DAT, regulating its activity negatively. In knockout GPR37 mice dopamine uptake and DAT surface expression in striatal membranes are both upregulated^{167, 168}. For some GPCRs it has been demonstrated the formation of complexes also with ion channels, such as the β 2-adrenergic receptor and the calcium activated potassium channel¹⁶⁹ or the calcium channel Cav1.2¹⁷⁰ or the complex between dopamine receptor D5 and the GABA_A ligand-activated channel. In the majority of these non-oGPCRs-ion channel complexes a ligand is not required since they are formed constitutively, suggesting that such complex might be also formed between oGPCRs and ion channels.

1.9 Experimental approaches to study G P C R

The modularity and shared topology of GPCRs allowed the development of experimental techniques that became fundamental for studying activation and signaling mechanisms. These techniques share the general property of improved temporal and spatial control of GPCR activation and signaling. This allows to dissect GPCR structural properties and partition common functional motifs and their role in physiological relevant processes.

One pioneering approach was the design, through targeted mutations, of GPCRs that respond only to synthetic ligands, called RASSL^{171,172,173,174}. This approach permits to activate selectively GPCRs by removing ligand dependence on the endogenous agonist(s) present in the tissue in which GPCRs are expressed. RASSL receptors were used to demonstrate that in the taste signal processing differently activated cell populations play a fundamental role rather than the activation of specific GPCRs^{175,176}.

This approach has been further used and developed also in neuroscience with the creation of a class of synthetic GPCRs called DREADDs^{177,178} able to be activated only by an inactive clozapine derivative. Collectively, these synthetic receptors have been used to study neurological process at the level of the CNS

and in the peripheral nervous system. The previously described approaches are based on a deep physiological and structural knowledge of the receptor studied. For many GPCRs a limited amount of information is available and this limitation reduces the use of the previously described methods. Novel methods allow to combine well-studied GPCRs with other GPCRs for which less information is available, in order to use the first as tool to study activation and signaling mechanisms of the latter.

1.9.1 Chimeric GPCRs as their use as functional probes

A chimeric GPCR is a synthetic protein created with DNA engineering from two different GPCRs that combines characteristics belonging to both parent receptors.

The chimeric approach is based on the hypothesis that GPCRs consist in first approximation of two substructures¹⁷⁹:

- The first is formed by the N-terminus, transmembrane domains and the extracellular loops (responsible for ligand binding).
- The second is formed by the intracellular loops (responsible for coupling with the G-Protein and activation of different intracellular signaling pathways).

Also, in this hypothesis these two substructures are topologically connected but functionally independent.

A direct consequence of this hypothesis is the possibility to create by DNA engineering a synthetic GPCR fusing ligand binding and G-Protein binding domains from two different GPCRs (i.e. **GPR \mathbf{A}** and **GPR \mathbf{B}**). This process would lead to the creation of a receptor that is able of being activated by **GPR \mathbf{A}** -agonists and transduce **GPR \mathbf{B}** -signal transduction. This approach has been used widely, with large library of synthetic receptor created and tested. Up to 2004 more than 100 chimeric GPCRs were cloned and verified to be expressed and/or functional¹⁷⁹.

Chimeric GPCRs have been engineered to determine which regions in the protein structure are responsible for the ligand binding process. Substitution of the N-terminus or of the extracellular loops and transmembrane domain has been used to modify the affinity of GPCRs to different agonists.

Substitution of intracellular loops and intracellular portion of transmembrane domains has been demonstrated to be effective in switching and tuning the coupling of chimeric GPCRs between the different G-Protein mediated signaling pathways. Initially limited to GPCRs belonging to the same family or class, the creation of chimeric GPCRs with parents GPCRs coming from different classes was first achieved by creating a β 2-adrenergic receptor-Frizzled2 chimera used to study the mechanism of WNT signaling, especially important in early development^{180,181}. There are at the moment no theoretical, experimental or bioinformatics tools precise enough to predict if a chimeric GPCR is going to have folding and/or expression or signaling issues. From literature, it looks important to preserve the two different substructures while assembling the chimeric receptor. There are examples in literature¹⁸² in which mixing of transmembrane domains belonging to the parents GPCRs leads to not functional chimeric GPCRs. However, it has to be taken in account that more not functional chimeras might have been engineered and tested, but not published. The concept that the preservation of the two substructures enhances the probability of conservation of the receptor functionality is in accordance with the available structural data that show how transmembrane domains are highly involved in the conformational changes related to GPCR and signal activation. Another strength of the chimeric approach is the conservation of selectivity in the G-Protein binding process. It has not been shown till now an example in literature in which the creation of a chimeric receptor leads to the activation of a G-Protein mediated signaling pathway not belonging to the parent GPCRs that donate the intracellular sequences supposed to interact with the G-protein. In comparison with other approaches like targeted mutagenesis, the chimeric approach has the advantage to give a quantitative analysis in the change in

properties of the GPCRs such as possibility to bind to new ligands or to signal with different G-Protein mediated pathway.

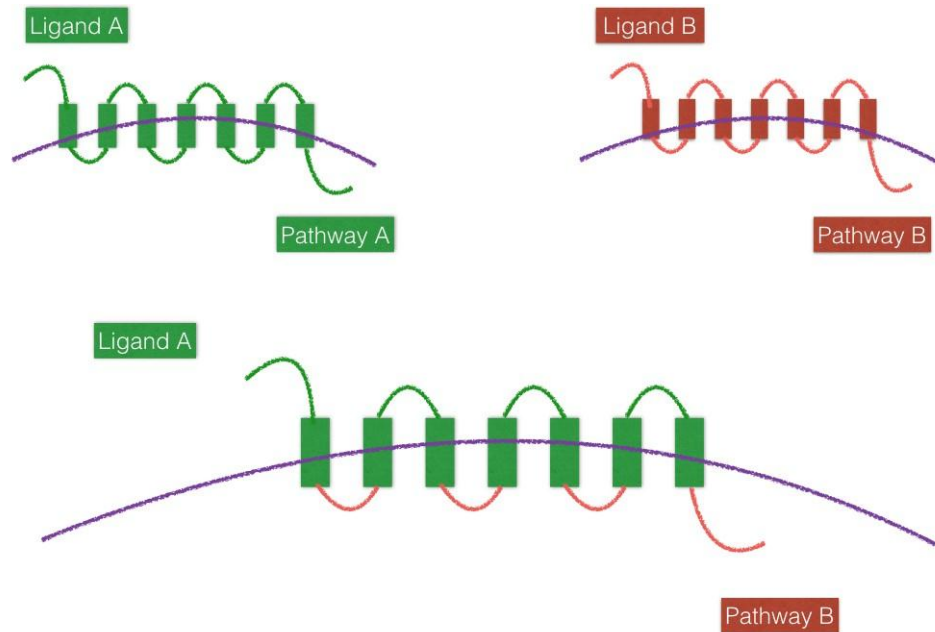


Figure 1.9 Chimeric approach for creating synthetic GPCRs with combined properties of parents GPCRs

1.9.2 Optogenetic control of GPCRs

Experimental approaches that lead to the control of GPCRs and their related G-Protein mediated signaling pathway beyond the use of endogenous or exogenous agonist or antagonist are fundamental for the study of the physiological processes that are mediated by GPCRs activation. Chimeric GPCRs can be powerful and useful to study those processes, but they might be subject to constraints when based on the use of a chemical as trigger for the activation of the synthetic chimeric GPCRs. In particular, (i) chemicals are subjected to diffusion processes that influence experimental spatial and temporal resolution, (ii) may have collateral side effects difficult to predict and (iii) oblige to control for possible toxic effects.

Light is one possible stimulus that is not influenced by the previously described limitations (together with temperature¹⁸³, magnetic fields¹⁸⁴⁻¹⁸⁷, ultrasonic

radiation¹⁸⁸⁻¹⁹⁰) and it has been largely used as a trigger for controlling biological processes.

The advantages of using light to modulate biological processes are (i) light allows to precisely control in time the experimental conditions, making possible to divide an experiment in two different states (ON and OFF state) and facilitating the interpretation of the data collected. (ii) modern optical techniques make possible to highly control the delivery of light, with spatial resolution that permit single cells activation (iii) light can be tuned to reduce at the minimum the side effects and damages to the biological system studied (phototoxicity).

Optogenetics is defined as a set of techniques based on the use of light to control biological processes. Light has been used more and more widely to modulate biochemical and second messenger pathways. Not all systems can be naturally modulated by light, and that in order to make an experiment controllable with light both genetic engineering and special experimental set up might be needed.

Three different approaches can be used in order to achieve optical control of a biological system:

- Insert a light-activated protein (i.e. Channelrhodopsin) and use its endogenous coupling properties to modulate the system activity.
- By using DNA engineering, modify in a light-sensitive manner one or more proteins involved in the process of study.
- Create light-sensitive chimeric GPCRs with equivalent signaling functions to the receptor on which control needs to be achieved.

In the case of GPCRs all approaches have been used. Improved DNA cloning techniques are facilitating the use of the chimeric approach with several protein families and larger number of receptors¹⁹¹.

Light-sensitive GPCRs naturally expressed in vertebrates and recently discovered microbial light-sensitive GPCRs represent a large ensemble of light-

sensitive proteins that can be use as template for the creation of light-sensitive chimeric GPCRs^{192,193}.

1.9.2.1 Light-sensitive GPCRs

The process in which the absorption of a photon from a protein activates a signal cascade is called phototransduction. Light-sensitive GPCRs are defined as opsins, and they represent the universal photoreceptor molecules of all visual system in the animal kingdom. The phototransduction process in the opsin is G-Protein mediated. Upon interaction with a photon (or a few photon) opsins undergo morphological changes that trigger the activation of G-Protein mediated signaling pathways¹⁹⁴.

The mammalian visual system is a good example to explain the mechanisms of phototransduction. Opsins are expressed both in cone and in rods (two different sets of photosensitive cells). Upon the opsin interaction with photons, the $G\alpha$ subunit detach from the $G\beta$ - γ subunit, and binds to its effector cyclic nucleotide phosphodiesterase¹⁹⁵ (PDE). The activation by the $G\alpha$ subunit of the PDE causes a decrease in intracellular concentration of cGMP, inducing the closing of cyclic nucleotide gated channels. Channel closure modifies the cell membrane potential, bringing the photosensitive cells to a state of hyperpolarization. Hyperpolarized cells released neurotransmitters to downstream cells, making the visual signal travelling till it reaches the ganglion cells that form the optical nerve, and as last step the brain.

Opsins can be divided in 6 subfamilies^{196,197,198}:

- Vertebrate opsins
- $G\alpha$ -o coupled opsins
- $G\alpha$ -s coupled opsins
- $G\alpha$ -q coupled opsins (found in invertebrates)
- Photoimerase opsins

- Neuropsins

The vertebrate opsins subfamily comprises visual and non-visual opsin with different spectral sensitivity, including four groups of cone opsin and one group of rod opsin. The four groups of cone opsins are divided according to the wavelength for which they are sensitive:

- The S group is sensitive to UV and violet light.
- The M1 group is sensitive to blue light.
- The M2 group is sensitive to green light.
- The L group absorbs red or green light and it can be considered strictly related to the opsins in the M2 group.

In the human genome, nine different genes code for opsins: one gene for a long wave sensitive opsin (OPN1LW), one gene for medium wave sensitive opsin (OPN1MW, with two isoforms OPN1MW2 and OPN1MW3), one gene for a short wave sensitive opsin (OPN1SW) and one coding for rhodopsin¹⁹⁹. The remaining five genes code for opsin not involved in the human vision: OPN3 (also known as encephalopsin), OPN4 (melanopsin), OPN5 (neuropsin), RRH (peropsin) and RGR (a retinal coupled GPCR).

Several hypotheses have been made about the physiological role played by non-visual opsins.

Encephalopsin (OPN3) was the first non-visual opsin discovered and it has the interesting feature of being expressed in cells and tissues classically believed not to be photosensitive. It is present in the brain (mostly in the hypothalamus) in the heart, lung, skeletal muscles, pancreas, kidney and placenta. It is supposed to play a role in circadian rhythms and in non-photosensitive processes such as asthma, and presents a peak of absorption in the blue-green region^{200,201}.

Melanopsin (OPN4) is considered to be a G α -q coupled opsin according to sequence analysis and experiments²⁰²⁻²⁰⁴. It presents an absorption maximum

around 480 nm and is mostly expressed in the photosensitive retinal ganglion cells (pRGCs). It also shows the interesting feature of having a bi-stable state, making the process of photoinduction reversible by light. pRGCs are involved in the stimulation of different brain regions such as the suprachiasmatic nuclei (SCN), the olivary pretectal nucleus (OPN) and the ventrolateral preoptic areas (VLPO).

It is supposed to be involved in the visual system, but not in the image-forming set of responses to light, but in processes such as the suppression of melatonin release, pupil constriction, circadian rhythms and related induction of sleep^{205,206,207}.

Neuroopsin (OPN5) is expressed in the eye, brain, testes and spinal cord in human. It is listed as a Class A oGPCR, although it is known to respond to light in the UV range. In a three-state activation system, the ground state can be excited with UV wavelengths (absorption peak at 380nm) to bring the protein to an excited state, which is stable in the dark and can be further activated by blue light²⁰⁸. Another light excitation (with wavelengths in the range of 635-690 nm) can bring back neuroopsin to its UV sensitive ground state. It has been demonstrated that UV activation of neuroopsin can trigger coupling of the receptor with the G α -I protein in mammalian cells, lowering the level of intracellular cAMP²⁰⁹⁻²¹².

RRH, also known as peropsin, it is localized in the apical microvilli of the Retinal Pigment Epithelium (RPE), in proximity with the photoreceptor of the outer segment of the human visual system. RRH has the property to use as chromophore all-trans-retinal, and to isomerize it to the 11-cis form. This is the opposite process that usually occur in the phototransduction process (i.e. in rhodopsin), where 11-cis retinal is isomerized by light to its all trans form. This photochemical property suggest that RRH might be involved in the machinery of retinal recycling, isomerizing all-trans-retinal to 11-cis retinal that can bind to other opsin express in the visual system²¹³⁻²¹⁵.

RGR, or Retinal G-Protein coupled receptor, is expressed mostly at the RPE, like RRH, but also in the Mueller cells of the neural retina. RGR has been

isolated and purified in the bovine RPE, showing both the properties to respond to UV and visible light and to bind to all-trans retinal but not to the 11-cis form. This, like in the case of the RRH, can suggest a role in the retinal recycling machinery, taking in account that the all-trans retinal get enzymatically bring back to their 11-cis form and supplied to other opsins^{216,217,218}.

1.9.2.2 Use of light-sensitive GPCRs in Optogenetic

There are several examples in literature of the use of endogenous or chimeric light-sensitive GPCRs.

The Korana group opened to the use of chimeric light-activated GPCR to control biological process, although their work does not contain any in vivo application²¹⁹. In order to prove a common activation mechanism for GPCRs (based on the structural information available at the time) the Korana group engineered several rhodopsin- β 2-adrenergic receptor chimeras. For each of the intracellular loops of the β 2-adrenergic receptor different candidate sequences to be cloned at specific sites of the rhodopsin structure were identified. In order to decide where to insert the intracellular loops of the β 2-adrenergic receptor in the rhodopsin sequence, the Korana group identified the boundaries between the transmembrane domain of rhodopsin and the intracellular domains of the β 2-adrenergic receptor. Cloning single and different combination of the β 2-adrenergic receptor intracellular loops in the rhodopsin sequence different versions of the rhodopsin- β 2 chimera were created. Comparing the light-stimulated signal with the one of the isopropanol activated β 2-adrenergic receptors it was suggested that the intracellular loops might have different roles in the coupling the β 2-adrenergic receptor with the G-Protein. The Korana group identified as minimal working chimera the one in which only the third intracellular loop of the β 2-adrenergic receptor is present in the rhodopsin structure, with only one sequence suited to create a functional chimera out of the six possible sequences for the third intracellular loop. The full rhodopsin- β 2- chimeric receptor, with all four extracellular loops belonging to the β 2- adrenergic receptor, showed activation half in magnitude in comparison with the

one obtained by stimulating the endogenous β 2-adrenergic receptor with 10 μ M Isoproterenol.

In addition to this, the Korana group showed that the replacement of the third intracellular loop in rhodopsin was already sufficient to drastically reduce the rhodopsin-G-protein mediated signaling pathways ($G\alpha$ -t1/2), while the replacement of other loops kept the signaling properties of rhodopsin intact. It has to be noticed that the results of the Korana group works have been later confirmed by the crystal structure of the β 2-adrenergic receptor solved by Rasmussen in 2011²¹.

The work of the Korana group on the rhodopsin- β 2-adrenergic receptor chimera is extremely important for several reasons. First, they used for the first time the chimeric approach to prove a common activation mechanism between GPCRs and to verify their modularity based on the information available on rhodopsin. Second, they opened the way to the application of chimeric GPCRs in vivo by proving that they can trigger a response strong enough to be candidate for an in vivo use.

Third, they showed how delicate is the choice of the sequences for loops replacement and the likelihood of getting a not-functional chimeric receptor.

In 2009, the results achieved by the Korana group were used by the Deisseroth group to engineer a set of light-activated chimeric GPCRs²²⁰, termed optoXRs. By sequence homology, Deisseroth and co-workers identified the same cutting sites in the sequence of the β 2-adrenergic receptor and the α 1-adrenergic receptor, getting a single candidate sequence for both the intracellular loops of rhodopsin and the other two amine receptors.

In comparison with the work of Korana, the optoXRs of Deisseroth achieved a light stimulation of the same order of magnitude of their relative ligand-activated receptors, although a different (less potent) agonist was used (10 μ M of Norepinephrine instead of 10 μ M Isoproterenol). The further step proved by Deisseroth paper was that the signal obtained by light stimulation of optoXRs was strong enough to trigger reward-related behavior (in the case of the light-

activated α 1-adrenergic chimeric receptor) and anxiety related behavior (in the case of the light-activated β 2-adrenergic chimeric receptor) in a mouse.

One other example of control of neuronal activity through the use of chimeric GPCR is represented by the rhodopsin-5-HT1a chimera engineered by Herlitze²²¹ group in 2010. The 5-HT1a is a metabotropic G-Protein coupled receptor linked to the $G\alpha$ -i/o signaling pathway.

In this case only the insertion of the C-terminus of the 5-HT1a in the rhodopsin structure it was sufficient to light activate the G-Protein related inward rectifying potassium channel and to cause a membrane hyperpolarization in the hippocampal neurons, comparable to the agonist induced response of the endogenous 5-HT1a. Also, the light-activated chimera is able to rescue 5-HT1a signals in neuronal slices of knockout mice, proving the possibility to use such tool in controlling serotonergic neuronal activity and behaviors in normal and disease-related murine models.

The repertoire of opsin in vertebrate and human offers the possibility to explore different wavelength sensitivities, a property that get even more important in vivo where tissue light absorption plays an important role.

Rhodopsin is not the only light-sensitive GPCRs that has been used as optogenetic tools.

Among the non-visual opsins, OPN3 (encephalopsin) has been shown to regulate cell migration in human orbital fat stem cells trough activation of MAPK and to down regulate the anti-apoptotic pathway in 5-Fluorouracil sensitive hepatocellular Carcinoma, as well as play a role as regulator of cAMP signaling²²².

Melanopsin (OPN4) has been used to create a synthetic light- regulated transcription device in order to enhance blood-glucose homeostasis in mice, by regulating calcium release in the ER and PKC-related activation of TRPC calcium pump²²³.

Neuroopsin (OPN5) has been used in Neuro2a and HEK293 cells to regulate cAMP decrease, calcium release and MAPK²¹⁰ activation upon illumination with UV light. In the design of optogenetic tools based on light-sensitive GPCRs, the potency of the light-induced signal has to be taken in account in order to think of possible in vivo uses. Opsins that show a bleach

resistant property can be used to repeat and sustain in time a low magnitude signal in order to achieve a light stimulated signal strong enough to be able to trigger the same biological responses of the relative agonist activated receptor. This is the case of the box jellyfish opsin²²⁴ (JellyOP). This opsin shows the property of trigger a reversible, high magnitude and reproducible increase of cAMP in mammalian cells, with both a spike-like behavior in the case of flashed illumination and a repeatable sustained level in case of repeated stimulation. This suggests that the JellyOP can be used as a promising optogenetic tool to regulate G α -s activity in mammalian cells and as a template for design of chimeric optogenetic tool.

1.9.3 Bioinformatics tool in GPCR functional characterization

The properties of GPCRs described in the previous sections (modularity, structural homology, ligand and G-Protein coupling mechanisms) have been mostly studied with either in vitro or in vivo techniques.

Modern technology actually allows us to use a third approach, an in silico approach, to explore the properties of GPCRs and ideally to predict specific characteristics of them such as candidate ligands or G-Protein coupling just by knowing the amino-acid sequence²²⁵.

There is nowadays a large variety of bioinformatics tools specialized in different aspects connected with GPCRs: GPCR predictors, ligand predictors, structural predictors and G-Protein coupling predictors.

The sequencing of a larger number of vertebrate genomes is increasing the number of homologues of known human GPCRs found in these vertebrates. The identification of new homologues, as well as the identification of new possible candidate genes for GPCRs is usually done based on sequence homology.

Multiple sequence alignments have been the base of GPCR discovery and classification. Historically, Muscle and ClustalW2 have been the most used software to perform this kind of alignment, while now Muscle has been proven to be faster and more stable than other software alternatives²²⁶⁻²²⁸.

In the last years the focus on using in silico tools for studying GPCRs has moved to the development of algorithms able to predict the coupling of GPCRs with one

or more G-Proteins. The in silico approach would give an estimate of the coupling based on sequence properties and supply a guide for experimental design to actually prove the coupling itself.

The idea behind the development of such coupling-algorithms is based on the modularity of GPCRs. The hypothesis is that specific amino acid sequences and topological features both in the receptor and in the G-protein structurally determine the GPCRs-G-Protein coupling. These features facilitate the interaction with a particular G α (in most of the cases) subunit. Crystal structures data and studies based on chimeric receptors suggest that the sequences responsible for G-Protein coupling are located in the cytoplasmic side of the receptor. In particular, the intracellular loops are supposed to play a major role in the G-Protein coupling process. The difficulty in understanding how this coupling might be influenced by amino acid sequences rely on different factors mostly concerning the description of the forces involved in the GPCR-G-protein coupling (i.e. chemical, electrical, quantum) and at which scale these forces acts (intracellular level, single loop, single amino acid etc.).

All these factors imply that studying the GPCR-G-Protein coupling cannot be limited to the description of the interaction as a two bodies problem, but requires a statistical approach. GPCRs are classified in different families according to structural properties; the same structural properties may allow a classification of GPCRs according to their coupling properties that goes beyond the experimental evidences. Algorithms that can be trained on a sample of GPCRs for which the G-Protein coupling information is known represent the best available approach to guess coupling properties for GPCRs for which this information is still missing. The training sample is needed in order to create statistical fingerprints of known GPCR-G-Protein interaction based on structural properties. These fingerprints can be applied on GPCRs not included in the training sample and use to guess G-Protein coupling properties for these receptors.

One other approach would be to consider the probability of a specific G-Protein coupling given some peculiar structural properties (i.e. specific amino acids in the intracellular loops) on a subset of GPCRs for which the coupling is known, and extend these probabilities to the whole ensemble of GPCRs (including the

ones with unknown coupling).

These two different approaches are based on two different mathematical tools: hidden Markov Models to create GPCR fingerprints and Bayesian statistics to calculate conditional coupling properties. In its simplest description, a hidden Markov model is a stochastic model that assumes that future states of a system depend only on the present state that is partially observable. Bayesian statistics estimate the degree of belief in a proposition before and after accounting for evidence and compute a possible distribution of outcomes.

2-Thesis aims and hypothesis

In section 1.9 I described how orphan GPCRs have physiological relevant functions in many different biological process. A large number of oGPCRs are involved in different diseases and this make them promising future targets for drug development. The lack of endogenous or exogenous ligands makes the development of drug targeting oGPCRs a complicate process. The standard deorphanization approaches uses in the past years have achieved some success in the deorphanization process, but the rate with which new ligands are discovered for oGPCR has significantly slowed down.

The approach I proposed is based on the contemporary use of chimeric GPCRs and optogenetic. My aim is to find answer to three fundamental questions related to oGPCRs:

- Are oGPCRs functional at all?
- If yes, which signaling pathways do they preferentially activate?
- It is possible to retrieve a possible ligand for the receptors still consider as orphan?

For some of the oGPCRs these questions have been partially addresses and in some cases positively answered, but there is still a large number of oGPCRs for which this questions remain nowadays still without an answer.

Till April 2011 IUPHAR listed 94 oGPCRs in the Class A subfamily: out of these 94 receptors, 29 genes were either identified as opsins or insert in one GPCR group and named accordingly. For the remaining 65 receptors, the known information is gene sequences and expression pattern, while few data are available about other properties (putative ligands, signaling pathways and so on). The previously mentioned three questions lead to a forth one: is there an alternative method to decipher activation properties and signaling pathway of oGPCRs and use this information to guess candidate endogenous agonist or to

design synthetic agonist?

My approach is based on the engineering of a complete light-activated library of chimeric receptor based on bovine rhodopsin with intracellular loops belonging to the 65 human Class A oGPCRs identified by the GPRXX nomenclature. This synthetic library shares the activation properties of bovine rhodopsin and would make possible to screen upon light activation the coupling properties of the selected 65 human Class A oGPCRs. A second library of light-activated chimeric receptors based on bovine rhodopsin and well-studied GPCRs will give the reference controls for light activation and G-Protein coupling of the light-activated oGPCRs.

Historically, the study of the coupling properties of GPCRs was mostly focus on the measurement of changes in concentration of second messenger such as cAMP, IP3, intracellular Ca^{2+} upon activation of different G-Proteins.

An ideal GPCR screening approach should be simple, nonradioactive, with a high signal-to-noise ratio, easy to handle (i.e. low number of reagents to add) and open for automation (i.e. use of 96/384/1536 well plate-formats). Screening for stimulation of cAMP by GPCR activation is generally straightforward²²⁹⁻²³¹ while use cAMP screening assay to monitor inhibition of cAMP generally required a more complicated approach (i.e. the use of forskolin for maximize the inhibition signal requiring preliminary titration experiments). Radiometric cAMP assays have been widely used, but are being replaced by fluorescence or luminescence-based assays. Alternative cAMP assays are based on ELISA (enzyme-linked immunoabsorbent assay) and FRET approaches. Intracellular

Ca^{2+} can be monitored using calcium-sensitive fluorescence dyes (such as Fura2AM) and automated real time CCD based fluorescence plate readers^{232,233}. Screening for G-protein mediated pathways that signal through different second messengers can be as well screen using promiscuous G- proteins³⁶.

In case of studies based on a few number of GPCRs this approach might be still competitive, although its lack in universality.

In fact, the measurement of each different second messenger implies the development of different reading systems and experimental setups that makes difficult if not impossible to compare signal potencies for different G-Proteins even for single GPCRs. Screening for changes in the intracellular concentration of second messenger is an approach more sensitive to G-Protein mediated pathway cross talking, and introduces a not removable source of noise in the data.

The necessity of different experimental setups and analysis for each second messenger makes this approach extremely difficult in case of screening of large libraries of receptor. My approach is based on the screening of GPCRs coupling properties using a reporter gene system. Reporter gene systems are indeed more suited for multiple screening of receptors for different reasons. This approach is based on the production of a reporter gene response to activation of a specific signaling cascade (and relative second messenger). The magnitude of the activation can be estimated monitoring the expression levels of the selected reporter protein.

The activation of different subunits of the G-Proteins enhance the production of second messengers in the intracellular matrix and activates gene transcription by various response elements such as the cAMP response element (CRE), nuclear factor of activated T-cells response element (NFAT-RE), serum response element (SRE), serum response factor response element (SRF-RE, a mutant form of SRE) and several others.

Reporter genes systems have been used to screen GPCRs signaling properties linked to cAMP or Ca²⁺ signaling due to their stability and sensitivity. Despite the concern related to the distance between the activation event and the reporter protein expression, reporter gene systems have the clear advantage to share a common reading system for all gene activation, considering that the quantity measured in this set up is one unique reporter protein.

The optogenetic stimulation of the 65 light-activated human Class A oGPCRs and their screen using gene report systems will allow me to prove functional

properties and G-Protein coupling preferences for the selected human oGPCR genes and allow the functional dissection of their physiological role, increasing the information available in the finding and design of appropriate agonists for these genes.

3 - Material and Methods

3.1 Engineering of human Class A oGPCR light-activated chimeras

3.1.1 Algorithm for the design of chimeric GPCRs

I adopted as basic principle for the creation of the chimeric GPCRs the domain swapping principle. The domain swapping principle is based on the exchange of sequences corresponding to the intracellular loops of to the acceptor GPCR with the sequences corresponding to the intracellular loops belonging to the donor GPCRs genes. The approach I used to create rhodopsin-based light-activated chimeric GPCRs was systematically designed in order to be used “off the shelf”, i.e. not dependent on the number of genes taken in consideration.

I chose bovine rhodopsin as the light-activated GPCR template for the creation of light-activated human Class A oGPCRs and control GPCRs. I made this choice based on previously published work (see Section 1.9.2.2) in which bovine rhodopsin was successfully used to engineer light-activated chimeric GPCRs. This choice is further supported by the fact that the all the GPCRs for which I created light-activated chimeric versions belong to the same GPCRs Class A subfamily. Lastly, among all class A GPCRs rhodopsin presents the unique feature of having a negligible constitutive activity (or in this case dark activity) thanks to the ionic lock between its TM3 and TM6 (see section 1.4.2). One of the strengths of the chimeric approach is that there are no limitations on the choice of genes to be used as parent GPCRs. In my case the choice of rhodopsin is definitely the best option for all previous listed reasons. However, the same chimeric algorithm, as well as the cloning and the experimental procedures described in the following sections, could be used with a different GPCR as acceptor GPCR (i.e. β 2-adrenergic receptor). Of course a different acceptor GPCR would change the properties of the chimeric GPCRs, for example introducing higher levels of constitutive activity or functional selectivity.

I first compared the amino acid and nucleotide sequences of the donor GPCRs (oGPCRs and control GPCRs) with the bovine rhodopsin sequence. I assigned to each sequence a unique identifier and using Igor Pro the sequences were randomized in order and then aligned using MUSCLE algorithm^{226,227}.

The alignment of the donor GPCR sequences with bovine rhodopsin allowed me to identify regions belonging to intracellular loops of the donor receptors. I used the works of Korana and Deisseroth groups to select in the rhodopsin amino acid sequence:

- The cutting sites belonging to regions at the border of the rhodopsin transmembrane domains.
- The amino acid and nucleotide sequence of intracellular loops both for bovine rhodopsin and all donor GPCRs.

I identified for each donor GPCRs four candidate sequences corresponding to the four different intracellular loops (IL1, IL2, IL3, and IL4). I verified the candidate sequences for each intracellular loop of each donor gene by comparison with the information deposited in the Uniprot database.

The domain swapping can be achieved in at least two different ways:

- Design in silico of different light-activated chimeric GPCRs for ordering as synthetic genes.
- Design of a common rhodopsin-based plasmid and use high-throughput cloning techniques to cut and paste the intracellular loops belonging to the donor GPCRs in the acceptor plasmid (mother plasmid).

In this work I chose to use the second approach for several reasons:

- The creation of a mother plasmid allows the further creation of more light-activated chimeric receptors.

- Currently available gene synthesis techniques are still expensive in comparison with the order of a single mother construct plus short gene fragments.

One key requirement was that high-throughput cloning techniques can be improved and automatized in such a way to make the creation of large complete libraries of synthetic chimeric receptors achievable in reasonably short amount of time and limited resources.

3.1.2 High-throughput cloning

I designed a common mother construct for the cloning of light-activated chimeric GPCRs based on the domain swapping principle. This mother construct is mostly constituted by the nucleotides sequences belonging to the rhodopsin extracellular loops, transmembrane domains and the N - terminus. I inserted at the beginning of the mother construct sequences for membrane integration and an anti-VSV-G epitope for antibody staining (for the complete sequence of the mother construct see Appendix, Figure 6.3). The VSV-G epitope²³⁴ represents the amino acid sequence YTDIEMNRLGK derived from the Vesicular Stomatitis viral glycoprotein. The epitope is located on the extracellular side of the mother construct and serves for checking membrane expression through antibody staining. In the rhodopsin sequence, in the same positions corresponding to the intracellular loops, I designed four artificial loops.

The artificial loops are designed in order be able to use the mother construct as template for the cloning of both the human Class A oGPCRs and the control GPCRs libraries. The cloning approach itself is based on the use of Typells restriction enzymes and the Golden Gate-cloning technique¹⁹¹.

Typells restriction enzymes cleave directionally outside of their recognition sequence and they recognize sequences that are continuous non-palindromic. They are made of two distinct domains, one for DNA binding and the other for DNA cleavage²³⁵. They are thought to bind to DNA as monomers for the most part, but to cleave DNA cooperatively, through dimerization of the cleavage domains of adjacent enzyme molecules. For this reason, some Typells

enzymes are much more active on DNA molecules that contain multiple recognition sites. The Golden Gate cloning technique is a high-throughput genetic engineering technique based on the use of Type IIs Restriction enzymes²³⁶. The presence of Type IIs restriction enzyme recognition sites in the DNA sequence that has to be cloned ("insert") in the acceptor plasmids implies multiple advantages in the cloning strategy:

- No restriction sites in the cloned gene ("seamless" cloning)
- Digestion and ligation happen in the same reaction step without the need for gel purification
- More than one insert can be cloned inside for each cloning step

The Golden Gate cloning approach had to be tailored to fit my needs. The sequence for the bovine rhodopsin-based mother construct was finalized considering the proposed cutting sites from Airan *et al.*²²⁰. Those cutting sites correspond to the start at the end of the transmembrane domains of bovine rhodopsin that enclose the intracellular loops (IL1, IL2, IL3 and IL4). The fake intracellular loops shared a common design with some specific difference among them in order to perform Golden Gate cloning:

- Each fake intracellular loop starts and ends with two sequences that are also present on each corresponding control and oGPCRs intracellular loop (i.e. every first intracellular loops of the control/orphan receptors will start and end with the same sequences present at the start and the end of the first fake intracellular loops in the mother construct).
- The start-end sequences are unique for each non-coding intracellular loop of the mother construct and this guarantee the conserved directionality in the insertion of the control/oGPCR intracellular loops.
- Each artificial loop contains a unique pair of Type IIs restriction enzymes sites in opposing direction. The presence of these sites allow the

insertion of the control/orphan intracellular loops and does not make possible the re-ligation of the fake insert that would be re-digested.

- An additional and unique analytical enzyme site is present in each fake intracellular loop to eliminate the plasmid in which one of more artificial loops were get re-ligated.

Loop	Start Overhang	End Overhang	Restriction sites	Analytical sites
I	CGTC	CTCA	GAGACC, GGTCTC - BsaI	ACCGGT - AgeI
II	GGTG	GCCA	GAGACG, CGTCTC - BsmBI	GCTAAGC - BlnI
III	CGGA	CGCA	GTCTTC, GAAGAC - BbsI	GATATC - EcoRV
IV	CGC/CGT	ACA	GAAGAGC, GCTCTTC - SapI	GCGGCCGC - NotI

Tab 3.1 Restriction enzymes and relative sequences (different of each of the four fake intracellular loops) contained in the rhodopsin-based mother construct

I performed the screening of the light-activate oGPCRs and control GPCRs libraries in HEK293 (**H**uman **E**mbrionic **K**idney) mammalian cell lines. Considering the use of a mammalian based screening system, I subcloned when necessary control GPCRs (in their full-length and light-activated form) as well as the 65 light-activated human Class A oGPCRs in a modified pcDNA3.1(-) mammalian expression vector. There are currently no off-the-shelf available mammalian expression vectors that are free from endogenous restriction sites for Typells enzymes in their sequence. The presence of these endogenous cutting site would make the use of Typells restriction enzymes impossible leading to unplanned cutting of the plasmid during the cloning process. For this reason, I modified pcDNA3.1(-) (from Invitrogen V79020) in its nucleotides sequence by site-direct mutagenesis to eliminate any endogenous Typells restriction sites. In the original pcDNA3.1(-) sequences six endogenous Typells restriction sites are present:

- BsaI (two sites)

- BbsI (one site)
- SapI (three sites)

I eliminated these six endogenous sites by single point mutation as follow:

Restriction Enzyme	Original Sequence	New Sequence
BsaI	gagacc	Gagaca
BbsI	gaagac	Gaagag
SapI	gaagagc	Gaagagc
SapI	gctc	gctcG

Table 3.2 List of single point mutations used to modify endogenous Typells restriction sites present in the pcDNA3.1(-) sequence

I subcloned the bovine rhodopsin-based mother construct in the modified pcDNA3.1 (-) using XhoI and EcoRI restriction sites. The intracellular loops belonging to the human Class A oGPCRs and control GPCRs were ordered in the form of oligonucleotides (Integrated DNA Technologies) and synthetic genes (Epoch Life Science).

In the case of the intracellular loops ordered as oligonucleotides, each intracellular loop came in the form of a forward and reverse oligonucleotide. Prior to insertion in the mother construct, I resuspended both oligonucleotides (forward and reverse) for each intracellular loop to a final concentration of 5ug/ul. I then mixed 0.5ul of each complementary oligonucleotide in 99ul of annealing buffer (10 mM Tris, pH 7.5-8.0, 50 mM NaCl, 1 mM EDTA in distilled water) and I heated the solution to 95°C for 15 min. Prior to use, I allowed the solution to slowly cool to room temperature. I performed the insertion of the intracellular loops in the mother construct using 96 well plates in order to being able to perform each cloning step in parallel for all light-activated human Class A oGPCR and control GPCRs. I tested different conditions in order to develop the optimal modified Golden Gate cloning protocol:

- Variation in the number of intracellular loops inserted for each cloning step.

- Variation in the number of incubation cycles for each cloning step.
- Variation in the duration of each single incubation cycle.
- Role of the analytical digest in the intracellular loops insertion efficiency.
- Role of the restriction enzymes heat inactivation in the intracellular loops insertion efficiency.

In the final set of conditions, I prepared the following mixture with a total reaction volume of 20ul for each cloning step (two for a total of four loops exchanged for each chimeric GPCR):

1. 100 ng uncut plasmid DNA (i.e. mother construct)
2. 7.8 ng each intracellular loops
3. The ratio between the mother construct plasmid and the intracellular loops was approximately 5:1
4. 1ul T4 DNA ligase
5. 2ul of Promega ligation buffer
6. 5 units of the first Typells restriction enzyme, depending on the intracellular loops chosen

I then incubated the mixture in a thermocycler for a first set of heating cycles:

Number of cycles	First time step	Temperature	Second time step	Temperature
11	2 minutes	37 degrees	2 minutes	37 degrees

Table 3.3 First set of thermocycles with duration and temperature of each cycles and total number of cycles

At the end of these first set of thermocycles, I added five units of the second restriction enzymes (always in accordance with the chosen intracellular loops), and started a second set of thermocycles:

Number of cycles	First time step	Temperature	Second time step	Temperature
11	2 minutes	37 degrees	1 minute	37 degrees

Table 3.4 Second set of thermocycles with duration and temperature of each cycles and total number of cycles

After the second set of thermocycles I heat inactivated the Typells restriction enzymes by increasing the mixture temperature to 50°C for 5 min and up to 80°C degrees for 10 min. I let cool down the mixtures at room temperature for at least half an hour. In order to reduce the amount of clones containing mother construct still having the artificial intracellular loops, I digested the PCR products with 5 units of an additional restriction enzyme (AgeI, BlnI, EcoRV or NotI corresponding to IL1, IL2, IL3, IL4).

I retransformed the digested PCR products into E. coli XL10 gold competent cells. In order to keep the 96 well format and the high-throughput approach of the cloning technique, I added 50ul E. coli XL10 gold competent cultures to each well of a 96 well plate PCR plate. I tested an aliquot of the cells need for each plate for competency by retransforming 1ng of pcDNA3.1(-) in 1ul and counting the number of colonies. I only continued with cultures/plates that yielded more than 1000 colonies for transforming the Golden Gate PCR products after storage at -80°C. I transformed Golden Gate PCR products using the 96 well PCR E. Coli XL10 competent cells plates and plated them in six well dishes I previously filled with LB media and ampicillin. I used glass beads in order to speed up the plating process (~3-4 glass beads for each well of the six well plates). After transforming, I minipreped 2 clones for each Golden Gate PCR products that were verified by Sanger sequencing (LGC Genomics). I selected only one positive clone for creating the libraries. The modified Golden Gate approach was generally extremely stable with an efficiency grated than 80%. The modified Golden Gate approach worked for most of the genes. In some specific cases, it was more difficult and in some other cases not possible to obtain positive clones using the general approach described before. In those cases, I applied modifications to the established protocol in order to increase intracellular loops insertion efficiency. One first modification I performed was to

add two intracellular loops in two different moments: first intracellular loops and relative Typells restriction enzyme before the first set of thermocycles and the second intracellular loops with relative Typells restriction enzymes before the second set of thermocycles. Also, since there are not constrain on the order of which intracellular loops can be inserted into the mother construct, I tested all possible permutation of two loops insertion. Both previous modifications allowed me to increase the number of positive clones obtained for the light- activated chimeric libraries. For some of the remaining genes that still presented difficulties in cloning, I engineered an alternative modified Golden Gate protocol, based on the principle of reducing the percentage of glycerol from the restriction enzymes in the total volume of the initial mixture. I set the total reaction volume to 32ul, consequently increasing the amount of Promega Ligase buffer to 3.2ul. I kept the quantity of mother construct, intracellular loops and relative ratio unmodified. This modified protocol allowed to test also the role of the analytical digest in the previously described cloning modified Golden Gate cloning protocol. I retransformed 1.5ul of the mixture prior digestion and I digested the remaining 30.5ul using the appropriate analytical enzymes as already described according to the standard Golden Gate protocol. The result was not conclusive, but no major improvement was reached when the analytical digest was omitted. For a few amount of light-activated human Class A oGPCRs both the original and the modified Golden Gate protocols did not give positive clones. In this case, in order to preserve the completeness of the light- activated orphan library, I ordered the corresponding genes were prepared using gene synthesis (Epoch Life Science).

3.2 Functional testing of light-activated chimeric GPCRs

3.2.1 Luciferase-based reporter plasmid for screening G-protein mediated signaling pathways

For the screening of GPCRs I used a gene reporter system based on different luciferases. This system has the advantage to be easily identifiable and quantifiable using the bioluminescence properties of the enzyme luciferase when interacting with the appropriate substrate luciferin. Among luciferases present in nature, the luciferase from *Photinus pyralis* (Firefly luciferase) and from *Renilla reniformis* (Renilla Luciferase) have been widely used in gene reporter systems considering the full characterization of their enzymatic reactions²³⁷. Luciferase-based gene reporter systems have the ability to test many signaling events by coupling a response element linked to the signal that has to be detected to the transcription of the luciferase gene. The intensity of the signal can be measured and quantified by bioluminescence. For GPCRs it is known that signal transduction mediated by the interaction with different G α subunits regulate different intracellular second messengers. Increase or decrease of intracellular level of these second messengers can up-or down-regulate gene transcription.

More specifically, in case of GPCRs the relation between second messengers and gene activation is well known and can be in good approximation described as follow²³⁸:

- Activity of GPCRs that modulate increase or decrease of intracellular concentrations of cAMP can be monitored by coupling luciferase transcription to a cAMP responsive element (**CRE**)^{239,240}
- Activity of GPCRs that modulate increase of intracellular concentration of calcium through IP3 (Ca²⁺) can be monitored by coupling luciferase transcription to the transcription factor Nuclear factor of activated T-cells (**NFAT**)^{241,242}

- Activity of GPCRs that interact with RhoGEF and RhoA can be monitored by coupling luciferase transcription to a modified serum response factor, sensitive only to RhoA activation (**SRE.L**)²⁴³
- Activity of GPCRs that modulate activation of the ERK1/2 pathway can be monitored by coupling luciferase transcription to the serum responsive element (**SRE**)²⁴⁴

The previous description is limited to the interaction between second messengers and transcription factors. To extend this description to the interaction between G-protein mediated pathways and transcription factors, it has to be taken in account the complexity of the G-protein mediated signal transduction. This complexity is actually an advantage, because it permits to have different choices of transcription factors to couple to luciferase to screen the same G-protein mediated pathway.

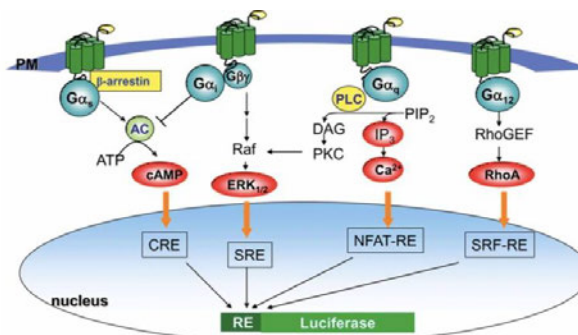


Figure 3.1 Mechanism of coupling between G-protein mediated pathways and luciferase gene response systems through different transcription factors (from Cheng *et al.*²³⁸)

For example, in case of Gα-q coupled GPCRs, their activity can be monitored using a NFAT responsive element (that will respond to raise of intracellular Ca²⁺ concentration trough IP3), or using a SRE responsive element (that will respond to PKC and consequent ERK1/2 activation). I decided to use three different Luciferase based reporter plasmids:

1 - A CRE reporter plasmid (Pgl4.29, Promega) sensitive to change in cAMP concentration and related to activation of G α -s mediated signaling pathways.

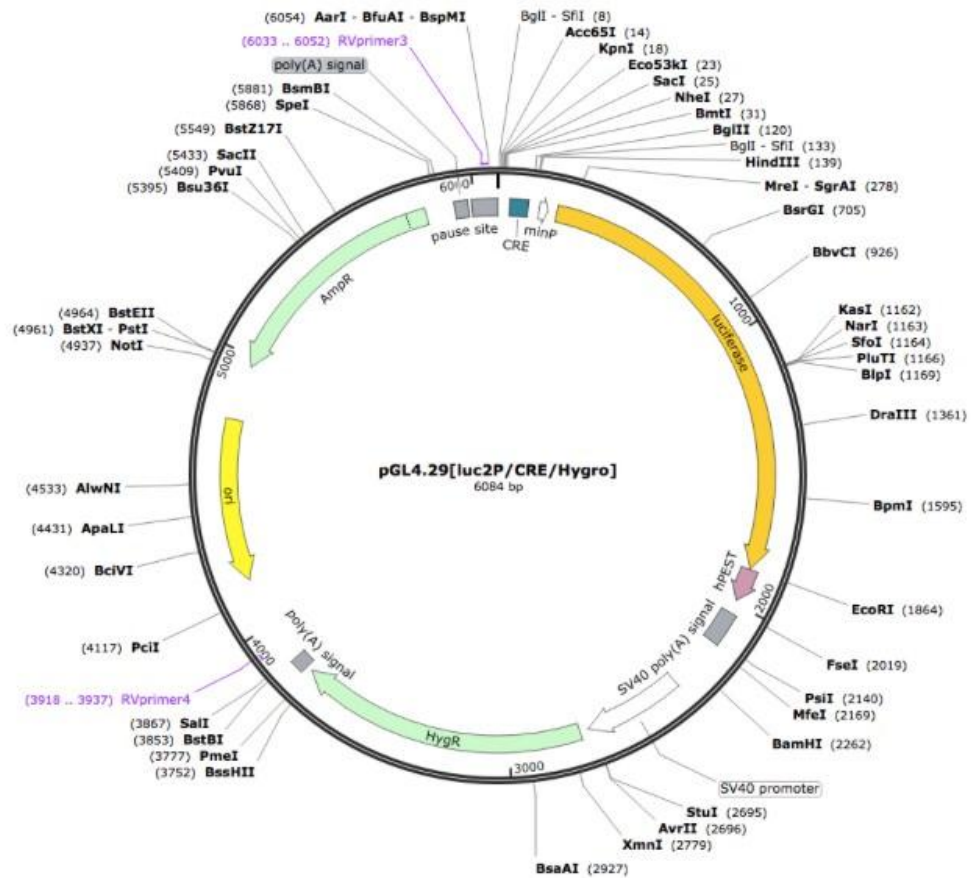


Figure 3.2 Vector map of the luciferase-based CRE reporter plasmid

2 - A SRE reporter plasmid (Pgl4.33, Promega) sensitive to activation of MAPK through β -arrestin and PKC and hypothetically related to activation of G α -q and G α -12/13 mediated signaling pathways.

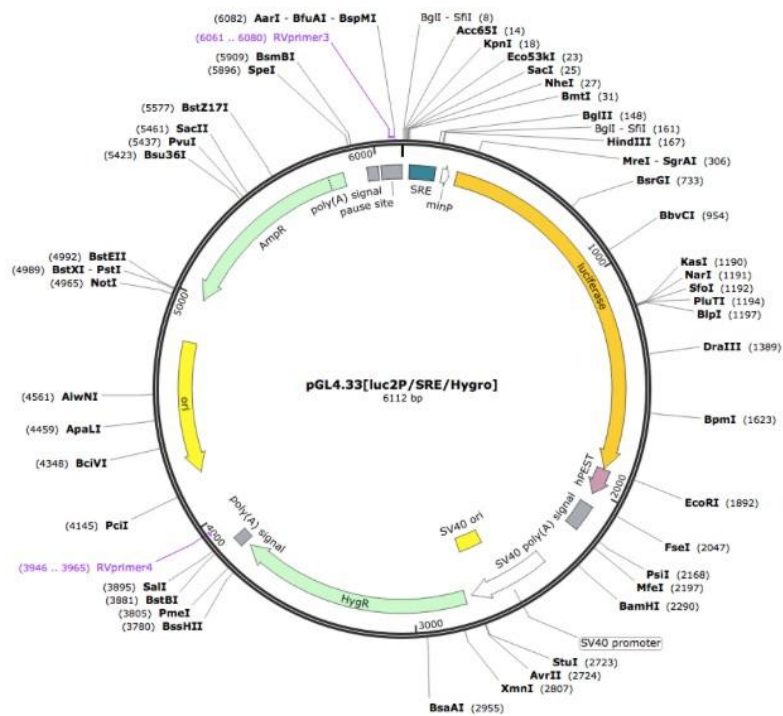


Figure 3.3 Vector map of the luciferase-based SRE reporter plasmid

3 - A SRE.L reporter sensitive to RhoA activation and hypothetically related to activation of $G\alpha$ -q mediated signaling pathways

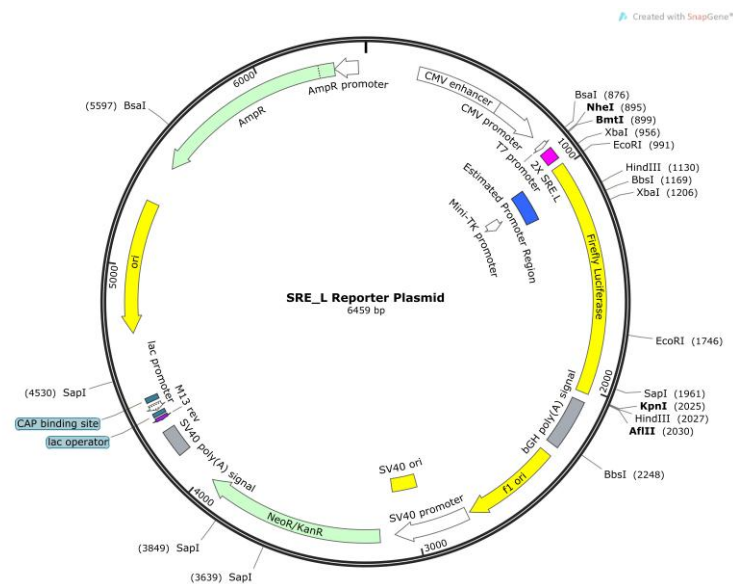


Figure 3.4 Vector map of the luciferase-based SRE.L reporter plasmid

I also used the CRE reporter to measure decrease in cAMP concentration by stimulating cAMP production using endogenously expressed receptors and estimate G α -i/o mediated signaling pathways. All previously described reporter plasmids are based on Firefly Luciferase as reporter protein, which expression changes only upon activation of one of the previously described G-protein mediated signaling pathways. Gene reporter systems based only on a single reporter protein (such as Luciferase) might be statistically noisy by not taking in account hidden variables such as transfection efficiency (especially when not working with stable cell lines) and cell number. To get an estimate of these hidden variables, I co-transfected together with the Firefly-based Luciferase reporter plasmid a second Luciferase reporter plasmid based on Renilla Luciferase. I subcloned the Renilla Luciferase reporter gene in pcDNA3.1(-) (between NheI and XbaI sites) and thus it contains the same promoter of the Firefly based reporter plasmids, with the difference that is constantly expressed proportionally to the number of positively transfected cells and it is not affected by activation of any G-protein mediated signaling pathways.

3.2.2 Experimental procedure

I screened all genes included in this study with one single reporter plasmid at time. The total duration of each experiment was 5 days. On DAY 1, I treated 96 well plates with transparent bottom (Greiner Bio- one) with poly-L-ornithine (PLO) in dilution 1: 25 in PBS (final concentration 1mM). I added 70ul of the PLO dilution to each 96 well plate, and either incubated at 37° for three hours or stored in the fridge overnight. Plates coated with this procedure could be used for as long as four weeks keeping their coating properties. Before cell seeding, I washed the 96 well plates with PBS in order to remove any residual PLO. When removing PLO (as well as for any other experimental steps concerning the change of media in the 96 well plates) I used a cell culture tip (volume 250ul) attached to a cell culture aspiration pump. I used the tip instead of a classic glass pipette for its larger sucking section that lower the sucking pressure at the contact between the tip and the

well plate and reduce both the amount of coating aspirated and the amount of cell detached during the different media changes. I seeded four 96 well plates with HEK 293 cell at the concentration of 50000 cells for 100ul (well). I cultured and seeded HEK293 cells in DMEM supplemented with 10% FBS, 100 U/ml penicillin and 0.1 mg/ml streptomycin in a humidified incubator (37 degrees Celsius, 5% CO₂).

24 hours after seeding (DAY 2) I changed the media to antibiotics-free DMEM supplemented with 5% FBS. The choice of antibiotic free media was due to the fact that cells were transfected by lipofection and antibiotics are proved to lower transfection efficiency and cell viability. Transfection was performed following a template 96 well plate that was applied to all four 96 well plate seeded with HEK293 cells. In the template each well corresponds to either:

- A single light-activated human Class A oGPCR
- A single light-activated chimeric control GPCR
- A single full-length agonist activated control GPCRs

Transfection was performed on a 96 well plate using lipofection and polyethylenimine solution (PEI, 1mg/ml in H₂O; Polysciences) as lipofection reagent. I tried different ratios between receptor plasmids, Firefly reporter plasmid and Renilla plasmid in order to achieve the best combination in terms of transfection and reporter efficiency. For PEI best transfection efficiency was reached for 100ng of DNA for 1ul of reagent.

I also tried different ratio between the receptor plasmids, the Firefly reporter plasmid and the Renilla plasmid, leading to the final choice of keeping a constant ratio of 1:1 between the receptor plasmid and the Firefly reporter plasmid and a 10:1 ratio between the Receptor-Firefly reporter plasmids and the Renilla plasmid.

Taking in account the previously described constrains, for each well, I mixed 75ng of receptor, 75ng of Firefly reporter plasmid and 7.5ng of Renilla plasmid with 25ul of Optimem-L and incubate for 5 minutes. In parallel I diluted 1ul of

PEI solution (1mg/ml in H₂O; Polysciences) in 25 ul Optimem-I (Life Technologies 519043) for each well. I combined the two solutions, incubated at room temperature for 20 min and then added to the cells using a multichannel pipette. After six hours, I changed the culture media to starve media (DMEM supplemented with 0.5% FBS and antibiotics).

On DAY 3, I incubated the cells overnight with 10uM of 9-cis retinal (Sigma) dissolved in DMEM supplemented with 0.5% FBS and antibiotics. The binding of rhodopsin with 11-cis retinal and its isomerization in all-trans form upon interaction with a photon is a necessary condition for the activation of the rhodopsin signal cascade. It has been shown in literature that HEK 293 cells contains the machinery for retinal recycling, but it is not yet clear if the level of endogenous 11-cis retinal contained in the HEK293 cells would be sufficient for activate light-stimulated chimeric receptors. 9-cis retinal is functionally equivalent to 11-cis retinal and allow rhodopsin activation upon light stimulation²⁴⁵. On DAY 4, I performed light and ligand stimulation. Out of the four plates prepared and transfected, I chose two plates as light plates and two as dark plates. Prior to start light and ligand stimulation, I changed media to CO₂ independent media supplemented with 0.5% FBS and antibiotics. I performed ligand-stimulation of control receptors and reporter-only transfected cells right before light stimulation with selected agonist and fixed concentrations. I carried out ligand and light stimulation in an incubator (Exoterra) modified with 450 light emitting diodes (300 LED IP65, SMD3528; 150 LED IP66, SMD5050, 465-470 nm and 525-530 nm wavelength ranges). The four 96 well plates were ligand and light stimulated at 37 degrees Celsius for six hours with blue and green light (400 $\mu\text{W}/\text{cm}^2$) or only blue light (280 $\mu\text{W}/\text{cm}^2$, for the SRE reporter, in order to avoid endogenous activation of green-sensitive opsin expressed in HEK293 cells). I shielded the two dark plates from light by wrapping them in aluminum foil. When testing for reduction of intracellular cAMP concentration using the CRE reporter plasmid, I stimulated the cells with NECA (500 nM) immediately (three to five minutes) before agonist

and light stimulation in order to increase intracellular levels of cAMP by activating endogenously expressed adenosine receptors (A2A, A2B)²⁴⁶.

Receptor(s)	Ligand	Final concentration
α 1AR β 2AR	Norepinephrine (NOR)	10 μ M ²²⁰
FFR3	Propionate (PPA)	10 mM ²⁴⁷
A2AR	Adenosine (NECA)	100 μ M ²⁴⁸
D1R D2R	Dopamine (DOP)	100 μ M ^{249, 250}
M2R M3R	Muscarine (MUSC)	100 μ M ²⁵¹
M1R	VU357017 (positive, allosteric modulator)	25 μ M ²⁵²

Table 3.5 List of agonist used for the ligand stimulation of endogenously expressed GPCRs and transiently transfected full-length control GPCRs

After six hours of (ligand and light) stimulation, I developed luminescence signals using the Dual-Glo system from Promega. The protocol I used for the Dual-Glo Luciferase assay was slightly modified in comparison with the one proposed from the manufacturer. Prior to use the Dual-Glo Promega kit, I removed the CO₂ independent media using the previously described procedure; I prepared the first reagent by mixing Firefly Luciferase buffer with the relative substrate. This buffer allows cell lysis and furnishes a proper substrate for reading Firefly luciferase values. I added 50ul of the Firefly substrate plus buffer to each well and I shook the plates manually plates for 10 minutes (covered with an aluminum foil to protect from light) in order to allow a complete lysis of the cells. I read Firefly values in a microplate reader (Biotech Synergy H1) using a luminescence fiber; intensity was integrated for 1 s for each measurement and I used an artificial software gain of 135 for every measurement.

After the Firefly measurement, I prepared the second reagent by mixing the Promega Stop&GLO substrate and buffer. 50ul of the mixture were added directly in the original 50ul of Firefly mixture. The STOP&GLO buffer has the

property to quench the Firefly luciferase and to act as a buffer for the Renilla luciferase. I shook again the plates for 10 minutes and I read Renilla values using a microplate reader with the same setting already described for the Firefly measurements.

3.3 Data Analysis for the luciferase-based screening platform

For the analysis of the luciferase assays, I normalized all Firefly values by the Renilla values for each well of the 96 well plates to take in account variations coming from cell number and transfection efficiency²⁵³. For each of the 96 well plates, I normalized the Firefly/Renilla values of each well with the average value of the non-agonist-stimulated control wells to consider the intrinsic variation of each plate and being able to compare between different plates.

I repeated each experiment three to five times. For each experiment, every 96 well plate was validated by first looking at the ratio of the agonist-stimulated control GPCRs versus the not agonist-stimulated control GPCRs. These controls were included on each plate and used as validation: if agonist control receptor did not show the expect induction between agonist and not agonist stimulation, the single plate was not taken in account in the overall experimental analysis for the specific reporter gene.

I used induction values calculated for light-activated control receptor as validation for the light-stimulation procedure. Average values were calculated for light-activated control GPCRs on both light plates (N=2) and dark plates (N=2). If light-activated control GPCRs did not show the expect induction between light state and dark state, the experiment was consider as not validated and not included in the overall average for the specific reporter plasmid.

I calculated averages of Firefly/Renilla ratios for each well on the total number of experiments for each different G-protein coupled pathway reporter plasmid. I used these values to identify orphan genes for which light activation was considered significant by calculating induction values defined as the ratio between Firefly/Renilla in light condition over dark condition.

I considered oGPCRs genes for which induction values were bigger than 2.5-fold as active (for CRE, SRE and SRE.L reporter plasmids), while for the NECA-stimulated CRE reporter plasmid significant light dependent induction was considered for genes in which values were lower than 0.7-fold.

3.4 Antibody staining of the light-activated chimeric oGPCRs

For antibody staining, I used a 96 well plates format following a similar procedure as described already in the previous section for the Luciferase assays. On DAY 1, I coated and seeded cells into a 96 well according to the protocol for the Luciferase functional assays. On DAY 2, I transfected all 65 light-activated Human Class A oGPCRs constructs plus rhodopsin as positive staining control following the procedure already described in the previous section. I considered not transfected cells plus primary antibody as negative staining control.

On DAY 3, cells were washed with DPBS (LifeTechnologies Inc.) two times for three minutes to remove any residual media and to decrease the chances of detach them in the following washing steps. I prepared 4% PFA solution from 95% PFA powder (Sigma) in PBS, and I used it to fix cells for 15 minutes at room temperature. PFA was used as fixation agent in order to not permeabilize the cell membrane; the not permeabilization of the cell membrane together with the location of the VSV-G epitope on the extracellular side of the mother construct allowed me to stain chimeric receptor that are expressed at the cell membrane. After fixation, I washed the cells four times for five minutes with DPBS; cells were later incubated 30 minutes in blocking buffer (1% BSA in DPBS, 50 ul/well) prior the incubation with primary antibodies (clone P5D4, Sigma, 1 hours at RT, 1:250 final dilutions in blocking buffer). I washed again the cells 3 times for 5 minutes' prior incubation with 30ul/well of anti-polyvalent biotinylated antibody for 10 minutes at RT.

After another washing step (2 times for 3 minutes with DPBS) I incubated cells with horse-radish peroxidase secondary antibody for 10 minutes at RT. I prepared a DAB mixture by adding 30 ul of DAB (Sigma, D6065) in 1 ml of DAB substrate (Sigma, D6190). After washing with DPBS (2 times for 3 minutes), I

added 40ul/well of DAB mixture and let incubate for 3 minutes at RT. I stopped the reaction adding 70ul/well of distilled water and I measured absorbance values at 450nm using a Synergy H1 plate reader for each well.

3.5 Bioinformatics tools for GPCRs-G-protein coupling prediction

At the moment in which this thesis is written, these are the algorithm published that claim to be able to decipher G-protein coupling for GPCRs:

- Cao, 2002: A **Naïve Bayes** model²⁵⁴
- Sreekumar, 2004: **hidden Markov** model²⁵⁵
- Yabuki, 2005: **hidden Markov** model plus support vector machine²⁵⁶
- Sgourakis, 2005: **hidden Markov** models and artificial neural networks²⁵⁷
- Sgourakis, 2005: refined **hidden Markov** model²⁵⁸
- Ono, 2006: **hidden Markov** model²⁵⁹
- Guo,2006: Autocross-Covariance Transform²⁶⁰

Some of these algorithms are available online, for the ones not published on public servers the authors were contacted in order to retrieve the original source code. The algorithms retrieved and used for this current work are:

- Yabuki, 2005: **hidden Markov** model plus support vector machine
 - o GRIFFIN
- Sgourakis, 2005: refined **hidden Markov** model
 - o PREDCOUPLE
- Sgourakis, 2005: **hidden Markov** models and artificial neural networks
 - o PREDCOUPLE2

These algorithms are based on Hidden Markov Models. In order to have an estimate of how good these algorithms perform on data set of well-known GPCRs there are two main parameters to take in account: the sensitivity of the algorithm and the specificity. Sensitivity is defined as the number of positive results confirmed as positive from experimental data, specificity is the number of negative results confirmed as negative by experimental data. In the case of GPCRs coupling, sensitivity is the ability to predict a G-protein coupled pathway for a GPCR that has been confirmed by experimental approaches, specificity take in account the number of predicted G-protein coupled pathways that are not verified in experimental data.

For the chosen algorithms:

- The **Griffin** algorithm is trained on a set of 682 GPCRs (of which 394 are olfactory receptors) and has a claimed sensitivity and specificity of on average more than 85 % on the training set
- The **Predcouple** algorithm is trained on 282 GPCRs and a “correct classification rate” of 91 %, predicting 6 out of 24 experimental verified promiscuous GPCRs coupling
- The **Predcouple2** algorithm is trained on 226 GPCRs with a claimed sensitivity of 100% and specificity of 92 % on the training dataset.

For all these algorithms, two different data set were prepared:

- One dataset containing well-studied GPCRs (overlapping with the training dataset of each algorithms) and the original sequences of the 65 chosen oGPCRs
- One dataset containing the sequences of the 65 light-activated Human Class A oGPCRs

I collected data for each of the dataset. For each control and oGPCR for which the algorithms were run I considered each pathway with a probability of coupling higher than 50 % as predicted coupling.

4 - Results

4.1 Human Class A oGPCR gene selection

94 genes in the human genome are currently listed and classified as human Class A oGPCRs. For all class 94 human Class A oGPCRs I retrieved both amino acid sequences and nucleotide sequences from the Uniprot database (<http://www.uniprot.org>). For GPR79 it was not possible to retrieve a deposited nucleotide sequence and it was excluded from the study. For a limited amount of genes, the nucleotide sequences were adapted to match the deposited protein sequence. I did not include 29 human oGPCR genes in this study either because they are currently considered as opsins (OPN3, OPN5) or because classified in one of the GPCRs subfamilies.

In this study I selected 65 genes for engineering of bovine rhodopsin-based chimeric receptors. These genes correspond to the human Class A oGPCRs genes currently identified by the GPRXX nomenclature according to the IUPHAR (I first checked the list in April 2011 and verified it again in April 2015 to keep track of any changes).

Using the algorithm described in the section 3.1, I designed and cloned for all selected 65 human Class A oGPCRs their respective light-activated chimeras based on bovine rhodopsin.

For one gene, GPR101, I was not able to retrieve a meaningful chimeric sequence and therefore this gene was excluded from the functional screening.

Identifier	Gene name	SwissProt/Uniprot ID
MO3	GPR1	P46091
MO4	GPR3	P46089
MO5	GPR4	P46093
MO6	GPR6	P46095
MO7	GPR12	P47775
MO8	GPR15	P49685
MO9	GPR17	Q13304
MO10	GPR18	Q14330
MO11	GPR19	Q15760

MO12	GPR20	Q99678
MO13	GPR21	Q99679
MO14	GPR22	Q99680
MO15	GPR25	O00155
MO16	GPR26	Q8NDV2
MO17	GPR27	Q9NS67
MO18	GPR31	O00270
MO19	GPR32	O75388
MO20	GPR33	Q49SQ1
MO21	GPR34	Q9UPC5
MO22	GPR35	Q9HC97
MO23	GPR37	O15354
MO24	GPR37L1	O60883
MO25	GPR39	O43194
MO26	GPR42	O15529
MO27	GPR45	Q9Y5Y3
MO28	GPR50	Q13585
MO29	GPR52	Q9Y2T5
MO30	GPR55	Q9Y2T6
MO31	GPR61	Q9BZJ8
MO32	GPR62	Q9BZJ7
MO33	GPR63	Q9BZJ6
MO34	GPR65	Q8IYL9
MO35	GPR68	Q15743
MO36	GPR75	O95800
MO37	GPR78	Q96P69
MO39	GPR82	Q96P67
MO40	GPR83	Q9NYM4
MO41	GPR84	Q9NQS5
MO42	GPR85	P60893
MO43	GPR87	Q9BY21
MO44	GPR88	Q9GZN0
MO45	GPR101	Q96P66
MO46	GPR119	Q8TDV5
MO47	GPR120	Q5NUL3
MO4	GPR132	Q9UNW8
MO49	GPR135	Q8IZ08
MO50	GPR139	Q6DWJ6
MO51	GPR141	Q7Z602
MO52	GPR142	Q7Z601
MO53	GPR146	Q96CH1
MO54	GPR148	Q8TDV2
MO55	GPR149	Q86SP6
MO56	GPR150	Q8NGU9
MO57	GPR151	Q8TDV0

MO58	GPR152	Q8TDT2
MO59	GPR153	Q6NV75
MO60	GPR160	Q9UJ42
MO61	GPR161	Q8N6U8
MO62	GPR162	Q16538
MO63	GPR171	O14626
MO64	GPR173	Q9NS66
MO65	GPR174	Q9BXC1
MO66	GPR176	Q14439
MO67	GPR182	O15218
MO68	GPR183	P32249

Table 4.1 List of oGPCRs selected for the luciferase-based functional screening with relative identifiers and SwissProt/Uniprot reference numbers

4.2 Control GPCR gene selection

There are currently several GPCRs for which both several agonists and G-Protein mediated activated signaling pathways are known. I chose a subset of control GPCRs taking in account coupling properties and available information in literature on their use in a chimeric form. I chose nine different well studied GPCRs as candidate genes for the creation of light-activated control chimeric GPCRs.

These genes were also used in their agonist-activated form to estimate the efficiency of their respective light-activated chimeras and to prove the preservation of coupling properties between agonist and light-activated control GPCRs.

The genes I selected as full-length control GPCRs (defining as full-length receptors being able to be chemically stimulated by their proper agonists) belong almost entirely to the human genome, with the only exception of the $\alpha 1$ adrenergic receptor ($\alpha 1AR$) whose original species is rat.

Receptor	Species	Predom. G coupling.	Expr. Vector	Source
$\beta 2$ -adrenergic receptor ($\beta 2AR$)	Human	G α -s	pcDNA3	Robert Lefkowitz (Duke Univ.) via Addgene, Inc. (14697)
$\alpha 1$ -adrenergic receptor ($\alpha 1AR$)	Rat	G α -q	pCMV5	Robert Lefkowitz (Duke Univ.) via Addgene, Inc. (45760)

Free fatty acid receptor 3 (FFR3)	Human	G α -i/o	pcDNA3	Graeme Milligan (Univ. of Glasgow)
Adenosine A2A receptor (A2AR)	Human	G α -s	endogenous	Atwood 2011
Dopamine receptor D1 (D1R)	Human	G α -s	pcDNA3.1(-)	MGC (MHS6278-202856822)
Dopamine receptor D2 (D2R)	Human	G α -i/o	pcDNA3.1(-)	MGC (MHS6278-202830262)
Muscarinic acetylcholine receptor M1 (M1R)	Human	G α -q and G α -s	pcDNA3.1(-)	Klaus Groschner (Med.Univ. of Graz)
Muscarinic acetylcholine receptor M2 (M2R)	Human	G α -i/o	pcDNA3.1(-)	MGC (MHS6278-211689788)
Muscarinic acetylcholine receptor M3 (M3R)	Human	G α -q	endogenous	Atwood 2011

Table 4.2 List of control GPCRs used in agonist and light-activated chimeric forms form with their specie of provenience, expression vector and origin information

Only two full-length control GPCRs are endogenously expressed in HEK293 cells according to Atwood *et al.*²⁴⁸, while all other full-length control GPCRs were transiently transfected using the mammalian expression pcDNA3.1(-), or equivalent mammalian expression vectors having a CMV promoter, in order to guarantee comparable expression efficiency (Table 4.2).

4.3 Validation of the luciferase-based reporter plasmids

I chose HEK293 cells to build the oGPCRs screening platform for the luciferase-based assays. According to Atwood *et al.*, HEK293 cells should theoretically express sufficient levels of G-Protein related proteins to activate G-Protein mediated intracellular cascades.

For each luciferase-based reporter plasmid I performed three different sets of experiments to validate the screening assay:

- I first agonist-stimulated HEK293 cells transfected with only the different luciferase-based reporter plasmids chosen for the screening of the G-

Protein mediated pathway and the Renilla plasmid. The set of agonists used was the same chosen for the stimulation of the ligand-activated control GPCRs. With this experiment I wanted to estimate efficiency of the reporter plasmids and the contribution of HEK293 cells endogenous GPCRs to background signals.

- Then, I stimulated HEK293 cells transiently transfected with the ligand-activated control GPCRs plus the Luciferase based reporter plasmid and the Renilla plasmid to estimate sensitivity and specificity of each reporter in recording increase in the Firefly/Renilla ratio due to agonist stimulation.
- Last, I light-stimulated the light-activated version of the control GPCRs to estimate the efficiency of the light stimulation experimental apparatus and the specificity and sensitivity of each reporter plasmid in recording light induced increase in the Firefly/Renilla ratios.

4.3.1 CRE reporter plasmid

I performed the validation of the CRE luciferase-based reporter plasmid performing the three different sets of experiments described in the previous section. The luciferase-based CRE reporter plasmid is supposed to be sensitive to rising in intracellular level of cAMP upon receptor activation. When not stated differently, HEK293 cells have always been transfected with the Renilla luciferase plasmid for all the experiments performed.

4.3.1.1 Agonist stimulation of endogenously expressed GPCRs

In a first set of experiments I stimulated endogenously expressed GPCRs in HEK293 cells transfected with the luciferase-based CRE reporter plasmid. I stimulated HEK293 cells using the set of agonists described in section 3.2.1 of the Material and Methods.

I performed these experiments to measure the response of HEK293 endogenously expressed GPCRs able to stimulate the CRE transcription factor.

I considered these responses as estimated background signals for the screening assay.

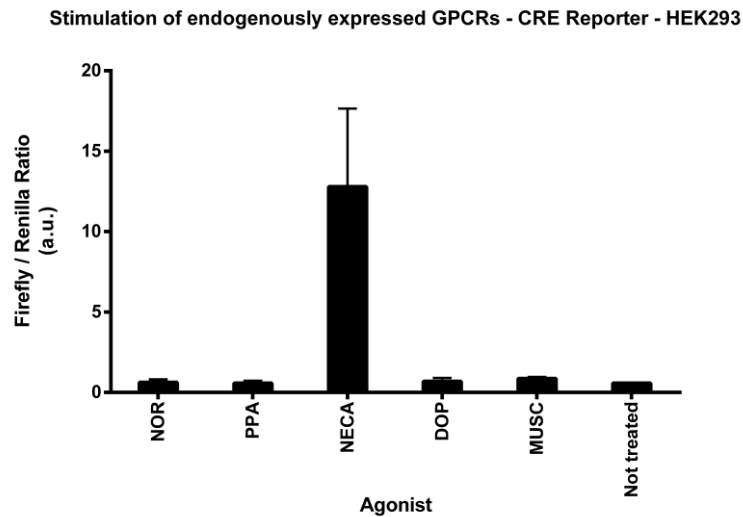


Figure 4.1 Agonist-stimulation of endogenously expressed GPCRs in HEK293 cells monitored using the luciferase-based CRE reporter plasmid

Only HEK293 cells stimulated with NECA showed a Firefly/Renilla ratio significantly higher in comparison with unstimulated cells. All other agonist shows Firefly/Renilla ratios not significantly higher of the ones recorded unstimulated cells.

The activation of the CRE reporter plasmid upon NECA stimulation is due to the stimulation of endogenously expressed GPCRs adenosine receptors A2A and A2B, as expected from literature.

Data represented in Figure 4.1 prove that:

- HEK293 cells levels of expression of G-Protein related proteins are sufficient to stimulate the CRE the reporter plasmid.
- The CRE reporter plasmid used is sensitive enough to detect signal coming from agonist stimulation of endogenously expressed GPCRs.
- The only significant signal background for the Luciferase-based CRE reporter plasmid is due to NECA stimulation of endogenously expressed

adenosine receptors (A2A, A2B), while no significant background signal is recorded for any of the other agonist used.

4.3.1.2 Agonist stimulation of transiently transfected full-length control GPCRs

I agonist-stimulated HEK293 cells transiently transfected with the full-length control GPCRs listed in Table 4.2 in order to estimate the sensitivity and specificity of the luciferase-based CRE reporter plasmid in detecting signals coming from transiently transfected full-length control GPCRs.

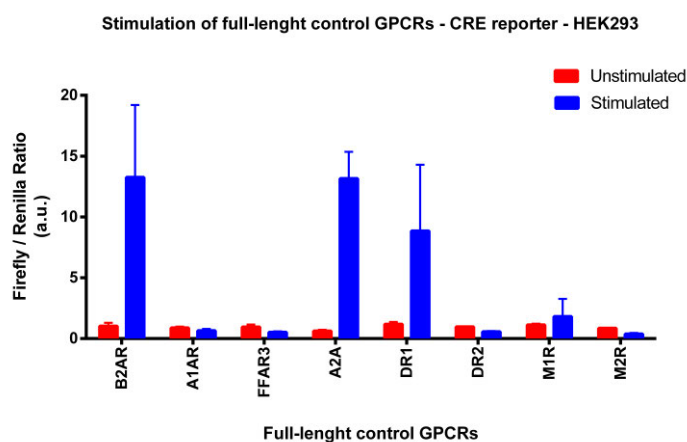


Figure 4.2 Agonist-stimulation of transiently transfected full-length control GPCRs in HEK293 cells monitored using the luciferase-based CRE reporter plasmid

HEK293 cells transiently transfected with full-length β 2-adrenergic receptor (B2AR) and Dopamine 1 (DR1) show a significant increase in the Firefly/Renilla ratio upon Norepinephrine (B2AR) and Dopamine (DR1) stimulation. Considering the results in Figure 4.1, the signals recorded from Norepinephrine and Dopamine stimulation are dependent only on the activation of transiently transfected B2AR and DR1 and have are not dependent on endogenously expressed GPCRs. HEK293 cells stimulated with NECA showed an activation comparable with the one shown in Figure 4.1.

HEK293 cells transfected with Muscarinic 1 receptor (M1R) showed a weak increase in the Firefly/Renilla ratio upon stimulation with Muscarine. All other HEK293 cells transiently transfected with full-length control GPCRs showed no

significant increase in the Firefly/Renilla ratio upon agonist stimulation in comparison with unstimulated cells.

Data shown in Figure 4.2 prove that the luciferase-based CRE reporter plasmid is enough sensitive to discriminate signal coming from transiently transfected agonist stimulated full-length control GPCRs. Also, the CRE reporter plasmid is activated only through agonist stimulation of GPCRs (transiently transfected and endogenously expressed) for which ability to increase intracellular level of cAMP has been previously proved.

4.3.1.3 Light-stimulation of transiently transfected light-activated control GPCRs

I light-stimulated HEK293 cells transiently transfected with light-activated control GPCRs (Table 4.2) following the light-stimulation procedure described in section 3.3 of the Material and Methods.

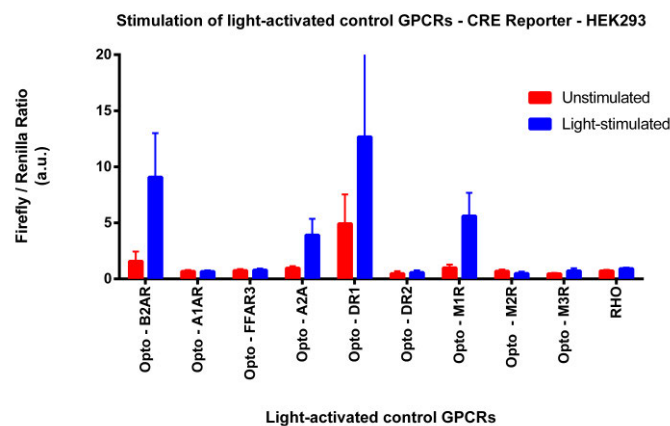


Figure 4.3 Light-stimulation of transiently transfected light-activated control GPCRs in HEK293 cells monitored using the luciferase-based CRE reporter plasmid

I considered the Firefly/Renilla ratio values in dark and light conditions for HEK293 cells transfected with rhodopsin (“RHO” column, Figure 4.3) as negative control, not expecting stimulation of the CRE transcription factor from the activation of $G\alpha$ -t1/2.

Light-activated control GPCRs show an activation pattern comparable with the agonist stimulation of their respective full-length genes (Figure 4.3 vs Figure

4.2). Light-activated B2AR, DR1 and A2A showed a significant increase in the Firefly/Renilla ratio values upon light-stimulation.

Light-activated M1R present a light-dependent CRE stimulation significantly higher in comparison with the one recorded from the agonist stimulation of the full-length M1R (Figure 4.2).

I stimulated HEK293 cells transiently transfected with the full-length M1R with CCH (Carbachol, not selective agonist) and VU357017 (selective M1R agonist) in order to prove that the light induced response in the light-activated M1R is neither an artifact created by the assay or an artificial coupling created by the chimeric M1R. HEK293 cells transfected only the luciferase-based CRE reporter plasmid were as well stimulated using CCH and VU357017 and considered as negative control.

M1R stimulation by CCH - CRE Luciferase Reporter

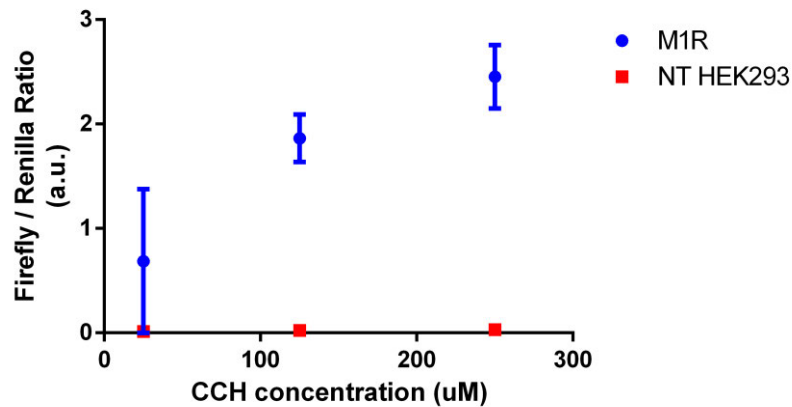


Figure 4.4 CCH stimulation of full-length M1R transiently transfected in HEK293 cells monitored using the luciferase-based CRE reporter plasmid

M1R stimulation by VU357017 - CRE Luciferase Reporter

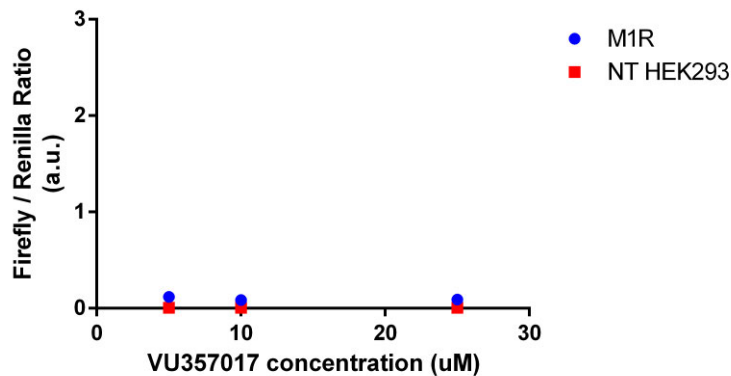


Figure 4.5 VU357017 stimulation of full-length M1R transiently transfected HEK293 cells monitored with the luciferase-based CRE reporter

HEK293 cells transiently transfected with the full-length M1R and stimulated with different concentrations of CCH shown Firefly/Renilla values significantly higher in comparison with HEK293 cells containing only the luciferase-based CRE reporter plasmid (Figure 4.4).

HEK293 cells transiently transfected with the full-length M1R and stimulated with different concentrations of VU35017 show no significant difference in the Firefly/Renilla ratio values in comparison with HEK293 cells only transfected with the luciferase-based CRE reporter plasmid (Figure 4.5).

The data represented in Figure 4.3, 4.4 and 4.5 suggest that the removal of the M1R ligand dependency in the light-activated M1R preserve the ability of the M1R intracellular loops to couple to G α -s subunits, increase intracellular levels of cAMP and subsequently activate the CRE transcription factor.

Data shown in Figure 4.3 prove that:

- The light stimulation procedure described in section 3.3 is sufficient to stimulate light-activated control GPCRs.
- The CRE reporter plasmid is sensitive enough to record light-dependent CRE activation by transiently transfected light-activated control GPCRs.
- The light-activated control GPCRs showed a light-dependent CRE activation pattern (Figure 4.5) comparable with the activation pattern of their respective full-length genes.

4.3.2 SRE.L reporter plasmid

I performed the same three sets of experiments describe in section 3.1 to validate the luciferase-based SRE.L reporter plasmid. This reporter plasmid is supposed to be sensitive to RhoA activation. Except for when stated differently, in the following experiments HEK293 cells were always transfected with the Renilla luciferase plasmid.

4.3.2.1 Agonist stimulation of endogenously expressed GPCRs

I agonist-stimulated HEK293 cells transfected with the luciferase-based SRE.L reporter plasmid in order to measure activation coming from agonist stimulation

of endogenously expressed GPCRs and estimate background signal for this screening assay.

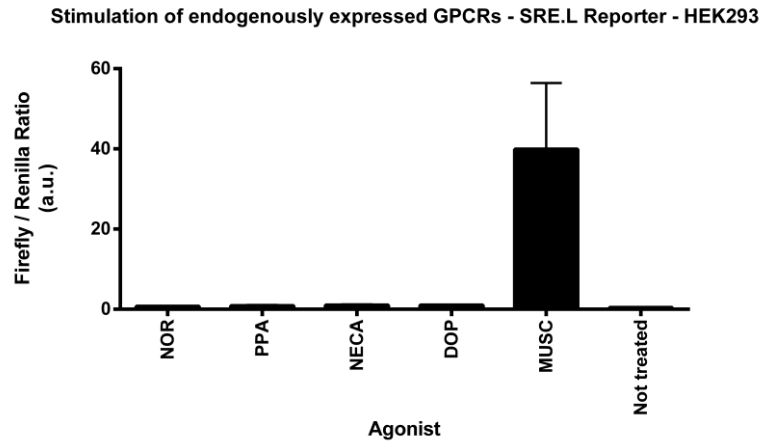


Figure 4.6 Agonist-stimulation of endogenously expressed GPCRs in HEK293 cells monitored using the luciferase-based CRE reporter plasmid

HEK293 cells stimulated with Muscarine show Firefly/Renilla ratio values significantly higher in comparison with same values measured for unstimulated cells, while all other agonists show values comparable with unstimulated cells.

According to the literature, HEK293 cells endogenously express a significant amount of Muscarine 3 receptor (M3R) supposed to be able to activate RhoA and consequently stimulate the SRE.L transcription factor.

Data shown in Figure 4.6 prove that the SRE.L reporter plasmid is sensitive enough to record signals coming from agonist stimulation of endogenously expressed GPCRs. Also, only Muscarine stimulated HEK293 cells show significant background signal coming from the activation of endogenously expressed M3R, while all other agonist shows comparable activation with unstimulated cells.

4.3.2.2 Agonist stimulation of transiently transfected full-length control GPCRs

I agonist-stimulated HEK293 cells transiently transfected with full-length control GPCRs and SRE.L reporter plasmid.

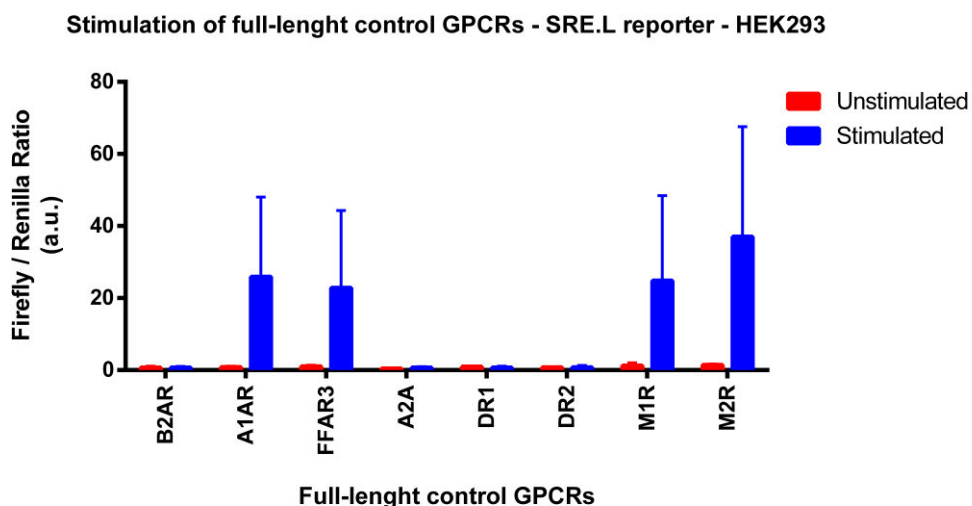


Figure 4.7 Agonist-stimulation of transiently transfected full-length control GPCRs in HEK293 monitored using the luciferase-based SRE.L reporter

HEK293 cells transiently transfected with α 1-adrenergic receptor (A1AR), free-fatty acid 3 receptor (FFAR3), Muscarinic 1 (M1R) and Muscarinic 2 (M2R) show significant increase in Firefly/Renilla ratio values upon agonist stimulation. All other transiently transfected full-length controls show Firefly/Renilla ratio values comparable between stimulated and unstimulated states. While the induction recorded for the A1AR and FFAR3 can be exclusively related to the activation of the transiently transfected full-length control GPCRs, the M1R and M2R induction need further analysis. The M1R is known to be $G\alpha$ -q coupled while the M2R is known to be $G\alpha$ -i/o coupled. The data for agonist stimulation of HEK293 cells only SRE.L reporter transfected (Figure 4.6) show that Muscarine is able to activate the endogenously expressed M3R in HEK293 cells. This suggests that the M1R and M2R responses upon Muscarine stimulation (Figure 4.7) might not be dependent on the agonist stimulation of transiently transfected M1R and M2R, but on the endogenous response of M3R.

4.3.2.3 Light stimulation of transiently transfected light-activated control GPCRs

I light-stimulated HEK293 cells transfected with light-activated control GPCRs following the procedure explained in section 3.2.

No dark activity is recorded in HEK293 cells transiently transfected with light-activated control GPCRs. Firefly/Renilla values for rhodopsin are comparable under dark vs. light condition.

Light stimulation conserves the activation pattern of the agonist stimulation for the A1AR and FFAR3 receptors, while light-activated M1R and M2R shown no light induced activation of the SRE.L reporter.

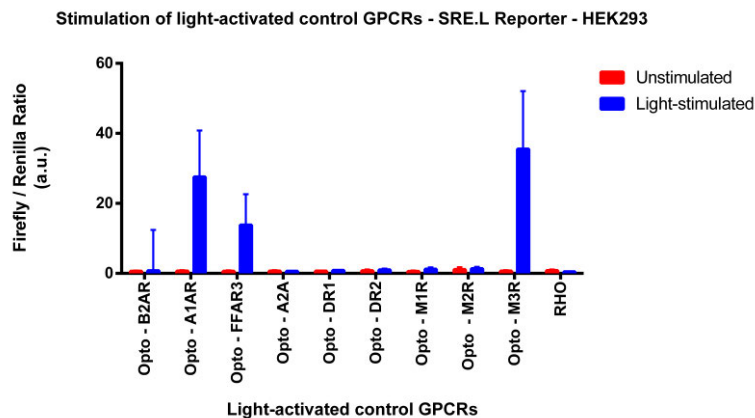


Figure 4.8 Light-stimulation of transiently transfected light-activated control GPCRs in HEK293 cells monitored using the luciferase-based SRE.L reporter plasmid

The absence of light-dependent stimulation of the SRE.L reporter plasmid by the light-activated M1R and M2R is in accordance with the hypothesis that the agonist dependent stimulation shown in Figure 4.6 for the M1R and M2R is due to the activation of endogenously expressed M3R, whose RhoA coupling and consecutive activation of the SRE.L responsive element is also confirmed by light activation of its corresponding light-activated chimera shown in Figure 4.10.

4.3.3 SRE reporter plasmid

To validated the luciferase-based SRE reporter plasmid I performed three sets of experiments described in section 4.1. The SRE reporter plasmid is supposed to be sensitive to MAPK and PKC activation. When not stated differently, HEK293 cells have to been considered always transfected with the Renilla plasmid.

4.3.3.1 Agonist stimulation of endogenously expressed GPCRs

I agonist-stimulated HEK293 cells transfected with the SRE reporter plasmid in order to record activity from stimulation of endogenously expressed GPCRs and estimate background signals for this reporter assay.

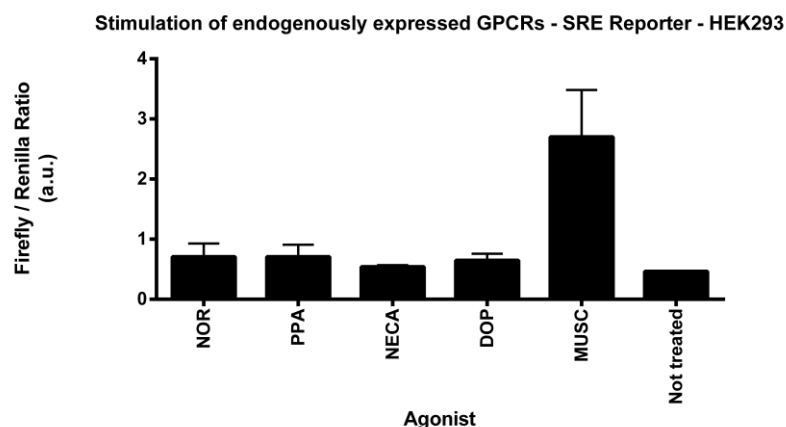


Figure 4.9 Agonist-stimulation of endogenously expressed GPCRs in HEK293 cells monitored using the luciferase-based SRE reporter

HEK293 cells stimulated with Muscarine show significant increase in the Firefly/Renilla ratio values in comparison with unstimulated cells, while all other agonist show Firefly/Renilla ratio values comparable with unstimulated cells. The activation by Muscarine of SRE reporter plasmid can be explained by the activation of the endogenously expressed M3R, like already shown in Figure 4.6 for HEK293 cells transfected with the SRE.L reporter plasmid.

4.3.3.2 Agonist stimulation of transiently transfected full-length control GPCRs

I agonist stimulated HEK293 cells transiently transfected with full-length control GPCRs. Agonist-stimulated HEK293 cells transiently transfected with A1AR, FFAR3, M1R and M2R full-length control GPCRs show significant increase in the Firefly/Renilla ratio upon agonist stimulation in comparison with unstimulated cells. In the case of the A1AR and FFAR3 the increase in the Firefly/Renilla ratio values in the stimulated states is due only to the activation of the transiently transfected full-length genes.

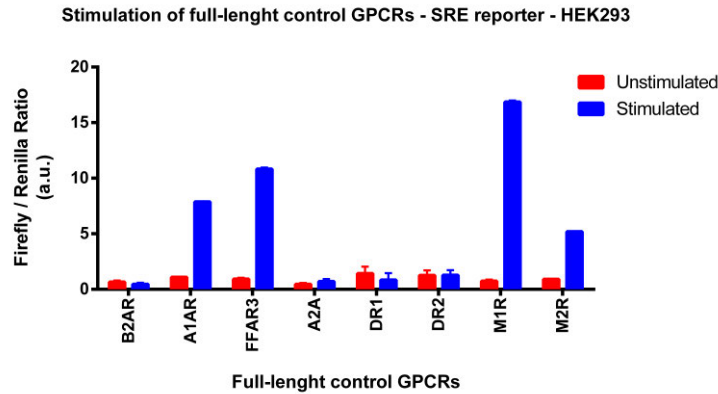


Figure 4.10 Agonist-stimulation of transiently transfected full-length control GPCRs in HEK293 cells monitored using the luciferase-based SRE reporter plasmid

The response of the M1R can be justified by agonist stimulation of the transiently transfected M1R receptor and the endogenously expressed M3R, while the response of the M2R receptor is entirely derived from the agonist stimulation of endogenously expressed M3R, as supported also by the results of the equivalent experiment performed using the SRE.L reporter plasmid (Figure 4.7)

4.3.3.3 Light stimulation of transiently transfected light-activated control GPCRs

I light-stimulated HEK293 cells transiently transfected with light-activated control GPCRs following the procedure described in section 3.1 of the Material and Methods.

Light-stimulated HEK293 cells transiently transfected with light-stimulated control GPCRs shown an activation pattern (Figure 4.11) comparable with the agonist-induced activation pattern of the respective full-length control genes (Figure 4.10) in the case of the A1AR, FFAR3 and M1R receptors.

The absence of signal from the light-activated M2R control GPCRs validate as M3R dependent the ligand induced activation shown in Figure 4.10. The agonist-induced response for cells transiently transfected with the M1R (Figure 4.10) can be considered as the sum of the endogenous stimulation of the M3R plus the stimulation of the transiently transfected M1R.

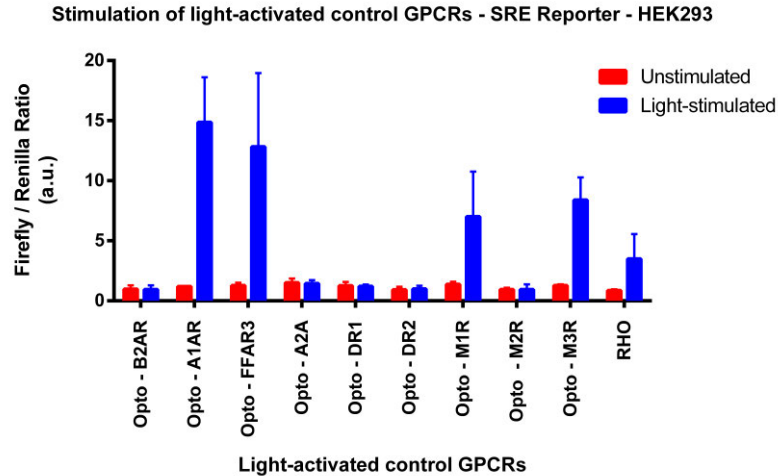


Figure 4.11 Light-stimulation of transiently transfected light-activated control GPCRs monitored using the luciferase-based SRE reporter

Figure 4.11 and 4.10 show that the SRE Luciferase reporter plasmid can be used to screen PKC and MAPK dependent G-Protein mediated pathways in the functional assay for the light-activated oGPCRs.

4.3.4 CRE reporter plasmid to monitor cAMP depletion

The luciferase-based CRE reporter plasmid can be used to screen for reduction of intracellular level of cAMP upon receptor activation. HEK293 cells can be pre-stimulated in order to increase intracellular levels of cAMP.

In theory pre-stimulated cells expressing receptor known to be $G\alpha$ -i/o couple will have at the end of the screening assay lower Firefly/Renilla ratio values in comparison with the other pre-stimulated cells.

In order to verify this hypothesis, I performed the three sets of experiments already performed for the other luciferase-based reporter plasmids, plus an additional experiment to estimate the right concentration of agonist to use for HEK293 pre-stimulation.

4.3.4.1 NECA dose response curve for pre-stimulation of HEK293 cells

As already shown for the validation of the luciferase-based CRE reporter plasmid HEK293 cells endogenously express a sufficient amount of adenosine receptors to stimulate production of cAMP upon NECA stimulation.

In a first set of experiments I tested different concentrations of NECA to stimulate endogenously expressed adenosine receptors A2A and A2B in HEK293 cells to increase the amount of intracellular cAMP levels.

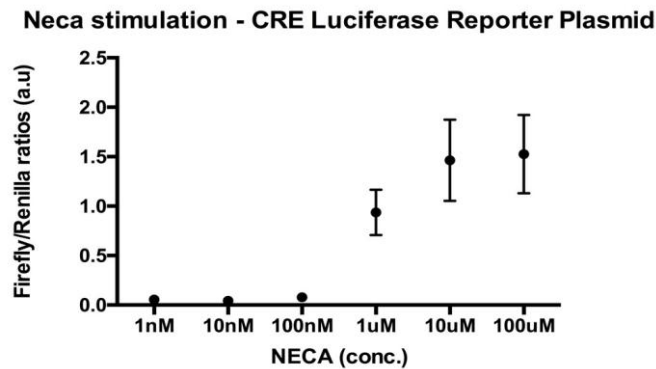


Figure 4.12 NECA stimulation (at different concentrations) of HEK293 cells monitored using the luciferase- based CRE reporter

Using different concentrations of NECA I was able to calculate a dose response curve for stimulation of endogenously expressed GPCRs in HEK293 cells transfected with the luciferase-based CRE reporter plasmid.

I chose 500nM as final concentration for HEK293 pre-stimulation with NECA considering this values as close to the NECA EC50.

4.3.4.2 Agonist stimulation of endogenously expressed GPCRs

I pre-stimulated HEK293 cells transfected with the luciferase-based CRE reporter plasmid with 500nm of NECA for five minutes (see section 3.2) prior agonist stimulation (following the same procedure used for previous luciferase- based reporter plasmids validations).

In this assay the values of the Firefly/Renilla ratios for control GPCRs that are known to decrease intracellular cAMP levels by coupling with $G\alpha$ -i/o subunits are supposed to be lower in the case of the ligand/light stimulated state in comparison with the unstimulated one.

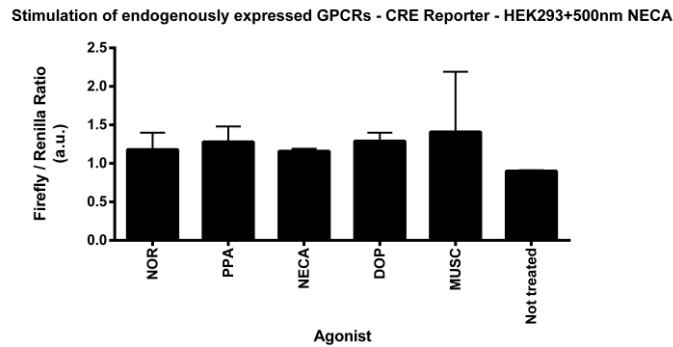


Figure 4.13 Agonist-stimulation of NECA prestimulated HEK293 cells monitored using the luciferase-based CRE reporter plasmid

All agonist stimulated HEK293 cells show Firefly/Renilla ratio values comparable with the values of HEK293 cells only pre-stimulated with 500 nm of NECA (Figure 4.15). No further CRE stimulation is recorded for any of the agonist-stimulated HEK293 cells, suggesting that HEK293 do not endogenously express sufficient levels of any Gα-i/o coupled GPCRs.

4.3.4.3 Agonist stimulation of transiently transfected full-length control GPCRs

I agonist-stimulated HEK293 transiently transfected with full-length control GPCRs after pre-stimulation with 500nM of NECA.

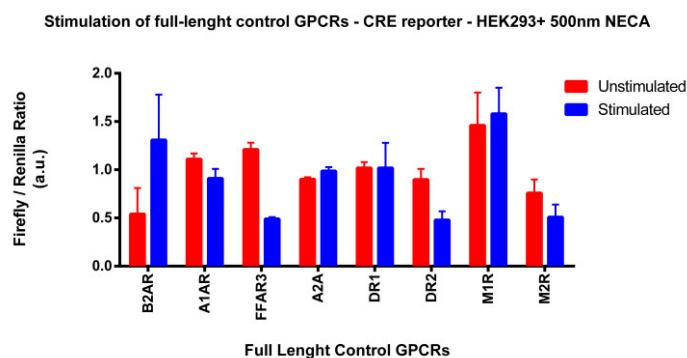


Figure 4.14 Agonist-stimulation of transiently transfected full-length control GPCRs in prestimulated HEK293 cells monitored using the luciferase-based CRE reporter plasmid

FFAR3, DR2 and M2R show lower values of Firefly/Renilla ratios in the agonist-stimulated state in comparison with the unstimulated state. These receptors are known by literature to be able to lower the amount of intracellular cAMP levels upon agonist stimulation. The FFAR3 receptor shows a strong reduction in cAMP levels that is in accordance with previously published work. All other control receptors show Firefly/Renilla ratio values comparable with the values of NECA pre-stimulated HEK293 cells.

Data shown in Figure 4.14 suggest that NECA pre-stimulation of HEK293 cells transfected with the luciferase-based CRE reporter plasmid is a valid approach to screen for decrease of intracellular level of cAMP upon agonist-stimulation of transiently transfected control GPCRs.

4.3.3.4 Light stimulation of transiently transfected light-activated control GPCRs

I light stimulated pre-stimulated HEK293 cells transiently transfected with light-activated control GPCRs.

The light-activated control GPCRs show a light-activation pattern in accordance to their respective ligand-activated receptors (Figure 4.14 vs. Figure 4.15)

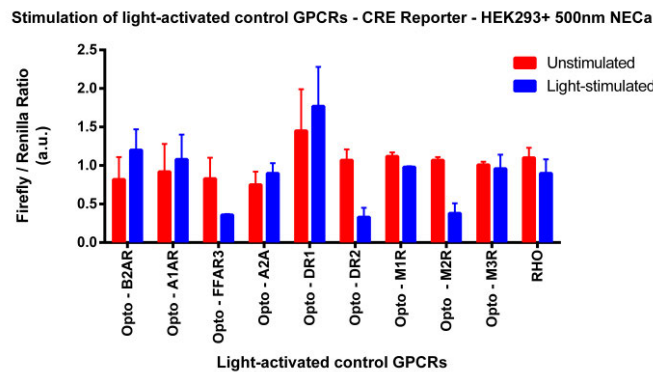


Figure 4.15 Light-stimulation of transiently transfected light-activated control GPCRs in prestimulated HEK293 cells using the luciferase-based CRE reporter

Light-activated FFAR3, D2R and M2R show a significant reduction in Firefly/Renilla ratios in the light-activated states in comparison with dark values,

while all other light-activated control GPCRs show Firefly/Renilla ratio values comparable for the in the dark and light state.

The data presented in Figure 4.14 and 4.15 show that is possible to record reduction of intracellular level of cAMP upon light-stimulation of light-sensitive control GPCRs $G\alpha$ -i/o coupled using HEK293 cells transfected with the luciferase-based CRE reporter plasmid and pre-stimulated with 500nM of NECA.

4.4 Functional screening of light-activated human Class A oGPCRs

The luciferase based reporter plasmid previously described for which I performed a full validation using both transiently transfected full-length and light-activated control GPCRs were used to set up the screening platform for all the selected 64 light-activated human Class A oGPCRs using HEK293 cells. The screening platform and the data analysis were set up following the procedure described in sections 4.2 and 4.3 of the Material and Methods. Only when not stated differently, HEK293 cells were always transfected with the Renilla plasmid for all the following described experiments.

4.4.1 CRE reporter

I transfected HEK293 cells with all 64 light-activated human Class A oGPCRs, CRE reporter. HEK293 cells were light stimulated according to procedure described in the section 3.1.1.

None of the 64 light-activated human Class A oGPCRs screened used the luciferase-based CRE reporter plasmid shows significant activity in the dark, with Firefly/Renilla ratios comparable to the ratios under dark condition of light-activated control receptors and rhodopsin shown in Figure 4.1, 4.2 and 4.3.

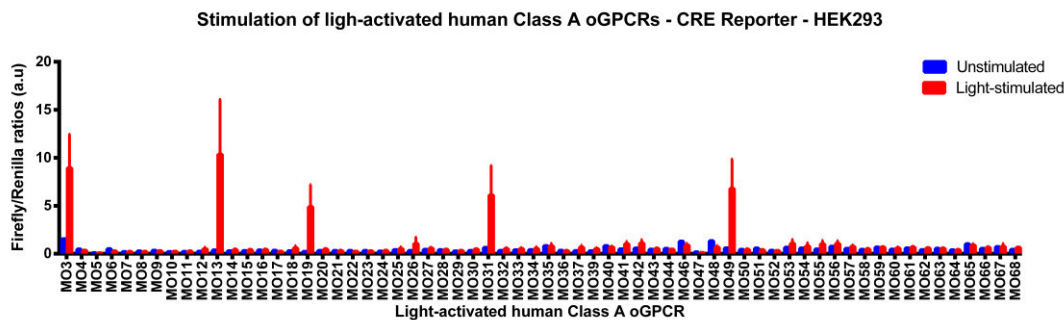


Figure 4.16 Light-stimulation of transiently transfected light-activated human Class A oGPCRs in HEK293 cells monitored using the luciferase-based CRE reporter

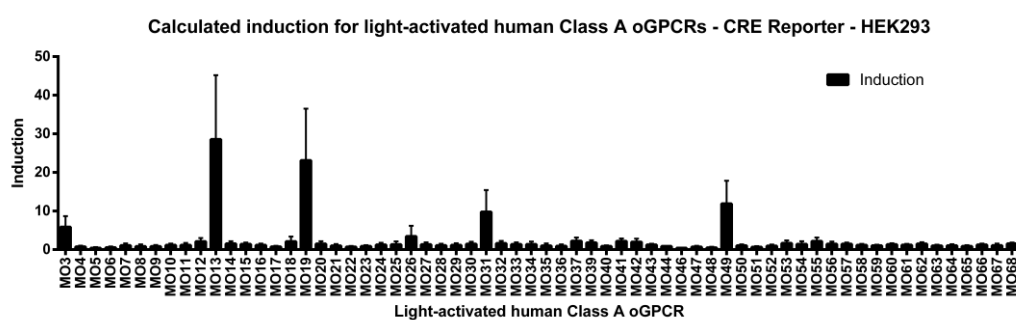


Figure 4.17 Induction values for light-stimulated human Class A oGPCRs calculated on the data collected using the luciferase-based CRE reporter

I calculated induction values from the data represented in Figure 4.16 (Figure 4.17) for all 64 light-activated human Class A oGPCRs by dividing Firefly/Renilla values after light stimulation with dark values. I set as threshold to identify strong activation from light-activated human Class A oGPCRs an induction value higher or equal to 2.5 (that implies more than a two-fold increase in the Firefly/Renilla ratio between light and dark conditions).

Six light-activated Class A oGPCRs show an induction value above the defined threshold:

Identifier	Gene Name	Induction value
MO3	Opto-GPR1	5.87
MO13	Opto-GPR21	28.55
MO19	Opto-GPR32	23.07
MO26	Opto-GPR42	3.45
MO31	Opto-GPR61	9.78

MO49	Opto-GPR135	11.89
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Table 4.8 Orphan genes for which significant light-dependent induction was measured using the luciferase-based CRE reporter

4.4.2 SRE.L reporter

I light-stimulated HEK293 cells transiently transfected with all 64 light-activated human Class A oGPCRs and the luciferase-based SRE.L reporter plasmid.

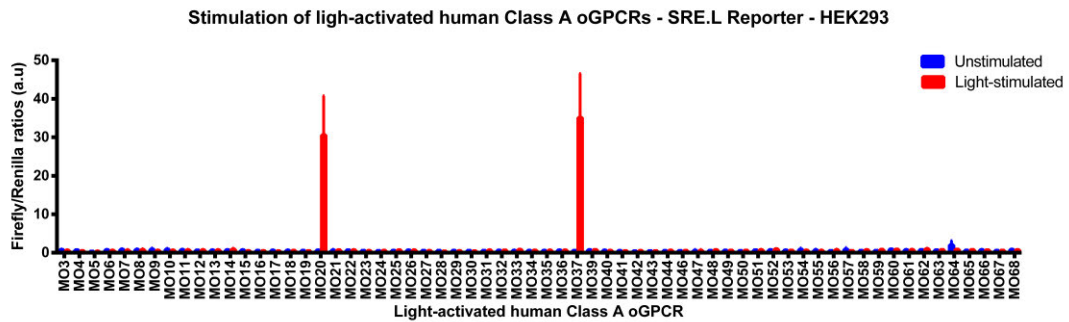


Figure 4.18 Light-stimulation of transiently transfected light-activated human Class A oGPCRs in HEK293 cells monitored using the luciferase-based SRE.L reporter

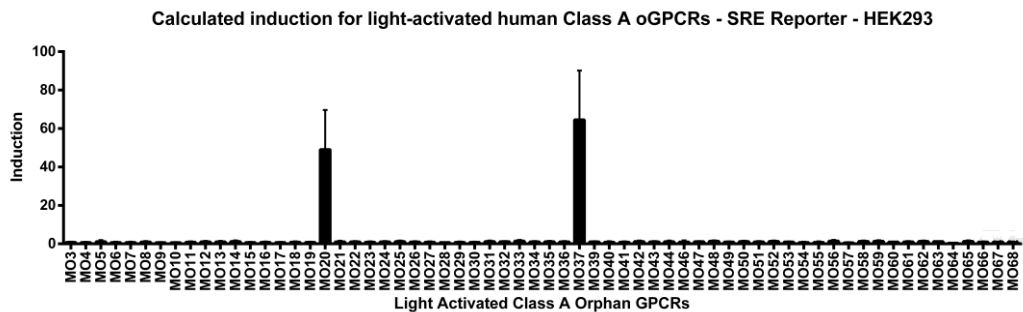


Figure 4.19 Induction values for light-stimulated human Class A oGPCRs calculated on the data collected using the luciferase-based SRE.L reporter

No light-activated human Class A oGPCRs shows significant activity in the dark, with Firefly/Renilla ratios comparable to the ratios under dark condition of light - activated control receptors and rhodopsin shown in Figure 4.7 and Figure 4.8. I calculated induction values from the data represented in Figure 4.20 for all 64 light-activated human Class A oGPCRs. I set as threshold to identify strong

activation from light-activated human Class A oGPCRs an induction value higher or equal to 2.5

Two light-activated human Class A oGPCRs show an induction value above the defined threshold, while the remaining 62 receptors do not show any significant light dependent activation:

Identifier	Gene Name	Induction value
MO20	Opto-GPR33	49.1
MO37	Opto-GPR78	64.5

Table 4.9 Orphan genes for which significant light dependent induction was measured in SRE.L reporter based screening assays

4.4.3 SRE reporter

I transfected HEK293 cells with all 64 light-activated human Class A oGPCRs, SRE reporter and Renilla luciferase plasmid. Cells were light stimulated following the procedure describe in section 3.2.1.

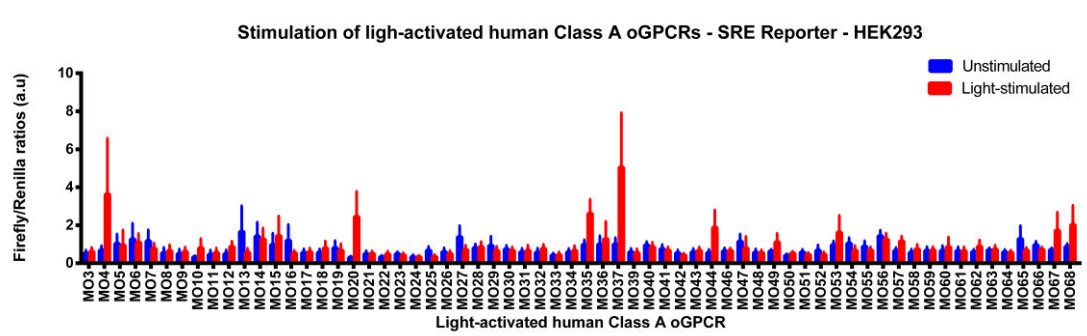


Figure 4.20 Light-stimulation of transiently transfected light-activated human Class A oGPCRs in HEK293 cells monitored using the luciferase-based SRE reporter

No light-activated chimeric orphan receptor shows significant activity in the dark, with Firefly/Renilla ratios comparable to the ratios under dark condition of light-activated control receptors and rhodopsin as shown in Figures 4.14 and 4.15 (Figure 4.20)

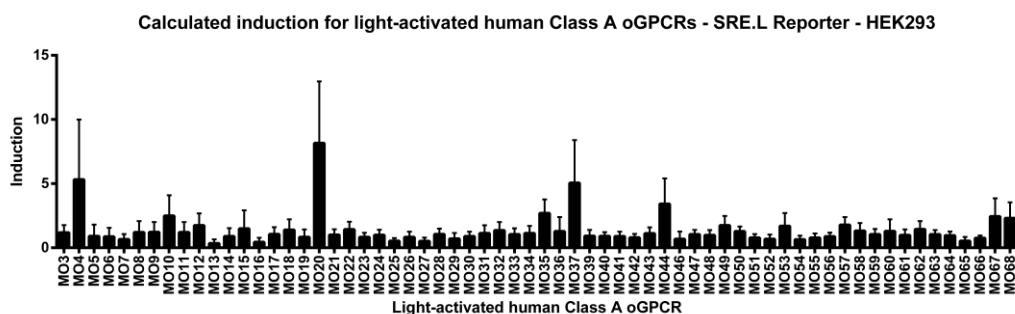


Figure 4.21 Induction values for light-stimulated human Class A oGPCRs calculated on the data collected using the luciferase-based SRE.L reporter

I calculated induction values from the data represented in Figure 4.20 (Figure 4.21) for all 64 light-activated chimeric Class A oGPCRs. I set as threshold to identify strong activation from light-activated Class A oGPCRs an induction value higher or equal to 2.5

Six light-activated human Class A oGPCRs show an induction value above the fixed threshold, while all remaining 58 GPCRs do not show any significant light dependent activation:

Identifier	Gene Name	Induction value
MO4	Opto-GPR3	5.32
MO10	Opto-GPR18	2.49
MO20	Opto-GPR33	2.69
MO35	Opto-GPR68	3.45
MO37	Opto-GPR78	5.05
MO44	Opto-GPR88	3.41

Table 4.10 Orphan genes for which significant light dependent induction was measured in SRE reporter based screening assays

4.4.4 CRE reporter plasmid and NECA prestimulation

I transfected HEK293 cells with all 64 light-activated human Class A oGPCRs. Cells were prestimulated with 500nm of NECA and then light-stimulated according to the procedure describe in section 3.2.1.

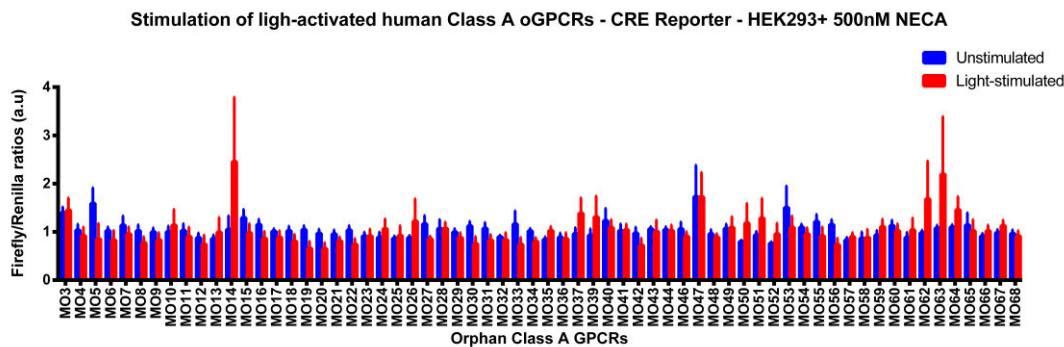


Figure 4.22 Light-stimulation of transiently transfected light-activated human Class A oGPCRs in prestimulated HEK293 cells monitored using the luciferase-based CRE reporter

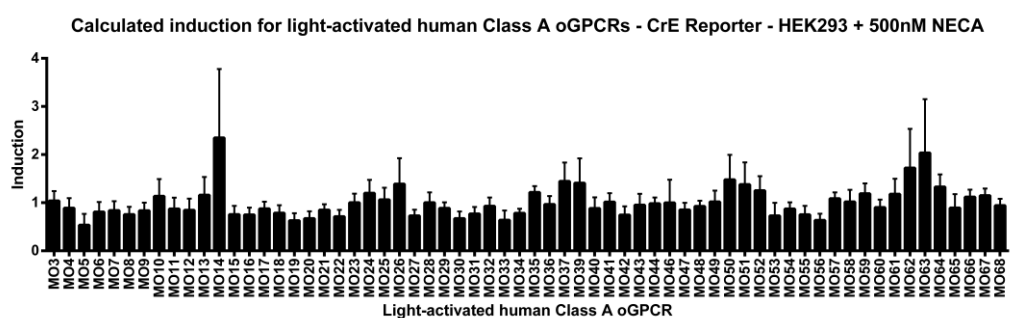


Figure 4.23 Induction values for light-stimulated human Class A oGPCRs calculated on the data collected using the luciferase-based CRE reporter after HEK293 NECA prestimulation

I calculated induction values from the data represented in Figure 4.22 for all 64 light-activated chimeric Class A oGPCRs (Figure 4.23). For this functional screening it is not possible to use the same induction threshold used for the previously described reporter plasmids. In this experimental setup, using the CRE reporter plasmid with NECA pre-stimulation, I expect a reduction in the Firefly/Renilla ratio values under light conditions in comparison with the dark values. I defined as new threshold a value of “reverse” induction (still calculated as Firefly/Renilla ratio value under light conditions divided for the same ratio under dark conditions) 0.7, which implies a minimum of 30% reduction between light and dark Firefly/Renilla ratios.

Six light-activated human Class A oGPCR show an induction value below the fixed threshold, while all the others 58 GPCRs do not show any significant light dependent decrease for intracellular cAMP levels:

Identifier	Gene Name	Induction value
MO5	Opto- GPR4	0.53
MO19	Opto- GPR32	0.63
MO20	Opto- GPR33	0.67
MO30	Opto- GPR55	0.67
MO33	Opto- GPR63	0.63
MO56	Opto- GPR150	0.64

Table 3.11 Orphan genes for which significant light dependent induction was measured in NECA prestimulated CRE reporter based screening assays

4.5 Antibody staining of all 64 light-activate human Class A oGPCRs

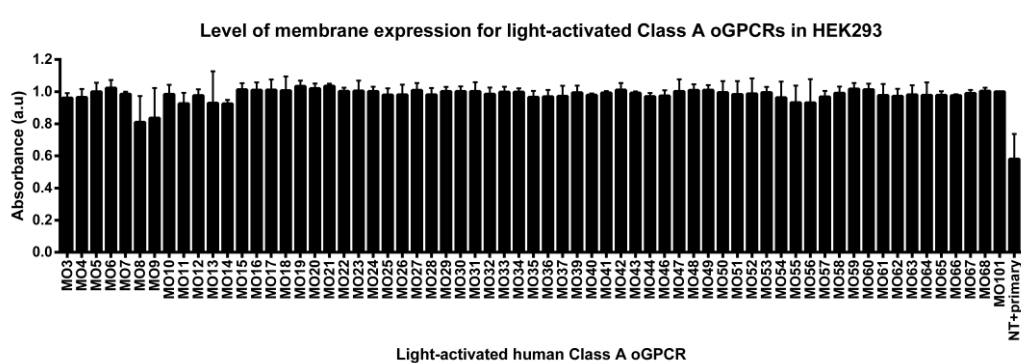


Figure 4.24 Absorbance normalized by the value of Rhodopsin (MO101) for the 64 light-activated Class A oGPCRs I transfected HEK293 cells with all 64 light-activated human Class A oGPCRs and bovine rhodopsin. Cells were light stimulated and later stained with an anti-VSVG antibody (see section 3.1) following the procedure described in section 3.3.

Absorbance values normalized for Rhodopsin (indicated with MO101 in Figure 4.24) for all 64 light-activated human Class A oGPCRs show significant transient expression in light stimulated HEK293 cells. The fixation technique used allows me to consider the absorbance values shown in figure 4.24 for all 64 light-activated human Class A oGPCRs has to be related mostly to expression of the light-activated human Class A oGPCRs on the cell membrane.

All 64 light-activated human chimeric human Class A oGPCRs show significant level of membrane expression in comparison with the positive control

rhodopsin, with the exception of Opto-GPR12 and Opto-GPR15 that show a lower but yet still significant expression level in comparison with expression level of rhodopsin and the negative control.

4.6 Validation of G-Protein coupling prediction algorithms

I used the PREDCOUPLE, PREDCOUPLE2 and GRIFFIN prediction algorithms to study in silico the predicted coupling of 64 light-activated human Class A oGPCRs chosen for this study, their corresponding complete orphan sequences and ligand and light-activated control GPCRs.

The first criterion I adopted to validate each single algorithm was the agreement between the predicted coupling for the control GPCRs and the coupling reporter by literature and the experiment I performed using Luciferase based reporter plasmids.

Secondly, I considered the agreement between the predicted couplings for the full-length 64 human Class A oGPCRs I selected for this work and their respective light-activated chimeric genes. According to the hypothesis on which my screening using chimeric receptor is based and according to the data shown for control GPCRs, the coupling between full-length GPCRs and their respective chimeric receptor has to be the same.

As third criterion I consider the overall agreement between the three different algorithms I used to study the coupling of orphan and control GPCRs. Although based on different mathematical and statistical approaches, the outcome for the predicted coupling for control GPCRs and oGPCRs in both their ligand and light-activated form should be algorithm independent.

4.6.1 Validation of the GRIFFIN algorithm

4.6.1.1 Full-length control GPCRs

I run the Griffin algorithm with the sequence of the full-length control GPCRs described in table 4.6 in order to estimate the algorithm performance with GPCRs for which coupling properties are already known.

Control Receptor	Predominant G. coupling(experimental)	Predicted G. Coupling
β 2 adrenergic receptor (β 2AR)	G α -s	G α -s
α 1 adrenergic receptor (α 1AR)	G α -q	G α -q
Free fatty acid receptor 3 (FFR3)	G α -i/o	G α -i/o
Adenosine A2A receptor (A2AR)	G α -s	G α -s
Dopamine receptor D1 (D1R)	G α -s	G α -s
Dopamine receptor D2 (D2R)	G α -i/o	G α -i/o
Muscarinic acetylcholine receptor M1 (M1R)	G α -q and G α -s	G α -q and G α -s
Muscarinic acetylcholine receptor M2 (M2R)	G α -i/o	G α -i/o
Muscarinic acetylcholine receptor M3 (M3R)	G α -q	G α -q

Table 4.12 Predicted G-Protein coupling for full-length control GPCRs according to the GRIFFIN algorithm

The Griffin algorithm scored a 9/9 of correct predictions when analyzing sequences of full-length control GPCRs, showing that is able to predict correct coupling when analyzing entire sequences of GPCRs genes.

4.6.1.2 Light-activated control GPCRs

I run the GRIFFIN algorithm on the sequences of the light-activated control GPCRs to check if the algorithm is able to predict the correct coupling of chimeric GPCRs for which I have proved preservation of coupling properties in the experiment described in section 4.3.1.3, 4.3.2.3, 4.3.3.4.

Light-activated control Receptor	Predominant G coupling (experimental)	Predicted G. Coupling
β 2 adrenergic receptor (β 2AR)	G α -s	G α -t1/2
α 1 adrenergic receptor (α 1AR)	G α -q	G α -t1/2
Free fatty acid receptor 3 (FFR3)	G α -i/o	G α -t1/2

Adenosine A2A receptor (A2AR)	G α -s	G α -t1/2
Dopamine receptor D1 (D1R)	G α -s	G α -t1/2
Dopamine receptor D2 (D2R)	G α -i/o	G α -t1/2
Muscarinic acetylcholine receptor M1 (M1R)	G α -q and G α -s	G α -t1/2
Muscarinic acetylcholine receptor M2 (M2R)	G α -i/o	G α -t1/2
Muscarinic acetylcholine receptor M3 (M3R)	G α -q	G α -t1/2

Table 4.13 Predicted G-Protein coupling for full-length control GPCRs according to the GRIFFIN algorithm

The Griffin algorithm scored a 0/9 of positive result when predicting G-Protein coupling for light-activated control GPCRs. All light-activated control GPCRS are predicted to be coupled to G α -t1/2 that is the G-Protein mediated pathway activated by rhodopsin.

This result suggests that the GRIFFIN algorithm is not able to distinguish between bovine rhodopsin and chimeric receptor for which bovine rhodopsin constitute the majority of their sequences.

4.6.1.3 Human Class A oGPCRs

I run the GRIFFIN algorithm on all 64 Human Class A oGPCRs both on their full sequences and in their respective light-activated version.

Gene name	Identifier	Full-length predicted coupling	Light-activated predicted coupling
GPR1	MO3	G α -q	G α -t1/2
GPR3	MO4	G α -s	G α -t1/2
GPR4	MO5	G α -q	G α -t1/2
GPR6	MO6	G α -s	G α -t1/2
GPR12	MO7	G α -s	G α -t1/2
GPR15	MO8	G α -q	G α -t1/2
GPR17	MO9	G α -q	G α -t1/2

GPR18	MO10	Gα-q	Gα-t1/2
GPR19	MO11	Gα-i/o	Gα-t1/2
GPR20	MO12	Gα-q	Gα-t1/2
GPR21	MO13	Gα-i/o	Gα-t1/2
GPR22	MO14	Gα-i/o	Gα-t1/2
GPR25	MO15	Gα-q	Gα-t1/2
GPR26	MO16	Gα-i/o	Gα-t1/2
GPR27	MO17	Gα-q	Gα-t1/2
GPR31	MO18	Gα-i/o	Gα-t1/2
GPR32	MO19	Gα-s	Gα-t1/2
GPR33	MO20	Gα-q	Gα-t1/2
GPR34	MO21	Gα-s	Gα-t1/2
GPR35	MO22	Gα-s	Gα-t1/2
GPR37	MO23	Gα-q	Gα-t1/2
GPR37L1	MO24	Gα-s	Gα-t1/2
GPR39	MO25	Gα-q	Gα-t1/2
GPR42	MO26	Gα-q	Gα-t1/2
GPR45	MO27	Gα-i/o	Gα-t1/2
GPR50	MO28	Gα-s	Gα-t1/2
GPR52	MO29	Gα-i/o	Gα-t1/2
GPR55	MO30	Gα-q	Gα-t1/2
GPR61	MO31	Gα-s	Gα-t1/2
GPR62	MO32	Gα-i/o	Gα-t1/2
GPR63	MO33	Gα-i/o	Gα-t1/2
GPR65	MO34	Gα-q	Gα-t1/2
GPR68	MO35	Gα-q	Gα-t1/2
GPR75	MO36	Gα-s	Gα-t1/2
GPR78	MO37	Gα-i/o	Gα-t1/2
GPR82	MO39	Gα-q	Gα-t1/2
GPR83	MO40	Gα-q	Gα-t1/2
GPR84	MO41	Gα-s	Gα-t1/2

GPR85	MO42	Gα-q	Gα-t1/2
GPR87	MO43	Gα-q	Gα-t1/2
GPR88	MO44	Gα-q	Gα-t1/2
GPR119	MO46	Gα-s	Gα-t1/2
GPR120	MO47	Gα-q	Gα-t1/2
GPR132	MO48	Gα-i/o	Gα-t1/2
GPR135	MO49	Gα-i/o	Gα-t1/2
GPR139	MO50	Gα-s	Gα-t1/2
GPR141	MO51	Gα-s	Gα-t1/2
GPR142	MO52	Gα-s	Gα-t1/2
GPR146	MO53	Gα-s	Gα-t1/2
GPR148	MO54	Gα-s	Gα-t1/2
GPR149	MO55	Gα-s	Gα-t1/2
GPR150	MO56	Gα-s	Gα-t1/2
GPR151	MO57	Gα-s	Gα-t1/2
GPR152	MO58	Gα-s	Gα-t1/2
GPR153	MO59	Gα-q	Gα-t1/2
GPR160	MO60	Gα-s	Gα-t1/2
GPR161	MO61	Gα-s	Gα-t1/2
GPR162	MO62	Gα-q	Gα-t1/2
GPR171	MO63	Gα-q	Gα-t1/2
GPR173	MO64	Gα-s	Gα-t1/2
GPR174	MO65	Gα-s	Gα-t1/2
GPR176	MO66	Gα-s	Gα-t1/2
GPR182	MO67	Gα-q	Gα-t1/2
GPR183	MO68	Gα-q	Gα-t1/2

Table 4.14 Coupling prediction for 64 human Class A oGPCRs in their full-length and light-activated forms according to the GRIFFIN algorithm

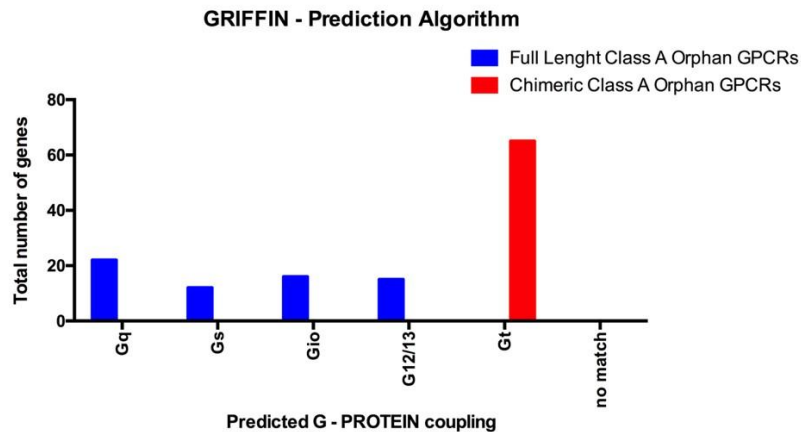


Figure 4.25 Predicted G-Protein coupling for 64 full-length and relative light-activated human Class A oGPCRs according to the Griffing Algorithm.

The GRIFFIN algorithm is able to predict a possible coupling for all 64 full-length human Class A oGPCRs sequences, while all respective light-activated version is predicted to be Gα-t1/2 coupled, as already shown in the previous section for light-activated control GPCRs.

This result confirm that the GRIFFIN algorithm is not sensitive enough to predict a reasonable coupling for light-activated chimeric receptor for which has been shown conservation of coupling properties (like in the case of light-activated control GPCRs) and to distinguish between rhodopsin based chimeric receptor and rhodopsin itself.

4.6.2 Validation of the PREDCOUPLE algorithm

4.6.2.1 Full-length control GPCRs

I run the PREDCOUPLE algorithm with the sequences of the full-length control GPCRs described in Table 3.6 in order to estimate the algorithm performance with full-length GPCRs for which coupling properties are already known.

Control Receptor	Predominant G-coupling (Experimental)	Predicted G-Coupling
β2 adrenergic receptor (β2AR)	Gα-s	Gα-s
α1 adrenergic receptor (α1AR)	Gα-q	Gα-q
Free fatty acid receptor 3 (FFR3)	Gα-i/o	Gα-i/o
Adenosine A2A receptor	Gα-s	Gα-s

(A2AR)		
Dopamine receptor D1 (D1R)	Gα-s	Gα-s
Dopamine receptor D2 (D2R)	Gα-i/o	Gα-i/o
Muscarinic acetylcholine receptor M1 (M1R)	Gα-q and Gα-s	Gα-q
Muscarinic acetylcholine receptor M2 (M2R)	Gα-i/o	Gα-i/o
Muscarinic acetylcholine receptor M3 (M3R)	Gα-q	Gα-q

Table 4.14 Predicted G-Protein coupling for full-length control GPCRs according to the PREDCOUPLE algorithm

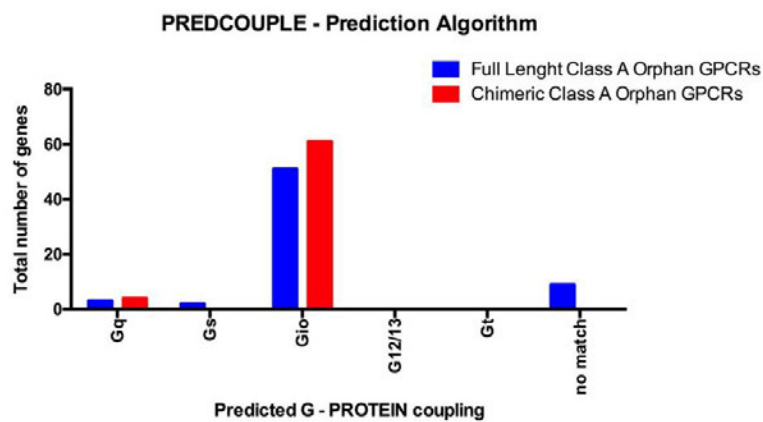


Figure 4.26 Predicted G-Protein coupling for 64 full-length and relative light-activated human Class A oGPCRs according to the PREDCOUPLE Algorithm.

The PREDCOUPLE algorithm scored a 9/9 of correct predictions when analyzing sequences of full-length control GPCRs, showing that is able to predict correct coupling when analyzing entire sequences of GPCRs genes.

4.6.2.2 Light-activated control GPCRs

I run the PREDCOUPLE algorithm on the sequences of the light-activated control GPCRs to check if the algorithm is able to predict the correct coupling of chimeric GPCRs for which I have proved preservation of coupling properties in the experiment described in section 4.3

Light-activated control Receptor	Predominant G coupling (experimental)	Predicted G. Coupling
β2 adrenergic receptor (β2AR)	Gα-s	Gα-s

α 1 adrenergic receptor (α 1AR)	G α q	G α -q
Free fatty acid receptor 3 (FFR3)	G α -i/o	G α -i/o
Adenosine A2A receptor (A2AR)	G α -s	G α -s
Dopamine receptor D1 (D1R)	G α s	G α -s
Dopamine receptor D2 (D2R)	G α -i/o	G α -i/o
Muscarinic acetylcholine receptor M1 (M1R)	G α -q and G α -s	G α -q
Muscarinic acetylcholine receptor M2 (M2R)	G α -i/o	G α -i/o
Muscarinic acetylcholine receptor M3 (M3R)	G α -q	G α -q

Table 4.15 Predicted G-Protein coupling for full-length control GPCRs according to the PREDCOUPLE algorithm

The PREDCOUPLE algorithm scored a 9/9 of positive result when predicting G-Protein coupling for light-activated control GPCRs. All light-activated control GPCRS are predicted to be coupled equivalently to their full-length respective genes and in accordance to what I proved with the experiment described in section

This result prove that the PREDCOUPLE algorithm is able to predict correctly coupling of light-activated control GPCRs and therefore to distinguish such receptor from bovine rhodopsin.

4.6.2.3 Human Class A oGPCRs

I run the PREDCOUPLE algorithm on all 64 human Class A oGPCRs both on their full sequences and their respective light-activated version

Gene name	Identifier	Full-length predicted coupling	Light-activated predicted coupling
GPR1	MO3	no match	G α -i/o
GPR3	MO4	G α -i/o	G α -i/o
GPR4	MO5	G α -i/o	G α -i/o

GPR6	MO6	Gα-i/o	Gα-i/o
GPR12	MO7	Gα-i/o	Gα-i/o
GPR15	MO8	Gα-i/o	Gα-i/o
GPR17	MO9	Gα-i/o	Gα-i/o
GPR18	MO10	Gα-i/o	Gα-i/o
GPR19	MO11	Gα-i/o	Gα-i/o
GPR20	MO12	Gα-i/o	Gα-i/o
GPR21	MO13	Gα-s	Gα-i/o, Gα-q
GPR22	MO14	Gα-i/o	Gα-i/o
GPR25	MO15	Gα-i/o	Gα-i/o
GPR26	MO16	Gα-i/o	Gα-i/o
GPR27	MO17	Gα-i/o	Gα-i/o
GPR31	MO18	Gα-i/o	Gα-i/o
GPR32	MO19	Gα-i/o	Gα-i/o
GPR33	MO20	Gα-i/o	Gα-i/o
GPR34	MO21	Gα-i/o	Gα-i/o
GPR35	MO22	Gα-i/o	Gα-i/o, Gα-q
GPR37	MO23	Gα-i/o	Gα-i/o
GPR37L1	MO24	Gα-i/o	Gα-i/o
GPR39	MO25	Gα-i/o	Gα-i/o
GPR42	MO26	Gα-i/o	Gα-i/o
GPR45	MO27	Gα-i/o	Gα-i/o
GPR50	MO28	Gα-q, Gα-i/o, Gα-s	Gα-q
GPR52	MO29	Gα-i/o	Gα-i/o
GPR55	MO30	Gα-i/o	Gα-i/o
GPR61	MO31	Gα-i/o	Gα-i/o
GPR62	MO32	Gα-i/o	Gα-i/o
GPR63	MO33	Gα-i/o	Gα-i/o
GPR65	MO34	Gα-i/o	Gα-i/o
GPR68	MO35	Gα-i/o	Gα-i/o
GPR75	MO36	no match	Gα-i/o
GPR78	MO37	Gα-i/o	Gα-i/o
GPR82	MO39	Gα-i/o	Gα-i/o
GPR83	MO40	Gα-i/o, Gα-q	Gα-i/o
GPR84	MO41	Gα-i/o	Gα-i/o
GPR85	MO42	Gα-s	Gα-i/o
GPR87	MO43	Gα-i/o	Gα-i/o
GPR88	MO44	Gα-i/o	Gα-i/o
GPR101	MO45	Gα-i/o	Gα-i/o
GPR119	MO46	Gα-i/o	Gα-i/o
GPR120	MO47	Gα-i/o	Gα-i/o
GPR132	MO4	Gα-i/o	Gα-i/o
GPR135	MO49	Gα-q	Gα-i/o, Gα-q
GPR139	MO50	Gα-i/o	Gα-i/o
GPR141	MO51	Gα-q, Gα-i/o	Gα-i/o, Gα-q

GPR142	MO52	no match	Gα-i/o
GPR146	MO53	no match	Gα-i/o
GPR148	MO54	no match	Gα-i/o
GPR149	MO55	Gα-i/o	Gα-i/o
GPR150	MO56	Gα-i/o	Gα-i/o
GPR151	MO57	no match found	Gα-i/o
GPR152	MO58	Gα-i/o	Gα-i/o
GPR153	MO59	probable no gpcr	Gα-i/o
GPR160	MO60	Gα-i/o	Gα-i/o
GPR161	MO61	no match	Gα-i/o
GPR162	MO62	no match	Gα-i/o
GPR171	MO63	Gα-i/o	Gα-i/o
GPR173	MO64	Gα-i/o	Gα-i/o
GPR174	MO65	Gα-i/o	Gα-i/o
GPR176	MO66	Gα-i/o	Gα-i/o
GPR182	MO67	Gq	Gα-i/o
GPR183	MO68	no match	Gα-i/o

Table 4.16 Predicted G-Protein coupling for full-length control GPCRs according to the PREDCOUPLE algorithm

The PREDCOUPLE algorithm is not able to predict a possible G-Protein coupling for 8 out of 64 for full-length human Class A oGPCRs, while a possible coupling is always predicted for all 64 light-activated oGPCRs.

Out of 64 human Class A oGPCRs genes, the PREDCOUPLE algorithm show no agreement between the predicted coupling for full-length oGPCR and light-activated oGPCR genes in 14 cases.

The agreement between the full-length and light-activated oGPCRs genes predicted coupling can be explained by noticing that most of the genes are in both cases predicted to couple one single G-protein mediated pathways, Gα-i/o.

4.6.3 Validation of the PREDCOUPLE2 algorithm

4.6.3.1 Full-length control GPCRs

I run the PREDCOUPLE2 algorithm with the sequences of the full-length control GPCRs described in table 3.6 in order to estimate the algorithm performance with full-length GPCRs for which coupling properties are already known.

Control Receptor	Predominant G-coupling (Experimental)	Predicted G-Coupling
β 2 adrenergic receptor (β 2AR)	G α -s	G α -s
α 1 adrenergic receptor (α 1AR)	G α -q	G α -q
Free fatty acid receptor 3 (FFR3)	G α -i/o	G α -i/o
Adenosine A2A receptor (A2AR)	G α -s	G α -s
Dopamine receptor D1 (D1R)	G α -s	G α -s
Dopamine receptor D2 (D2R)	G α -i/o	G α -i/o
Muscarinic acetylcholine receptor M1 (M1R)	G α -q and G α -s	G α -q
Muscarinic acetylcholine receptor M2 (M2R)	G α -i/o	G α -i/o
Muscarinic acetylcholine receptor M3 (M3R)	G α -q	G α -q

Table 4.17 Predicted G-Protein coupling for full-length control GPCRs according to the PREDCOUPLE2 algorithm

The PREDCOUPLE2 algorithm scored a 9/9 of correct predictions when analyzing sequences of full-length control GPCRs, showing that is able to predict correct coupling when analyzing entire sequences of GPCRs genes.

4.6.3.2 Light-activated control GPCRs

I run the PREDCOUPLE2 algorithm on the sequences of the light-activated control GPCRs to check if the algorithm is able to predict the correct coupling of chimeric GPCRs for which I have proved preservation of coupling properties in the experiment described in section 4.3.

Light-activated control Receptor	Predominant G-coupling (Experimental)	Predicted G-Coupling
β 2 adrenergic receptor (β 2AR)	G α -s	G α -s
α 1 adrenergic receptor (α 1AR)	G α -q	G α -q
Free fatty acid receptor 3 (FFR3)	G α -i/o	G α -i/o
Adenosine A2A receptor (A2AR)	G α -s	G α -s
Dopamine receptor D1 (D1R)	G α -s	G α -s
Dopamine receptor D2 (D2R)	G α -i/o	G α -i/o
Muscarinic acetylcholine receptor M1 (M1R)	G α -q and G α -s	G α -q
Muscarinic acetylcholine receptor	G α -i/o	G α -i/o

M2 (M2R)		
Muscarinic acetylcholine receptor M3 (M3R)	Gα-q	Gα-q

Table 4.18 Predicted G-Protein coupling for full-length control GPCRs according to the PREDCOUPLE2 algorithm

The PREDCOUPLE2 algorithm scored a 9/9 of positive result when predicting G-Protein coupling for light-activated control GPCRs. All light-activated control GPCRS are predicted to be coupled equivalently to their full-length respective genes and in accordance to what I proved with the experiment described in section 4.3.

This result prove that the PREDCOUPLE2 algorithm is able to predict correctly coupling of light-activated control GPCRs and therefore to distinguish such receptor from bovine rhodopsin.

4.6.3.3 Human Class A oGPCRs

I run the PREDCOUPLE2 algorithm on all 64 human Class A oGPCRs both on their full sequences and in their respective light activated version.

Gene name	Identifier	Full-length predicted coupling	Light-activated predicted coupling
GPR1	MO3	Gα-q, Gα-i/o	Gio, Gα-q
GPR3	MO4	Gα-s, Gio	Gα-q, Gio
GPR4	MO5	Gio	Gio
GPR6	MO6	Gα-s	Gio, Gα-q, Gα-s
GPR12	MO7	Gα-s, Gio	Gα-q, Gio, Gα-s
GPR15	MO8	Gio, Gα-q, Gα-12/13	Gio, Gα-q, Gα-12/13
GPR17	MO9	Gio	Gio
GPR18	MO10	Gio	Gα-q, Gio
GPR19	MO11	Gα-q, Gio	Gα-q, Gio
GPR20	MO12	Gα-q, Gα-12/13, Gs	Gα-s, Gio
GPR21	MO13	Gio, Gα-s	Gio
GPR22	MO14	Gio, Gα-s, Gα-12/13	Gio
GPR25	MO15	Gio, Gα-12/13	Gio
GPR26	MO16	Gio, Gα-q	Gio, Gα-s
GPR27	MO17	Gio, Gα-q	Gio, Gα-q
GPR31	MO18	Gio	Gio

GPR32	MO19	Gio, Gα-q	Gio, Gα-q
GPR33	MO20	Gα-q	Gα-q, Gio
GPR34	MO21	Gio, Gα-q	Gio
GPR35	MO22	Gα-q, Gα-12/13, Gio	Gα-q, Gα-12/13, Gio
GPR37	MO23	Gα-q, Gαio, Gas	Gα-q, Gαio
GPR37L1	MO24	Gio, Gα-s	Gio, Gα-q
GPR39	MO25	Gα-q	Gio, Gα-q
GPR42	MO26	Gio, Gα-q	Gio
GPR45	MO27	Gio	Gio, Gα-q
GPR50	MO28	Gio, Gα-s	Gio, Gα-s
GPR52	MO29	Gio, Gα-q	Gio
GPR55	MO30	Gio, Gα-q	Gio, Gα-q
GPR61	MO31	Gα-s, Gio	Gα-s, Gio
GPR62	MO32	Gα-s, Gα-q, Gα-12/13	Gio, Gα-s
GPR63	MO33	Gio, Gα-q	Gα-q, Gio
GPR65	MO34	Gio, Gα-q	Gα-q, Gio
GPR68	MO35	Gio	Gio
GPR75	MO36	Gio	Gio
GPR78	MO37	Gα-s, Gα-q	Gio, Gα-s
GPR82	MO39	Gα-q, Gio, Gα-12/13	Gα-q, Gio
GPR83	MO40	Gio, Gα-q	Gio, Gα-q
GPR84	MO41	Gio, Gα-s, Gα-12/13	Gio
GPR85	MO42	Gio, Gα-q	Gio
GPR87	MO43	Gio, Gα-q	Gio, Gα-q
GPR88	MO44	Gα-s, Gio	Gio, Gα-s
GPR119	MO46	Gio, Gα-q	Gio, Gα-q, Gα-12/13
GPR120	MO47	Gα-q, Gα-12/13, Gα-s, Gio	all - nothing
GPR132	MO4	Gio, Gq	Gα-q, Gio, Gα-s
GPR135	MO49	Gα-io, Gα-q	Gα-q, Gio
GPR139	MO50	no match	Gα-q, Gio
GPR141	MO51	Gα-q, Gio	Gio, Gα-q, Gα-12/13
GPR142	MO52	Gα-q, Gio, Gα-12/13, Gα-s	Gio
GPR146	MO53	Gio, Gα-q, Gα-12/13	Gα-q, Gio
GPR148	MO54	Gio	Gio
GPR149	MO55	Gio	Gio, Gα-q
GPR150	MO56	Gio, Gα-q, Gα-s	Gio
GPR151	MO57	Gio	Gio, Gα-s
GPR152	MO58	Gio	Gio
GPR153	MO59	probable no gpcr	Gio, Gα-q
GPR160	MO60	Gio, Gα-q	Gio
GPR161	MO61	Gio	Gio
GPR162	MO62	Gα-q, Gio	Gα-q, Gio
GPR171	MO63	Gα-q, Gio, Gα-12/13	Gio, Gα-q, Gα-12/13
GPR173	MO64	Gα-q, Gio, Gα-s	Gα-q, Gio
GPR174	MO65	Gio, Gα-q	Gio, Gα-q

GPR176	MO66	Gα-s	Gio, Gα-q, Gα-s
GPR182	MO67	Gα-q, Gio, Gα-12/13	Gα-q, Gio, Gα-12/13
GPR183	MO68	Gα-q, Gio	Gio, Gα-q

Table 4.19 Predicted G-Protein coupling for 64 human Class A human oGPCRs in their full-length and light-activated form according to the PREDCOUPLE2 algorithm

The PREDCOUPLE2 algorithm is able to predict a possible G-Protein coupling for all 64 full-length and light-activated orphan GPCRs.

Out of 64 human Class A oGPCRs genes, the PREDCOUPLE algorithm show no agreement between the predicted coupling for full-length oGPCR and light-activated oGPCR genes in 11 cases.

The agreement between the full-length and light-activated oGPCRs genes predicted coupling is helped by the ability of the PREDCOUPLE2 algorithm to propose more than one single possible pathways.

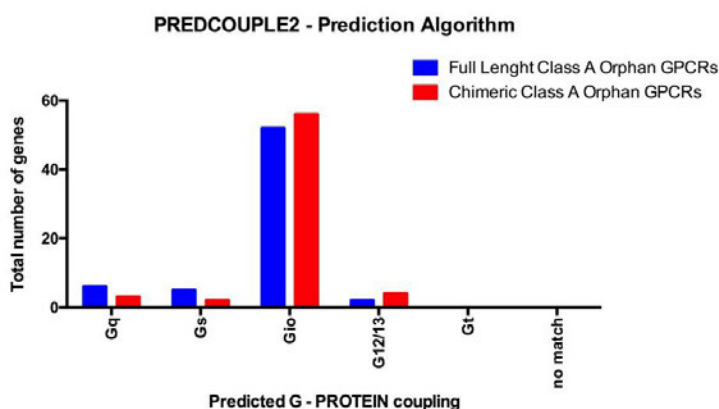


Figure 4.27 Predicted G-Protein coupling for 64 full-length and relative light-activated human Class A oGPCRs according to the Predcouple2 Algorithm

4.6.4 Comparison between the different algorithms

I defined for each control and oGPCRs in both full-length and light-activated chimeric form the agreement between the predicted couplings between different algorithms as the superposition between the predicted couplings for the two most probable pathways.

In the case of full-length control GPCRs, there is full agreement both considering only the most probable pathways and the two most probable

pathways considering PREDCOUPLE vs GRIFFIN and PREDCOUPLE2 vs GRIFFIN.

In the case of the light-activated control GPCRs, there is no agreement between the PREDCOUPLE, PREDCOUPLE 2 and GRIFFIN, and this due to the fact that for the GRIFFIN algorithm all light-activated chimeric receptors (control and oGPCRs) are considered to conserve the coupling properties of rhodopsin.

I did not perform the agreement analysis between the PREDCOUPLE and the PREDCOUPLE 2 being two different version of the same algorithm, and thus a strong agreement between the predicted couplings of these two algorithm would be less significant.

In Figure 4.27 and 4.28 the number of positive coupling (superposition between the different algorithms) considering only the main predicted pathways and negative coupling (no superposition between the different algorithms) are shown for PREDCOUPLE vs GRIFFIN and PREDCOUPLE2 vs. GRIFFIN for the full-length 64 human Class A oGPCRs.

In the case of PREDCOUPLE vs GRIFFIN there is high disagreement between the predicted couplings for full-length oGPCRs both considering only the main predicted pathways or the two most probable. This disagreement is present also when comparing PREDCOUPLE2 vs GRIFFIN, although in the case of the PREDCOUPLE vs GRIFFIN, I got more positive than negative coupling.

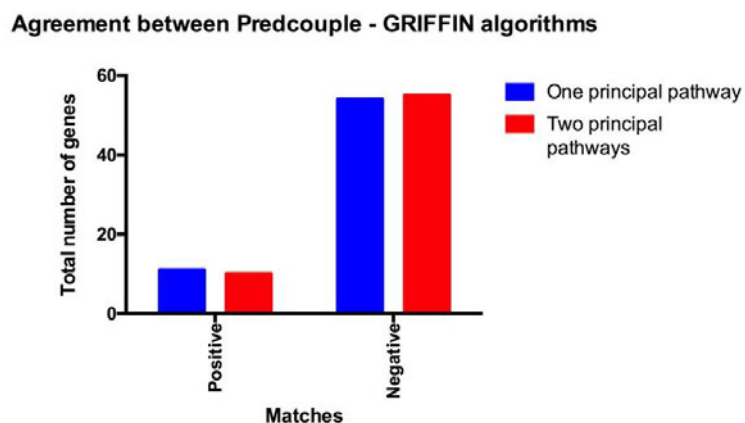


Figure 4.28 Number of positive and negative matches between the Predcouple and Griffin Algorithms for principal and first two principal predicted G-Protein coupling for 64 full-length and relative light-activated human Class A oGPCRs

Agreement between Predcouple2 - GRIFFIN algorithms

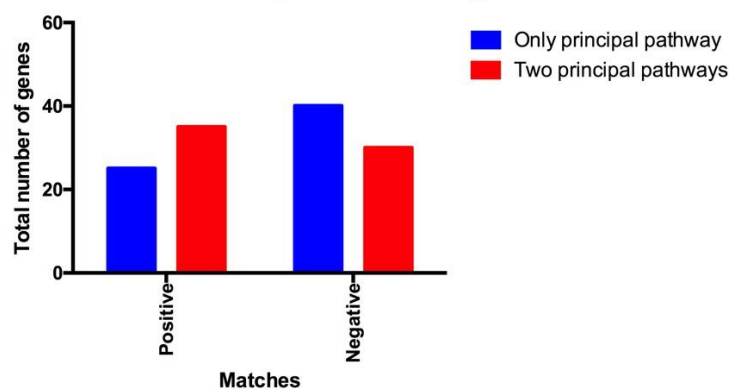


Fig 4.29 Number of positive and negative matches between the Predcouple and Griffin Algorithms for principal and first two principal predicted G-Protein coupling for 65 full-length and relative light-activated chimeric Class A oGPCRs

5 - Discussion

Orphan GPCRs (oGPCRs) represent a valuable target in drug discovery due to their proven and potential role in many diseases. Till now, exploiting of oGPCRs in drug development was limited by the insufficient amount of information about these receptors, including limited knowledge about their signaling and structural properties.

Notably, in some cases non signaling functions or ligand independent functions have been proposed for oGPCRs, but it still remains a question about if and what signaling cascades these receptors activate once stimulated by an agonist.

I have shown that the chimeric approach is a new approach to increase the amount of information available about the functional and signaling properties of orphan GPCRs and guide drug discovery into exploring new possible therapeutic approaches.

Although the design of chimeric GPCRs has been largely focused in the last 15 years on the study their molecular functions, this approach has been limited by the lack of a systematic protocol in order to design, clone and test large libraries of chimeric receptors. Also, the limited amount of data about the functionality of chimeric GPCRs has brought doubts about the validity of the domain swapping dogma and more generally on the idea that GPCRs can be considered as receptors in which the ligand interaction and the signal transduction are two related independent processes. Also, for the large number of chimeric GPCRs engineered in the past, a platform for a complete screening of all G-Protein mediated signaling pathways was missing, leaving the concern that functional chimeric GPCRs might show original unwanted coupling properties in comparison with their full-length receptors. In this work I demonstrated that such a systematic approach to the design, clone and screen large libraries of chimeric receptors is possible.

Indeed, the “chimeric algorithm” described in this thesis allows creating libraries of chimeric GPCRs in a step-by-step process from sequence retrieval till the generation of the synthetic genes.

The gene reporter system based on the use of luciferase-based reporter plasmids allowed screening for several G-Protein mediated pathways for a large number of chimeric receptor at the same time. For all G-Protein mediated pathways different methods are currently available. However, they have the inconvenient of being based on different readouts. This implies that, while screening for activation of different G-Protein pathways, results coming from different assays cannot be easily compared.

The testing platform build on the use of luciferase based gene reporter plasmids has the unique advantage of unifying in one single output signals coming from different signaling pathways. In fact, one of the main problems when screening large libraries of receptors that can activate different signaling pathways, such as GPCRs, is comparing results coming from different screening systems.

The reliability of the luciferase-based assays is testified by the results on ligand-activated control GPCRs, which show activation pattern in accordance with previously available data, implying that the platform is able to correctly detect and distinguish G-Protein mediated signaling pathways.

The reliability of the “chimeric algorithm” is testified by the results achieved with the testing of the light-activated control GPCRs library.

Light-activated version of full-length control GPCRs designed following the “chimeric algorithm” show intact functionality and specificity, excluding most of the concern regarding the generation of chimeric GPCRs such as loss of functionality or creation/deletion of signaling cascades.

The cloning approach based on the design of a common mother construct for the creation of all genes of a synthetic library can be translated for application with any other GPCRs, such as GPCRs or light sensitive opsin that might present more convenient properties. Bi stable opsins as well as protein that present a close life cycle can be used following the same approach to create libraries of light-activated receptors tuned to fit to different experimental

settings. One of the biggest concerns at the beginning of this work was to develop a screening platform that allows me to overcome the issue of not having a proper positive control while testing the light-activated human Class A oGPCRs. The coherence between the screening data belonging to full-length control GPCRs and their relative light-activated chimeric versions allow me to propose that the signaling data collected from the light-activated human Class A oGPCRs reflect the signaling properties of their relative full-length genes.

Out of the 64 light-activated human Class A oGPCRs tested for G-Protein mediated pathways, I observed in total 19 receptor-pathway couplings in the HEK293 cell line. Considering that G-Protein coupling properties can be cell- type dependent, these results strongly suggested that human Class A oGPCRs might still conserve intact functional properties and are able to signal through G- Protein mediated pathways even if I was not able to detect a significant activation in HEK293 cells. Fourteen different light-activated human Class A oGPCRs designed according the chimeric algorithm show significant activation of one or more luciferase-based reporter plasmids.

Light-activated human Class A oGPCR	Luciferase-based reporter plasmid activated	Possible second messengers activated
Opto-GPR1	CRE	cAMP é
Opto-GPR3	SRE	PKC and MAPK/ERK
Opto-GPR4	CRE + NECA	cAMP ê
Opto-GPR18	SRE	PKC and MAPK/ERK
Opto-GPR21	CRE	cAMP é
Opto-GPR32	CRE	cAMP é
Opto-GPR33	SRE.L, SRE, CRE + NECA	RhoA, PKC and MAPK/ERK, cAMP ê
Opto-GPR42	CRE	cAMP é
Opto-GPR55	CRE + NECA	cAMP ê
Opto-GPR63	CRE + NECA	cAMP ê
Opto-GPR68	SRE	PKC and MAPK/ERK
Opto-GPR78	SRE	PKC and MAPK/ERK
Opto-GPR88	SRE	PKC and MAPK/ERK
Opto-GPR135	CRE	cAMP é

Table 5.1 List of light-activated human Class A oGPCRs with significant activation of one or more luciferase-based reporter plasmid upon light stimulation.

The functional data I collected can be compared to the already available information for the receptors listed in table 4.1. Constitute activity and intensity and localization of oGPCR expression are important factors in order to estimate oGPCR possible physiological roles. Information coming from knockout and knockdown studies are as well fundamental.

Especially taking in account the importance of GPCRs in drug discovery, the availability of murine knockout models is extremely important in understanding the physiological functional roles of GPCRs and oGPCRs and to observe disease-related phenotypes.

In the following table are collected the available KO murine models (in the form of Embryonic Stem (ES) cells or stable murine strains) with relative phenotype (when observed). In Appendix II, references reporting phenotypes are collected (from the International Mouse Phenotyping Consortium (IMPC) and the Jackson Laboratories database).

	Gene	ES	Mice	Phenotype	Phenotype description
1	GPR1	YES	YES	YES	Metabolic-glutamate intolerance
2	GPR2 (Ccr10)	YES	Under Production	YES	Behavior, Immune response, Growth
3	GPR3	YES	Under Production	YES	Behavior, Metabolism
4	GPR4	YES	Under Production	Proposed	Cardiovascular system, Homeostasis, Aging, Respiration
5	GPR6	YES	Under Production	Proposed	Behavior, Nervous system
6	GPR7 (Npbwr1)	NO	YES	Proposed	Behavior, Growth, Liver and Biliary system
7	GPR14 (Uts2r)	YES	YES	Proposed	Cardiovascular system, Muscular system
8	GPR17	YES	YES	Proposed	Behavior, Immune system, Aging, Nervous system
9	GPR18	YES	Under Production	NO	NO
10	GPR19	YES	YES	Proposed	Behavior
11	GPR20	YES	YES	YES	Behavior, Nervous system, Immune system, Aging
12	GPR21	YES	Under Production	Proposed	Behavior, Growth, Metabolism, Immune system
13	GPR22	YES	YES	YES	Cardiovascular system, Metabolism
14	GPR23 (Lpar4)	YES	YES	Proposed	Embryogenesis, Growth, Immune system, Aging, Cardiovascular system
15	GPR24 (Mchr1)	YES	NO	Proposed	Behavior, cardiovascular system, growth, nervous system
16	GPR26	YES	Under Production	Proposed	Behavior, Metabolism, Growth
17	GPR27	NO	Under Production	NO	NO
18	GPR30	YES	Under Production	YES	Cardiovascular system, Growth, Immune system, Biliary system

19	GPR31b	YES	Under Production	NO	NO
20	GPR33	YES	YES	YES	Nervous system (abnormal gait)
21	GPR34	YES	YES	YES	Immune system, Nervous system, Vision
22	GPR35	YES	YES	NO	NO
23	GPR37	YES	Under Production	Proposed	Behavior, Growth, Nervous system
24	GPR3711	YES	Under Production	Proposed	Behavior, Nervous system, Vision
25	GPR39	NO	YES	Proposed	Digestion, Growth, Metabolism
26	GPR40 (Ffar1)	YES	YES	YES	Behavior, Metabolism, Biliary system, Nervous system, Taste
27	GPR41 (Ffar3)	YES	NO	Proposed	Cardiovascular system, Growth, Metabolism, Nervous system
28	GPR43 (Ffar2)	YES	YES	Proposed	Digestive system, Growth, Metabolism, Immune system, Aging
29	GPR44 (Ptgdr2)	YES	NO	Proposed	Hematopoietic system, Metabolism, Immune system
30	GPR45	YES	NO	NO	NO
31	GPR48 (Lgr4)	YES	NO	Proposed	Digestive system, Embryogenesis, Growth, Metabolism, Immune system, Aging, Nervous system, Vision
32	GPR49 (Lgr5)	YES	Under Production	Proposed	Behavior, Digestive system, Growth, Metabolism, Aging,
33	GPR50	YES	YES	YES	Behavior, Growth, Metabolism
34	GPR51 (Gabbr2)	NO	YES	Proposed	Behavior, Growth, Metabolism, Aging, nervous system
35	GPR54 (Kiss1r)	YES	YES	YES	Behavior, Growth, Digestive system, Metabolism, Immune system, Aging, Nervous system
36	GPR55	YES	YES	YES	Metabolism, Immune system, Skeleton
37	GPR56 (Adgrg1)	NO	Under Production	Not confirmed	Behavior, Nervous system
38	GPR58 (Taar2)	YES	YES	NO	NO
39	GPR61	NO	YES	Proposed	Metabolism (aldosterone)
40	GPR62	YES	Under Production	NO	NO
41	GPR63	YES	YES	NO	NO
42	GPR64 (Adgrg2)	YES	Under Production	Proposed	Metabolism, Reproduction
43	GPR65	YES	YES	YES	Immune system, Hematopoietic system, Skeleton
44	GPR66 (Nmur1)	YES	YES	YES	Metabolism
45	GPR68	NO	Under Production	Proposed	Hematopoietic system, Metabolism, Immune system, Tumorigenesis
46	GPR69 (Lancl1)	YES	Under Production	Proposed	Metabolism, Immune system, Nervous system
47	GPR70 (Tas1r1)	YES	Under Production	Proposed	Nervous system, Reproduction, Taste/Olfaction
48	GPR71 (Tas1r2)	YES	Under Production	Proposed	Nervous system, Taste/Olfaction
49	GPR73 (Prokr1)	YES	YES	YES	Behavior, Cardiovascular system, Metabolism
50	GPR7311 (Prokr2)	YES	YES	Proposed	Behavior, Growth, Metabolism, Aging, Nervous system,

51	GPR74	NO	Under Production	Proposed	Nervous system
52	GPR75	YES	Under Production	NO	NO
53	GPR77 (C5ar2)	YES	Under Production	Proposed	Behavior, Metabolism, Biliary system, Aging
54	GPR80 (Oxgr1)	YES	YES	Proposed	Metabolism, Immune system, Renal system
55	GPR81 (Hcar1)	YES	NO	Proposed	Metabolism
56	GPR83	YES	Under Production	Proposed	Behavior, Hematopoietic system, Immune system
57	GPR84	YES	YES	Proposed	Hematopoietic system, Immune system
58	GPR85	YES	Under Production	Proposed	Behavior, Growth, Nervous system
59	GPR86 (P2ry13)	YES	YES	Proposed	Digestive system, Metabolism, Biliary system, Skeleton
60	GPR87	YES	YES	Proposed	Limbs, Digits, Tail, Skeleton
61	GPR88	YES	YES	Proposed	Behavior, Nervous system
62	GPR89	YES	Under Production	Proposed	Growth, Metabolism, Immune system, Aging, Pigmentation, Reproduction
63	GPR90 (Mrgprh)	YES	Under Production	NO	NO
64	GPR91 (Sucnr1)	YES	Under Production	Proposed	Hematopoietic system, Immune system, Renal system
65	GPR93 (Lpar5)	YES	YES	YES	Behavior, Nervous system
66	GPR97	YES	NO	NO	NO
67	GPR98 (Adgrv1)	YES	YES	YES	Behavior, Hearing system, Aging, Nervous system, Vision
68	GPR100 (Rxfp4)	YES	YES	YES	Behavior, Growth
69	GPR101	YES	YES	NO	NO
70	GPR103 (Qrfpr)	YES	YES	Proposed	Skeleton
71	GPR106 (Rxfp2)	YES	YES	YES	Reproduction, Skeleton
72	GPR107	YES	YES	YES	Hematopoietic system, Metabolism, Aging
73	GPR108	YES	YES	NO	NO
74	GPR110 (Adgrf1)	YES	Under Production	NO	NO
75	GPR111 (Adgrf2)	YES	NO	NO	NO
76	GPR112 (Adgrg4)	YES	Under Production	NO	NO
77	GPR114 (Adgrg5)	YES	YES	NO	NO
78	GPR115 (Adgrf4)	YES	YES	NO	NO
79	GPR116 (Adgrf5)	YES	YES	YES	Growth, Hematopoietic system, Metabolism, Immune system, Aging, Respiratory system
80	GPR119	YES	YES	NO	NO
81	GPR120 (Far4)	YES	YES	Proposed	Growth, Metabolism, Biliary system, Nervous system, Taste/Olfaction
82	GPR123 (Adgra1)	YES	YES	NO	NO

83	GPR124	NO	YES	Proposed	Cardiovascular system, Digestive system, Growth, Aging, Nervous system, Respiratory system
84	GPR125 (Adgra2)	YES	Under Production	NO	NO
85	GPR126 (Adgrg6)	YES	NO	Proposed	Behavior, Growth, Metabolism, Aging, Nervous system
86	GPR127	YES	YES	NO	NO
87	GPR128 (Adgrg7)	YES	YES	NO	NO
88	GPR131 (Gpbar1)	YES	YES	YES	Behavior, Growth, Metabolism, Biliary system
89	GPR132	YES	Under Production	Proposed	Growth, Hematopoietic system, Immune system, Respiratory System
90	GPR133	YES	YES	NO	NO
91	GPR136 (Opn5)	NO	Under Production	NO	NO
92	GPR137	YES	Under Production	NO	NO
93	GPR137b	YES	YES	NO	NO
94	GPR137c	YES	NO	NO	NO
95	GPR139	YES	YES	NO	NO
96	GPR142	YES	YES	NO	NO
97	GPR143	YES	NO	Proposed	Nervous system, Pigmentation, Vision
98	GPR146	YES	NO	NO	NO
99	GPR149	YES	Under Production	Proposed	Behavior, Reproduction
100	GPR150	YES	NO	NO	NO
101	GPR152	YES	YES	NO	NO
102	GPR153	YES	Under Production	NO	NO
103	GPR154 (Npsr1)	YES	YES	Proposed	Metabolism, Respiration
104	GPR155	YES	NO	NO	NO
105	GPR156	YES	YES	NO	NO
106	GPR157	YES	NO	NO	NO
107	GPR158	YES	YES	NO	NO
108	GPR160	YES	NO	NO	NO
109	GPR161	YES	NO	Proposed	Behavior, Embryogenesis, Aging, Nervous system, Vision
110	GPR162	YES	YES	NO	NO
111	GPR165	NO	Under Production	NO	NO
112	GPR171	YES	NO	NO	NO
113	GPR172b (Slc52a2)	YES	YES	NO	NO
114	GPR175)	YES	YES	NO	NO
115	GPR176	YES	YES	NO	NO
116	GPR178	YES	YES	NO	NO
117	GRP179	YES	Under Production	Proposed	Vision
118	GPR180	YES	Under Production	Proposed	Cardiovascular system, Metabolism
119	GPR182	YES	YES	NO	NO

120	GPR183	YES	YES	YES	Hematopoietic and Immune system
121	GRM1	NO	Under Production	YES	Behavior, Growth, Hearing, metabolism, Immune system, Aging, Nervous system
122	GRM2	YES	Under Production	YES	Behavior, Metabolism, Nervous system
123	GRM3	YES	YES	YES	Behavior, Nervous system
124	GRM4	NO	Under Production	Proposed	Behavior, Nervous system
125	GRM5	NO	Under Production	YES	Behavior, Growth, Nervous system
126	GRM6	YES	YES	YES	Nervous system, Vision
127	GRM7	YES	NO	YES	Behavior, Metabolism, Aging, Nervous system
128	GRM8	YES	YES	YES	Behavior, Growth, Metabolism, Nervous system
129	GPRC2a	YES	YES	YES	Behavior, Growth, Metabolism, Immune system, Aging Vision
130	GPRC5a	YES	NO	YES	Immune system, Respiration, Tumorigenesis
131	GPRC5b	YES	YES	YES	Behavior, Aging

Table 5.2 List of GPCRs (including oGPCRs) belonging to different subfamilies (Class A, Adhesion and Class C) for which at least one KO model is available or under development.

The data in table 4.2 show that for the moment a consistent amount of murine KO models are currently available for GPCRs. This might change in the future thanks to the CRISP/CAS9 technique that shortens both costs and time of development of stable KO strains^{261,262}. For the oGPCRs for which I detected a significant stimulation of one or more luciferase-based reporter plasmids the previously mentioned information is also available. For some specific cases possible agonist and related activated second messengers are proposed in single studies, explaining why these genes are still formally considered as oGPCRs (see table 5.3 for genes and references).

In the following paragraphs, for each oGPCRs for which I detected at least one possible G-Protein coupling, I will summarize what is known and what my result add to it.

GPR1 is currently considered a chemerin receptor, although an agreement on this is still missing. Chemerin is a chemoattractant protein that plays an active role in recruitment of dendritic cells and macrophages to inflammation sites. A chemerin-dependent activation of RhoA has been reported for GPR1, not recorded in my assays. However, the light-activated GPR1 showed significant activation of the CRE luciferase-based plasmid, suggesting that GPR1

increases intracellular levels of cAMP. Modifications of intracellular level of cAMP are required for regulation of actin based cell migration and chemotaxis. Thus activation of the CRE luciferase-based reporter plasmid is in agreement with the hypothesis of the involvement of this receptor in inflammation and migration-related biological processes. GPR3 is expressed in oocytes and it is supposed to play a role in the communication between oocytes and the surrounding stromal tissue. It has been proved its ability to increase cAMP in oocytes without the interaction with a ligand (constitutive activity), although Sphingosine 1-phosphate (S1P) has been proposed as putative ligand. Recently, it has been suggested that GPR3 might play a role in the Alzheimer's disease²⁶³. It has been determined that the absence of GPR3 alleviated the cognitive deficits and reduced amyloid pathology in four different d i s e a s e s - relevant mouse models of Alzheimer. Furthermore, GPR3 was found to be elevated in postmortem brain tissue from a subset of patient suffering of Alzheimer²⁶⁴. The activation of the CRE luciferase-based reporter system by the light-activated GPR3 supports the hypothesis that this receptor might modify intracellular level of cAMP, not only in oocytes. For this receptor, as well as for all other oGPCRs involved in diseases, the conservation of the activated pathway in literature and in my screening assay open to different considerations. The look for a possible agonist or antagonist for GPR3 could be direct to ensemble of molecules that have been proved to act as ligand for similar GPCR that modify as well intracellular level of cAMP. The screening could be limited even more by considering only molecules present in the native tissue of GPR3 or similar GPCRs, conserving the approach of the already described orphan strategy. On the other hand, both the information coming from my screening assay and confirm by literature might move the therapeutic approach from GPR3 through the pathway activated by the receptor itself. My results suggest that the role of cAMP regulation in Alzheimer disease should be further investigate and that this second messenger could be considered at therapeutic target.

GPR4 is considered to be a proton-sensing GPCR. This class of GPCRs is supposed to be activated usually upon pH drops to values between 6.2-6.8. The study of proton-sensing GPCRs is still challenging (although different knockout murine models are available, see table 5.2) for the redundancy of this class of receptors that usually call for multiple gene deletions. Previous studies proved the ability of GPR4 to activate different G-protein mediated pathways, while in my screening assay the light-activated GPR4 is proved to lower significantly intracellular level of cAMP. pH modification is involved in inflammatory processes. The light-activated GPR4 would allow investigating further the role of this specific proton-sensing GPCR in tissue where different other proton-sensing GPCRs are simultaneously expressed. It is interesting to notice that this receptor, being involved in pH sensing and (directly to indirectly) to inflammatory states shown ability to modify intracellular level of cAMP in my screening assay, raising considerations similar to the ones related to GPR3. GPR18 is supposed to be able increase intracellular level of cAMP upon activation with lipoamino acids and cannabinoids. The hypothesis that GPR18 upon stimulation with different ligands might be able to modify cAMP intracellular levels fit with the available data about its possible physiological roles. GPR18 is considered involved in cell migration²⁸⁰, macrophage apoptosis²⁸¹ and it has been proposed a role in controlling the reconstitution of the mouse small intestine intraepithelial lymphocytes²⁸². I found activation of the SRE reporter by the Opto-GPR18, while no signal was detected in experiments with the CRE luciferase-based reporter plasmid. Indeed, activation of the ERK1/2 pathway by GPR18 has been reported in the control of hypotension in rats. Also, the MAPK/ERK1/2 pathway is involved in cell proliferation and cell death, and as previously described GPR18 might be linked to macrophage apoptosis.

Gene	Tissue Localization	KO (ES or mice)	Phenotype	Possible agonists	Second messengers
GPR1	Ubiquitous	YES	YES	Chemerin	RhoA, ROCK ²⁶⁵
GPR3	Ubiquitous	YES	Not confirmed	S1-P	cAMP ²⁶⁶
GPR4	Ubiquitous	YES	Not confirmed	Protons	cAMP, RhoA, PKC ^{267, 268,269}
GPR18	Ubiquitous	YES	Not confirmed	Lipoamino acids	cAMP ^{270, 271}
GPR21	Ubiquitous	YES	Not confirmed	No information available	PKC ²⁷²
GPR32	Arterial/venous tissue	No		No information available	No information available
GPR33	Thyroid, lung, spleen, thymus	YES	YES	No information available	cAMP ²⁷³
GPR42	No signal in human tissue	No		Propionate	cAMP ²⁷⁴
GPR55	Brain and digestive system	YES	YES	Cannabinoid ligands	PKC and MAPK/ERK1 ²⁷⁵
GPR61	CNS and testes	YES	Not confirmed	No information available	cAMP ¹⁵⁵
GPR63	Ubiquitous	YES	No	Sphingosine 1-phosphate	No Information available
GPR68	Ubiquitous	YES	YES	Sphingosylphosphorylcholin, Benzodiazepine, Protons	cAMP, PKC ^{276,277, 278}
GPR78	Brain and placenta	NO		Constitute activity	cAMP ²⁷⁹
GPR88	Central Nervous System and trachea	YES	YES	No information available	No information available
GPR135	Ubiquitous, but especially CNS	No		No Information available	No information available
GPR150	Mainly CNS	YES	Not confirmed	No Information available	No information available

Table 5.3 List of human class A oGPCRs that show significant activation of one or more luciferase-based reporter plasmid including information about tissue expression, presence of a murine knockout with significant phenotype, list of possible candidate agonists and G-protein mediated pathway for which coupling was demonstrated using different assays.

I found a significant number of light-activated human Class A oGPCRs able to activate directly or inversely the CRE reporter plasmid, implying their ability to modify intracellular cAMP levels, fundamental in regulating actin based cell migration, chemotaxis and in general important for the control of inflammatory processes.

GPR32 and GPR33 belong to this group of light-activated oGPCRs that activate the CRE reporter plasmid.

GPR32 has been proposed to be sensitive to resolvins, a family of lipid mediators involved in temper the inflammatory response. More specifically, GPR32 seems to be involved in inflammatory processes localized in the lungs, such as inflammatory signaling in human airway epithelial cells and in the TGF- β 1 induced epithelial mesenchymal transition of lung cancer cells.

GPR33, although still classified as an oGPCRs, is considered by sequence homology as a chemoattractant receptor; its inactivation in humans, different great apes and rodent species as well as the presence of an intact allele in geographically restricted human populations suggest that this gene was undergoing positive selection in the last million years²⁷³.

Our data proves signaling functions for the intact light-activated GPR33 both in cAMP and internalization related G-Protein mediated pathways, strengthening the hypothesis of an active role of GPR33 in leucocyte chemotaxis and pathogen entry, like similar chemoattractant receptors, although further internalization studies might be needed in order to verify this hypothesis.

GPR42 can be considered the oGPCRs included in my screening with the most limited amount of information available. Expression data for this oGPCR are not available as well as KO models. It has been suggested its ability to increase levels of intracellular cAMP after stimulation with Propionate, ability recorded also in my data for the Opto-GPR42²⁸³.

Unlike GPR42, GPR55 is an oGPCR for which the available information justifies its involvement in several different physiological roles. It has been shown for GPR55 the ability to activate PKC and MAPK mediated pathways. These pathways are involved in cell proliferation: indeed, for GPR55 it has been

proposed a role in neuronal growth as well as in angiogenesis. In my screening Opto-GPR55 reversely activates the CRE luciferase-based reporter plasmid, the ability of GPR55 to modify intracellular level of cAMP might strengthen the hypothesis that this oGPCRs is involved in the inflammatory response and migration-related molecular processes. In fact, it has been shown that GPR55 is involved in intestinal inflammation, in lipid accumulation and consequent rise of inflammatory states and in the process of cancer angiogenesis in ovarian carcinoma. Actually, the role of GPR55 is not limited to the angiogenic process, but it has been shown that GPR55 promotes cancer cell proliferation, metastasis formation in colon cancer and in general GPR55 is considered a novel tumorigenic target²⁸⁴. All previous considerations suggest that GPR55 might be able to activate different G-protein mediated pathways and play a relevant role in different physiological processes.

GPR61 is known to be constitutive active and to have the ability to increase intracellular levels of cAMP. Opto-GPR61 significantly activate the CRE luciferase-reporter plasmid, confirming the coupling properties of this oGPCR. From a functional point of view, little is known about GPR61; the current hypothesis suggests a role of GPR61 in metabolism and in the regulation of aldosterone secretion.

Although for GPR63 candidate agonists were identified²⁶³, limited amount of information is available on its involvement in any relevant physiological processes. Opto-GPR63 was able to significantly reduce the amount of intracellular cAMP, suggesting that this oGPCR might possible be involved in inflammatory processes or, in general, in biological processes involving cell migration.

For GPR68 new information about possible agonist was recently retrieved using approaches based on homology models, leading to the identification of benzodiazepine as novel not-selective agonist. GPR68 is considered to be a proton-sensing GPCR (like the previously described GPR4) involved in different physiological processes related to acidosis, such as inflammation and the regulatory processes of the acidic tumor microenvironment. Dendritic cells

expressing GPR68 show inhibited migration properties in acidic environments. GPR68 controls the activity of proton transport proteins in epithelial cells and plays a specific role in asthma, regulating the contraction of airways in respect to change in pH²⁸⁵. For GPR68 example of cAMP and PKC mediated pathway activation are present in literature. In my screening the Opto-GPR68 activated the SRE luciferase-based reporter plasmid, while no significant activation was measured for the CRE luciferase-based reporter. The data of my screening compared with previously known data about GPR68 suggest that the ability of GPR68 to activate different G-protein mediated pathway might be related not only on the ligand and tissue dependency, but also on the difference between homeostatic and inflammatory conditions.

GPR78 presents a unique feature among the oGPCRs for which I recorded a significant light-dependent activation in my screening. In fact, it is the only gene expressed in humans, but not in mice. GPR78 has been suggested to be constitutive active in HEK293 cells, increasing the amount of intracellular cAMP levels. In my screening actually two different reporter plasmid were significantly activated by the Opto-GPR78, the SRE and the SRE.L luciferase-based reporter plasmid, while no significant activation was measured for the luciferase-based CRE reporter plasmid. This suggest that possibly the increase of cAMP level related to constitutive activity of GPR78 might not be related to this receptor function.

Most of the oGPCRs positive in my screening were found to have either inflammation-cAMP related signaling functions or cell growth-apoptosis related functions. Actually, oGPCRs were believed to be involved in high-order brain functions both taking in account the difficulties in finding both proper candidate agonists and, as shown in table 4.2, clear phenotypes in mouse KO studies. In the case of GPR88, the hypothesis of its implication in high-order brain function, more specifically disease models, is still valid. Mice lacking GPR88 exhibit a lower basal level of dopamine, which is a fundamental regulator of brain activity^{137,138}. GPR88 is supposed to be involved in disorders of the CNS such as the bipolar disorder (BD) and schizophrenia¹³⁹. Relation between GPR88

and these mental illnesses were found in different human populations where the relation was analyzed in triads formed by parents and child. In my screening, opto-GPR88 activates the SRE luciferase-based reporter plasmid, indicating the ability of GPR88 to activate either PKC or MAPK mediated pathways. However, how the activation of these specific pathways might lead to the development of severe physiological disease is difficult to estimate.

GPR135 and GPR150 can be considered a similar case to GPR42. Also for this oGPCR very little is known apart from its expression pattern in human. No possible candidate agonist is available, as well as hypothesis about their physiological role. Opto-GPR135 activates the CRE reporter plasmid, implying the ability of GPR135 to increase intracellular level of cAMP. The Opto-GPR150 decreased the CRE luciferase-based signal of NECA pre-stimulated cells, implying the ability of GPR150 to decrease intracellular level of cAMP. The absence of KO models as well as putative agonists makes the light-activated version of these oGPCRs a promising approach to dissect their physiological roles in the native tissues.

What implications does this research result have? For the light-activated human Class A oGPCRs for which I did not detect functional coupling a conserved functionality cannot be excluded. Being the G-Protein coupling dependent on the intracellular concentration of G-Protein related proteins, those light-activated human oGPCRs for which no significant coupling was detected in HEK293 cells could still activate canonical and non-canonical pathways in other cell types and tissues.

This data inspire further experiments in which light-activated Class A human oGPCRs can be tested in native tissue/organs, allowing to dissect their physiological roles. In fact, the light-activated oGPCRs may for the first time allow to test in vitro and in vivo the functional properties of this class of GPCRs using all advantages the Optogenetic approaches.

The data I collected allow to prioritize the study of oGPCRs in specific disease models by knowing their signaling properties before elucidating their activation mechanism and identifying proper agonists.

More generally, the approach described in this work permits to further elucidate the role of G-Protein dependent specific signaling pathways and second messenger. The creation of light-activated versions of known GPCRs will allow establishing a technique in which these pathways can be turned ON and OFF. This might allow in further studies to relate specific phenotypes to signaling pathways.

Finally, the rhodopsin-based library of chimeric GPCRs I designed may allow investigating structure properties of GPCRs for which current structure knowledge is limited; in fact, the techniques and the results achieved in crystallization of rhodopsin in its active and inactive form, as well as a coupled taste with the G-Protein can be as well used to obtain structural information about orphan GPCRs and verified their coupling properties by crystallization studies.

In summary, the chimeric algorithm as well as the luciferase-based platform represent a new approach for elucidating functional properties for oGPCRs for which little is known besides sequences and expression pattern.

The alternative approach based on the study of gene sequences using bioinformatics tools such as G-Protein prediction algorithms based on different mathematical and statistical tools in order to predict G-Protein coupling is far from being able to substitute functional testing. In fact, the algorithms tested in this work, when they do not fail in distinguish full-length GPCRs from their respective light-activated chimeric receptors, give not coherent results, showing a prediction pattern dependent on the mathematical or statistical approaches used to calculate the prediction. Also, these algorithms do not take in account differences in the topological localization of specific sequences when predicting G-Protein coupling, and approximate properties with a degree of detail not sufficient for elaborate proper predictions.

The main aim of this work was to answer three questions:

- ***Are orphan GPCRs functional at all?***
- ***If yes, which signaling pathways do they activate?***

- ***It is possible to retrieve a possible ligand for the receptors still consider as orphan?***

My results show that some Class A oGPCRs are functional and able to activate G-Protein mediated pathways in light-activated chimeras. The stability and reliability of both the chimeric algorithm and the assay strongly suggest that the signaling properties recorded for the light-activated human Class A oGPCRs reflect the signaling properties of their respective full-length genes. My results suggest that further investigation is needed for those light-activated human Class A oGPCRs for which no significant G-Protein coupling was recorded, with necessary testing in native tissues. The chimeric approach and my library of light-activated Class A human oGPCRs allow to overcome the necessity for information about activation properties and agonist for oGPCRs by creating a class of signaling-equivalent synthetic receptor that can be used in vitro and in vivo to elucidate signaling properties and physiological roles of this fundamental class of receptors.

6 - Appendix I

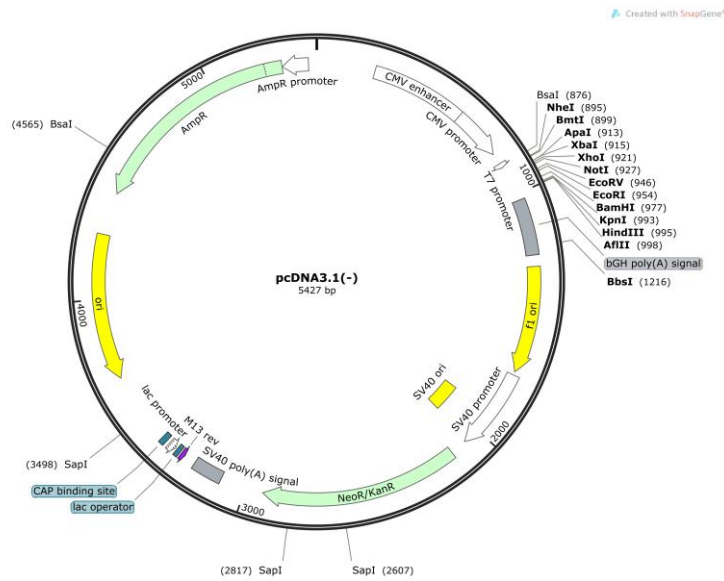


Figure 6.1 Vector map of pcDNA3.1(-) constructed from its original sequence, including endogenous *Typell*s restriction enzyme sites

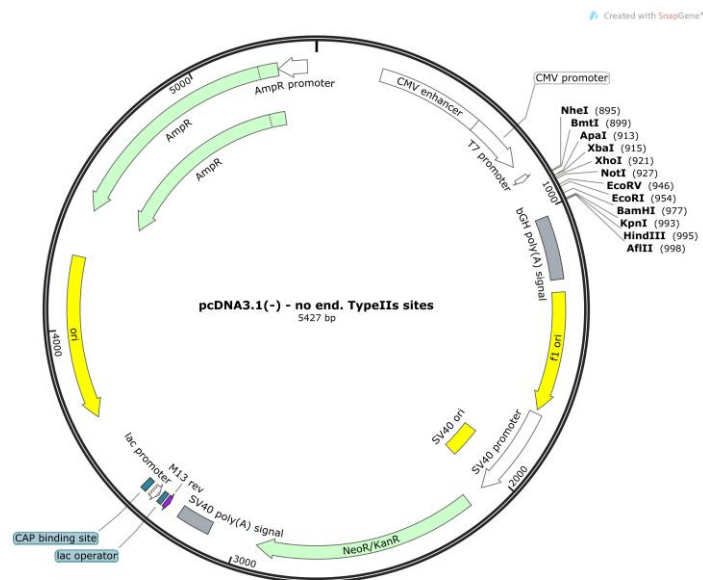


Figure 6.2 Vector map of pcDNA3.1(-) used for the cloning of the light-activated control GPCRs and light-activated human Class A oGPCRs, after the removal of the endogenous *Typell*s restriction enzymes sites

CTCAGGaccatgaaAcgatcatcgcctgagctacatcttctgctggtattcgccatgtacaccgatatagagatgaacagcgtgggaagatag
cctcatgaacgggacgggccccaaacttctacgtgcttctccaacaagcggcggtggtgagcagccctcgaggccccagtaactactggc
ggagccatggcagttctccatgctggcgcctacatgcttctgctgatcatgcttggcttcccatcaacttctcaagctgtagctagagaaccagt
ccagcaACCGGTcaagaagctgggtctccctcaactacactgctcaacctggcggtggcagacctctcatggtGtctggggggttaccaccacc
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tgggtgctctggccatgagcggtagctggtggtgtagcggcaagcccatGCTAAGCgagcaacttccggtctcggccatcatggggctgctca
cctgggtcatggtctggcctgtgcccgcgccccctctgctgggtggtccaggtacatcccggaggcagcagtgctcgtgctggggattgactactaca
cgccccacgaggaAaccaacaatgagtcgctctacatgctggtggtccacttcatcatcccctgattgtcatattctctgctacggAcaagt
cttcgctggtggtGATATCcaacgtcaagggaagcagcagcagtgatcatcatggtcatgcttctctaatctgctggctgcccctacgctgggggtg
cgttctacatcttaccatcagggtctgacttggccccatctcatgaccatcccggcttcttctgcaagacttctgcccgtctacaaccccgta
tctacatcatgatgaacaagcagttccgCagaagcactgcatggtCGGCCGCCaccactctcgctctctacagaAaccagccaagtggcctgca
cTAAGAATTC

xxxxx: XhoI recognition site, Anti-VSV-G sequence, signaling peptide, EcoRI recognition site
xxxxx: Overhangs for intracellular loops insertion
xxxxx: TypeIIs restriction enzymes sites
xxxxx: Bovine Rhodopsin sequence
xxxxx: Analytical enzymes sites
xxxxx: Single point mutation to remove endogenous TypeIIs restriction enzymes sites

Figure 6.3 Sequence of the mother construct used for the creation of the light-activated control GPCRs and light-activated human Class A oGPCRs

Name	Sequence
Opto-GPR1	MRTIIALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYV PFSNKTGVVRS PFEAPQYYLAE PWQFSMLAAYMFL LIMLG FPINFLTYLVTFGKWKKT VLN YILLNLAVADLFM VFGGFTTLYTSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLAIE RYVVVVIHPVLSHRHRTLKNAIMGVAFTWVMALACAAPPLV GWSRYIPEGMQCSCGIDYYPHEETN NSESVIYMFVVFHFIIP LIVIFFCYGC LIFKVKRSILISSRHFRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVII IMMNKQFRARFRSSVAEILKYTLWEVSCSGTVSEQLRNS ETKNLCLLETAQTETSQVAPA*
Opto-GPR3	MRTIIALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYV PFSNKTGVVRS PFEAPQYYLAE PWQFSMLAAYMFL LIMLG FPINFLTYLVIVGTPAFRAPLNYI LLNLAVADLFM VFGGFTTLYTSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLAIE ERYVVVYNALTYSETTVTRAIMGVAFTWVMALACAAPPLV GWSRYIPEGMQCSCGIDYYPHEETN NSESVIYMFVVFHFIIP PLIVIFFCYGCICRIVCRHAQQIALQRHLLPASHYVATR KGI RMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIP AFFAKTSAVYNPVIIIMMNKQFRKVLWAVCCSSSKIPFRSRSPSDV TETSQVAPA*
Opto-GPR4	MRTIIALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYV PFSNKTGVVRS PFEAPQYYLAE PWQFSMLAAYMFL LIMLG FPINFLTYVAVRQVQRNELNYI LLNLAVADLFM VFGGFTTLYTSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLAIE ERYVVVAHPLRFARLRVKTAIMGVAFTWVMALACAAPPLV GWSRYIPEGMQCSCGIDYYPHEETN NSESVIYMFVVFHFIIP PLIVIFFCYGCILRAVRGSVSTERQEKAKIRRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYN PVIIIMMNKQFRSDVAKALHNLRLFLASDKPQEMANASLTLETPLTSKR NSTAKAMTQSWAATPPSQDGVQLKMLPPAQTE TSQVAPA*
Opto-GPR6	MRTIIALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYV PFSNKTGVVRS PFEAPQYYLAE PWQFSMLAAYMFL LIMLG FPINFLTYVIASTPALRTP LNYI LLNLAVADLFM VFGGFTTLYTSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLAIE ERYVVVYNALTYYSRRTLLGAIMGVAFTWVMALACAAPPLV GWSRYIPEGMQCSCGIDYYPHEETN NSESVIYMFVVFHFIIP PLIVIFFCYGRICQVVRHAHQIALQHC LAPPFLAATRKGVRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIP AFFAKTSAVYNPVIIIMMNKQFRALWLLCGCFQSKVFPFRSRSPSEVTETSQVAPA*
Opto-GPR12	MRTIIALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYV PFSNKTGVVRS PFEAPQYYLAE PWQFSMLAAYMFL LIMLG FPINFLTYLVIFHNPSLRAPLNYI LLNLAVADLFM VFGGFTTLYTSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLAIE ERYVVVYALTYHSERTVTFAIMGVAFTWVMALACAAPPLV GWSRYIPEGMQCSCGIDYYPHEETN NSESVIYMFVVFHFIIP PLIVIFFCYGCICRIVCRHAQQIALQRHLLPASHYVATR KGI RMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIP AFFAKTSAVYNPVIIIMMNKQFRKALCLICCGCIPSSLAQRARS PSDV TETSQVAPA*
Opto-GPR15	MRTIIALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYV PFSNKTGVVRS PFEAPQYYLAE PWQFSMLAAYMFL LIMLG FPINFLTYLVLFHFKPGSRRLNYI LLNLAVADLFM VFGGFTTLYTSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLAIE ERYVVVVVWVSRKFRRTDCAIMGVAFTWVMALACAAPPLV GWSRYIPEGMQCSCGIDYYPHEETN NSESVIYMFVVFHFIIP PLIVIFFCYGCIAARKLCAHYQQSGKHNKLLKKSIRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSA VYNPVIIIMMNKQFRRAIVHCLCPCCLKNYDFGSS TETS DSHLTKALSTFIHAEDFARRRKR SVSLTETSQVAPA*
Opto-GPR17	MRTIIALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYV PFSNKTGVVRS PFEAPQYYLAE PWQFSMLAAYMFL LIMLG FPINFLTYVIFIRDHKS GTP LNYI LLNLAVADLFM VFGGFTTLYTSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLAIE ERYVVVHPVKSLKLRRLPLYAIMGVAFTWVMALACAAPPLV GWSRYIPEGMQCSCGIDYYPHEETN NSESVIYMFVVFHFIIP PLIVIFFCYGLIIRSLRQGLRVEKRLKTKAVRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYN PVIIIMMNKQFRHALCNLLCGKRLKGGPPSPFEGKTNESLSAKSEL TETSQVAPA*
Opto-GPR18	MRTIIALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYV PFSNKTGVVRS PFEAPQYYLAE PWQFSMLAAYMFL LIMLG FPINFLTYLVFVSC TTKRRT LNYI LLNLAVADLFM VFGGFTTLYTSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLAIE ERYVVVQPKYAKELKNTCKAIMGVAFTWVMALACAAPPLV GWSRYIPEGMQCSCGIDYYPHEETN NSESVIYMFVVFHFIIP PLIVIFFCYGVIIHNLHGR TSKLKPVKERSIRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAV YNPVIIIMMNKQFRARVISVMLYRNYLRSMRKRFSRSGSLRSLNSINSEMLTETSQVAPA*
Opto-GPR19	MRTIIALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYV PFSNKTGVVRS PFEAPQYYLAE PWQFSMLAAYMFL LIMLG FPINFLTYVIVHRSRRTQSTLNYI LLNLAVADLFM VFGGFTTLYTSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLAIE ERYVVVVYPLSKVRSREKAKAIMGVAFTWVMALACAAPPLV GWSRYIPEGMQCSCGIDYYPHEETN NSESVIYMFVVFHFIIP PLIVIFFCYGVKVIKIWRIGTDGRVTRTMNIVPRTKVKTRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIP FFAKTSAVYNPVIIIMMNKQFRRMKELFCMSSMKCYRSNAYTITTSRMAKKNVVGISELPSMAKTIKDSIYDSFDREAK

	EKKLAWPINSNPNTFVTETSQVAPA*
Opto-GPR20	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVFCRTRAKTPLNYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA ERYVVVVRPEGSRRCRQPACAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI PLIVIFFCYGRIMCALSRLHQRGRQRVRAMRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAV YNPVIYIMMNKQFRATVRGLFGQHGEREPSSGDVVMHRSSKSGSRHHILSAGPHALTQALANGPEATEETSQVAPA*
Opto-GPR21	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVHFCAPLLNHHTLNYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA IERVVVTKPLTYNTLVTPWRAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI IPLIVIFFCYGNIFRICQOHTKDISERQARFSSQSGETGEVQACPKRYARMVIMVIAFLICWLPYAGVAFYIFTHQGSDF GPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRRLKRLSGAMCTSCASQTTANDPYTVRSKGPLNGCHIETSQVAPA*
Opto-GPR22	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVCMKSNLINSVLNYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA IERVVVVKPANRILTMGRAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI LIVIFFCYGKILQALNIRIGTRFSTGQKKKARKKKTISLTTQHEATDMSQSSGGRNVVFGVRTSVSIVIALRRRAVKRHRERR ERQKRVRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRKVLKSKMKRRV SIVEADPLPNNAVIHNSWIDPKRNNKIFEDSEIREKCLVQVVTDTETSQVAPA*
Opto-GPR25	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVLAGRRGPRRLNLYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA IERVVVVKLEEARPLRTPRCAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI PLIVIFFCYGRISRRRLRRPHVGRARRNSLRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNP VIYIMMNKQFRARALDGCAGTRGLARRISSASSLSRDDSSVFCRAQAANTASASWTEETSQVAPA*
Opto-GPR26	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVLAGRRGPRRLNLYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA IERVVVVKLEEARPLRTPRCAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI PLIVIFFCYGKILQALNIRIGTRFSTGQKKKARKKKTISLTTQHEATDMSQSSGGRNVVFGVRTSVSIVIALRRRAVKRHRERR ERQKRVRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRKVLKSKMKRRV SIVEADPLPNNAVIHNSWIDPKRNNKIFEDSEIREKCLVQVVTDTETSQVAPA*
Opto-GPR27	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVIVRERSLHRALNLYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA ERYVVVAHHRFYAERLAGWPCAAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI IPLIVIFFCYGHRDRKMRPARLVPAVSHDWTFHGPGATGQAANWTAGFGRGPTPALVGRIPRAGPEGARRLLVLEEFK EKRLCRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRDCFRAQFPCCQSPR TTQATHPCDLKIGILTEETSQVAPA*
Opto-GPR31	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVFLFRVRVWVPLNYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA ERYVVVHPRKLVNLSQQAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI PLIVIFFCYGGIIRALQKRLREPEKQPKLQRAQRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAV YNPVIYIMMNKQFRSSRYRVRVHTLGRGQQAEPDFNPRDSYSTETSQVAPA*
Opto-GPR32	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVTFVRMARTVNLNYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA RYVVVLPVWALNHRVQRAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI LIVIFFCYGLIRAKLLREGWVHANRPKRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIY IMMNKQFREKFFQSLTSALARAFGEEEFSSCPRNAPRETETSQVAPA*
Opto-GPR33	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVLRKMKQTVNLNYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA RYVVVLPVWALNHRVQRAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI LIVIFFCYGRVASKVKERSLFSKSKPFRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIY IMMNKQFRKVFKKSILALFESTFSEDSSVERTQTETSQVAPA*
Opto-GPR34	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVFLGIHRKRNSLNYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA ERYVVVNRISQQRKAITTKQAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI PLIVIFFCYGKIGKLLNRISKRRSKFPNSGKYATTARMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKT SAVYNPVIYIMMNKQFRKIMCQLLFRFQGEPSRSESTSEFKPGYSLHDTSVAVKIQSSSKSTTETSQVAPA*
Opto-GPR35	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVFCRTRAKTPLNYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA ERYVVVVRPEGSRRCRQPACAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI PLIVIFFCYGKILQALNIRIGTRFSTGQKKKARKKKTISLTTQHEATDMSQSSGGRNVVFGVRTSVSIVIALRRRAVKRHRERR ERQKRVRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRKVLKSKMKRRV SIVEADPLPNNAVIHNSWIDPKRNNKIFEDSEIREKCLVQVVTDTETSQVAPA*
Opto-GPR37	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVVCNHNYMRSILNYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA IERVVVTVNQMYEMIENCSAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI PLIVIFFCYGVTARKIRKAEKACTRGNKRQIQLESQMNRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKT KTSAVYNPVIYIMMNKQFRRAFMECCCCCEECIQKSSSTVSDDDNEYTELELSPFSTIRREMSFTASVGHCTETSQV APA*
Opto-GPR37L1	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVWVHYSYLLKALNLYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA IERVVVTVNQMYEMIENCSAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI PLIVIFFCYGVTARKIRKAEKACTRGNKRQIQLESQMNRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKT KTSAVYNPVIYIMMNKQFRRAFMECCCCCEECIQKSSSTVSDDDNEYTELELSPFSTIRREMSFTASVGHCTETSQV APA*
Opto-GPR39	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVVLQKKGYLQKELNYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA ERYVVVCHPFRYKAVSGPQCAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI PLIVIFFCYGMMQVLMKSKGSLAGGTRPPQLRSESEESRTARRQITRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPI FMTIPAFFAKTSAVYNPVIYIMMNKQFRFVQVQLCCRLSQHANHEKRLRVHAHSTDSARFVRQPLLFASRRQSSARRT EKIFLSTFQSEAE PQSKSQSLSELSLEPNSGAKPANSAAENGFEHEVTEETSQVAPA*
Opto-GPR42	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVPPFSNKTGVVRSPEAPQYLAEPWFQFSLMAYMFLMLG FPINFLTYVFGKLRCPVALNLYILLNLAVADLFMVFGGFTTTLTYSLHGYPVFGPTGCNLEGGFATLGGIEIALWSLVVLA IERVVVVAHPLWYKTRPRLQQAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYPHEETNNEFSVIMYFVVFHFI IPLIVIFFCYGRVWILGRGSHRRQRVARMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNP VIYIMMNKQFRADFHELLRRLCGLWQWQESSMELKEQKGGEEQRA DRPAERKTSSEHSQCGTGGQVACENTETSQVAPA *

Opto-GPR45	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVYVYQRPAMRSALNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE ERYVVVVQRQDKLNPRRAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI VIFFCYGCILNTRVKNVAVRHNQSDSLDLRQLTRAGLRRLQRQQQVSDLSFKTKAFRVMVIIMVIAFLICWLPYAGVAFYIF THQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFREACIELLPQTFQILPKVPERIRRRIQPSTVYVCNENQSAVTETS QVAPA*
Opto-GPR50	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVVTNKKLRLNSLNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE ERYVVVCHSLQYERIFSVRNAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI PLIVIFFCYGRIWTKVLAARDPAGQNDPNQLAEVRNFRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAK TSAVYNPVIYIMMNKQFRREYWTIFHAMRHPIIFFSGLISDIEMQEARLARARAHARDQAREQDRAHACPAVEETPMNVR NVPLPGDAAAGHPDRASGHPKPHSRSSAYARKSASTHKSASFVSHSKAASGHLKPVSGHSPASGHKPSATVYPKPASVHFKA DSVHFKGDSVHFKPDVHFKPASSNPKPIIGHVVSAGSHSKSAFSAATSHPKPTTGHKIPATSHAEPPTADYKPKPATTSHPK PTAADNPELSASHCPEIPAIAHVPVSDSDLPESASSPAAGFTKPAASQLESDDIADLPDPTVVTSTNDYHDVVVIDVEDDP DEMAVTETSQVAPA*
Opto-GPR52	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVVFHFCAPLLHHYTLNLYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE ERYVVVTKPLSYNQVLTWPCRAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI IPLIVIFFCYGHIFKICRQHTKEINDRRARFPSEVDSRETHGSPDRRYARMVIIMVIAFLICWLPYAGVAFYIFTHQGSDF FGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRLGLRLRSETMCTSCMCVKDQEAQEPKPRKRANSCSITETSQVAPA*
Opto-GPR55	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVVFSTFLKRNRPDYAALNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLV VLAIERVYVVRYPLLVSHLRSRKAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFH FHIPLIVIFFCYGRSIIHLLGRDHTQDWWQKACIRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAK TSAVYNPVIYIMMNKQFRMNIARHRPSRVQLVQDOTTISRGTETSQVAPA*
Opto-GPR61	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVIAKTPALRKLNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE RYVVVVHMPRYEVRMTLGLAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI LIVIFFCYGSMFRVARVAAMQHGLPMTWETPRQRSELSRSTMTVSSGAPQTPHRTFGGKKAARMVIIMVIAFLICWLP YAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRGELSKQVCFKPAPEEELRPLPSREGSIEENFLQF LQGTGCPSESWSRPLPSFKQEPFAVDFRIPGQIAEBTSEFLEQQLTSDIIMSDSYLRPAASPRLESTETSQVAPA*
Opto-GPR62	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVVLRTPLGRDLNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE RYVVVVHPLRPGSRPPAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI LIVIFFCYGGIFVVARAALRPPRARGSRRLHSDLSRLSILPPLRPLRPGGKAARMVIIMVIAFLICWLPYAGVAFYIFTHQ SDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRALGRLSRRALPGVPRACTPQAWHPRALLQCRPPGPAVGESEAPE QTPPELAGGRSPAYQGPPESSLSTETSQVAPA*
Opto-GPR63	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVYVYQKAAAMRSALNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE ERYVVVVQRQDKLNPRRAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI VIFFCYGGILNTRHNLRIHSYPEGICLSQAKLGLMSLQRPQMSIDMGFKTRAFRMIIMVIAFLICWLPYAGVAFYIF THQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRDACLDMMPKSKFLLPQLPGHTKRRIRPSAVYVCGEHRVTVETS QVAPA*
Opto-GPR65	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVYVYQKAAAMRSALNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE ERYVVVVYPLKFFFLTRRFAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI PLIVIFFCYGKQYQAVRHKNKATENKEKRIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYN PVIYIMMNKQFRYDMWNILKFKCTGRCNTSQRQRKRLSVSTKDTMELEVLLETETSQVAPA*
Opto-GPR68	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVYVYQKAAAMRSALNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE ERYVVVAHPRFRHQFRTLKAAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI IPLIVIFFCYGGILRAVRRSHGTQKSRKQIQRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYN PVIYIMMNKQFRDLARLRGACLAFLTCRSTGRAREAYPLGAPASGKSGAQGEEPELLTKLHPAFQTPNSPGSGGFPTGRL ATETSQVAPA*
Opto-GPR75	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVYVYQKAAAMRSALNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE AIERVYVVLGKQPNRTHAESFPCAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI IPLIVIFFCYGMIAQTLRKNQVRKCPVITVDASRPQPFMGPVQGGGDPIQCAMPALYRNQNYNKLQHVQTRGYTKSPNQ LVTPAASRLQLVSAINLSTAKDSKAVRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIY IMMNKQFRKVLWCLQYIGLGFCCQKTRLRAMGKGNLEVRNRSKSHHETNSAYMLSPKQKQKFDQACGPHSKESMVS PISAGHQCGQSSSTPINTRIEPYYSINSSPSQEBESSPCNLQPVNSFGFANSYIAMHYHTNDLVQVEYDSTSAKQIPVPSVT ETSQVAPA*
Opto-GPR78	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVYVYQKAAAMRSALNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE IERVYVVVPLRQYRARRHCQRMQDVTMKAALALLADLHPSVRQCLIQKRRRHRATRMVIIMVIAFLICWLPYAGVAFYI FTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRQVLGAMVHRLKRTPRPASTHSSLDVAGMVHQLKRTPRPAS THNGSVDTENDSCLQHTTETSQVAPA*
Opto-GPR82	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVYVYQKAAAMRSALNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE ERYVVVYCYEKIFYGHLKFRQPNFAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI IPLIVIFFCYGQVHRVARRHCQRMQDVTMKAALALLADLHPSVRQCLIQKRRRHRATRMVIIMVIAFLICWLPYAGVAFYI FAKTSAVYNPVIYIMMNKQFRKTYLNFYTKNSAHMQSYGTETSQVAPA*
Opto-GPR83	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVYVYQKAAAMRSALNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE ERYVVVHMLPKPRISTKAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI IPLIVIFFCYGRVAKKLWLCNMIGDVTTEQYFALRRKKKTIIRMVIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAF AKTSAVYNPVIYIMMNKQFRIELKALLSMCQRPPKQEDRPPSPVPSFRVAVTEKNDGQRAPLANNLLPTSQLSGKTDLS VEPIVTMSTETSQVAPA*
Opto-GPR84	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWQFSMLAAYMFLLLIMLG FPINFLTYVYVYQKAAAMRSALNYILLNLAVADLFMVFGGFTTTLTYSLHGYFVFGPTGCNLEGGFFATLGGIEIALWSLVVLAIE ERYVVVAHPLKFPQVSAKGAIMGVAFTWVMALACAAPPLVWWSRYIPEGMQCSCGIDYYPHEETNNESFVIYMFVVFHFI IPLIVIFFCYGLIHRQVKRAAQALDQYKLRQASIHNSHVARTEAMPGRFQELDSRLSAGGSPGIESISAPVSAATTQTLGDS SEVDQINSKRAKQMAEKSPPEASAKAQIKGARRAPDSSSEFGKVTMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPI FMTIPAFFAKTSAVYNPVIYIMMNKQFRQAYGISILKGRPRSFRHLHTEETSQVAPA*

Opto-GPR85	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYLVVKDKTLHRLALNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I RYVVVVAHHRFYTKRLETFWTAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I PLIVIFFCYGHD RRKMPVQFVAAVSQNWT FHGPGASGQAAANWLAGFGRGPTPTLLGI RQNANTTRRRLLV LDEFKMEK RISRMVI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFFAKTSAVYNPVIYIMMNKQFRRCFSTLLYCRKSRLP REPYCVITETSQVAPA*
Opto-GPR87	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYLVVFFHIRNKTS LNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I E RYVVVVKPFGDSRMYSI TFAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I P LIVIFFCYGAI SRY IHKSSRQFISQSSRKRKHNRMI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFFAKTSAV YNPVIYIMMNKQFRRLFKKSNI RTRSES IRSLSQSVRRSEVRIYDYDTV TETSQVAPA*
Opto-GPR88	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYLVVSSFRKLQTT LNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I ERYVVVRAPATYQALYQRRAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I PLIVIFFCYGGIVRRVSVKRVS LNFHLLHQLPFGCARMVI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFFA KTSAVYNPVIYIMMNKQFRRSVRSVLPVGVGDAAAA AVAATAVPAVSAQQLGTRAAGQHW TETSQVAPA*
Opto-GPR119	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYLVVLL IHKNDGLNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I ERYVVVKQPFYRLKIMSGFVAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I PLIVIFFCYGDM LKIASMSHQ I RMEHAGAMAGGYSRPTSPDFKALRMI IMVIAFLICWLPYAGVAFY IFTHQGSDFGP IFMTI PAFFAKTSAVYNPVIYIMMNKQFRRLQLYHMLGVKVKVLT SFLFLSARNCGERPRESSCHVITISSEFDGTETSQ VAPA*
Opto-GPR120	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYLVVARRRRR GALNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I E RYVVVHLQRGVRGRRRAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I P LIVIFFCYGKILQ TSEHLLDARAVVTHSEITKASRKR LTVSLAYSESHQIRV SQDDFR LFRMVI IMVIAFLICWLPYAGVAF Y IFTHQGSDFGPIFMTI PAFFAKTSAVYNPVIYIMMNKQFRWKIIFCCFWFPEKGA I LDT SFTSQRN DLSI ISG TETSQVAPA *
Opto-GPR132	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYVALLQVLQGNV LNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I ERYVVVVALESRRRRRRTAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I PLIVIFFCYGRIFRSIKQSMGLSAAQKAKV KRMVI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFFAKTSAVYN PVIYIMMNKQFRQEVSR IHKGNKEWSMRTDVTR LTRHSRDT EELQSPVALADHYTFSRPHVPPGSPCKALIEESCTETSQV APA*
Opto-GPR135	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYLVVKHRQLRTV LNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I ERYVVVVRPREKIGRRRAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I P LIVIFFCYGHICKTVRLSDVRVRPVNTYARVLRFFSEVRTRMVI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFF AKTSAVYNPVIYIMMNKQFRRNREEGYTRNVDAFLPSQGPGLQARSRLRNRYANRLGACNRMS SSSNPSAGVADGVAWMA RKNPVVLF CREGPEPEPVTA VTKQPKSEAGDTS L TETSQVAPA*
Opto-GPR139	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYLVLSQLVARRQK LNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I ERYVVVCHPLKYHTVSYPARAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I PLIVIFFCYGIVYKLRKSNFR LRGYTGKTRMVI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFFAKTSAVYN PVIYIMMNKQFR TMAAATLKAFFKQKQPVQFYTNHNSITSSPWI SPANSHCI KMLVYQYDKNGKPIKVPSTETSQVAP A*
Opto-GPR141	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYLVVKMNTSRV LNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I E RYVVVKCKDKVFEYRKLAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I P LIVIFFCYGIMLMVQKLRHSLLSHQEFWAQRMI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFFAKTSAVYNP VIYIMMNKQFRQKI IGLWNCVLCR TETSQVAPA*
Opto-GPR142	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYVLARLATRTRRPN LNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I ERYVVVCHPLHRAASSPGR AIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I IPLIVIFFCYGAI I HRLRRRGRSGLQPRVKGSTRMVI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFFAKTSAV YNPVIYIMMNKQFRATVRQV IHDAYL PCTLASQPEGMAAKPVMEPPGLPTGA EVTETSQVAPA*
Opto-GPR146	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYLVNLHASKASMTMLNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I ERYVVVALPRTYMASVYNAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I P LIVIFFCYGLLSRVRREDT PLDRDTGRLEPSAHRMVI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFFAKTSAV YNPVIYIMMNKQFRSKLQRLMKK L PCGDRHCS PDHMGVQOV L TETSQVAPA*
Opto-GPR148	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYVILRNQRLRQELNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I ERYVVVHPLRYS L FMSHGAAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I PLIVIFFCYGRIYAEAKTSGI WQGYSRARGTLRMI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFFAKTSAV YNPVIYIMMNKQFRQLLGMVRGHLPSRRHQAI FTISTETSQVAPA*
Opto-GPR149	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYVLLKQNR T V LNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVVLA I E RYVVVHRGVGSQTASRRSGAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I P LIVIFFCYGEISRGASIPGTPPTAGRVVLS PEDAPGFLRRSGGCS P S S DTVFGGAPAAAGAEACRRENRTLYGTRSF T VSAQKRMVI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFFAKTSAVYNPVIYIMMNKQFRLSFQKSYGIYKIA HEDYDDDENSI FYHNLMSSECTTKDQRDRNRI FNAIKVEISTT PSLDSS TQRGINKCNTDI TEAKQDSNNKDAFSDK TGGDINYEETTFSEGPERRLSHEESQKPD LSDWEWCRSKSERTPRORSYALAI PLCAFQGTVLSHAPTGTKTLSTLSTYEVSA EGQKITPASKKIEVYRSKSVGHEPNSESSSTFVDTSVKIHLEVLEICDNEEALDTVLSI SNISSQSTQVRSPSLRYSRKEN RFVCDLGETASYS LFLPTSNPDGDI NIS I P DTV AHRQNSKRQHQRDGYQE IQLLNKAYRKEEESGSTETSQVAPA*
Opto-GPR150	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYVLCGGGFPWAGPKRRK LNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSL VLAIERYVVVRLPHGRPLPAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I PLIVIFFCYGHLLSVWVHRPQAPAAAAPWSASPGRAPAPSALPRAKQVSRMVI IMVIAFLICWLPYAGVAFY IFTHQGSDFG GPIFMTI PAFFAKTSAVYNPVIYIMMNKQFRRLKRLRGLS LCCAPQGADEEGPRGHQALYRQRWPHPHYHARREPLDEG GLRPPPPRRLPSCSCESAFTETSQVAPA*
Opto-GPR151	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFPFSNKTGVVRS PFEAPQY LAEPWQFSMLAAYMFL L IMLG FPINFLTYVLLHNAWKGKPSMLNY ILLNLAVADLFMVFGGFTTTLTYSLHG YFVFGPTGCNLEGGFATLGG EIALWSLVV LAIERYVVVSDPAKQVSIHNAYAIMGVAFTWVMALACAAPPLVGWSRY IPEGMCQSCGIDYYPHEETNNE SFVIYMFVVFH I I PLIVIFFCYGRAYDQCKKRGTQTQNLNRQIRSKQVTRMVI IMVIAFLICWLPYAGVAFY IFTHQGSDFGPIFMTI PAFFAKT

	SAVYNPVIYIMMNKQFREGKGVWKMWITKKPPTVSESQETPAGNSEGLPDKVPSPEPASIPKEKFPSSPSSGKGKTEKAE IPIPLPDVEQFWHERDTPVSVQDNDPIPEWEHEDQETGEGVKTETSQVAPA*
Opto-GPR152	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWFQFSLMAYMFLIMLG FPINFLTYLVAGSQARHGAGTRLNLYLLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGGFATLGGELIALWSLVVLA AIERYVVVLCPHWYPGHRPVRLAIMGVAFTWVMALACAAPPLVGVWSRYIPEGMQCSCGIDYYPHEETNNEFSVIYMFVVFH I I PLIVIFFCYGLTQATACRTRCHRQQQPAACRGFARMVI IMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTI PAFFAKTS AVYNPVIYIMMNKQFRTLLRSVLSFAALCEERFSGFTPTPEPQTQDSEGP TLPEPMAEAQSQMDPVAQPQVNPPLQPRSD PTAQPQLNPTAQPQSDPTAQPQLNMQPQSDSVAQPQADTNVQTPAPAASSVPSPCDEASPTPSSHTPGALEDPATPPAS EGESPSSTPPEAAPGAGPTTETSQVAPA*
Opto-GPR153	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWFQFSLMAYMFLIMLG FPINFLTYLVVGAQKQKWKPLNYLLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGGFATLGGELIALWSLVVLA AIERYVVVCPVNYRLSNAKQKQAIMGVAFTWVMALACAAPPLVGVWSRYIPEGMQCSCGIDYYPHEETNNEFSVIYMFVVFH I I PLIVIFFCYGLTAVQVGRQADRRRAFTVPTIIVVEDAQGKRSSIDGSEPAKTLQRVMVIIMVIAFLICWLPYAGVAFYIFTHQ GSDFGPIFMTI PAFFAKTS SAVYNPVIYIMMNKQFRADLKAVREKCMALMANDEESDDETSLEGGISPDVLVRLSDYGYGGD FVALDRMAKYEISALEGGGLPQLYPLRPLQEDKMQYLQVPPTRRFSHDDADVMAAVPLPAFLAFTHQGSDFGPIFMTI PAFFAKTS ERRRASLLAFAEDAPPSRARRRRAESLLSLRPSALDSGPRGARDSPPGSPRRRPPGPRASASALLPDAFALTAFCCEPQAL RRPPGPFPAAPADGADPGEAFTPPSSAQRSPGPRPSAHSHAGSLRPLGSLASWGEPPGLRAAGGGGSTS SFLSSPSESSGY ATLHSDSLGSASTETSQVAPA*
Opto-GPR160	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWFQFSLMAYMFLIMLG FPINFLTYLVTLGMRKNTCQNLNYLLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGGFATLGGELIALWSLVVLA AIERYVVVSKTTLKSFCKQKLFYFAIMGVAFTWVMALACAAPPLVGVWSRYIPEGMQCSCGIDYYPHEETNNEFSVIYMFVVFH I I PLIVIFFCYGRITSYMNETILYFPFSSHSYTVRSKRMVI IMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTI PA FFAKTS SAVYNPVIYIMMNKQFRKLDIGLPLDFVNWKCCFIPLTIPNLEQIEKPI SIMICTETSQVAPA*
Opto-GPR161	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWFQFSLMAYMFLIMLG FPINFLTYLVLYKKSLLTLLNYLLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGGFATLGGELIALWSLVVLA AIERYVVVLYPMVYPMKITGNRAIMGVAFTWVMALACAAPPLVGVWSRYIPEGMQCSCGIDYYPHEETNNEFSVIYMFVVFH I I PLIVIFFCYGIFRVARVKARKVHCGTIVVEEDAQRTGRKNSSTSTSSGSRRAAFQGVYSAQCCKALRMVI IMVIAFLI CWLPAAGVAFYIFTHQGSDFGPIFMTI PAFFAKTS SAVYNPVIYIMMNKQFRKELLGMCFCGDRYREPFVQRQRTSRLSISN RITDLGLSPHLTALMAGGQPLGHSSGDTGTFCSQSDGTDMMLEDYTDSDNPPSHCTCPKRRSSVTFEDEVQIEKAAK NSILHVKAEBHKLSDSYAASLAKAIEABEAKINLFGGEALPGVLVARTVFGGGFGRRSRTLVSQRLQLSIEEGDLVLAEE QRTETSQVAPA*
Opto-GPR162	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWFQFSLMAYMFLIMLG FPINFLTYLVISAKQKHKPLNYLLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGGFATLGGELIALWSLVVLA AIERYVVVRWPVNYRLSNAKQKQAIMGVAFTWVMALACAAPPLVGVWSRYIPEGMQCSCGIDYYPHEETNNEFSVIYMFVVFH I I PLIVIFFCYGLTWARPRRQARRVGGGGTKAGGPGALGTRPAFEVPAIIVVEDARGKRSSLDGSESAK TSLQRVMI IMV AFLICWLPYAGVAFYIFTHQGSDFGPIFMTI PAFFAKTS SAVYNPVIYIMMNKQFRADVTVYSAQCCKALRMVI IMVIAFLI YAEGRVCKVRFDANGATGPGSRDPAQVQLLPGRHMLFPPLERVHYLQVPLSRRLSHDETNI FSTPREPFGFLHKWSSDDIR VLPQSRALGGPPEYLGRHRLEDEEABEGGLASLRQFLESGLVSGGGPPRGPFRREITTFIDETPLPSP TASP HSPRRRPLGLSPRRLSLGSPESRAVGLPLGLSAGRRCSLTGGEESARAWGGSWGPNPI FQTLTLETETSQVAPA*
Opto-GPR171	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWFQFSLMAYMFLIMLG FPINFLTYLVFIQKNTNHRCLNYLLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGGFATLGGELIALWSLVVLA AIERYVVVTHSCKIYRIQEPGFAIMGVAFTWVMALACAAPPLVGVWSRYIPEGMQCSCGIDYYPHEETNNEFSVIYMFVVFH I I PLIVIFFCYGLVIRQLYRNKNDENYPNVKKALRMVI IMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTI PAFFAKTS NFVIYIMMNKQFRSKVTE T FASP KETKAQEKELRCENNATE T S Q V A P A *
Opto-GPR173	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWFQFSLMAYMFLIMLG FPINFLTYLVVLERALHKAALNYLLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGGFATLGGELIALWSLVVLA AIERYVVVAHHRFYAKRMTLWTAIMGVAFTWVMALACAAPPLVGVWSRYIPEGMQCSCGIDYYPHEETNNEFSVIYMFVVFH I I PLIVIFFCYGRHRKMGKPAQMVPAISQNWTFHGPGATGQAANWIAAGFGRGMPMP TLLGIRQNGHSAARLLGMDEVBGEKQ LGRMVI IMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTI PAFFAKTS SAVYNPVIYIMMNKQFRKCLRT HAPCWTGGAPA PREPYCVMTETSQVAPA*
Opto-GPR174	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWFQFSLMAYMFLIMLG FPINFLTYLVFYGYMKETKRLNYLLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGGFATLGGELIALWSLVVLA AIERYVVVMPYFRFDCKQKYDAIMGVAFTWVMALACAAPPLVGVWSRYIPEGMQCSCGIDYYPHEETNNEFSVIYMFVVFH I I PLIVIFFCYGKTVLSQDKYPMQDLGKQKALRMVI IMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTI PAFFAKTS YNPVIYIMMNKQFRRLSRQDLHDSIQLHAKS FVSNHTASTMTPELCTETSQVAPA*
Opto-GPR176	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWFQFSLMAYMFLIMLG FPINFLTYLVTCRTTTFVKSVLNYLLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGGFATLGGELIALWSLVVLA AIERYVVVLYPLERKISDAKAIMGVAFTWVMALACAAPPLVGVWSRYIPEGMQCSCGIDYYPHEETNNEFSVIYMFVVFH I I PLIVIFFCYGLIRRALASQKQKVI I AALRTPQNTISIPYASQREAEHLRMVI IMVIAFLICWLPYAGVAFYIFTHQGSDFGPI FMTI PAFFAKTS SAVYNPVIYIMMNKQFRKCLIGTLVQLHHRYSRRNVSTGSGMAEASLEPSIRSGSGLLEMFHIGQQQIFK PTEDEESEAKYIGSADFQAKEI FSTCLGEGQGPQFAPSAPPLSTVDSVQVAPAAPVEPETFPDKYSLOFGFGPFELPQW LSETRNSKKRLLPLGNTPEELIQTKVQKVRERKMSRNKVSIFPKVDSTETSQVAPA*
Opto-GPR182	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWFQFSLMAYMFLIMLG FPINFLTYLVNWRGSGRAGLLNYLLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGGFATLGGELIALWSLVVLA AIERYVVVTSASPSWQRYQHRVRAAIMGVAFTWVMALACAAPPLVGVWSRYIPEGMQCSCGIDYYPHEETNNEFSVIYMFVVFH I I PLIVIFFCYGLTACRLRQPGQPKSRHRMVI IMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTI PAFFAKTS PVIYIMMNKQFRGRLNNAVHYLPKQDKAGTCASSSSCSTQHSIIITKGDSPAAAAPHPEPSLQAHLLPNTSPISPT QFLTPTSTETSQVAPA*
Opto-GPR183	MKTI IALSYIFCLVFAMYTDIEMNRLGKDSLMMNGTEGPNFYVFPFSNKTGVVRSPEAPQYYLAEFPWFQFSLMAYMFLIMLG FPINFLTYLVIVQNRKINSNLNYLLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGGFATLGGELIALWSLVVLA AIERYVVVHPLRYNKIKRIEHAIMGVAFTWVMALACAAPPLVGVWSRYIPEGMQCSCGIDYYPHEETNNEFSVIYMFVVFH I I PLIVIFFCYGQICCKLFRQAKQNLTEKSGVKNKALRMVI IMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTI PAFFAKT SAVYNPVIYIMMNKQFRKVMRMLKRVSVS ISSAVKSAPEENSREMTETQMMIHSKSSNGKTETSQVAPA*

Table 6.1 Amino acid sequences of all light-activated human Class A oGPCRs created using the chimeric algorithm described in section 2.1

	<p>CCTGGGTCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGCCTGTG CGGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTCATCATC CCCCGATTGTGCATATTTCTGCTACGGATGCATTTGCAAGGAAGCTGTGGCCCATTTACGAGCAATCAGGAAAGCAACA AAAAGCTGAAGAAATCTATACGCATGGTGTATCATGGTTCATCGCTTTCTTAATCTGCTGGCTGCCCTACGCTGGGGTGGC GTTCTACATCTTACCACATCAGGGCTCTGACTTTGGCCCCATCTTCATGACCATCCGGCTTTCTTTGCCAAGACTTTGCC GTCTACAAACCCCGTTCATCTACATCATGATGAACAAGCAGTTCCGCGGGCCATTGTCCACTTTGGCCCTTGGCCCTGAAAA ACTATGACTTTGGGAGTAGCACTGAGACATCAGATAGTCACTTCACTAAGGCTCTCTCCACTTCATTCATGCAGAAGATTT TGCCAGGAGGAGGAGGCTGTGTCTACTCACAGAAACCAGCCAAAGTGGCGCTGCCTAA</p>
Opto-GPR17	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCTTTAGTTGTACCACCAAGAAGAGAACCACGCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCCCTTACACCTCTCTGACGGGTACTTCGCTTTTGG GCCACGGGTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCCATGCTTCAATC GAGCGGTACGTGGTGGTGTACAGCCGAAGTACGCCAAGAAGCTTAAAAACACGTGCAAGGCCATCATGGCGTGCCTTCA CCTGGGTCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGTCTGTG CGGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTGGTCCATTCATC CCCCGATTGTGCATATTTCTGCTACGGAGTCAATTATTCATAATCTCTTCCAGGCAGGACGCTAAGCTGAACCCAAAG TCAAGGAGAAGTCCATACGCATGGTGTATCATGGTTCATCGCTTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTT CTACATCTTCAACCATCAGGGCTCTGACTTTGGCCCCATCTTCATGACCATCCCGCTTTCTTTGCCAAGACTTCTGCGT TACAACCCGTCATCTACATCATGATGAACAAGCAGTTCCGCCACGCCCTGTGCAACTTGTCTGTGGCAAAAGCTCAAGGCCCGC CCCCAGCTTCGAAGGAAACCAACGAGAGCTCGTGTGAGTGCAGGCTGACAGAAACAGCCAAAGTGGCGCTGCCTAA</p>
Opto-GPR18	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCTTTAGTTGTACCACCAAGAAGAGAACCACGCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCCCTTACACCTCTCTGACGGGTACTTCGCTTTTGG GCCACGGGTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCCATGCTTCAATC GAGCGGTACGTGGTGGTGTACAGCCGAAGTACGCCAAGAAGCTTAAAAACACGTGCAAGGCCATCATGGCGTGCCTTCA CCTGGGTCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGTCTGTG CGGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTGGTCCATTCATC CCCCGATTGTGCATATTTCTGCTACGGAGTCAATTATTCATAATCTCTTCCAGGCAGGACGCTAAGCTGAACCCAAAG TCAAGGAGAAGTCCATACGCATGGTGTATCATGGTTCATCGCTTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTT CTACATCTTCAACCATCAGGGCTCTGACTTTGGCCCCATCTTCATGACCATCCCGCTTTCTTTGCCAAGACTTCTGCGT TACAACCCGTCATCTACATCATGATGAACAAGCAGTTCCGCCACGCCCTGTGCAACTTGTCTGTGGCAAAAGCTCAAGGCCCGC GAAGCATGCGCAGAAAAGTTCCGATCTGGTAGTCTACGGTCACTAAGCAATATAAACAGTGAATGTTAAACAGAAACCG CAAAGTGGCGCTGCCTAA</p>
Opto-GPR19	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCTTTAGTTGTACCACCAAGAAGAGAACCACGCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCCCTTACACCTCTCTGACGGGTACTTCGCTTTTGG GCCACGGGTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCCATGCTTCAATC GAGCGGTACGTGGTGGTGTATCTCTGAGCTTCAAGTGTCCAGAGAAAAGCCAAAGGCCATCATGGCGTGCCTTCA CCTGGGTCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGTCTGTG CGGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTGGTCCATTCATC CCCCGATTGTGCATATTTCTGCTACGGAAAGTCAATAAATATATTTGGAGAATAGGCACAGATGGCCGAACGGTGAAGG GGACAAATGAACATTTGCCCTCGGACAAAAGTGAACAAATATCCGCATGGTGTATCATGGTTCATCGCTTTCTTAATCTGCTG GCTGCCCTACGCTGGGGTGGCGTTTACATCTTCAACCATCAGGGCTCTGACTTTGGCCCCATCTTCATGACCATCCCGCT TTCTTTGCCAAGACTTCTGCGTCTACAACCCGTCATCTACATCATGATGAACAAGCAGTTCCGCGAGGGATGAAGAGAG CTTTTTGCATGCTCTATGAAATGTTACCAGAAAGTGCCTATACTATCAACAAGTTCAAGGATGGCCAAAAAAACTA CGTTGGCATTTAGAAATCCCTTCCATGGCCAAAATATTACAAAGACTCGATCTATGACATCTTGGTGGTCCATTCATC GAAAAAAGCTTGTCTGGCCATTAACTCAAATCCACAAATACTTTTGTACAGAAACAGCCAAAGTGGCGCTGCCTAA</p>
Opto-GPR20	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCTTTAGTTGTACCACCAAGAAGAGAACCACGCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCCCTTACACCTCTCTGACGGGTACTTCGCTTTTGG GCCACGGGTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCCATGCTTCAATC GAGCGGTACGTGGTGGTGTGCGGCCGAAGGCTCCCGCCGCTGCCCGCAGCCTGCCTGTGCCATCATGGCGTGCCTTCA CCTGGGTCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGTCTGTG CGGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTGGTCCATTCATC CCCCGATTGTGCATATTTCTGCTACGGAGCAGTATGTTGTGACTGTGCGGCCGGGTCTGCTCCACAGGGTGCAGC GCCGCGTGGGGCCATGCGCATGGTGTATCATGGTTCATCGCTTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTT CTACATCTTCAACCATCAGGGCTCTGACTTTGGCCCCATCTTCATGACCATCCCGCTTTCTTTGCCAAGACTTCTGCGT TACAACCCGTCATCTACATCATGATGAACAAGCAGTTCCGCCACGCCCTCCGAGGCTCTTCCGCCAGCAGGAGCGGT AGCCACGAGCGGTGACGTGGTCAAGTGCACAGGAGCTCCAAGGCTCAGGCCGTATCATCTCTTCAAGTGCAGCCGCTCA CGCCCTCACCCAGGCCCTGGCTAATGGGCCGAGGCTACAGAAACAGCCAAAGTGGCGCTGCCTAA</p>
Opto-GPR21	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCTTTAGTTGTACCACCAAGAAGAGAACCACGCTCAACTACATCTGCTCAACC ACCTGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCCCTTACACCTCTCTGACGGGTACTTCGCTTTTGG TGGCCACGGGTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCCATGCTTCAATC ATCGAGCGGTACGTGGTGGTGTAAACCTTAACTATAAATCTCTGTTTACCCCTGGAGGCCATCATGGCGTGCCTT TCACTGGTCAATGGCTCTGGCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGTCTG GTGCGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTGGTCCATTCATC ATCCCCGATTGTGCATATTTCTGCTACGGAAACATCTCCGCATCTGCCAACAGCACAAAGGACATCAGCGAAAGGC AAGCCCGTTACGACAGCCAGAGTGGGGAGTGGGAAAGTGCAGGCTGTCTGATAAGCCATGCCCCATGCGGATCAT CATGGTTCATCGCTTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTCTACATCTTCAACCATCAGGGCTCTGACTTT GGCCCATCTTCAATGACCATCCCGCTTTCTTTGCCAAGACTTCTGCGTCTACAACCCGTCATCTACATCATGATGAACA AGCAGTTCCGCGAGGACTAAAGCCCTTCCAGGGCTATGTGACTTTCTGTGCAAGTGCAGATCAGCCACAGCCCTTCA CACAGTTAGAAGCAAGGCCCTTCTAATGGATGTATATCACAGAAACAGCCAAAGTGGCGCTGCCTAA</p>

Opto-GPR22	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCCGAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGCTTACTGTCATGAAATCCAACCTTAATCAACTCTGTCTCAACTACATCTGCTCA ACCTGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCTCTACACCTCTCTGCACGGGTACTTCTGCTT TGGGCCACGGGCTGCAACCTGGAGGGCTTCTTGGCCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGGCC ATCGAGCGGTACGTGGTGGTAAACCTGCAACCGAATTCTGACAATGGGCAGAGCCATCATGGGCTGCGCTTCACT GGTTCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGTCTGCTGGC GATTGACTACTACGCCCCACGAGGAAACCAACAATGAGTCTTCTGTCATCTACATGTTCTGGTCCACTTCACTATCCCC CTGATTTGTCATATTTCTTCTGCTACGGAAAAATACTCAGGCTCTTAATATTCGAATAGGCACAGAAATTTCAACAGGCGA AGAAGAAGCAAGAAAGAAAAGCAATTTCTTAACCACACAACATGAGGCTACAGACTGTCCACAAGCAGTGGTGGGAG AAATGTAGTCTTTGGTGAAGAATCTCAGTTCTGTAATAATTGCCCTCCGGCGAGCTGTGAAACGACCCGTGAACGACGA GAAAGCAAAAGAGAGTGTCCGCATGGTATCATATGTCATCGCTTTCCTAATCTGCTGGCTGCCCTACCTGCTGGGTGG CGTTCTACATCTTACCCTCAGGGCTCTGACTTGGCCCCATCTTCAATGACCATCCCGGCTTCTTTCGCAAGACTTCTG CGTCTACAACCCCGTCTACATCATGATGAACAAGCAGTTCGCAAGGCTTGTAAAAGTAAAATGAAAAGCGAGTTGTT TCTATAGTAGAAGCTGATCCCCGCTAATAATGCTGTAATACACAACCTTGGATAGATCTAAAAGAAAACAAAAAATTA CCTTTGAAGATAGTGAATAAGAGAAAAATGTTTGTGCTCAGGTTGTACAGACACAGAAACAGCAAGTGGCGCTGCG CTAA</p>
Opto-GPR25	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCCGAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGCTTCTGGCCGGGCGGCGGGCCCGGCGGCTGCTCAACTACATCTGCTCAAC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGCACGGGTACTTGTCTTGG GCCCCAGGGCTGCAACCTGGAGGGCTTCTTGGCCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGAAGTCTGTCAGGCGAGGCGCACTGCGCACCCCGCGCTGCGCCATCATGGGCTGCCCTTCA CCTGGTTCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGGCTGTG CGGGATTGACTACTACGCCCCACGAGGAAACCAACAATGAGTCTTCTGTCATCTACATGTTCTGGTCCACTTCACTATC CCCCGATTTGTCATATTTCTTCTGCTACGGACGCTTCTGCGCCGCTGCGAGCGCCCGCCGACGCTGGGTGGGCGCGGAGA ACTCGCTGCGCATGGTATCATATGGTTCATCGCTTTCCTAATCTGCTGGCTGCCCTAGCTGCTGCTTCTACATCTT CACCCTCAGGGCTCTGACTTGGCCCCATCTTCAATGACCATCCCGGCTTCTTGGCAAGACTTCTGCGCTACAACCCC GTCATCTACATCATGATGAACAAGCAGTTCGCGCCCGGGCGCTGGACGGGCGCTGGGGCGCACCGGCGCTGGCGCGAA GGATCAGTTTCAAGCTCTCGCTCTCCAGGGACAGACTTCCGTTTCCGTTTCCGCGGCGCCAGGCGCGAACAACCTGCTCGG CTCTGGACAGAAACAGCAAGTGGCGCTGCCCTAA</p>
Opto-GPR26	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCCGAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGCTTCTGTCACAGCGCGACATCCGCGCGCAGGCGCTCAACTACATCTGCTCA ACCTGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGCACGGGTACTTGTCTTGG TGGGCCACGGGCTGCAACCTGGAGGGCTTCTTGGCCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGGCC ATCGAGCGGTACGTGGTGGTGGTTCCTGGTGGTACCGGGCCAAAGTGGCCTCCGCGACCCCATCATGGGCTGCCCT TCACTGGGTACATGGCTCTGGCCTGTGCCGCGCCCCCTCGTGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGGCTC GTGCGGATTGACTACTACGCCCCACGAGGAAACCAACAATGAGTCTGTTCTCATCTACATGTTCTGGTCCACTTCACT ATCCCCCTGATTTGTCATATTTCTTCTGCTACGGAAAGGTGCTCAAGGTGGCCGCTTCCATTTGCAAGCGCATTCGACGTGATCA CCATGACAGCGCTGGTGTGCTGCTGGTGTGCTGACCCCAAGTGTGCGGGAACGCTGTCTGGAGGGCGGAGCCGACACA GCGAGCCACCGCATGGTATCATATGGTTCATCGCTTTCCTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTCTTACATC TTCACCCATCAGGGCTCTGACTTGGCCCCATCTTCAATGACCATCCCGGCTTCTTGGCAAGACTTCTGCGCTTACAAC CCGTCATCTACATCATGATGAACAAGCAGTTCGCGCAAAAGTTCGCAAGGAGATCTGAACAGGCTCTGCAACAGCCCTCAT CCACTCTCTGGCCTCACAGCGACTCTCACAGCCAGAACATTCTGCCGTTGTCTGAGACAGAAACAGCAAGTGGCGCT GCCTAA</p>
Opto-GPR27	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCCGAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGCTTCTGTCAGCGTGTGCGGGGAGCGAGCTGCAACCGCCCTCAACTACATCTGCTCA TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGCACGGGTACTTGTCTTGG GCCCCAGGGCTGCAACCTGGAGGGCTTCTTGGCCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGCGCACACCGCTTCTATGACAGCGCCTGCGCCGCTGGCCGCTGGTGGTGGTGGTGGTGGTGG CCTTCACTGGGTATGGCTCTGGCCTGTGCCGCGCCCCCTCGTGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGT CTGCTGCGGGATTGACTACTACGCCCCACGAGGAAACCAACAATGAGTCTGTTCTGTCATCTACATGTTCTGGTCCACTT ATCATCCCCCTGATTTGTCATATTTCTTCTGCTACGGACACGACCGCGCAAGATGCGGCCCGCGCCTGGTGGCCGCTCA GCCAGACTGGACCTTCCAGCGCCCGGGCGCCACCGCCAGGCGCGCCCAACTGGAGGGGGGCTTGGCCCGGGGCCAC GCCGCCCGGCTTGTGGGCATCCGCGCCGAGGGCGGGCGCGCGCGCCCTCTCTGCTGGAAAGATTCAGAGC GAGAAGGGCTGTGCCGATGGTATCATATGGTTCATCGCTTTCCTAATCTGCTGGCTGGCTGCTGCTGCTGGGTGGCTTCT ACATCTTACCCATCAGGGCTCTGACTTGGCCCCATCTTCAATGACCATCCCGGCTTCTTGGCAAGACTTCTGCGCTCTA CAACCCCGTCTACATCATGATGAACAAGCAGTTCGCGACTGCTTCAAGGGCCAGTTCCTGCTGCCAGAGCCCGG ACCACCCAGGCGACCCATCCCTGCGACTTGAAGGCATTTGGTTTAAACAGAAACAGCCAAAGTGGCGCTGCCCTAA</p>
Opto-GPR31	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCCGAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGCTTCTTCTGTTCCGGGTGAGGGTGTGGAAGCCGCTCAACTACATCTGCTCAAC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGCACGGGTACTTGTCTTGG GCCCCAGGGCTGCAACCTGGAGGGCTTCTTGGCCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGTCCACCTCGGCTTAAGTCAACCTGCTGTTCTCTCAGGCGCCATCATGGGCTGCCCTTCA CCTGGTTCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGTCTGCTG CGGGATTGACTACTACGCCCCACGAGGAAACCAACAATGAGTCTTCTGTCATCTACATGTTCTGGTCCACTTCACTATC CCCCGATTTGTCATATTTCTTCTGCTACGGAGGCATCATAGGGCTTCCAGAAAAGACTCCGGAGGCTGAGAAAAGCCCA AGCTTACGGGGCCAGCGCATGGTATCATATGGTTCATCGCTTTCCTAATCTGCTGGCTGCCCTACGCTGGGTGGCGCT CTACATCTTACCCATCAGGGCTCTGACTTGGCCCCATCTTCAATGACCATCCCGGCTTCTTGGCAAGACTTCTGCGCTC TACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCGCGAGCTTCTATCGAGGGTGTTCACACCTTCCGAGGCAAA GGAGGCGAGCAGAGCCCGAGATTCAACCCAGAGACTCTTATTCACAGAAACAGCCAAAGTGGCGCTGCCCTAA</p>
Opto-GPR32	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCCGAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGCTTCTGTCAGCGTGTGCGGGGAGCGAGCTGCAACCGCCCTCAACTACATCTGCTCA TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGCACGGGTACTTGTCTTGG GCCCCAGGGCTGCAACCTGGAGGGCTTCTTGGCCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGTCCACCTCGGCTTAAGTCAACCTGCTGTTCTCTCAGGCGCCATCATGGGCTGCCCTTCA CCTGGTTCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGTCTGCTG CGGGATTGACTACTACGCCCCACGAGGAAACCAACAATGAGTCTTCTGTCATCTACATGTTCTGGTCCACTTCACTATC CCCCGATTTGTCATATTTCTTCTGCTACGGAGGCATCATAGGGCTTCCAGAAAAGACTCCGGAGGCTGAGAAAAGCCCA AGCTTACGGGGCCAGCGCATGGTATCATATGGTTCATCGCTTTCCTAATCTGCTGGCTGCCCTACGCTGGGTGGCGCT CTACATCTTACCCATCAGGGCTCTGACTTGGCCCCATCTTCAATGACCATCCCGGCTTCTTGGCAAGACTTCTGCGCTC TACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCGCGAGCTTCTATCGAGGGTGTTCACACCTTCCGAGGCAAA GGAGGCGAGCAGAGCCCGAGATTCAACCCAGAGACTCTTATTCACAGAAACAGCCAAAGTGGCGCTGCCCTAA</p>

	<p>CGAGGCCCGCAGTACTACCTGGCCGAGCCATGGCAGTTTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCCACAGCTGTACGCTCTGCAGAAAGGATACTGCAGAAAGGACTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTCACCACCACCCTTACACCTCTCTGCACGGGTACTTCTGTTGG GCCACGGGTGCAACTGGAGGGTCTTTGGCCACTTGGGCGGTGAAATGCACTGTGGTCCTTGGTGGCTCTGGCCATC GAGCGGTACGTGGTGTGTACCCCTTACAGTACAAGGCTGTGTGGGACCTTGGCAGCCATCATGGGCTGCCTTCA CCTGGGTATGGCTCTGGCTGTGCCCGCCCCCTCGTCGGCTGGTCCAGGTACATCCGGAGGCTGACAGTGTCTGTG CGGATTGACTACTACAGCCCCACGAGGAAACCAAAATGAGTCGTTCGTATCTACATGTTCTGGTCCACTTACATATC CCCCGATTGTACATATTTCTGTACGGAATGATGACAGTGTCTGATGAAAAGCCAGAAAGGCTCGCTGGCCGGGGCAGC GGCTCCGACAGTGAAGAAAGTCCGAGAGCCAGAGAGCAGGACCCGACAGGAGCAGACCATCCGATGGTATCATATGGT CATCGCTTTCCTAATCTGTGGCTGCCCTACGCTGGGTGGCTTCTACATCTTACCACATCAGGGCTCTGACTTGGCC ATCTTACATGACCATCCGGCTTCTTTGCCAAGACTTCTGCCGTCTACAACCCCGTCATCTACATGATGAAACAAGCAGT TCCGGCGGGTGTTCGTGACGGTGTGTGCTGCCCTGTGCTGCAGCACGCCAACCCAGAGAAAGCCCTGCGCTACATG GCATCCACCACCAGCAGCGCCCGCTTTGTGACGCGCCGCTTGTCTGTGCGCTCCCGCCGACCTCTCTGCAAGGAACT GAGAAATTTTCTAAGCACTTTTCAGAGCGAGCCGAGCCCAAGTCAAGTCCAGTCAATGAGTCTGTGAGTCTGAGTCA CAAATCAGGCGCAAACAGCAATTTCTGCTGCAGAGAATGGTTTTTCAGGAGCATGAAGTTACAGAAACAGCCAAAGTGGC GCTTGCCTAA</p>
Opto-GPR42	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACCTGGCCGAGCCATGGCAGTTTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCCACAGCTGTACGCTTTTGTGGCAAGCTGCGGTGGCCCGCGGTGGCCGCTGCTGCTGCTCA ACCTGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCCTTACACCTCTCTGCACGGGTACTTCTGCTT TGGGCCACGGGTGCAACTGGAGGGTCTTTTGGCCACTTGGGCGGTGAAATGCACTGTGGTCCTTGGTGGTCTGGCC ATCGAGCGGTACGTGGTGGTGGCCACCACCTGTTGTAACAAGACCCGCGCGAGGCTGGGGCGGCTGCTGCTGCTGCT TCACCTGGGTATGGCTTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGACGAGTGT GTGGGGGATTGACTACTACAGCCCCACGAGGAAACCAAAATGAGTCGTTCGTATCTACATGTTCTGGTGGTCCACTTCA ATCCCCGATTGTATATTTCTGTGCTACGAGCCCTGGTGTGGATCTCCGACAGAGGGGCGGACCCGCGGACAGGAA GGGTGGCGGCATGGTATCATCATGGTTCATCGCTTTCCTAATCTGCTGGTGGCTACGCTGGGTGGCGTTCATACCTT CACCATCAGGGCTCTGACTTTGGCCCATCTTTCATGACCATCCCGCTTTCTTTGCCAAGACTTCTGCCGTTCACAAACCT GTACATACATCATGATGAACAAGCAGTTCGCGCCGACTTTCATGAGCTGCTGAGGAGTGTGTGGTGGTCTGAGTGGC GGCAGCAGGAGAGCAGCATGGAGTGAAGGAGCAGAAGGAGGGAGGAGCAGAGAGCGGACCGACCGTGAAGAAAGAC CAGTGAACACTCAGAGGGCTGTGAACCTGGTGGCCAGGTGGCTGTGCTGAAAACACAGAAACAGCAAGTGGCGCTGCC TAA</p>
Opto-GPR45	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACCTGGCCGAGCCATGGCAGTTTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCCACAGCTGTACGCTGTACAGAGGCGGCTATGCGCTCGGCCCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCCTTACACCTCTCTGCACGGGTACTTCTGCTTTGG GCCACGGGTGCAACTGGAGGGTCTTTTGGCCACTTGGGCGGTGAAATGCACTGTGGTCCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGTCCAGCGCCAGGACAAGCTGAACCCGCGCAGGGCCATCATGGGCTGCGCTTCACTGGGTCA TGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGACGAGTGTCTGGCGGGATGA CTACTACAGCCCCACGAGGAAACCAAAATGAGTCGTTCGTATCTAATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT GTCATATTTCTGCTACGGATGCATCTCAACACGGTCCGCAAGAAGCCGTCGCGGTGCACAACAGCTCGGACAGCCTGG ACCTGGCGCAGCTCACAGGGGCGGGCTTGGCCGCTTGCAGCGGAGCAACAGGTCACGCTGGACTTGGAGTTCAGAGCCAA GGCCTTCCGATGGTATCATCATGGTCACTTTCCTAATCTGCTGGCTGCCCTACGCTGGGTGGCCTTACATCTTTC ACCCATCAGGGCTCTGACTTTGGCCCATCTTTCATGACCATCCCGCTTTCTTTGCCAAGACTTCTGCCGTTCACAAACCG TCATCTACATCATGATGAACAAGCAGTTCGCGAGGGCTGCATAGAGTTGCTGCCCCAGACCTTCCAAATCTCCCCAAAGT GCCTGAGCGGATCCGAAGGAGAAATCCAGCCAAAGCACAGTCTACGTGTGCAATGAAAACAGCTCTGCGGTTACAGAAACAGC CAAGTGGCGCTGCCTAA</p>
Opto-GPR50	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACCTGGCCGAGCCATGGCAGTTTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCCACAGCTGTACGCTGTACGACGAAAGCAAGAGTCCCGAATTTCTCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCCTTACACCTCTCTGCACGGGTACTTCTGCTTTGG GCCACGGGTGCAACTGGAGGGTCTTTTGGCCACTTGGGCGGTGAAATGCACTGTGGTCCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGTCCAGCAGCCAGGACAAGCTGAACCCGCGCAGGGCCATCATGGGCTGCGCTTCACTGGGTCA CCTGGGTATGGCTCTGGCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGACGAGTGTCTGGT CGGATTGACTACTACAGCCCCACGAGGAAACCAAAATGAGTCGTTCGTATCTACATGTTCTGGTGGTCCACTTCAATCAT CCCCGATTGTACATATTTCTGTACGGAAGGACTTGGACCAAAAGTGTGGCGGGCCGTGACCTGACGGGCGAAGTCTGT ACAACCAACTTGTGAGGTTCGCAATTTTCGATGGTATCATCATGGTATCGCTTTCTTAATCTGCTGGTGGTGGTGGTGG TGGGTGGCGTTCATACATCTTACCACATCAGGGCTCTGACTTTGGCCCATCTTTCATGACCATCCCGCTTCTTTGCCAAG ACTTCTGCCGTTCACAAACCCGCTCATCTACATCATGATGAACAAGCAGTTCGCGAGAGAACTGGACCATCTTTCATGCTA TGGCGCACCTATCATATTTCTTCTGCTGCCCTCATCAGTATGATTTCTGAGATGACAGGAGGCGCCATCCCTGGCGCCCG TGCCATGCTCGGACCAAGCTCGTGAACAAGCCGTGCCCATGCTGTCTGCTGCTGGAGGAAACCCGATGAATGTCCGG AATGTTCCATTACCTGGTGTGCTGAGCTGGCCACCCGACCGTGCCTTGGCCACCCTAAGCCCAATTCCAGATCTCTCT CTGCTATCGCAAACTGGCTTACCCACCAAGTCTGCTTTAGCCACTCCAAGGCTGCCCTGGTCACTCCAAAGCTTGT CTCTGGCCACTCCAAGCTGCTCTGGTCAACCAAGTCTGCCACTGTCTACCTAAGCTGCTCTGTCCATTTCAAGGCT GACTCTGTCCATTTCAAGGGTACTCTGTCCATTTCAAGCCTGACTCTGTTCATTTCAAGCCTGCTTCCAGCAACCCCAAGC CCATCACTGGCCACCATGTCTCTGCTGGCAGCCACTCCAAGTCTGCTTCAGTGTGCCACAGCCACCTTAAACCCACAC TGGCCACATCAAGCCAGCTACCAGCCATGCAGAGCCACCACCTGTGACTATCCCAAGCTGCCACTACAGCCACCCCTAAG CCCCTGCTGCTGACAACCCGAGCTCTGCTCCATTTGCCCGAGATCCCTGCCATTTGCCACCCTGTGCTGAGCACA GTGACCTCCCTGAGTCGGCTCTAGCCCTGCCGCTGGGCCCCAAGCCTGCTGCCAGCCAGCTGGAGTCTGACACCCTCG TGACCTTCTGACCTACTGTAGTCACTACCAGTACCAATGATTAACATGATGCTGCTGGTATTGATGTTGAAGATGATCTT GATGAAATGGCTGTGACAGAAACAGCCAAAGTGGCGCTGCCTAA</p>
Opto-GPR52	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACCTGGCCGAGCCATGGCAGTTTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCCACAGCTGTACGCTTTTTCATGTTGCTCCACTGTTACATCATATACTCAACTACATCTGCTTCA ACCTGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCCTTACACCTCTCTGCACGGGTACTTCTGCTT TGGGCCACGGGTGCAACTGGAGGGTCTTTTGGCCACTTGGGCGGTGAAATGCACTGTGGTCCTTGGTGGTCTGGCC ATCGAGCGGTACGTGGTGGTGAACAAGCCTTTCTTACAATCAACTGGTACCCCTTGTGCCGCTCATGCGGCGCATGCGCT TCACCTGGGTATGGCTTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGACGAGTGT GTGGGGATTGACTACTACAGCCCCACGAGGAAACCAAAATGAGTCGTTCGTATCTACATGTTCTGGTGGTCCACTTCAATCAT ATCCCCGATTGTACATATTTCTGTACGGACACATTTTCAAATTTGCCGTCAGCACACCAAGAGATAAATGACCGAA GGGCCCCGATTCCCTAGTCAAGGAGTATCTTCCAGAGAGACTGGACACAGCCCTGACCTGCGTACGCCCGCATGGTGT CATCATGGTATCGCTTTCCTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTTCATCATCTTACCACATCAGGGCTGTGAC</p>

	TTTGGCCCCATCTTCATGACCATCCCGGCTTCTTTGCCAAGACTTCTGCCGTCTACACCCTGCATCTACATCATGATGA ACAAGCAGTTCCGCCTAGGCCCTCCGAAGGCTGTCTGAGACAATGTGCACATCTGTATGTGTGAAGGATCAGAAAGCACA AGAACCACAACTAGGAAACGGGCTAATTTCTTGGCTCCATTACAGAAACAGCCAAAGTGGCCCTGCCTAA
Opto-GPR55	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCTTTAGCACCCTCCTTAAGAACAGGTGGCCCGATTATGCTGCCCTCAACTACA TCTTGCCTCAACTGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTCCACCACCCTCTACACCTCTCTGCACGGGTA CTTCGTCTTTGGGCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCCGCTGAAATTCGACTGTGGTCTTGGTG GTCCTGGCCATCGAGCGGTACGTGGTGGTGGTACCCGCTACTGGTGAGCCACCTCCGGTCCCGCAGGAAGGCCATCATGG GCGTCCGCTTCACTGGTTCATGGCTCTGGCCTGTGCCGCGCCCCCTCTCGTGGTGGTCCAGGTACATCCCGAGGGCAT GCAGTGTCTGTGGGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCTGTGCTCATCTACATGTTCTGGTGC CACTTCATCATCCCCCTGATTGTATATTTCTTCTGCTACGGAAGGAGCATCCACATCTGCTGGCCGCGGAGATCACACCC AGGACTGGTGCAGCAGAAAGCCTGCATCCGCATGGTATCATCATGGTTCATCGCTTTCTCAATCTGCTGGTGGCTCACG GCGGTGGCGTTCTACATCTTCACTTCCACCATCAGGGCTCTGACTTTGGCCCATCTTACATGACCATCCCGCTTTCTTGGCAAG ACTTCTGCCGTCTACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCGCGATGAACATCAGGCGCCACCGCCCTCCA GGTCCAGCTGGTCTGCAGGACACCGATCTCCCGGGCACAGAAACAGCCAAAGTGGCCCTGCCTAA
Opto-GPR61	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCTTCGCCAAGACGCTGCCCTCCGAAAACCTACATGTTCTGCTGATCATGCTTGGC CCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTCCACCACCCTCTACACCTCTCTGCACGGGTACTTCGTCTTTGGGCC CACGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCTGGCCATCGAG CGGTACGTGGTGGTGGTCCACCCATGGCTACGAGGTGGCCATGACGCTGGGGCTGGCCATCATGGGCTTCCGCTTCACTT GGTTCATGGCTGTGGCCTGTGCCGCGCCCCCTCTCGTGGTGGTCCAGGTACATCCCGAGGGCATGCACTGCTGCTGGCGG GATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCTGTGCTCATCTACATGTTCTGGTGGTCTTCACTCATCCCC CTGATTGCTATTTCTTCTGCTACGGAAGCATGTTCCGAGTGGCCCGTGGTGGCCATGCAGCAGGGCCGCTGCCACGT GGATGGAGACACCCCGGCAACGCTCCGAATCTCTCAGCAGCCGCTCCACGATGGTCCACGCTCGGGGGCCCCAGAGCCAC CCCACCCGGAGCTTTGGGGGAGGAAAGCAGCAGCATGGTATCATCATGGTTCATGCTGGTCTGGTGGTCTGGCCTGGCC TACGCTGGGTGGCGTCTACATCTTCAACCATCAGGGCTCTGACTTTGGCCCATCTTACATGACCATCCCGGCTTTCTTTG CCAAGACTTCTGCCGTCTACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCGCGGGGAGTGGAGCAAGCAGTTTGT CTGCTTCTCAAGCCAGTCCAGAGGAGGAGCTGAGGCTGCCAGCCGGGAGGGCTCCATGGAGGAACTTCAGGCAACTCTC CTTCCAGGGACTGGTGTCTTCTGAGTCTGGGTTTCCCGACCCCTACCCAGCCCAAGCAGGAGCCACCTGCTGTGACT TTCGAATCCAGGCCAGATAGCTGAGGAAACCTCTGAGTTCCTGGAGCAGCAACTCACAGCCGACATCATGCTGAGACAG CTACCTCCGCTCTGCCGCTCAACCCGGCTGGAGTCAACAGAAACAGCCAAAGTGGCCCTGCCTAA
Opto-GPR62	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCTGTGCTGCGCAGCCGGACTGCGCGACCTCAACTACATCTGTCTAACCTGG CCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTCCACCACCCTCTACACCTCTCTGCACGGGTACTTCGTCTTTGGGCC CACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCTGGCCATCGAG CGGTACGTGGTGGTGGTGCACCCGCTGCCGCGAGGCTCGCGCCCGCCGCCATCATGGGCTGGCTTCACTGGTTCATGG CTCTGGCCTGTGCCGCGCCCCCTCTCGTGGTGGTCCAGGTACATCCCGAGGGCATGCACTGCTGCTGGCGGATGACTA CTACACGCCCCACGAGGAAACCAACAATGAGTCTGTGCTCATCTACATGTTCTGGTGGTCTTCACTCATCCCTGATTGTC ATATTTCTGCTACGAGGACATCTTCTGGTGGCGGCTCGCGCTGCCCTGAGGCCCCACGCGCGCGCGGGTCCCGAC TCCACTCGGACTCTCTGGATAGCCGCTTTCCATCTTGGCCGCGCTCCGGCTCGCTTCCCGGGGCAAGGCGCCCGCAT GGTATCATCATGGTTCATGCTTTCTCAATCTGCTGGCTGCCCTACGCTGGGGTGGCGTTCATCATCTTCACTCCCTGAGG TCTGACTTTGGCCCATCTTCAATGACCATCCCGGCTTTCTTTGCCAAGACTTCTGCGCTTACAACCCGCTCATCTACATCA TGATGAACAAGCAGTTCGCTTGGCACTGGGCGGCTTCTCTCGCGTGCATGCTGGACCTGTGGCGGCTGCACTCCGCA AGCCTGGCACCCGCGGCACTCTTGAATGCCCTCCAGAGGCCCCACAGAGGGCCCTGCGGTGGGCTTCTGAGGCTCCAGAA CAGACCCCGAGTGGCAGGAGGCGGAGCCCGCATACCAGGGCCACCTGAGAGTCTCTCTCCACAGAAACAGCCAAAG TGGCCCTGCCTAA
Opto-GPR63	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCTTTACAAAAGCTGCCATGAGGCTGCACTTCACTCACTCCCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTCCACCACCCTCTACACCTCTCTGCACGGGTACTTCGTCTTTGG GCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGTCTCTGGCCATC GAGCGGTACGTGGTGGTGGTCCAGAGGAGGATAAGCTAAACCCATATAGAGCCATCATGGGCTCCGCTTCACTGGGTCA TGGCTTGGCCTGTGCCGCGCCCCCTCTCGTGGTGGTCCAGGTACATCCCGAGGGCATGCACTGCTGCTGGCGGATTTGA CTACTACACGCCCCACGAGGAAACCAACAATGAGTCTGTGCTCATCTACATGTTCTGGTGGTCCACTTCACTCATCCCC TGATGCTATTTCTGCTACGAGGACACTCAACCCCTTGGCAACAATGCCTTGGAGATCCAGGATGATGAGGATAT GCCTCAGCCAGGCCAGCAACTGGGCTCATGAGTCTGCAGAGGCTTTCAGATGAGCATGACATGGGCTTTAAAACAGC TGCCTTCCGATGGTATCATCATGGTTCATGCTTTCTCAATCTGCTGGCTGCCCTACGCTGGGGTGGGCTTCTACATCTT ACCCATCAGGGCTCTGACTTTGGCCCATCTTCAATGACCATCCCGGCTTTCTTTGCCAAGACTTCTGCGCTCAACACCCCG TCATCTACATCATGATGAACAAGCAGTTCGCGATGCTTGCCTGGACATGATGCTTAAGTCTTCAAGTPTTTGGCGAGCT CCCTGGTACACAAAGCGACGGATACGCTTAGTGTCTATGTGTGGGAAACATCGGACGGTGGTACAGAAACAGC CAAGTGGCCCTGCCTAA
Opto-GPR65	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCTTTACAAAAGCTGCCATGAGGCTGCACTTCACTCACTCCCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTCCACCACCCTCTACACCTCTCTGCACGGGTACTTCGTCTTTGG GCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGTCTCTGGCCATC GAGCGGTACGTGGTGGTGGTCCAGAGGAGGATAAGCTAAACCCATATAGAGCCATCATGGGCTCCGCTTCACTGGGTCA TGGCTTGGCCTGTGCCGCGCCCCCTCTCGTGGTGGTCCAGGTACATCCCGAGGGCATGCACTGCTGCTGGCGGATTTGA CTACTACACGCCCCACGAGGAAACCAACAATGAGTCTGTGCTCATCTACATGTTCTGGTGGTCCACTTCACTCATCCCC TGATGCTATTTCTGCTACGAGGACACTCAACCCCTTGGCAACAATGCCTTGGAGATCCAGGATGATGAGGATAT GCCTCAGCCAGGCCAGCAACTGGGCTCATGAGTCTGCAGAGGCTTTCAGATGAGCATGACATGGGCTTTAAAACAGC TGCCTTCCGATGGTATCATCATGGTTCATGCTTTCTCAATCTGCTGGCTGCCCTACGCTGGGGTGGGCTTCTACATCTT ACCCATCAGGGCTCTGACTTTGGCCCATCTTCAATGACCATCCCGGCTTTCTTTGCCAAGACTTCTGCGCTCAACACCCCG TCATCTACATCATGATGAACAAGCAGTTCGCGATGCTTGCCTGGACATGATGCTTAAGTCTTCAAGTPTTTGGCGAGCT CCCTGGTACACAAAGCGACGGATACGCTTAGTGTCTATGTGTGGGAAACATCGGACGGTGGTACAGAAACAGC CAAGTGGCCCTGCCTAA
Opto-GPR68	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT

	CGAGGCCCGCAGTACTACCTGGCGGAGCCATGGCAGTTCTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCCCTACGCTGTACGTCGGCTACCTGCAGATCAAGGCC GGAACGAGCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGCACGGGTACTTCGCTTTGG GCCACGGGTGCAACTGGAGGGTCTTTGGCCACCTTGGCGGTGAAATGCACTGTGGTCTTGGTGGCTTGGCCATC GAGCGGTACGTGGTGGCCATCCCTCCGCTTCCACCAGTTCCGACCCTGAAGCGGCCATCATGGCGTTCGCTTCA CCTGGTTCATGGCTTGGGCTTGGCCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGGAGGCTGCGAGTCCGTGTG CGGATTGACTACTACAGCCCCACGAGGAAACCAAAATGAGTCGTTCTGTCATCTACATGTTCTGGTCCACTTACATC CCCCGATTGTCATATTTCTTCTGCTACGGAGGATCTTGCCTGGCGCTGGCCGGAGCCAGGCACCAGAAAAGCCGAAG ACCAGATCCAGCGCATGGTATCATATGGTTCATCGCTTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCTTCTACAT CTTACCACCTCAGGGCTGACTTTGGCCCCATCTCATGACCATCCCGCTTCTTTGCCAAGACTTCTGCCGTCAACA CCCTCATCTACATCATGATGAACAAGCAGTTCCGCGGAGCTGGCCGCTCCGCGGGCTGGCTGGCTTCTTCTCACT GCTCCAGGACCGGCCGGCCAGGAGGCTTACCCTGGGTGGCTGGCCGAGGCTCCGGGAAAAGCGGGCCAGGGTGAAG GCCGAGCTGTTGACCAAGCTCCACCCGGCTTCCAGACCCTTAATCGCCAGGCTGGCGGGTCCCCACGGCAGGTTG GCCACAGAACCGCAAGTGGCGCTGCCTAA
Opto-GPR75	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCCCTACGCTGTACGCTTTTTTCGATCCAGCCTTCCAGAAATTCAGAAACCACTCAACTACATCTGCT TCAACTTGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGCACGGGTACTTCTGT CTTTGGGCCACGGGCTGCAACTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCAGATGTTGCTGGTGGTGGCTG GCCATCGAGCGGTACGTGGTGGTGTGGGAAACAGCCTAATCGCACGGCTCCTTTCCCTGCGCCATCATGGCGTGGCT TCACCTGGGTTCATGGCTTGGCTGTGCCGCCCCCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGCGCATCGAGTGCCTC GTGGGGATTGACTACTACAGCCCCACGAGGAAACCAAAATGAGTCGTTCTGTCATCTACATGTTCTGGTGGTCCACTTCACT ATCCCCCTGATTGTCATATTTCTTCTGCTACGGAATGATTGCTCAGACCTTCCGGAAGAAGCCTCAAGTCAGAAAGTGGCCCC CTGTAATACAGTCATGCTTCCAGACACAGCCTTTCATGGGGTCCCTGTGCAGGAGGTGGAGATCCCATCCAGTGTGC CATGCCGCTCTGTATAGGAACCAAGAAATTAACAACAACCTGCAGCAGCTTACAGCCGTGAAATTCAGAAAGTGGTGGTGGT CTGGTCAACCCCTGCAGCAAGCCGACTCCAGCTCGTATCAGCCATCAACTTCCACTGCCAAGGATTCAGAAAGCCGTGGCA TGGTGCATCATGTTGTCATCGCTTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTTCATCATCTTCAACCCATCAGGG CTCTGACTTTGGCCCATCTTCTATGACCATCCCGCTTCTTTGCCAAGACTTCTGCGCTGTACAAACCCGCTCATCTACATC ATGATGAACAAGCAGTTCCGAGGAAAGTGTCTGGTGCCTCAATACATAGGCTGGTTTTTTCTGCTGCAACAAAAGA CTCGACTTCCAGCCATGGGAAAGGAAACCTCGAAGTCAACAGAAACAATCTCCCATCATGAAAACAACCTTGCCTACAT GTTATCTCAAAAGCCACAGAAAGAAATTTGGAGCCAGGCTTGGGCCAAGTCAATCAAAAGAAATGATGGTGGTGGTGGT ATCTCTGCTGGACATCAACACTGTGGTCCAGCAGCTCGACCCCATCAACACTCGGATTGACCTTACTACAGCATCTATA ACAGCAGCCCTTCCAGGAGGAGAGCCCATGTAACCTTACAGCCAGTAAACTCTTTGGATTGGCAATTCATATATTGC CATGCAATATACACCACTAATGACTTAGTGCAGGAATATGACAGCACTTACAGCAAGCAGATTCCAGTCCCTCCGTGATA GAAACCGCAAGTGGCGCTGCCTAA
Opto-GPR78	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCCCTACGCTGTACGCTTGCCTTACAGCCGAGAGCTCCGCACTCGAGCCCTCAACTACATCTGCTCA ACCTGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGCACGGGTACTTCTGCTT TGGGCCACGGGCTGCAACTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCAGTGTGGTCTTGGTGGTCTGGCC ATCGAGCGGTACGTGGTGGTGGCTTCCCATGCGCTACGCCGGAGCCCTGCGACCGCGCTTATGCCATCATGGCGTGGCT TCACCTGGTTCATGGCTTGGCTGTGCCGCCCCCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGCGCATCGAGTGCCTC GTGGGGATTGACTACTACAGCCCCACGAGGAAACCAAAATGAGTCGTTCTGTCATCTACATGTTCTGGTGGTCCACTTCACT ATCCCCCTGATTGTCATATTTCTTCTGCTACGGACAGGTGCACCGGTGGCAGCAGACTGCCAGGCGATGGACACCGTCA CCATGAAGCGCTCGCGCTCGCCAGTGCACCCAGTGTGGCGAGCCCTGCCTCATCCAGCAGGCTCCAGCCCGCCGCA CCGCGCCACCCGATGGTATCATATGGTTCATCGCTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTTCATCATC TTCACCCATCAGGGCTGACTTTGGCCCATCTTTCATGACCATCCCGCTTCTTTGCCAAGACTTCTGCGCTTACAAC CCGTCATCTACATCATGATGAACAAGCAGTTCCGCAAGTCCGCGCCGATGGTGCACCCGCTTCTGTAAGAGAACCCCGCG CCCAGCATCCACCCATGACAGCTCTCTGGATGGCGGATGGTGCACAGCTGCTGAAGAGAACCCCGCGCCAGGCTTC ACCCACAACGGCTCTGTGGACACAGAGAATGATTCTGCTGCAGCAGACACACAGAAACCGCAAGTGGCGCTGCCT AA
Opto-GPR82	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCCCTACGCTGTACGCTTTTTTAACAATAAGTAAATAACATCACTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGCACGGGTACTTCTGCTTTGG GCCACGGGCTGCAACTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCAGTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGTGCTATGAGAAAATATTTATGGCCATTTACTGAAAAAATTTCCGAGCCCAACTTTGCCATCA TGGCGTCCGCTTACCTGGTTCATGGCTTGGCTGTGCCGCCCCCCCCCTCGTCGGCTGGTCCAGGTACATCCCGGAGGG CATGCACTGCTCGTGGGGATTGACTACTACAGCCCCACGAGGAAACCAAAATGAGTCGTTCTGTCATCTACATGTTCTGGT GTCCACTTACATCCCTGATTGTCATATTTCTTCTGCTACGGATCTTTGTAAGCCATCTGAGAAAAAATGAAAGCTGTA CGTCCATATGAGAAAGATTTGACTTACAGTTCTGTGGCATGGTATCATATGGTTCATCGCTTTCTTAATCTGCTGGCT GCCCTACGCTGGGTGGCTTCTACATCTTACCCATCAGGGCTCTGACTTTGGCCCATCTTATGACCATCCCGCTTCT TTTGCCAAGACTTCTGCCCTTACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCCGCAAAACATATATAATCTCT TTACAAAGTCTAATTCAGCACATATGCAATCATATGGTACAGAAACCGCAAGTGGCGCTGCCTAA
Opto-GPR83	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCCCTACGCTGTACGCTATCTTCAAGAACCAGCGAATGCACTCGGCCCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGCACGGGTACTTCTGCTTTGG GCCACGGGCTGCAACTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCAGTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGTGCTATGAGAAAATATTTATGGCCATTTACTGAAAAAATTTCCGAGCCCAACTTTGCCATCA TGGCGTCCGCTTACCTGGTTCATGGCTTGGCTGTGCCGCCCCCCCCCTCGTCGGCTGGTCCAGGTACATCCCGGAGGG CATGCACTGCTCGTGGGGATTGACTACTACAGCCCCACGAGGAAACCAAAATGAGTCGTTCTGTCATCTACATGTTCTGGT GTCCACTTACATCCCTGATTGTCATATTTCTTCTGCTACGGATCTTTGTAAGCCATCTGAGAAAAAATGAAAGCTGTA CGTCCATATGAGAAAGATTTGACTTACAGTTCTGTGGCATGGTATCATATGGTTCATCGCTTTCTTAATCTGCTGGCT GCCCTACGCTGGGTGGCTTCTACATCTTACCCATCAGGGCTCTGACTTTGGCCCATCTTATGACCATCCCGCTTCT TTTGCCAAGACTTCTGCCCTTACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCCGCAAAACATATATAATCTCT TTACAAAGTCTAATTCAGCACATATGCAATCATATGGTACAGAAACCGCAAGTGGCGCTGCCTAA
Opto-GPR84	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCTGGTGGCAGCCCTT

	<p>CGAGGCCCGCAGTACTACCTGGCCGAGCCATGGCAGTTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCCCTCAGCTGTACGCTTTGGCCATCCAGCCCAAGCTCCGTACCAGCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGACGGGTACTTCTGCTTTGG GCCACGGGTGCAACTGGAGGGGTTCTTGGCCACCTTGGCGGTGAAATGCACTGTGGTCCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGCCACCCTAAGCTTTTTCCCAAGTTTTCAGTGCCAAAGGGGCCATCATGGCGTGCCTTCA CCTGGGTATGGCTTGGGCTGTGGCCGCCCCCCCCCTGCTGGCTGGTCCAGGTACATCCCGGAGGCTGCTGGTGTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTGCTCATCTACATGTTGCTGGTCCACTTACATC CCCCGATTGTCATATTTCTTCTGCTACGGACTCATCCACCAGGTCAAACGAGCAGCAGGACTGGACCAATACAAGT TGGCAGAGGCAAGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTTTCCAGGAGCTGGACAGCAG GTTAGCATCAGGAGGACCCAGTGGGGGATTTCATCTGAGCCAGTCAGTGTGCCACCACCCAGCCCTGGAAGGGGACTCA TCAGAAAGTGGGAGATCAGATCAACAGCAAGAGGCAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGATCTGCCAAGGCC AGCCAAATTAAGGAGCCAGAAGGGCTCCGGATTCTTTCATCGAAATTTGGGAAGGTGACTCGCATGGTATCATGTTGTC CGCTTTCCTAATCTGCTGGCTGCCCTACGCTGGGGTGGCGTTCATACATCTCACCCATCAGGGCTGACTTTGGCCCCATC TTCATGACCATCCCGGCTTCTTTCGCAAGACTTCTGCCGCTTACAACCCCGTATCTACATCATGAAACAAGCAATTC GCCAAGCATATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATACAGAAACCAGCCAAAGTGGCCGCTGC CTAA</p>
Opto-GPR85	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCGTGGTGGCAGCCCCCT CGAGGCCCGCAGTACTACCTGGCCGAGCCATGGCAGTTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCGCCATCAACTTCCCTCAGCTGTACGTCCTAGTGAAGATAAGACTTTGCATAGAGCAGCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGACGGGTACTTCTGCTTTGG GCCACGGGTGCAACTGGAGGGGTTCTTGGCCACCTTGGCGGTGAAATGCACTGTGGTCCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGCCATCACCGCTTCTATACAAGAGGCTGACCTTTGGAGCGCCATGCTGGTGGTCTGGCCATC CCTGGTTCATGGCTTGGCCTGTGCCGCGCCCCCCCCCTGCTGGCTGGTCCAGGTACATCCCGGAGGGCATGCAAGTGTGCTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTGCTCATCTACATGTTGCTGGTCCACTTACATC CCCCGATTGTCATATTTCTTCTGCTACGGACAGCATCGAAGAAAATGAGCCAGTCCAGTTTCTAGCAGCTCAGCCAGAG ACTGGACTTTTCATGGTCTGGAGCCAGTGGCCAGGCAAGTGCATTTGGTATGAGGATTGGGAAGGGTCCACACCACC CACCTTCTGGGCATCAGGCAAAATGCAAAACCCAGGAGGCAAGGCTATTGGTCTTACAGGATGCAAAATGAGGAAA AGAATCAGCCGATGGTATCATCATGCTGCTTCTTCTAATCTGCTGGCTGCCCTAGCCAGGCTGGCTTTCATGACT TCACCCATCAGGGCTCTGACTTTGGCCCCATCTTTCATGACCATCCCGGCTTCTTTCGCAAGACTTCTGCCGCTTACAACC CGTTCATCATCATGATGAACAAGCAGTTCGGCCGCTGTTTCAGCACACCTCTTTCATGCAAGAAATCCAGGTTACCA AGGAACTTACTGTGTTATAACAGAAACAGCCAAAGTGGCCGCTGCCTAA</p>
Opto-GPR87	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCGTGGTGGCAGCCCCCT CGAGGCCCGCAGTACTACCTGGCCGAGCCATGGCAGTTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCGCCATCAACTTCCCTCAGCTGTACGCTTTTTCCACATTAGGAATAAAACCAGCTCAACTACATCTGCTCAACCCTGG CCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGACGGGTACTTCTGCTTTGGGCC CACGGGTGCAACTGGAGGGGTTCTTGGCCACCTTGGCGGTGAAATGCACTGTGGTCCTTGGTGGTCTGGCCATCAG CGGTACGTGGTGGTGGTCAAGCCATTTGGGACTCTCGGATGTACAGCATAACCTTGGCCATCATGGGCTGCGCTTACCT GGGTTCATGGCTTGGCCTGTGCCGCGCCCCCCCCCTGCTGGCTGGTCCAGGTACATCCCGGAGGGCATGCAAGTGTGCTGCGG GATTGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTGCTCATCTACATGTTGCTGGTCCACTTTCATGACT CTGATTGTCATATTTCTTCTGCTACGGAGCCATATCCAGGTACATCCACAATCCAGCAGGCAATTCATAAGTCAAGCC GAAAGCGAAAACATAACCGCATGGTATCATCATGCTGCTTTCCTAATCTGCTGGCTGCCCTACGCTGGGTGGCCGTT CTACATCTTCAACCATCAGGGCTCTGACTTTGGCCCCATCTTTCATGACCATCCCGGCTTTCATGACCATCCCGGCTTTCGCT TACAAACCCGCTCATCTACATCATGATGAACAAGCAGTTCGCGAAGGCTGTTCAAAATAAATAATCAGAACAGGAATG AAAGCATCAGATCACTGCAAAAGTGTGAGAAATCGGAAGTTCGCATATATATGATTACATGATGTACAGAAACCAGCCAA AGTGGCCGCTGCCTAA</p>
Opto-GPR88	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCGTGGTGGCAGCCCCCT CGAGGCCCGCAGTACTACCTGGCCGAGCCATGGCAGTTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCGCCATCAACTTCCCTCAGCTGTACGTCGTTGCTTCCGAAAGTGCAGACCACCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGACGGGTACTTCTGCTTTGG GCCACGGGTGCAACTGGAGGGGTTCTTGGCCACCTTGGCGGTGAAATGCACTGTGGTCCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGCCGCGCCCCCCTACCAGGCGCTGTACCAGGGCCACGCCATCATGGGCTGCGCTTCA CCTGGTTCATGGCTTGGCCTGTGCCGCGCCCCCCCCCTGCTGGCTGGTCCAGGTACATCCCGGAGGGCATGCAAGTGTGCTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTGCTCATCTACATGTTGCTGGTCCACTTTCATCATC CCCCGATTGTCATATTTCTTCTGCTACGGAGCATGCTGCGCCGCTGCTGTCAGGCTCAAGCGGGTCAAGCTGCTCAACT TCCACTGCTGACCAAGTGGCCGGCTGCGCCGATGGTATCATCATGCTGCTTTCCTAATCTGCTGGTGGCCCTA CGTGGGTGGGCTTTCATCTTCAACCATCAGGGCTCTGACTTTGGCCCCATCTTTCATGACCATCCCGGCTTTCGCTTTGGCC AAGACTTCTGCCGCTTACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCGCGCGCTCCGCTGGCTCAGTCTGCCG GCGTGGCGACGCGCGCGCGCTGCGCTTGGCCACAGCCGCTGCCCGCAGTGTCCAGGCGCAACTGGGACCCCGCGCCG GGCCAGCACTGGACAGAAACCAGCTGCCTAA</p>
Opto-GPR119	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCGTGGTGGCAGCCCCCT CGAGGCCCGCAGTACTACCTGGCCGAGCCATGGCAGTTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCGCCATCAACTTCCCTCAGCTGTACGTCGTTGCTTCCGAAAGTGCAGACCACCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGACGGGTACTTCTGCTTTGG GCCACGGGTGCAACTGGAGGGGTTCTTGGCCACCTTGGCGGTGAAATGCACTGTGGTCCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGAAGCAGCCCTCCGCTACTTGAAGATCATGAGTGGTTCGTTGGCCATCATGGGCTGCGCTTCA CCTGGTTCATGGCTTGGCCTGTGCCGCGCCCCCCCCCTGCTGGCTGGTCCAGGTACATCCCGGAGGGCATGCAAGTGTGCTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTGCTCATCTACATGTTGCTGGTCCACTTTCATCATC CCCCGATTGTCATATTTCTTCTGCTACGGAGCATGCTCAAGATTGCCATGACAGCAGCAGAGATTCGAAAGATGAAAC ATGCAGGAGCCATGGCTGGAGTTATCGATCCCCAGGACTCCAGGACTTCAAAGCTCTCCGATGGTATCATCATGTTG CATGCTTTCTAATCTGCTGGCTGCCCTACGCTGGGGTGGCGTTCATCATCTTCAACCATCAGGGCTTTCGCTTTGGCCCC ATCTTCATGACCATCCCGGCTTCTTTCGCAAGACTTCTGCCGCTTACAACCCCGTATCTACATCATGATGAACAAGCAGT TCCGCTGACGCTTACCACATGGCCCTAGGATGAAAGGTTGCTCACCTTCCAGCTATTCCTCTCTTCTGCGCCAGGAATTG TGGCCAGAGAGGCCAGGGGAAAGTTCCTGTCATCATGCTCACTATCTCCAGCTCAGAGTTTGAATGACAGAAACCAGCCAA GTGGCCGCTGCCTAA</p>
Opto-GPR120	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCGTGGTGGCAGCCCCCT CGAGGCCCGCAGTACTACCTGGCCGAGCCATGGCAGTTCCATGCTGGCCGCCTACATGTTCTGCTGATCATGCTTGGC TTCGCCATCAACTTCCCTCAGCTGTACGTCGTTGCTTCCGAAAGTGCAGACCACCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGACGGGTACTTCTGCTTTGG GCCACGGGTGCAACTGGAGGGGTTCTTGGCCACCTTGGCGGTGAAATGCACTGTGGTCCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGAAGCAGCCCTCCGCTACTTGAAGATCATGAGTGGTTCGTTGGCCATCATGGGCTGCGCTTCA CCTGGTTCATGGCTTGGCCTGTGCCGCGCCCCCCCCCTGCTGGCTGGTCCAGGTACATCCCGGAGGGCATGCAAGTGTGCTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTGCTCATCTACATGTTGCTGGTCCACTTTCATCATC CCCCGATTGTCATATTTCTTCTGCTACGGAGCATGCTCAAGATTGCCATGACAGCAGCAGAGATTCGAAAGATGAAAC ATGCAGGAGCCATGGCTGGAGTTATCGATCCCCAGGACTCCAGGACTTCAAAGCTCTCCGATGGTATCATCATGTTG CATGCTTTCTAATCTGCTGGCTGCCCTACGCTGGGGTGGCGTTCATCATCTTCAACCATCAGGGCTTTCGCTTTGGCCCC ATCTTCATGACCATCCCGGCTTCTTTCGCAAGACTTCTGCCGCTTACAACCCCGTATCTACATCATGATGAACAAGCAGT TCCGCTGACGCTTACCACATGGCCCTAGGATGAAAGGTTGCTCACCTTCCAGCTATTCCTCTCTTCTGCGCCAGGAATTG TGGCCAGAGAGGCCAGGGGAAAGTTCCTGTCATCATGCTCACTATCTCCAGCTCAGAGTTTGAATGACAGAAACCAGCCAA GTGGCCGCTGCCTAA</p>

	GGGTCAATGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGCCTGTCGCGG GATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTTCATCATCCCC CTGATTGTCAATATTTCTGCTACGGAATAATTTTACAGACCTCGGAACACCTCCTGGATCGCAAGAGCTCTGCTACTCACA GTGAGATCACAAGGCGATCAAGGAAGAGGCTCACGGTAAAGCTGGCCTACTCGGAGAGCCACAGATCCCGGTGCCAGCA GGACTTCCGGCTGTCCGCATGGTATCATCATGGTATCGCTTTCCTAATCTGCTGGCTGCCCTACGCTGGGGTGGCGTTC TACATCTTACCCTACAGGCTCTGACTTTGGCCCCATTTTCATGACCATCCCGCTTTCCTTGGCCAAAGACTCTGCGCTT ACAACCCCGTCATCTACATCATGATGAACAAGCAGTTCCGCTGGAAGAAATTTTGTCTGCTTCTGGTCCAGAAAAGGG AGCCATTTAAACAGACACATCTGTCAAAGAAATGACTTGTGATTATTTCTGGCACAGAAAACAGCCAAGTGGCGCTGCC TAA
Opto-GPR132	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTCTCCACAAGACGGGCGTGGTGGCGAGCCCTT CGAGGCCCGCGAGTACTACTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCCTTGTGAAGCACCAGGAGCTCCGACCCGTCACACTTCACTTCACTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTCCACCACCCTTACACCTCTGACAGGGTACTTCTGCTTTGG GCCACGGGCTGCAACCTGGAGGGCTTCTTGGCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGTGCGCCCGCGGGGAGAAGATCGCCCGCGCCGCGCCATCATGGGCTGCCCTTCACTTCACTT CCGGCTTGGCCTGTGCGCGCCCGCTCGTGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGCCTGTCGCGGAT TGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTTCATCATC CCCCTGATTGTCAATTTCTGCTACGGACGGATTTTCAGGAGCATCAAGCAGAGCATGGGCTTAAAGCGCTGCCAGAAGG CCAAGGTGAAGCGCATGGTGTATCATGTTGTCATCGCTTTCCTAATCTGCTGGCTGCCCTACGCTGGGCTGGCTGTCA CTTCACCCTACAGGGCTGACTTTGGCCCCATTTTCATGACCATCCCGCTTTCCTTGGCAAGACTTCTGCCGTCTACAAC CCGCTCATCTACATCATGATGAACAAGCAGTTCCGCCAAGAAGTGTCCAGAAATCCATAAGGGGTGGAAGAGGTGTCATGA AAACAGCTCACAGGCTCACCCACAGCAGGAGCACCAGGAGCTGCAGTGCCTGGCCGTGCCAGTCCAGACCACTACCTT CTTCCAGGCCGTGCACCCACAGGGTACCATTGCCCTGCAAGAGGCTGATTGAGGAGTCTGTACAGAAAACAGCCAAGTG CGCCTGCCTAA
Opto-GPR135	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTCTCCACAAGACGGGCGTGGTGGCGAGCCCTT CGAGGCCCGCGAGTACTACTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCCTTGTGAAGCACCAGGAGCTCCGACCCGTCACACTTCACTTCACTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTCCACCACCCTTACACCTCTGACAGGGTACTTCTGCTTTGG GCCACGGGCTGCAACCTGGAGGGCTTCTTGGCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGTGCGCCCGCGGGGAGAAGATCGCCCGCGCCGCGCCATCATGGGCTGCCCTTCACTTCACTT CCGGCTTGGCCTGTGCGCGCCCGCTCGTGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGCCTGTCGCGGAT TGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTTCATCATC CCCCTGATTGTCAATTTCTGCTACGGACACATCTGCAAGACGGTGGCCTGTGCGACGTGCGCGGTGGAACACTTCAAG GCGCGGTGCTGGCCTTCTCAGCGAGGTGCGCACCGCATGGTGTATCATGGTATCGCTTTCCTAATCTGCTGGTGGC CTACGCTGGGGTGGCCTTTCATCTTACCCTACAGGGCTGACTTTGGCCCCATTTTCATGACCATCCCGCTTTCCTT GCCAAGACTTCTGCCGTCTACAACCCCGTTCATCTACATCATGATGAACAAGCAGTTTCGCGCAGCGGAGGGGTAACC GGACTAGGAATGTGGACGCTTCTGCCAGCCAGGGCCCGGTCTGCAAGCCAGAAGCCGAGTGCCTTCGAAACCGCTA TGCCAAACCGGCTGGGGCCCTGCAACAGGATGTCCTTTCCAACCCCGCAGCGGAGTGGCAGGGGACGTTGCCATGTGGGCC CGCAAAAATCCAGTTGACTTTTCTGCGGAGAGGGACCCACAGAGCCGTTGACCGCAGTACCAAAACAGCTAAATCCGAAG CTGGGGATACCAGCTCACAGAAACAGCCAAGTGGCGCTGCCTAA
Opto-GPR139	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTCTCCACAAGACGGGCGTGGTGGCGAGCCCTT CGAGGCCCGCGAGTACTACTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCCTTGTGAAGCACCAGGAGCTCCGACCCGTCACACTTCACTTCACTCAACC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTCCACCACCCTTACACCTCTGACAGGGTACTTCTGCTTTGG GCCACGGGCTGCAACCTGGAGGGCTTCTTGGCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGTGCGCCCGCTCAAGTACCACACGGTGTATACCCAGCCCGCCATCATGGGCTGCCCTTCA CTTGGTTCATGGCTCTGGCCTGTGCCGCGCCCGCTCGTGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGCCTG TGCGGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTTCATCATC CCCCTGATTGTCAATTTCTGCTACGGAAATCATTGTGTACAAGCTCAGGAGGAAAAGCAATTTTCGGCTCCGTGGCTACT CCACGGGAAAACCCCGCATGGTGTATCATGTTGTCATCGCTTTCCTAATCTGCTGGCTGCCCTACGCTGGGTTGGGTT CTTACATTTACCCTACAGGGCTGACTTTGGCCCCATTTTCATGACCATCCCGCTTTCCTTGGCAAGACTTCTGCCGTC TACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCCGCACCATGGCAGCCCGCCAGCTCAAGGCTTTCCTAAGTGC AGAAGCAACCTGTACAGTTCTACACCAATCATAACTTTTCCATAAAGTACCCCTGGATCTCGCCGCAAACTCACACTG CATCAAGATGCTGGTGTACCAGTATGACAAAATGAAAACCTATAAAGTATCCCGACAGAAAACAGCCAAGTGGCGCT GCCTAA
Opto-GPR141	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTCTCCACAAGACGGGCGTGGTGGCGAGCCCTT CGAGGCCCGCGAGTACTACTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCCTTGTGAAGCACCAGGAGTCACTGCTCAACTTCACTTCACTTCACTTGG CCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTCCACCACCCTTACACCTCTGACAGGGTACTTCTGCTTTGGGCC CACGGGCTGCAACCTGGAGGGCTTCTTGGCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGGCCATCGAG CCGTACGTGGTGGTGTCAAGTGAAGACAAAGTGAATTTACAGAAAACCTGGCCATCATGGGCTGCCCTTCACTTGGG TCCATGGCTCTGGCCTGTGCCGCGCCCGCTCGTGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGCCTGTCGCGGAT TGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTTCATCATC CCCCTGATTGTCAATTTCTGCTACGGAAATCATTGTGTACAAGCTCAGGAGGAAAAGCAATTTTCGGCTCCGTGGCTACT CCACGGGAAAACCCCGCATGGTGTATCATGTTGTCATCGCTTTCCTAATCTGCTGGCTGCCCTACGCTGGGTTGGGTT CTTACATTTACCCTACAGGGCTGACTTTGGCCCCATTTTCATGACCATCCCGCTTTCCTTGGCAAGACTTCTGCCGTC TACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCCGCACCATGGCAGCCCGCCAGCTCAAGGCTTTCCTAAGTGC AGAAGCAACCTGTACAGTTCTACACCAATCATAACTTTTCCATAAAGTACCCCTGGATCTCGCCGCAAACTCACACTG CATCAAGATGCTGGTGTACCAGTATGACAAAATGAAAACCTATAAAGTATCCCGACAGAAAACAGCCAAGTGGCGCT GCCTAA
Opto-GPR142	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTCTCCACAAGACGGGCGTGGTGGCGAGCCCTT CGAGGCCCGCGAGTACTACTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCCTTGTGAAGCACCAGGAGTCACTGCTCAACTTCACTTCACTTGG CCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTCCACCACCCTTACACCTCTGACAGGGTACTTCTGCTTTGGGCC CACGGGCTGCAACCTGGAGGGCTTCTTGGCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGGCCATCGAG CCGTACGTGGTGGTGTCAAGTGAAGACAAAGTGAATTTACAGAAAACCTGGCCATCATGGGCTGCCCTTCACTTGGG TCCATGGCTCTGGCCTGTGCCGCGCCCGCTCGTGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGCCTGTCGCGGAT TGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTTCATCATC CCCCTGATTGTCAATTTCTGCTACGGAAATCATTGTGTACAAGCTCAGGAGGAAAAGCAATTTTCGGCTCCGTGGCTACT CCACGGGAAAACCCCGCATGGTGTATCATGTTGTCATCGCTTTCCTAATCTGCTGGCTGCCCTACGCTGGGTTGGGTT CTTACATTTACCCTACAGGGCTGACTTTGGCCCCATTTTCATGACCATCCCGCTTTCCTTGGCAAGACTTCTGCCGTC TACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCCGCACCATGGCAGCCCGCCAGCTCAAGGCTTTCCTAAGTGC AGAAGCAACCTGTACAGTTCTACACCAATCATAACTTTTCCATAAAGTACCCCTGGATCTCGCCGCAAACTCACACTG CATCAAGATGCTGGTGTACCAGTATGACAAAATGAAAACCTATAAAGTATCCCGACAGAAAACAGCCAAGTGGCGCT GCCTAA

	GCACCTTTGGCATCACAGCCAGAGGGCATGGCGGCGAAGCCTGTGATGGAGCCTCCGGGACTCCCCACAGGGGCAAGTGCAC AGAAACCAGCAAGTGGCGCTGCCTAA
Opto-GPR146	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCGTGGTGGCGAGCCCTT CGAGGCCCCGAGTACTACCTGGCGGAGCCATGGCAGTTCTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCATCAACTTCTCAGCTGTACGTCTCTGCGGAACCAACGGCTCGCAGGAGCTCAACTACATCTGCTCAAC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTCACCACCACCTTCTACACCTCTCTGCACGGGTACTTCGCTTTGG GCCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGCACTGCCGGGACCTACATGGCCAGCGTGTACACACCGCATCATGGCCGTTCGCTTGGG TCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGTCTGTCGGGAT TGACTACTACAGCCCCACGAGGAAACCAACATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTCATCATCCCCCTG ATTGTATATTTCTTGTACTGGACTACTTCCCGCGTCCGAGGGAGACACGCCCTGGACCGGGACACGGGCGGCTGG AGCCCTCGGCACACAGGGCATGGTGTATCATATGGTTCATCGCTTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTT CTACATCTTACCCTCAGGGCTCTGACTTTGGCCCATCTTTCATGACCATCCGGCTTTCTTTGCCAAGACTTCTTGGCGTC TACAAACCCGCTCATCTACATCATGATGAACAAGCAGTTCCGAGCAAGTCCAAACGGCTGATGAAAAGCTGCCCTGGGGG ACCGGCACTGCTCCCGGACCAATGGGGGTGCACAGGTGCTGGCGACAGAAACCAGCAAGTGGCGCTGCCTAA
Opto-GPR148	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCGTGGTGGCGAGCCCTT CGAGGCCCCGAGTACTACCTGGCGGAGCCATGGCAGTTCTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCATCAACTTCTCAGCTGTACGTCTCTGCGGAACCAACGGCTCGCAGGAGCTCAACTACATCTGCTCAAC TGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTCACCACCACCTTACACCTCTCTGCACGGGTACTTCGCTTTGGG GCCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGTCCACTGCGTACCTTCTCTCATGTCCTTCCATGGGGTCCATCATGGCGCTGCCTTCA CCTGGTTCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGTCTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTCATCATC CCCCGATTGTATATTTCTTGTACTCGGAAGGATCTATGACAGGCCAAGACTTCAGGCATCTGGGGGACGGGTATTTCCC GGGCCAGGGGACCCCTGGCATGGTGTATCATATGGTTCATCGCTTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTT CTACATCTTACCCTCAGGGCTCTGACTTTGGCCCATCTTTCATGACCATCCGGCTTTCTTTGCCAAGACTTCTGGCGTC TACAAACCCGCTCATCTACATCATGATGAACAAGCAGTTCCGCGCAGCTGTGGCGATGGTTCGGGGCCACCTCCATCCAGGA GGCACCAGGCCATCTTACCATTTCACAGAAACCAGCAAGTGGCGCTGCCTAA
Opto-GPR149	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCGTGGTGGCGAGCCCTT CGAGGCCCCGAGTACTACCTGGCGGAGCCATGGCAGTTCTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCATCAACTTCTCAGCTGTACGTCTCTGCGGAACCAACGGCTCGCAGGAGCTCAACTACATCTGCTCAACCTGG CCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTCACCACCACCTTACACCTCTCTGCACGGGTACTTCGCTTTGGGG CACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCTGGCCATCGAG CGGTACGTGGTGGTGCACAGAGGTGTGGGGAGCCAGACGCTCCAGAAGTTCGGGCGCCATCATGGCCGCTCCGCTTCACT GGGTATGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGGAGGCATGCAGTGTCTGTCGGG GATTGACTACTACAGCCCCACGAGGAAACCAACATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTCATCATCCCC CTGATTGTATATTTCTTGTACTGGAGAAATTTCCCGTGGAGCTTCAATTTCTGGGACCCCTCTACTGGGGGAGAGTGG TTTCCCTGTCCCGAGGATGCTCCAGGCCGAGTGTGCCGCGCTCTGGGGATGCTCTCCGAGCTCCGAGCTCCAGGCTTGGC ACCGGGTGGCCCGCTGCCGCTGGGGTGAAGCTGCAGGCGTGAAGACCGGGGACTCTCTATGGCACCAGGAGCTTCACC GTGAGCTAGCGCAGAGCGCATGGTGTATCATATGGTTCATCGCTTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGT TCTACATCTTACCCTCAGGGCTCTGACTTTGGCCCATCTTTCATGACCATCCCGGCTTTCTTTGGACGGGTACTTCGCTT CTACAAACCCGCTCATCTACATCATGATGAACAAGCAGTTCCGCTTATCTTCAAAAAGTTATGGATTATAAAAATAGCA CATGAAGATTACTATGATGATGATGAAATTTCCATATTTCTATCACAACCTGATGAATCTGAGTGTGAAACTCAAAAAGCC CTCAGAGAGACAACCGTAACATCTTCAATGCTATAAAGTAGAAATCAGCACCACCGCCCTCTCTGGACGGGTACTTCCAA AGGCATCAACAAATGCACAAATACTGATATTACAGAAGTAAACAGGATTCACAAACAAAAGGATGCGTTTTCTGACAAA ACAGGAGGTGATATTAACATGAAGAAACTACCTTTTCTGAAGGGCCAGAAAGAGGCTGTCTCATGAAGAGAGTCAAAAAC CAGATCTTTCAGACTGGGAGTGGTGTAGGAGTAATCAGAAAGAACCCCTCGTCAGCGTTCGCTTATGCGCTTACGCTTCC CTTGTGTGATTTCCAGGGGACTGTGCTCTCCATGCACTACAGGAAACCCCTATCTCTTTCTACCTATGAGGTAAGGCCA GAAGGGCAAAAATAACTCCAGCCTTAAGAAAATAGAAGTCTATCGATCCAAAAGTGTGGCCATGAACAAAACCTCAGAA ATTCTTATCCAGTGTGGACACCCAGTGTGAAAATACACTTGGAGGTTCTTGAATTTGTGATAATGAAGGGCTTGGGA CACTGTGCAATCATTAAGTAAATCAGTCACTCCACACAAGTCAAGTCTCCATCCCTACGTTTACCTCAGGAAAGAAAAC AGATTTGTTTCATGTGACCTAGGGGAAACAGCCTCATACTCCCTTTTTTTGGCCACCAGTAATCCTGATGGTGTATTAATA TCTCCATTCAGACACAGTGAAGACACAGGCAAGCAAGTAAAGGAGCATCAAGAGAGGGATGGCTACAGGAGAAAAT CCAGTTGTTAAATAAAGCTTACAGAAAAGAGAGGAGAAAGCAAGGATGACAGAAACCAGCAAGTGGCGCTGCCTAA
Opto-GPR150	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCGTGGTGGCGAGCCCTT CGAGGCCCCGAGTACTACCTGGCGGAGCCATGGCAGTTCTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCATCAACTTCTCAGCTGTACGTCTCTGCGGCGGGCGGGCCCTGGGGGGCCCAAGCGTGCAGGCTCAACT ACATCTGCTCAACCTTGCACCTTGCACCTTTCATGGTGTTCGGGGGCTTCACCACCACCTCTGCACCGG GTACTTCTGCTTTGGGCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGGGGTGAAATTCGACTGTGGTCTT GTGGTCTGGCCATCGAGCGGTACGTGGTGGTGGGCTCCCGCACGGCCGGCCGCTGCCCGCCATCATGGCGTTCGCTTCA CCTGGGTATGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGTCTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTCATCATC CCCCGATTGTATATTTCTTGTACTCGGACACCTACTCTCCGCTGTGGTGGCGCACGGCCCGCAGGCCCCCGGCTGCAG CGCCCTGGTCGGCGAGCCAGGTTCAGGCCCTTGGCCCGCAGCGGCTGCCCGCGCCAAAGGTGACGGCCGATGGTGTAT CATGGTTCATCGCTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTTCATCATCTTACCCTCAGGGCTCTGACTTT GGCCCATCTTTCATGACCATCCCGGCTTTCTTTGCCAAGACTTCTGCCCTTACAAACCCGCTCATCTACATCATGATGAACA AGCAGTTCCCGCAGACAGCTGGCGAAGCGGCTGGGCTCTCTGCTGCGCGCCGAGGGAGGCGGAGGACGAGGAGGGGCC CCGGGGCCACAGGCGCTTACCGCCAAAGCTGGCCCAACCTCATATACCATGCTCGCGGGAAACCGCTGGACGAGGGC GGCTTGGCGCCACCCCTCCGCGCCCCAGACCCCTGCCTTGTCTTGGCAAAGTGCCTTACAGAAACCAGCAAGTGGCGC CTGCCTAA
Opto-GPR151	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGAGCGGGCGTGGTGGCGAGCCCTT CGAGGCCCCGAGTACTACCTGGCGGAGCCATGGCAGTTCTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCATCAACTTCTCAGCTGTACGTCTCTTCAATGCTTGGAAAGGAAAGCCATCCATGCTCAACTACATCTGCT TCAACTGGCCGTGGCCGACCTTTCATGGTGTTCGGGGGCTTCACCACCACCTTACACCTCTCTGCACGGGTACTTCGT CTTTGGGCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCGACTGTGGTCTTGGTCCCTG GCCATCGAGCGGTACGTGGTGGTGGTGGGAGCCAGCAAGTGAATTCACAACTACCGCCATCATGGCGTCCGCTTCA CCTGGTTCATGGCTCTGGCCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGTCTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACATGAGTCGTTTCGTCATCTACATGTTCTGGTCCACTTCATCATC CCCCGATTGTATATTTCTTGTACTCGGACACCTACTCTCCGCTGTGGTGGCGCACGGCCCGCAGGCCCCCGGCTGCAG CGCCCTGGTCGGCGAGCCAGGTTCAGGCCCTTGGCCCGCAGCGGCTGCCCGCGCCAAAGGTGACGGCCGATGGTGTAT CATGGTTCATCGCTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTTCATCATCTTACCCTCAGGGCTCTGACTTT GGCCCATCTTTCATGACCATCCCGGCTTTCTTTGCCAAGACTTCTGCCCTTACAAACCCGCTCATCTACATCATGATGAACA AGCAGTTCCCGCAGACAGCTGGCGAAGCGGCTGGGCTCTCTGCTGCGCGCCGAGGGAGGCGGAGGACGAGGAGGGGCC CCGGGGCCACAGGCGCTTACCGCCAAAGCTGGCCCAACCTCATATACCATGCTCGCGGGAAACCGCTGGACGAGGGC GGCTTGGCGCCACCCCTCCGCGCCCCAGACCCCTGCCTTGTCTTGGCAAAGTGCCTTACAGAAACCAGCAAGTGGCGC CTGCCTAA

	<p>GGTGGCGTTTACATCTTACCCATCAGGGCTCTGACTTTGGCCCATTTTCATGACCATCCCGGCTTTCTTTGCCAAGACT TCTGCCGTCTACAACCCCGTCACTACATCATGATGAACAAGCAGTTCCGGAAGGCTTGAAGGCTGTATGAAATGGATGA TAACAAAAAACCCTCCAACCTGTCTCAGAGTCTCAGGAAACACCAAGCTGGCAACTCAGAGGGCTCCCTGACAAGGTTCCATC TCCAGAATCCCCAGCATCCATACCAGAAAAAGAGAAACCCAGCTCTCCCTCCTTGGCAAGGGGAAAACTGAGAAAGCAGAG ATTCCCATCTTCTGACGTAGAGCAGTTTGGCATGAGAGGACACAGTCCCTTCTGTACAGGACAATGCCATATCCCTT GGAAACATGAAGATCAAGAGACAGGGGAAAGTGTAAACAGAAACAGCCAAAGTGGCCGCTGCCTAA</p>
Opto-GPR152	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCATCAACTTCTCAGCTGTACGTGCGCCGCTCCAGGCGCCGATGGAGCTGGCAGCCGACTCAACTACATCTCTGC TCAACCTGGCCGTGGCCGACTTCTCATGTTGTTCCGGGGCTTACCACCACCTCTACACCTCTCTGCACGGGTACTTCGT CTTTGGGCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGT GCCATCGAGCGGTACGTGGTGGTGTGTGCCACACTGGTACCTGGGACCGCCAGTCCGCTGGCCATCATGGCGTGC CCTTCACTGGGTCATGGCTCTGGCCTGTGCCGCGCCCTTCTGCTGGTGGTCCAGGTACATCCCGAGGGCATGCAGTGC CTCGTGGGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCTGTTGCTCATCTACATGTTCTGGTGGTCTT ATCATCCCCCTGATGTTGATATCTTCTGTACGGACTCACCCAGGCCACAGCTGTGCGACCTGCCACGCCAACAGCAGC CCGAGCTTCCCGGGCTTCCGCCGATGGTGTATCATATGCTATGCTTTCCATCTGCTGGTCCCTTCCATCTGCTGGGCT GGCGTCTACATCTTACCACATCAGGGCTCTGACTTTGGCCCATCTTTCATGACCATCCCGCTTTCTTTGCCAAGACTTCT CCGCTTACAAACCCCTCATCTACATCATGATGAACAAGCAGTTCCGCACTTGTGCGCTCCGTCTCTGCTTCCGCTGGC CAGCTTCTGCGAGGAGCGCCGCGGAGCTTACGCCCACTGAGCCACAGACCAGCTAGATTTGCTGGTCCACTTCACTTCC AGAGCCGATGGCAGAGGCCAGTACAGATGGATCCTGTGGCCAGCCTCAGGTGAACCCACACTCCAGCCACGATCGGAT CCCACAGCACAGCCACAGTGAACCTACGGCCAGCCACAGTCCGATCCCACAGCCAGCCACAGTGAACCTCATGGCC AGCCACAGTCAAGTTCTGTGGCCAGCCACAGGACAGACTAACCTCCAGACCCCTGCACTTCCAGCTTCTGTCAGGCT TCCCTGTGATGAAGCTTCCCCAACCCATCTCGCATCTACCCAGGGGCTTGGAGACCCAGCCACACTCCTGCTCT GAAGGAAAAGCCCGCAGCAGCAGCCCGCAGAGCGGCCCGGGCGCAGGCCCCACGACAGAAACAGCCAAAGTGGCGCTG CCTAA</p>
Opto-GPR153	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCATCAACTTCTCAGCTGTACGTGCTTGGCGCAAGCAGAAGAAGTGAAGCCCTCAACTACATCTCTGCTCAACC TGGCCGTGGCCGACTTCTCATGTTGTTCCGGGGCTTACCACCACCTTCTACACCTCTCTGCACGGGTACTTCGTCTTTGG GCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTTGGCCATC GAGCGGTACGTGGTGGTGTGTGCCCTGTCAACTACCGATTGAGCAATGCCAAGAAGCAGGCCATCATGGCGTGCCTTCA CCTGGGTCATGGCTCTGGCCTGTGCCGCGCCCTTCTGCTGGTGGTCCAGGTACATCCCGAGGGCATGCAGTGTCTGTG CGGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCTGTTGCTCATCTACATGTTCTGGTGGTCCACTCATC CCCCGTGATGATATTTCTTCTGCTACGGAACGCTGGCCGTGACGGTGGGCGCCAGGCCAGCCCGGCTTCACTGCTGC CATGGTGTATCATATGTTGCTTCTTCTAATCTGCTGGTGCCTACGCTGGGTTGGTGGTCCACTTCACTCAG GGCTGTACTTTGGCCCATCTTTCATGACCATCCCGCTTCTTTGCCAAGACTTCTGCGCTTACAACCCGCTCATCTACA TCATGATGAACAAGCAGTTCCCGCTGACTTCAAGCTGTCCGGGAGAAGTGCATGGCCCTCATGGCCACACAGCAGGAGT AGACGATGAACACAGCTTGAAGGTTGGCATCTCCCGGACTGGTGTGGAGCGCTCCCTGAGTCCCTGAGTCCCTGAGGCTGAT TTTGTGGCCCTAGATAGGATGGCAAGTATGAGATCTCCGCCCTGGAGGGGGCTGCCCGACTTACCACCTGCAGCCCT TGCAGGAGGACAAGATGAATAACCTGCAAGTCCCGCCACCGCGGCTTCTCCACAGCAGTCCGGACGTGTGGGCGCCGCT CCGCTGCCCGCTTCTGCTGGCGCTGGGGCTCCGGCGAGGACTTGGCCGCTTGGCGGCTTCCACTTCACTTCACTTCA GAGCGCGCCGCGCCAGCTTCTGGCTTCCGGGAGGACGACCACCTCCCGCGCGCCGCGCTCGGCCAGAGCCCTGCT TGTGCTGGCCCTCGCCCTGGATAGCGCCCGCGGGGAGCCCGACTCGCCCGCCGCGCCGCGCCGCGCCGCGCCGCG GCCCGGCCCGCTCCGCTCGCCCTGGCCCTGCTGCGCCGAGCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCG CGCCCGCCCGCCGGGCTTCCCGCTGCGCCCGCCCGCCCGCAGCCGAGATCCCGGAGGCGCCGACGCCCCAAGCA GCGCCAGCGGAGCCAGGGCCACGCCCTTCCGCACTCGCACGCGGCTCTCTGCGCCCGGCTGAGCGCGTGTGGG CGAGCCCGGGGGCTCGCGCGCCGCGGGCGGGGAGCACCAGCAGCTTCTGAGTCCGATCTTGAAGCTTCCGAGCTTCCG GCCAGCTGCACCTCGACTCGCTGGGCTCCGCGTCCACAGAAACAGCCAAAGTGGCGCTGCCTAA</p>
Opto-GPR160	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCATCAACTTCTCAGCTGTACGTGCTTGGCGCAAGCAGAAGAAGTGAAGCCCTCAACTACATCTCTGCTCAACC TCAACCTGGCCGTGGCCGACTTCTTACGTTGTTCCGGGGCTTACCACCACCTTACACCTCTCTGCACGGTACTTCGT CTTTGGGCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTGT GCCATCGAGCGGTACGTGGTGGTGTCTAAAACAACCAAGCTTTCATTTAAGTGTCAAAAATTTATTTATTTCCGCTCATG GCTCGCTTCACTGGGTGATGGCTCTGGCTGTGCCGCGCCCTTCCGCTGGTCCAGGTACATCCCGAGGCGATCCGAGG GCATGAGTGTGCTGGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCTGTTGCTCATCTACATGTTGTTG CACTTCACTATCCCCCTGATTGTCATATTTCTTCTGTACGGAAGGATAACTTCTATATGAATGAAACTATCTTATATTTT CTTTTCACTCCACTCCAGTTACTTACTGTGAGATCTAAAACAACGATGGTGTATCATATGCTGCTGCTGCTGCTGCT GCTGCCCTACGCTGGGTTGGCTTCTACATCTTACCACATCAGGGCTCTGACTTTGGCCCATCTTTCATGACCATCCCGGCT TCTTTGCCAAGACTTCTGCCGCTACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCCGCTTAAAGACATTTGAT TACCTTTGGATCCATTTGCAACTGGAAGTGTCTGCTTCACTTCACTTACAATTCCTAATCTTGAAGCAATTTGAAAGCTGAT ATCAATAATGATTTGTACAGAAACAGCCAAAGTGGCGCTGCCTAA</p>
Opto-GPR161	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCAGCCCTT CGAGGCCCGCAGTACTACTTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCATCAACTTCTCAGCTGTACGTGCTTGTACAAGAAGTCTACTCTTCAACCTCTCAACTACATCTCTGCTCAACC TGGCCGTGGCCGACTTCTTACGTTGTTCCGGGGCTTACCACCACCTTACACCTCTCTGCACGGGATCTTCGTCTTTGG GCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGGCGGTGAAATGCACTGTGGTCTTGGTGGTCTTGGCCATC GAGCGGTACGTGGTGGTGTGTACCCATGTTGTACCCATGAAGATCACAGGAAACCGGGCCATCATGGCGTGCCTTCA CCTGGGTCATGGCTCTGGCCTGTGCCGCGCCCTTCCGCTGGTCCAGGTACATCCCGAGGCGATCCGAGGCTGCTGCTG CGGGATTGACTACTACACGCCCCACGAGGAAACCAACAATGAGTCTGTTGCTCATCTACATGTTGTTGTTGCTCATCATC CCCTGATTGTCATATTTCTTCTGTACGGATTCTTCCGCTGGCCAGGTCAGGCAAGGTCAGGTCAGTGGTGGCAGC TCCGTCATGTTGAGGAGGATGCTCAGAGGACCGGGAGGAAAGTCCAGCACCTCCACTCTTCCAGGCAAGGAGGAA TGCCTTTCCAGGTTGGTGTACTCGGCCAACAGTGAAGCCCTCCGATGGTGTATCATATGTTGATCATGCTTCTCAATC TGCTGGTGCCTTACGCTGGGTTGGCTTCTACATCTTACCACATCAGGGCTCTGACTTTGGCCCATCTTTCATGACCATC CGGCTTTCTTTGCCAAGACTTCTGCGCTTACACCCCGTCACTACATCATGATGAACAAGCAGTTCCGCTTAAAGACATTTGAT GGGATCACAGACTGGGCTGTCCCAACCTCACTGCGCTCATGGCAGTGGACAGCCCTCCAGGCTTCCAGGCAAGGAGCAGC GGGACACTGGCTTACGCTGCTCCAGGACTCAGGACAGATATGATGCTGCTTGGAGTACACGCTGTGATGACAACCTTCC CTCTCACTGCACTTGGCCACCAAGAGAGGAGTCCGGTACATTTGAGGATGAAGTGAACAATAAAGAGGCTGCCAAG AACTCGATTTCTCATGTGAAGCTGAATACACAAGTCTTGGACAGTACGACAGCAAGCTTGGCCAAAGCATTGAGGCGG</p>

	AAGCCAAATCAACTTATTTGGGGAGGAGGCTTTGCCAGGGTCTTGGTTACAGCACGGACTGTCCCGGGGGCGGCTTCGGGGCCGAGGAGCAGAACTCTTGTGAGCCAGAGGTCAGTTGACAGCATCGAAGAAAGGAGATGTTTTAGCTGCCGAGCAGAGAACAGAAACAGCCAAAGTGGCGCTGCCTAA
Opto-GPR162	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAAAGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGCCAGCCCCTCGAGGCCCGCAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGCTTCCCACTCAACTTCCCTACGCTGTACGTCTTTATACAGAAGAATACGAATACAGGTGTCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTCACCACCACCTCTACACCTCTCTGCACGGGTACTIONTCTGCTTTGGGCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATGCACTGTGGTCCTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGCCACCACCGCTTCTACGCCAAGCGCATGACACTCTGGACGCCATCATGGGCGTGCCTTCA CCTGGGTATGGCTCTGGCCTGTGCCCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGCCTGTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTCTGTCATCTACATGTTCTGGTCCACTTCATCATC CCCCTGATTTGCATATTTCTTCTGCTACGGAACACTGTGGGCCCGCCCCGAGGGCTCGGCAGGCCGAGAGTGGGGGTG GTGGGGGACAAAGCGGGTGGCCAGGGCCTTGGGTACCCGGCCAGCTTTTGGAGTACCAGCCATTGGTGGAGGATGC AGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGCCAGCCCCT CGAGGCCCGCAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCACTCAACTTCCCTACGCTGTACGTCTTTATACAGAAGAATACGAATACAGGTGTCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTCACCACCACCTCTACACCTCTCTGCACGGGTACTIONTCTG GCCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATGCACTGTGGTCCTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGCCACCACCGCTTCTACGCCAAGCGCATGACACTCTGGACGCCATCATGGGCGTGCCTTCA CCTGGGTATGGCTCTGGCCTGTGCCCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGCCTGTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTCTGTCATCTACATGTTCTGGTCCACTTCATCATC CCCCTGATTTGCATATTTCTTCTGCTACGGACTTGTAAATTCGACAGCTCTACAGAAACAAAGATAATGAAATTACCCAAATG TGAAGAGGGCTTCCCGATGGTATCATGATCATGATCATGCTTCTTAACTTCTGCTGGCTGCCTGAGGCTGGGGTGGGCTCTA CATCTTACCCTCAGGGCTGACTTTGGCCCATCTTATGACCATCCGGCTTTCTTTGCCAAGACTTCTGCCGTCTAC AACCCGCTCATCTACATCATGATGAACAGGAGTTCGGCTCAAAGTCACTGAGACTTTTGCCTCACTAAAGAAACCAAGG CTTCAAGAAAGAAATTAAGATGTGAAATAATGCAACAGAAACAGCCAAAGTGGCGCTGCCTAA
Opto-GPR171	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAAAGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGCCAGCCCCT CGAGGCCCGCAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCACTCAACTTCCCTACGCTGTACGTCTTTATACAGAAGAATACGAATACAGGTGTCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTCACCACCACCTCTACACCTCTCTGCACGGGTACTIONTCTG GCCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATGCACTGTGGTCCTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGCCACCACCGCTTCTACGCCAAGCGCATGACACTCTGGACGCCATCATGGGCGTGCCTTCA CCTGGGTATGGCTCTGGCCTGTGCCCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGCCTGTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTCTGTCATCTACATGTTCTGGTCCACTTCATCATC CCCCTGATTTGCATATTTCTTCTGCTACGGACTTGTAAATTCGACAGCTCTACAGAAACAAAGATAATGAAATTACCCAAATG TGAAGAGGGCTTCCCGATGGTATCATGATCATGATCATGCTTCTTAACTTCTGCTGGCTGCCTGAGGCTGGGGTGGGCTCTA CATCTTACCCTCAGGGCTGACTTTGGCCCATCTTATGACCATCCGGCTTTCTTTGCCAAGACTTCTGCCGTCTAC AACCCGCTCATCTACATCATGATGAACAGGAGTTCGGCTCAAAGTCACTGAGACTTTTGCCTCACTAAAGAAACCAAGG CTTCAAGAAAGAAATTAAGATGTGAAATAATGCAACAGAAACAGCCAAAGTGGCGCTGCCTAA
Opto-GPR173	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAAAGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGCCAGCCCCT CGAGGCCCGCAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCACTCAACTTCCCTACGCTGTACGTCTTTATACAGAAGAATACGAATACAGGTGTCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTCACCACCACCTCTACACCTCTCTGCACGGGTACTIONTCTG GCCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATGCACTGTGGTCCTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGCCACCACCGCTTCTACGCCAAGCGCATGACACTCTGGACGCCATCATGGGCGTGCCTTCA CCTGGGTATGGCTCTGGCCTGTGCCCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGCCTGTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTCTGTCATCTACATGTTCTGGTCCACTTCATCATC CCCCTGATTTGCATATTTCTTCTGCTACGGACTTGTAAATTCGACAGCTCTACAGAAACAAAGATAATGAAATTACCCAAATG TGAAGAGGGCTTCCCGATGGTATCATGATCATGATCATGCTTCTTAACTTCTGCTGGCTGCCTGAGGCTGGGGTGGGCTCTA CCCATCAGGGCTCTGACTTTGGCCCATCTTATGACCATCCGGCTTTCTTTGCCAAGACTTCTGCCGTCTACAACCCGCT CATCTACATCATGATGAACAGGAGTTCGGCTCAAAGTCACTGAGACTTTTGCCTCACTAAAGAAACCAAGG CTTCAAGAAAGAAATTAAGATGTGAAATAATGCAACAGAAACAGCCAAAGTGGCGCTGCCTAA
Opto-GPR174	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAAAGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGCCAGCCCCT CGAGGCCCGCAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCACTCAACTTCCCTACGCTGTACGTCTTTATACAGAAGAATACGAATACAGGTGTCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTCACCACCACCTCTACACCTCTCTGCACGGGTACTIONTCTG GCCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATGCACTGTGGTCCTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGCCACCACCGCTTCTACGCCAAGCGCATGACACTCTGGACGCCATCATGGGCGTGCCTTCA CCTGGGTATGGCTCTGGCCTGTGCCCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGCCTGTG CGGGATTGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTCTGTCATCTACATGTTCTGGTCCACTTCATCATC CCCCTGATTTGCATATTTCTTCTGCTACGGAACCGCTTTCCTAACTTCTGCTGGCTGCCTACGCTGGGGTGGGCTCTA CATCTACATCATGATGAACAGGAGTTCGGCTCAAAGTCACTGAGACTTTTGCCTCACTAAAGAAACCAAGG CTTCAAGAAAGAAATTAAGATGTGAAATAATGCAACAGAAACAGCCAAAGTGGCGCTGCCTAA
Opto-GPR176	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAAAGGATAGCCTCATGAACGGGACCGAGGGCCCAAACCTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGCCAGCCCCT CGAGGCCCGCAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTGCTGATCATGCTTGGC TTCCCACTCAACTTCCCTACGCTGTACGTCTTTATACAGAAGAATACGAATACAGGTGTCTCAACTACATCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTCACCACCACCTCTACACCTCTCTGCACGGGTACTIONTCTG GCCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATGCACTGTGGTCCTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGCTTATCCACTGGAGAGGAAATATCTGATGCAAGGCCATCATGGGCGTGCCTTCACTGGG TCATGGCTCTGGCTGTGCCCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAGTGCCTGTGCGGGAT TGACTACTACAGCCCCACGAGGAAACCAACAATGAGTCGTTCTGTCATCTACATGTTCTGGTCCACTTCATCATC CCCCTGATTTGCATATTTCTTCTGCTACGGAACCGGTTTTATCACTGCAAGATAAATATCCCATGGCCAAAGATCTTGGG AGAAACAGAAAGCCTTGGCATGGTGTATCATGATCATGATCATGCTTCTTAACTTCTGCTGGCTGCCTACGCTGGGTGGGCTT CTACATCTTACCCTCAGGGCTGACTTTGGCCCATCTTATGACCATCCGGCTTTCTTTGCCAAGACTTCTGCCGTCT ACAACCCGCTCATCTACATCATGATGAACAGGAGTTCGGCAGGCGGCTTTCAAGACAAGATTTGATGACAGCATCCAA CTTCAAGAAAGAAATTAAGATGTGAAATAATGCAACAGAAACAGCCAAAGTGGCGCTGCCTAA

	GCAAGTGTGATAGGGACCTGGTGAACCTACACCACCGATACAGTCGCCGTAATGTGGTACAGGAGTGGCATGGC TGAGGCCAGCCTGGAACCCAGCATACCTCGGGTAGCCAGCTCCTGGAGATGTCCACATTTGGCCAGCAGCATCTTTAAG CCCACAGAGGATGAGGAAGAGAGTGGCCCAAGTACATTTGGTTCAGCTGACTTCCAGGCCAAGGAGATATTTAGCCTGCC TGGAGGGAGAGCAGGGGCCACAGTTTGGCCCTCTGCCACCCCTGAGCAGTGGACTCTGTATCCAGGTTGGCCAGCGGC AGCCCTGTGGAACCTGAAACATTCCTGATAAGTATTCCTGCAGTTTGGCTTTGGCCCTTTTGGATTGCCTCCTCAGTGG CTCTCAGAAACCCGAAACAGCAAGAGCGGCTGCTTCCCCCTTTGGCAACACCCAGAGGAGCTGATCCAGAGCAAGGTGC CCAAGGTAGGCAGGGTGGAGCGGAAGTGAAGCAAAATAAAGTGAGCATTTTCCAAAGGTGGATTCCACAGAAACCAG CCAAGTGGCCCTGCCTAA
Opto-GPR182	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCCAGCCCTT CGAGGCCCGCAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCAACTGGCGCGGCTCAGGCCGGGACGGGCTGCTCAACTACATCTCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCCACCTTACACCTCTCTGCACGGGTACTTCTGCTTTGG GCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTGCACTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTACACGCGCTCCCCCTCTGGCAGCGTTACCAGCACCGAGTGGCGCGGCGCCATCATGGGCG TCGCTTCACTGGGTCATGGCTGTGGCTGTGGCGGCCCTCTGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCA GTGCTCTGTGGGATTGACTACTACACGCCACGAGGAACCAACAATGAGTCTGCTGCTACATGTTCGTGGTGCAC TTTATCATCCCCCTGATTGTATATTCTTCTGCTACGGACTGACAGCCTGCCGGCTGGCGGACGCAGGACAACCCAAAGAGCC GGCGCCACTGCCGATGGTGTATCATGTTGTCATCGCTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCTGCTACAT CTTCCACCATCAGGGCTGTGACTTTGGCCCATCTTATGACCATCCCGGCTTCTTTGGCAAGACTTCCGCTTACAC CCCGTCACTACATCATGATGAACAAGCAGTTCGGCGGCCGCTCCTGAATGCTGTAGTCCATTACCTTCTTAAGGACCAGA CAAAGGGGGGACATGCGCCTCTCTCTCTCTGTTCCACCCAGCATTCCATCATCACCAAGGCTGATAGCCAGCCTGC TGCAGCAGCCCCCACCCTGAGCCAAAGCTGAGCTTTCAGGCACACCAATTGGTTCCAATACTTCCCCATCTCTCCACT CAGCCTCTTACACCAGCACAGAAACCAGCCAAGTGGCGCTGCCTAA
Opto-GPR183	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTGCCATGTACACCGATATAGAGATGAACAGGCTGGGAA AGGATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCTCCAACAAGACGGGCGTGGTGGCCAGCCCTT CGAGGCCCGCAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGC TTCCCCATCAACTTCTCAGCTGTACGTCAACTGGCGCGGCTCAGGCCGGGACGGGCTGCTCAACTACATCTCTGCTCAACC TGGCCGTGGCCGACCTTCTCATGGTGTTCGGGGGCTTACCACCCACCTTACACCTCTCTGCACGGGTACTTCTGCTTTGG GCCACGGGCTGCAACCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTGCACTGTGGTCTTGGTGGTCTGGCCATC GAGCGGTACGTGGTGGTGGTACACGCGCTCCCCCTCTGGCAGCGTTACCAGCACCGAGTGGCGCGGCGCCATCATGGGCG TCGCTTCACTGGGTCATGGCTGTGGCTGTGGCGGCCCTCTGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCA GTGCTCTGTGGGATTGACTACTACACGCCACGAGGAACCAACAATGAGTCTGCTGCTACATGTTCGTGGTGCAC TTTATCATCCCCCTGATTGTATATTCTTCTGCTACGGACTGACAGCCTGCCGGCTGGCGGACGCAGGACAACCCAAAGAGCC GGCGCCACTGCCGATGGTGTATCATGTTGTCATCGCTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCTGCTACAT CTTCCACCATCAGGGCTGTGACTTTGGCCCATCTTATGACCATCCCGGCTTCTTTGGCAAGACTTCCGCTTACAC CCCGTCACTACATCATGATGAACAAGCAGTTCGGCGGCCGCTCCTGAATGCTGTAGTCCATTACCTTCTTAAGGACCAGA CAAAGGGGGGACATGCGCCTCTCTCTCTGTTCCACCCAGCATTCCATCATCACCAAGGCTGATAGCCAGCCTGC TGCAGCAGCCCCCACCCTGAGCCAAAGCTGAGCTTTCAGGCACACCAATTGGTTCCAATACTTCCCCATCTCTCCACT CAGCCTCTTACACCAGCACAGAAACCAGCCAAGTGGCGCTGCCTAA

Table 6.2 Nucleotide sequences of all light-activated human Class A oGPCRs created using the chimeric algorithm described in section 3.1

Name	Sequence
Opto-B2AR	MKTI IALSYI FCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFFSNKTVVRS PFEPQYYLAE PWQFSMLAAYMFL L IMLGFPI NFLTLVYIAKFERLQTVLNY ILLNLAVADLFMVFGGFTTTL YTS LHGYFVFGPTGCNLEGFATLGGEIALWSLVVLA IERYVVV TSPFKYQSL LTKNKAIMGVAF TWMALACAAPLVGWSRY IPEGMQCSCGIDYYPHEETNNESFVI YMFVVFH I IPLIVIFFCY GRVYVAKRQLQK I DKSEGRFHS PNLQVEQDGRSGHLRRSSK FCLKEHKALRMVI IMVIAFLICWLPYAGVAFY I FT HQGSD F GPIFMT I PAFFAKTS AVYNPVI YIMMNKQFR I AQE LLLRRSSSKAYGN YGSSNNGKTDYMG EASGCQLQGEKESERL CEDPP GTESFVNCQGT VPSLSLDSQGRNCSTNDSPLTETSQVAPA*
Opto-A1AR	MKTI IALSYI FCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFFSNKTVVRS PFEPQYYLAE PWQFSMLAAYMFL L IMLGFPI NFLTLVYVACHRHLSVNLNY ILLNLAVADLFMVFGGFTTTL YTS LHGYFVFGPTGCNLEGFATLGGEIALWSLVVLA IERYVVV SYPLRYPTIVTQRRIMGVAF TWMALACAAPLVGWSRY IPEGMQCSCGIDYYPHEETNNESFVI YMFVVFH I IPLIVIFFCY GRVYVAKRESRGLKSLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKT HFSVRLLKFSREKKAARMVI IMVIAFLICWLPYA GVAFY I FT HQGSD F GPIFMT I PAFFAKTS AVYNPVI YIMMNKQFRKAFQNV LRIQCLCRKQSSKHALGY T LHPPSQAVEGQH KDM VRIPVGSRETFYRISKTDGVCEWKFSSMPRGSARI TVSKDQSSCTTARVRSKSLFQVCCVGPSTPSLDKNHQVPTIKVHT I SL SENGEEV TETSQVAPA*
Opto-FFR3	MKTI IALSYI FCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFFSNKTVVRS PFEPQYYLAE PWQFSMLAAYMFL L IMLGFPI NFLTLVYVFGKLRQRFPVNLNY ILLNLAVADLFMVFGGFTTTL YTS LHGYFVFGPTGCNLEGFATLGGEIALWSLVVLA IERYVV VAHPLWYKTRPRLGQIMGVAF TWMALACAAPLVGWSRY IPEGMQCSCGIDYYPHEETNNESFVI YMFVVFH I IPLIVIFFCY YGRVLWILGRGGSHRRQRVARMVI IMVIAFLICWLPYAGVAFY I FT HQGSD F GPIFMT I PAFFAKTS AVYNPVI YIMMNKQFR DFHELLRRLCGLWGQWQESSMELKEQKGGEEQRADRP AERKTS EHSQCGGTGGQVACAESTETSQVAPA*
Opto-A2A	MKTI IALSYI FCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFFSNKTVVRS PFEPQYYLAE PWQFSMLAAYMFL L IMLGFPI NFLTLVYVWLNLSNLQVNLNY ILLNLAVADLFMVFGGFTTTL YTS LHGYFVFGPTGCNLEGFATLGGEIALWSLVVLA IERYVVV RIPLRYNGLVTGTRIMGVAF TWMALACAAPLVGWSRY IPEGMQCSCGIDYYPHEETNNESFVI YMFVVFH I IPLIVIFFCY GRIFLAARRQLQMESQPLPGERARSTLQKEVHARMVI IMVIAFLICWLPYAGVAFY I FT HQGSD F GPIFMT I PAFFAKTS AVYNP PVI YIMMNKQFRQTFRKI IRSHVLRQVEPFKAAGTSARVLA AHGSDGEQVSLRLNGHPGWANGSAPHERRPNGYALGLVSGG SAQESQNTGLPDVELLSHELKGVCEPPGLDDPLAQD GAGVSTETSQVAPA*
Opto-D1R	MKTI IALSYI FCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFFSNKTVVRS PFEPQYYLAE PWQFSMLAAYMFL L IMLGFPI NFLTLVYVIRFRHLRSKVLNY ILLNLAVADLFMVFGGFTTTL YTS LHGYFVFGPTGCNLEGFATLGGEIALWSLVVLA IERYVV VSSPFQYERKMT PKAIMGVAF TWMALACAAPLVGWSRY IPEGMQCSCGIDYYPHEETNNESFVI YMFVVFH I IPLIVIFFCY YGSYIRIAQKQIRRI SALERA AVHAKNCQT T TGNPNV ECSQSESSFKMSFKRETKVLRMVI IMVIAFLICWLPYAGVAFY I FT QGSDFGPIFMT I PAFFAKTS AVYNPVI YIMMNKQFRKAFSTLLGCYRLCPTTNNAIETV S INNNGAVMFS SHHEPRGSI SKDCNL VYLL PHAVGSS EDL KREEAGGI PKPLEKLS PALSVI LDYD TDV SLEKI QPVT HSGQHS TTETSQVAPA*
Opto-D2R	MKTI IALSYI FCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFFSNKTVVRS PFEPQYYLAE PWQFSMLAAYMFL L IMLGFPI NFLTLVYVSRKALQTT LNY ILLNLAVADLFMVFGGFTTTL YTS LHGYFVFGPTGCNLEGFATLGGEIALWSLVVLA IERYVVV AMPLYNTRYSSKRAIMGVAF TWMALACAAPLVGWSRY IPEGMQCSCGIDYYPHEETNNESFVI YMFVVFH I IPLIVIFFCY YKIIYVLRKRRKRVNTRKSSRAFRANLKT PLKGNCTHPEDMKLCTVIMKSN GSFVNRRRMDAARQAQLEMEMLSSTSPPERT RYSPIPPSHHQLTLPDP SHHGLHSPNDSPAKPEKNHAKI VNPRIAKFFE I QTM PNGKTRTSLK TMSRRKLSQQEKKATRMV I I MVIAFLICWLPYAGVAFY I FT HQGSD F GPIFMT I PAFFAKTS AVYNPVI YIMMNKQFRKAFMKI LHCTETSQVAPA*

Opto-M1R	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFFSNKTGVVRS PFEAPQY YLAEPWQFSMLAAYMFL L IMLGFPI NFLTLVYFVKVNTLKVNLNY ILLNLAVADLFMVFVGGFTTTLTYSLHGYFVFGPTGCNLEGFATLGGEIALWLSLVLA IERYVVV TRPLSYRAKRTPRRAIMGVAFTWVMALACAAPPLVWGSRY IPEGMQCSCGIDYYPHEETNNESFV IYMFVVFH I I PLIVIFFCY GR IYRE TENRARELALQ GSETPGKGGGSSSSSSERSQP GAEGSPETPPGCCRCR APRLLQAYSWK EEEEEDEGSMESLTSSEG E EPGSEVVIKMPMDPEAQA PTKQPPRSSPNTVKRPTKKGRDRAGKQKPRGKEQLAKRKTFSLVKEKKAAR MVI IMVIAFLICW LPYAGVAFY I FTHQGSDFGPI FMTI PAFFAKTSAVYNPVI YIMMNKQFRDTFRLLLLCRWDKRRWRKI PKRPGSVHRTPSRQCTE TSQVAPA*
Opto-M2R	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFFSNKTGVVRS PFEAPQY YLAEPWQFSMLAAYMFL L IMLGFPI NFLTLVYFVKVNTLKVNLNY ILLNLAVADLFMVFVGGFTTTLTYSLHGYFVFGPTGCNLEGFATLGGEIALWLSLVLA IERYVVV TKPLTYPVKRTTKMAIMGVAFTWVMALACAAPPLVWGSRY IPEGMQCSCGIDYYPHEETNNESFV IYMFVVFH I I PLIVIFFCY GHISRASKSR IKKDKKEPVANQDPVSPSLVQGRIVKPNNNMPSDDGLEHNKI QNGKAPRDPVTEN CVQGEKESNDSTSVSA VASNM RDDEITQDENTVSTSLGHSKDENSKQTCIRIGTKTKPSDSCPTNTTVEVVGSSGQNGDEKQNI VARKI VKMTKQPAKKK PPSRREKVKTRMVI IMVIAFLICWLPYAGVAFY I FTHQGSDFGPI FMTI PAFFAKTSAVYNPVI YIMMNKQFRDTFRLLLLCRWDKRRWRKI NIGATR TETSQVAPA*
Opto-M3R	MKTI IALS YIFCLVFAMYTDIEMNRLGKDSL MNGTEGPNFYVFFSNKTGVVRS PFEAPQY YLAEPWQFSMLAAYMFL L IMLGFPI NFLTLVYFVKVNTLKVNLNY ILLNLAVADLFMVFVGGFTTTLTYSLHGYFVFGPTGCNLEGFATLGGEIALWLSLVLA IERYVVV TRPLTYRAKRTTKRAIMGVAFTWVMALACAAPPLVWGSRY IPEGMQCSCGIDYYPHEETNNESFV IYMFVVFH I I PLIVIFFCY RPTLTKETKREKLAGLQAGTEAETENFVHPTGSSRSYSLQYQSMKRSNRKRYGRCHFVFTTKSWKPSSEQMDQDHS SSS WNNNDAAA SLENSASSDEEDIGSETRAIYS I VLKLPGHST I LNSTKLPSSDNLQVPEELGMVDLEKADK LQAQKSVDDGGSFP KSFSLPIQL EASVDTAKTSDVNSSVSGKSTATLPLSFK EATLAKRFALKTRSQITKRRKMSLVKEKKAAR MVI IMVIAFLICWLP YAGVAFY I FTHQGSDFGPI FMTI PAFFAKTSAVYNPVI YIMMNKQFRDTFRLLLLCRWDKRRWRKI PKRPGSVHRTPSRQCTE TETSQVAPA*

Table 6.3 Amino acid sequences of all light-activated control GPCRs created using the chimeric algorithm described in section 3.1

Name	Sequence
Opto-B2AR	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAAAGG ATAGCCCTCATGAACGGGACCGAGGGCCCAAACTTCTACGTGCCTTCTCCAAACAGACGGGCGTGGTGCCGAGCCCTTCGAGGC CCCGCAGTACTACCTGGCGGAGCCATGGCAGTTCCTCATGTGCGCCGCTACATGTTCTCTGCTGATCATGCTTGGCTTCCCATC AACTTCTCACGCTGTACGCTTGTGGGCAAGCTGCAGCGCCGCTCAACTACATCTGCTCAACTGGCCGTGGCCGTGGCCG ACCTTCTCATGGTGTTCGGGGGCTTACCACCACCTCTACACCTCTCTGCACGGGTACTTCGCTTCTGGGCCACGGGCTGCAA CCTGGAGGGCTTCTTTGCCACCTTGGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCTGGCCATCGAGCGGTAGCTGGTGGT ACATCGCCATTCAAATACCAGAGCTCTGACCAAGAAATAAGGCCATCATGGGCGTGCCTTCACTGGGTATGGCTTGGCCCT GTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAAGTCTCGTGGGGATGACTACTACACGCCCA CGAGGAAACCAAAATGAGTCGTCATCATGTTCTGGTCCACTTCATCATCCCCCTGATTGTCATATTTCTTCTGCTAC GAAAGGGTGTTCAGGTGGCCAAAAGGCAGCTCCAGAAGATAGACAAATCTGAGGGAAGATTCCACTKCCCCAACCTCGCCGAG TGGAGCAGGATGGGCGGAGTGGGCACGGACTCCGAAGTCTTCAAAGTCTGCTTGAAGGAGCACAAGCCCTCCGCATGTTGAT CATCATGGTTCATCGCTTCTTAATCTGCTGGCTGCCTACGCTGGGTGGCGTTCATCATCTCACCCATCAGGGCTGACTTT GGCCCATCTTTCATGACCATCCCGGCTTTCTTTGCCAAGACTTCTGCGGCTTACAACCCCGTCACTCATCATGATGAACAAG AGTTCGCGATTCCTTCCAGGAGCTTCTATGCTCCGAGGCTCTTCAAAGCTTATGGGAACGGCTACTCCAGCAACAGTAA TGGCAAAACAGACTACATGGGAGGCGAGTGGATGTCAGCTGGGCGAGGAAAAGAAAGTGAACGGCTGTGTGAGGACCCCA GGCAGGAAAGCTTTGTGAAGTGTCAAGGTACTGTGCTTAGCCTTAGCCTTGAATCCCAAGGGAGGAAGTGTAGTACAAATGACT CACCCTGACAGAAACAGCAAGTGGCGCTGCCTAA
Opto-A1AR	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAAAGG ATAGCCCTCATGAACGGGACCGAGGGCCCAAACTTCTACGTGCCTTCTCCAAACAGACGGGCGTGGTGCCGAGCCCTTCGAGGC CCCGCAGTACTACCTGGCGGAGCCATGGCAGTTCCTCATGTGCGCCGCTACATGTTCTCTGCTGATCATGCTTGGCTTCCCATC AACTTCTCACGCTGTACGCTTGTGGGCAAGCTGCAGCGCCGCTCAACTACATCTGCTCAACTGGCCGTGGCCGTGGCCG ACCTTCTCATGGTGTTCGGGGGCTTACCACCACCTCTACACCTCTCTGCACGGGTACTTCGCTTCTGGGCCACGGGCTGCAA CCTGGAGGGCTTCTTTGCCACCTTGGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCTGGCCATCGAGCGGTAGCTGGTGGT AGTCAACCCCTGCGTACCAACCATCGTCACCCAGAGGGCCATCATGGGCGTGCCTTCACTGGGTATGGCTTGGCCCT GTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAAGTCTCGTGGGGATGACTACTACACGCCCA CGAGGAAACCAAAATGAGTCGTCATCATGTTCTGGTCCACTTCATCATCCCCCTGATTGTCATATTTCTTCTGCTAC GGCAGCTTACGTTGGTGGCCAAAAGGGAGAGCCGGGCTCAAGTCTGGCTCAAGACCGGACCAAGTCCGACTCGGAGCAAGTGA CGCTCCGCATCCATCGGAAAAACGCCCGGAGGAGGAGCGGGATGGCCAGCGCCAAAGACCAAGACGCACTTCTCAGTGGGCT CCTCAAGTTCCTCCGGGAGAAAGCGGCCGATGGTATCATGTTGTCATGCTTCTTCAATCTGCTGGCTGCCCTACGCT GGGTGGCGTTCATCATCTTACCCATCAGGGCTCTGACTTTGGCCCATCTTCATGACCATCGGCTTCTTTGCCAAGACTT CTGCCGTCAACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCGCAAGGCTTTCAGAAATGCTTGTGAAATCCAGTGTCT GTGCAGAAAGCAGTCTCCAAACATGCCTGGGCTACACCTGCACCCGCGCCAGCGAGCGCGTGAAGGGCAACACAAGCAATG TTCGCTACCCGTTGGGATCAAGAGAACTTCTACAGGATCTCAAGACCGGATGGCGTGTGTGAATGAATAATTTTCTTCC TGCCCGTGGATCTGCCAGGATTACAGTGTCAAAGACCAATCTCTGTACACAGCCCGGTTGAGAAGTAAAAGCTTTTGTGA GGTCTGCTGCTGTAGGGCCCTCAACCCCGACCTTGAACAAGAACATCAAGTTCACACCATTAAGGTTCCACCATCTCCCTC AGTGAGAACGGGAGGAAGTCCACAGAAACAGCAAGTGGCGCTGCCTAA
Opto-FFR3	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAAAGG ATAGCCCTCATGAACGGGACCGAGGGCCCAAACTTCTACGTGCCTTCTCCAAACAGACGGGCGTGGTGCCGAGCCCTTCGAGGC CCCGCAGTACTACCTGGCGGAGCCATGGCAGTTCCTCATGTGCGCCGCTACATGTTCTCTGCTGATCATGCTTGGCTTCCCATC AACTTCTCACGCTGTACGCTTGTGGGCAAGCTGCAGCGCCGCTCAACTACATCTGCTCAACTGGCCGTGGCCGTGGCCG CCGACCTTCTCATGGTGTTCGGGGGCTTACCACCACCTCTACACCTCTCTGCACGGGTACTTCGCTTCTGGGCCACGGGCTG CAACTGGAGGGCTTCTTTGCCACCTTGGGCGGTGAAATTCGACTGTGGTCTTGGTGGTCTGGCCATCGAGCGGTAGCTGGTGGT GTGGCCACCCACTGTGGTACAAGACCCGGCAGGCTGGGCGAGGCAATCATGGGCGTGCCTTCACTGGGTATGGCTTGG CCTGTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGAGGGCATGCAAGTCTCGTGGGGATGACTACTACACGCC CCACGAGGAAACCAAAATGAGTCGTCATCATGTTCTGGTCCACTTCATCATCCCCCTGATTGTCATATTTCTTCTGCTG TACGACCGCTGGTGTGATCTCGGCAGAGGGGCGAGCCCGCGGAGAGGGTGGCGCATGGTATCATCATGGTCA TCGCTTTCTTAATCTGCTGGCTGCCCTACGCTGGGTGGCGTTCATCATCTTACCCATCAGGGCTCTGACTTTGGCCCATCTT CATGACCATCCCGGCTTTCTTTGCCAAGACTTCTGCCGTCTACAACCCGCTCATCTACATCATGATGAACAAGCAGTTCGCGCC GACTTTCATGAGTGTGAGGAGTGTGTGGCTCTGGGCGAGTGGCAGCAGGAGAGCAGCATGGAGTGAAGGAGCAGAAAG GAGGGAGGAGGAGAGAGCGGACCGACCGCTGAAAGAAAGACCAAGTGAACACTCAGAGGCTGTGGAATGGTGGCCAGGTGGC CTGTGCTGAAAGCAGCAGAAACAGCAAGTGGCGCTGCCTAA
Opto-A2A	ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGGAAAGG ATAGCCCTCATGAACGGGACCGAGGGCCCAAACTTCTACGTGCCTTCTCCAAACAGACGGGCGTGGTGCCGAGCCCTTCGAGGC

	<p>CCCGCAGTACTACCTGGCGGAGCCATGGCAGTTTCCATGTGGCCGCTACATGTTCTGCTGATCATGCTTGGCTTCCCCATC AACTTCTCACGCTGTACGTGTGGCTCAACAGCAACCTGCAGAACCTCAACTACATCTGCTCAACTGGCCGTGGCCG ACCTTCTTACGTTGGTTCGGGGCTTCCACCACCTCTACACCTCTCTGCAACGGGTACTTCTGCTTGGCCGACGGGCTGCAA CCTGGAGGGCTTCTTTGCCACCTTGGGGCGTGAATTGCACCTGTGGTCTTGGTGGTCTGGCCATCGAGCGGTACGTGGTGGT CGCATCCCGCTCCGGTACAATGGCTTGGTACCAGCAGAGGGCCATCATGGCGTCCGCTTCACTGGTGTGCTGGCTTGGCC GTGCCCGCCCCCTCGTGGCTGGTCCAGGTACATCCCGAGGGGCATGCAAGTGTCTGGCGGGATGCACTACACGCCCCA CGAGAAACCAACAATGAGTCGTTCGTACATACATGTTCTGGTCCACTTTCATCATCCCCCTGATTGTATATTCTCTGTCTAC GGACGGATCTTCTGGCGGCGCAGCAGCTGAAGCAGATGGAGAGCCAGCTTCTGCCGGGGAGCGGGCAGCGTCCACACTGC AGAAGGAGGTCCATGCTCGCATGGTGTATCATCATGTCATGCTTTCCTAATCTGCTGGCTGCCCTACCGTGGGGTGGCGTTCTA CATCTTACCCATCAGGGCTGTACTTGGCCCCATCTCATGACCATCCCGCTTCTTTCGCAAGACTTCTGCCCTCACAAC CCGCTCATACATCATGATGAACAAGCAGTTCCCGCAGACCTTCCGCAAGATCATTCCAGCCAGCTCTCGAGGAGCAAGAAC CTTTCAGGCAGCTGGCACCAGTCCCGGGTCTTGGCAGCTCATGGCAGTACGGAGAGCAGGTGACGCTCCGGCTCAACGGCCA CCCGCAGGAGTGTGGGCCAACGGCAGTGTCCACCCTGAGCGGAGGGCCAAATGGCTATGCCCTGGGGTGGTGGAGGG AGTGCACAAGAGTCCAGGGGAACAGGGCTCCAGAGCTGGAGCTCCTTAGCCATGAGCTCAAGGGAGTGTCCAGAGCCCC CTGGCTTAGATGACCCCTGGCCAGGATGGAGCAGGAGTGTCCACAGAAACCAGCCAAGTGGCGCTGCCTAA</p>
Opto-D1R	<p>ATGAAAACGATCATCGCCCTGAGTACATCTTCTGCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGAAAGG ATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCTTCTTCCAACAAGACGGGCGTGGTGGCGAGCCCTTCGAGGC CCCGCAGTACTACCTGGCGGAGCCATGGCAGTTCTCCATGTGGCCGCTACATGTTCTGCTGATCATGCTTGGCTTCCCCATC AACTTCTCACGCTGTACGTGTATCAGGTTTGCACACCTGCGGTCCAAAGGTGCTCAACTACATCTGCTCAACTGGCCGTGG CCGACTTCTCATGGTGTTCGGGGCTTCCACCACCTCTACACCTCTCTGCAACGGGTACTTCTGCTTGGGGCCAGGGCTG CAACTGGAGGGCTTCTTTGCCACCTTGGGGCGTGAATTGCACCTGTGGTCTTGGTGGTCTGGCCATCGAGCGGTACGTGGT GTGTCAGCCCTTTCAGTATGAGAGGAAGTACTCCGAAGGCAGCCATCATGGCGTCCGCTTCACTGGGTGATGGCTTGG CCTGTCCCGCCCCCTCGTGGCTGGTCCAGGTACATCCCGAGGGGCATGCAAGTGTCTGGCGGGTACTACTACAGCC CCACGAGGAAACCAACAATGAGTCGTTCGTACATCATGTTCTGGTCCACTTTCATCATCCCCCTGATTGTATATTCTTCTGC TAGGAAAGTATACAGAGGATGGCCAGAAAGCAATCCGGCGCATCTCAGCTTTCGAGAGGGCAGCAGTCCATGCCAAGAACTGCC AGACCCACAGGTAAATGGAAACCTGTCAATGCTTCAATCAGAAAGTTCCTTAAAGATGTCTTAAAGAGGCAATAAGT CCTGGCATGGTGTATCATGTTCTGCTTTCCTAATCTGCTGGTCCCTACGCTGGGTGGCGTCTACATCTTCAACCAT CAGGGCTCTGACTTTGGCCCCATCTTATGACCATCCCGCTTCTTTCGCAAGACTTCTGGCGTCAACAACCCGATCATAC TCATGATGAACAAGCAGTTCGCAAGGCATCTGACCCCTTTCAGGATGCTTAGAGATCTGCTCCACAGAAATAGCATGATA GACTGTAAGCATCAACAACAACGGGGCTGTGATGTTTCCAGCCACCATGAGCCCGAGGCTCCATCTCAAGGACTGTAATCTG GTTTACTGATCCCTCATGCTGTGGGCTCCTTTCGAGGACTGAAAGGGAGGAGGCGGGTGGCATACCTAAGCCACTGGAGAGG TGTCCCGGCTTATCGGTATATTGGACTATGACACCGATGCTCTCTAGAAAAGATCCAAACCCGTTACCCACAGCGGACAGCA TTCAACCACAGAAACCAGCCAAGTGGCGCTGCCTAA</p>
Opto-D2R	<p>ATGAAAACGATCATCGCCCTGAGTACATCTTCTGCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGAAAGG ATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCTTCTTCCAACAAGACGGGCGTGGTGGCGAGCCCTTCGAGGC CCCGCAGTACTACCTGGCGGAGCCATGGCAGTTCTCCATGTGGCCGCTACATGTTCTGCTGATCATGCTTGGCTTCCCCATC AACTTCTCACGCTGTACGTGTATCAGGAGAAAGGCTTTCAGACACCTCAACTACATCTGCTCAACTGGCCGTGGCCG ACCTTCTCATGGTGTTCGGGGCTTCCACCACCTCTACACCTCTCTGCAACGGGTACTTCTGCTTGGGGCCAGGGCTGCAA CCTGGAGGGCTTCTTTGCCACCTTGGGGCGTGAATTGCACCTGTGGTCTTGGTGGTCTGGCCATCGAGCGGTACGTGGTGGT GCATGCTTATGTTGATAAACACAGCTACAGCTCCAAAGCGCCAGCCATCATGGCGTCCGCTTCACTGGGTGATGGCTTGG CCTGTCCCGCCCCCTCGTGGCTGGTCCAGGTACATCCCGAGGGGCATGCAAGTGTCTGGCGGGTACTACTACAGCC CCACGAGGAAACCAACAATGAGTCGTTCGTACATCATGTTCTGGTCCACTTTCATCATCCCCCTGATTGTATATTCTTCTGC TAGGAAAAATATACATGTTCTCCGCAAGCGTCCGAAGCGGGTCAAACCAAGCGTAGCAGCCGAGCTTTCAGAGCCAACTGA AAACCCACTCAAGGGCAACTGTACCCACCTGAGGACATGAAACTCTGACCCGTTATCATGAAGCTAATGGGATTTCCAGT GAACAGCGGAGAATGGATGCTGCCCGCAGCTCAGGAGCTGAAATGGAGATGCTGTCAAGCACCAGCCCCCAGAGAGGACC CGGTATAGCCCCATCCCTCCAGTCAACCCAGCTCACTTCCCGATCCATCCCAACAGGCTTACATAGCAACCCCTGACAGT CTGCCAAACCAGAAAGAAATGGGCATGCCAAGATTGTCAATCCAGGATTCGCAAGTTCCTTGAAGATCCAGACCATGCCAAATGG CAAAACCCGACTCCCTTAAAGCAGTGTAGCCCGAGGAGCTTCCAGCAGAGGAGAAGAAAGCCACTCGCATGGTGTATCAT ATGGTATCGCTTTCCTAATCTGCTGGTCCCTACGCTGGGGTGGCGTTCATACATCTTCAACCATCAGGGCTCTGACTTTGGCC CCCTCTCATGACCATCCCGCTTCTTTCGCAAGACTTCTGCCGCTTCAACACCCGCTCATCTACATCATGATGAACAAGAGGAT CCGCAAGGCCTTCATGAAGATCTTGCACAGAAACCAGCCAAGTGGCGCTGCCTAA</p>
Opto-M1R	<p>ATGAAAACGATCATCGCCCTGAGTACATCTTCTGCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGAAAGG ATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCTTCTTCCAACAAGACGGGCGTGGTGGCGAGCCCTTCGAGGC CCCGCAGTACTACCTGGCGGAGCCATGGCAGTTCTCCATGTGGCCGCTACATGTTCTGCTGATCATGCTTGGCTTCCCCATC AACTTCTCACGCTGTACGTCTTCAAGGTCAACACGGAGCTCAAGACAGTCTCAACTACATCTGCTCAACTGGCCGTGGCCG ACCTTCTCATGGTGTTCGGGGCTTCCACCACCTCTACACCTCTCTGCAACGGGTACTTCTGCTTGGGGCCAGGGCTGCAA CCTGGAGGGCTTCTTTGCCACCTTGGGGCGTGAATTGCACCTGTGGTCTTGGTGGTCTGGCCATCGAGCGGTACGTGGTGGT ACTGGCCCCCTGAGTACCGTCCAAAGCGCACACCCCGCGGGCCATCATGGCGTCCGCTTCACTGGGTGATGGCTTGGCCT GTGCCCGCCCCCTCGTGGCTGGTCCAGGTACATCCCGAGGGGCATGCAAGTGTCTGGCGGGATGCACTACACGCCCCA CGAGAAACCAACAATGAGTCGTTCGTACATACATGTTCTGGTCCACTTTCATCATCCCCCTGATTGTATATTCTTCTGTAC GGACGATCTACCGGGAGACAGAAACCGAGCAGGGAGCTGGCAGCCCTTTCAGGCTCCGAAACGCCAGGCAAGGGGTGGCA CGACAGCAGCTCAGAGAGGTCCAGCAGGGCTGAGGGCTCACCAGACTCTCCAGCCGCTTCCAGCCGCTTCCGCTGGCGGGC CCCCAGGCTGTGCAGGCTACAGCTGGAAGGAAAGAGGAAAGAGGACGAAAGCTCCATGGAGTCCCTCATCTCAGAGGGA GAGGAGCTGGCTCCGAAGTGGTGTCAAGATGCCAATGGTGGACCCCGAGGCACAGGCCCCCAAGCAGCCCCCAGGAGCT CCCCAATACAGTCAAGAGGCGACTAAGAAAGGGCGTGTACGAGTGGCAAGGGCCAGAAAGCCGGAAGAGGAGCAGCTGGC CAAGCGGAAACCTTCTCGTGGTCAAGGAGAAGAGGGCGCTCGCATGGTGTATCATGTTGTATCATGTTCTTCTAATCTGTCTG CTGCCCTACGCTGGGGTGGGTTTACATCTTCAACCATCAGGGCTCTGACTTTGGCCCCATCTCATGACCATCCCGCTTCT TTGCCAAGACTTCTGCCGCTTCAACACCCGCTCATCTACATCATGATGAACAAGAGTTCGCGGGATTTCCGCTGTCTGCT TTGCCCTGGGACAAGAGGCGCTGGCCAAAGATCCCAAGCGCCCTGGCTCCGTCACCCGCTTCCCTCCCGCAATGACAGAA ACCAGCAAGTGGCGCTGCCTAA</p>
Opto-M2R	<p>ATGAAAACGATCATCGCCCTGAGTACATCTTCTGCTGGTATTTCGCCATGTACACCGATATAGAGATGAACAGGCTGGAAAGG ATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCTTCTTCCAACAAGACGGGCGTGGTGGCGAGCCCTTCGAGGC CCCGCAGTACTACCTGGCGGAGCCATGGCAGTTCTCCATGTGGCCGCTACATGTTCTGCTGATCATGCTTGGCTTCCCCATC AACTTCTCACGCTGTACGTCTTAAAGTCAACACGGAGCTCAAGACAGTCTCAACTACATCTGCTCAACTGGCCGTGGCCG ACCTTCTCATGGTGTTCGGGGCTTCCACCACCTCTACACCTCTCTGCAACGGGTACTTCTGCTTGGGGCCAGGGCTGCAA CCTGGAGGGCTTCTTTGCCACCTTGGGGCGTGAATTGCACCTGTGGTCTTGGTGGTCTGGCCATCGAGCGGTACGTGGTGGT ACAAACCTTGCACCTACCCAGTCAAGCGGACCCAAATAAGGCATCATGGCGTCCGCTTCACTGGGTGATGGCTTGGCCT GTGCCCGCCCCCTCGTGGCTGGTCCAGGTACATCCCGAGGGGCATGCAAGTGTCTGGCGGGATGCACTACACGCCCCA CGAGAAACCAACAATGAGTCGTTCGTACATCATGTTCTGGTCCACTTTCATCATCCCCCTGATTGTATATTCTTCTGTAC GGACATATCCCGAGCCAGCAAGAGCAGGATAAAGAAAGGACAAGAAAGGAGCTTTCGCAACCAAGCCCGTTCCTCAAAGT TGTGTAAGAAAGGATAGTGAAGCAACAAATAACACATGCCAGCAGTACGATGGCTGGAGCAACAACAAATCCAGAAATGG CAAGCCCCAGGATCCTGTGACTGAAACTGTGTTTCAGGGAGAGGAGAAGGAGCTCCAAATGACTCCACTCAGTCACTGCT GTTGCCCTAATATGAGAGATGATGAAATAACCCAGGATGAAACACAGTTCCTACTTCCCTGGCCATTCCAAAGATGAGAACT CTAAGCAACATGCATCAGAAATGGCACCAGCCCAAAAGTGAATCATGTACCCCAACTAATACCCCGTGGAGGTAGTGGG GTCTCAGTCAAGATGGAGATGAAAAGCAGAAATTTAGCCCGCAAGATTGTGAAGATGACTAAGCAGCCTGCAAAAAGAA</p>

	<p>CCTCCTCCTCCCGGAAAAGAGTACCCGCATGGTGATCATCATGGTCATCGCTTTCCTAATCTGCTGGCTGCCCTACGCTG GGTGGCGTTTACATCTTACCCATCAGGGCTCTGACTTTGGCCCCATCTTCATGACCATCCCGGCTTTCTTTGCCAAGACTTC TGCCGCTACAACCCCGTCATCTACATCATGATGAACAAGCAGTTCCGCAAAACCTTTAAACACCTTCTCATGTGTCATTATAAG AACATAGGCGCTACAAGGACAGAAACAGCCAAAGTGGCGCCTGCCTAA</p>
Opto-M3R	<p>ATGAAAACGATCATCGCCCTGAGCTACATCTTCTGCCTGGTATTCCGCATGTACCCGATATAGAGATGAACAGGCTGGGAAAAG ATAGCCTCATGAACGGGACCGAGGGCCAAACTTCTACGTGCCTTTCCAAACAGACGGGCGTGGTCCGACGCCCTTCGAGGC CCGCGACTACTACCTGGCGGAGCCATGGCAGTTCTCCATGCTGGCCGCTACATGTTCTCTGCTGATCATGCTTGGCTTCCCATC AACTTCTCACGCTGTACGCTTTAAGGTCACAAGCAGCTGAAGACGGTCTCAACTACATCTCTGCTCAACTGGCCGTGGCCG ACCTCTTCATGGTGTTCGGGGGCTTACCACCACCTTACACCTCTCTGCACGGGTACTTCGTCTTTGGGCCACCGGGCTGCAA CCTGGAGGGCTTCTTTGCCACCTTGGCGGTGAAATTCACATGTGGTCTTGGTGGTCTTGGCCATCGAGCGGTACGTGGTGGT ACGAGGCGCTCACGTACCAGCCAAACGAACAACAAAGAGAGCCATCATGGCGCTGCCTTCACTGGTCTGCTGCTGGCTTGGCC GTGCCGCGCCCCCTCGTCGGCTGGTCCAGGTACATCCCGGAGGGCATGCAGTGTCTGCGGGATTGACTACTACAGCCCCA CGAGAAACCAACAATGAGTCGTTCGTTCATCATGTTCTGGTCCACTTCATCATCCCCCTGATGTGTATATTCTTCTGTAC GGAAGGATCTATAAGGAACTGAAAAGCCTACCAAGAGCTTGGTGGCTGCAAGCTTGGGACAGAGGCAGAGACAGAAAAT TTGTCCACCCACGGGCACTTTCGAAGCTGCAGCAGTTACGAACTTCAACAGCAAGCATGAAACGCTCCAAACAGGAGGAAGTA TGCCCGCTGCCACTTCTGGTTTCAACAACAAGAGCTGGAAACCCAGCTCCGAGCAGATGGACCAAGACACAGCAGCAGTACAGT TGGAACAACAATGATGCTGCTGCCTCCCTGGAGAATCCCGCTTCTCCGACGAGGAGGACATTGGCTCCGAGACGAGAGCCATCT ACTCCATCTGCTCAAGCTTCCGGTCCAGCACCATCTCAACTCCACCAAGTTACCTCATCGGACAACTGCAGGTGCCTGA GGAGGAGCTGGGATGGTGGACTTGGAGAGGAAAGCCGACAAGCTGCAGGCCAGAGAGCGTGGACGATGGAGGCAGTTTCCCA AAAAGCTTCTCAAGCTTCCATCCAGCTAGAGTCAGCCGTGGACACAGCTAAGACTTCTGAGCTCAACTCTCAGTGGGTAAAG GCACGGCCACTTACCTCTGTCTTCAAGGAAGCCACTCTGGCCAAAGGTTTGTCTGAAAGCCAGAAGTCAAGTCACTAAGCG GAAAAGGATGCTCCTGGTCAAGGAGAAGAAAGCGGCCGATGGTGCATCATGGTGCATGCTTTCTAATCTGCTGGCTGCC TAGCCTGGGGTGGCTTCTACATCTTACCCATCAGGGCTCTGACTTTGGCCCATCTTCATGACCATCCCGCTTTCTTTGCCA AGACTTCTGCCGTCTACAACCCCGTCTCATCATCATGATGAACAAGCAGTTCCGACCACTTTCAAGATGCTGCTGTGTGCCA GTGTGACAAAAAAGAGGGCCAAAGCAGCAGTACCAGCAGACAGTCCGTCATTTTCAACAGCGCCACCCGAGCAGGCTT ACAGAAACCGCAAGTGGCGCTGCCTAA</p>

Table 6.4 Nucleotide sequences of all light-activated control GPCRs created using the chimeric algorithm described in section 3.1

Gene name	CRE		SRE		SRE.L		CRE+stim.	
	Dark	Light	Dark	Light	Dark	Light	Dark	Light
Opto-GPR1	1.52 ± 0.42	8.94 ± 3.52	0.52 ± 0.17	0.61 ± 0.22	0.74 ± 0.25	0.57 ± 0.20	1.39 ± 0.12	1.45 ± 0.26
Opto-GPR3	0.45 ± 0.16	0.33 ± 0.07	0.68 ± 0.23	3.63 ± 2.95	0.63 ± 0.19	0.44 ± 0.17	1.03 ± 0.13	0.92 ± 0.18
Opto-GPR4	0.47 ± 0.18	0.294 ± 0.07	1.61 ± 1.00	1.84 ± 1.36	0.67 ± 0.25	0.50 ± 0.38	0.60 ± 0.12	0.36 ± 0.11
Opto-GPR6	0.49 ± 0.26	0.25 ± 0.08	1.26 ± 0.84	1.09 ± 0.46	0.69 ± 0.21	0.51 ± 0.20	1.02 ± 0.08	0.83 ± 0.2
Opto-GPR12	0.19 ± 0.08	0.2 ± 0.06	1.17 ± 0.58	0.76 ± 0.30	0.8 ± 0.28	0.58 ± 0.27	1.14 ± 0.19	0.95 ± 0.15
Opto-GPR15	0.26 ± 0.14	0.21 ± 0.07	0.54 ± 0.29	0.65 ± 0.31	0.77 ± 0.25	0.73 ± 0.32	1.02 ± 0.13	0.77 ± 0.13
Opto-GPR17	0.32 ± 0.10	0.27 ± 0.08	0.49 ± 0.25	0.6 ± 0.24	0.87 ± 0.34	0.54 ± 0.17	1 ± 0.08	0.83 ± 0.15
Opto-GPR18	0.19 ± 0.06	0.22 ± 0.06	0.32 ± 0.07	0.8 ± 0.49	0.87 ± 0.28	0.56 ± 0.21	1 ± 0.12	1.14 ± 0.33
Opto-GPR19	0.21 ± 0.08	0.24 ± 0.09	0.46 ± 0.23	0.55 ± 0.25	0.73 ± 0.22	0.63 ± 0.28	1.03 ± 0.14	0.9 ± 0.21
Opto-GPR20	0.23 ± 0.03	0.49 ± 0.20	0.49 ± 0.20	0.86 ± 0.29	0.59 ± 0.15	0.64 ± 0.24	0.88 ± 0.10	0.74 ± 0.19
Opto-GPR21	0.36 ± 0.07	10.36 ± 5.73	1.66 ± 1.36	0.57 ± 0.22	0.62 ± 0.19	0.64 ± 0.22	0.86 ± 0.08	0.99 ± 0.31
Opto-GPR22	0.27 ± 0.09	0.41 ± 0.12	1.41 ± 0.74	1.27 ± 0.59	0.69 ± 0.18	0.86 ± 0.31	1.05 ± 0.29	2.45 ± 1.34
Opto-GPR25	0.29 ± 0.08	0.4 ± 0.08	0.97 ± 0.61	1.44 ± 1.03	0.64 ± 0.22	0.45 ± 0.15	1.29 ± 0.17	0.98 ± 0.19
Opto-GPR26	0.36 ± 0.10	0.41 ± 0.09	1.2 ± 0.84	0.54 ± 0.14	0.53 ± 0.17	0.44 ± 0.15	1.15 ± 0.11	0.86 ± 0.15
Opto-GPR27	0.32 ± 0.10	0.23 ± 0.04	0.56 ± 0.20	0.59 ± 0.21	0.58 ± 0.17	0.41 ± 0.15	1.01 ± 0.06	0.89 ± 0.14
Opto-GPR31	0.27 ± 0.11	0.57 ± 0.27	0.56 ± 0.19	0.79 ± 0.38	0.57 ± 0.21	0.51 ± 0.17	1.02 ± 0.10	0.8 ± 0.15
Opto-GPR32	0.21 ± 0.07	4.89 ± 2.32	0.81 ± 0.38	0.67 ± 0.36	0.54 ± 0.16	0.44 ± 0.13	1.04 ± 0.09	0.66 ± 0.15
Opto-GPR33	0.31 ± 0.14	0.46 ± 0.10	0.3 ± 0.07	2.45 ± 1.33	0.62 ± 0.16	30.56 ± 10.2 3	0.97 ± 0.09	0.65 ± 0.13
Opto-GPR34	0.3 ± 0.11	0.3 ± 0.09	0.49 ± 0.16	0.5 ± 0.14	0.61 ± 0.27	0.65 ± 0.16	0.95 ± 0.09	0.81 ± 0.09
Opto-GPR35	0.32 ± 0.11	0.22 ± 0.04	0.33 ± 0.08	0.47 ± 0.16	0.63 ± 0.16	0.64 ± 0.21	1.03 ± 0.10	0.74 ± 0.12
Opto-GPR37	0.3 ± 0.08	0.25 ± 0.07	0.5 ± 0.11	0.41 ± 0.13	0.53 ± 0.12	0.47 ± 0.16	0.91 ± 0.08	0.91 ± 0.15
Opto-GPR37L1	0.25 ± 0.08	0.31 ± 0.09	0.33 ± 0.11	0.33 ± 0.08	0.49 ± 0.13	0.5 ± 0.19	0.89 ± 0.11	1.06 ± 0.20

Opto-GPR39	0.39 ± 0.19	0.51 ± 0.21	0.67 ± 0.21	0.35 ± 0.10	0.52 ± 0.15	0.63 ± 0.19	0.87 ± 0.05	0.92 ± 0.21
Opto-GPR42	0.3 ± 0.14	1.05 ± 0.68	0.59 ± 0.21	0.49 ± 0.18	0.61 ± 0.15	0.6 ± 0.20	0.88 ± 0.05	1.22 ± 0.46
Opto-GPR45	0.43 ± 0.16	0.56 ± 0.12	1.38 ± 0.60	0.71 ± 0.24	0.53 ± 0.13	0.48 ± 0.15	1.16 ± 0.18	0.85 ± 0.07
Opto-GPR50	0.4 ± 0.16	0.43 ± 0.06	0.81 ± 0.20	0.86 ± 0.28	0.51 ± 0.15	0.34 ± 0.12	1.07 ± 0.19	1.07 ± 0.13
Opto-GPR52	0.26 ± 0.09	0.3 ± 0.07	0.93 ± 0.49	0.65 ± 0.24	0.54 ± 0.15	0.45 ± 0.17	0.99 ± 0.07	0.88 ± 0.11
Opto-GPR55	0.32 ± 0.12	0.46 ± 0.09	0.74 ± 0.2	0.66 ± 0.20	0.5 ± 0.15	0.4 ± 0.10	1.12 ± 0.10	0.75 ± 0.15
Opto-GPR61	0.62 ± 0.17	6.11 ± 3.10	0.58 ± 0.2	0.66 ± 0.29	0.51 ± 0.15	0.62 ± 0.18	1.07 ± 0.12	0.82 ± 0.12
Opto-GPR62	0.32 ± 0.09	0.51 ± 0.14	0.57 ± 0.22	0.77 ± 0.22	0.55 ± 0.16	0.6 ± 0.11	0.89 ± 0.04	0.83 ± 0.15
Opto-GPR63	0.37 ± 0.11	0.51 ± 0.13	0.42 ± 0.12	0.44 ± 0.16	0.53 ± 0.18	0.78 ± 0.16	1.16 ± 0.28	0.74 ± 0.15
Opto-GPR65	0.39 ± 0.15	0.53 ± 0.21	0.59 ± 0.19	0.67 ± 0.26	0.54 ± 0.14	0.58 ± 0.16	1.02 ± 0.05	0.8 ± 0.08
Opto-GPR68	0.81 ± 0.45	0.78 ± 0.31	0.97 ± 0.27	2.61 ± 0.76	0.52 ± 0.15	0.58 ± 0.17	0.84 ± 0.05	1.02 ± 0.09
Opto-GPR75	0.33 ± 0.14	0.30 ± 0.08	0.99 ± 0.45	1.28 ± 0.93	0.61 ± 0.18	0.62 ± 0.15	0.89 ± 0.09	0.86 ± 0.13
Opto-GPR78	0.29 ± 0.05	0.65 ± 0.24	1 ± 0.34	5.05 ± 2.87	0.54 ± 0.12	35.1 ± 11.47	0.96 ± 0.13	1.38 ± 0.32
Opto-GPR82	0.28 ± 0.07	0.50 ± 0.14	0.59 ± 0.19	0.54 ± 0.21	0.68 ± 0.17	0.71 ± 0.15	0.93 ± 0.14	1.31 ± 0.43
Opto-GPR83	0.81 ± 0.18	0.67 ± 0.14	0.95 ± 0.19	0.86 ± 0.25	0.56 ± 0.22	0.51 ± 0.16	1.23 ± 0.26	1.09 ± 0.17
Opto-GPR84	0.47 ± 0.09	1.02 ± 0.27	0.75 ± 0.23	0.67 ± 0.19	0.49 ± 0.16	0.45 ± 0.13	1.03 ± 0.14	1.04 ± 0.12
Opto-GPR85	0.55 ± 0.15	1.10 ± 0.38	0.54 ± 0.16	0.43 ± 0.10	0.39 ± 0.10	0.49 ± 0.15	0.97 ± 0.13	0.72 ± 0.15
Opto-GPR87	0.44 ± 0.09	0.53 ± 0.09	0.59 ± 0.18	0.66 ± 0.18	0.44 ± 0.12	0.45 ± 0.13	1.06 ± 0.05	1 ± 0.24
Opto-GPR88	0.52 ± 0.08	0.44 ± 0.04	0.55 ± 0.17	1.88 ± 0.92	0.48 ± 0.15	0.55 ± 0.19	1.04 ± 0.06	1.02 ± 0.12
Opto-GPR119	1.27 ± 0.45	0.87 ± 0.23	0.64 ± 0.17	0.67 ± 0.14	0.47 ± 0.09	0.52 ± 0.10	1.06 ± 0.14	0.9 ± 0.10
Opto-GPR120	0.69 ± 0.18	0.48 ± 0.20	1.78 ± 0.79	1.59 ± 1.02	1.22 ± 0.54	0.80 ± 0.64	0.65 ± 0.24	0.77 ± 0.19
Opto-GPR132	1.33 ± 0.43	0.66 ± 0.20	0.57 ± 0.18	0.55 ± 0.15	0.5 ± 0.11	0.69 ± 0.17	0.96 ± 0.09	0.89 ± 0.07
Opto-GPR135	0.57 ± 0.12	6.78 ± 3.09	0.64 ± 0.09	1.11 ± 0.45	0.58 ± 0.14	0.55 ± 0.14	1.07 ± 0.10	1.09 ± 0.23
Opto-GPR139	0.42 ± 0.09	0.43 ± 0.11	0.41 ± 0.08	0.53 ± 0.11	0.46 ± 0.11	0.55 ± 0.12	0.8 ± 0.03	1.18 ± 0.41
Opto-GPR141	0.55 ± 0.13	0.37 ± 0.08	0.58 ± 0.15	0.45 ± 0.12	0.63 ± 0.16	0.68 ± 0.20	0.93 ± 0.08	1.28 ± 0.41
Opto-GPR142	0.33 ± 0.12	0.3 ± 0.05	0.67 ± 0.29	0.46 ± 0.14	0.7 ± 0.17	0.91 ± 0.19	0.76 ± 0.04	0.95 ± 0.23
Opto-GPR146	0.65 ± 0.15	1.06 ± 0.43	0.96 ± 0.21	1.62 ± 0.89	0.6 ± 0.17	0.58 ± 0.12	1.5 ± 0.45	1.09 ± 0.24
Opto-GPR148	0.55 ± 0.13	0.78 ± 0.39	1.05 ± 0.29	0.68 ± 0.25	0.81 ± 0.4	0.58 ± 0.16	1.09 ± 0.07	0.95 ± 0.13
Opto-GPR149	0.46 ± 0.10	1.01 ± 0.39	0.88 ± 0.3	0.69 ± 0.17	0.66 ± 0.28	0.54 ± 0.18	1.21 ± 0.15	0.91 ± 0.19
Opto-GPR150	0.74 ± 0.26	1.05 ± 0.32	1.43 ± 0.31	1.26 ± 0.33	0.48 ± 0.12	0.7 ± 0.23	1.15 ± 0.10	0.73 ± 0.14
Opto-GPR151	0.52 ± 0.09	0.75 ± 0.18	0.65 ± 0.17	1.17 ± 0.25	0.87 ± 0.49	0.49 ± 0.12	0.83 ± 0.06	0.9 ± 0.09
Opto-GPR152	0.42 ± 0.08	0.48 ± 0.10	0.56 ± 0.17	0.74 ± 0.26	0.52 ± 0.10	0.68 ± 0.16	0.87 ± 0.13	0.88 ± 0.17
Opto-GPR153	0.67 ± 0.15	0.67 ± 0.09	0.66 ± 0.21	0.69 ± 0.18	0.54 ± 0.12	0.75 ± 0.19	0.93 ± 0.10	1.1 ± 0.16
Opto-GPR160	0.44 ± 0.04	0.58 ± 0.15	0.67 ± 0.26	0.86 ± 0.51	0.87 ± 0.13	0.83 ± 0.13	1.13 ± 0.12	1.02 ± 0.15
Opto-GPR161	0.57 ± 0.08	0.67 ± 0.13	0.66 ± 0.21	0.65 ± 0.21	0.7 ± 0.18	0.74 ± 0.20	0.88 ± 0.11	1.04 ± 0.25
Opto-GPR162	0.39 ± 0.1	0.57 ± 0.08	0.61 ± 0.13	0.88 ± 0.34	0.73 ± 0.14	0.95 ± 0.24	0.98 ± 0.06	1.68 ± 0.79
Opto-GPR171	0.54 ± 0.09	0.54 ± 0.11	0.70 ± 0.10	0.73 ± 0.21	0.63 ± 0.12	0.74 ± 0.13	1.08 ± 0.06	2.19 ± 1.20
Opto-GPR173	0.37 ± 0.09	0.38 ± 0.09	0.59 ± 0.14	0.57 ± 0.13	1.98 ± 1.18	0.8 ± 0.11	1.1 ± 0.06	1.46 ± 0.27
Opto-GPR174	1.01 ± 0.23	0.87 ± 0.19	1.28 ± 0.69	0.68 ± 0.16	0.55 ± 0.17	0.74 ± 0.09	1.14 ± 0.26	1.02 ± 0.23
Opto-GPR176	0.53 ± 0.12	0.64 ± 0.12	0.96 ± 0.2	0.72 ± 0.13	0.67 ± 0.22	0.65 ± 0.14	0.91 ± 0.06	1.02 ± 0.12

Opto-GPR182	0.71 ± 0.18	0.75 ± 0.32	0.7 ± 0.11	1.72 ± 0.96	0.52 ± 0.15	0.56 ± 0.11	0.98 ± 0.07	1.13 ± 0.12
Opto-GPR183	0.43 ± 0.09	0.65 ± 0.07	0.88 ± 0.16	2.02 ± 1.01	0.76 ± 0.23	0.68 ± 0.18	0.96 ± 0.08	0.91 ± 0.11

Table 6.2 Mean induction values for each light-activated human Class A oGPCRs for the different luciferase-based gene reporters used for the functional screening (section 4.2, 4.3)

7-Appendix II

GPR1

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GPR37

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GPR3711

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