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Alternative Splicing of G-protein Coupled Receptors: Relevance to Pain Management

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Abstract

Drugs that target G-protein coupled receptors (GPCRs) represent the primary treatment strategy for patients with acute and chronic pain; however, there is substantial individual variability in both the efficacy and adverse side effects associated with these drugs. Variability in drug responses is, in part, due to individuals' diversity in alternative splicing of pain-relevant GPCRs. GPCR alternative splice variants often exhibit distinct tissue distribution patterns, drug binding properties, and signaling characteristics that may impact disease pathology as well as the size and direction of analgesic effects. Here, we review the importance of GPCRs and their known splice variants to the management of pain.

Pain is a multidimensional sensory and emotional experience that can generally be categorized into one of four types¹. *Nociceptive pain* is an acute response to environmental stimuli that warns of potential or actual tissue damage. In the event of actual damage, inflammatory and/or neuropathic pain may occur. *Inflammatory pain* occurs in response to damage of tissues and infiltration of immune cells, while *neuropathic pain* occurs in response to damage of nerves. Inflammatory and neuropathic pain typically serve to promote wound healing and repair; however, in many cases, the pain outlasts the stimulus and becomes chronic. Unlike inflammatory and neuropathic pain, *functional or idiopathic pain* is characterized by perpetual abnormalities in sensory processing that occur in the absence of direct inflammation or nerve damage.

Acute and chronic pain are primarily treated with pharmacological agents that promote analgesia. The principle target of a variety of analgesic drugs including opioids, cannabinergics, and anti-depressants is g-protein coupled receptors (GPCRs). Upon activation, GPCRs initiate molecular changes resulting in excitation or inhibition of nerve, immune, and glial cells important for the onset and maintenance of pain. While the critical role of GPCRs in pain biology and management is well established, reliably effective

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therapeutics with minimal side effects are lacking. Inter-individual variability in response to a given analgesic is largely due to variation at the genetic level. Of particular interest are genetic variants in alternative splice regions that alter protein coding of the mRNA, giving rise to proteins which differ in form and function (i.e., alternative splice variants). This review highlights the importance of alternative splicing in the regulation of GPCRs involved in the transmission and modulation of pain.

GPCRs are Relevant for the Treatment of Pain

The human genome encodes approximately 800 distinct GPCRs, 70% of which contribute to pain or pain-related phenotypes². GPCRs interact with a tremendous variety of signaling mediators, ranging from small molecules to large peptides and proteins. Although each receptor has the ability to induce a range of functional intracellular changes, all GPCRs possess a distinct and evolutionarily conserved architecture. Each canonical or classic receptor is comprised of seven transmembrane (7TM) proteins that span the cellular membrane. These transmembrane proteins are interconnected by intracellular and extracellular loops (Figure 1). In addition, there are amino acid chains known as N-terminus and C-terminus tails, which are attached to the first and last transmembrane, respectively. As alluded by its name, every GPCR is coupled to a g-protein, which acts as a molecular switch to regulate cellular activity. (Table 1).

The resulting structure created by the transmembrane segments and loops provides interactive sites where ligands can bind. Ligands that bind to their receptor and initiate cell signaling are referred to as agonists. Upon binding, agonists produce a conformational change of the GPCR and subsequent uncoupling of the associated g-protein. Once uncoupled, the g-protein separates into two subunits (the alpha (α) and beta/gamma (β/γ) subunits), each of which initiates a chain of molecular reactions that affect cellular activity³. Depending on the type of g-protein, the initiated downstream effects can promote cellular excitation or inhibition (Table 1). In general, agonists that activate pain-relevant GPCRs coupled to G_s typically produce pain, while those coupled to G_i typically inhibit pain². Other ligands, known as antagonists, compete with agonists for the GPCR binding site and impede g-protein uncoupling and downstream signaling events. Because of their ability to modulate cellular activity at each step of the pain pathway, GPCRs represent a popular pharmacologic target for the management of clinical pain. In fact, over 60% of commonly prescribed analgesics work by binding to GPCRs³. Table 2 provides a summary of these GPCRs (opioid, cannabinoid, adrenergic, and serotonergic receptors) along with their associated g-protein, endogenous ligands, and analgesic compounds.

Opioid receptors are among the most well known GPCRs that regulate the transmission and perception of pain. There are four opioid receptor subtypes, including: the mu opioid receptor (MOR-1), the delta opioid receptor, the kappa opioid receptor, and the nociceptin receptor. Of these subtypes, MOR-1 is the classic receptor responsible for analgesic responses to endogenous endorphins as well as exogenous drugs. Upon agonist binding to MOR-1, its associated $G_{\alpha i}$ protein is activated and produces cellular inhibition of pronociceptive neurons⁹. For this reason, opioids are used in the management of acute pain (such as that associated with surgery) as well as chronic pain disorders such as low back

pain, extremity pain, and osteoarthritis¹⁰. Opioid antagonists, usually co-administered with opioid agonists to reduce the development of unwanted opioid side effects, are also capable of producing analgesia independently of MOR-1¹¹.

Cannabinoid receptors share similar signaling properties with MOR-1, making them attractive targets for clinical pain management. There are two cannabinoid (CB) receptor subtypes, CB₁ and CB₂, both of which couple to G_{αi}. CB receptors play a significant role in promoting analgesia in response to endocannabinoids such as 2-arachidonoylglycerol (2-AG) and anandamide. Commercially available CB agonists such as nabilone and tetrahydrocannabinol, which bind to both CB subtypes, are used to treat fibromyalgia and neuropathic pain¹².

Adrenergic receptors, which mediate the physiological responses to epinephrine (Epi) and norepinephrine (NE), represent another frequently targeted class of GPCRs. The adrenergic superfamily includes three subtypes respectively of α₁ARs (α_{1A}AR, α_{1B}AR, α_{1D}AR), α₂ARs (α_{2A}AR, α_{2B}AR, α_{2C}AR), and βARs (β₁ARs, β₂ARs, β₃ARs). The α₂AR couples to G_{αi} and promotes analgesia *via* cellular inhibition. Hence α₂AR agonists such as trazodone are used to promote analgesia. In contrast, α₁AR, which is coupled to G_{αq}, facilitates cellular excitation of pronociceptive neurons, resulting in increased pain signaling. The βARs also facilitate pain signaling *via* G_{αs} signaling. To attenuate their excitatory contributions, α₁AR and βARs are commonly used to treat a range of chronic pain disorders such as migraine, neuropathic pain, and fibromyalgia.

Finally, serotonin receptors, which mediate physiological responses to the monoamine serotonin (5-HT) play an important role in pain management⁸. The serotonin superfamily is quite large, including seven general members: 5-HT₁ (5-HT_{1A}, 5-HT_{1B}, 5-HT_{1D}, 5-HT_{1E}, 5-HT_{1F}), 5-HT₂ (5-HT_{2A}, 5-HT_{2B}, 5-HT_{2C}), 5-HT₃, 5-HT₄, 5-HT₅, 5-HT₆, and 5-HT₇. With the exception of the 5-HT₃ receptor, a ligand-gated ion channel, all 5-HT receptors are GPCRs. The effects of the 5-HT receptor family on pain are heavily dependent upon the receptor subtype. Triptans target G_{αi}-coupled 5-HT₁ receptors, which promote analgesia *via* cellular inhibition, and normalize vascular changes associated with migraine headache¹³. Antidepressants promote chronic synaptic serotonin release that causes the downregulation of G_{αq} coupled 5-HT₂ receptors, thus attenuating their excitatory contributions to pain signaling. 5-HT antagonists that target 5-HT₄ receptors in the central nervous system and the gastrointestinal (GI) tract are used in the treatment of migraine¹⁴ and IBS¹⁵. Meanwhile, the net effect of 5-HT₇ activation on pain is highly dependent on the location of the receptor. Activation of 5-HT₇ receptors on peripheral nerve terminals produces pain^{16,17}, while activation in midbrain structures such as the periaqueductal gray alleviates pain associated with nerve injury¹⁸.

While these conventional therapeutics are able to alleviate pain, their efficacy is limited to a subset of the population¹⁹. Additionally, their use is constrained by adverse side effects, such as altered mental state, nausea, constipation, sedation, and life-threatening respiratory depression. Variability in patient response and side-effect profiles is, in part, due to diversity in alternative splicing of GPCRs expressed in tissues that regulate pain processing. By expanding our understanding of GPCR alternative splice variants and their associated

pharmacodynamic responses, we will be able to better predict patient-centered treatment outcomes.

Alternative Splicing Adds to the Diversity of GPCR Signaling

Alternative splicing is an important mechanism of gene regulation, affecting approximately 90% of all genes within the human genome²⁰. A single gene is able to generate exponential protein coding capabilities *via* alternative splicing. Prior to alternative splicing, a gene is first transcribed into precursor messenger ribonucleic acid (pre-mRNA). The pre-mRNA sequence contains short protein coding regions known as exons. Interspersed between the exons are longer non-coding regions known as introns (Figure 2). Before the sequence can be translated to produce protein, the introns and alternative exons within pre-mRNA are removed, or spliced, and the constitutive exons are brought together, resulting in the canonical mRNA transcript ready for protein synthesis. When alternative splicing occurs, however, the pre-mRNA is edited such that constitutive exons are removed from, or introns are retained, in the final mRNA transcript. The most common type of alternative splicing within the human genome is exon skipping²¹. Here, constitutive exons are excluded from the final mRNA transcript. Another common type of alternative splicing is splice site selection, in which the portion of an exon is spliced out due the presence of a nucleotide sequence that facilitates splicing activity²¹. Intron retention is another type of alternative splicing in which an intron remains in the final mRNA transcript. Each type of alternative splicing will render an mRNA transcript and corresponding protein that is structurally different than the canonical protein produced from the standard template.

Accumulating evidence suggests that alternative splicing significantly adds to the functional diversity of the human genome and that variations in these processes produce pathological states²². The presence of multiple GPCR splice variants allows for essential, precisely regulated differences in expression (e.g., tissue-specific expression)²³, as well as in agonist binding²⁴, agonist-induced internalization²⁵, and intracellular signaling dynamics^{25,26}. Some alternative splice variants even display functional characteristics opposite to the canonical form²⁷⁻²⁹. Polymorphisms that alter the ratio of functionally distinct protein isoforms through alternative splicing may produce changes in the direction of pain-relevant GPCR pharmacodynamics (e.g. coupling to stimulatory vs. inhibitory G protein effector systems), yet remain understudied. A PubMed search of “alternative splicing pain” yields only 87 relevant original research articles. Most are focused on ion channels such as voltage-gated calcium channels³⁰ and transient receptor potential channels^{31,32}, with only 12 articles focusing on GPCRs. This is an important area of study as identification of GPCR splice variants differentially expressed in individuals with altered pain perception and/or analgesic responses will help elucidate novel targets for the development of individualized treatment strategies.

Functional GPCR Alternative Splice Variants

Examples of alternative splice variants of pain-relevant GPCRs that exhibit diversity in expression and signaling profiles include the aforementioned MOR-1, cannabinoid receptors, adrenergic receptors, and serotonin receptors. Of additional interest are

nociceptin, prostaglandin and neurokinin receptors, which are not targeted by common analgesics but are critical for the induction and modulation of pain. Accumulating evidence from *in vitro*, pre-clinical, and clinical studies suggests that alternative splicing of these and other GPCR transcripts adds additional layers of complexity to GPCR signaling and pharmacodynamics responses. (Table 3).

Opioid receptors

The pharmacologic manipulation of the mu opioid receptor is an essential component of clinical pain treatment. Although the signaling characteristics of MOR-1 are well established, we are just beginning to understand the complex nature of genetic variants that contribute to alternative splicing. At least 20 MOR-1 splice variants have been identified in mouse and human genomes²⁵, suggesting an array of potentially functional consequences that may occur with opioid administration.

Pre-clinical studies within the past 15 years have begun to reveal the functional properties of specific MOR-1 splice variants. Pasternak and coworkers provide evidence that the gene expression of *MOR-1* splice variants represent compensatory responses to chronic opioid administration that stabilize or diminish the development of tolerance⁹⁰ Other studies have shown that the presentation of some unwanted side effects are due to the activation of MOR-1 splice variants. For example, Liu and colleagues have demonstrated that because of its distinct C-terminus, the splice variant MOR-1D dimerizes with the gastrin-releasing peptide receptor in the mouse spinal cord to produce opioid-induced itch³³ Another splice variant known as MOR-1K, a truncated receptor lacking the N-terminus and first transmembrane, has been implicated in the paradoxical increase in pain sensitivity known as opioid-induced hyperalgesia (OIH). In contrast to MOR-1 which typically couples to $G\alpha_i$, MOR-1K couples to $G\alpha_s$ to activate adenylyl cyclase (AC) and increase intracellular calcium, thus engaging pro-nociceptive signaling events that likely drive OIH²⁹. A subsequent preclinical study in mice revealed that genetic knockdown of *MOR-1K* hindered the development of OIH and unmasked opioid analgesia⁹¹.

Additional studies investigating the functional characteristics of MOR-1 splice variants provide evidence that a set of these receptors promote opioid analgesia by providing exclusive binding sites for different opioids. Transgenic mice lacking exon 11, an exon that provides an alternative promoter region for the MOR transcript, demonstrated substantial reductions in the analgesic efficacies of heroin, fentanyl, and the morphine metabolite morphine-6 β -glucuronide²⁴, suggesting that exon-11 containing variants play a critical role in opioid analgesia. Exon 11-containing splice variants also mediate the analgesic effects of iodobenzoylnaltrexamide (IBNtxA), a novel synthetic opioid that produces ten times the analgesic efficacy of morphine without producing respiratory distress, dependence, tolerance, or GI distress in rodents^{36,40,92}. MOR-1 splice variants also promote analgesia by enhancing canonical receptor function. Single-transmembrane splice variants MOR-1R and MOR-1S structurally enhance MOR-1 function by stabilizing the canonical 7TM receptor at the cellular membrane⁴². Collectively, these studies highlight the importance of MOR-1 alternative splice variants in mediating opioid analgesia, as well as side effects such as tolerance, itch, and OIH.

Although few preclinical studies have examined the nociceptin receptor (ORL-1), it may also play an influential role in opioid analgesia. Majumdar and colleagues demonstrate that the exon 11 splice variant MOR-1G dimerizes with ORL-1 to provide a binding site for novel opioid IBNtxA⁹³, suggesting that ORL-1 interacts with MOR-1 splice variants to provide specific opioid binding sites. The contribution of ORL-1 to splice variant signaling is further complicated by the existence of its own splice variants, ORL-1_{Long} and ORL-1_{Short}⁹⁴. Thus far, ORL-1_{Short} has been implicated in the regulation of the canonical receptor, indicating a possible influence over ORL-1 function.

Cannabinoid receptors

Both the CB₁ and CB₂ receptors undergo alternative splicing to yield variants differing at their N-terminal region. The CB_{1a} variant is truncated by 61 amino acids, with the first 28 amino acids completely different from the canonical CB₁⁴⁹. While its tissue distribution largely overlaps with that of CB₁, CB_{1a} exhibits decreased agonist binding and activity, which might be due to a lack of two glycosylation sites typically important for signal transduction⁹⁵. The CB_{1b} variant lacks the first 33 N-terminus amino acids and although it overlaps with CB₁ in a number of tissues, its abundant expression in fetal brain suggests it may play an important role in development⁴⁸. Similar to CB_{1a}, CB_{1b} exhibits decreased agonist binding and activity.

The CB₂ variants are generated through the use of alternate promoters located upstream of the major coding exon 3⁵³. The gene *CB_{2A}* is initiated from the more distal promoter and includes exons 1a and 1b spliced to exon 3, while *CB_{2B}* is initiated from the more proximal promoter and includes exon 2 spliced to exon 3. The CB_{2A} variant is predominantly expressed in testes and at lower levels in spleen and brain. In contrast, the CB_{2B} variant is predominantly expressed in spleen with very low expression in brain and no expression in testes. These tissue-specific distribution patterns may indicate specialized roles for the different splice variants with respect to pain modulation, immune response, and spermatogenesis.

Adrenergic receptors

Adrenergic receptors play a key role in pain processing as well as cognition and cardiovascular function. While α_2 ARs, β_1 ARs, and β_2 ARs are highly relevant to the modulation of pain by endogenous and exogenous agonists, the genes encoding these receptors are intronless and not subject to alternative splicing. Among the remaining adrenergic receptors, the α_{1A} AR subtype has been most extensively studied with respect to alternative splicing.

The human *α_{1A} AR* gene locus is comprised of over 8 exons and codes for 15 known splice variants⁹⁶. The canonical receptor is generated through splicing exon 1 (coding for the N-terminus and transmembranes [TM] 1 to 6) together with exon 2 (coding for TM7 and the C-terminus). Four C-terminus splice variants (α_{1A-2} , α_{1A-3} , α_{1A-4} , α_{1A-5}) have been identified that are generated through the use of additional acceptor sites at varying locations within, and distal to, exon 2. The α_{1A-2} , α_{1A-3} , and α_{1A-4} variants exhibit ligand binding properties and tissue distribution profiles similar to α_{1A} AR, although α_{1A-3} and α_{1A-4} are absent in

kidney⁵⁴⁻⁵⁷. In contrast to $\alpha_{1A}AR$ that couples to $G\alpha_q$, these variants couple to $G\alpha_i$ so as to inhibit AC activity⁷. This diversity in $\alpha_{1A}AR$ signaling may contribute to differential responses to α_1AR antagonists used in the treatment of pain.

In addition, eleven 6TM variants (α_{1A-6} , α_{1A-7} , α_{1A-8} ... α_{1A-16}) have been identified that are generated through exon skipping. These variants lack TM7 and their C-terminal tails are located extracellularly⁵⁶. The truncated 6TM variants are expressed in similar tissues as $\alpha_{1A}AR$, but are localized exclusively within the cell and unable to bind α_1AR agonists or directly mediate signal transduction. The 6TM variants do, however, impair $\alpha_{1A}AR$ ligand binding and trafficking to the cell surface. Thus, $\alpha_{1A}AR$ 6TM variants likely play a significant physiological role by modifying the function and expression of their parent 7TM receptors.

One $\alpha_{1B}AR$ splice variant has also been identified in human brain⁵⁸. The $\alpha_{1B}AR$ protein is generated through splicing of exons 1 and 2. In contrast to the canonical receptor, the $\alpha_{1B-2}AR$ includes an immediately adjacent sequence following exon 1 in its coding sequence and excludes exon 2 that codes for TM7. Tseng-Crank and colleagues also identified low levels of a truncated $\alpha_{1D}AR$ transcript, however the result was inconclusive and naturally occurring $\alpha_{1D}AR$ variants were not observed⁵⁸. More work is required to determine the potential functional role of $\alpha_{1B}AR$ and $\alpha_{1D}AR$ variants.

The β_3AR is primarily known for its ability to regulate energy metabolism and thermogenesis⁵⁸, though evidence for its ability to promote functional and neuropathic pain is emerging^{61,63,97}. The gene encoding β_3AR undergoes alternative splicing within the coding region to yield two C-terminal splice variants differing with respect to tissue expression, g-protein signaling profiles, and regulatory properties^{57,64,98}. The $\beta_{3A}AR$ and $\beta_{3B}AR$ splice variants contain completely unique terminal chains that are 13 and 17 amino acids long, respectively. The $\beta_{3A}AR$ is primarily enriched in fat tissue and couples exclusively to $G\alpha_s$, while the $\beta_{3B}AR$ is primarily enriched in brain and couples to both $G\alpha_s$ and $G\alpha_i$. In addition, the $\beta_{3A}AR$ exhibits increased agonist-induced extracellular acidification, a measure of cAMP-independent cellular activity. Their unique tissue distribution and signaling profiles, together with the known functional role of β_3ARs , could indicate that $\beta_{3A}ARs$ play a greater role in lipolysis/thermogenesis and that $\beta_{3B}AR$ in brain mediate pain. While these studies were conducted in mouse, it is important to note that the human β_3AR contains a significant number of genetic variants that are predicted to regulate alternative splicing^{65,66}.

Serotonin receptors

Serotonin receptors play a key role in pain processing as well as mood and GI function⁸. Of the 5-HT₁ (A, B, D-F), 5-HT₂ (A-C), 5-HT₄, 5-HT₅, 5-HT₆, and 5-HT₇ GPCR family members, the 5-HT_{2A}, 5-HT_{2C}, 5-HT₄, 5-HT₆, and 5-HT₇ receptors are known to undergo alternative splicing.

The human 5-HT₂ receptor subtypes (5-HT_{2A}, 5-HT_{2B}, and 5-HT_{2C}) couple to $G\alpha_q$ proteins to promote the transient release of intracellular calcium. One truncated splice variant of 5-HT_{2A} (5-HT_{2A-tr}) has been identified that utilizes alternate splice donor and acceptor sites to

yield a 3TM receptor with 57 unique amino acids in the C-terminal region⁶⁴ The 5-HT_{2A-tr} is co-expressed with 5-HT_{2A} in most brain tissues, however is unable to couple to the calcium pathway. Two truncated splice variants of 5-HT_{2C} (5-HT_{2CT} and 5-HT_{2C-R-COOH}) have also been identified. Similar to 5-HT_{2A-tr}, the 5-HT_{2CT} variant utilizes alternate splice donor and acceptor sites to yield a 3TM receptor with 19 unique amino acids in the C-terminal region⁶⁵ The 5-HT_{2C-R-COOH} variant retains an extra 90 nucleotides from intron 5 in the TM4 splice site, resulting in a 3TM receptor with a short C-terminus⁶⁶. Compared to the canonical 5-HT_{2C} receptor, the truncated variants exhibit similar expression patterns but have impaired 5-HT ligand binding and G-protein coupling^{65,66}. While the relative importance of these truncated 5-HT₂ splice variants in humans remains unknown, they are conserved in rat and mouse⁶⁶ where their expression levels increase following nerve injury⁹⁹.

The 5-HT₄ receptor couples preferentially to G_{αs} and, while widely expressed, the highest levels are found in intestine⁷⁴. Agonists targeting 5-HT₄ are beneficial in alleviating abdominal pain associated with irritable bowel syndrome. Of all the 5-HT receptors, 5-HT₄ possesses the greatest diversity in alternative splicing. At least ten splice variants have been identified that vary with respect to their tissue distribution and function. Nine C-terminus variants (5-HT_{4a}, 5-HT_{4b}, 5-HT_{4c}, 5-HT_{4d}, 5-HT_{4e}, 5-HT_{4f}, 5-HT_{4g}, 5-HT_{4i}, 5-HT_{4n}) have been identified that are identical up to amino acid Leu358, after which they vary in sequence and length⁷⁵. Additionally, one variant (5-HT_{4h}) has been identified that includes exon h coding for 14 additional amino acids in the second extracellular loop⁷⁰ The 5-HT_{4a}, 5-HT_{4b}, 5-HT_{4c}, and 5-HT_{4e} variants are expressed in most tissues, with distribution patterns similar to the canonical form^{74,75}. In contrast, the 5-HT_{4f} variant is found in the brain and GI tract, but absent in the heart and other tissues²² Meanwhile, the 5-HT_{4d} and 5-HT_{4h} variants are expressed exclusively in the GI tract^{70,72,75}. While all of the 5-HT₄ splice variants display typical ligand binding properties, some show notable functional differences. Both of the GI-specific 5-HT_{4d} and 5-HT_{4h} variants have a tendency to recognize 5-HT antagonists as partial agonists^{70,78} Furthermore, the 5-HT_{4d} variant exhibits a remarkable 20-fold increase in cAMP formation following application of the 5-HT₄ agonist renzapride⁷⁸ The 5-HT_{4b} variant is unique in its able to couple to G_{αi} as well as G_{αs} proteins, suggesting its diverse signaling capabilities in the GI tract, brain, and other tissues⁶⁸ In the absence of ligand binding, the majority of C-terminus variants exhibits heightened constitutive AC activity^{67,69,73,76-78}. The ability of GPCRs to increase basal AC activity has been previously reported and can result in physiological functions of the receptor that are largely independent of endogenous ligands or exogenous drugs¹⁰⁰. Collectively, these studies illustrate the high degree of tissue and signaling specificity for a number of 5-HT₄ splice variants that may be represent attractive targets for the development of new more selective drugs for the treatment of irritable bowel syndrome among other conditions.

The 5-HT₆ receptor is unique in that it is expressed almost exclusively in the central nervous system⁸. A 3TM splice variant of 5-HT₆ (5-HT_{6-tr}) has been identified in brain that is generated through different splice donor and acceptor sites⁸⁰. The corresponding receptor includes the TM1-3 and 10 unique amino acids in its C-terminus. In contrast to 5-HT₆, the expression of 5-HT_{6-tr} is limited to substantia nigra and caudate. The 5-HT_{6-tr} receptor is able to translocate to the membrane, yet unable to bind serotonin. This splice variant may

have a yet-to-be-determined function or be indicative of abnormalities due to pathologic state.

The 5-HT₇ receptor is expressed on primary afferent nociceptors, as well as in pain-relevant brain regions where it couples to G_{αs} to mediate the transmission and modulation of pain. Three splice variants of 5-HT₇ (5-HT_{7a}, 5-HT_{7b}, 5-HT_{7d}) have been identified that are all generated through alternative splicing of the second intron located near the C-terminal coding region. The 5-HT_{7a} and 5-HT_{7b} variants have tissue expression profiles and functional characteristics similar to the canonical receptor, though 5-HT_{7b} has been shown to exhibit significantly higher constitutive AC activity when expressed in stable cell lines¹⁰¹. The 5-HT_{7d} variant is predominantly expressed in smooth muscle tissues such as the heart and GI tract⁸² and displays unique functional characteristics. Compared to the canonical 5-HT₇ receptor and the 5-HT_{7a} and 5-HT_{7b} variants, the 5-HT_{7d} variant displays agonist-independent internalization (even in the presence of antagonist) and associated reductions in agonist-induced AC activity⁸⁵. It has been suggested that differences in the functional characteristics of 5-HT₇ variants is due to specific features of their carboxyl tails, leading to differential interactions with protein partners that mediate their activity, trafficking, and/or internalization^{85,102}

Prostaglandin E Receptor 3

Prostaglandins, such as prostaglandin E₂, are a product of cyclooxygenase (COX) that facilitate pain transmission through binding to the prostaglandin E receptor 3 (EP₃ receptor). Activation of the G_{αi}-coupled EP₃ receptor has been shown to produce analgesia¹⁰³, but also to promote HIV-induced inflammation¹⁰⁴ and sensitization of trigeminal nociceptors¹⁰⁵. These contradictory effects may be due to the presence of EP₃ splice variants. Six C-terminus splice variants (EP_{3A...F}) have been identified, to date. Of these, the EP_{3C} receptor exhibits the most unique signaling characteristics as it is able to couple to G_{αs} as well as G_{αi}⁸⁶. The dual coupling of the EP_{3C} variant to different g-proteins may explain the ability of EP₃ ligands to produce both analgesia and hyperalgesia.

Neurokinin-1 Receptor

Neurokinin-1 receptors (NK-1Rs) are targets for the endogenous pro-pain ligand substance P. Their activation results in G_{αq}-mediated increases in intracellular calcium levels and production of pro-inflammatory cytokines⁸⁹. Alternative splicing of the NK-1R yields a truncated variant (NK-1R_{truncated}) that lacks the C-terminus and has functional properties that differ from the canonical receptor. Unlike NK-1R, activation of the NK-1R_{truncated} variant does not result in increased levels of calcium or nuclear activity of factor-κB (NF-κB). Instead, activation of NK-1R_{truncated} results in decreased phosphorylation of protein kinase C (PKC) and levels of interleukin-8. A recent clinical study has demonstrated the utility of an NK-1R antagonist in the treatment of chronic pain conditions and anxiety¹⁰⁶. Results from functional studies of the NK-1R_{truncated} variant suggest that splice variant-specific agonists may also be useful for pain management.

Clinical Relevance of Functional Gene Regulatory Events

Given the extensive list of alternative GPCR splice variants and their known impact on signaling and pharmacodynamics, it is expected that these variants have important clinical implications for pain management. Major strides in both preclinical and clinical research are still needed before we can reliably predict a patient's treatment response based on their splice variant expression profile. Such strides have been made, however, in the study of another type of gene variation, single nucleotide polymorphisms (SNPs). Like alternative splicing, SNPs within key pain-related genes can result in changes that subsequently affect the encoded protein. For example, SNPs in the gene encoding catechol-o-methyltransferase (COMT; an enzyme that metabolizes catecholamines) are indicative of abnormalities in COMT function and predictive of chronic pain risk and treatment response. Human genetic association studies have shown that the rs4680 SNP, alone or in combination with other nearby SNPs, is predictive of temporomandibular disorder (TMD) and fibromyalgia onset^{107,108}. Subsequent molecular studies demonstrated that these SNPs alter the thermostability and/or structure of the *COMT* transcript¹⁰⁹, explaining why patients with functional pain disorders^{110–112} and exacerbated postoperative pain^{113–116} exhibit decreased levels of COMT alongside increased levels of catecholamines. Preclinical studies further revealed that elevated levels of epinephrine/norepinephrine resulting from low COMT activity, lead to increased pain through activation of β ARs^{117,118}. Coming full circle, results from a randomized controlled trial demonstrated that the β AR antagonist propranolol provides significant pain relief for pain patients who carry the SNPs associated with decreased levels of COMT¹¹⁹. Together, these findings highlight the impact of gene regulation on pain as well as the utility of genetic and protein biomarkers in identifying a subgroup of patients who will benefit from specific therapies.

In a similar fashion, we believe that measurement of alternative GPCR splice variants can be used as a diagnostic tool to provide personalized pain treatment. This is already being done in cancer. *In vitro* studies examining the role of NK-1R alternative splicing in breast cancer cells demonstrated that overexpression of the NK-1R_{truncated} variant promotes tumorigenesis^{120,121}. A complementary clinical study further demonstrated that individuals with overexpression of the *NK-1R_{truncated}* variant were at increased risk for colitis-associated carcinoma, while expression levels of the canonical *NK-1R* remained consistent between cases and controls¹²².

Just as the study of alternative splicing is beginning to inform diagnosis and management of patients with cancer, the study of alternative splicing in pain-relevant GPCRs has great potential to advance the current state of clinical care for patients with chronic pain. Additionally, this line of inquiry may lead to the advent of new pain therapies such as IBNtxA, a novel opioid analgesic specifically targeting 6TM mu opioid splice variants¹²³.

Conclusion

G-protein coupled receptors play a major role in modulating the activity of a chorus of cells involved in the transmission, modulation and perception of pain. For this reason, GPCRs are the primary target of many pharmacologic interventions used in the management of acute

and chronic pain. Nonetheless, the use of these medications is limited due to variability in analgesic efficacy and side effect profiles. These limitations are partly attributed to genetic differences that influence alternative splicing of pain-relevant GPCRs. The functional importance and implications of the diversity of GPCRs in contributing to the pathophysiology of clinical pain is just beginning to emerge. More research, especially in the clinical arena, is necessary to further investigate the functions of specific GPCR splice variants, as well as the dynamic interactions between multiple variants of the same canonical receptor, within the context of pain. This line of inquiry will evolve our understanding of pain mechanisms and inform the design of new and clinically useful drugs that target specific alternative splice variants altered in a subset of patients.

Abbreviations

2-AG	2-Arachidonoylglycerol
5-HT	5-Hydroxytryptamine
AC	Adenylyl Cyclase
cAMP	Cyclic Adenosine Monophosphate
CB	Cannabinoid
COMT	Catechol-O-Methyltransferase
Epi	Epinephrine
GPCR	G-protein Coupled Receptor
GI	Gastrointestinal
IBNtxA = IBS	Irritable Bowel Syndrome
mRNA	messenger ribonucleic acid
MOR-1	Mu Opioid Receptor
NE	Norepinephrine
NK-1R	Neurokinin-1 Receptor
OIH	Opioid-induced Hyperalgesia
ORL-1	Nociceptin receptor
PKC	Protein Kinase C
SNP	Single Nucleotide Polymorphism
TM	Transmembrane
αAR	Alpha adrenergic receptor
βAR	Beta adrenergic receptor

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Questions

1. Which of the following medications is NOT a mu opioid receptor agonist?
 - a. Morphine
 - b. Fentanyl
 - c. Hydrocodone
 - d. **Naloxone**
 - e. Methadone

2. Which 5-HT receptor is exclusively targeted by triptans?
 - a. **5-HT1**
 - b. 5-HT2
 - c. 5-HT4
 - d. 5-HT6
 - e. 5-HT7

3. What is the most common form of alternative splicing in humans?
 - a. Intron Retention
 - b. **Exon Skipping**
 - c. Alternative 3' Splice Site
 - d. Alternative 5' Splice Site
 - e. Exon Retention

4. Which MOR-1 splice variant contributes to opioid-induced itch?
 - a. MOR-1A
 - b. **MOR-1D**
 - c. MOR-1G
 - d. MOR-1K

- e. MOR-1S
5. The α_{1A-2} , α_{1A-3} , and α_{1A-4} variants exhibit the same binding capabilities as the α_{1A} receptor. Unlike the canonical receptor, these splice variants couple to $G_{\alpha i}$ instead of $G_{\alpha s}$. This change in g-protein coupling is due to alternative splicing of what receptor region?
- a. N-terminus
 - b. Extracellular loop 1
 - c. **C-terminus**
 - d. 1st transmembrane
 - e. Intracellular loop 1

Learning Objectives: On completion of this article, you should be able to (1) explain the importance of GPCRs to pain signaling and modulation; (2) explain the basic concepts of alternative splicing; and (3) describe how individual variability in alternative splicing of GPCRs may contribute to variability in the nature of pain as well as responses to analgesic drugs.

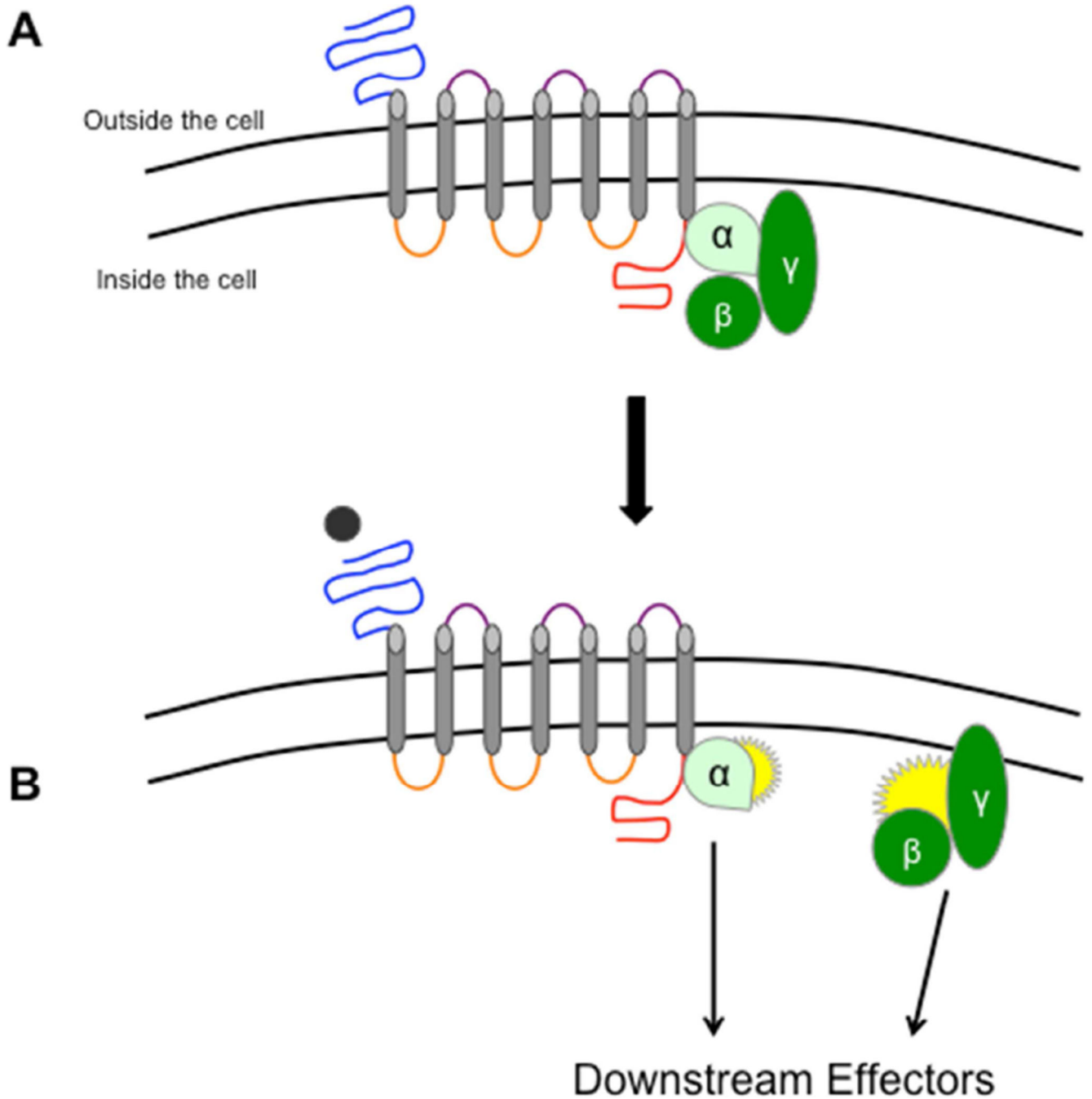


Figure 1. GPCR structure and function. A) A g-protein coupled receptor (GPCR) is composed of seven transmembranes (grey) interconnected by three intracellular (orange) and three extracellular (purple) loops. On the end of the first and last transmembrane are the N-terminus (blue) and C-terminus (red), respectively. As its name suggests, a GPCR is bound to a tri-meric g-protein composed of alpha (α) and beta/gamma (β/γ) subunits. B) When a ligand (black) binds to a GPCR, the associated g-protein separates into the α and β/γ subunits. These subunits then stimulate a variety of downstream effectors that produce

changes in cellular activity (see Table 1). Abbreviations: GPCR = G-Protein Coupled Receptor

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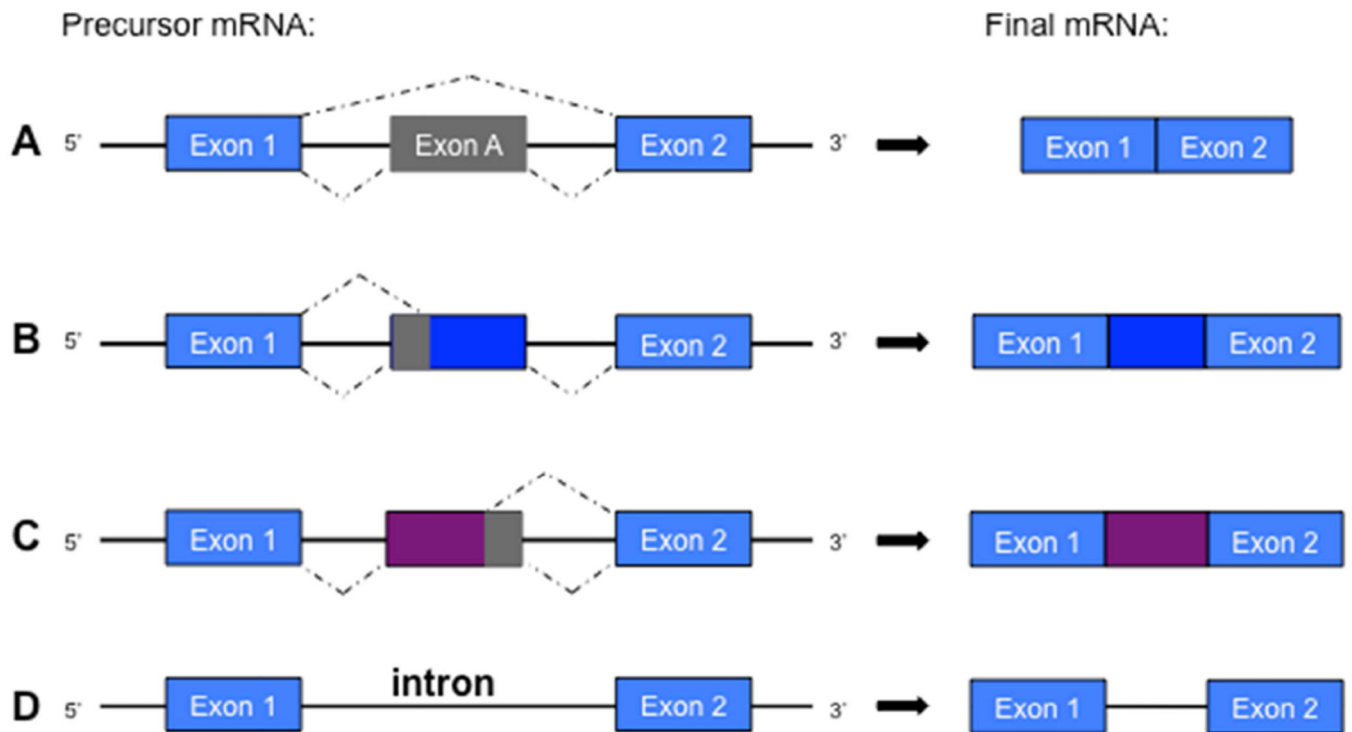


Figure 2.

Different types of alternative splicing. The most common type of alternative splicing in animals is A) exon skipping, in which a constitutive exon is spliced from the final mRNA transcript. Alternative B) 3' and C) 5' splice sites provide additional junctions within an exon, resulting in partial splicing of the exonic mRNA sequence. D) Intron retention is a rare type of alternative splicing that occurs when an intron remains within the final mRNA transcript. Abbreviations: mRNA = Messenger Ribonucleic Acid

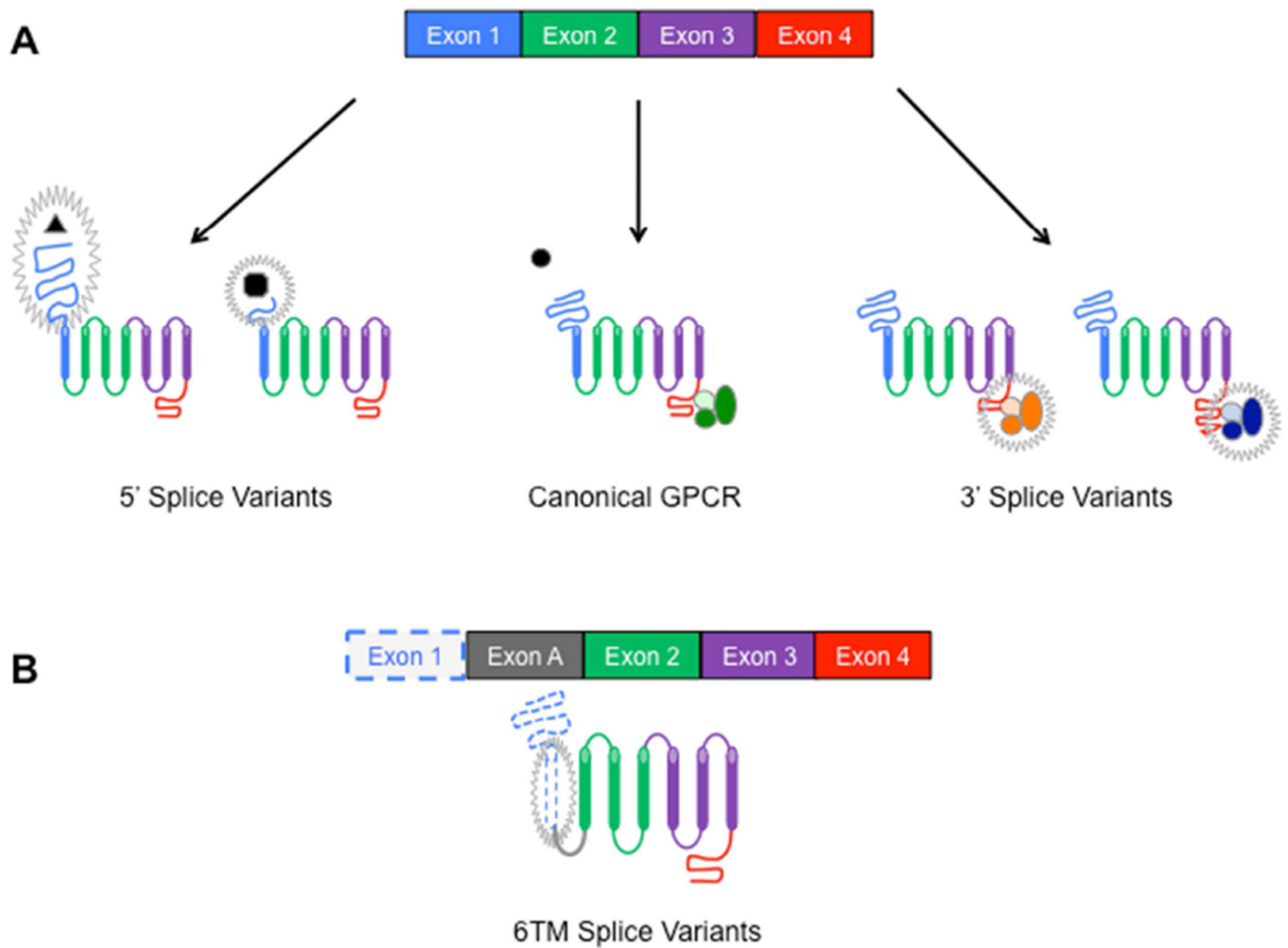


Figure 3. Structural variations in GPCRs as a result of alternative splicing. Exons within the mRNA transcript serve as coding regions for specific sections of protein. Alternative splicing events that change or remove exonic sequences can produce GPCR splice variants with corresponding changes in protein composition and/or structure. A) For example, splicing events that lead to alterations in exon 1 can yield GPCRs with truncated N-termini that affect ligand binding, while events that lead to alterations in exon 4 can yield GPCRs with truncated C-termini that affect g-protein coupling and signaling. B) Splicing events can also lead to skipping of an exon that codes for an unit of the GPCR, such as a transmembrane, thus yielding a truncated GPCR lacking the encoded section, such as a 6 transmembrane (6TM) splice variant. Abbreviations: GPCR = G-Protein Coupled Receptor; TM = Transmembrane

Table 1

Common G-proteins and Their Intracellular Effects.

G protein	Effectors	Overall Impact
G α_s	activates adenylyl cyclase \rightarrow \uparrow cAMP ^a	cellular excitation (pro-nociceptive)
G α_q	activates PLC β \rightarrow \uparrow intracellular Ca ⁺⁺ levels	cellular excitation (pro-nociceptive)
G $\alpha_{i/o}$	inhibits adenylyl cyclase \rightarrow \downarrow cAMP	cellular inhibition (anti-nociceptive)

^a Abbreviations: cAMP = cyclic adenosine monophosphate; Ca = calcium; PLC β = phospholipase C β .

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Table 2

GPCRs Commonly Targeted for Clinical Pain Management.

GPCR	G-protein	Endogenous Ligands	Prescribed Analgesics			Known Splice Variant
			Reuptake Inhibitors	Agonist	Antagonist	
Mu-Opioid Receptor						
MOR-1^a	Gα ₁ ⁴	α-endorphin β-endorphin γ-endorphin		Alfentanil Buprenorphine Codeine Fentanyl Hydrocodone Hydromorphone Levorphanol Meperidine Methadone Morphine Oxycodone Oxymorphone Remifentanyl Sufentanil Tapentadol Tramadol	Naloxone Naltrexone	Yes
Cannabinoid (CB) Receptors						
CB1	Gα ₁ ⁵	2-AG Anandamide LPI NADA OAE		Nabilone THC	Cannabidiol	Yes
CB2	Gα ₁ ⁵			Nabilone THC	Cannabidiol	Yes
Adrenergic (AR) Receptors						
α ₁ AR	Gα _q ⁶	Epinephrine Norepinephrine	Amiripityline (NET) Despiramine (NET) Desvenlafaxine (NET) Duloxetine (NET) Levorphanol (MAO) Meperidine (NET) Nortriptyline (NET) Tapentadol (NET) Venlafaxine (NET)		Amiripityline Promethazine Nortriptyline Trazodone	Yes
α ₂ AR	Gα ₁ ⁶			Clonidine	Trazodone	No
β ₁ AR	Gα _s ⁷				Atenolol Nadolol Metoprolol Propranolol Timolol	No

GPCR	G-protein	Endogenous Ligands	Prescribed Analgesics			Known Splice Variant
			Reuptake Inhibitors	Agonist	Antagonist	
β_2 AR	G_{α_s} , G_{α_i} , G_{α_7}				Nadolol Propranolol Timolol	No
β_3 AR	G_{α_s} , G_{α_7}				Nadolol Propranolol Timolol	Yes
Serotonin (5-HT) Receptors						
5-HT ₁	G_{α_i} , G_{α_8}	Serotonin	Amitriptyline (SERT) Desipramine (SERT) Desvenlafaxine (SERT) Duloxetine (SERT) Levorphanol	Almotriptan Dihydroergotamine Eletriptan Frovatriptan Naratriptan Rizatriptan Sumatriptan Zolmitriptan	Trazodone	No
5-HT ₂	G_{α_c} , G_{α_4}		(MAO) Nortriptyline (SERT) Trazodone (SERT) Venlafaxine (SERT)	Dihydroergotamine Methylergometrine Mosapride	Amitriptyline Nortriptyline Promethazine Trazodone	Yes
5-HT ₄	G_{α_s} , G_{α_8}				Amitriptyline Nortriptyline Trazodone	Yes
5-HT ₆	G_{α_s} , G_{α_8}				Amitriptyline Nortriptyline Trazodone	Yes
5-HT ₇	G_{α_s} , G_{α_8}				Amitriptyline Trazodone	Yes

Abbreviations: 2-AG = 2-Arachidonoylglycerol; 5-HT = Serotonin; CB = Cannabinoid; LPI = Lysophosphatidylinositol; MAO = Monooxygenase; MOR-1 = Mu Opioid Receptor; NADA = N-Arachidonoyl Dopamine; NET = Norepinephrine Transporter; OAE = Viridhamine (OAE); SERT = Serotonin Transporter; THC = Tetrahydrocannabinol; α AR = Alpha adrenergic receptor; β AR = Beta adrenergic receptor

Table 3

Signaling, Tissue Distribution, and Function of Known GPCR Splice Variants.

Receptor Variants	G-protein	Tissue Distribution	Functional Characteristics
Opioid Receptors			
MOR-1	Gα _i ⁴	brain, spinal cord > adrenal gland > small intestine ³⁴	
C-term variants			OP binding → analgesia ³⁸
MOR-1A		brain ³⁵	OP binding → analgesia ³⁸
MOR-1B		brain ³⁵	OP binding → analgesia ³⁸
MOR-1C		brain ³⁵ ; agonist-induced reduction ³⁶	OP induced itch ³³
MOR-1D	Gα _i ³³	brain ³⁵	OP binding → analgesia ³⁸
MOR-1E		brain ³⁵	OP binding → analgesia ³⁸
MOR-1F		brain ³⁵	?
MOR-1O		brain ³⁵	?
MOR-1P		brain ³⁵	?
MOR-1U		brain ³⁵	?
MOR-1V		brain ³⁵	?
MOR-1W		brain ³⁵	?
MOR-1X		brain ³⁵	OP binding → analgesia ³⁹
MOR-1Y		brain ³⁵	
N-term variants		brain ³⁵	Novel opioid binding ⁴⁰ OP binding → analgesia ⁴¹
MOR-1G		brain ³⁵	OP binding → analgesia ⁴¹
MOR-1H		brain ³⁵	OP binding → analgesia ⁴¹
MOR-1I		brain ³⁵	contributes to OIH
MOR-1J	Gα _s ²⁹	brain ³⁵	OP binding → analgesia ⁴¹
MOR-1K		brain ³⁵	?
MOR-1L		brain ³⁵	?
MOR-1M		brain ³⁵	
MOR-1N			?
Single TM variants		brain ³⁵	Stabilization of MOR-1 ⁴² Stabilization of MOR-1 ⁴²
MOR-1Q		brain ³⁵	?
MOR-1R		brain ³⁵	?
MOR-1S		brain ³⁵	?
MOR-1T		brain (human neuroblastoma cell line) ³⁷	?
MOR-1Z		brain (human neuroblastoma cell line) ³⁷	
MOR-1SV1			
MOR-1SV2			

Receptor Variants	G-protein	Tissue Distribution	Functional Characteristics
ORL-1	Gα _i ⁴³	brain, immune cells, GI tract ⁴⁴	↓ agonist binding ⁴⁶ ?
ORL-1 _{Short}		brain > testis > heart, kidneys, muscle,	
ORL-1 _{Long}		spleen, thymus ⁴⁵ brain > testis > muscle, spleen ⁴⁵	
Cannabinoid Receptors			
CB1	Gα _i ⁵	brain, sc, DRG > pituitary > heart, lung, uterus, testis, spleen, tonsils ⁴⁷	↓ agonist binding, ↓GTPγS activity ⁴⁸ ↓ agonist binding, ↓GTPγS activity ⁴⁸
N-term variants			
CB1a		similar distribution to CB1+ kidney ^{48,49}	
CB1b		fetal brain > GI tract, uterus, muscle > adult brain ⁴⁸	
CB2	Gα _i ⁵	immune cells/tissues > glia and macrophages in brain/sc ^{47,50-52}	? ?
N-term variants			
CB2A		testis > spleen, leukocytes > brain ⁵³	
CB2B		spleen > leukocytes ⁵³	
Adrenergic Receptors			
α_{1A}	Gα _q ⁶	liver, heart, brain > prostate, kidney, bladder ⁶	pharmacology similar to α _{1A} ^{7,54,55,57} impair α _{1A} binding & cell surface expression ⁵⁶
C-term variants	Gα _i ⁷	liver, heart > prostate, kidney ^{54,55}	
α _{1A-2}	Gα _i ⁷	liver > heart, prostate (absent in kidney) ^{54,55}	
α _{1A-3}	Gα _i ⁷	liver, heart > prostate, (absent in kidney) ^{54,55}	
α _{1A-4}			
α _{1A-5}			
6TM variants (-TM7)		liver, heart, hippocampus, and prostate; expressed intracellularly ⁵⁶	
α _{1A-6}			
α _{1A-7}			
α _{1A-8}			
α _{1A-9}			
α _{1A-10}			
α _{1A-11}			
α _{1A-12}			
α _{1A-13}			
α _{1A-14}			
α _{1A-15}			
α _{1A-16}			

Receptor Variants	G-protein	Tissue Distribution	Functional Characteristics
α_{1B} 6TM variant (-TM7) α_{1B-2}	$G\alpha_q$ ⁶	liver, heart, brain (including cortex) ⁶ expressed in hippocampus, but absent in cortex ⁵⁸	?
β_3 C-term variants β_{3a} (mouse) β_{3b} (mouse)	$G\alpha_s$, $G\alpha_i$ ^{59,60} $G\alpha_s$ ^{7,61} $G\alpha_s, G\alpha_i$ ^{7,61}	fat, immune cells/tissues > GI tract, DRG ^{59,62} fat > ileum > brain ⁶³ brain > fat, ileum ⁶³	? ? ?
Serotonin Receptors			
5-HT_{2A} 6TM variant (-TM4) 5-HT _{2A-tr}	$G\alpha_q$ ⁸	cortex, hippocampus, brainstem, olfactory > basal ganglia, limbic ⁸ hippocampus, caudate, corpus collosum, amygdala, substantia nigra ⁶⁴	impaired 5-HT-induced Ca ⁺⁺ signaling ⁶⁴
5-HT_{2C} 6TM variant (-TM4) 5-HT _{2CT} C-term variant 5-HT _{2AC-R-COOH}	$G\alpha_q$ ⁸	choroid plexus, striatum, hippocampus, hypothalamus, olfactory, sc ^{8,65} choroid plexus, striatum, hippocampus, hypothalamus, olfactory, sc ⁶⁵ sc, cortex, cerebellum, medulla, caudate, amygdala, corpus collosum ⁶⁶	impaired 5-HT ligand binding ⁶⁵ impaired 5-HT ligand binding ⁶⁶
5-HT₄ C-term variants 5-HT _{4a} 5-HT _{4b} 5-HT _{4c} 5-HT _{4d} 5-HT _{4e} 5-HT _{4f} 5-HT _{4g} 5-HT _{4i} 5-HT _{4n} 2 nd EL loop variant	$G\alpha_s$ ⁸ $G\alpha_s$ ⁶⁷ $G\alpha_s$, $G\alpha_i$ ^{67,68} $G\alpha_s$ ⁶⁷ $G\alpha_s$ ⁶⁷ $G\alpha_s$ ⁶⁹ $G\alpha_s$ ⁷⁰ $G\alpha_s$ ⁷¹ $G\alpha_s$ ⁷² $G\alpha_s$ ⁷³ $G\alpha_s$ ⁷⁰	intestine > brain > pit > uterus, testis > spleen > heart, kidney, lung, sc ⁷⁴ intestine, brain > pit > uterus, testis > heart > spleen, lung, sc ⁷⁴ intestine, brain > pit > uterus > heart, spleen, lung, sc ⁷⁴ intestine > pit > brain > uterus, testis, heart, spleen, sc ⁷⁴ ileum, colon, but absent in brain ^{73,75} brain > testis > sc > intestine, pit, heart, prostate ileum, colo ⁷⁵ brain, ileum, colon ⁷⁵ brain, heart, ileum, colon ⁷⁵ brain, ileum, colon, heart ⁷⁵	 \uparrow constitutive AC activity, \uparrow isomerization, \downarrow agonist internalization ^{76,77} \uparrow constitutive AC activity ⁶⁷ \uparrow constitutive AC activity ⁶⁷ 20-fold \uparrow in agonist-induced cAMP activity ⁷⁸ \uparrow constitutive AC activity ⁶⁹ ? ? \uparrow constitutive AC activity ⁷⁹ antagonist GR113808 acts as partial

Receptor Variants	G-protein	Tissue Distribution	Functional Characteristics
5-HT _{4h}		brain, heart, oesophagus ⁷⁵ GI tract ⁷⁰	agonist ⁷⁰
5-HT₆ 6TM variant (-TM4) 5-HT _{6-tr}	Gα _s ⁸	cortex, hippocampus, olfactory, striatum, amygdala, acumbens ⁸ cortex, hippocampus, cerebellum, thalamus, substantia nigra, caudate ⁸⁰	impaired binding to 5-HT and LSD ⁸⁰
5-HT₇ C-term variants 5-HT _{7a} 5-HT _{7b} 5-HT _{7d}	Gα _s ⁸ Gα _s ⁸¹ Gα _s ⁸² Gα _s ⁸²	brain, heart, GI tract, muscle, kidney, astrocytoma, glia ^{83,84} brain, heart, GI tract, spleen, lung, astrocytoma, glia ^{81,83,84} brain, heart, GI tract, spleen, lung, astrocytoma, glia ⁸²⁻⁸⁴ heart, GI tract, ovary, testis, spleen, lung, astrocytoma ⁸³	? ↑ constitutive AC activity ⁸² exhibit agonist-independent internalization ⁸⁵
Prostaglandin E Receptors			
EP₃ C-term variants EP3 _{AI} EP3B/II EP3C/III EP3D EP3E EP3F	Gα _i ⁸⁶ Gα _i Gα ₁₂ ⁸⁶ Gα _i Gα ₁₂ ⁸⁶ Gα _i , Gα _s ⁸⁶ ? ? ?	Kidney> uterus>stomach> brain, thymus, heart, spleen ⁸⁶ ? ? ? ? ? ?	↓ constitutive AC activity ⁸⁶ ↓ AC activity ⁸⁶ ↓ or ↑ constitutive AC activity ⁸⁶ ? ? ?
Neurokinin Receptor			
NK-1R NK-1R _{truncated}	Gα _{q/11} ⁸⁷ ?	brain, GI tract, lung, thyroid, immune cells ⁸⁸ ?	Impaired SP-induced calcium release ⁸⁹

Abbreviations: 5-HT = serotonin; AC = adenylyl cyclase; N-term = amino terminus; Ca⁺⁺ = calcium; C-term = carboxyl terminus; cAMP = cyclic adenosine monophosphate; EL = extracellular loop; GI = gastrointestinal; LSD = lysergic acid