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Perspective

GABA-Activated Ligand Gated Ion Channels: Medicinal Chemistry and Molecular Biology

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1. Introduction

GABA (**1**, 4-aminobutanoic acid, γ -aminobutyric acid) is the major inhibitory neurotransmitter in the brain and is essential for the overall balance between neuronal excitation and inhibition. GABA influences neurons via a large number of receptor subtypes which are grouped on the basis of their pharmacology under three major classes of receptors: GABA_A, GABA_B, and GABA_C receptors. GABA_A and GABA_C receptors are ligand gated ion channels, while GABA_B receptors are G-protein coupled receptors. This Perspective compares and contrasts aspects of the medicinal chemistry and molecular biology of GABA_A and GABA_C receptors. The molecular diversity of these ligand gated ion channels represents important challenges for medicinal chemists in the design of subunit-specific therapeutic agents.

GABA_A receptors were reviewed in the *Journal of Medicinal Chemistry* by Krogsgaard-Larsen and colleagues¹ in 1994 in a Perspective titled "GABA_A Receptor Agonists, Partial Agonists, and Antagonists: Design and Therapeutic Prospects". There continues to be extensive investigations of GABA_A receptors, particularly with respect to their modulation by important drugs, such as the benzodiazepines, ethanol, general anesthetics, barbiturates, and a wide range of chemically diverse substances. Johnston² has described GABA_A receptors as "the most complicated of the superfamily of ligand-gated ion channels in terms of the large number of receptor subtypes and also the variety of

ligands that interact with specific sites on the receptors." There are many excellent, extensive reviews on aspects of GABA_A receptors.^{1,3–10} GABA_C receptors appear to be much simpler than GABA_A receptors, but they have not been studied anywhere nearly as intensively as GABA_A receptors.^{11–16}

1.1. Ligand Gated Ion Channels. Ligand gated ion channels (LGICs) mediate fast synaptic transmission via the movement of ions through channels gated by neurotransmitters such as acetylcholine and GABA. These receptors are very different from G-protein coupled receptors (GPCRs) that were the subject of a recent Perspective in the *Journal of Medicinal Chemistry*.¹⁷ The nicotinicoid superfamily of LGICs encompasses several families of receptors including nicotinic acetylcholine receptors, 5-HT₃ receptors, GABA_A receptors, GABA_C receptors, strychnine-sensitive glycine receptors, and some invertebrate anionic glutamate receptors. Other superfamilies of LGICs include the excitatory glutamate receptors (with subfamilies of NMDA, AMPA, and kainate receptors) and the ATP receptors (which currently consist of a single family). From the nicotinicoid superfamily of LGICs, the most studied and best understood of this class of receptors is the nicotinic acetylcholine receptors, while the GABA_A receptors appear to be the most complex and the GABA_C receptors the simplest.¹⁸

Members of the nicotinicoid superfamily are considered to be pentamers composed of protein subunits likely to have been derived from a common ancestor.^{18–20} As illustrated in Figure 1A, each subunit has a large extracellular N-terminal domain which incorporates

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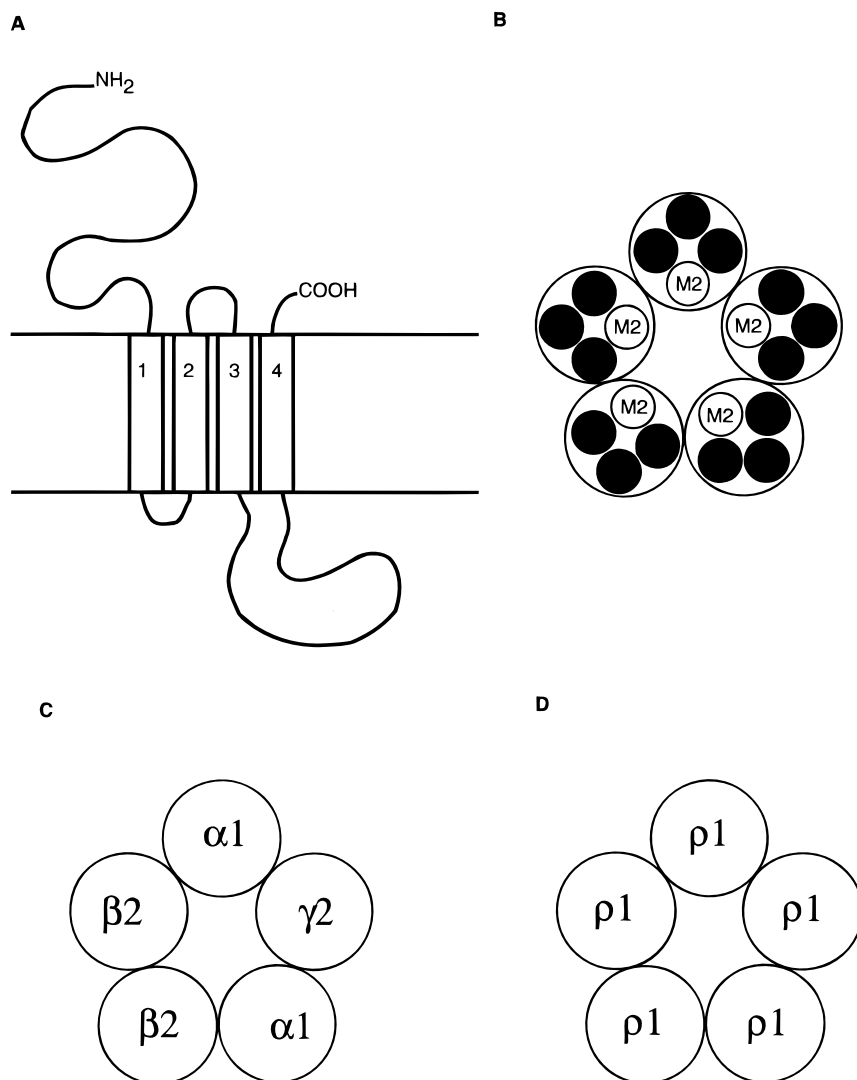


Figure 1. Representations of GABA-activated ligand gated ion channels: A, general structure of one of the five protein subunits showing four membrane spanning regions; B, pentameric arrangement of the protein subunits showing the second membrane spanning region lining the pore of the ion channel; C, heteromeric makeup of a GABA_A receptor with two $\alpha 1$, two $\beta 2$, and one $\gamma 2$ protein subunits; and D, homomeric makeup of a GABA_C receptor with five $\rho 1$ protein subunits.

part of the agonist/antagonist-binding site, followed by three membrane spanning domains (M1–3), an intracellular loop of variable length and a fourth membrane spanning domain (M4), and the C-terminal end being extracellular. Each subunit arranges itself such that the second membrane spanning domain (M2) forms the wall of the channel pore (Figure 1B) and the overall charge of the domain determines whether the channel conducts anions or cations. Both GABA_A and GABA_C receptors are GABA-gated chloride ion channels causing inhibition of neuronal firing, with GABA_A receptors being heteromeric, i.e., composed of different subunits (e.g. $\alpha 1$, $\beta 2$, and $\gamma 2$ subunits as illustrated in Figure 1C) and GABA_C receptors being homomeric (e.g. composed exclusively of $\rho 1$ subunits, Figure 1D). The cytoplasmic loop (Figure 1A), between the third and fourth transmembrane domains (M3 and M4), is believed to be the target for protein kinases, required for subcellular targeting and membrane clustering of the receptor.

The hierarchy within the nicotinicoid superfamily of LGICs as described by Le Novere and Changeux¹⁸ is as follows: the first rank is the family defined by the endogenous ligand responsible for channel opening; the

second rank is the subfamily defined by the ability to form endogenous receptors together; and the last rank is the tribe. In the present context of the GABA-activated LGIC family, GABA_A and GABA_C receptors are subfamilies, while the tribes are the protein subunits that show substantial sequence identity, e.g., the six α subunits, the four β subunits, etc., and the three ρ subunits.

The optimized alignment of the human GABA_A $\beta 1$ and GABA_C $\rho 1$ amino acid sequences from Le Novere and Changeux¹⁸ shows overall 172 matching amino acids between these proteins equating to an optimized sequence identity of 36%. Similar matching between human GABA_A $\alpha 1$ and human GABA_C $\rho 1$ sequences shows significantly less sequence identity: overall 128 matching amino acids, 28% optimized sequence identity, about 50% identity in the transmembrane spanning domains, and 44% identity in a 71-amino acid sequence of the N-terminal extracellular domain.

1.2. Recombinant Receptors: Complementary Structure–Activity Studies. The ability to express functional receptors composed of proteins of known amino acid sequence in suitable biological cells, e.g., frog

oocytes or human embryonic kidney (HEK) cells, that do not normally express such receptors has revolutionized our understanding of LGICs. Cloning studies have yielded a variety of sequence-related nucleotides that code for a variety of closely related membrane-bound LGIC receptors. When injected into appropriate cells, these cells will express functional LGIC recombinant receptors that can be studied by conventional electrophysiological recording techniques, e.g., two-electrode voltage clamp studies, or by radioligand binding studies. This technology enables structure–activity studies on a series of related compounds to be carried out on clearly defined receptor subtypes.

The native nucleotides coding for these receptors may be subjected to site-directed mutagenesis or cutting and splicing techniques to produce mutants or chimeras. On injection into appropriate cells, these nonnative nucleotides may produce mutant or chimeric receptors that have different functional properties to the native receptors. This technology thus enables systematic variation of the receptors themselves and can be used to delineate which amino acid residues are responsible for the pharmacological and physiological properties of the receptors.

Structure–activity relationship (SAR) studies involving structural variations of both the ligands and their receptor targets (termed complementary structure–activity studies)²¹ play important roles in drug development, being vital to the discovery of drugs that interact selectively with particular native and mutant receptor subtypes. Inheritable mutations in the nicotinic acid superfamily of LGICs, including GABA_A receptors, have been identified.²²

1.3. How GABA Activates LGICs. Ligand binding to LGICs has been generally considered to be diffusion-limited, i.e., fast, with binding affinity being primarily determined by the rate of ligand dissociation. This appears to be the case for nicotinic LGICs where the binding of acetylcholine is almost as fast as that predicted if the rate-limiting step is the diffusion of acetylcholine into its binding site. Two recent studies on GABA-activated LGICs suggest, however, that GABA binds orders of magnitude more slowly to GABA_A and GABA_C receptors than expected for relatively free diffusion.

Jones et al.²³ used patch clamping of rat hippocampal neurons in culture to study what defines ligand affinity at these native GABA_A receptors. Their results indicate that a ligand-specific energy barrier between unbound and bound states determines GABA_A receptor selectivity. They quantitatively model this barrier by requiring the participation of movable elements within a flexible binding site. Their flexible binding-site model envisages the binding site behaving as a pair of mobile ‘arms’ attached to fixed ‘anchor’ sites by spring-like tethers. Binding is diffusion-limited only if the ligand is long enough to span the distance between these wells. Shorter agonists bind more slowly because the arms must move to accommodate them, which requires activation energy. The model explicitly requires the ligand to perform thermodynamic work and implies that only nondiffusion-limited ligands can be agonists because otherwise they cause no movement of the receptor. Successful agonist binding involves the coordinated

motion of separate parts of the receptor, and variations of a fraction of an angstrom or a single hydrogen bond cause quite large changes in affinity.

Chang and Weiss²⁴ studied the relationship between agonist binding and channel gating by measuring radioligand binding of GABA agonists to single oocytes expressing recombinant human $\rho 1$ GABA_C receptors and directly correlating the binding kinetics with electrophysiological measurements. They showed that the association rate for GABA is 4 orders of magnitude slower than diffusion, indicating that GABA has restricted access to its binding site. They interpret their results in terms of a minimalist five-state model involving the sequential binding of three agonist molecules to the receptor and a transition to the open channel. Chang and Weiss²⁴ envisage the channel opening locking the agonist molecules onto the GABA_C receptor. Colquhoun²⁵ has raised some problems of interpretation with this study. For example, there seems to be about 10 times as many binding sites as the number of receptors inferred from the maximum current. However, Colquhoun²⁵ is enthusiastic about the overall interpretation that the GABA agonist remains bound while the receptor is active, i.e., while the channel is open.

The GABA_A receptor activation model of Jones et al.²³ involves ligand-induced changes in a dynamic receptor, while the GABA_C receptor activation model of Chang and Weiss²⁴ involves the receptor changing between at least five different states in the presence of an activating ligand. Each model involves much slower binding of agonists than that allowed by diffusion and consequently much slower dissociation of bound agonists in order to accommodate what can be measured as equilibrium affinity constants. The five different states envisaged by Chang and Weiss²⁴ possibly equate to low-energy states of a dynamic receptor as envisaged by Jones et al.,²³ although there are significant differences between the channel properties of GABA_A and GABA_C receptors (see section 2.1).

2. Similarities and Differences between the GABA_A and GABA_C LGIC Subfamilies

GABA_A and GABA_C receptors are classified as subfamilies of the GABA LGIC family on the basis of their significant physiological, pharmacological, and molecular biological differences.

The protein subunits that make up the GABA_A and GABA_C LGIC subfamilies show up to 36% optimized sequence identity overall and up to 73% sequence identity in the transmembrane spanning regions.¹⁸ They are clearly derived from common ancestral proteins in the nicotinic acid superfamily.

The two subfamilies can be distinguished on the basis of their different channel properties, the availability of selective agonists, antagonists, and modulators, the different chromosomal localization of the genes coding for the protein subunits of the two subfamilies and the reluctance of these subunits to coexpress in functional receptors, and the different proteins that anchor the protein complexes to the cytoskeleton. A summary of these differences follows (Table 1), some aspects being covered in more detail in later sections.

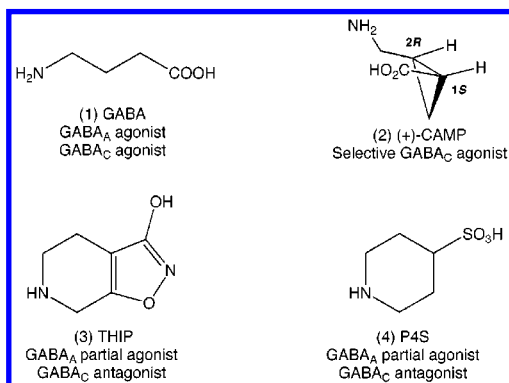
2.1. Channel Properties. The mean channel open time for GABA_A receptors is less than that of GABA_C

Table 1. Differences between GABA_A and GABA_C Receptors

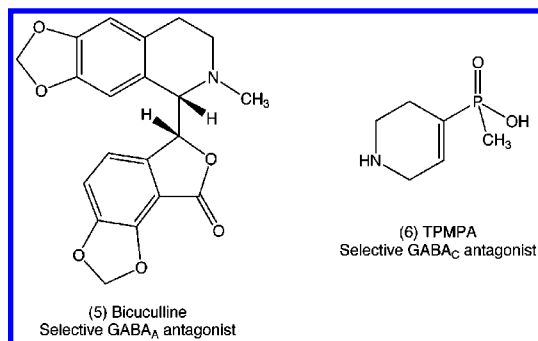
	GABA _A receptors	GABA _C receptors
channel type	Cl ⁻ channel	Cl ⁻ channel
conductance	27–30 pS	7–8 pS
mean channel open time	25–30 ms	150–200 ms
GABA concentrations	10–100 μ M	1 μ M
channel composition	heterooligomeric	homooligomeric
subunit composition	α 1–6, β 1–4, γ 1–3, δ , ϵ , θ	ρ 1–3
chromosomal location of coding genes	chromosomes 1, 4, 5, 15, and X	chromosomes 3 and 6
selective agonist	not known	(+)-CAMP
selective antagonist	bicuculline	TPMPA
potency order of common agonists	muscimol > GABA > TACA	TACA > GABA > muscimol
modulators	benzodiazepines, barbiturates, and steroids	not known
anchoring protein	GABARAP	MAP-1B

receptors. GABA_A receptor gated chloride channels desensitize more readily and are activated and closed more quickly than GABA_C receptor gated chloride channels.^{26–28}

2.2. Selective Agonists. (+)-CAMP (**2**, 1*S*,2*R*-2-(aminomethyl)cyclopropanecarboxylic acid) is a selective agonist for GABA_C receptors being inactive at GABA_A receptors.²⁹ No equivalent selective GABA_A agonist is yet known that does not also have a significant agonist/antagonist action at GABA_C receptors. However, THIP (**3**, 4,5,6,7-tetrahydroisoxazolo[4,5-*c*]pyridin-3-ol) and P4S (**4**, piperidine-4-sulfonic acid) are partial agonists at GABA_A receptors and competitive antagonists at GABA_C receptors.³⁰



2.3. Selective Antagonists. Bicuculline (**5**) and TPMPA (**6**, (1,2,5,6-tetrahydropyridin-4-yl)phosphinic acid) are selective competitive antagonists for GABA_A and GABA_C receptors, respectively. Bicuculline is some 5000 times more potent as an antagonist at GABA_A receptors than at GABA_C receptors,³⁰ while TPMPA is at least 100 times more potent as an antagonist at GABA_C receptors than at GABA_A receptors.³¹ Some phosphinic acid analogues of GABA that are inactive at GABA_A receptors (and agonists at GABA_B receptors) are potent GABA_C antagonists.³⁰



2.4. Modulators. GABA_A receptors are modulated by barbiturates, benzodiazepines, and neurosteroids,² whereas GABA_C receptors are insensitive to these agents.¹²

2.5. Subunit Expression. The protein subunits that can coexpress to make up recombinant GABA_A receptors do not coexpress with any of the GABA_C protein subunits to form functional heteromeric receptors. GABA_A receptor protein subunits do not form functional homomeric receptors, whereas GABA_C receptor protein subunits do. Distinct GABA_A and GABA_C receptor responses can be observed in the same native neurons²⁷ and in recombinant expression systems.³⁰

2.6. Chromosomal Location of Coding Genes. The genes coding for GABA_A subunit proteins show $\alpha\beta\gamma/\epsilon$ clustering on human chromosomes 1, 4, 5, 15, and X (see section 3.1), whereas the genes coding for GABA_C subunit proteins ρ 1 and ρ 2 are found on human chromosome 6^{32–34} and the gene for ρ 3 is on human chromosome 3.³⁵

2.7. Anchoring Proteins. Different proteins, GABA_A receptor-associated protein (GABARAP)³⁶ and microtubule-associated protein 1B (MAP-1B),³⁷ anchor GABA_A and GABA_C subunits respectively to the cytoskeleton.

2.8. IUPHAR Recommendations Regarding the Nomenclature of Subtypes of GABA_A Receptors. The International Union of Pharmacology (IUPHAR) has formed a Nomenclature Committee to attempt to rationalize the nomenclature of pharmacologically important receptors. Most of the receptor nomenclature reports thus far have been concerned with GPCRs. The IUPHAR report on GABA_A receptors⁸ was the first major report on LGICs. It was a task that the committee appeared to take on with some trepidation. They state that the 'combinatorial principle of receptor construction introduces a higher order of complexity. This complexity renders the recognition of the structures of receptor subtypes in their natural setting extremely difficult (in fact, at present, usually unattainable). Thus, it is not possible to construct a classification comparable with the comprehensive scheme for native receptor subtypes obtained in the previous articles of this series.' The IUPHAR committee notes that theirs is "a provisional version" of recommendations and recognizes "its limitations are considerable".

The proposals made by the IUPHAR committee largely address the issue of the wide variety of effects of benzodiazepines on GABA_A receptors. The major criteria for their classification are the pharmacological effects of various benzodiazepines together with the protein subunit composition of recombinant receptors

that exhibit specific responses to benzodiazepines and related drugs. They identify six major types of benzodiazepine responses and thus recommend that the subtypes of the GABA_A receptor should be designated as a series: GABA_{A1}, GABA_{A2}, GABA_{A3}, GABA_{A4}, GABA_{A5}, and GABA_{A6}. They then address the issue that not all GABA_A receptors are influenced by benzodiazepines and propose that benzodiazepine-insensitive GABA_A receptors be known as GABA_{A0} receptors.

The IUPHAR committee noted the sequence similarities between GABA_A receptor subunits and what are currently classified as GABA_C receptor subunits and recommended that the latter be reclassified as benzodiazepine-insensitive GABA_A receptors. Thus what are now widely referred to in the literature as GABA_C receptors would be classified as GABA_{A0r} receptors – 0 for benzodiazepine-insensitivity and r for being comprised of a ρ subunit. The justification for this appears to be solely the sequence similarities between the GABA_A receptor protein subunits and the GABA_C receptor subunits as discussed above in section 2. They note that “selective antagonists have been the most powerful operational tools for discriminating subtypes in other receptor classes”; unfortunately they appear to have overlooked the discovery of TPMPA (**6**) as a selective GABA_C receptor antagonist in 1996.³⁸

GABA_A and GABA_C receptors are clearly distinguished on the basis of the selective antagonists bicuculline (**5**) and TPMPA (**6**) for GABA_A and GABA_C receptors, respectively. Furthermore, the IUPHAR classification minimizes the significance of the reluctance of GABA_C receptor subunits to coexpress with GABA_A receptor subunits in functional recombinant receptors, the clear evidence in the retina for functionally distinct native GABA_A and GABA_C receptors on the same neurons, and the substantial physiological and pharmacological differences between GABA_A and GABA_C receptors.

The IUPHAR classification as applied to benzodiazepine-sensitive, bicuculline-sensitive GABA-activated LGICs is a welcome initiative. However, we reject the inclusion of GABA_C receptors in the GABA_A receptor classification as provisionally recommended by Barnard et al.⁸ and prefer the classification on GABA_A and GABA_C receptors as distinct subfamilies of the family of GABA-activated LGICs (as used by Darlison and Albrecht,⁴ Le Novère and Changeux,¹⁸ and Bormann³⁹).

We consider that the principles enunciated by Barnard et al.⁸ for the GABA_A receptor subfamily could well be applied to the GABA_C receptor subfamily as TPMPA-sensitive, bicuculline-insensitive GABA-activated LGICs being called GABA_{Cr1}, GABA_{Cr2}, or GABA_{Cr3} receptors to designate them being composed of $\rho 1$, $\rho 2$, or $\rho 3$ subunits.

3. GABA_A Receptors

3.1. GABA_A Receptor Subunits. GABA_A receptors are considered heterooligomeric receptors. To date, at least 16 human GABA_A receptor proteins have been described, and these have been classified under five distinct subfamilies of protein subunits termed α , β , γ , δ , and ϵ . There are six α subunits, four β subunits with two splice variants, three γ subunits with two splice variants, one δ subunit, and one ϵ subunit.^{2,21,40} Recently

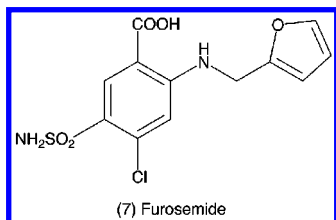
a θ subunit has been described.⁴¹ There is approximately 30% sequence identity between the subunit classes and approximately 70% sequence identity between subunit subtypes. If all possible combinations of isoforms containing 2α , 2β , and one other class were represented in native pentameric GABA_A receptors, then more than 2000 different GABA_A receptors could exist in vivo.² Barnard et al.⁸ suggested a maximum of the order of 800 combinations. It is quite unlikely that these extraordinary numbers of GABA_A receptor subtypes exist in vivo; however, a significant number do exist that can be differentiated pharmacologically as well as by subunit composition.

McKernan and Whiting⁴² concluded that the number of major subtypes of GABA_A receptors was probably less than 10, with the $\alpha 1\beta 2\gamma 2$ subtype accounting for 43%, $\alpha 2\beta 2/3\gamma 2$ 18%, and $\alpha 3\beta \gamma 2/\gamma 3$ 17% on the basis of immunoprecipitation studies, but this has been challenged by Sigel and Kannenberg⁴³ in that receptor subtypes that are difficult to solubilize, e.g., anchored receptors, are under-represented in immunoprecipitation studies. Barnard et al.⁸ discuss the difficulties of a variety of methods for determining GABA_A receptor subtypes in situ, while Darlison and Albrecht⁴ address the issue of “GABA_A Receptor Subtypes: Which, Where and Why?” Subunit mutant and receptor gene knockout animals can provide evidence of the importance of particular subunits of GABA_A receptors.^{44–46} Clearly, the availability of a range of subunit-specific drugs would greatly aid in our understanding of the relative importance of the various GABA_A receptor subunit proteins and their preferred combinations.

3.2. Structural Diversity of Chemicals Acting on GABA_A Receptors. Johnston² proposed that there were at least 11 different structurally specific sites on GABA_A receptors. The 11 sites were (1) agonist sites, which also recognize competitive antagonists; (2) picrotoxinin sites, which also interact with γ -butyrolactones, caprolactams, and some insecticides; (3) sedative–hypnotic barbiturate sites; (4) neuroactive steroid sites; (5) benzodiazepine sites; (6) ethanol sites; (7) stereoselective sites for inhalation anesthetics; (8) furosemide sites; (9) sites for Zn²⁺ ions; (10) sites for other divalent cations; and (11) sites for La³⁺ ions. In addition, 3 other possible sites were noted: (a) phospholipid sites; (b) phosphorylation sites involving specific protein kinase activities; and (c) sites involved in the interaction of GABA_A receptors and microtubules that may anchor receptor clusters at postsynaptic membranes. Furthermore, it was clear that several of the proposed sites, e.g., the benzodiazepine and steroid sites, could be further subdivided.

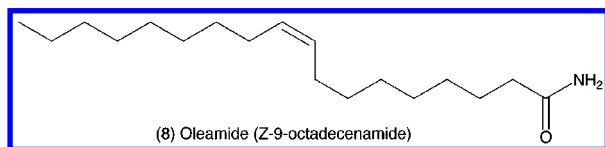
The structural diversity of chemicals acting on GABA_A receptors suggests that these receptors do indeed have a large number of sites that recognize specific chemical patterns. Some of the sites may be associated with specific protein subunits; e.g., the diuretic furosemide (**7**) appears to act on sites specifically associated with $\alpha 6$ subunits⁴⁷ – indeed an important medicinal chemistry target is the discovery of subunit-specific agents. Studies on chimeric $\alpha 1$ and $\alpha 6$ subunits and site-directed mutagenesis of these and $\beta 2/3$ subunits indicate that particular amino acid residues in transmembrane

domains 1 and 2 are important in the specificity of the GABA receptor antagonist action of furosemide.⁴⁸



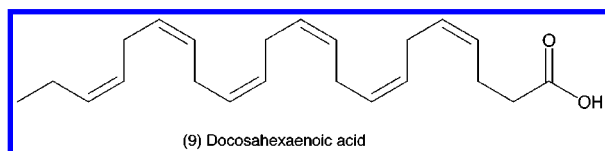
There has been significant recent interest in a number of structural classes of chemicals that influence GABA_A function. These include endogenous substances found in vertebrates, natural products found in herbal preparations, and new chemical entities.

3.2.1. Oleamide and Related Fatty Acid Derivatives. The brain lipid, oleamide (8) (Z-9-octadecenamide), accumulates in the CSF of sleep-derived cats suggesting that it may be an endogenous sleep-inducing factor. Oleamide enhanced the effects of GABA on rat cultured cortical neurons with an EC_{50} of 15 μM .⁴⁹ In studies on recombinant GABA_A receptors expressed in *Xenopus* oocytes, oleamide enhanced the effects of GABA only on benzodiazepine-sensitive receptors containing a $\gamma 2$ subunit, but its enhancing action was not sensitive to the specific benzodiazepine antagonist flumazenil.^{49,50} Oleamide and related compounds are being intensively investigated for use in sleep therapy.



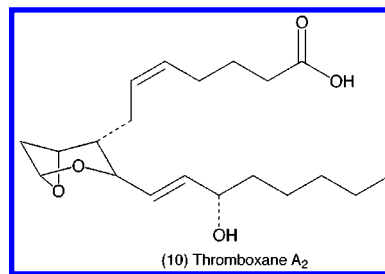
Oleic acid does not directly influence GABA_A receptor function, nor does the endogenous cannabinoid anandamide (*N*-arachidonyl ethanolamide).⁵¹

Docosahexaenoic acid (9) has complex effects of recombinant GABA_A receptors, accelerating desensitization at 0.1 μM , enhancing peak amplitude at 1 μM , and gradually suppressing peak amplitude at 3 μM . Oleic acid had no effect, while arachidonic acid mimicked the effect of docosahexaenoic acid.⁵² 13-L-Hydroxylinoleic acid and a variety of food additives enhanced the action of GABA on recombinant GABA_A receptors.⁵³

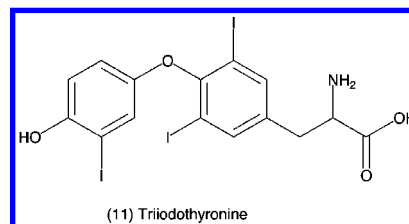


The arachidonic acid metabolite, thromboxane A₂ (10), and several analogues inhibit the action of GABA on GABA_A receptors.⁵⁴

3.2.2. Thyroid Hormones. Thyroid hormones antagonize GABA_A receptor function. The most potent is L-triiodothyronine (11), a noncompetitive inhibitor with an IC_{50} of 7 μM .⁵⁵ Studies on recombinant GABA_A receptors show that the effect requires only $\alpha 1$ and $\beta 2$ subunits and that it was not blocked by the benzodiazepine antagonist flumazenil. This work suggests a non-genomic action of thyroid hormones, which are known to be released from nerve terminals, on GABA_A recep-



tors. L-Triiodothyronine also had a direct channel-gating action (EC_{50} 23 μM) that was blocked by picrotoxin but insensitive to bicuculline.



3.2.3. Peptides and Proteins. The peptide hormone, somatostatin-14, and GABA are known to be colocalized in some CNS neurons and to modulate reciprocally each other's release. Studies on TBPS binding to GABA_A receptors indicate that somatostatin interacts with these receptors in the micromolar range,⁵⁶ but functional studies on GABA_A receptors have yet to be reported.

Waglerin-1, a 22-amino acid peptide purified from the venom of Wagler's pit viper, modulated the action of GABA on hypothalamic neurons.⁵⁷ It enhanced the action of GABA on 78 and suppressed on 44 of 141 neurons examined. The potentiation could be blocked by the benzodiazepine antagonist flumazenil. The suppression was competitive and positively correlated with inhibition of GABA responses by Zn^{2+} ions, suggestive that waglerin-1 is a competitive antagonist of GABA_A receptors that lack γ subunits. This suggests that waglerin has subunit-specific actions on GABA_A receptors, acting as a benzodiazepine-like positive modulator on some receptors and as a competitive antagonist on other receptors.

Amyloid- β protein is the major component of the amyloid deposition that characterizes Alzheimer's disease. Studies on *Aplysia* neurons have shown that amyloid- β fragments 1–40 and 25–35, but not 1–16, inhibit GABA-activated responses, indicating that this activity resides in amino acid residues 17–40 of amyloid- β .⁵⁸ Studies on mammalian GABA_A receptors have yet to be reported.

Insulin promotes the rapid translocation of GABA_A receptors from the intracellular compartment to the plasma membrane in transfected HEK cells.⁵⁹ This requires the presence of the $\beta 2$ subunit. In CNS neurons, insulin increases the expression of GABA_A receptors on postsynaptic and dendritic membranes.

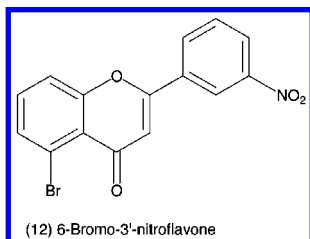
A new cellular protein, GABARAP, that links GABA_A receptors via $\gamma 2$ subunits to the cytoskeleton has been identified.³⁶ GABARAP binds to GABA_A receptors in vitro and in vivo. Its highly positive charged N-terminus features a putative tubulin-binding motif suggesting a mechanism for the targeting and clustering of GABA_A receptors at synapses.

The microtubule depolymerizing agent, colchicine, is a competitive antagonist of recombinant $\alpha 1\beta 2\gamma 2L$ GABA_A receptors expressed in *Xenopus* oocytes.⁶⁰ Other depolymerizing agents, such as nocodazole and vinblastine, did not influence these GABA_A receptors, and the polymerizing agent, taxol, did not affect colchicine inhibition of GABA responses.

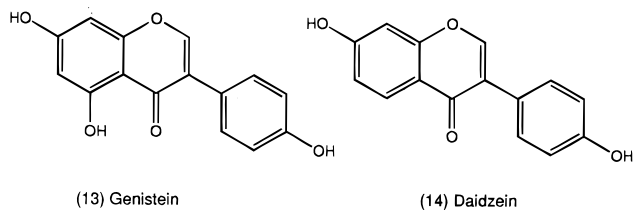
3.2.4. Nitric Oxide and Nitrous Oxide. The diffusible endogenous factor, nitric oxide, directly influences recombinant GABA_A receptor function. It acted as a GABA antagonist on $\alpha 1\beta 2\gamma 2s$ receptors, while on $\alpha 1\beta 2$ receptors it was inactive at low concentrations and enhanced GABA action at high concentrations.⁶¹ Nitric oxide also has indirect actions on GABA_A receptors acting via protein kinase G and A.⁶²

The gaseous anesthetic, nitrous oxide, enhances the action of GABA on GABA_A receptors in a manner similar to other anesthetic agents.⁶³

3.2.5. Flavonoids. Neuroactive flavonoids have been described as a new family of benzodiazepine receptor ligands.^{64,65} Flavonoids isolated from plants used in traditional medicine as tranquilizers have specific actions on the benzodiazepine sites of GABA_A receptors. Unlike the benzodiazepines, they have anxiolytic effects not associated with myorelaxant, sedative, or amnesic actions. Combinatorial chemistry has yielded synthetic flavonoids such as 6,3'-dinitroflavone and 6-bromo-3'-nitroflavone (**12**) that have high affinity (K_i 1.5–30 nM) for GABA_A receptors.⁶⁵ SAR studies on recombinant GABA_A receptors indicate that 6-methylflavone is a benzodiazepine antagonist.⁶⁶ Molecular modeling analysis of 3'- and 4'-substituted flavones has allowed further development of a comprehensive pharmacophore model of the interaction of benzodiazepines and related compounds with GABA_A receptors.⁶⁷

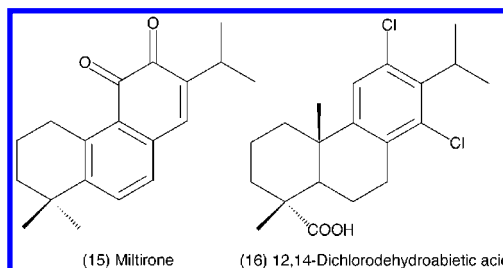


The isoflavones, genistein (**13**) and daidzein (**14**), have been shown to directly inhibit the action of GABA on recombinant GABA_A receptors; this action is independent of the well-known tyrosine kinase inhibitory action of genistein (**13**), since daidzein (**14**) is not a tyrosine kinase inhibitor.⁶⁸



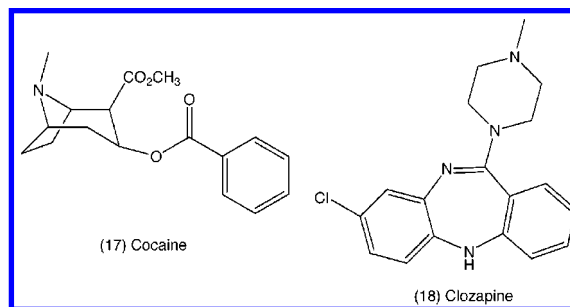
3.2.6. Terpenoids. A range of terpenoids are known to modulate GABA_A receptors. Miltirone (**15**) is the most potent of a series of diterpene quinolones from the Chinese medicinal herb *Salvia miltiorrhiza* that positively modulate GABA_A receptors.⁶⁹ Quantitative struc-

ture–activity relationship (QSAR) studies have been carried out on 28 picrotoxane terpenoids, including picrodendrin, that noncompetitively block rat brain GABA_A receptors, to reveal significant differences between the ionotropic GABA receptors in rat brain and houseflies.⁷⁰ 12,14-Dichlorodehydroabiatic acid (**16**), a fish toxin which is produced from the diterpene carboxylic acid dehydroabiatic acid in the bleaching of wood pulp, is a potent noncompetitive antagonist of GABA_A receptors.⁷¹

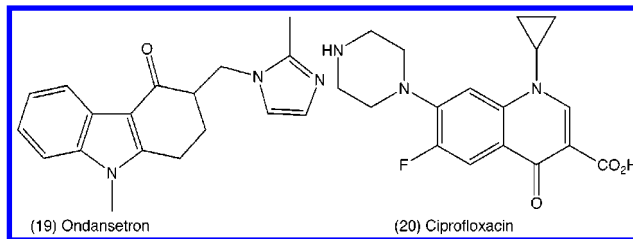


3.2.7. Miscellaneous Therapeutic Agents. A variety of therapeutic agents known for their effects on other receptors also have actions on GABA_A receptors. These actions on GABA_A receptors may contribute to side effects of the therapeutic agents and provide structural leads for the development of more specific agents.

The GABA_A receptor antagonist action (IC_{50} 127 μ M) of cocaine (**17**) may contribute to cocaine-induced seizures.⁷² Clozapine (**18**) and some other antipsychotic drugs may preferentially block the same subset of GABA_A receptors.⁷³ The dehydro derivative of the antidepressant, pirlindole, is a GABA_A receptor antagonist (EC_{50} 12 μ M).⁷⁴



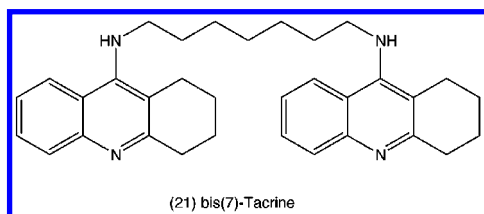
The 5-HT₃ receptor antagonist, ondansetron (**19**), is a noncompetitive antagonist (IC_{50} 10 μ M) of GABA_A receptors; this action may be the basis of ondansetron-induced seizures.⁷⁵



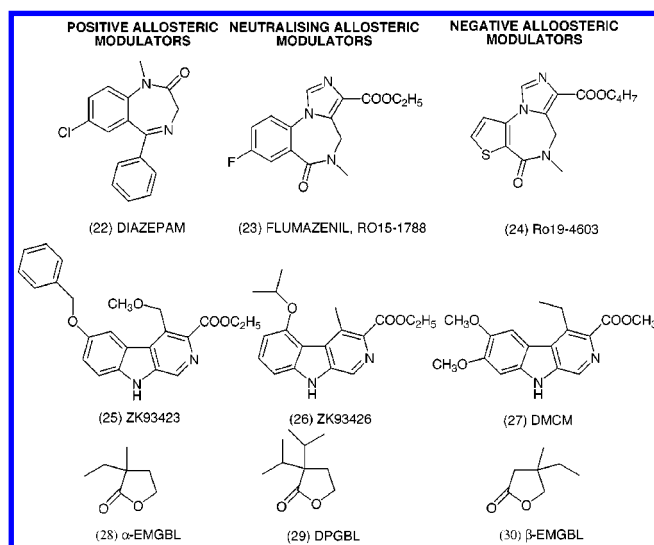
Quinolone antibacterial agents, such as ciprofloxacin (**20**), that have convulsant side effects are GABA_A receptor antagonists; the increased incidence of convulsions induced by these quinolones administered concomitantly with nonsteroidal antiinflammatories, such

as felbinac, is consistent with such antiinflammatories potentiating the GABA_A receptor antagonist action of the quinolones.^{76,77}

bis(7)-Tacrine (1,7-*N,N*-heptylenebis(9,9'-amino-1,2,3,4-tetrahydroacridine)) (**21**) is a potential Alzheimer's disease drug on the basis of its superior acetylcholinesterase inhibition and memory-enhancing potency relative to tacrine. It is a competitive GABA_A receptor antagonist (IC₅₀ 6 μ M), some 18 times more potent than tacrine on these receptors.⁷⁸



3.3. Benzodiazepines and Related Compounds as Allosteric Modulators of a Subset of GABA_A Receptors. The discovery in 1975 that the therapeutic effects of the then most widely prescribed of all drugs, the benzodiazepines, were related to modulation of GABA receptors^{79,80} continues to have a profound influence on the study of GABA_A receptors. A range of diverse chemicals have been found to interact with what became known as benzodiazepine receptors, including diazepam (**22**), flumazenil (**23**), some β -carbolines (**25–27**), and γ -butyrolactones (**28–30**). New concepts about receptor modulation were realized ('inverse agonists', positive and negative modulators) and new generations of drugs developed (e.g. the imidazopyridine, zolpidem (**31**)).



GABA receptors became known as GABA/Bz receptors, and subtypes of these receptors were described (BZ₁ and BZ₂). These terms should no longer be used as we now know that (a) benzodiazepines act on many other receptors unrelated to GABA_A receptors, (b) benzodiazepines interact with only one of several regulatory sites on GABA_A receptors, and (c) GABA_A receptors exist that are insensitive to modulation by benzodiazepines.⁸

Benzodiazepines have no direct action on mammalian GABA_A receptors. They act to enhance the action of

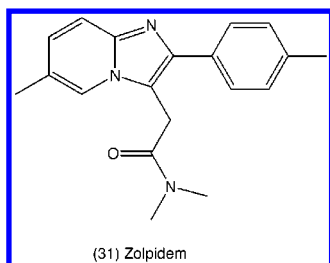
GABA by increasing the frequency of GABA-activated channel openings⁸¹ and by increasing channel conductance.⁸² The discovery of agents, such as 6,7-dimethoxy-4-ethyl- β -carboline-3-carboxylate (**27**, DMCM), that decreased the action of GABA on GABA_A receptors led to the concept of benzodiazepine 'inverse agonists'.⁸³ Interestingly, DMCM (**27**) was initially described as having 'negative efficacy' at benzodiazepine receptors⁸⁴ – this is a more accurate terminology than 'inverse agonist' as strictly benzodiazepines are allosteric modulators of GABA_A receptors rather than agonists or 'inverse agonists'. True inverse agonists have been described in constitutively active G-protein coupled receptors, such as β 2-adrenoceptors.⁸⁵

Puia et al.⁸⁶ introduced the terms 'positive allosteric modulator' and 'negative allosteric modulator' to accurately describe what are commonly but incorrectly described as 'agonists' and 'inverse agonists' when referring to the actions of benzodiazepines on GABA_A receptors. Johnston² introduced the term 'neutralizing allosteric modulator' for benzodiazepine 'antagonists', such as flumazenil (**23**, Ro15-1788). The term 'allosteric' is justified on the basis of GABA agonists and competitive antagonists binding to GABA_A receptors at sites different from those that bind benzodiazepines and related modulators. The classification of these modulatory actions should be made on the basis of functional assays in which the concentrations of agonists and modulators are systematically varied. This enables the relative potencies and efficacies of positive and negative allosteric modulators to be established and thus to classify some modulators as, e.g., partial positive allosteric modulators, if their maximal modulation of agonist responses is less than that of other modulators.

The effects of benzodiazepines on GABA_A receptors are complexly dependent on subunit composition as excellently reviewed by Barnard et al.⁸ In general, the γ 2 subunit is required for the most widely observed effects of benzodiazepines on native GABA_A receptors, consistent with γ 2 subunits being much more abundant in brain than γ 1 and γ 3 subunits. Positive allosteric modulation is reduced when γ 2 is replaced by γ 1 or γ 3 in recombinant GABA_A receptors and negative allosteric modulators become positive allosteric modulators.^{86,87} In addition, flumazenil (**23**) changes from a neutralizing allosteric modulator to a positive allosteric modulator when γ 2 is replaced by γ 1.⁸⁸ If γ is replaced by δ or ϵ , the GABA_A receptors are insensitive to benzodiazepines.^{89–91}

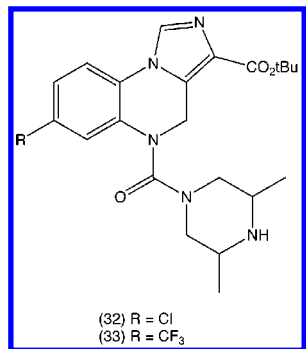
The importance of the γ 2 subunit in GABA_A receptors for benzodiazepine effects is demonstrated by transgenic mice that lack the gene coding for γ 2 subunits and whose GABA_A receptors are insensitive to benzodiazepines.⁹² A single amino acid on the γ 2 subunit has a profound influence on the effects of the benzodiazepines.⁹³ Mutating threonine 142 to serine changes the action of flumazenil from a neutralizing to a positive allosteric modulator and doubles the potencies of diazepam (**22**), flunitrazepam, and clonazepam as positive allosteric modulators, whereas responses to zolpidem (**31**) and alpidem are halved by this mutation. The agonist effects of GABA and the modulatory effects of barbiturates and neurosteroids were not influenced by this mutation. The nature of the α subunit in GABA_A

receptors also has a major influence on benzodiazepine action (see Barnard et al.⁸), whereas the β subunit has little influence.⁹⁴



The development of subunit-specific modulators of GABA_A receptors is an important medicinal chemistry target with the objective of discovering better therapeutic agents that do not have either the unwanted side effects or the full range of therapeutic actions of the traditional benzodiazepines. These side effects include dependence, potentiation of the effects of ethanol, mild ataxia, and mild amnesia. Agents selective for one of the four major therapeutic actions of benzodiazepines, i.e., anxiolytic, sedative–hypnotic, anticonvulsant, and muscle-relaxant actions, are much sought after. The widely prescribed sedative–hypnotic drug, zolpidem (31), is an imidazopyridine that has only minor anxiolytic, muscle relaxant, and anticonvulsant properties and may bind selectively to some benzodiazepine sites on particular GABA_A receptor subtypes,^{95,96} though its amnesic side effects appear to be similar to those of traditional benzodiazepines.⁹⁷

There have been many extensive QSAR studies on benzodiazepines and related compounds using activity data generated from studies on what we now know to be mixed populations of GABA_A receptors.^{98–100} Some recent studies have used activity data using recombinant GABA_A receptors of known subunit composition. Thus, Huang et al.¹⁰¹ measured the binding affinities for a series of imidazobenzodiazepines at five different GABA_A receptors and carried out QSAR studies using comparative molecular field analysis (CoMFA). Jacobsen et al.¹⁰² carried out binding and functional studies on a series of 61 piperazine imidazo[1,5-*a*]quinoxaline ureas on $\alpha 1\beta 2\gamma 2$ recombinant GABA_A receptors to develop two urea-based compounds (32, 33) that were partial positive allosteric modulators with good anxiolytic properties and minimal benzodiazepine-type side effects.

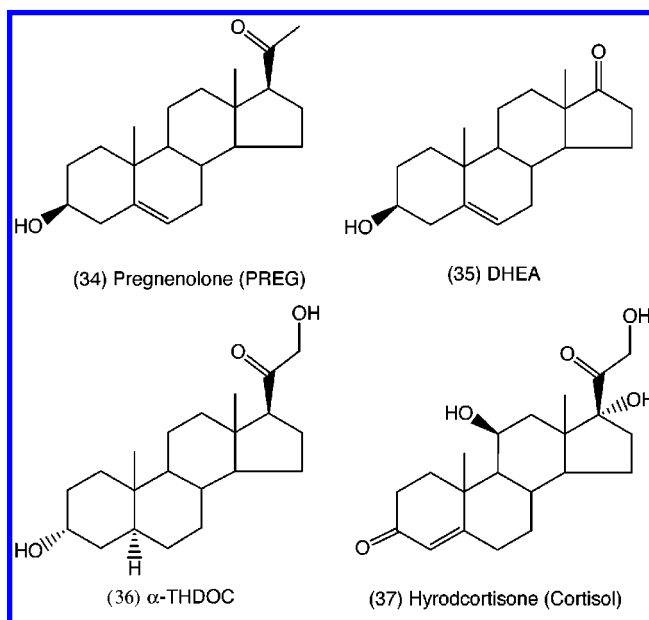


3.4. Steroid Modulation of GABA_A Receptors.

Neuroactive steroids are potent, selective allosteric modulators of GABA_A receptors. These steroids include neurosteroids that are synthesized in the brain and may

serve as endogenous anxiolytic and analgesic agents, steroids such as corticosteroids that are produced elsewhere in the body, and a variety of synthetic steroids. Studies on recombinant GABA_A receptors provide evidence for a subunit-selective heterogeneity of steroid sensitivity,^{103,104} although steroid modulation appears to be a general property of most GABA_A receptors unlike benzodiazepine modulation.² Neuroactive steroids also modulate NMDA receptors¹⁰⁵ and calcium channels associated with G-protein receptors.¹⁰⁶

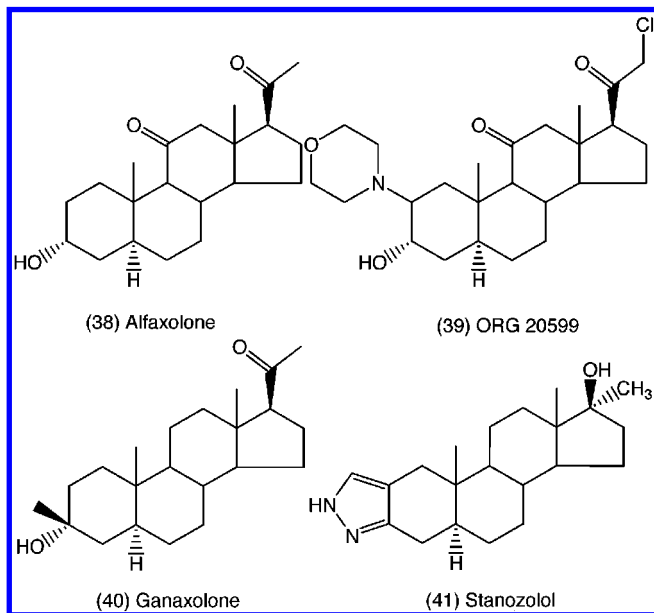
Neurosteroids synthesized in the brain and neuroactive steroids imported into the brain from the periphery represent important endogenous agents for influencing brain function by modulating the activation of GABA_A receptors.¹⁰⁷ They include pregnenolone (34, PREG), dehydroepiandrosterone (35, DHEA), their sulfates, and their reduced metabolites such as 3 α ,21-dihydroxy-5 α -pregnan-20-one (36, α -THDOC). The brain levels of α -THDOC (36), among the most potent known steroid modulators of GABA_A receptors, increase during stress; this increase is prevented by adrenalectomy indicating that the adrenals are the source of α -THDOC.¹⁰⁸ The adrenal steroids, hydrocortisone (37, cortisol) and cortisone, are also potent modulators of GABA_A receptors.^{109,110}



Steroid modulation of GABA_A receptors is enantioselective indicating that steroids act at specific sites on GABA_A receptors rather than via nonenantioselective interactions with membrane lipids.¹¹¹ Nilsson et al.,¹¹² however, found that this was not true for all steroids, observing enantioselectivity for DHEA (35) but not for pregnenolone sulfate or 3 α ,5 β -3-hydroxypregnan-20-one sulfate. Some evidence has been produced to indicate that the neuroactive steroids might modulate GABA_A receptors via the picrotoxinin site in the chloride channel,¹¹³ but studies on mutant GABA_A receptors that are insensitive to picrotoxinin show that PREG sulfate and DHEA sulfate do not require a functional picrotoxinin site to modulate GABA_A receptors.¹¹⁴ Although many of the actions of neuroactive steroids are similar to those of barbiturates on GABA_A receptors, steroids and barbiturates interact with different sites on GABA_A recep-

tors.¹¹⁵ Neuroactive steroids appear to modulate GABA_A receptors only from the extracellular domain, being inactive on intracellular administration.¹¹⁶

Synthetic steroids that modulate GABA_A receptors show promise as therapeutic agents. The steroid anesthetic alfaxolone (**38**, 3 α -hydroxy-5 α -dihydropregnane-11,20-dione) is no longer used in human medicine but has provided a lead for the development of new steroid derivatives. Thus, CCD-3693, an orally active analogue of pregnanolone, shows promise as a sedative–hypnotic agent;¹¹⁷ some water-soluble 2 β -morpholinyl steroids (e.g. **39**) are intravenous anesthetic agents,¹¹⁸ and the steroid analogue, ganaxolone (**40**), is an orally active anticonvulsant.¹¹⁹



Anabolic steroids used to enhance sporting performance are known to modulate GABA_A receptors. The steroids include DHEA (**35**, an endogenous steroid whose use is permitted in major league baseball but is banned in many other sports) and stanozolol (**41**).^{113,120}

Many neuroactive steroids have bidirectional activity on GABA_A receptors, acting as positive allosteric modulators at low concentrations and as negative allosteric modulators at higher concentrations (e.g. PREG and its sulfate¹²¹). Epipregnanolone (3 β -hydroxy-5 β -pregnan-20-one) is able to block the positive modulating action of neuroactive steroids suggesting that the bidirectional activity results from interactions with more than one class of modulatory site for steroids on GABA_A receptors.^{122,123} This is supported by the opposing effects of some 3 α -hydroxy (positive modulation) and 3 β -hydroxy (negative modulation) steroids.¹²⁴ Steroid partial positive modulators ('partial agonists'), such as 3 α ,21-dihydroxy-5 β -pregnan-20-one, have been noted.¹²⁵

4. GABA_C Receptors

4.1. GABA_C Receptor Subunits. GABA_C receptors are considered to be both homooligomeric and pseudoheterooligomeric receptors comprised of ρ subunits. To date, up to five different ρ subunits have been cloned, including two from human retinal cDNA library ($\rho 1$ and $\rho 2$)^{32,126} with two $\rho 1$ splice variants,¹²⁷ three from rat ($\rho 1$ – $\rho 3$),^{128–131} two from chick ($\rho 1$ and $\rho 2$),¹³² five from

white perch ($\rho 1$ – $\rho 5$),¹³³ and two from mouse ($\rho 1$ and $\rho 2$)¹³⁴ retinæ. These subunits are often referred to as GABA_A receptor subunits because they show 30–40% sequence identity with other GABA_A receptor subunits.²¹ This level of subunit similarity is comparable with GABA_A receptor subunits; however, it is also comparable with other LGIC subunits such as glycine and nicotinic acetylcholine receptor subunits. The ρ subunits have approximately 60–70% sequence identity between each other^{32,130,135,136} and have between 85% and 99% sequence identity among species.

4.2. Composition of GABA_C Receptors. ρ Subunits do not coassemble with the classical GABA_A receptor subunits. Coexpression of ρ subunits with the GABA_A receptor subunits $\alpha 1$, $\beta 2$, and $\gamma 2$ expressed in *Xenopus* oocytes and with the β subunit of the glycine receptor in HEK 293 cells showed no detectable alterations in whole cell currents.¹⁴ Furthermore, coimmunoprecipitation experiments using human $\rho 1$ and $\rho 2$ subunits with $\alpha 1$, $\alpha 5$, and $\beta 1$ GABA_A receptor subunits showed no interaction between these subunits in vitro.¹³⁷ Thus, ρ subunits do not combine with the classical GABA_A receptor subunits. It has been shown that the N-terminal region of the subunits directs the assembly of either ρ or GABA_A receptor subunits into homooligomeric GABA_C and heterooligomeric GABA_A receptors.¹³⁷ Thus, GABA_C receptors are physically and functionally different from GABA_A or glycine receptor subunits.

The human $\rho 1$ and $\rho 2$ subunits form homooligomeric receptors when expressed in oocytes, with different physiological yet similar pharmacological properties. Whole cell currents generated by human $\rho 2$ receptors are an order of magnitude lower than currents generated by $\rho 1$ receptors,^{136,138} yet they have a pharmacological profile similar to that of expressed $\rho 1$ receptors. This suggests that the amino acid residues important for most aspects of GABA receptor agonist action may not be among those that differ between $\rho 1$ and $\rho 2$ subunits, including the 20% amino acid difference in the N-terminal region.¹³⁵ Chimera constructs between human $\rho 1$ and $\rho 2$ subunits have shown that the N-terminus of the $\rho 1$ subunit contains subunit assembly signals that aid $\rho 1$ subunits to form more efficient homooligomeric receptors than $\rho 2$ subunits.^{139,140}

Even though there is high sequence identity between the rat and human $\rho 2$ subunits, the rat $\rho 2$ subunit does not appear to form homooligomeric receptors when expressed in *Xenopus* oocytes. However, it can assemble with the rat $\rho 1$ subunit to form pseudoheterooligomeric receptors in oocytes, with similar pharmacology to native GABA_C receptors in the rat retina.¹²⁸ The rat $\rho 3$ subunit forms both homooligomeric¹⁴¹ as well as pseudoheterooligomeric receptors by assembling with other ρ subunits. The increasing evidence that rat and human $\rho 1$ and $\rho 2$ subunits, as well as rat $\rho 3$ subunits, combine to form pseudoheterooligomeric receptors^{128,142} with physical properties distinct from homooligomeric receptors indicates that GABA_C receptors are heterogeneous in vivo.

4.3. Site-Directed Mutagenesis Studies on GABA_C Receptors. Site-directed mutagenesis studies have been used to study the structure–function of $\rho 1$ GABA_C receptors. The $\beta 2$ GABA_A receptor subunit has been shown to have the highest sequence identity with the

$\rho 1$ GABA_C receptor subunit (approximately 50%). Thus, much of the site-directed mutagenesis studies of $\rho 1$ GABA_C receptors have been directed at comparisons with similar studies on the $\beta 2$ GABA_A receptor subunit.²⁸ Five amino acid residues (Y198, Y200, Y241, T244, and Y247), located between the N-terminal extracellular cysteine loop and the first transmembrane spanning domain, were shown to be involved in GABA-mediated activation at homooligomeric $\rho 1$ GABA_C receptors.²⁸ The amino acid residues were conservatively mutated, and these mutations significantly impaired GABA-mediated activation. These residues were grouped in two domains that corresponded in position to the putative agonist-binding domains previously identified for the $\beta 2$ subunit of the $\alpha 1\beta 2\gamma 2$ GABA channels. Y198, T244, and Y247 correspond directly with the amino acid residues identified for GABA activation in the $\beta 2$ subunit, while Y200 and Y241 do not.²⁸ The latter residues correspond to important residues identified for glycine receptor activation.

A single amino acid residue in the M2 region which corresponds to threonine 314 (T314) has been shown to confer picrotoxinin sensitivity to rat $\rho 1$ GABA_C receptors expressed in *Xenopus* oocytes.¹²⁸ GABA_C receptors in the rat retina are insensitive to picrotoxinin, while $\rho 1$ GABA_C receptors, expressed in *Xenopus* oocytes, are sensitive to picrotoxinin. However, coexpressing $\rho 1$ and $\rho 2$ subunits in oocytes produces a novel GABA receptor with similar pharmacology to native GABA_C receptors in the rat retina indicating that pseudoheterooligomeric GABA_C receptors may exist in vivo. Mutation of T314 to a methionine on the $\rho 1$ subunit resulted in a receptor that was insensitive to picrotoxinin.

GABA_A receptors containing a β subunit are potentiated by the presence of low concentrations of barbiturate anesthetics, while GABA_C receptors are not. Chimeric constructs using $\beta 2$ and $\rho 1$ subunits were made to identify the region(s) of the β subunit that confers barbiturate sensitivity, and these were found to be located on the M3 domain. Further studies using site-directed mutagenesis identified a single amino acid residue, tryptophan 328 (W328), which is located on the M3 domain to confer barbiturate sensitivity of the $\rho 1$ subunit when replaced by a hydrophobic residue.^{143,144}

4.4. Channel Properties of GABA_C Receptors. GABA_C receptors differ from GABA_A receptors in many significant ways. GABA_C receptors are more sensitive than GABA_A receptors to GABA. In studies using single-channel electrophysiological recordings with outside-out patches from rat retinal bipolar cells, GABA_C receptors conducted less current and were 7 times more sensitive to GABA receptors than GABA_A receptors (at GABA_C receptors, EC₅₀ 4 μ M; at GABA_A receptors, EC₅₀ 27 μ M).²⁶ The mean channel open time for GABA_C receptors in bipolar cells is approximately 5 times longer than for GABA_A receptors.²⁶ GABA_C receptors have slower activation times. They do not readily desensitize with maintained GABA application and have slower closing times than GABA_A receptors consisting of $\alpha 1$, $\beta 2$, and $\gamma 2$ subunits expressed in *Xenopus* oocytes.²⁸

4.5. Distribution of GABA_C Receptor Subunits. The use of reverse transcriptase PCR, Northern blot, and in situ hybridization techniques has shown that rat $\rho 1$ and $\rho 2$ mRNAs are located predominantly in the

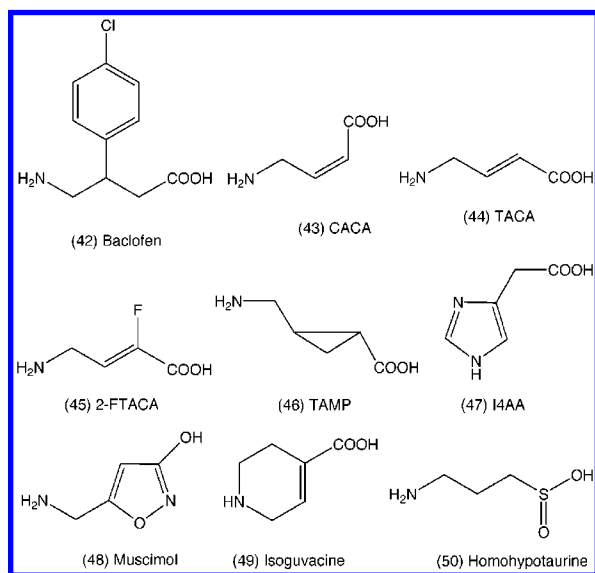
retina. However, rat $\rho 2$ mRNA is also found in most brain areas.^{145–151} The $\rho 3$ mRNA expression pattern is different from the expression pattern of $\rho 1$ and $\rho 2$ mRNAs in rat brain. $\rho 3$ mRNA has lower expression levels in the retina and stronger expression levels in the hippocampus.¹⁵⁰ RT-PCR and in situ hybridization have also been used to determine the expression patterns of $\rho 1$ and $\rho 2$ subunits in the brains of 1-day-old chicks.^{132,152} Transcripts were present in the cerebellum, optic tectum, epithalamus, and nucleus pretectalis. Furthermore, mRNA patterns show that the genes expressing $\rho 1$ and $\rho 2$ subunit exist on different populations of cells.¹⁵² RT-PCR showed that human ρ subunits are heterogeneously expressed in the CNS. Whereas the $\rho 1$ subunit is confined mainly to the retina, the $\rho 2$ subunit is present in all brain regions tested, including the cerebellum, thalamus, and temporal and frontal cortices.¹⁴²

Immunohistochemical studies have shown that ρ subunits are localized to rod bipolar cell axons where the GABAergic amacrine cells form synapses in the rat retina.^{14,16,145–147,149,153} Clusters of these subunits have been shown to occur on postsynaptic sites. Many other receptor subunits including GABA_A and glycine receptor subunits are also found on rod bipolar cell axons; however, these do not colocalize with ρ subunits.¹⁴⁹ The distribution of GABA_C receptors in the retina and in other parts of the visual pathway indicates that these receptors are involved in the temporal processing of visual information.^{154,155}

4.6. Compounds Acting on GABA_C Receptors. The initial studies on GABA receptor classification began when the naturally occurring alkaloid, bicuculline (5), and its derivative, bicuculline methochloride, were shown to block the inhibitory actions of GABA in the spinal cord.^{156–160} By 1981, it had been shown that baclofen (42), a lipophilic analogue of GABA that crosses the blood–brain barrier, had similar agonist effects as GABA in the CNS. However, these effects could not be blocked by bicuculline (5). Thus, evidence was emerging that GABA receptors were heterogeneous and that not all GABA receptors were antagonized by bicuculline (5). The GABA_A/GABA_B classification was developed to distinguish GABA receptors that were (a) inhibited by bicuculline and insensitive to baclofen (42) and (b) activated by baclofen (42) and insensitive to bicuculline (5). These bicuculline-resistant receptors were classified as GABA_B receptors and the original bicuculline-sensitive receptors were termed GABA_A receptors.

At this time, a series of conformationally restricted analogues of GABA, which included CACA (43, *cis*-4-aminocrotonic acid) and TACA (44, *trans*-4-aminocrotonic acid), were tested for their depressant effects on GABA receptors located on spinal interneurons of the cat under pentobarbitone anesthesia.¹⁶⁰ CACA and TACA were designed to reduce the number of conformations that GABA can attain in order to identify which conformations bind to GABA receptors in the spinal cord. CACA (43) is a conformationally restricted analogue of GABA held in a folded conformation, while TACA (44) is a conformationally restricted analogue of GABA held in the extended conformation. It was shown that the depressant effect of TACA (44) but not CACA (43) was inhibited by bicuculline methochloride.¹⁶⁰

CACA (**43**) continued to depress the firing of spinal interneurons in the presence of bicuculline methochloride. Furthermore, the glycine receptor antagonist, strychnine, did not inhibit the depressant effect of CACA. Thus, CACA had no effect on glycine receptors in the spinal cord.¹⁶⁰ Andrews and Johnston¹⁶¹ therefore postulated that folded conformations of GABA activated a population of GABA receptors that were insensitive to bicuculline and extended conformations of GABA activated GABA receptors that were sensitive to bicuculline. CACA (**43**) was also shown to depress the firing of Renshaw cells in the cat spinal cord, yet baclofen (**42**) had relatively little effect on these cells. It seemed likely, therefore, that CACA (**43**) and baclofen (**42**) acted at different receptors. In addition to CACA and baclofen, several other conformationally restricted analogues of GABA have been shown to have bicuculline-insensitive depressant actions in the spinal cord. These include (\pm)-CAMP ((\pm)-*cis*-2-(aminomethyl)cyclopropanecarboxylic acid),¹⁶² T2ACHC (*trans*-2-aminocyclohexanecarboxylic acid),¹⁶³ and T3ACHC (*trans*-3-aminocyclohexanecarboxylic acid).¹⁶³



Both CACA and (\pm)-CAMP failed to displace the binding of [3 H]baclofen to rat cerebellar membranes.¹⁶⁴ On the basis of these results, the existence of a class of bicuculline-insensitive binding sites for GABA that are insensitive to baclofen was proposed, and these sites could be termed GABA_C receptors.¹⁶⁴ For some time, the GABA_C receptor classification was not accepted and the term non-A non-B was used instead to describe bicuculline-insensitive, baclofen-insensitive receptor sites.¹⁶⁵ However, studies of the effects of CACA in a variety of neuronal preparations link CACA to receptors that are activated by GABA and are distinct from the classical GABA_A and GABA_B receptors.^{27,30,166,167} Thus, popularity of classifying these receptors as GABA_C receptors has grown.

Expression of poly(A)⁺ RNA from mammalian retinæ injected into *Xenopus* oocytes generated two pharmacologically distinct GABA receptors, consisting of a bicuculline-sensitive component (GABA_A component) and a bicuculline-insensitive and baclofen-insensitive component (GABA_C component).³⁰ The GABA_A component was blocked by bicuculline, and the remaining

current (GABA_C component) was used to determine a structure–activity profile. The most potent GABA_C receptor agonists in this study were found to be TACA (**44**, K_D 0.6 μ M) and GABA (K_D 1.7 μ M),³⁰ while CACA (**43**) was shown to be a moderately potent, selective partial agonist.³⁰

GABA_C receptors were detected electrophysiologically in rod bipolar cells from rat retina. These receptors were insensitive to bicuculline (**5**) and baclofen (**42**) but were activated by CACA (**43**) after coapplication of GABA (**1**) with 100 μ M bicuculline (**5**) to abolish the GABA_A component.²⁷ It was found that GABA_C receptors were more sensitive to GABA and the channel opened for longer periods with maintained agonist application, compared to GABA_A receptors.²⁶

GABA_C receptors were also detected in white perch retina on rod-driven horizontal cells (H4) but not bipolar cells, which were shown to contain GABA_A receptors.¹⁶⁷ Differences between the two receptor types were detected by applying GABA to both types of cells. First, the bipolar cells showed rapid desensitization, while at rod-driven horizontal cells desensitization was not observed.¹⁶⁷ Further studies showed that GABA_C receptors were found on cone-driven but not rod-driven horizontal cells isolated from catfish retinae¹⁶⁸ as well as in bass retinal bipolar cells.¹⁶⁹ GABA receptors on bipolar terminals in tiger salamander retinae were also shown to conduct chloride ions with similar pharmacology to GABA_C receptors.^{170,171}

For a long time, CACA (**43**) was believed to be a selective partial agonist for GABA_C receptors. Unlike TACA (**44**), it is neither a substrate for nor an inhibitor of GABA:2-oxoglutarate aminotransferase in extracts of rat brain mitochondria, nor does it influence the activity of glutamate decarboxylase in rat brain extracts.¹² However, uptake studies have shown that CACA (**43**) acts as a weak inhibitor of β -alanine uptake in rat cerebral cortex slices.¹⁷² CACA (**43**) is a weak substrate for a transporter that transports GABA, β -alanine, and nipecotic acid in glial cells isolated from guinea-pig retina.¹⁷³ Furthermore, CACA (**43**) stimulates the passive release of [3 H]GABA and [3 H] β -alanine by heteroexchange from slices of rat cerebellum, cerebral cortex, and spinal cord, without influencing potassium-evoked release.¹⁷⁴ CACA (**43**) is only 10 times weaker as a substrate for the transporter than as a partial agonist at the GABA_C receptors. This transporter may be related to the GAT-3 protein, a GABA transporter located predominantly on glial cells in the CNS.¹⁷⁴

To date, the most selective agonist at GABA_C receptors is (\pm)-CAMP, more specifically (+)-CAMP (**2**),²⁹ while TPMPA (**6**) is the most selective antagonist at these receptors.^{31,38}

4.6.1. GABA_C Receptor Agonists and Partial Agonists. SAR studies have been carried out on GABA_C receptors in a variety of systems, which include GABA_C receptors on rod horizontal cells of white perch retina as well as bovine retinal RNA³⁰ and human homooligomeric $\rho 1$ and $\rho 2$ cRNAs expressed in *Xenopus* oocytes.^{135,138,175–177} From these studies, GABA (**1**), TACA (**44**), 2-FTACA (**45**, 2-fluoro-*trans*-4-aminocrotonic acid), and (\pm)-CAMP were shown to be agonists, while TAMP (**46**, *trans*-2-(aminomethyl)cyclopropanecarboxylic acid), CACA (**43**), imidazole-4-acetic acid (**47**,

I4AA), muscimol (**48**), isoguvacine (**49**), and homohypotaurine (**50**) were shown to be partial agonists at GABA_C receptors. The order of agonist/partial agonist potency at GABA_C receptors can be summarized as follows: TACA > GABA > muscimol \approx 2-FTACA > homohypotaurine > I4AA > TAMP \gg (\pm)-CAMP \approx CACA > isoguvacine. At GABA_A receptors, the order of potency is muscimol \gg GABA \approx TACA > isoguvacine \gg CACA. From these SAR studies, it appears that the partially folded conformation of GABA that activates GABA_C receptors is similar to the conformation which TACA, CACA, and (\pm)-CAMP can attain. However, a more extended conformation of GABA is required to activate GABA_A receptors, and this conformation is inaccessible to CACA.

CACA (**43**), which was the first compound to distinguish GABA_C receptors from GABA_A receptors, is a moderate partial agonist at human ρ 1 and ρ 2 receptors expressed in *Xenopus* oocytes (EC₅₀(ρ 1) 74 μ M; EC₅₀(ρ 2) 70 μ M) and shows 70–80% of the efficacy of GABA.^{135,175} The potency and efficacy of CACA at these receptors is similar to those found in GABA_C receptors derived from bovine retinal RNA expressed in *Xenopus* oocytes³⁰ but not to those found in white perch retinae using patch clamp electrophysiology. These results indicate that GABA_C receptors in the retina may consist of ρ subunits and are heterogeneous. Other differences were also observed with the pharmacology of native GABA_C receptors in white perch retina compared to those expressed in oocytes. Isoguvacine (**49**) is an agonist in the perch retina, while in *Xenopus* oocytes it is a partial agonist; I4AA (**47**) is a pure antagonist in the retina but a partial agonist in oocytes; THIP (**3**) is less potent as an antagonist in the retina than in oocytes; and muscimol (**48**) has a lower efficacy in the retina than in oocytes. The differences in the pharmacology observed in the white perch retina and in oocytes may be attributed to differences in species, receptor heterogeneity, or phosphorylation states that may influence pharmacological actions.

Muscimol (**48**) is an analogue of GABA where the carboxylic acid moiety of GABA is replaced by an isoxazole ring system. It has two low-energy conformations, one in an extended and one in a partially folded conformation. Muscimol (**48**) is widely used as a pharmacological tool to study GABA_A receptors. However, muscimol is a potent partial agonist, albeit weaker than GABA, at both human ρ 1 (K_D 2.3 μ M) and ρ 2 (K_D 1.4 μ M) GABA_C receptors expressed in oocytes,^{135,175} bovine retinal RNA expressed in oocytes,³⁰ and rod horizontal cells of white perch retina.¹⁶⁷ Muscimol is more potent at GABA_C than GABA_A receptors expressed in oocytes.^{30,135,175} Therefore, one requires caution when using muscimol (**48**) to study GABA_A receptors.

The sulfinic acid analogue of GABA, homohypotaurine (**50**), is a potent partial agonist at ρ 1 GABA_C receptors expressed in *Xenopus* oocytes (EC₅₀ 4.6 μ M), albeit weaker than GABA, activating 69% of the maximal response produced by GABA.¹⁷⁷ Thus, the sulfinic acid group appears to reduce the ability of homohypotaurine to activate the channel of ρ 1 GABA_C receptors in oocytes.

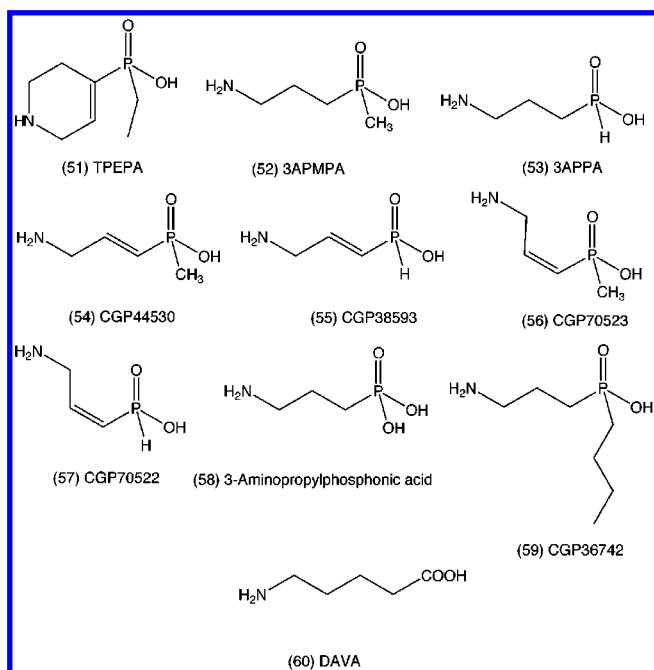
TACA (**44**) is approximately 120 times more potent than CACA (**43**) at homooligomeric ρ 1 and ρ 2 GABA_C

receptors expressed in *Xenopus* oocytes. It has a high efficacy, activating 95% of the maximal response produced by GABA, and is the most potent agonist at GABA_C receptors expressed in oocytes (EC₅₀(ρ 1) 0.6 μ M; EC₅₀(ρ 2) 0.4 μ M^{135,175}). Halogeno and methyl substituents on the C2, C3, and C4 positions of TACA produced a marked reduction in both the efficacy and affinity of the compound for ρ 1 GABA_C receptors expressed in oocytes.¹⁷⁷ Out of the C2, C3, and C4 positions, only the C2 position of TACA tolerated any form of substitution. 2-FTACA (**45**), substituted with a fluoro group at the C2 position, is a potent agonist (EC₅₀ 2.43 μ M), albeit weaker than the parent compound, TACA (EC₅₀ 0.44 μ M), at human ρ 1 GABA_C receptors expressed in *Xenopus* oocytes. It has a high efficacy, activating 90% of the maximal response produced by GABA.¹⁷⁷ Other substituents including a methyl group at the C2 position markedly reduced both the affinity and activity of the compound for this receptor. Substituents on the C2 position of GABA, including chloro, methyl, and methylene substituents, also reduced the affinity and activity for human ρ 1 GABA_C receptors expressed in *Xenopus* oocytes. These results indicate that larger substituents on the C2 position may interact unfavorably with the receptor protein when undergoing receptor activation.¹⁷⁷

TAMP (**46**) is a moderately potent partial agonist with low efficacy at ρ 1 and ρ 2 GABA_C receptors expressed in *Xenopus* oocytes (EC₅₀(ρ 1) 20 μ M; EC₅₀(ρ 2) 17.5 μ M^{135,175}). TAMP activates ρ 1 and ρ 2 GABA_C receptors by 25% and 43% of the maximal response produced by GABA, respectively.^{135,175} In contrast to TAMP, (\pm)-CAMP is a moderately potent full agonist at ρ 1 and ρ 2 GABA_C receptors (EC₅₀(ρ 1) 68.0 μ M; EC₅₀(ρ 2) 34.5 μ M^{135,175}). CAMP has no effect in inhibiting [³H]GABA uptake in cortical slices and thus may be the most selective agonist at GABA_C receptors.¹⁶²

4.6.2. Competitive GABA_C Receptor Antagonists. TPMPA (**6**) and TPEPA (**51**, 1,2,5,6-tetrahydropyridine-4-ylethylphosphinic acid) are the most selective GABA_C receptor antagonists to date. These compounds were developed from the observation that isoguvacine, a conformationally restricted analogue of TACA held in a partially folded conformation, has activity at both GABA_A and GABA_C receptors but no activity at GABA_B receptors. Thus, the tetrahydropyridine ring distinguishes GABA_B from GABA_C receptors but does not distinguish GABA_A from GABA_C receptors. As discussed previously, the methylphosphinic acid group can distinguish GABA_C from GABA_A receptors. Thus by incorporating a tetrahydropyridine ring system with either a methylphosphinic or ethylphosphinic moiety, potent and selective antagonists at GABA_C receptor were developed.^{31,38} TPMPA is twice as potent as TPEPA, which further establishes that an increase in the alkyl group on the alkylphosphinic acid reduces GABA_C receptor affinity. TPMPA is more than 100 times more selective in blocking ρ 1 GABA_C receptors than in blocking GABA_A receptors from rat cerebral cortex poly-(A⁺) RNA expressed in *Xenopus* oocytes.³¹ At GABA_B receptors, TPMPA is a weak agonist when measured by whole-cell patch recordings from pyramidal neurons in rat hippocampal slices.³¹ TPMPA is more than 500 times more selective in blocking ρ 1 GABA_C receptors expressed in *Xenopus* oocytes than in activating GABA_B

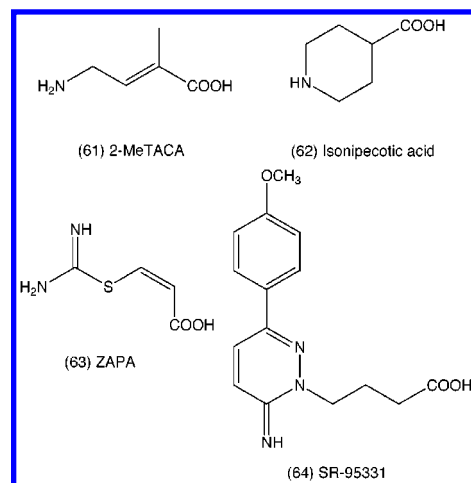
receptors.³¹ Furthermore, TPMPA was found to be 8 times weaker at $\rho 2$ than at $\rho 1$ GABA_C receptors expressed in *Xenopus* oocytes.¹³⁸ TPMPA has been shown to block responses in the neonatal rat spinal cord providing evidence for the involvement of GABA_C receptors in synaptic transmission in this tissue.¹⁷⁸



From SAR studies, many GABA_C receptor antagonists have been identified. These include a variety of phosphinic, methylphosphinic, and phosphonic acids (**52**–**59**), DAVA (**60**, δ -aminovaleric acid, K_B 20 μ M), 2-MeTACA (**61**, 2-methyl-*trans*-4-aminocrotonic acid, K_B 45 μ M), P4S (**4**, piperidine-4-sulfonic acid, K_B 81 μ M), 3-aminopropylphosphonic acid (**58**, K_B 10 μ M), isonipecotic acid (**62**, K_B > 100 μ M), and THIP (**3**, K_B 32 μ M). Other compounds such as strychnine (K_B 69 μ M), ZAPA (**63**, *Z*-3-[(aminoiminomethyl)thio]prop-2-enoic acid, K_B 19 μ M), and SR-95331 (**64**, gabazine, 2-(3-carboxypropyl)-3-amino-6-(*p*-methoxyphenyl)pyridazinium bromide, K_B 35 μ M) are also moderately potent GABA_C receptor antagonists at bovine retinal poly(A)⁺ RNA expressed in *Xenopus* oocytes.³⁰ The order of potency for competitive antagonists at GABA_C receptors is as follows: methylphosphinic acids \geq phosphinic acids > 3-APA > ZAPA \approx DAVA > THIP \approx SR-95331 > 2-MeTACA > strychnine > P4S > isonipecotic acid.

P4S (**4**) is the sulfonic acid analogue of isoguvacine. It was first developed as a GABA_A receptor ligand and appears to have similar potency as GABA in activating GABA_A receptors from rat cortex RNA expressed in *Xenopus* oocytes (K_D 104 μ M).³⁰ However, this compound is a partial agonist, activating rat brain GABA_A receptors expressed in *Xenopus* oocytes by <30% of the currents produced by GABA.³⁰ P4S produced no response on its own but was shown to be a moderately potent antagonist at GABA_C receptors from retinal RNA expressed in oocytes.³⁰

Phosphonic acid analogues of GABA, such as 3-aminopropylphosphonic acid (**58**), differentiate between GABA_A and GABA_C receptors. 3-Aminopropylphosphonic acid is a moderately potent inhibitor of GABA_C



receptors. This compound has no clear action as an agonist or antagonist at GABA_A receptors from rat cortex RNA expressed in *Xenopus* oocytes.³⁰ However, 3-aminopropylphosphonic acid is not selective for GABA_C receptors. It has weak depressant effects on the CNS that is insensitive to bicuculline, and it acts as a partial agonist at peripheral GABA_B receptors. Like 3-aminopropylphosphonic acid, 4-aminobutylphosphonic acid had little effect on GABA_A receptors. It is a weak inhibitor of GABA_B receptors but only has weak inhibitory effects on GABA_C receptors. 2-Aminoethylphosphonic acid is largely inactive at GABA_C receptors.³⁰

To date, the most potent classes of GABA_C receptor antagonists are the methylphosphinic acid analogues, followed by the phosphinic acid analogues, of GABA. The most potent GABA_C antagonist is 3APMPA (**52**, (3-aminopropyl)methylphosphonic acid). The phosphinic acid analogue of GABA, 3APPA (**53**, 3-aminopropylphosphonic acid), is approximately 3 times weaker than 3APMPA ((3-aminopropyl)methylphosphonic acid). Thus, the methyl group may either bind to a small hydrophobic pocket on the binding site and/or alter the pK_A to improve binding. Similar results were observed with the methylphosphinic and phosphinic acid analogues of TACA, CGP44530 (**54**, (*E*-3-aminoprop-1-en-1-yl)methylphosphonic acid) and CGP38593 (**55**, (*E*-3-aminoprop-1-en-1-yl)phosphonic acid) respectively, and the methylphosphinic and phosphinic acid analogues of CACA, CGP70523 (**56**, (*Z*-3-aminoprop-1-en-1-yl)methylphosphonic acid) and CGP70522 (**57**, (*Z*-3-aminoprop-1-en-1-yl)phosphonic acid) respectively.¹⁷⁶ The methylphosphinic acids CGP44530 (**54**) and CGP70523 (**56**) were more potent antagonists than the corresponding phosphinic acid analogues CGP38593 (**55**) and CGP70522 (**57**). However, the unsaturated methylphosphinic and phosphinic acid analogues were weaker than the corresponding saturated analogues.¹⁷⁶

3APMPA (**52**), 3APPA (**53**), CGP44530 (**54**), CGP38593 (**55**), and CGP70523 (**56**) are not selective GABA_C receptor antagonists as they all activate GABA_B receptors. However, the methylphosphinic and phosphinic acid moieties dramatically reduce affinity for GABA_A receptors. Thus, the methylphosphinic and phosphinic acid substituents are able to differentiate GABA_A from GABA_C receptors but not from GABA_B receptors. This could be attributed to the different pK_A activity between the carboxylic and phosphinic acids, as well as the orientation which the different acid groups can attain.

The phosphinic acid moiety is tetrahedral, while the carboxylic acid moiety is planar. The relative lack of selectivity of the methylphosphinic and phosphinic acid analogues of TACA and particularly of CACA is unexpected but may be explained by the higher degree of rotational freedom between the C2 and C3 bonds and between the phosphorus and C1 bonds. Thus, these compounds are more likely to attain conformations that bind to both GABA_B and GABA_C receptors.¹⁷⁶

An increase in the size of the alkyl group on the alkylphosphinic acid moiety reduces the affinity at GABA_C receptors. CGP36742 (**59**, (3-aminopropyl)butylphosphinic acid) is a moderately potent antagonist, while CGP35348, the diethoxymethyl analogue of GABA, has no effect at GABA_C receptors.¹⁷⁶

4.6.3. Noncompetitive GABA_C Receptor Antagonists. Picrotoxinin and the related chloride channel inhibitor, *t*-butylbicyclophosphorothionate (TBPS), blocked homooligomeric $\rho 1$ GABA_C receptors expressed in *Xenopus* oocytes. However, these compounds were 30 and 250 times weaker at GABA_C than GABA_A receptors expressed in *Xenopus* oocytes.²⁶ The picrotoxinin sensitivity of GABA_C receptors derived from $\rho 1$ and $\rho 2$ subunits has been found to be dependent on agonist concentration, as picrotoxinin may be a use-dependent antagonist interacting with open chloride channels. Furthermore, studies have shown that a single amino acid residue in the M2 region of the $\rho 2$ subunit confers picrotoxinin sensitivity.^{128,179,180} Coexpression of $\rho 1$ and $\rho 2$ subunits in *Xenopus* oocytes gives rise to functional receptors with picrotoxinin insensitivity¹²⁸ similar to native GABA_C receptors in rat retina.²⁶ Thus pseudoheteromeric as well as homomeric GABA_C receptors may exist in vivo.

4.6.4. GABA_C Receptor Modulators. GABA_C receptors are not modulated by benzodiazepines, steroids, or barbiturates, and in fact little is known about GABA_C receptor modulators. GABA_C receptors in rat bipolar cells have been shown to be modulated by protein kinase C.¹⁸¹ Furthermore, low micromolar concentrations of glycine have also been shown to modulate the effect of a submaximal concentration of GABA at $\rho 1$ GABA_C receptors expressed in *Xenopus* oocytes.¹⁸² However, at millimolar concentrations, glycine directly activates these receptors. Glycine modulation of GABAergic synapses may play an important role in synaptic transmission.¹⁸²

4.7. Differences between GABA_C Receptor Subtypes. Some SAR differences between human $\rho 1$ and $\rho 2$ receptor subtypes have been noted. These include the intrinsic activity (calculated as a percentage of the maximum whole cell current produced by a maximum dose of GABA) of the partial agonist, I4AA (**47**), being 7-fold higher at $\rho 2$ than $\rho 1$ receptors.¹³⁵ I4AA is an analogue of GABA where the amino group of GABA has been replaced by an imidazole ring. Due to a resonance charge distribution between the two nitrogens of the imidazole ring system, there is a weakening of the charge at the basic end of the molecule. I4AA is a moderately potent partial agonist (EC₅₀ 16 μ M), with low intrinsic activity (*I*_m 3%) at $\rho 1$ GABA_C receptors expressed in *Xenopus* oocytes.¹⁷⁵ However, it is a more potent antagonist at this receptor (*K*_B 1.5 μ M), with an affinity similar to that of GABA at $\rho 1$ GABA_C recep-

tors.¹³⁸ I4AA was shown to activate $\rho 2$ GABA_C receptors expressed in *Xenopus* oocytes. It is a potent partial agonist (EC₅₀ 3 μ M) with a higher intrinsic activity for the $\rho 2$ (*I*_m 38%) than the $\rho 1$ GABA_C receptors.^{135,138,175}

2-MeTACA (**61**) is a moderately potent inhibitor of $\rho 1$ GABA_C receptors expressed in *Xenopus* oocytes (*K*_B 45 μ M). In contrast, 2-MeTACA (**61**) activates the human $\rho 2$ GABA_C receptor subtype (EC₅₀ 101 μ M) by 34% of the maximal response produced by GABA.¹³⁸ Although receptor binding was less favorable at the $\rho 2$ compared to the $\rho 1$ GABA_C receptors, steric interaction between the C2 substituent and the receptor protein may play an important role in activation. Thus, 2-MeTACA (**61**) can pharmacologically distinguish between the human $\rho 1$ and $\rho 2$ homooligomeric GABA_C receptor subtypes.¹³⁸

5. Future Directions

While great progress has been made in our understanding of the medicinal chemistry and molecular biology of GABA-activated ligand gated ion channels over the past decade, this has been achieved without significant input from combinatorial chemistry, high-throughput screening, or structure-based drug design. We can expect important advances from these key strategies in the future, with structural leads coming from the side effects of other drugs and from herbal extracts. In addition, genomics will reveal links between specific GABA receptor gene products and neurological disorders, which will provide specific targets for drug development via complementary SAR studies.

While some classic combinatorial chemistry was carried out on benzodiazepines, this did not lead to better modulators of GABA-activated ligand gated ion channels but rather to novel agents that interact with other classes of receptors, e.g., cholecystokinin receptors.¹⁸³ The only reported use of combinatorial chemistry for the development of new GABA receptor agents has been the generation of small libraries of flavones by solution-phase combinatorial chemistry that have yielded novel flavone derivatives that modulate GABA receptors.¹⁸⁴ The great chemical diversity of agents acting on GABA-activated ligand gated ion channels described in this Perspective should provide significant opportunities for the application of combinatorial chemistry to the discovery of new agents with selective actions on the various subtypes of these receptors.

The high-throughput screening of agents acting on ligand gated ion channel receptors has proved difficult. Limited success has been achieved using binding assays, but functional assays are needed to differentiate between agonists, partial agonists, antagonists, and modulators of these receptors. High-throughput screening functional assays have been described for ligand gated cation channel receptors such as nicotinic acetylcholine receptors¹⁸⁵ and the NMDA subtypes of ionotropic glutamate receptors,¹⁸⁶ but no high-throughput functional assays have been described thus far for ligand gated anion channel receptors such as ionotropic GABA receptors. The development of such assays is highly desirable.

An important strategic question for high-throughput functional assays for GABA-activated ligand gated ion channels is what protein subunit combinations should

be used in the primary screens? Given that the discovery of subunit-specific GABA receptor ligands is a major goal, it may be that particular target receptor subtypes will have to be selected on the basis of, for example, association with a specific genetic disorder. To achieve the desired specificity, only compounds that have no or very little interaction with the ubiquitous subtypes of GABA receptors will be of interest. This means that new structural classes of test compounds will need to be developed, e.g., by screening diverse combinatorial libraries, by following structural leads from the side effects of other drugs such as the apparent selectivity of the diuretic furosemide (7) for particular amino acids in $\alpha 6$ GABA receptor subunits,⁴⁸ and from herbal extracts. Many herbal extracts have been reported to influence the activity of GABA-activated ligand gated ion channels: e.g., extracts of Ginkgo biloba¹⁸⁷ and ginseng.¹⁸⁸

Structure-based drug design depends on the availability of good structural data for the target receptor. High-resolution structural information on ligand-gated ion channels is rather sparse, but the determination of the crystal structure of a ligand-binding region of an ionotropic glutamate receptor in a complex with the agonist kainate¹⁸⁹ suggests that similar information will be soon forthcoming for GABA-activated ligand gated ion channels. Molecular modeling of receptor sites is another approach which has been applied to nicotinic acetylcholine receptors¹⁹⁰ and to GABA-activated ligand gated ion channels,¹⁹¹ while methods are being developed for predicting the location of ligand-binding sites on protein surfaces.¹⁹² The relatively simple homomeric GABA_C receptors would appear to be excellent targets for high-resolution structural data by crystal studies and molecular modeling.

Pharmacogenomics is regarded as one of the 'hottest' fields in biotechnology today.¹⁹³ Genetic polymorphisms in receptors and other drug targets are being linked to individual differences in drug efficacy, metabolism, and side effects.¹⁹⁴ The era of 'one drug fits all patients' is seen as about to give way to individualized therapy matching a patient's unique genetic makeup with an optimally effective drug.¹⁹³ High-throughput analysis of differential gene expression, via 'DNA chips' and other technology, is now a reality.¹⁹⁵ While mutations of receptors in disease states appear to be relatively uncommon, inheritable mutations GABA_A receptors have been identified.²² Disruption of the gene coding for the $\beta 3$ GABA_A receptor subunit has been associated with Angelman syndrome, a neurodevelopmental disorder characterized by mental retardation and epilepsy.¹⁹⁶ Knockout mice that lack this gene exhibit electroencephalograph abnormalities, seizures, and behavioral characteristics typically associated with Angelman syndrome.¹⁹⁶ Rett syndrome, an X-linked dominant neurodevelopmental disorder, may involve the gene coding for the $\alpha 3$ GABA_A receptor subunit,¹⁹⁷ while a number of studies have linked polymorphisms in the genes coding for the $\alpha 6$, $\beta 1$, $\beta 2$, and $\gamma 2$ GABA_A receptor subunits with alcohol dependence syndrome and Korsakoff's psychosis.^{198,199} The genes coding for $\rho 1$ and $\rho 2$ GABA_C receptor subunits are located in a region of chromosome 6q that contains loci for inherited disorders of the eye.³⁵ These studies indicate that genetic disor-

ders of GABA-activated ligand gated ion channels may represent key therapeutic targets and that the development of drugs acting on abnormal GABA receptor gene products is an important endeavor. Site-directed mutagenesis studies of recombinant GABA receptors show that changing even a single amino acid residue can have major effects on drug sensitivity. For example, changing T328 to a hydrophobic amino acid confers barbiturate sensitivity on the $\rho 1$ GABA_C subunit.^{143,144} Thus, meaningful pharmacogenomics in relation to drugs acting on GABA-activated ligand gated ion channels is a distinct possibility, with complementary SAR studies²¹ involving structural variations of both the ligands and their receptor targets playing a vital role.

6. Conclusion

This Perspective highlights the remarkable structural diversity of natural and synthetic chemicals that interact with GABA_A receptors to alter their function in the brain. While medicinal chemistry studies on GABA_C receptors are just beginning, it is already clear that GABA_C receptors are very different from GABA_A receptors in terms of agonist and antagonist structural profiles. Both subfamilies of GABA-activated ligand-gated ion channels are targets for drug development, with major advances likely to result from the interactive application of combinatorial chemistry, high-throughput screening, structure-based drug design, and genomics.

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