

## **Non-classical Pharmacology of the Dopamine Transporter: Atypical Inhibitors, Allosteric Modulators and Partial Substrates**

Kyle C. Schmitt, Richard B. Rothman and Maarten E.A. Reith

*Department of Neurosurgery, New York University School of Medicine, New York, New York (K.C.S.); Departments of Pharmacology and Psychiatry, New York University School of Medicine, New York, New York (M.E.A.R.); Medicinal Chemistry Section of the Intramural Research Program, National Institute on Drug Abuse, National Institutes of Health, Baltimore, MD (R.B.R).*

## Running Title Page

**Running title:** Pleiotropic Characteristics of DAT Ligands

**Corresponding author:** Kyle C. Schmitt, Ph.D., Department of Neurosurgery, New York University School of Medicine, 455 First Ave, Public Health Labs (8<sup>th</sup> Floor), New York, New York 10016, USA; phone: 212.263.5177; fax: 212.689.0334; email: [kyle.schmitt@nyumc.org](mailto:kyle.schmitt@nyumc.org).

**Text Pages:** 27

**Main Text Words (Including Figure Legends):** 5380

**Tables:** None

**Figures:** 3 (Main Text) and 3 (Supplemental Material)

**Abstract:** 250 words

**References:** 67

**ABBREVIATIONS:** ADHD, attention deficit/hyperactivity disorder;  $\beta$ -CFT, 2 $\beta$ -carbomethoxy-3 $\beta$ -(4-fluorophenyl)tropane;  $\beta$ -CIT, 2 $\beta$ -carbomethoxy-3 $\beta$ -(4-iodophenyl)tropane; DA, dopamine; DAT, dopamine transporter; ENAP, (*N*-ethyl)-1-(2-naphthyl)-propan-2-amine; GBR12909, 1-(2-[*bis*(4-fluorophenyl)methoxy]ethyl)-4-(3-phenylpropyl)-piperazine; JHW007, (*N*-butyl)-3 $\alpha$ -[*bis*(4-fluorophenyl)methoxy]tropane; LeuT, leucine transporter; MPP<sup>+</sup>, 1-methyl-4-phenylpyridinium; NAP, 1-(2-naphthyl)-propan-2-amine; NET, noradrenaline transporter; NSS, neurotransmitter sodium symporter; RTI-371, 3 $\beta$ -(4-methylphenyl)-2 $\beta$ -[3-(4-chlorophenyl)isoxazol-5-yl]tropane; SERT, serotonin transporter; SoRI-9084, (*N*-benzhydryl)-2-phenylquinazolin-4-amine; SoRI-20040, (*N*-diphenylethyl)-2-phenylquinazolin-4-amine; SoRI-20041, (*N*-diphenylpropyl)-2-phenylquinazolin-4-amine; TM, transmembrane domain.

**Recommended Section:** JPET Perspectives in Pharmacology Review

## **Abstract**

The dopamine transporter (DAT) is a sodium-coupled symporter protein responsible for modulating the concentration of extraneuronal dopamine in the brain. The DAT is a principle target of various psychostimulant, nootropic and antidepressant drugs, as well as certain drugs used recreationally, including the notoriously addictive stimulant cocaine. DAT ligands have traditionally been divided into two categories: cocaine-like inhibitors and amphetamine-like substrates. Whereas inhibitors block monoamine uptake by the DAT, but are not translocated across the membrane, substrates are actively translocated and trigger DAT-mediated release of dopamine by reversal of the translocation cycle. As both inhibitors and substrates increase extraneuronal dopamine levels, it is often assumed that all DAT ligands possess an addictive liability equivalent to cocaine. However, certain recently developed ligands—such as “atypical” benztropine-like DAT inhibitors with reduced or even a complete lack of cocaine-like rewarding effects—suggest that addictiveness is not a constant property of DAT-affecting compounds. These atypical ligands do not conform to the classical preconception that all DAT inhibitors (or substrates) are functionally and mechanistically alike. Instead, they suggest the possibility that the DAT exhibits some of the ligand-specific ‘pleiotropic’ functional qualities inherent to G-protein-coupled receptors. That is, ligands with different chemical structures induce specific conformational changes in the transporter protein, which can be differentially transduced by the cell, ultimately eliciting unique behavioral and psychological effects. The present overview discusses compounds with conformation-specific activity, useful not only as tools for studying the mechanics of dopamine transport, but also as leads for medication development in addictive disorders.

## Introduction

The dopamine transporter (DAT) is a transmembrane protein that regulates dopaminergic signaling in the central nervous system. DATs help to modulate the concentration of extraneuronal dopamine by actively shuttling released transmitter molecules back across the plasma membrane into dopaminergic neurons, where they can be sequestered for later reuse or enzymatic catabolism. Dopaminergic signaling is involved in many aspects of brain function, most notably cognition, motor function, affect, motivation, behavioral reinforcement and economic analysis (reward prediction and valuation) (Greengard, 2001; Montague and Berns, 2002; Salamone et al., 2009). As such, perturbation of DAT function is implicated in a number of neuropsychiatric disorders: ADHD, Parkinson's disease, depression, anhedonia and addictive/compulsive disorders (Gainetdinov and Caron, 2003; Felten et al., 2011; Kurian et al., 2011). The DAT is also of significant pharmacological interest, as it is a target of several popular medications and a number of recreational drugs. Notable clinically used DAT ligands include psychostimulants (e.g. dextroamphetamine, methylphenidate and modafinil), antidepressants (e.g. bupropion) and certain anorectics (e.g. phendimetrazine, a prodrug that is converted to the DAT ligand phenmetrazine *in vivo*). Interaction with the DAT also underlies the powerful reinforcing and locomotor stimulant effects of cocaine, one of the most prominent drugs of addiction (reviewed in Gainetdinov and Caron, 2003 and Schmitt and Reith, 2010).

Like its fellow monoaminergic siblings—the neuronal serotonin and noradrenaline transporters (SERT and NET, respectively)—the DAT is a member of the neurotransmitter/sodium symporter (NSS) protein superfamily. NSS proteins utilize the electrochemical potential energy inherent to the inwardly-directed transmembrane Na<sup>+</sup> gradient to facilitate the thermodynamically unfavorable process of moving substrate molecules against their concentration gradient (Gether et al., 2006; Forrest et al., 2011). Ligands acting at the DAT and other NSS proteins have historically been divided into two categories: inhibitors and substrates. Inhibitors are compounds that bind to the symporter and impede substrate

translocation, but are themselves not transported inside the cell (cocaine, for example, is a prototypical monoamine transporter inhibitor). Substrates, in contrast, are actively translocated across the plasma membrane into the cytosolic compartment. Substrates (particularly exogenous substrates like amphetamine and phenmetrazine) are also referred to as “releasers,” as the uptake of substrates can provoke *efflux* of cytosolic transmitter molecules via reversal of the symport cycle (for review, see Robertson et al., 2009). Reverse transport by the DAT depends upon the concentration of intracellular Na<sup>+</sup> (Khoshbouei et al., 2003)—which is increased by the sodium influx accompanying uptake of amphetaminergic substrates, thereby promoting dopamine efflux (Sitte et al., 1998). In addition to releasing dopamine by reverse transport, exogenous substrates also inhibit dopamine uptake by competing with dopamine for access to unoccupied DATs. Hence, despite having virtually orthogonal mechanisms of action, both DAT inhibitors and substrates act to increase extracellular dopamine levels.

Owing to their effects on extraneuronal dopamine, it was originally assumed that all DAT-affecting drugs would elicit behavioral effects identical to those of cocaine—that is, they would be readily self-administered, strong psychomotor stimulants with extremely high addictive liability, differing solely in potency (Ritz et al., 1987; Bergman et al., 1989; Cline et al., 1992; Katz et al., 2000). However, a multitude of studies conducted over the past 10-15 years indicate that this notion is incorrect: while certain DAT inhibitors do produce the anticipated cocaine-like behavioral reactions, various ‘atypical’ DAT inhibitors—such as benztropine, modafinil and vanoxerine (GBR12909)—have far milder reinforcing and locomotor stimulant properties, particularly in humans (Søgaard et al., 1990; Carroll et al., 2009; Vosburg et al., 2010). Moreover, exceptionally potent dopamine uptake inhibitors that exhibit no reinforcement efficacy whatsoever in animal models have also been reported, indicating that addictiveness is not a constant property of DAT inhibitors (Desai et al., 2005; Li et al., 2011). Fig. 1 shows a number of examples of both cocaine-like (Fig. 1A) and atypical DAT inhibitors (Fig. 1B). Similar to the demonstration of atypical DAT inhibitors, recent investigation of substrate-like ligands

revealed compounds with unique ‘partial substrate’ properties (Rothman et al., 2012). Like traditional ‘full’ substrates (e.g. amphetamine), partial substrates are translocated by the DAT, but are significantly less effective at inducing reverse transport (DAT-mediated substrate efflux). Examples of compounds that act as either full or partial substrates are given in Figs. 2A and 2B, respectively.

While the categorization of ligands like atypical inhibitors and partial substrates has challenged the notion that DAT ligands are functionally homogeneous, the molecular mechanism underlying this newly discovered heterogeneity is still poorly understood. Recent studies comparing cocaine-like and atypical DAT inhibitors suggest that the behavioral and phenomenological effects of a particular ligand are contingent upon *how* the compound interacts with the transporter. Inhibitors with differing chemical structures exert unique conformational effects on the transporter, stabilizing the protein in different structural states upon binding (Reith et al., 2001; Loland et al., 2008; Schmitt and Reith, 2011) and the nature of these conformational effects, can, in turn, influence an inhibitor’s rewarding effects (Loland et al., 2008; Li et al., 2011). The finding that different DAT ligands induce specific conformational changes—which are somehow differentially transduced by the cell, ultimately eliciting distinct downstream effects—suggests the possibility that NSS proteins exhibit some of the ligand-specific ‘pleiotropic’ functional qualities inherent to G-protein-coupled receptors (reviewed in Urban et al., 2007). In parallel with this insight has come evidence that NSS protein membrane trafficking is dynamically and rapidly regulated by interaction with substrates and other ligands (for review, see Schmitt and Reith, 2010). These findings have led to tacit speculation that NSS proteins can function as both transporters and as receptor-like sensors (‘transceptors’), with respective intra- and extracellular substrate-binding domains serving as real-time detectors of substrate concentration on both sides of the plasma membrane (Taylor, 2009; Kriel et al., 2011). In this review, we discuss the conformation-specific activity of certain DAT ligands, with an emphasis on potential protein/ligand interaction mechanisms. As there is no direct DAT

crystallographic structure available, much of our discussion is based upon the wealth of structural data provided by crystals of prokaryotic NSS family members in various conformations—such as LeuT, a bacterial leucine transporter from *Aquifex aeolicus* (Yamashita et al., 2005)—and subsequent homology models developed from these prokaryotic structures by our laboratory and others.

### **The Conformational Cycle of the NSS Protein Family**

One of the first proposed mechanisms for secondary active transport was the alternating access model of Jardetzky, published nearly a half-century ago. According to this model, for a membrane protein to be capable of electrochemical-coupled active transport, it needed to fulfill three structural requirements: (1) it must contain a cavity in the core of the protein large enough to accommodate a binding site for associated substrate(s), (2) it must be able to adopt two different conformations—in which the substrate-binding cavity is alternatively open to the extracellular space and the cytosolic space, respectively and (3) the substrate-binding cavity must exhibit differing affinities for its cognate ligand(s) when the protein exists in the respective outward- and inward-facing conformations (Jardetzky, 1966). The transition between conformations would be accomplished via a chemical reaction contingent upon substrate binding to the outward-open state. This reaction would then trigger the rearrangement of the transporter, simultaneously closing off external access to the binding site whilst exposing the site to the intracellular milieu. As the affinity of the central binding site for its transported substrate(s) dropped following allosteric re-arrangement of the transporter to the inward-facing state, substrate molecules would naturally dissociate away from the tiny binding cavity into the larger volume of the cytosol by diffusion (due to the binding cavity's diminutive volume, the apparent local concentration of substrate(s) would be many orders of magnitude greater than that of the entire intracellular volume).

Upon elucidation of the prototypical 12TM structure inherent to the NSS superfamily with the crystallization of LeuT, this “exceeding subtle” model has proven to be astoundingly accurate

(Yamashita et al., 2005). Consonant with the alternating access model, the LeuT structure revealed a hydrophobic substrate-binding pocket in the center of the plasma membrane. Residues within partially unwound, flexible regions of TMs 1 and 6 and certain residues of TMs 3 and 8 interact to form this transmembrane cavity, which is large enough to accommodate two Na<sup>+</sup> ions and a variety of different amino acid substrates (Singh et al., 2008). In the original LeuT/leucine crystal, the central substrate-binding pocket (dubbed the S1 site) is protected from both the periplasmic and cytoplasmic space by 'gating' networks—proximal residue side chains that are linked to one another via salt-bridging (joint hydrogen and ion-pair bonding), cation- $\pi$  bonding and aromatic  $\pi$ -stacking interactions (Yamashita et al., 2005). These gating residues are critical for functional substrate translocation and are highly conserved throughout the entire NSS protein family. The gating residue networks move as a group, functioning as intracellular and extracellular lids that occlude the hydrophobic S1 site from water infiltration upon binding of ions and substrate (Nyola et al., 2010; Forrest et al., 2011). Hence, in addition to the two low-energy conformations predicted by Jardetzky (outward-open and inward-open), LeuT revealed a third low-energy state: a dually occluded, substrate-bound intermediate. In the DAT, the extracellular gate is formed by strong hydrogen/ionic interactions (a salt-bridge) between residues Arg85 and Asp476 and a  $\pi$ -cation interaction between Arg85 and the aromatic residue Phe320. In addition, the charged side chain of Asp79 forms a hydrogen bond with the hydroxyl moiety of Tyr156, helping the two aromatic rings of Tyr156 and Phe320 form a lid that obstructs a substrate molecule bound at the S1 site (the LeuT residue corresponding to Asp79 is the neutral Gly24, as the bound substrate leucine provides a necessary charged carboxyl moiety). The composition of the S1 site is exceptionally well conserved amongst the DAT, NET and SERT, suggesting that their respective substrates bind in a similar orientation, with substrate selectivity determined by subtle differences in local hydrophobic/hydrophilic character (Koldsø et al., 2013). The intracellular gate consists of a salt-bridge interaction between Arg60 and



Asp436 and a  $\pi$ -cation interaction between Arg60 and Tyr335, with the side chain of Glu428 helping to stabilize the gate via a hydrogen bond with the hydroxyl group of Tyr335. Fig. 3A depicts the relative configuration of the gating residue networks in the occluded, outward- and inward-facing transporter conformations.

Single-molecule dynamics studies, molecular simulations and subsequent crystals of LeuT in outward-open and inward-open conformations have since hinted at a plausible mechanism for substrate translocation. A schematic demonstrating the conformational cycle of the DAT—based upon the proposed conformational dynamics of LeuT—is presented in Fig. 3B. Starting from an ion/substrate-free (apo) outward-facing state, binding of Na<sup>+</sup> ions promotes a more stabilized outward-facing conformation with a fully open extracellular gate, primed to bind substrate (Claxton et al., 2010; Krishnamurthy and Gouaux, 2012). Subsequent binding of substrate at the S1 site increases the probability of salt-bridge formation between extracellular gating residues, helping to close the extracellular gate. Substrate binding at the S1 site also induces conformational changes in TM helices, particularly TM1, which are propagated to the intracellular gate via a cascade of allosteric interactions, breaking salt bridge and cation- $\pi$  interactions between the cytoplasmic gating residues of TMs 1, 6 and 8 and causing the inner portion of TM1 to flex upward and away from TM6 (Zhao et al., 2010; 2011). Finally, as the transporter completes the shift to an inward-facing state, release of Na<sup>+</sup> ions is promoted by water penetration into the interior vestibule, hydration of the binding sites and ultimately by release of the substrate into the cytosol (Zhao and Noskov, 2011; Zhao et al., 2011). Putative substrate interaction pockets and permeation paths for the DAT modeled in the outward-facing, occluded and inward-facing states are highlighted in Fig. 3A. The complete substrate permeation pathway—rendered as an overlay following superposition of the three respective modeled DAT conformations—is shown in Supplemental Fig. 1. The procedures employed in modeling the different DAT conformations are detailed in the Supplemental Methods.

Since the proposal of the alternating access model, it has traditionally been assumed that NSS proteins possess a single, centrally localized substrate interaction site. However, Javitch and colleagues presented evidence of a novel variation in this mechanism in LeuT (Shi et al., 2008). The authors proposed that binding of a second leucine molecule to a high-affinity allosteric secondary site (termed the S2 site) in the extracellular vestibule of the transporter—located 11 Å above the primary (S1) substrate site (see Supplemental Fig. 1)—helps to trigger the conformational shift from an occluded to an inward-facing state and is required for cytosolic release of Na<sup>+</sup> and leucine from the primary site. The S2 site is rather promiscuous and has been shown to bind compounds from a diverse array of structural classes, including tricyclic antidepressants (Zhou et al., 2007), fluoxetine and other selective SERT inhibitors (Zhou et al., 2009) and alkyl-glucoside detergents (Quick et al., 2009). Tricyclics bind to the S2 site with relatively low (>10 μM) affinity and act as LeuT inhibitors, stabilizing the protein in an occluded conformation nearly identical to the original LeuT/leucine crystal (Zhou et al., 2007). The nature of the S2 site in LeuT and its relevance to NSS protein function is the subject of contentious debate (see *e.g.* Quick et al., 2012 and the rebuttal of Wang and Gouaux, 2012). While molecular simulations and radioligand dissociation assays suggest the presence of a high-affinity secondary site, no crystallographic evidence of LeuT with a substrate-like molecule occupying the S2 site has been found. Our recent investigation of bivalent phenethylamines (novel DAT ligands bearing two substrate-like moieties linked by a flexible polymethylene spacer) show increasing binding potency (up to 82-fold greater than parent monovalent substrates) as the spacer approaches a critical length of roughly 10-12 Å, consonant with the distance separating the S1 and S2 sites in LeuT (Schmitt et al., 2010). Computational modeling of the potent bivalent ligands bound to the DAT indicated simultaneous occupancy of both the S1 and putative S2 sites (see Supplemental Fig. 2). These data support the idea that multiple substrate-interaction sites exist in a single DAT protein; however, they do not enable any

conclusions to be made regarding the affinity of substrates for the S2 site or the purported need for S2 site occupancy to achieve translocation (Shi et al., 2008; Shan et al., 2011).

### **Partial Substrates and Allosteric Modulators: Differential Effects on Uptake Versus Efflux**

Building upon the concepts introduced with the alternating access model of transporter function, one of the earliest explanations of DAT-mediated substrate efflux was the facilitated exchange model (Robertson et al., 2009). According to this model, when an extracellular substrate (e.g. amphetamine) is taken up via the DAT, a cytosolic dopamine molecule can bind to the now inward-facing DAT and ‘hitch a ride’ during reorientation of the transporter to an outward-facing conformation. If the facilitated exchange model is correct, then one might expect that any differences amongst substrates in their ability to induce efflux would be strictly determined by their uptake kinetics: that is, uptake and efflux would be expected to co-vary directly. However, more recent studies suggest that uptake and efflux of substrates are two mechanistically distinct processes that can be differentially regulated. During a previous chemical library screen for potential NSS ligands, we found several 4-quinazolinamine derivatives (see Fig. 2C for structures) that bind to the DAT with moderate (1-5  $\mu\text{M}$ ) affinity and exhibit a novel mechanism of action as DAT ligands: partial allosteric modulation of transporter function (Pariser et al., 2008; Rothman et al., 2009). Each of the 4-quinazolinamine ligands (SoRI-9084, SoRI-20040 and SoRI-20041) inhibited the binding of the phenyltropane radioligand [ $^{125}\text{I}$ ] $\beta$ -CIT; however, none of the SoRI ligands exhibited a classical dose-dependent competitive binding profile. At equilibrium, a sufficient concentration of a competitive DAT inhibitor (such as cocaine) will block virtually 100% of the binding of another competitive inhibitor (in this case, [ $^{125}\text{I}$ ] $\beta$ -CIT), yet each of the SoRI compounds showed a ceiling in their ability to inhibit [ $^{125}\text{I}$ ] $\beta$ -CIT binding to the DAT, with maximum efficacy ( $E_{\text{max}}$ ) ranging from 40-60%. The allosteric modulators increased the  $K_{\text{D}}$  value and decreased the  $B_{\text{max}}$  value for [ $^{125}\text{I}$ ] $\beta$ -CIT binding and also slowed the dissociation rate of prebound [ $^{125}\text{I}$ ] $\beta$ -CIT, further suggesting that

these ligands do not compete for the same binding site as  $\beta$ -CIT (Pariser et al., 2008). In addition, each of the compounds inhibited uptake of [ $^3$ H]DA by the DAT, but with a similar asymptotic ceiling in their effect (unlike competitive inhibitors, which produce complete inhibition of uptake). Perhaps most importantly, while two of the quinazolinamine modulators (SoRI-9804 and SoRI-20040) partially inhibited *both* uptake of [ $^3$ H]DA (forward transport) and DAT-mediated release of preloaded [ $^3$ H]DA (reverse transport), the third compound (SoRI-20041) similarly inhibited substrate uptake, but had no appreciable effect on efflux (Rothman et al., 2009). This compound is the first DAT ligand that has been shown to differentially affect substrate uptake versus release, indicating that the two functional modes of substrate translocation are unique and that it is possible to design compounds that selectively affect a single part of the NSS translocation cycle. In addition, SoRI-20041 and the other 4-quinazolinamine ligands demonstrate that DAT activity can be partially modulated in a non-competitive, saturable (*i.e.* allosteric) and functionally selective manner, akin to a G-protein-coupled receptor.

The fascinating finding that SoRI-20041 partially inhibits [ $^3$ H]DA uptake primarily via a decrease in the maximal uptake rate ( $V_{max}$ )—but does not alter amphetamine-induced, DAT-mediated efflux of either [ $^3$ H]DA or [ $^3$ H]MPP<sup>+</sup>—suggests that SoRI-20041 influences DAT function via an allosteric binding site distinct from the canonical S1 substrate site. One can speculate that SoRI-20041 subtly alters the conformation of the DAT such that inward transport of substrate is impaired, but outward efflux of substrate is not. At the present time, it is not possible to define how SoRI-20041 does this on a molecular level. However, it seems likely that SoRI-20041 could prove to be a useful tool for further research into the alternating access model and the impact that auxiliary binding sites (such as the putative S2 site discussed above) have on forward and reverse substrate translocation. The ability of these partial allosteric modulators to decrease the affinity and maximal binding potential of cocaine-like phenyltropane stimulants via interaction with an orthogonal binding site also suggests that such compounds could serve as worthwhile leads for designing cocaine addiction therapeutics.

Another line of evidence for the selective modulation of reverse transport comes from our recent report that different DAT substrates can have variable efficacies for inducing DAT-mediated efflux of the labeled substrate [<sup>3</sup>H]MPP<sup>+</sup>. For example, whereas the full substrate naphthylaminopropane (NAP, the (2-naphthyl)-analogue of amphetamine, also known as PAL-278; see Fig. 2A for structure) produced complete efflux of preloaded [<sup>3</sup>H]MPP<sup>+</sup> from rat synaptosomes within 30 minutes ( $E_{\max} \approx 100\%$ ), *N*-ethyl-naphthylaminopropane (ENAP, also known as PAL-1045; see Fig. 2B) was unable to elicit complete [<sup>3</sup>H]MPP<sup>+</sup> release within the experimental time window (efflux reached a plateau, with  $E_{\max} = 78\%$ ). Similarly, while the empathogen 3,4-methylenedioxyamphetamine (MDA) is a full DAT substrate (Rothman et al., 2009), the ethyl analogue 3,4-methylenedioxy-*N*-ethylamphetamine (MDEA) behaved as a partial substrate, with an  $E_{\max}$  value of roughly 65%. Importantly, the plateau in transporter-mediated [<sup>3</sup>H]MPP<sup>+</sup> efflux was insurmountable; merely increasing the concentration of a partial substrate did not produce complete release. In addition, the attenuated response observed for partial substrates in [<sup>3</sup>H]MPP<sup>+</sup> release assays was also demonstrated *in vivo*: whereas NAP produced clear dose-dependent increases in locomotor stimulation and extraneuronal DA levels in rats, ENAP showed a flat dose-response curve (Rothman et al., 2012). However, the question of whether or not the attenuated monoamine-releasing effect of partial substrates like ENAP is genuinely consequential *in vivo* will require further tests of such compounds in relevant behavioral assays such as self-administration, drug discrimination and conditioned place preference.

Although the molecular mechanisms that might explain the observation of partial release remain enigmatic, the DAT-mediated [<sup>3</sup>H]MPP<sup>+</sup> efflux experiments do provide some critical information. In particular, partial DAT substrates—such as ENAP (PAL-1045)—stimulate efflux at a slower rate than full DAT substrates such as amphetamine. One possible interpretation of these findings is that partial substrates are less effective at promoting the conformational changes in the DAT protein required for the overall process of alternating exchange. This would

result in an overall slower turnover rate of the exchange process, a slowed efflux of [<sup>3</sup>H]MPP<sup>+</sup> and a lower efficacy in the release assay during the typical 30 minute time course. It should also be noted that the existence of partial substrates is not limited to the DAT, as both SERT and NET partial substrates were identified as well (Rothman et al., 2012).

### **Atypical Uptake Inhibitors: Conformation-Specific Binding Mechanisms**

There is ample evidence that different classes of DAT inhibitors preferentially bind to (or induce upon binding) distinct transporter conformational states and such conformation-specific activity has been recently posited to affect the addictive liability of a given ligand (Loland et al., 2008). Conformation-specific DAT interaction was first suggested by the finding that cocaine and benztropine differentially affect the vulnerability of extracellular-facing DAT cysteine residues towards reaction with membrane impermeant sulfhydryl reducing reagents—indicating that these inhibitors stabilize different transporter conformations (Reith et al., 2001). Similarly, binding of cocaine-like compounds was shown to protect DAT transmembrane arginine residues from covalent reaction with phenylglyoxal, whereas benztropine-like compounds failed to impact phenylglyoxal reactivity (Volz et al., 2004). Whole-cell binding studies performed in the presence of Zn<sup>2+</sup> (a DAT modulator that loosely binds the extracellular face of the transporter, stabilizing an outward-facing conformation), or in the absence of extracellular Na<sup>+</sup> (which increases the relative number of inward-facing DATs) further hint at specific conformational effects that vary depending upon the structure of the bound inhibitor (Loland et al., 2002; Schmitt and Reith, 2011). For example, the affinity of cocaine-like inhibitors for displacement of [<sup>3</sup>H]β-CFT binding is strongly decreased in the wake of extracellular Na<sup>+</sup>-depletion, but binding of GBR12909, modafinil and JHW007 (Fig. 1B) is only nominally impacted (and binding of 3α-benzoyloxytropine is actually *increased*). This suggests that unlike cocaine-like ligands, atypical ligands do not require an outward-facing transporter in order to bind (Kopajtic et al., 2010; Schmitt and Reith, 2011).

In order to more easily screen the conformational binding preference of various ligands, investigators have employed mutagenesis to create DAT mutants with altered conformational equilibrium. For instance, we found that mutation of certain residues in the extracellular vestibule—either Trp84 to leucine or Asp313 to asparagine (W84L and D313N, respectively)—interferes with the DAT's transition between conformational states, biasing the transporter toward an outward-facing conformation (Chen et al., 2001; 2004). As these mutations promote an open-to-out DAT state, a compound's WT/mutant binding ratio can indicate whether the compound preferentially interacts with a more open, outward-facing conformation or a more closed (inward-facing or occluded) conformation. Each of these mutations considerably increased the affinity of cocaine and related 3 $\beta$ -aryltropanes, as well as the classical DAT inhibitor methylphenidate (Fig. 1A). However, the mutations displayed negligible or opposite effects on the binding affinity of benztropine, GBR12909, bupropion, modafinil and 3 $\alpha$ -benzoyloxytropane (Fig. 1B), as well as DAT substrates like dopamine and amphetamine (Schmitt et al., 2008; 2010). Loland and colleagues have also utilized a conformationally biased mutant DAT—in which the intracellular gating network residue Tyr335 was mutated to alanine (Y335A)—in order to investigate the relationship between inhibitor binding mechanism and cocaine-like effects (Loland et al., 2008). By disrupting a critical  $\pi$ -cation interaction needed for closure of the cytoplasmic gate, the Y335A mutation gives rise to a predominantly inward-facing transporter (Kniazeff et al., 2008). In the Y335A mutant, binding of cocaine-like compounds was essentially ablated; but binding of benztropine, JHW007 and modafinil was less impacted, giving further credence to the idea that benztropine-like atypical inhibitors preferentially interact with the inward-facing conformational state of the DAT (Loland et al., 2008; 2012). Notably, compounds that exhibited a cocaine-like loss of binding at the Y335A mutant more readily substituted for cocaine in rat drug discrimination tests and were more potent locomotor

stimulants in mice, demonstrating a correlation between conformational preference and cocaine-like behavioral effects.

It is worth noting, however, that additional factors (other than DAT conformational selectivity) may underlie the reduced cocaine-like effects observed in behavioral tests of certain atypical DAT inhibitors. One factor thought to impact the rewarding efficacy of a given psychostimulant is the rate at which the compound enters the brain and interacts with the DAT—compounds with a rapid onset of action tend to exhibit greater addictive potential than those with a slower onset rate (Wee et al., 2006). Even cocaine itself was found to have lower reinforcing efficacy in a primate progressive-ratio self administration paradigm when injected over a period of 10 minutes as opposed to a period of 10 seconds (Woolverton and Wang, 2004). It has thus been argued, for example, that the relatively slow DAT association kinetics observed for the benztropine-derived atypical inhibitor JHW007 is responsible for its lack of cocaine-like behavioral effects (Desai et al., 2005). However, a recent study of newer benztropine analogs that do not induce cocaine-like place preference or locomotor stimulation, but also have rapid onset rates, suggests that onset rate is not the sole determinant of a ligand's behavioral profile (Li et al., 2011).

In addition to kinetic differences, another theory proposed for the differential effects of cocaine-like and atypical DAT inhibitors is that atypical inhibitors engender few cocaine-like behavioral responses not because of their unique DAT binding profile, but instead due to interaction with additional targets other than the DAT. For example, antagonism of neuronal  $\sigma$  receptors is thought to contribute to the activity of the atypical DAT ligand rimcazole in reducing cocaine-induced locomotion and self-administration, with sigmaergic inhibition proposed to blunt potential locomotor stimulant effects mediated by DAT inhibition (Hiranita et al., 2011). In another case, the DAT-selective phenyltropane RTI-371 (3 $\beta$ -(4-methylphenyl)-2 $\beta$ -[3-(4-chlorophenyl)isoxazol-5-yl]tropane)—which, unlike most 3 $\beta$ -phenyltropanes, does not promote



locomotor stimulation—was found to be a positive allosteric modulator of the cannabinoid CB<sub>1</sub> receptor (Navarro et al., 2009). As CB<sub>1</sub> receptor agonists tend to decrease locomotor activity, it is possible that this potentiation of cannabinoid activity contributes to the lack of locomotor stimulation seen with some atypical DAT ligands.

### **Conclusions: Molecular Mechanisms of Action for Atypical DAT Ligands**

The structural basis of the differential interaction of cocaine-like and atypical DAT inhibitors is currently unknown, as is the molecular mechanism of more exotic ligands, such as the newly discovered 4-quinazolinamine-based allosteric modulators and 'partial substrate' monoamine releasers. The response that a given ligand has towards certain conformationally biasing mutations and ionic conditions offers some insight, but not specific structural information. Molecular modeling studies suggest that cocaine,  $\beta$ -CFT and methylphenidate promote an outward-facing conformation by breaking a critical hydrogen bond between the side chains of DAT residues Asp79 and Tyr156 (demonstrated in Supplemental Fig. 3A), impeding closure of the extracellular gating network and preventing the transporter from transitioning from an open-to-out state to an occluded state (Beuming et al., 2008; Schmitt and Reith, 2011). By contrast, binding models for the atypical inhibitors benztropine, modafinil and bupropion, as well as the substrates dopamine, amphetamine and 3,4-methylenedioxy-*N*-methylamphetamine (MDMA) reveal a preserved Asp79-Tyr156 bond (see Supplemental Fig. 3B), indicating that these ligands do not prevent the DAT from transitioning to an occluded conformation (Bisgaard et al., 2011; Schmitt and Reith, 2011). The fact that atypical inhibitors facilitate a closed-to-out state implies that they affect the transporter conformation in a manner more akin to substrates than to cocaine-like ligands, but unlike true substrates are not translocated into the intracellular milieu.

While our DAT modeling studies indicate that atypical ligands like modafinil and GBR12909 stabilize an occluded transporter state, the biochemical studies do not allow us to discriminate between an occluded or a more inward-facing state. It is conceivable that certain DAT ligands stabilize a true inward-facing state by interacting with a cytosol-accessible binding pocket (see

Supplemental Fig. 1). There is evidence that the psychedelic-like polycyclic tryptamine ibogaine acts in this manner at both the SERT and DAT, stabilizing an open-to-in, cytoplasmic-facing state of the transporter (Jacobs et al., 2007; Bulling et al., 2012). Interestingly, the recent crystallization of another 12TM prokaryotic membrane transporter protein—the L-carnitine/ $\gamma$ -butyrobetaine exchanger CaiT—indicated substrate interaction with three distinct binding domains: one in the center of the protein, one in the extracellular vestibule (akin to the S1 and S2 sites, respectively) and another located at the base of the *intracellular* vestibule, approximately 6 Å below the S1 site, directed towards the cytosol (Tang et al., 2010). The presence of such a site has led to speculation that NSS proteins possess a symmetrical intracellular secondary substrate site—that is, an “S3 site” (highlighted in Supplemental Fig. 1). Demonstration of an intracellular S3 site might help unravel the mechanism underlying the differences between substrates in their efficacy as releasers. For example, partial substrate ligands such as ENAP and MDEA may dissociate from the cytosolic S3 site at a slower rate than full substrates like amphetamine and NAP. Ibogaine itself could also be hypothesized to act as a SERT/DAT partial substrate—albeit one that is translocated so slowly that it effectively functions as an uptake inhibitor upon interaction with the transporter protein.

It is possible that altering the conformation of the DAT in different manners can trigger different downstream cellular signaling events. In this case, binding of particular ligand increases the probability that the transporter will adopt a given conformation and that ligand-specific conformation would then be transduced via DAT interaction partners and associated scaffolding proteins. The second-messaging cascades downstream of the DAT have not been completely elaborated at this time, but a vast array of DAT-interacting proteins has been detected (Eriksen et al., 2010; Hadlock et al., 2011). DAT interaction partners include membrane scaffolding and trafficking proteins, cytosolic kinases, phosphatases and other signaling proteins, G-protein-coupled receptors and receptor tyrosine kinases. These interaction partners are capable of altering surface DAT levels in real time and can even

selectively modulate particular DAT functions, such as reverse transport (reviewed in Eriksen et al., 2010). Further study of ligands with conformation-specific activity—including effects on putative signaling proteins downstream of the DAT—will help reveal the nature of the ‘transceptor’ function of NSS proteins and could also lead to improved medications for depression, ADHD, cocaine addiction and other monoamine-linked disorders.

### **Authorship Contributions**

*Wrote or contributed to the writing of the manuscript:* Schmitt, Reith, Rothman

Additional figures and a summary of computational methods are available online as Supplemental Materials.

## References

- Bergman J, Madras BK, Johnson SE and Spealman RD (1989) Effects of cocaine and related drugs in nonhuman primates. III. Self-administration by squirrel monkeys. *J Pharmacol Exp Ther* **251**:150–155.
- Beuming T, Kniazeff J, Bergmann ML, Shi L, Gracia L, Raniszewska K, Newman AH, Javitch JA, Weinstein H, Gether U, et al. (2008) The binding sites for cocaine and dopamine in the dopamine transporter overlap. *Nat Neurosci* **11**:780–789.
- Bisgaard H, Larsen MAB, Mazier S, Beuming T, Newman AH, Weinstein H, Shi L, Loland CJ, and Gether U (2011) The binding sites for benzotropines and dopamine in the dopamine transporter overlap. *Neuropharmacology* **60**:182–190.
- Bulling S, Schicker K, Zhang YW, Steinkellner T, Stockner T, Gruber CW, Boehm S, Freissmuth M, Rudnick G, Sitte HH, et al. (2012) The mechanistic basis for noncompetitive ibogaine inhibition of serotonin and dopamine transporters. *J Biol Chem* **287**:18524–18534.
- Carroll FI, Blough BE, Abraham P, Mills AC, Holleman JA, Wolckenhauer SA, Decker AM, Landavazo A, McElroy KT, Navarro HA, et al. (2009) Synthesis and biological evaluation of bupropion analogues as potential pharmacotherapies for cocaine addiction. *J Med Chem* **52**:6768–6781.
- Chen N, Vaughan RA, and Reith ME (2001) The role of conserved tryptophan and acidic residues in the human dopamine transporter as characterized by site-directed mutagenesis. *J Neurochem* **77**:1116–1127.
- Chen N, Zhen J, and Reith MEA (2004) Mutation of Trp84 and Asp313 of the dopamine transporter reveals similar mode of binding interaction for GBR12909 and benzotropine as opposed to cocaine. *J Neurochem* **89**:853–864.
- Claxton DP, Quick M, Shi L, de Carvalho FD, Weinstein H, Javitch JA, and Mchaourab HS (2010) Ion/substrate-dependent conformational dynamics of a bacterial homolog of neurotransmitter:sodium symporters. *Nat Struct Mol Biol* **17**:822–829.
- Cline E, Scheffel U, Boja JW, Carroll FI, Katz JL and Kuhar MJ (1992) Behavioral effects of novel cocaine analogs: a comparison with in vivo receptor binding potency. *J Pharmacol Exp Ther* **260**:1174–1179.
- Desai RI, Kopajtic TA, Koffarnus M, Newman AH, and Katz JL (2005) Identification of a dopamine transporter ligand that blocks the stimulant effects of cocaine. *J Neurosci* **25**:1889–1893.
- Eriksen J, Jørgensen TN, and Gether U (2010) Regulation of dopamine transporter function by protein-protein interactions: new discoveries and methodological challenges. *J Neurochem* **113**:27–41.
- Felten A, Montag C, Markett S, Walter NT, and Reuter M (2011) Genetically determined dopamine availability predicts disposition for depression. *Brain Behav* **1**:109–118.
- Forrest LR, Krämer R, and Ziegler C (2011) The structural basis of secondary active transport

- mechanisms. *Biochim Biophys Acta* **1807**:167–188.
- Gainetdinov RR and Caron MG (2003) Monoamine transporters: from genes to behavior. *Annu Rev Pharmacol Toxicol* **43**:261–284.
- Gether U, Andersen PH, Larsson OM, and Schousboe A (2006) Neurotransmitter transporters: molecular function of important drug targets. *Trends Pharmacol Sci* **27**:375–383.
- Greengard P (2001) The neurobiology of slow synaptic transmission. *Science* **294**:1024–1030.
- Hadlock GC, Nelson CC, Baucum AJ, Hanson GR, and Fleckenstein AE (2011) Ex vivo identification of protein-protein interactions involving the dopamine transporter. *J Neurosci Meth* **196**:303–307.
- Hiranita T, Soto PL, Kohut SJ, Kopajtic T, Cao J, Newman AH, Tanda G, and Katz JL (2011) Decreases in cocaine self-administration with dual inhibition of the dopamine transporter and  $\sigma$  receptors. *J Pharmacol Exp Ther* **339**:662–677.
- Jacobs MT, Zhang YW, Campbell SD, and Rudnick G (2007) Ibogaine, a noncompetitive inhibitor of serotonin transport, acts by stabilizing the cytoplasm-facing state of the transporter. *J Biol Chem* **282**:29441–29447.
- Jardetzky O (1966) Simple allosteric model for membrane pumps. *Nature* **211**:969–970.
- Katz JL, Izenwasser S, and Terry P (2000) Relationships among dopamine transporter affinities and cocaine-like discriminative-stimulus effects. *Psychopharmacology* **148**:90–98.
- Khoshbouei H, Wang H, Lechleiter JD, Javitch JA, and Galli A (2003) Amphetamine-induced dopamine efflux. A voltage-sensitive and intracellular  $\text{Na}^+$ -dependent mechanism. *J Biol Chem* **278**:12070–12077.
- Kniazeff J, Shi L, Loland CJ, Javitch JA, Weinstein H, and Gether U (2008) An intracellular interaction network regulates conformational transitions in the dopamine transporter. *J Biol Chem* **283**:17691–17701.
- Koldsø H, Christiansen AB, Sinning S, and Schiøtt B (2013) Comparative modeling of the human monoamine transporters: similarities in substrate binding. *ACS Chem Neurosci* **4**:295–309.
- Kopajtic TA, Liu Y, Surratt CK, Donovan DM, Newman AH, and Katz JL (2010) Dopamine transporter-dependent and -independent striatal binding of the benzotropine analog JHW007, a cocaine antagonist with low abuse liability. *J Pharmacol Exp Ther* **335**:703–714.
- Kriel J, Haesendonckx S, Rubio-Teixeira M, Van Zeebroeck G, and Thevelein JM (2011) From transporter to transceptor: signaling from transporters provokes re-evaluation of complex trafficking and regulatory controls: endocytic internalization and intracellular trafficking of nutrient transceptors may, at least in part, be governed by their signaling function. *Bioessays* **33**:870–879.
- Krishnamurthy H and Gouaux E (2012) X-ray structures of LeuT in substrate-free outward-open and apo inward-open states. *Nature* **481**:469–474.

- Kurian MA, Li Y, Zhen J, Meyer E, Hai N, Christen HJ, Hoffmann GF, Jardine P, von Moers A, Mordekar SR, et al. (2011) Clinical and molecular characterisation of hereditary dopamine transporter deficiency syndrome: an observational cohort and experimental study. *Lancet Neurol* **10**:54–62.
- Li SM, Kopajtic TA, O'Callaghan MJ, Agoston GE, Cao J, Newman AH, and Katz JL (2011) N-substituted bupropion analogs: selective dopamine transporter ligands with a fast onset of action and minimal cocaine-like behavioral effects. *J Pharmacol Exp Ther* **336**:575–585.
- Loland CJ, Desai RI, Zou MF, Cao J, Grundt P, Gerstbrein K, Sitte HH, Newman AH, Katz JL, and Gether U (2008) Relationship between conformational changes in the dopamine transporter and cocaine-like subjective effects of uptake inhibitors. *Molecular Pharmacol* **73**:813–823.
- Loland CJ, Mereu M, Okunola OM, Cao J, Prisinzano TE, Mazier S, Kopajtic T, Shi L, Katz JL, Tanda G, et al. (2012) R-modafinil (armodafinil): a unique dopamine uptake inhibitor and potential medication for psychostimulant abuse. *Biol Psychiatry* **72**:405–413.
- Loland CJ, Norregaard L, Litman T, and Gether U (2002) Generation of an activating Zn<sup>2+</sup> switch in the dopamine transporter: mutation of an intracellular tyrosine constitutively alters the conformational equilibrium of the transport cycle. *Proc Natl Acad Sci* **99**:1683–1688.
- Montague PR and Berns GS (2002) Neural economics and the biological substrates of valuation. *Neuron* **36**:265–284.
- Navarro HA, Howard JL, Pollard GT, and Carroll FI (2009) Positive allosteric modulation of the human cannabinoid (CB) receptor by RTI-371, a selective inhibitor of the dopamine transporter. *Br J Pharmacol* **156**:1178–1184.
- Nyola A, Karpowich NK, Zhen J, Marden J, Reith ME, and Wang DN (2010) Substrate and drug binding sites in LeuT. *Curr Opin Struct Biol* **20**:415–422.
- Pariser JJ, Partilla JS, Dersch CM, Ananthan S, and Rothman RB (2008) Studies of the biogenic amine transporters. 12. Identification of novel partial inhibitors of amphetamine-induced dopamine release. *J Pharmacol Exp Ther* **326**:286–295.
- Quick M, Shi L, Zehnpfennig B, Weinstein H, and Javitch JA (2012) Experimental conditions can obscure the second high-affinity site in LeuT. *Nat Struct Mol Biol* **19**:207–211.
- Quick M, Winther AML, Shi L, Nissen P, Weinstein H, and Javitch JA (2009) Binding of an octylglucoside detergent molecule in the second substrate (S2) site of LeuT establishes an inhibitor-bound conformation. *Proc Natl Acad Sci* **106**:5563–5568.
- Reith ME, Berfield JL, Wang LC, Ferrer JV, and Javitch JA (2001) The uptake inhibitors cocaine and bupropion differentially alter the conformation of the human dopamine transporter. *J Biol Chem* **276**:29012–29018.
- Ritz MC, Lamb RJ, Goldberg SR, and Kuhar MJ (1987) Cocaine receptors on dopamine transporters are related to self-administration of cocaine. *Science* **237**:1219–1223.
- Robertson SD, Matthies HJG, and Galli A (2009) A closer look at amphetamine-induced reverse

transport and trafficking of the dopamine and norepinephrine transporters. *Mol Neurobiol* **39**:73–80.

- Rothman RB, Dersch CM, Ananthan S, and Partilla JS (2009) Studies of the biogenic amine transporters. 13. Identification of "agonist" and "antagonist" allosteric modulators of amphetamine-induced dopamine release. *J Pharmacol Exp Ther* **329**:718–728.
- Rothman RB, Partilla JS, Baumann MH, Lightfoot-Siordia C, and Blough BE (2012) Studies of the Biogenic Amine Transporters. 14. Identification of Low Efficacy "Partial" Substrates for the Biogenic Amine Transporters. *J Pharmacol Exp Ther* **341**:251–262.
- Salamone JD, Correa M, Farrar AM, Nunes EJ, and Pardo M (2009) Dopamine, behavioral economics, and effort. *Front Behav Neurosci* **3**:13.
- Schmitt KC, Mamidyala S, Biswas S, Dutta AK, and Reith MEA (2010) Bivalent phenethylamines as novel dopamine transporter inhibitors: evidence for multiple substrate-binding sites in a single transporter. *J Neurochem* **112**:1605–1618.
- Schmitt KC and Reith MEA (2010) Regulation of the dopamine transporter: aspects relevant to psychostimulant drugs of abuse. *Ann NY Acad Sci* **1187**:316–340.
- Schmitt KC and Reith MEA (2011) The Atypical Stimulant and Nootropic Modafinil Interacts with the Dopamine Transporter in a Different Manner than Classical Cocaine-Like Inhibitors. *PLoS ONE* **6**:e25790.
- Schmitt KC, Zhen J, Kharkar P, Mishra M, Chen N, Dutta AK, and Reith MEA (2008) Interaction of cocaine-, benztropine-, and GBR12909-like compounds with wild-type and mutant human dopamine transporters: molecular features that differentially determine antagonist-binding properties. *J Neurochem* **107**:928–940.
- Shan J, Javitch JA, Shi L, and Weinstein H (2011) The substrate-driven transition to an inward-facing conformation in the functional mechanism of the dopamine transporter. *PLoS ONE* **6**:e16350.
- Shi L, Quick M, Zhao Y, Weinstein H, and Javitch JA (2008) The mechanism of a neurotransmitter sodium symporter—inward release of Na<sup>+</sup> and substrate is triggered by substrate in a second binding site. *Mol Cell* **30**:667–677.
- Singh SK, Piscitelli CL, Yamashita A, and Gouaux E (2008) A competitive inhibitor traps LeuT in an open-to-out conformation. *Science* **322**:1655–1661.
- Sitte HH, Huck S, Reither H, Boehm S, Singer EA, and Pifl C (1998) Carrier-mediated release, transport rates, and charge transfer induced by amphetamine, tyramine, and dopamine in mammalian cells transfected with the human dopamine transporter. *J Neurochem* **71**:1289–1297.
- Søgaard U, Michalow J, Butler B, Lund Laursen A, Ingersen SH, Skrumsager BK, and Rafaelsen OJ (1990) A tolerance study of single and multiple dosing of the selective dopamine uptake inhibitor GBR12909 in healthy subjects. *Int Clinical Psychopharmacol* **5**:237–251.

- Tang L, Bai L, Wang WH, and Jiang T (2010) Crystal structure of the carnitine transporter and insights into the antiport mechanism. *Nat Struct Mol Biol* **17**:492–496.
- Taylor PM (2009) Amino acid transporters: éminences grises of nutrient signalling mechanisms? *Biochem Soc Trans* **37**:237–241.
- Urban JD, Clarke WP, Zastrow von M, Nichols DE, Kobilka B, Weinstein H, Javitch JA, Roth BL, Christopoulos A, Sexton PM, et al. (2007) Functional selectivity and classical concepts of quantitative pharmacology. *J Pharmacol Exp Ther* **320**:1–13.
- Volz TJ, Kim M, and Schenk JO (2004) Covalent and noncovalent chemical modifications of arginine residues decrease dopamine transporter activity. *Synapse* **52**:272–282.
- Vosburg SK, Hart CL, Haney M, Rubin E, and Foltin RW (2010) Modafinil does not serve as a reinforcer in cocaine abusers. *Drug and Alcohol Dependence* **106**:233–236.
- Wang H and Gouaux E (2012) Substrate binds in the S1 site of the F253A mutant of LeuT, a neurotransmitter sodium symporter homologue. *EMBO Rep* **13**:861–866.
- Wee S, Carroll FI, and Woolverton WL (2006) A reduced rate of in vivo dopamine transporter binding is associated with lower relative reinforcing efficacy of stimulants. *Neuropsychopharmacology* **31**:351–362.
- Woolverton WL and Wang Z (2004) Relationship between injection duration, transporter occupancy and reinforcing strength of cocaine. *Eur J Pharmacol* **486**:251–257.
- Yamashita A, Singh SK, Kawate T, Jin Y, and Gouaux E (2005) Crystal structure of a bacterial homologue of Na<sup>+</sup>/Cl<sup>-</sup>-dependent neurotransmitter transporters. *Nature* **437**:215–223.
- Zhao C and Noskov SY (2011) The role of local hydration and hydrogen-bonding dynamics in ion and solute release from ion-coupled secondary transporters. *Biochemistry* **50**:1848–1856.
- Zhao Y, Terry D, Shi L, Weinstein H, Blanchard SC, and Javitch JA (2010) Single-molecule dynamics of gating in a neurotransmitter transporter homologue. *Nature* **465**:188–193.
- Zhao Y, Terry DS, Shi L, Quick M, Weinstein H, Blanchard SC, and Javitch JA (2011) Substrate-modulated gating dynamics in a Na<sup>+</sup>-coupled neurotransmitter transporter homologue. *Nature* **474**:109–113.
- Zhou Z, Zhen J, Karpowich NK, Goetz RM, Law CJ, Reith MEA, and Wang DN (2007) LeuT-desipramine structure reveals how antidepressants block neurotransmitter reuptake. *Science* **317**:1390–1393.
- Zhou Z, Zhen J, Karpowich NK, Law CJ, Reith MEA, and Wang DN (2009) Antidepressant specificity of serotonin transporter suggested by three LeuT-SSRI structures. *Nat Struct Mol Biol* **16**:652–657.



**Footnotes (Financial Support)**

\* This work was supported by the National Institutes of Health, National Institute on Drug Abuse [Grant R01 DA019676], National Institute on Mental Health [Grant R01 MH083840] and by the Intramural Research Program of NIDA, NIH, Baltimore, MD 21224.

## Legends to Figures

**Fig. 1.** Chemical structures of example cocaine-like and atypical DAT inhibitors. Whereas classical cocaine-like DAT inhibitors (*A*) stabilize an open-to-out transporter conformation, atypical inhibitors (*B*) stabilize a more inward-facing (closed-to-out) conformational state.

**Fig. 2.** Chemical structures of various DAT ligands that act as either substrates/releasers (*A* and *B*) or partial allosteric modulators (*C*). *A*, traditional DAT substrates, which exhibit full maximal efficacy in promoting monoamine release via DAT-mediated efflux (reverse transport). *B*, recently characterized “partial” DAT substrates, which promote DAT-mediated efflux at a slower rate than full substrates, giving them a lower efficacy ceiling as monoamine releasers. *C*, novel 4-quinazolinamine compounds that partially inhibit both [<sup>125</sup>I]β-CIT binding and dopamine uptake in a non-competitive and saturable manner, indicative of an allosteric modulatory effect. Of the 4-quinazolinamines, SoRI-20041 is unique in that affects substrate uptake without impacting efflux, demonstrating that it is possible to design functionally selective DAT modulators.

**Fig. 3.** *A*, computational models of the DAT, demonstrating the configuration of the extra- and intracellular gating networks and the substrate permeation pore in the open-to-out, occluded and open-to-in conformational states. Formation and disruption of salt bridges and π-cation interactions between residues in the two gating networks (labeled and rendered as highlighted yellow sticks) underlies the “alternating access” translocation mechanism. As the gates are reciprocally opened and closed, the respective periplasmic and cytoplasmic substrate permeation pores (rendered as a translucent molecular surface, with hydrophobic regions in green, polar regions in purple and solvent-exposed regions in red) grow significantly, facilitating water infiltration and diffusion of the substrate. *B*, an illustration of the putative substrate

translocation cycle for the DAT protein. In the absence of bound ions or ligands, the transporter protein exists in dynamic flux between outward- and inward-facing states. Binding of Na<sup>+</sup> at the S1 site stabilizes a fully outward-facing conformation with an open extracellular gate, primed to bind substrate molecules. Substrate binding at the S1 site induces closure of the extracellular gate, establishing an occluded conformation (closed-to-out). It has been suggested that interaction of a second substrate molecule with the S2 site helps facilitate opening of the intracellular gating network, giving rise to a fully inward-facing (open-to-in) conformation capable of releasing the S1-bound substrate and ions; however, no crystallographic evidence for simultaneous interaction of two substrate molecules with an NSS protein has been found.

Figure 1.

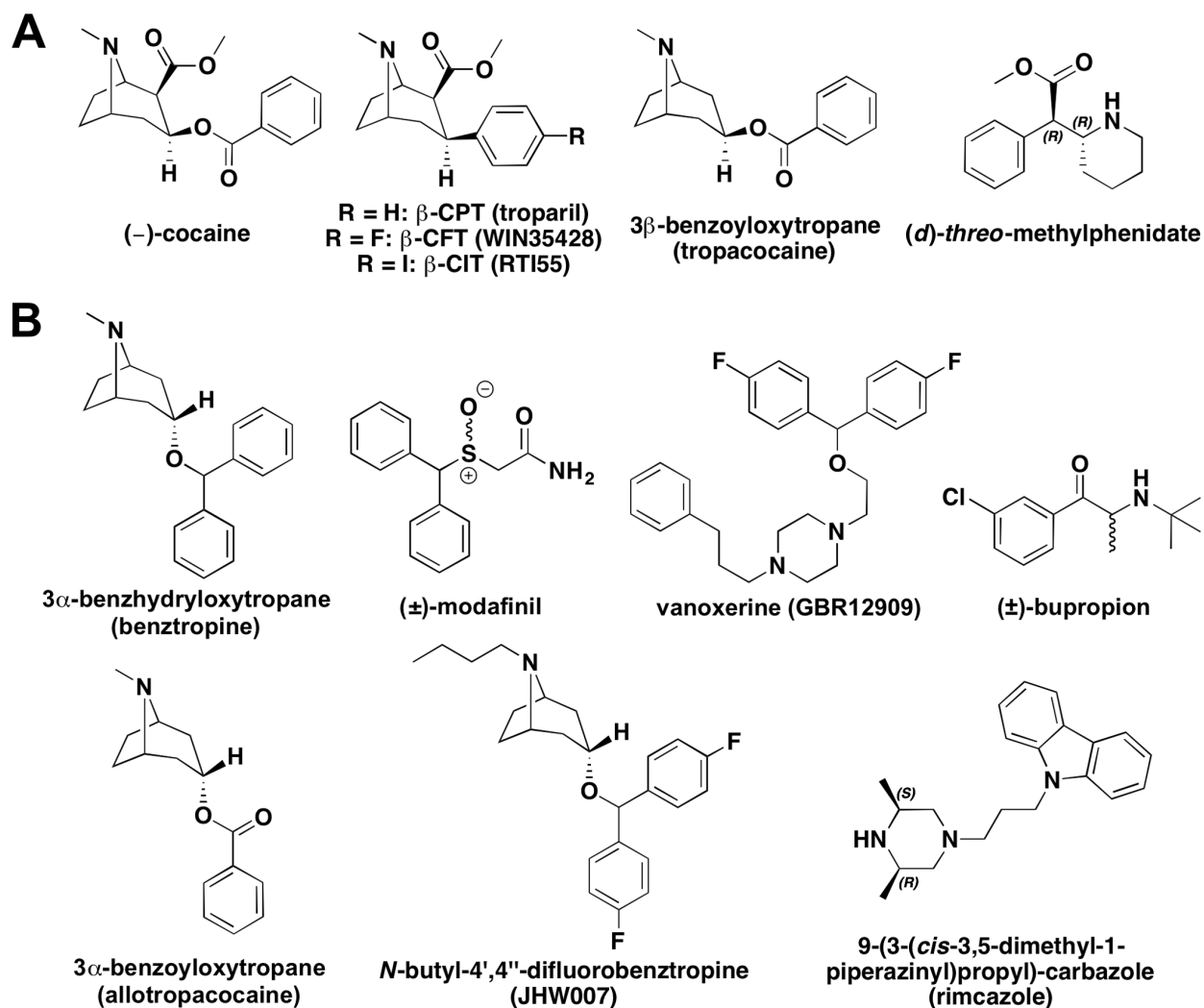


Figure 2.

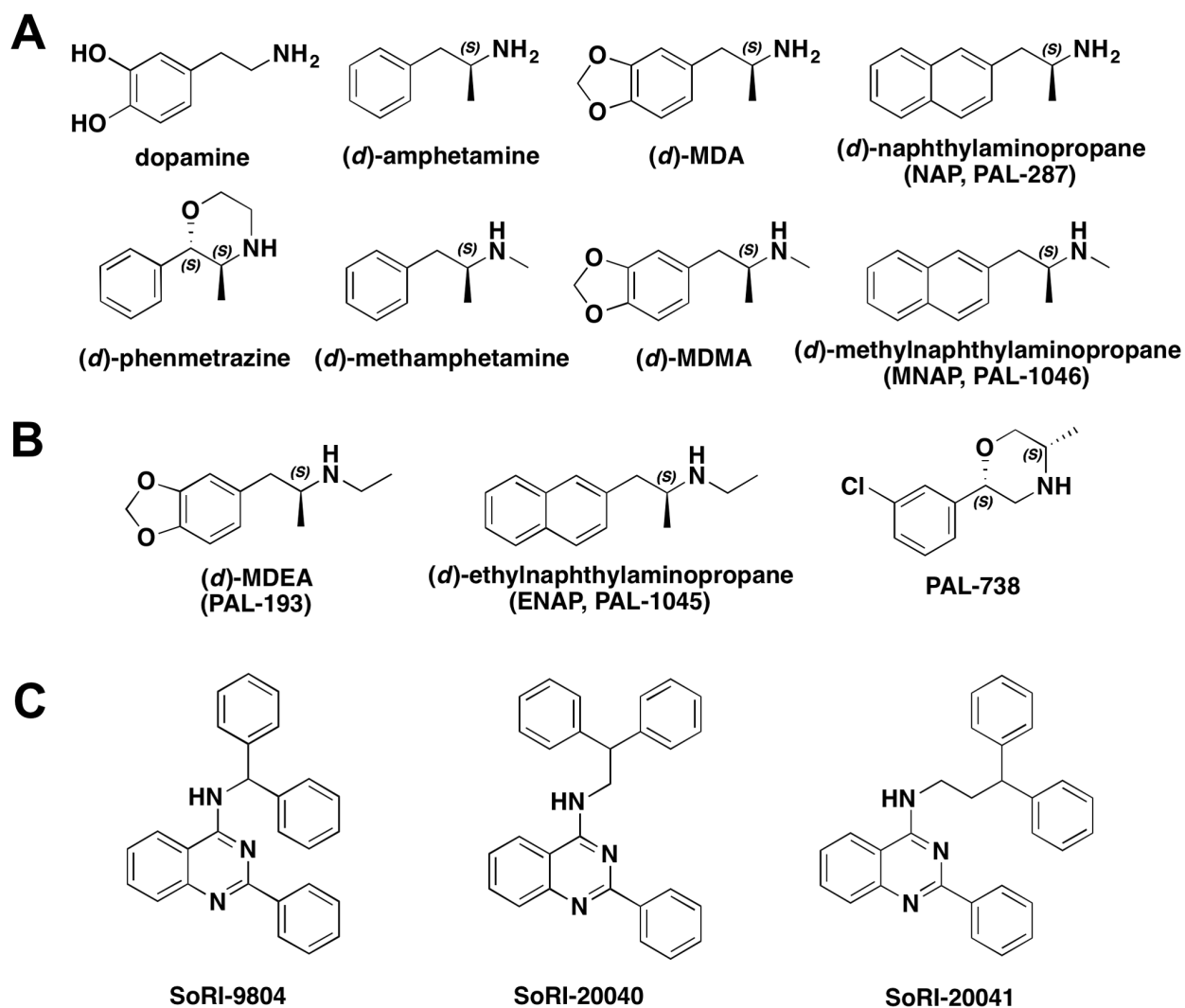
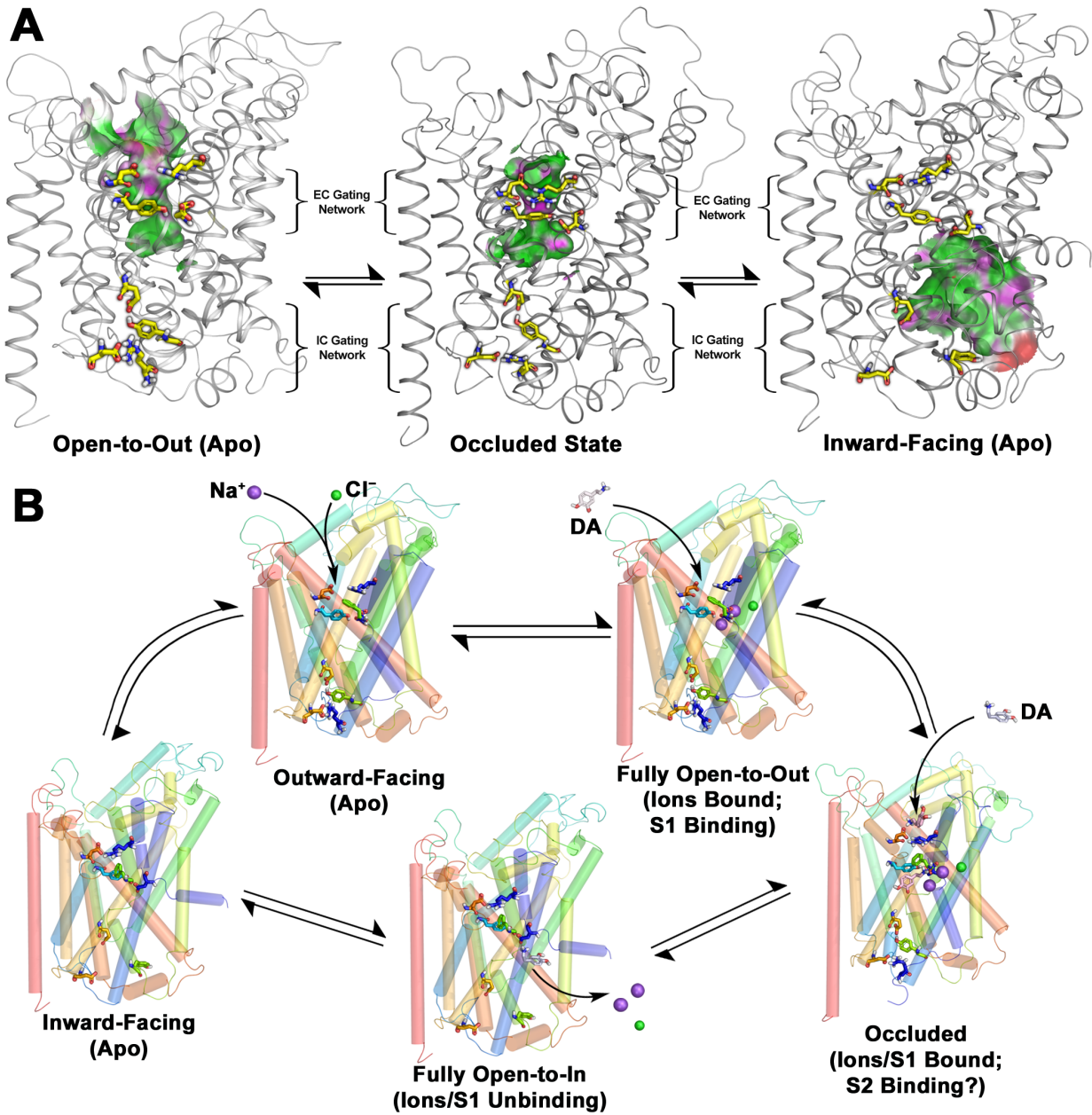
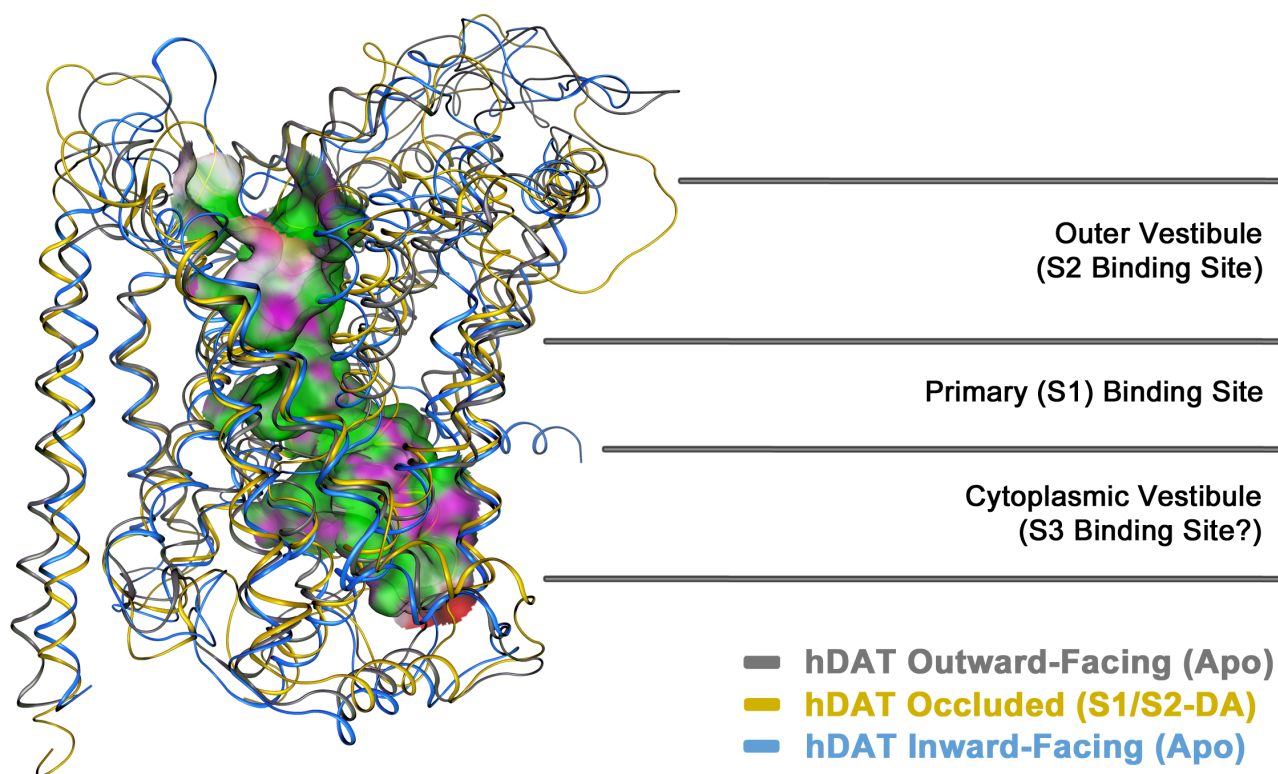


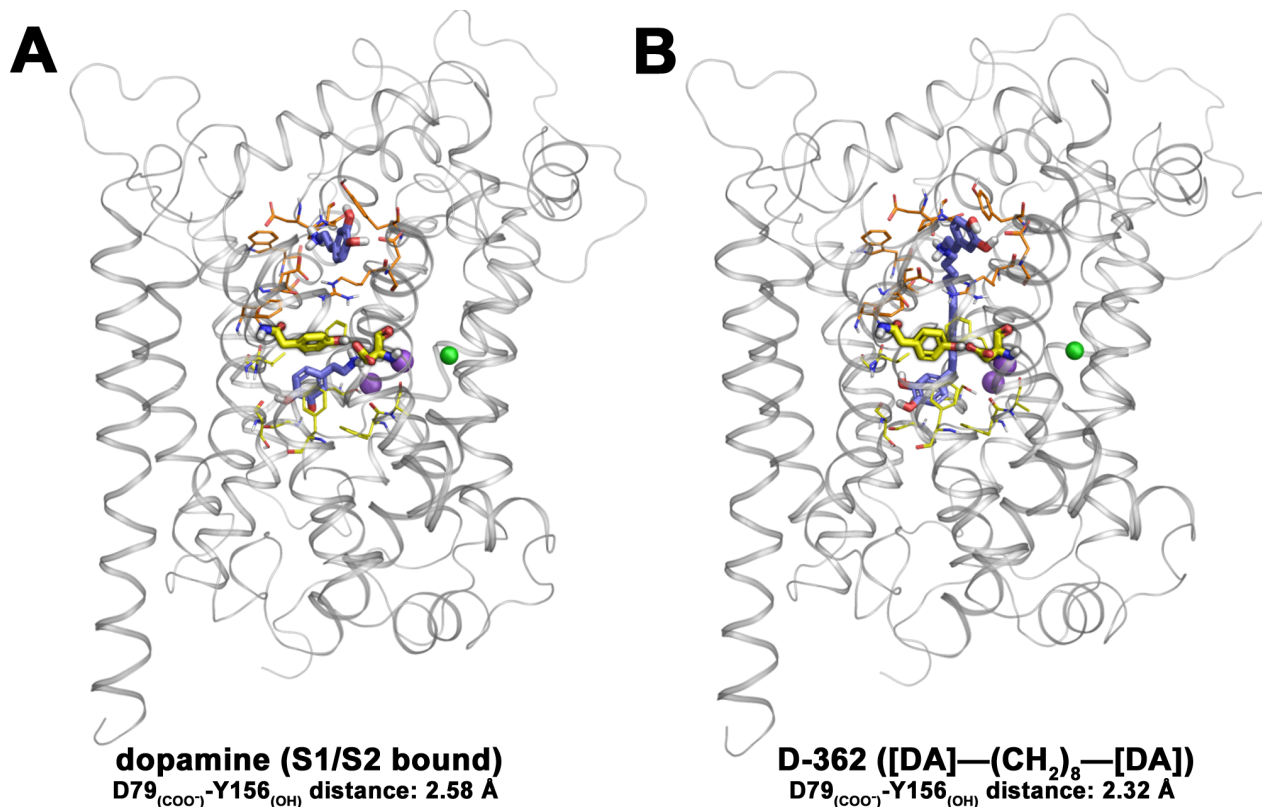
Figure 3.



## Supplemental Figures

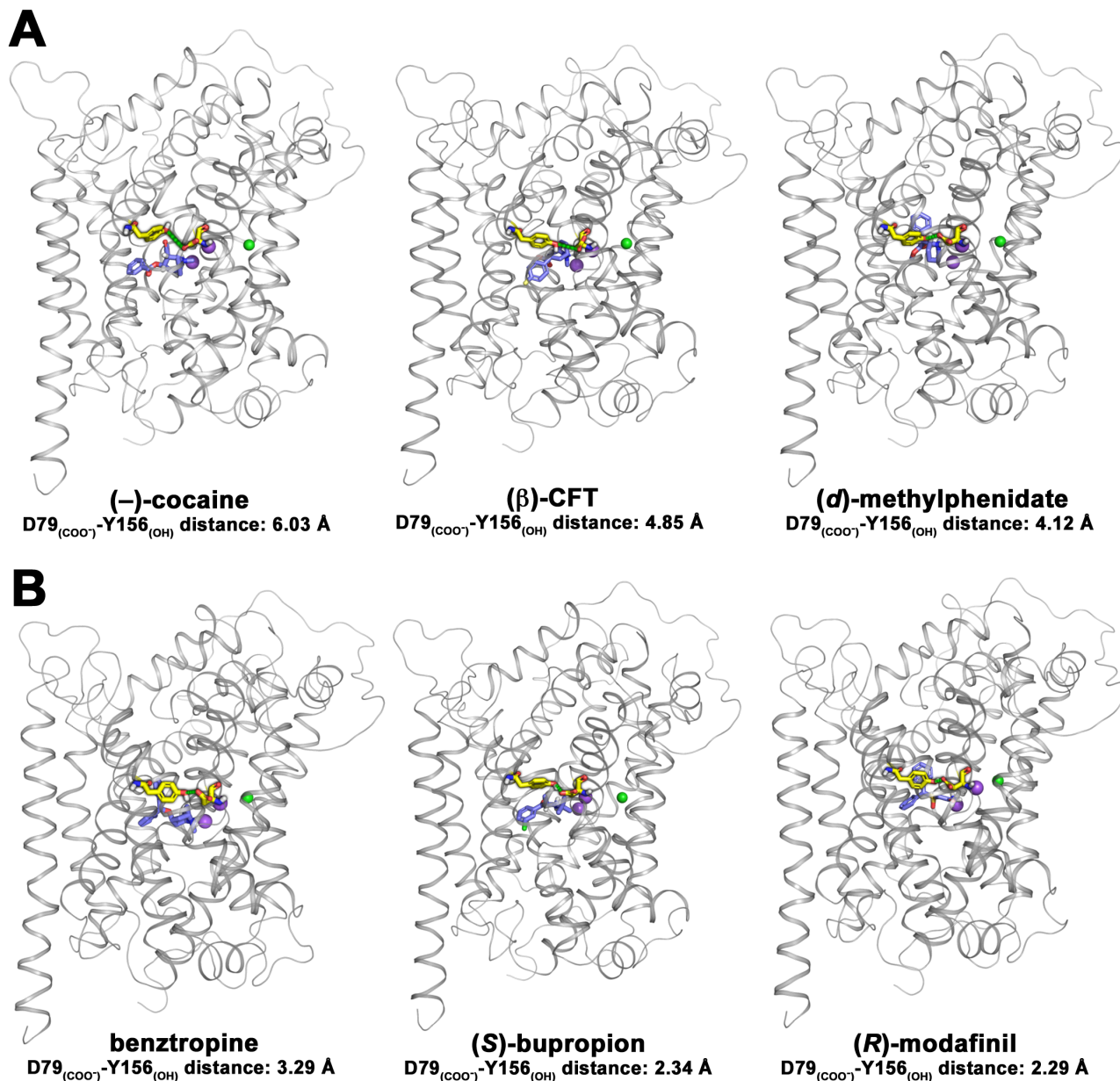


**Fig. S1.** Overlay illustration of the major DAT conformational states and putative substrate binding domains. The models were constructed based upon crystal structures of the bacterial NSS protein LeuT in each of the three respective conformations (described in the Supplemental Methods). The DAT is displayed as the superposition of the outward-facing (gray ribbons), occluded (gold ribbons) and inward-facing (light blue ribbons) models, following global structural alignment. Ligand binding pockets are rendered as translucent molecular surfaces and are overlaid to reveal the complete substrate permeation pathway (individual ligand binding domains for each of the three models are shown in Fig. 3 of the main text). The surface of the permeation pore is colored-coded based upon the local hydrophobic character—strongly hydrophobic regions are green, polar regions are purple and hydrophilic regions range from light pink to red, depending upon the extent of solvent exposure. The RMSD value for backbone  $C_{\alpha}$  atoms of the three conformations is 4.67 Å, with TM1 and the intra- and extracellular loop regions exhibiting the greatest geometric divergence. The most striking structural changes are observed in the inward-facing conformation, where the cytoplasmic-facing portion of TM1 is tilted acutely upwards, towards the plane of the plasma membrane. This outward pivot appears to give rise to the intracellular portion of the substrate permeation pathway, allowing cytosolic waters to interact with the S1-bound substrate and ions. Putative secondary ligand interaction sites in the respective extracellular and cytosolic vestibules are labeled. These auxiliary substrate interaction sites are likely transiently occupied by a substrate molecule as it moves along the permeation pore; however, substrate binding at the S2 site in the extracellular vestibule has also been theorized to play an integral role in the symport cycle of NSS proteins (Shi et al., 2008). In addition, interaction with a potential “S3 site”—located slightly below the S1 site in the cytosolic permeation pathway—may underlie the unique ability of ibogaine to inhibit the SERT and the DAT by stabilizing a fully inward-facing transporter conformation (Jacobs et al., 2007; Bulling et al., 2012).



**Fig. S2.** Final energy-minimized poses of model DAT/ligand complex with either dopamine (**A**) or its spacer-linked bivalent derivative D-362 (**B**) occupying both the S1 and S2 binding sites. Major residues lining the S1 site (F76, A77, D79, S149, V152, G153, Y156, F320, F326, S422 and G426) are shown as thin sticks with yellow carbon atoms, aside from the critical residues D79 and Y156, which are displayed as thick sticks and highlighted for visibility. Selected residues that are theorized to contribute to the S2 site (R85, Y88, F155, I159, W162, D313, D385, G386, P387 and D476) are shown as thin sticks with orange carbon atoms. The ligands are illustrated as thick sticks with light blue carbon atoms and the co-transported ions are shown as either purple (Na<sup>+</sup>) or green (Cl<sup>-</sup>) colored spheres. (**A**) Configuration of the DAT with two molecules of dopamine bound simultaneously at the S1 and S2 sites. (**B**) Binding mode of the bivalent phenethylamine ligand D-362, which incorporates two dopamine moieties linked at the amine nitrogen atoms by a flexible octamethylene spacer. D-362 acts as a potent DAT inhibitor and exhibits approximately 80-fold greater binding affinity than its monovalent parent in whole-cell [<sup>3</sup>H]CFT displacement assays, suggesting cooperative interaction with multiple binding sites (Schmitt et al., 2010). In the docking model, the catecholamine heads of D-362 are oriented such that they interact with the respective S1 and S2 sites in a manner similar to dopamine. For both DAT/ligand models, the terminal distance between the side chain carbonyl and hydroxyl oxygen atoms of residues D79 and Y156 is less than 3.5 Å (indicative of an intact hydrogen bond), suggesting that upon binding, the ligands enable the DAT to shift from an open-to-out conformation to an occluded state with a closed extracellular gate. In addition, the docking model of D-362 implies that the cavity connecting the central S1 site with the extracellular vestibule (and S2 site) is large enough to house relatively bulky spacer-linked molecules.





**Fig. S3.** Final energy-minimized poses of model DAT/ligand complexes with cocaine-like inhibitors (**A**) and atypical inhibitors (**B**) docked at the primary (S1) binding site. The ligands are illustrated as thick sticks with light blue carbon atoms and the co-transported ions are shown as purple ( $\text{Na}^+$ ) and green ( $\text{Cl}^-$ ) colored spheres. Residues D79 and Y156 are displayed as highlighted thick sticks with yellow carbon atoms and the terminal distance between the side chain carbonyl and hydroxyl oxygen atoms of the residues is indicated below each panel. (**A**) Binding of (-)-cocaine and the cocaine-like inhibitors  $\beta$ -CFT and methylphenidate disrupts the hydrogen bond between D79 and Y156 (interatomic distance  $>3.5$  Å), suggesting that these DAT ligands impede closure of the extracellular gating network and thus promote an open-to-out conformational state. (**B**) In contrast, docking models of the atypical inhibitors benztropine, bupropion and modafinil reveal a preserved D79-Y156 hydrogen bond (the interatomic distance is less than 3.5 Å in each case), suggesting that atypical inhibitors bind to the DAT in a more substrate-like manner than cocaine-like inhibitors and do not prevent the transporter from transitioning to a closed-to-out, occluded conformation.

## Supplemental Methods

The hDAT homology models were constructed based upon crystal structures of the bacterial NSS protein LeuT<sub>Aa</sub> in the respective outward-facing (Singh et al., 2008; PDB ID 3F3A), tricyclic-bound occluded (Zhou et al., 2007; PDB ID 2QJU) and inward-facing (Krishnamurthy and Gouaux, 2012; PDB ID 3TT3) conformational states. We have previously described the protocols employed in generation of the occluded state DAT homology model (Schmitt et al., 2010; Schmitt and Reith, 2011). Aside from certain minor modifications in the preparation of the corresponding LeuT template structure (detailed below), the outward-facing and inward-facing models were developed using similar procedures. Homology models were designed according to the revised NSS-family protein amino acid sequence alignment proposed by Beuming *et al.* (2006). Compared to the original familywise alignment for prokaryotic and eukaryotic NSS proteins (Yamashita et al., 2005), the revision incorporates a number of manual optimizations to account for regions of low sequence conservation. For each DAT model, the amino acid sequence of the LeuT crystal template was shorter than that of the DAT—hence, parts of the DAT intracellular N- and C-termini chains were not considered in the modeling process. The occluded state model incorporates residues Glu56 – Arg588, whereas the outward-facing and inward-facing models include residues Arg60 – Ser586 and Lys66 – Ser586, respectively. In addition, all waters, crystallization detergents (such as  $\beta$ -octylglucoside molecules) and ligands present in the template LeuT crystal structures were not incorporated into the DAT models.

In the case of the inward-facing LeuT structure, a monoclonal antibody fragment (6A10 Fab) that binds the cytosolic face of the transporter was co-crystalized with LeuT, in order to stabilize the labile inward-open conformation for X-ray diffraction (Krishnamurthy and Gouaux, 2012). This antibody fragment was removed from the inward-facing LeuT template file (PDB ID 3TT3) prior to homology modeling. In addition to the antibody fragment, the inward-open LeuT crystal structure also possessed three single-residue mutations relative to the other LeuT templates—Thr354 to Val (T354V), Ser355 to Ala (S355A) and Tyr268 to Ala (Y268A). These mutations were performed in order to weaken one of the sodium binding sites (T354V and S355A) and the intracellular gating network (Y268A), shifting the conformational equilibrium of the transporter toward a maximally inward-facing state. As these are well-conserved, structurally integral residues in the NSS family, we performed *in silico* “reverse mutagenesis”—reverting the mutant residues back to those of the original wildtype LeuT—prior to using the template for homology modeling of the inward-facing DAT. The mutant residue side-chains were replaced with the respective wildtype side-chains using the Rotamer Explorer tool of the Molecular Operating Environment (MOE) 2009.10 program (Chemical Computing Group; Montreal, Canada). For each target residue, we selected a top

scoring, low energy rotamer and then performed successive rounds of localized energy minimization with the AMBER99 forcefield, first to the residue atoms themselves and then to the side-chains of adjacent residues (those within a 4.5 Å radius). Following each mutagenesis operation, we screened the protein structure to ensure there were no interatomic clashes or backbone geometric distortions.

The three DAT models were generated by homology modeling using the MODELLER algorithm (<http://salilab.org/modeller/manual/>) and for each conformation, the resultant lowest energy structure was imported into MOE. The Protonate3D function in MOE was used to calculate residue protonation states and assign hydrogen atom coordinates, with partial charges assigned according to the AMBER99 forcefield. For the occluded conformation DAT model, the sodium ions were manually placed based upon their location in LeuT, but allowed to move freely during energy minimization and optimization rounds, as previously described (Schmitt and Reith, 2011). The DAT chloride ion was initially placed at a position corresponding to the side-chain carboxyl moiety of Glu290 in the occluded LeuT structure (see Forrest et al., 2007 and Zomot et al., 2007 for further discussion). Sodium and chloride ions were not integrated into the outward-facing and inward-facing DAT models, as they were intended to represent ligand-free (apo) transporter states. In order to refine residue stereochemistry and relieve any steric clashes, models were subjected to several rounds of energy minimization, employing the AMBER99 forcefield and the generalized Born (GB/VI) implicit solvation model as implemented in MOE (Labute, 2008). For each DAT model, stereochemical consistency was continuously evaluated using the PROCHECK algorithm (Laskowski et al., 1993; <http://www.ebi.ac.uk/thornton-srv/software/PROCHECK/>) and with Ramachandran plots produced by MOE. Ligand binding sites in the DAT models were identified with the Site Finder tool implemented in MOE and used to generate molecular surfaces depicting the substrate permeation pathway (Fig. 3 and Supplemental Fig. 1).

## Supplemental References

- Beuming T, Shi L, Javitch JA, and Weinstein H (2006) A comprehensive structure-based alignment of prokaryotic and eukaryotic neurotransmitter/Na<sup>+</sup> symporters (NSS) aids in the use of the LeuT structure to probe NSS structure and function. *Molecular Pharmacol* **70**:1630–1642.
- Bulling S, Schicker K, Zhang YW, Steinkellner T, Stockner T, Gruber CW, Boehm S, Freissmuth M, Rudnick G, Sitte HH, et al. (2012) The mechanistic basis for noncompetitive ibogaine inhibition of serotonin and dopamine transporters. *J Biol Chem* **287**:18524–18534.
- Forrest LR, Tavoulari S, Zhang YW, Rudnick G, and Honig B (2007) Identification of a chloride ion binding site in Na<sup>+</sup>/Cl<sup>-</sup>-dependent transporters. *Proc Natl Acad Sci* **104**:12761–12766.
- Jacobs MT, Zhang YW, Campbell SD, and Rudnick G (2007) Ibogaine, a noncompetitive inhibitor of serotonin transport, acts by stabilizing the cytoplasm-facing state of the transporter. *J Biol Chem* **282**:29441–29447.
- Krishnamurthy H and Gouaux E (2012) X-ray structures of LeuT in substrate-free outward-open and apo inward-open states. *Nature* **481**:469–474.
- Labute P (2008) The generalized Born/volume integral implicit solvent model: estimation of the free energy of hydration using London dispersion instead of atomic surface area. *J Comput Chem* **29**:1693–1698.
- Laskowski R, MacArthur M, Moss D, and Thornton J (1993) PROCHECK: a program to check the stereochemical quality of protein structures. *J Applied Crystallography* **26**:283–291.
- Schmitt KC, Mamidyala S, Biswas S, Dutta AK, and Reith MEA (2010) Bivalent phenethylamines as novel dopamine transporter inhibitors: evidence for multiple substrate-binding sites in a single transporter. *J Neurochem* **112**:1605–1618.
- Schmitt KC and Reith MEA (2011) The Atypical Stimulant and Nootropic Modafinil Interacts with the Dopamine Transporter in a Different Manner than Classical Cocaine-Like Inhibitors. *PLoS ONE* **6**:e25790.
- Shi L, Quick M, Zhao Y, Weinstein H, and Javitch JA (2008) The mechanism of a neurotransmitter sodium symporter—inward release of Na<sup>+</sup> and substrate is triggered by substrate in a second binding site. *Mol Cell* **30**:667–677.
- Singh SK, Piscitelli CL, Yamashita A, and Gouaux E (2008) A competitive inhibitor traps LeuT in an open-to-out conformation. *Science* **322**:1655–1661.
- Yamashita A, Singh SK, Kawate T, Jin Y, and Gouaux E (2005) Crystal structure of a bacterial homologue of Na<sup>+</sup>/Cl<sup>-</sup>-dependent neurotransmitter transporters. *Nature* **437**:215–223.
- Zhou Z, Zhen J, Karpowich NK, Goetz RM, Law CJ, Reith MEA, and Wang DN (2007) LeuT-desipramine structure reveals how antidepressants block neurotransmitter reuptake. *Science* **317**:1390–1393.
- Zomot E, Bendahan A, Quick M, Zhao Y, Javitch JA, and Kanner BI (2007) Mechanism of chloride interaction with neurotransmitter:sodium symporters. *Nature* **449**: 726–730.