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Molecular Basis for Selective Serotonin Reuptake Inhibition by the Antidepressant Agent Fluoxetine (Prozac)[S]

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ABSTRACT

Inhibitors of the serotonin transporter (SERT) are widely used antidepressant agents, but the structural mechanism for inhibitory activity and selectivity over the closely related norepinephrine transporter (NET) is not well understood. Here we use a combination of chemical, biological, and computational methods to decipher the molecular basis for high-affinity recognition in SERT and selectivity over NET for the prototypical antidepressant drug fluoxetine (Prozac; Eli Lilly, Indianapolis, IN). We show that fluoxetine binds within the central substrate site of human SERT, in agreement with recent X-ray crystal structures of LeuBAT, an engineered monoamine-like version of the bacterial amino acid transporter LeuT. However, the binding orientation of fluoxetine is reversed in our experimentally supported model compared with the LeuBAT structures, emphasizing the need for careful experimental verification when extrapolating findings from crystal structures of bacterial transporters to human relatives. We find that the selectivity of fluoxetine and nisoxetine, a NET selective structural congener of fluoxetine, is controlled by residues in different regions of the transporters, indicating a complex mechanism for selective recognition of structurally similar compounds in SERT and NET. Our findings add important new information on the molecular basis for SERT/NET selectivity of antidepressants, and provide the first assessment of the potential of LeuBAT as a model system for antidepressant binding in human transporters, which is essential for future structure-based drug development of antidepressant drugs with fine-tuned transporter selectivity.

Introduction

The early recognition of the serotonin (5-hydroxytryptamine) transporter (SERT) and the norepinephrine transporter (NET) as important targets for antidepressant drugs fostered extensive drug discovery efforts dedicated to the design and synthesis of compounds selectively targeting SERT and/or NET (Kristensen et al., 2011). In 1986, fluoxetine (Prozac; Eli Lilly, Indianapolis, IN) was approved as one of the first selective serotonin reuptake inhibitors (SSRIs) for the treatment of depression, and it has since become widely acknowledged as a breakthrough drug for depression (Wong et al., 1995, 2005). Unlike the tricyclic antidepressants (TCAs), fluoxetine and other SSRI drugs are highly selective for SERT, and today the SSRIs remain among the most widely prescribed antidepressant drugs (Waitekus and Kirkpatrick, 2004; Bauer et al., 2008).

Although compounds targeting SERT and NET have had important clinical significance for several decades, the molecular details underlying binding of antidepressants to these transporters are not clearly understood. Structural information of SERT and NET is still lacking, but X-ray crystal structures of the bacterial homolog LeuT (Yamashita et al., 2005; Krishnamurthy and Gouaux, 2012) have proved to be excellent structural templates for its mammalian counterparts and facilitated identification of the location and structure of ligand-binding sites in human transporters (Beuming et al., 2008; Celik et al., 2008; Andersen et al., 2009, 2010; Kaufmann et al., 2009; Koldsø et al., 2010, 2013a; Sinning et al., 2010; Plenge et al., 2012; Severinsen et al., 2012, 2013). Structures of LeuT have also provided direct insight into the binding mechanism of antidepressants. SSRIs and TCAs bind LeuT with low affinity to a site (denoted S2) located in an extracellular facing vestibule (Fig. 1) (Singh et al., 2007; Zhou et al., 2007, 2009), leading to the proposal that antidepressant drugs also bind to the S2 site in human transporters (Zhou et al., 2007, 2009). In contrast, recent structures of LeuBAT, an engineered version of LeuT with residues from SERT inserted into the central substrate site (denoted S1), and the dopamine transporter (DAT) from *Drosophila melanogaster*, displayed high-affinity binding of antidepressants within the central S1

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ABBREVIATIONS: β-CIT, (−)-2β-carbomethoxy-3β-(4-iodophenyl)tropane; DAT, dopamine transporter; IFD, induced-fit docking; NET, norepinephrine transporter; RMSD, root-mean-square deviation; SAR, structure-activity relationship; SERT, serotonin transporter; SSRI, selective serotonin reuptake inhibitor; TCA, tricyclic antidepressant; TM, transmembrane helix; WT, wild-type.

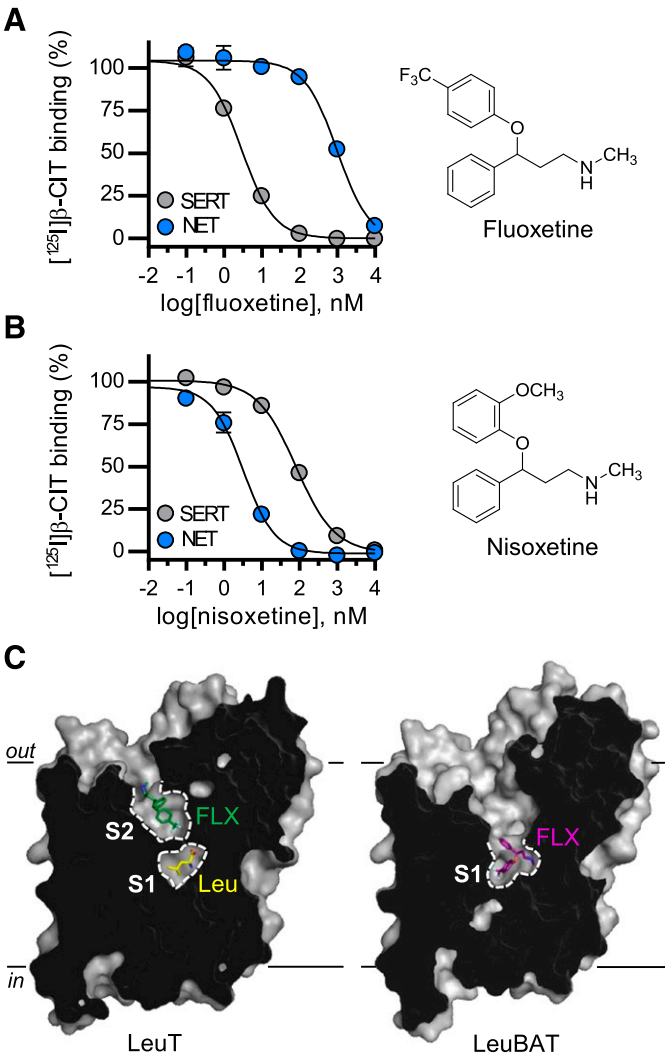


Fig. 1. (A and B) Chemical structure and pharmacological characterization of the SSRI fluoxetine (A) and the NET selective congener nisoxetine (B). The binding affinities of fluoxetine and nisoxetine toward SERT (filled gray circles) and NET (filled blue circles) were determined in an [^{125}I]β-CIT competition binding assay. Data points represent mean ± S.E.M. from triplicate determinations. (C) Left: cross-sectional illustration of the crystal structure of LeuT in complex with the substrate leucine (C-atoms shown in yellow) in the central S1 site and fluoxetine (FLX) (C-atoms shown in green) in the vestibular S2 site (PDB ID 3GWW). Right: cross-sectional illustration of the crystal structure of LeuBAT in complex with fluoxetine (C-atoms shown in magenta) in the central S1 site (PDB ID 4MM8).

site (Fig. 1) (Penmatsa et al., 2013; Wang et al., 2013). Combined with biochemical studies showing that most SSRIs inhibit SERT in a competitive manner (Graham et al., 1989; Koe et al., 1990; Apparsundaram et al., 2008), and several residues located within the S1 site of SERT and NET have been shown to be important for binding of SSRIs (Barker et al., 1999; Henry et al., 2006; Mason et al., 2007; Walline et al., 2008; Andersen et al., 2009, 2010; Koldsø et al., 2010; Sørensen et al., 2012), LeuBAT and *Drosophila* DAT seem to represent improved structural frameworks for studying the molecular pharmacology of human transporters compared with LeuT.

Fluoxetine has been cocrystallized together with both LeuT and LeuBAT, and these studies have provided ambiguous insight into the binding mechanism of this important SSRI drug. Whereas fluoxetine binds to the S2 site in LeuT, it binds to the S1 site in LeuBAT (Fig. 1) (Zhou et al., 2009; Wang et al., 2013). Surprisingly few biochemical studies have addressed the location of the fluoxetine binding site in human SERT, but it has been found that binding of fluoxetine is chloride-dependent and highly sensitive toward mutation of Ile172 to Met (Henry et al., 2006; Walline et al., 2008; Tavoulari et al., 2009; Sørensen et al., 2012). As Ile172 and the chloride binding site are both located within the central part of SERT, these observations are consistent with the S1 binding mode found in LeuBAT. However, both effects have been proposed to be allosterically induced (Walline et al., 2008; Tavoulari et al., 2009), and do thus not unequivocally pinpoint the location of the fluoxetine binding site. In contrast, nisoxetine, a structural congener of fluoxetine with selectivity for NET, was recently proposed to bind in the S2 site of NET (Wang et al., 2012). Given the structural similarity between nisoxetine and fluoxetine (Fig. 1) it is tempting to believe that they share the same binding site in SERT and NET, respectively. Here we have used a combination of chemical, biological, and computational approaches to decipher the molecular basis for binding of fluoxetine in SERT and selectivity over NET. Our study finds that fluoxetine binds within the S1 site of SERT and allows for the first assessment of LeuBAT as a model system for directly revealing the binding mode of antidepressants in human transporters.

Materials and Methods

Synthesis. A complete description of the synthesis and full characterization of fluoxetine, nisoxetine, and analogs 7–11 are found in Supplemental Methods.

Molecular Biology. As expression vectors, pcDNA3.1 and pCI-IRES-neo–containing human SERT and NET, respectively, were used (Kristensen et al., 2004; Andersen et al., 2011). Generations of point-mutants in SERT and NET were performed by site-directed mutagenesis using the QuikChange mutagenesis kit (Stratagene, La Jolla, CA). Multiple mutants were generated by introducing one or more mutations into existing mutants using site-directed mutagenesis. The mutations were verified by DNA sequencing of the entire gene (GATC Biotech, Constance, Germany). Synthetic cDNA encoding the two 15-fold mutants SERT-(NET S1) and NET-(SERT S1) was purchased from GeneArt (Thermo Fisher Scientific, Waltham, MA) and subcloned into the pCI-IRES-neo expression vector as detailed previously (Andersen et al., 2011).

Transport Assays and Radioligand Binding Experiments. [^{3}H]5-Hydroxytryptamine and [^{3}H]dopamine uptake measurements in COS-7 cells expressing wild-type (WT) and mutant forms of SERT and NET, and binding of [^{125}I]-labeled β-CIT [(−)-2β-carbomethoxy-3β-(4-iodophenyl)tropane] to membranes of COS-7 cells expressing WT and mutant forms of SERT and NET were performed essentially as described (Andersen et al., 2011; Sørensen et al., 2012). Detailed descriptions of the functional uptake assay and the radioligand binding assay are provided in Supplemental Methods.

Computational Methods. The *R*- and *S*-enantiomers of fluoxetine were docked into homology models of human SERT and NET, which were generated and validated as described previously (Koldsø et al., 2013b). To allow for protein flexibility during docking calculations, the induced-fit docking (IFD) workflow within the Schrödinger software suite (Schrödinger LLC, 2011; Sherman et al., 2006) was used. To address the binding of fluoxetine both in the central S1 site and the S2 site in the extracellular facing vestibule, two different types of IFD calculations were set up for each transporter. *R*- and *S*-fluoxetine were docked into the transporters utilizing the endogenous substrate bound to the S1 site as the binding site definition, with the default settings for the size of the binding site (a box measuring 26 × 26 × 26 Å^3 as the outer boundary for ligand and an inner box of 10 × 10 × 10 Å^3,

which should include the center of the ligand). These IFDs are termed small. In separate calculations, IFDs were performed where the binding site was defined from residues within the S1 site (SERT: Asp98 and Ile172; NET: Asp75 and Val148) in addition to S2 site residues (SERT: Arg104 and Glu493; NET: Arg81 and Asp473). In these IFDs, which are termed large, the inner box dimensions were increased to $20 \times 20 \times 20$ Å^3. Additionally, Trp80 of NET was mutated to Ala during the initial docking stage, since this residue was blocking the S2 site. The aligning residue in SERT (Trp103) is pointing away from the S2 site in the homology model and accordingly there was no need for mutation of this residue during initial docking. The maximum number of output structures was set to 20, and the recovered binding poses were ranked according to their XP GScores and Emodel scores. The XP GScore is an empirical scoring function that accounts for the interaction energy between the ligand and the protein and approximates the ligand binding free energy, while the Emodel score is a combination of the XP GScore, the nonbonded interactions, and the internal strain of the ligand (Friesner et al., 2004). The docking results have been divided into structural clusters based on heteroatom root-mean-square deviation (RMSD) < 2 Å in each docking. The structural clusters identified in each docking setup were further divided into global clusters. The global clusters were defined based on an RMSD < 2.3 Å between the heteroatoms of fluoxetine. A model of fluoxetine binding in SERT (a representative binding mode from the dominating SERT-Cluster 1) is provided as Supplemental Material.

Results

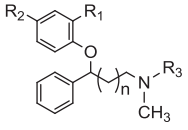
Structure-Activity Relationship Study. Fluoxetine and nisoxetine share a substituted 3-aryloxy-3-phenylpropan-1-amine skeleton, and are distinguished by their substitution on the phenoxy ring only. Where fluoxetine has a CF_3 group in the *para* position, nisoxetine has a methoxy group in the *ortho* position (Fig. 1). To delineate the role of these two diverging structural elements for activity at SERT and NET, we designed and prepared derivatives of fluoxetine and nisoxetine with different substituents on the phenoxy ring (Table 1) (see Supplemental Methods). Furthermore, the length and methyl substitution patterns of the aminoalkyl chain of SSRIs and TCAs have previously been shown to be important determinants for activity and selectivity toward SERT and NET (Owens et al., 1997; Andersen et al., 2009). To investigate the role of the aminoethyl chain of fluoxetine for activity and selectivity toward SERT and NET, we also prepared analogs of fluoxetine with modifications around this chain (Table 1) (see Supplemental Methods).

The binding affinities of the synthesized compounds were determined by displacing binding of the [^{125}I]-labeled cocaine analog β-CIT to human SERT and NET transiently expressed in membranes from COS-7 cells. As expected, fluoxetine had a high affinity toward SERT and selectivity over NET (7 versus 887 nM), whereas nisoxetine had a high affinity toward NET and selectivity over SERT (4 versus 167 nM) (Fig. 1; Table 1). Hence, as recognized from early structure-activity relationship (SAR) studies, *ortho* substitution of the phenoxy ring appears to confer selectivity toward NET, whereas substituents in the *para* position induce selectivity toward SERT (Wong et al., 1975). However, the analog with an unsubstituted phenoxy ring (compound 8) displayed comparable affinity toward NET as nisoxetine (4 versus 12 nM) whereas the analog with both *ortho* and *para* substitution (compound 9) had similar binding affinity toward SERT as fluoxetine (7 versus 4 nM) (Table 1), showing that the *ortho* substituent is a minor determinant for selective binding in NET over SERT. In contrast, the CF_3 substituent is essential for high-affinity binding in SERT and greatly reduces binding in NET (Table 1), thus showing that this substituent is the main determinant for the distinct selectivity profiles observed for fluoxetine and nisoxetine. In agreement with previous SAR studies of fluoxetine (Wong et al., 1975; Horng and Wong, 1976), we found that addition of an *N*-methyl group to fluoxetine (as in compound 7) reduced affinity toward SERT (7 versus 37 nM) but increased the selectivity for SERT over NET (127- versus 286-fold). Extending the aminoalkyl chain of fluoxetine with one methylene group (as in compound 10) had a minor effect on the affinity for SERT (7 versus 12 nM) but increased the selectivity over NET (127- versus 279-fold). The *N*,*N*-dimethyl analog of homofluoxetine (compound 11) had low activity toward both SERT and NET. The length and substitution pattern of the aminoalkyl chain on fluoxetine are

TABLE 1

Binding affinities of fluoxetine and nisoxetine derivatives at SERT and NET

The binding affinities at human SERT and NET were determined in an [^{125}I]β-CIT competition binding assay, and the selectivity ratio was calculated as K_i(NET WT)/K_i(SERT WT).



Compound	R_1	R_2	R_3	n	SERT WT	NET WT	SERT/NET Selectivity
					nM		
Fluoxetine (1)					7 ± 2	887 ± 115	127
S-Fluoxetine (*S*-1)	H	CF_3	H	1	3 ± 1	1324 ± 246	389
R-Fluoxetine (*R*-1)					5 ± 1	572 ± 67	108
Nisoxetine (2)	OCH_3	H	H	1	167 ± 31	4 ± 1	0.02
N-Methylfluoxetine (7)	H	CF_3	CH_3	1	37 ± 4	10,563 ± 1131	286
Des-CF_3-fluoxetine (8)	H	H	H	1	157 ± 29	12 ± 2	0.08
2-OCH_3-fluoxetine (9)	OCH_3	CF_3	H	1	3 ± 1	125 ± 22	45
Homofluoxetine (10)	H	CF_3	H	2	12 ± 1	3352 ± 593	279
N-Methylhomofluoxetine (11)	H	CF_3	CH_3	2	992 ± 34	7958 ± 1196	8

thus important determinants for binding and SERT/NET selectivity; this has also been observed for other SSRIs and TCAs (Owens et al., 1997; Andersen et al., 2009). Fluoxetine is a racemate consisting of a 1:1 mixture of *R*- and *S*-enantiomers and, unlike other antidepressant drugs that are highly enantioselective, the two enantiomers of fluoxetine have similar binding affinities for SERT (Wong et al., 1985). We determined the binding affinities of the *R*- and *S*-enantiomers of fluoxetine at SERT and NET and found the two enantiomers to be 389- and 108-fold selective toward SERT over NET, respectively, thereby showing that the stereochemistry of fluoxetine is an important determinant for SERT/NET selectivity (Table 1). In summary, our SAR analysis demonstrates that minor modifications of the chemical scaffold of fluoxetine can improve the affinity toward SERT and increase the selectivity over NET, whereas none of the compounds tested had greater affinity for NET or improved selectivity over SERT compared with nisoxetine.

Molecular Docking. To create models of possible binding modes of fluoxetine in SERT and NET, we performed IFD calculations of *R*- and *S*-fluoxetine into homology models of human SERT and NET. The SERT and NET homology models were constructed using LeuT as template (Koldsø et al., 2013b). Previous LeuT-based models of TCA binding in human SERT (Sinning et al., 2010) have proved to be very predictive when compared with the recent structure of the eukaryotic *Drosophila* DAT in complex with the TCA nortriptyline (Penmatsa et al., 2013) (Supplemental Fig. 1). Specifically, we observed the aromatic lid (Tyr176/Phe335) to be broken in our IFD calculations of fluoxetine in human SERT, showing that the outward-occluded LeuT structure can be used as template for human SERT and still provide an inhibitor-bound transporter model in an outward-open conformation. Furthermore, the overall structure of *Drosophila* DAT is very similar to that of LeuT, emphasizing that the LeuT-fold is conserved from prokaryotic to eukaryotic transporters, and together these findings substantiate the continued use of LeuT as a structural template for human transporters in the study of drug binding. Initially, IFD calculations were confined to the S1 binding site of SERT and NET (denoted small IFDs). In separate runs, the entire S1/S2 region was included in the docking calculations (denoted large IFDs). The docking results have been divided into clusters based on heteroatom RMSD < 2 Å, and further mapped into global clusters describing common binding modes by comparison of all clusters obtained from both small and large IFDs of both enantiomers of fluoxetine (Fig. 2; Table 2). The global clusters were defined based on RMSD < 2.3 Å between the heteroatoms of fluoxetine.

Overall, we observed three global clusters of fluoxetine binding in SERT. In the most prevalent binding mode identified in SERT-Cluster 1 (containing 89% of the poses obtained) (Table 2), fluoxetine is located almost entirely within the central S1 site except for the CF_3-substituted phenyl ring, which protrudes out toward the S2 site (Fig. 2A). In agreement with the similar binding affinities of *R*- and *S*-fluoxetine for SERT (Table 1), the XP GScores are also very similar for the two enantiomers. Additionally, a significant overlap between the two enantiomers in SERT-Cluster 1 is seen, where the amine of fluoxetine is anchored between Tyr95 and Asp98 on transmembrane helix (TM) 1, and the unsubstituted phenyl ring is located close to Ile168, Ile172, and Phe341 on TM3. Two minor global clusters of fluoxetine binding were also obtained

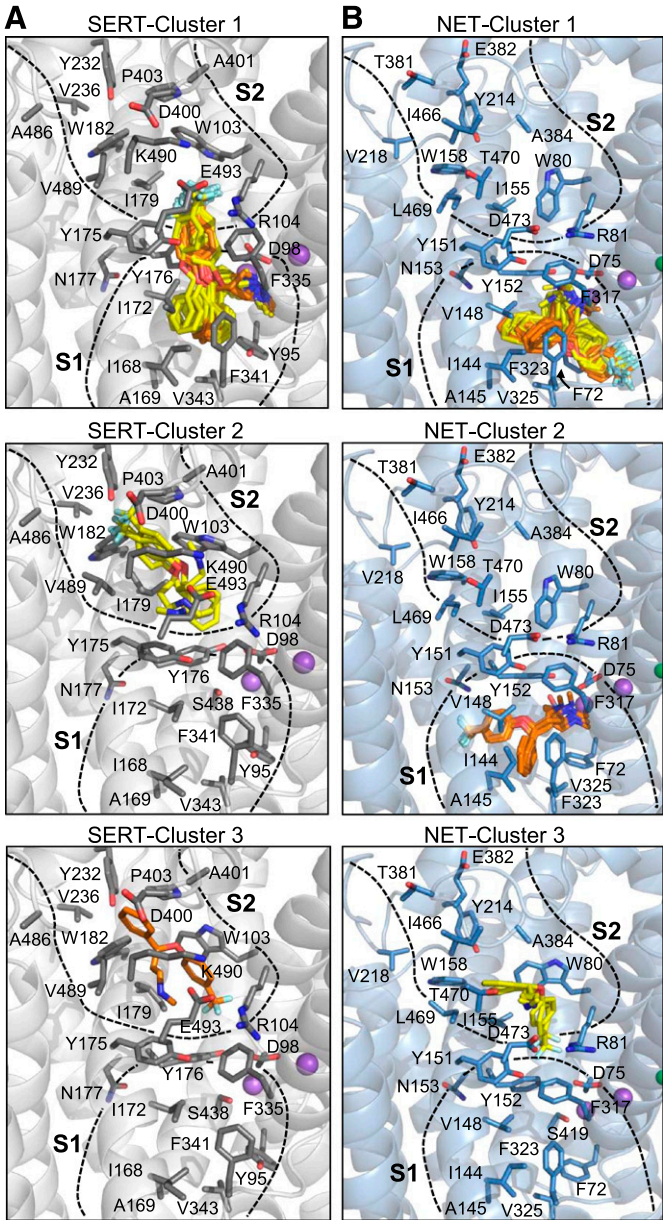


Fig. 2. (A and B) Global binding clusters obtained from IFD simulations of *R*-fluoxetine (C-atoms shown in yellow) and *S*-fluoxetine (C-atoms shown in orange) into homology models of SERT (A) and NET (B). The two dominating binding clusters (SERT-Cluster 1 and NET-Cluster 1) represent 89 and 67% of all *R*- and *S*-fluoxetine poses obtained from IFD simulations into SERT and NET, respectively (Table 2). Note that the *R*- and *S*-enantiomers are completely overlapping in the two dominating binding clusters, whereas only a single enantiomer is found in the minor binding clusters (SERT-Cluster 2–3 and NET-Cluster 2–3). Selected residues in proximity of the proposed binding clusters are shown as stick representations, and the sodium and chloride ions are shown as magenta and green spheres, respectively. The stippled lines indicate the curvature of the S1 and S2 sites.

(SERT-Cluster 2 and SERT-Cluster 3; 9 and 2%, respectively, of the poses obtained) (Table 2). In these two clusters, fluoxetine is exclusively located in the S2 site and the amine of the ligand is located close to Glu493 from TM10 in both clusters (Fig. 2A).

From IFD calculations in NET, we also found three global clusters of fluoxetine binding. In the dominating binding mode (NET-Cluster 1; 63% of the poses obtained) (Table 2), fluoxetine is located in the S1 site below an aromatic lid

TABLE 2

Results from SERT and NET docking calculations

The IFD setup is mentioned (either Small or Large). It is indicated if the cluster is located within the S1 or S2 site in addition to the cluster name for that setup. The number of poses in each cluster is listed with respect to the total number of poses. The average XP Gscore is listed with the standard deviation indicated in brackets. Also, the average Emodel score is listed with the standard deviation in brackets, and last it is listed in which global cluster the setup cluster belongs to.

Protein	IFD	Compound	S1 or S2 Site	Cluster	#Pose/#Total Poses	Avg. XP GScore	Avg. Emodel	Global Cluster
						kcal/mol		
hSERT	Small	*R*-Fluoxetine	S1	S1-C1	20/20	−11.7 (0.5)	−74.0 (9.5)	SERT-Cluster 1
				Outliers	0/20			
		S-Fluoxetine	S1	S1-C1	19/19	−11.5 (0.7)	−71.0 (8.1)	SERT-Cluster 1
				Outliers	0/19			
	Large	*R*-Fluoxetine	S2	S2-C1	4/4	−11.0 (0.4)	−65.2 (3.2)	SERT-Cluster 2
				Outliers	0/4			
		S-Fluoxetine	S1	S1-C1	1/2	−12.3 (-)	−81.4 (-)	SERT-Cluster 1
			S2	S2-C1	1/2	−11.0 (-)	−61.8 (-)	SERT-Cluster 3
				Outliers	0/2			
hNET	Small	*R*-Fluoxetine	S1	S1-C1	16/17	−10.6 (1.3)	−69.8 (5.8)	NET-Cluster 1
				Outliers	1/17			
		S-Fluoxetine	S1	S1-C1	12/19	−11.4 (0.6)	−69.1 (5.0)	NET-Cluster 1
			S1	S1-C2	6/19	−9.9 (0.3)	−55.3 (5.6)	NET-Cluster 2
				Outliers	1/19			
	Large	*R*-Fluoxetine	S1	S1-C2	2/5	−10.6 (0.5)	−53.0 (5.8)	NET-Cluster 2
			S2	S2-C1	2/5	−10.9 (0.2)	−66.8 (1.8)	NET-Cluster 3
				Outliers	1/5			
		S-Fluoxetine	S1	S1-C1	3/8	−11.7 (0.0)	−74.8 (0.7)	NET-Cluster 1
			S1	S1-C2	4/8	−10.0 (0.2)	−57.0 (2.4)	NET-Cluster 2
				Outliers	1/8			

(Tyr152/Phe317) (Fig. 2B). The amine of fluoxetine is coordinated by Asp75, the CF_3-substituted phenyl ring is located just above Phe72, and the unsubstituted phenyl ring is located close to Ile144, Val148, and Phe323. There is a significant overlap between the two enantiomers of fluoxetine in NET-Cluster 1, which is in agreement with the comparable binding affinities of the enantiomers toward NET (Table 1). Two minor global clusters were also obtained from IFDs in NET (NET-Cluster 2 and NET-Cluster 3; 24 and 4%, respectively, of the poses obtained) (Table 2). In NET-Cluster 2, fluoxetine is binding exclusively in the S1 site with the amine and unsubstituted phenyl ring located at similar positions as found in NET-Cluster 1, and in NET-Cluster 3 fluoxetine is binding in the S2 site in a similar pose as found in SERT-Cluster 3 (Fig. 2). NET-Cluster 1 and NET-Cluster 2 are not similar to any of the binding modes observed for fluoxetine within the S1 site of SERT.

Experimental Validation of Suggested Binding Modes of Fluoxetine in SERT. To distinguish between the three obtained clusters of fluoxetine binding in SERT, we performed a mutational analysis of residues within 6 Å of the predicted binding modes to determine their role in fluoxetine binding. In total, 59 point mutations across 27 different positions in the S1 and S2 sites of SERT were included in the study. Nine mutants rendered the transporter nonfunctional and were not studied further (Supplemental Table 1). The inhibitory potency (K_i) of fluoxetine was determined at each of the 50 functional point-mutants across 24 different positions (Fig. 3; Supplemental Table 1). At five positions (Tyr95, Asp98, Ile168, Ile172, Asn177), point mutations induced >10-fold shifts in the K_i value for fluoxetine (ranging from 11- to 79-fold), suggesting these residues are key determinants for fluoxetine binding in SERT. As all five residues are located within the S1 site of SERT, these results suggest that SERT-Cluster 1 represents the bioactive binding conformation of fluoxetine in SERT. This is in accordance with IFD calculations that also indicated fluoxetine to have the tightest binding in this cluster (Table 2), most significantly revealed in the Emodel scores. In contrast, mutations of residues within the S2 site generally induced <3-fold shifts in fluoxetine K_i (Fig. 3; Supplemental Table 1), thus speaking against the binding modes predicted in SERT-Cluster 2 and SERT-Cluster 3. Notably, an ionic interaction between the amine of fluoxetine and the negatively charged side-chain of the S2 residue Glu493 on TM10 is predicted in the two minor binding clusters (Fig. 2A). However, removing the negatively charged side-chain by the E493A mutation had no significant effect on the potency of fluoxetine (Fig. 3; Supplemental Table 1). Furthermore, mutations of six hydrophobic residues within the S2 site (Trp103, Ile179, Trp182, Tyr232, Val236, and Val489) that seem to be important for the overall shape of the extracellular vestibule of SERT, generally only led to small shifts (<3-fold) in fluoxetine K_i (Fig. 3; Supplemental Table 1), substantiating that SERT-Cluster 2 and SERT-Cluster 3 do not represent the bioactive binding conformation of fluoxetine in SERT. Interestingly, TM10 residues have previously been suggested to have an important role for inhibitor binding within the S1 site of *Drosophila* and human DAT (Bisgaard et al., 2011; Penmatsa et al., 2013). Here we show that mutation of residues in TM10 of SERT (Ala486, Val489, Lys490, and Glu493) induce <3-fold changes in the potency of fluoxetine (Fig. 4; Supplemental Table 1), suggesting that TM10 residues in DAT have a more important role in inhibitor binding than TM10 residues in SERT. The amino group of fluoxetine was found to have a key role for high-affinity binding in SERT (Table 1). According to data from SERT-Cluster 1,

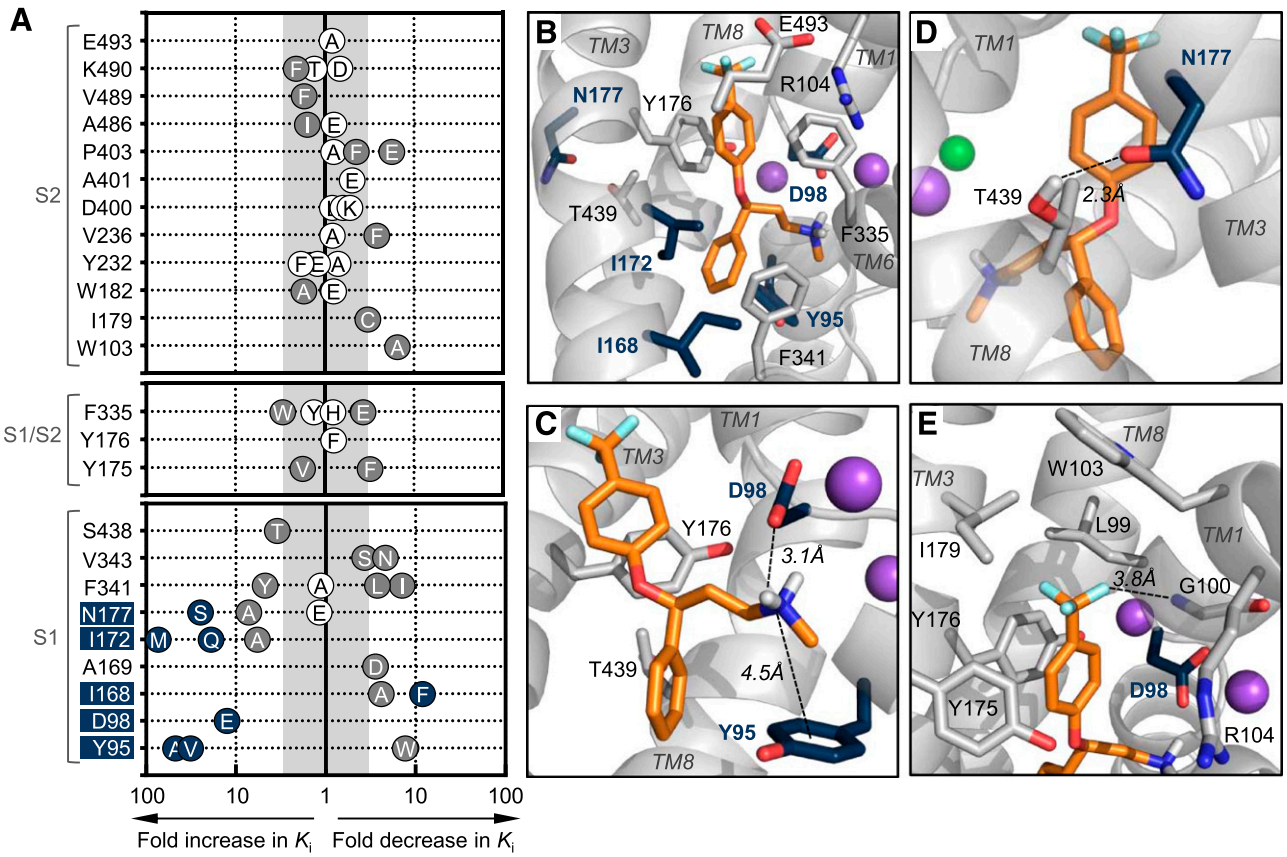


Fig. 3. (A) Graphical summary of the fold-change in fluoxetine potency (shown on *x*-axis) induced by point mutations at various positions in the S1 and S2 sites and in the S1/S2 interface (shown on *y*-axis). The fold-change is calculated as K_i(WT SERT)/K_i(mutant) or K_i(mutant)/K_i(WT SERT) for mutations increasing or decreasing the potency of fluoxetine, respectively. The gray shaded region indicates <3-fold change in fluoxetine potency. Open circles specify that the mutations do not significantly affect the K_i value for fluoxetine compared with WT SERT, whereas gray and blue shading of data points specify a significant change ($P < 0.01$; Student's *t* test). Mutations producing >10-fold changes in K_i and their corresponding positions are highlighted in blue. Fluoxetine K_i, substrate K_m, and functional activity of the mutations are shown in Supplemental Table 1. (B–E) Close-up views of a representative binding pose of *S*-fluoxetine (C-atoms shown in orange) in SERT from the dominating SERT-Cluster 1. Selected binding site residues are shown as stick representations. Positions where mutation induced >10-fold change in fluoxetine K_i are highlighted in blue. Sodium and chloride ions are shown as magenta and green spheres, respectively.

the amine forms direct interactions with Tyr95 and Asp98 on TM1, similar to what has previously been observed for escitalopram (Koldsø et al., 2010). Accordingly, the D98E mutation induced a 12-fold loss of potency for fluoxetine, and removal of the aromatic ring of Tyr95 (Y95A and Y95V) induced a 40-fold loss of potency for fluoxetine (Fig. 3; Supplemental Table 1). Interestingly, when substituting Tyr95 for Trp (Y95W) we found a significant 8-fold gain of potency (Fig. 3; Supplemental Table 1). Since Trp is a better cation–π interaction partner than Tyr (Gallivan and Dougherty, 1999), the gain of potency induced by Y95W suggests a cation–π interaction between the amine of fluoxetine and the aromatic side-chain of Tyr95. The I168F mutation induced an 11-fold gain of potency for fluoxetine (Fig. 3; Supplemental Table 1), which is likely induced by aromatic interactions between the inserted Phe and the unsubstituted phenyl ring of fluoxetine in the lower part of the S1 site (Figs. 2 and 3). Previously, the I172M mutation was shown to decrease fluoxetine potency (Henry et al., 2006; Walline et al., 2008; Thompson et al., 2011; Sørensen et al., 2012). Here, we show that mutation of Ile172 to Ala, Gln, and Met induced 6- to 79-fold loss of potency for fluoxetine, and we corroborate earlier findings that Ile172 plays a key role in recognition of fluoxetine (Fig. 3; Supplemental Table 1). Mutation of Asn177 on TM3 to Ala or Ser induced 7- and 25-fold loss of potency for fluoxetine, respectively. In contrast, the N177E mutation did not significantly affect fluoxetine K_i (Fig. 3; Supplemental Table 1), indicating that a side-chain bearing a carbonyl group in this position is important for recognition of fluoxetine. In SERT-Cluster 1, Asn177 is located >6.5 Å away from fluoxetine but interacts with Thr439 through an H-bond (Fig. 3). Hence, the N177A and N177S mutations might affect fluoxetine K_i in an indirect manner by modulating the overall shape of the S1 pocket by disruption of the H-bond between TM3 and TM8. The CF_3 substituent of fluoxetine was found to be a key determinant for obtaining high-affinity binding in SERT (Table 1). In SERT-Cluster 1, the CF_3-substituted phenyl ring is located in a hydrophobic pocket with a direct interaction between the CF_3 group and the backbone of Gly100 and aromatic π–π stacking interactions with Tyr176 (Fig. 3). Backbone interactions are notoriously difficult to address by conventional mutagenesis, and we have previously shown that SERT is very sensitive to mutation of Tyr176 (Andersen et al., 2010). Only the conservative Y176F mutation has so far been found to be functionally tolerated, and it had no significant effect on fluoxetine K_i (Fig. 3; Supplemental Table 1). Therefore, as an alternative approach to probe specific interactions between the CF_3-substituted phenyl ring of fluoxetine and SERT, we tested nisoxetine,

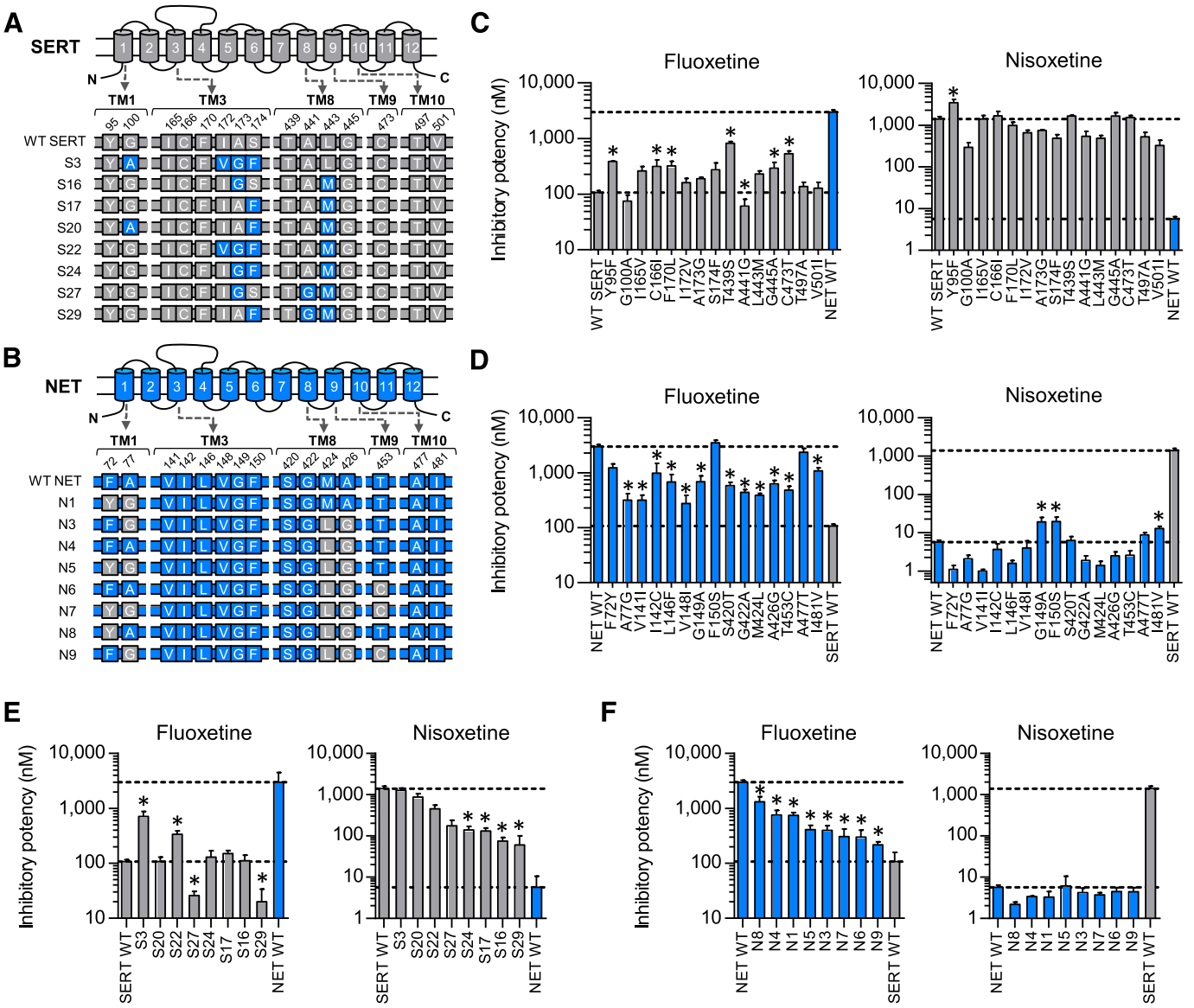


Fig. 4. (A and B) Topology diagram of SERT (A) and NET (B) illustrating the identity, TM location, and numbering of the 15 nonconserved SERT/NET residues within 6 Å of the putative S1 site, and a graphical representation of selected multiple SERT and NET mutants (see also Supplemental Fig. 2; Supplemental Tables 3, and 4). SERT mutants are shown on a gray background with mutations indicated in blue (A), and NET mutants are shown on a blue background with mutations indicated in gray (B). (C–F) Inhibitory potency of fluoxetine and nisoxetine at single point-mutants in SERT (C) and NET (D) and at multiple mutants in SERT (E) and NET (F). The inhibitory potency of fluoxetine and nisoxetine was determined in a functional uptake inhibition assay, and data represent mean ± S.E.M. from at least three independent experiments each performed in triplicate (Supplemental Tables 3 and 4). The stippled lines indicate the potency of the inhibitors at WT transporters. Asterisks denote significantly different K_i values compared with WT transporters ($P < 0.01$; Student's t test).

des-CF_3-fluoxetine (compound 8), and 2-OCH_3-fluoxetine (compound 9) at selected S1 mutations that induce significant changes in fluoxetine K_i (Supplemental Table 2). Nisoxetine, compound 8, and compound 9 have different aromatic substituents than fluoxetine, and we thus envisioned that if the substituted phenyl ring of fluoxetine interacts with one of the mutated residues, the analogs would be differentially affected by the mutation compared with fluoxetine. However, the potency of fluoxetine and the three analogs were generally affected to the same level across the tested mutations (Supplemental Table 2), thereby indirectly substantiating that the CF_3-substituted phenyl ring is located in the hydrophobic pocket, potentially engaging in backbone and aromatic stacking interactions that are difficult to address by site-directed mutagenesis. In summary, our mutational analysis establishes the S1 site as the primary binding site for fluoxetine in SERT and identifies SERT-Cluster 1 as the most likely binding mode model.

Molecular Determinants for SERT/NET Selectivity. We next sought to identify specific residues within SERT and NET that determine the distinct selectivity of fluoxetine and nisoxetine. We have shown that nonconserved SERT/NET residues within the S1 site dictate the selectivity for citalopram (Andersen et al., 2011). Accordingly, we hypothesized that the molecular determinants for fluoxetine and nisoxetine selectivity are also found among these residues. We have previously mutated each of the 15 nonconserved SERT/NET residues found within 6 Å of the S1 site to the aligning residue in the other transporter, resulting in 15 individual

SERT-to-NET mutations in SERT and 15 individual NET-to-SERT mutations in NET (Fig. 4; Supplemental Fig. 2) (Andersen et al., 2011). To systematically probe for the individual contribution of these nonconserved S1 residues for the selectivity of fluoxetine and nisoxetine, we determined the inhibitory potency of the two inhibitors at the 15 SERT-to-NET and the 15 NET-to-SERT mutations (Fig. 4; Supplemental Tables 3 and 4). For six of the SERT-to-NET mutations in SERT, the potency of fluoxetine was significantly decreased (3- to 7-fold). None of the SERT mutants induced an increase in the potency of nisoxetine (Fig. 4; Supplemental Table 3). In contrast, 12 of the 15 NET-to-SERT mutants in NET increased fluoxetine potency (3- to 11-fold), whereas only three mutants decreased the potency of nisoxetine (2- to 3-fold) (Fig. 4; Supplemental Table 4). Hence, as observed for citalopram (Andersen et al., 2011), inhibitor selectivity can be modulated, but is not controlled by a single nonconserved residue within the S1 site. Next, we combined the single point-mutants into a set of 30 multiple SERT-to-NET mutants in SERT (designated S1–S30) and 17 multiple NET-to-SERT mutants in NET (designated N1–N17) (Fig. 4; Supplemental Tables 3 and 4). The design of these mutants was initially directed by results from single point mutants and later combined with results from multiple mutants and with the binding poses obtained from IFD calculations. Functional uptake activity was retained for 29 of the 30 multiple SERT mutants and for 10 of the 17 multiple NET mutants (Supplemental Tables 3 and 4). The nonfunctional mutants were not studied further. For fluoxetine, a significant loss of potency (3- to 11-fold) was observed for eight of the multiple SERT mutants (Fig. 4; Supplemental Table 3). Mutations within the Ile172/Ala173/Ser174 motif on TM3 was included in the five multiple mutants that displayed the largest loss of potency, suggesting that this motif is an important determinant for the selectivity of fluoxetine. Interestingly, combining mutations in the Ile172/Ala172/Ser174 motif with A441G and L443M (as in S27, S28, and S29) induced a significant gain of potency for fluoxetine (Fig. 4; Supplemental Table 3), indicating that A441G and L443M hold a positive role for binding of the SSRI. For nisoxetine, seven of the multiple SERT mutants induced a significant gain of potency (10- to 24-fold). Combining mutations within the Ile172/Ala173/Ser174 motif with A441G and L443M on TM8 induced the largest gain of nisoxetine potency, indicating that residues on TM3 and TM8 are cooperative determinants for binding of nisoxetine in SERT. The 3-fold S29 mutant (SERT-S174F-A441G-L443M) had the largest effect, and rendered SERT 24-fold more sensitive to nisoxetine than SERT WT (60 versus 1422 nM), showing that key determinants for nisoxetine selectivity are located within the S1 site of SERT.

Determination of the potency of nisoxetine at the 10 functional multiple NET mutants surprisingly showed that all retained WT potency of the NET selective ligand (Fig. 4; Supplemental Table 4). These data strongly suggest that, in contrast to SERT, nonconserved S1 residues do not define the inhibitory potency of nisoxetine in NET. In contrast, all multiple NET-to-SERT mutants induced a significant gain of fluoxetine potency (2- to 14-fold) (Fig. 4; Supplemental Table 4). Mutations in TM1 (F72Y and A77G), TM8 (M424L and A426G), and TM9 (Thr453) were found to be most important for improving inhibitory potency of fluoxetine in NET. Specifically, the 4-fold N9 mutant (NET-A77G-M424L-A426G-T453C) induced the largest effect and rendered NET 14-fold more sensitive toward fluoxetine than NET WT (2993 versus 217 nM). Hence, nonconserved residues within the S1 site of SERT and NET are key determinants for the selectivity of fluoxetine, which are supportive of our proposed binding mode of fluoxetine (Fig. 2).

Interchanging Binding Sites between SERT and NET. Interchanging nonconserved residues within the S1 site of SERT and NET modulated the potency of fluoxetine and nisoxetine. However, the selectivity was not fully reversed by any of the tested mutants. We therefore generated a series of mutant constructs in which all nonconserved residues in the S1 site and/or all nonconserved residues in the S2 site were simultaneously interchanged between SERT and NET, and thereby in principle transplanting these binding sites from SERT into NET and vice versa. Hereby, three SERT constructs containing NET S1: SERT-(NET S1), NET S2: SERT-(NET S2), and NET S1/S2: SERT-(NET S1S2), in addition to two NET constructs containing SERT S1: NET-(SERT S1) and SERT S2: NET-(SERT S2) were created (Fig. 5; Supplemental Fig. 2; Supplemental Table 5). Additionally, we created two constructs in which all nonconserved residues within 6 Å of the predicted binding mode of fluoxetine (SERT-Cluster 1) were interchanged—SERT-(NET S1S2i) and NET-(SERT S1S2i), respectively. For a detailed description of mutant constructs, see Supplemental Fig. 2 and Supplemental Table 5.

Initially, we performed saturation binding analysis on membrane preparations from COS-7 cells expressing WT and mutant transporters and found that all SERT constructs bind [^{125}I]β-CIT, whereas only NET WT and NET-(SERT S2) showed specific [^{125}I]β-CIT binding (Fig. 5; Supplemental Table 5). Consistent with saturation binding analyses, confocal imaging of green fluorescent protein–tagged variants of WT and mutant transporters showed that the two NET constructs that do not bind [^{125}I]β-CIT—NET-(SERT S1) and NET-(SERT S1S2i)—were primarily retained within intracellular compartments (Supplemental Fig. 3). Next, we determined the binding affinities of fluoxetine and nisoxetine at the S1/S2 constructs that bind [^{125}I]β-CIT in a competition binding assay. For fluoxetine, insertion of NET S1 into SERT induced a 15-fold decrease in binding affinity (7 versus 102 nM), whereas insertion of the NET S2 site did not affect binding of fluoxetine (Fig. 5; Supplemental Table 5). Interestingly, the decreased binding affinity of fluoxetine in SERT-(NET S1) was reversed by simultaneous insertion of S2 site (Fig. 5; Supplemental Table 5). The binding affinity of nisoxetine was increased by 6-fold after inserting the S1 site from NET into SERT (167 versus 29 nM), whereas insertion of the S2 site had no significant effect on nisoxetine. Insertion of both the S1 and S2 sites from NET into SERT improved the binding affinity of nisoxetine to a similar level as observed when the S1 site was inserted alone (15 versus 29 nM), showing that residues located in the S1 site of SERT are key determinants for the selectivity of nisoxetine.

Similar detailed analysis was not possible for NET, since only the NET-(SERT S2) construct could bind [^{125}I]β-CIT. Interestingly, the binding affinity of nisoxetine was decreased almost to the same level as observed in SERT WT by inserting SERT S2 into NET (167 versus 104 nM compared with 4 nM at NET WT). Together with our initial analysis, which showed

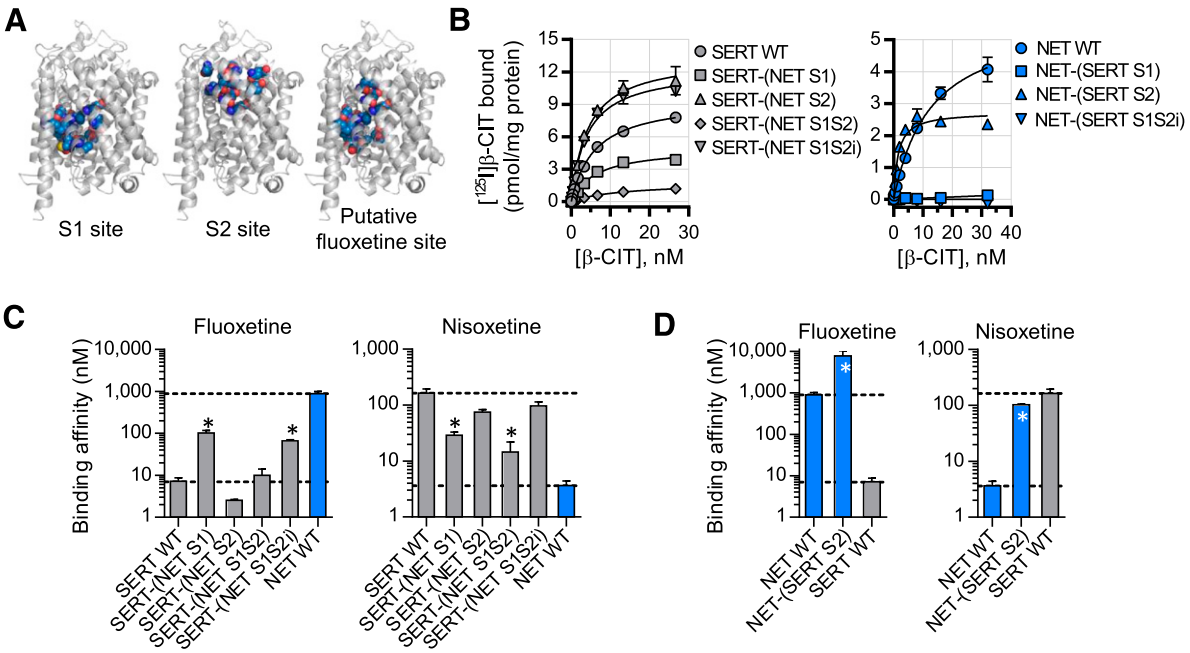


Fig. 5. (A) Location of nonconserved SERT/NET residues within 6 Å of the S1 site (left), S2 site (middle), and the putative fluoxetine binding site (right) shown on a homology model of SERT (see Supplemental Fig. 2 and Supplemental Table 5 for specific residues). (B) Saturation binding curves for [^{125}I]β-CIT binding to COS-7 membranes expressing WT and mutant forms of SERT (left) and NET (right) where all nonconserved residues within 6 Å of putative binding regions have been interchanged (for K_d and B_{max} values, see Supplemental Table 5). Data points represent mean ± S.E.M. from duplicate determinations. (C and D) The binding affinities of fluoxetine and nisoxetine were determined in an [^{125}I]β-CIT competition binding assay at WT and mutant forms of SERT (C) and NET (D), and data represent mean ± S.E.M. from at least three independent experiments each performed in duplicate (Supplemental Table 5). The stippled lines indicate the binding affinities of fluoxetine and nisoxetine at WT transporters. Asterisks denote significantly different K_i values compared with WT transporters ($P < 0.01$; Student's t test).

nonconserved S1 residues in NET to have a minor role in the selectivity of nisoxetine, this result suggested that nonconserved residues in the S2 site of NET are key determinants for the selectivity of nisoxetine. In summary, our mutational analysis of nonconserved SERT/NET residues supports the view that the selectivity of fluoxetine for SERT over NET is largely determined by nonconserved residues within the S1 site of both SERT and NET. This interpretation is fully in accordance with our proposed IFD models of fluoxetine binding within the S1 site in the two transporters. In contrast, we found that the selectivity of nisoxetine for NET over SERT is controlled by nonconserved residues in different regions of SERT (S1 residues) and NET (S2 residues). Differentiation between direct and indirect effects in mutagenesis studies is inherently difficult. Mutations can induce long-range allosteric effects that perturb a distinct binding site or induce a shift in the conformational equilibrium of the transporter that changes the temporal accessibility to the binding site. Thus, the mutational analyses do not allow us to conclusively specify the location of the nisoxetine binding site in SERT or NET, but they suggest that there is a complex mechanism for selective recognition of inhibitors in SERT and NET.

Discussion

The models of fluoxetine binding in human SERT and NET produced in the present study are based on X-ray crystal structures of LeuT and have been constructed using well-established procedures that have been implemented for modeling of other important monoamine transporter inhibitors (Andersen et al., 2010; Koldsø et al., 2010; Sinning et al., 2010; Severinsen et al., 2013). Very recently, *Drosophila* DAT and LeuBAT were crystallized in complex with antidepressants (Penmatsa et al., 2013; Wang et al., 2013). These X-ray crystal structures offer a new platform for understanding ligand interactions that have obvious potential to further push the field toward more reliable and realistic models of antidepressant binding in human transporters. However, both *Drosophila* DAT and LeuBAT are inactive in transport, and their pharmacological profiles seem to be a hybrid of the human SERT, NET, and DAT. Thus, to assess the potential of LeuBAT and *Drosophila* DAT for studying the molecular pharmacology of human transporters, it is critically important to establish similarities and discrepancies between *Drosophila* DAT and LeuBAT and their human relatives. For this purpose, comparison of our present fluoxetine model with the X-ray crystal structure of LeuBAT in complex with fluoxetine therefore provides an excellent first opportunity for assessment of the potential of LeuBAT as a model system for SSRI binding in human transporters. First and foremost, our proposed binding model of fluoxetine in SERT (SERT-Cluster 1) is in agreement with the LeuBAT structure (Wang et al., 2013) by showing that the inhibitor binds within the S1 site (Figs. 2 and 3). The observed S1 binding modes in LeuBAT and our SERT model correlate very well with our experimental validation, and can explain two key findings from the mutational analysis. Firstly, fluoxetine potency is largely affected by mutations in the S1 site (up to 79-fold loss-of-potency), whereas mutations in the S2 site generally induce <3-fold changes in fluoxetine K_i (Fig. 3; Supplemental Table 1). Secondly, our mutational analysis suggests a cation–π interaction between Tyr95 and the amino group

of fluoxetine, which is in agreement with our binding model showing that the amino group of fluoxetine is anchored between Tyr95 and Asp98 in the S1 site of SERT. A similar interaction is also observed in LeuBAT, where the amino group of fluoxetine is coordinated by the aligning residues (Tyr21 and Asp24, respectively) within the S1 site (Wang et al., 2013). Together with experimentally validated models showing other SERT inhibitors to also be anchored within the S1 site (Andersen et al., 2010; Koldsø et al., 2010; Sinning et al., 2010; Combs et al., 2011; Severinsen et al., 2013), this is in contrast to previous structural studies of LeuT in complex with antidepressants, that proposed SSRIs and TCAs to bind in the S2 site (Zhou et al., 2007, 2009). Hence, although crystal structures of LeuT have provided seminal improvements for our understanding of the overall structure and function of SERT and NET, our results emphasize that LeuBAT is an improved model system compared with LeuT for understanding the mechanism of drug binding in human transporters.

However, we do observe differences between fluoxetine binding in our model compared with the LeuBAT structure. Specifically, although the amine of fluoxetine is anchored similarly between the Tyr and Asp residues, the orientation of the two aromatic moieties of the inhibitor is reversed in our model compared with the LeuBAT structure (Fig. 6). While the CF_3-substituted phenyl ring binds between TM3 and TM8 in the LeuBAT structure, it is protruding up toward the S2 site in our model. Notably, neither from IFDs in SERT nor in NET did we identify any poses of fluoxetine in an orientation similar to the one in the LeuBAT structure (Fig. 2). Furthermore, observations from our mutational analysis of SERT are difficult to reconcile with the orientation of the two aromatic moieties of fluoxetine as found in LeuBAT. Specifically, the CF_3 group of fluoxetine is sandwiched in a groove between TM3 and TM8 in LeuBAT (Wang et al., 2013). In contrast, in our SERT model we observed an H-bond between the carbonyl group on the Asn177 side-chain and the hydroxyl group of the Thr439 side-chain, which is not conserved in LeuBAT. This H-bond constrains flexibility of TM3 and TM8 and does not allow a similar binding mode of the CF_3 group of fluoxetine in SERT (Fig. 6). Accordingly, we found that mutations of Asn177 and Thr439 induce a marked loss of potency for fluoxetine (Figs. 3 and 4), likely due to disruption of the H-bond and thereby the overall shape of the binding site rather than affecting direct interactions with the inhibitor. Also, if fluoxetine adopts the same binding mode in SERT as found in LeuBAT, Asn177 would be pointing directly toward the CF_3 group of the SSRI (Fig. 6). Thus, introduction of a negative charge into this subsite would likely cause an electrostatic repulsion with the electronegative CF_3 group, and thereby induce a loss of potency for fluoxetine. Notably, the N177E mutation had no effect on fluoxetine potency (Fig. 3), and since the H-bond to Thr439 can be preserved in the N177E mutant, this provides further support for our proposed binding model. Additionally, mutation of Ile179 in SERT has previously been shown to induce a marked loss of potency for fluoxetine (Zhou et al., 2009). This is in good agreement with our binding model, in which Ile179 is located within 3.5 Å from fluoxetine and points directly toward the subsite where the CF_3 group of fluoxetine binds (Fig. 6). In contrast, if fluoxetine adopts a similar binding mode in SERT as found in LeuBAT, Ile179 would be located >6.5 Å away from the inhibitor (Fig. 6), making it less likely that mutation at this site will have a pronounced effect on fluoxetine potency. Overall, even though fluoxetine shares the same binding site in human SERT and LeuBAT, our experimentally supported binding model of fluoxetine in SERT suggest that the SSRI has distinct binding modes in human and bacterial transporters, emphasizing the continued need for careful experimental validation when extrapolating findings from LeuBAT to human transporters.

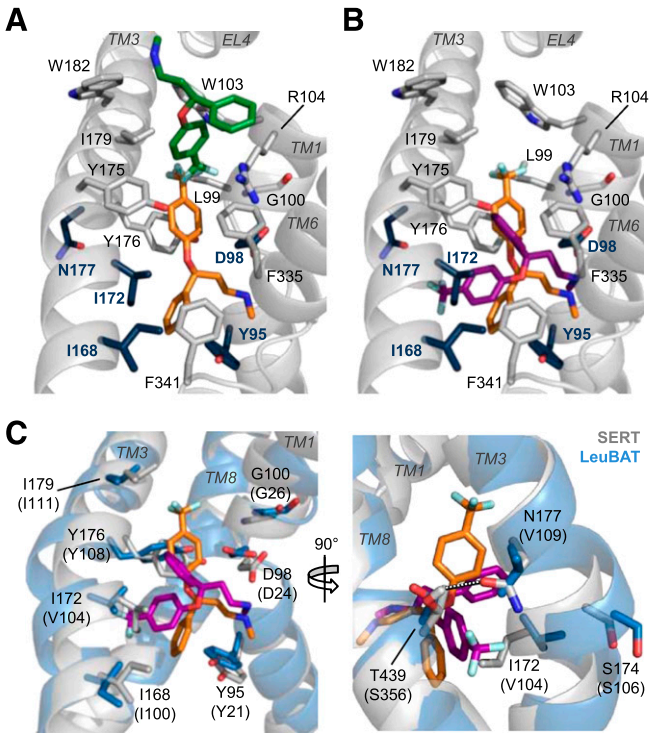


Fig. 6. (A and B) Superimposition of a representative binding pose of fluoxetine (C-atoms shown in orange) in SERT from the dominating SERT-Cluster 1 (same binding pose as shown in Fig. 2, B–E) and the binding mode of fluoxetine (C-atoms shown in green) in LeuT (PDB ID 3GWW) (A) and fluoxetine (C-atoms shown in magenta) in LeuBAT (B). The overlays are shown on the SERT model. Selected residues in proximity of the proposed binding clusters are shown as stick representations. Positions where mutations induce >10-fold changes in fluoxetine potency are highlighted in dark blue. (C) Superimposition of a representative binding pose of fluoxetine (C-atoms shown in orange) in SERT (shown in gray) and the binding mode of fluoxetine (C-atoms shown in magenta) in LeuBAT (shown in blue). Selected residues in proximity of the proposed binding clusters are shown as stick representations. Numbering and identity of LeuBAT residues are shown in brackets. H-bond between SERT residues Asn177 and Thr439 is indicated by stippled lines.

Our study provides novel insight into the molecular determinants for selective nisoxetine binding in NET by showing that nonconserved residues within the S2 site are important for high-affinity nisoxetine binding in NET (Figs. 4 and 5). Mutation of residues outside the S1 site in NET has previously been found to affect binding of nisoxetine (Paczkowski et al., 2007; Wenge and Bönisch, 2013). In addition, cocaine-like compounds, which are believed to bind in the S1 site of monoamine transporters (Beuming et al., 2008), display noncompetitive binding with nisoxetine in NET (Zhen et al., 2012). Together, these observations indicate that nisoxetine binds outside the S1 site, and are thus supportive of a recent model suggesting that nisoxetine binds to the S2 site in NET (Wang et al., 2012). However, nisoxetine is also affected by

mutations of S1 residues in NET (Mason et al., 2007; Sørensen et al., 2012), and the recent structures of *Drosophila* DAT and LeuBAT showed a common inhibitor binding site to be located within the central S1 site (Penmatsa et al., 2013; Wang et al., 2013). Taken together, it seems most likely that the high-affinity binding site for nisoxetine is located within the S1 site in NET, and that the selectivity is determined by nonconserved residues lining the S2 site that nisoxetine needs to permeate to reach the central S1 site. In contrast, we find that the molecular determinants that underlie the lower potency of nisoxetine in SERT are primarily located among nonconserved residues within the S1 site of this transporter (Figs. 4 and 5). This is in agreement with previous findings for other S1 residues in SERT that have been shown to be important for recognition of nisoxetine in SERT (Walline et al., 2008; Sørensen et al., 2012). Hence, in contrast to fluoxetine, where S1 residues in both SERT and NET control binding and selectivity (Figs. 3 and 4), selective binding of nisoxetine is controlled by residues in separate regions of the two transporters. Interestingly, the same pattern has also been found for the SSRI escitalopram and the structurally closely related NET selective inhibitor talopram (Andersen et al., 2011). Thus, the finding that the selectivity of seemingly closely related inhibitors is controlled by residues located in different regions of two closely related transporters suggests a complexity of the molecular pharmacology of monoamine transporters that warrants further studies.

In summary, our findings add important new information on the molecular basis for SERT/NET selectivity of antidepressants and provide the first assessment of the potential of LeuBAT as a model system for antidepressant binding to human transporters. Along with a growing number of other LeuT-derived models of inhibitor binding, we can now begin to understand the differences and similarities among the inhibitory mechanisms of antidepressants in a structural context. This is essential for establishing a useful framework for structure-based drug development of future monoamine transporter drugs with fine-tuned transporter selectivity.

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Authorship Contributions

Participated in research design: Andersen, Koldsø, Schiøtt, Strømgaard, Kristensen.

Conducted experiments: Andersen, Stuhr-Hansen, Zachariassen, Koldsø.

Performed data analysis: Andersen, Koldsø, Schiøtt, Strømgaard, Kristensen.

Wrote or contributed to the writing of the manuscript: Andersen, Koldsø, Schiøtt, Strømgaard, Kristensen.

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