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Article

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Dopamine D_4 Receptor-Selective Compounds Reveal Structure-Activity Relationships that Engender Agonist Efficacy

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KEYWORDS. Dopamine D_4 receptor, partial agonist, antagonist, phenylpiperazine, cognition, molecular modeling and simulation

ABSTRACT

The dopamine D_4 receptor (D_4R) plays important roles in cognition, attention, and decision making. Novel D_4R-selective ligands have promise in medication development for neuropsychiatric conditions, including Alzheimer's disease and substance use disorders (SUD). To identify new D_4R-selective ligands, and to understand the molecular determinants of agonist efficacy at D_4R, we report a series of eighteen novel ligands based on the classical D_4R agonist A-412997 (**1**, 2-(4-(pyridin-2-yl)piperidin-1-yl)-*N*-(*m*-tolyl)acetamide). Compounds were profiled using radioligand binding displacement assays, β-arrestin recruitment assays, cAMP inhibition assays, and molecular dynamic computational modeling. We identified several novel D_4R-selective ($K_i \leq 4.3$ nM and >100-fold vs. other D_2-like receptors) compounds with diverse partial agonist and antagonist profiles, falling into three structural groups. These compounds highlight receptor-ligand interactions that control efficacy at D_2-like receptors and may provide insights to targeted drug discovery leading to a better understanding of the role of D_4Rs in neuropsychiatric disorders.

INTRODUCTION

The dopamine D_4 receptor (D_4R) is a G protein-coupled receptor and a member of the D_2-like subfamily of dopamine receptors (including D_2R, D_3R and D_4R). D_2-like receptors have high sequence homology and share a $G_{\alpha i/o}$-coupled signaling mechanism, but differ substantially in localization within the brain and at the subcellular level.[1] Compared with D_2Rs and D_3Rs, D_4Rs have the lowest level of expression in the brain, and show a unique distribution pattern with most located in the prefrontal cortex (PFC) and hippocampus. The other D_2-like receptors are primarily in the striatum, basal ganglia and pituitary gland regions; regions associated D_2R-targeting antipsychotic drugs and the motor and endocrine side-effects commonly observed with them.[2-3] In contrast, D_4Rs expressed in PFC and hippocampus affect attention, exploratory behavior,[3] and performance in novel object recognition[4-5] and inhibitory avoidance[6] cognitive tasks. Therefore, pharmacological activation of D_4Rs may be useful to treat cognitive deficits associated with schizophrenia[7-10] and ADHD.[10-11] Additional research has explored D_4R agonism as a strategy to reduce the adverse effects of opioid drugs like morphine.[12-13] D_4R antagonism may be useful to treat substance use disorders (SUDs), particularly psychostimulant addiction, and L-DOPA-induced dyskinesias.[10, 14-20] The importance of targeting D_4Rs in treating these complex pathologies, especially in regards to the extent of receptor activation or inhibition, remains unknown, partially due to a lack of suitable compounds for investigating these pathways.

A-412997 (**1**, 2-(4-(pyridin-2-yl)piperidin-1-yl)-*N*-(*m*-tolyl)acetamide, Figure 1) was initially characterized as a "full agonist" (83% intrinsic activity) at D_4R, with high selectivity over D_2R and D_3R and *in vivo* effects that included induction of penile erection in rats.[21-22] Subsequent *in vivo* evaluations showed improved cognitive performance in social recognition tasks, novel object recognition tasks, and 5-trial repeated acquisition inhibitory avoidance tasks following treatment

by **1** (or similar D_4R agonists PD168077 (**2**) and CP226269 (**3**)); suggesting an important role for D_4R signaling in mediating short-term memory and cognition.[5, 23]

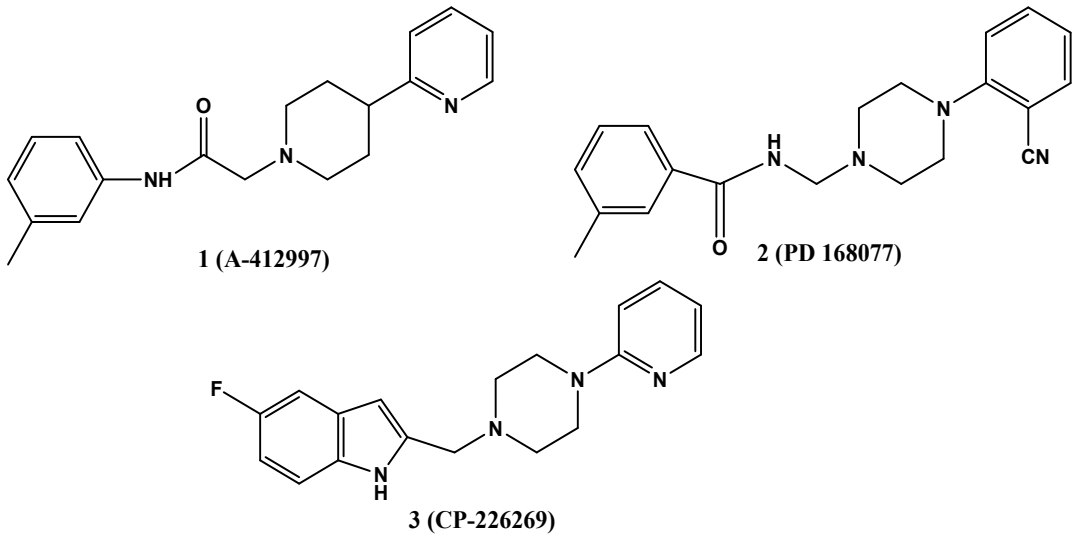


Figure 1. Three classic D_4R-selective partial agonists.

The goals of this study were to develop new D_4R agonists with a range of efficacy levels and to identify the molecular components that engender ligand efficacy at D_4R. To that end, we employed a rational drug design strategy incorporating classic structure-activity relationship (SAR) analysis around lead compound **1**. These studies were enhanced by detailed *in silico* molecular dynamics simulations exploiting the recently reported crystal structure of D_4R.[24] Furthermore, comparative analyses were done using the D_3R crystal structure[25] and the recently reported D_2R structure.[26]

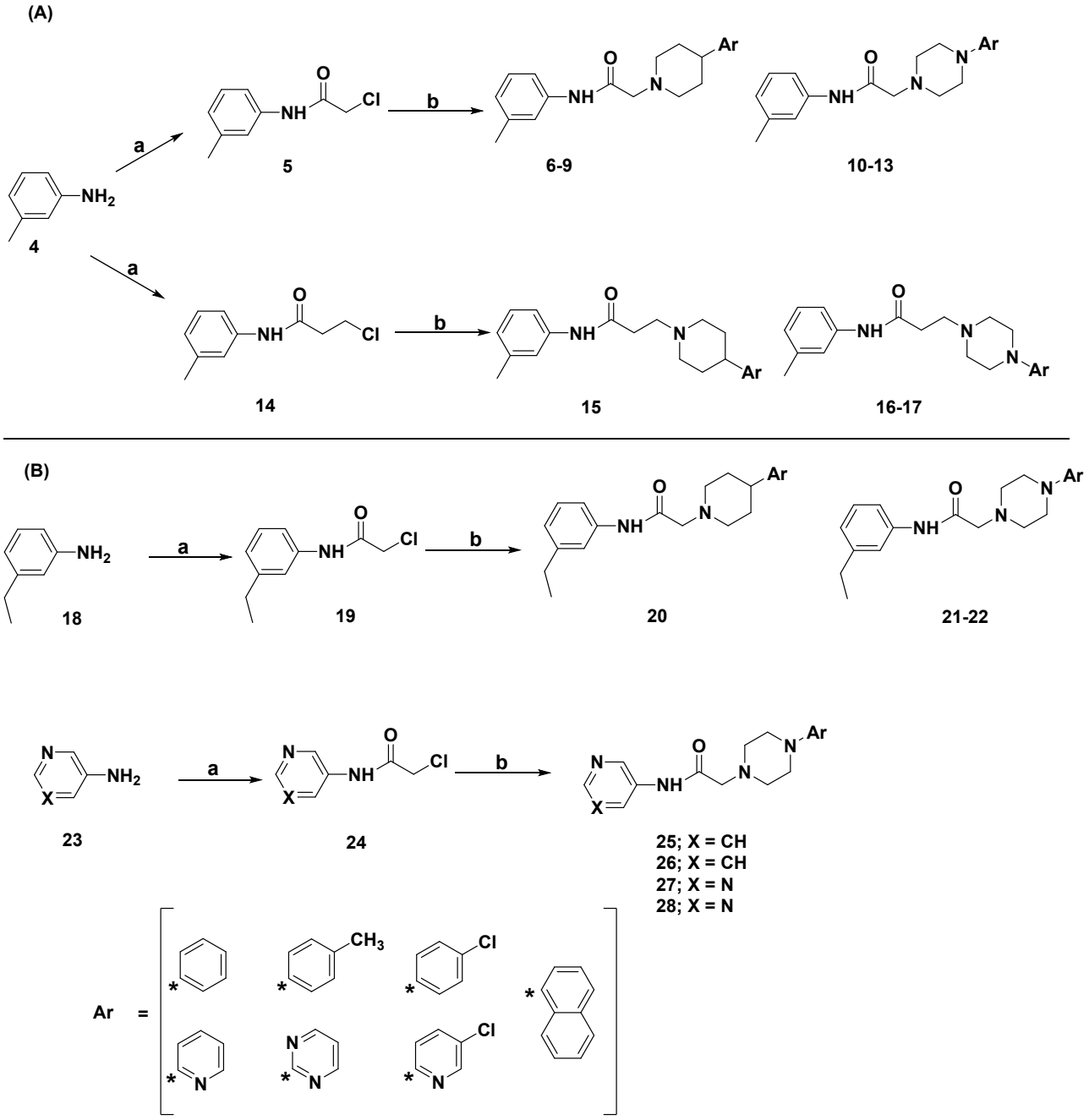
We synthesized a library of analogues primarily featuring modifications in the phenylpiperidinyl region of **1**, with additional variations in linker chain length and substitutions on the amidylphenyl region. Following extensive *in vitro* analyses, including binding and functional studies, we determined that selected modifications resulted in novel analogues with improved subtype

selectivity. Furthermore, we identified three classes of modifications that resulted in altered efficacy profiles at all D_2-like receptors. In order to determine key receptor-ligand interactions, and identify the molecular substrates of a putative "efficacy switch," the library was docked in receptor models of D_2R, D_3R, and D_4R using molecular dynamics simulations.

CHEMISTRY

Ligands were synthesized as outlined in Scheme 1 using routine N-alkylation reactions previously reported.[21, 27] The commercially available *m*-toluidine **4** was converted to intermediate 2-chloro-*N*-(*m*-tolyl)acetamide **5** by reacting with 2-chloroacetyl chloride in the presence of triethylamine and ethyl acetate at room temperature.[28] Using the same procedure, intermediates **14**, **19**, and **24** were synthesized in a similar manner, as indicated in Scheme 1, with either a one- or two-carbon linker. The intermediate compounds **5**, **14**, **19**, and **24** were used to alkylate different commercially available arylpiperazine or arylpiperidine amines in the presence of K_2CO_3 in CH_3CN under reflux conditions to yield the desired target compounds **6**–**9**, **10**–**13**, **15**–**17**, **20**–**22**, and **25**–**28**, respectively, with the exception of the synthesis of 1-(naphthalen-1-yl)piperazine which was previously reported[29] via nucleophilic substitution reaction with naphthalen-1-amine.

Scheme 1. Synthesis of 2-(4-(pyridin-2-yl)piperidin-1-yl)-*N*-(*m*-tolyl)acetamide analogues[a]



[a] Reagents and Conditions: (a) Triethylamine, EtOAc, RT; (b) CH_3CN, K_2CO_3, Reflux, appropriate arylpiperazine or arylpiperidine.

PHARMACOLOGICAL RESULTS AND DISCUSSION

Structure-Activity Relationships at Dopamine D_2-Like Receptors.

A primary objective of this study was to design ligands with high D_4R binding affinity and subtype selectivity. The compound **1** and several designed analogs are shown in Figure 2. In order to obtain D_4R ligands with high affinity and selectivity, using compound **1** as our lead compound, we employed three modification strategies, creating 2-(piperidin-4-yl)pyridinyl analogs, altering the linker chain length, and creating *N*-(*m*-tolyl)acetamide analogs.

Of note, when **1** was evaluated in two different functional assays, its profile was clearly that of a *partial* agonist rather than a full agonist as it is often described in the literature. In the agonist mode for both the cAMP accumulation and β-arrestin recruitment assays, **1** had an E_{max} of 61.9% and 22.5%, respectively, when normalized to dopamine.

The 2-pyridine moiety of **1** was replaced with a phenyl in **6**, *para*-tolyl in **7**, 4-chlorophenyl in **8**, and 5-methylpyridin-2-yl in **9**. The piperidine attached to the linker chain was replaced with a piperazine to form **10**, replaced with a pyrimidine to form **11**, replaced with a 5-chloropyridin-2-yl to form **12**, and replaced with a naphthyl substituent to obtain **13**. To evaluate the contribution of the alkyl chain to the binding affinity and selectivity, we synthesized alkyl chain length analogs of compounds **1**, **10** and **11**, adding an extra methylene to the linker chain in compounds **15**, **16**, and **17**, respectively. Finally, we probed the contribution of the *N*-(3-methylphenyl)acetamide moiety via replacement of the methyl with ethyl (compounds **20**, **21** and **22**, compared to compounds **1**, **10**, and **12**, respectively) or replaced of the entire *N*-(3-methylphenyl)acetamide moiety with heteroaromatics (compounds **25-28**).

In order to best evaluate comparative affinities, two different radioligands were used in competition binding studies: [^{3}H]*N*-methylspiperone, a high-affinity D_2-like antagonist, and [^{3}H]-(*R*)-(+)-7-OH-DPAT, a D_2-like agonist. Importantly, the binding affinities of D_2-like agonists and high-efficacy partial agonists are considerably higher when competing against an agonist radioligand because high-affinity agonist binding incorporates an efficacy measure in that the greater the efficacy for inducing G protein coupling, the greater the "apparent" affinity will be. On the other hand, antagonist binding, and competition for it, is unlinked from efficacy and therefore unbiased. Therefore, because these radioligands probe different receptor states, they provide complimentary views of ligand binding,[30] which are particularly valuable when examining affinity of partial agonists.

Several modifications of **1** resulted in modest improvements in D_4R affinity as measured by competition assays with [^{3}H]*N*-methylspiperone (up to ~3-fold) and [^{3}H]-(*R*)-(+)-7-OH-DPAT (up to ~3-fold). However, marked improvements in D_4R selectivity over D_2R and D_3R resulted from a variety of modifications, typically driven by a loss of affinity at D_2R and D_3R.

2-pyridine substitutions resulted in a potency gain when the piperidinyl moiety was replaced with piperazinyl (e.g., **10** and **21**). Adding an extra methylene to the linker chain, as in compounds **15**, **16**, and **17**, significantly diminished D_4R affinity and selectivity. These results are consistent with previous studies that determined the importance of carboxamide linker length for D_2-like receptor selectivity.[31] Replacement of the methyl with an ethyl at the *N*-(3-methylphenyl)acetamide moiety (compounds **20**, **21** and **22**) did not substantially alter affinity or selectivity for D_4R compared to methyl analogues **1**, **10**, and **12**, respectively. Replacement of the entire *N*-(3-methylphenyl)acetamide moiety with heteroaromatics (compounds **25-28**) uniformly led to loss of affinity and selectivity.

Overall, we noted three broader classes of modifications with distinct binding and efficacy profiles across the D_2-like receptors; as outlined in Figure 2, these include 1) substitution of the piperidine ring for piperazine, 2) substitution of the pyridine ring with a phenyl or napthyl moiety, and 3) *para*-substituted pyridine rings. These classes formed the basis for further structure-activity relationship profiling and modeling studies using molecular dynamics simulations.

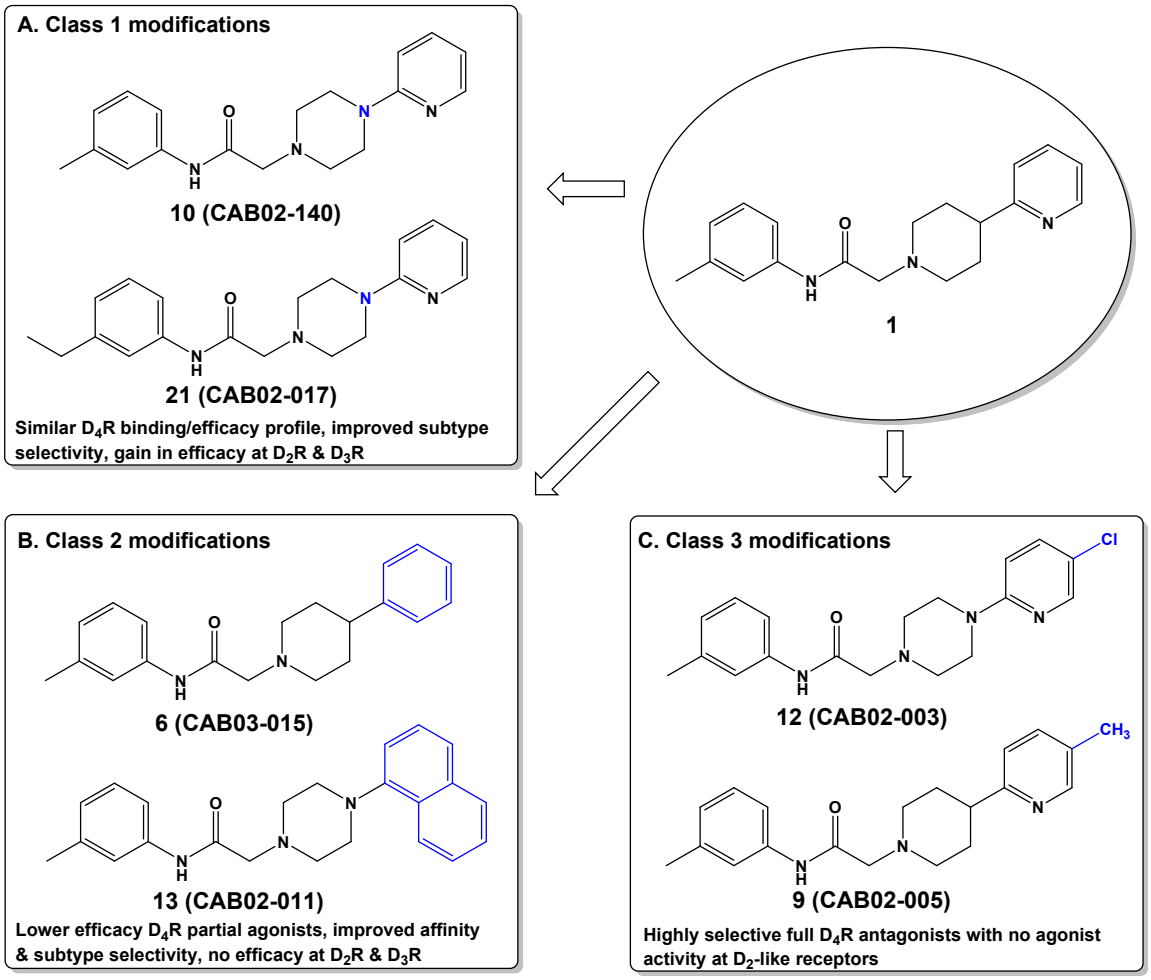
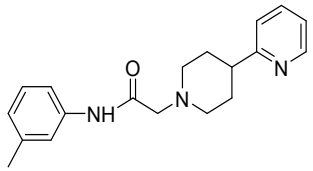
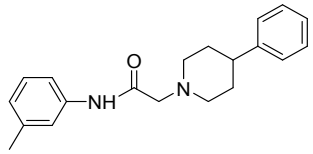
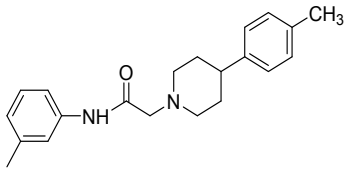
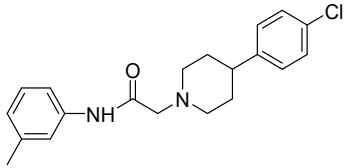
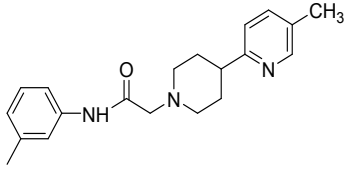


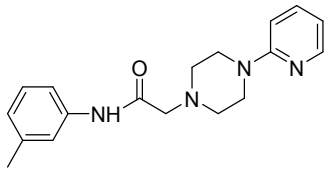
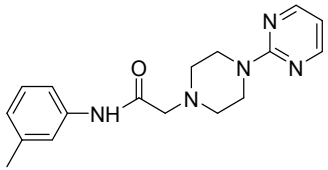
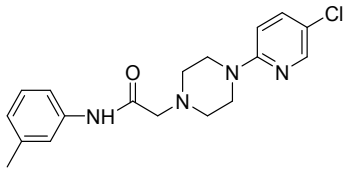
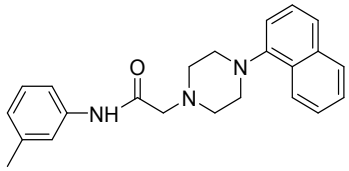
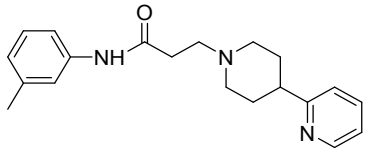
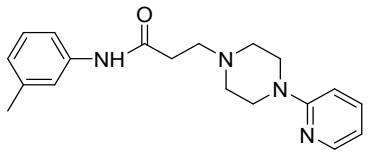
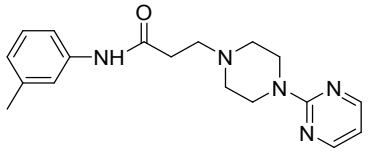
Figure 2. Three classes of modifications to the structure of **1** resulting in differing binding and efficacy profiles at D_2-like receptors. A. Substitution of piperidine ring for piperazine induced a gain of efficacy at D_2R and D_3R with insubstantial changes to D_4R efficacy. B. Substitution of the pyridine ring with a phenyl or napthyl moiety produced modest D_4R subtype selectivity

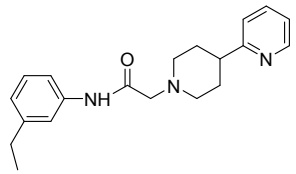
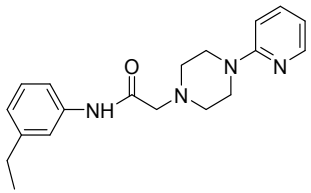
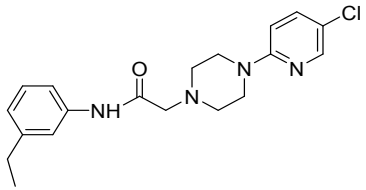
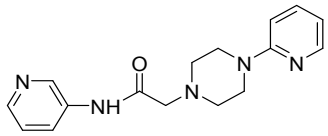
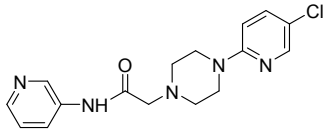
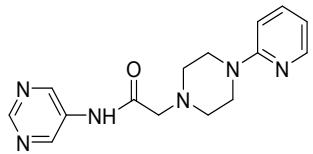
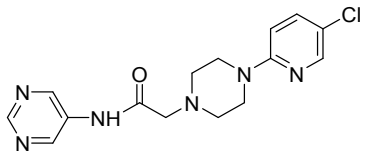
improvements and lowered partial agonist efficacy at D_4R with no agonist activity at D_2R or D_3R. C. *para*-substituted pyridine rings produced highly D_4R-selective antagonists.

The parent compound, **1**, showed 115-fold and 31-fold higher affinity for D_4R over D_2R and D_3R, respectively, as measured by [^{3}H]*N*-methylspiperone competition. When examined using [^{3}H]-(*R*)-(+)-7-OH-DPAT competition, **1** had higher affinity at all subtypes (consistent with an agonist radioligand being displaced by a compound that favors the activated receptor[30]), and showed a similar selectivity profile of 64-fold and 42-fold higher affinity for D_4R over D_2R and D_3R, respectively. Full binding results are presented in Table 1. Functional characterization revealed **1** to be a partial agonist at D_4R as measured in β-arrestin assays (E_{max} = 22.5%, EC_{50} = 473 nM) (Figure 3A and B) and cAMP inhibition assays (E_{max} = 61.9%, EC_{50} = 2.7 nM) (Figure 3B and C). The higher efficacy observed in the cAMP assay is likely due to spare receptors and/or amplification of cAMP accumulation vs. recruitment of β-arrestin. Consistent with a partial agonist profile, **1** and related analogs were partial antagonists when run in antagonist mode (Figure 3B and D), blocking function to a similar degree as their maximal agonist activity. This would be expected for a compound that is a partial agonist that maintains affinity for the orthosteric part of the receptor thereby acting as a partial antagonist in antagonist assays. Importantly, **1** showed no measurable agonist response on D_2R-mediated β-arrestin recruitment but behaved as a low affinity full antagonist (Figure 3E). Furthermore, **1** has very low potency and efficacy at the D_3R (Figure 3F). Complete functional results are presented in Tables 2 and 3. These data indicate that **1** is a potent and highly selective partial agonist at the D_4R.

Table 1. Human dopamine D_2-like receptor binding data in HEK293 membranes for ligands with varying arylpiperazine and arylamide moieties.[a]

Compound	Structure	K_i (nM) ± SEM [^{3}H]*N*-methlyspiperone					K_i (nM) ± SEM [^{3}H]7-OH-DPAT				
		D_2R	D_3R	D_4R	D_2R/D_4R	D_3R/D_4R	D_2R	D_3R	D_4R	D_2R/D_4R	D_3R/D_4R
1; A-412997[21-22]		6250 ± 375	1680 ± 446	54.2 ± 7.01	115	31	251 ± 72.2	167 ± 38.8	3.95 ± 1.41	64	42
6; (CAB03-015)[22]		821 ± 34.9	433 ± 137	25.8 ± 9.01	32	17	127 ± 35.8	777 ± 141	1.4 ± 0.42	91	555
7; (CAB02-007HP)		7824 ± 347	3681 ± 1237	110.4 ± 55	71	33					
8; (CAB02-009HP)		>50,000	26,320 ± 12,028	115.2 ± 42	>434	228					
9; (CAB02-005HP)		>50,000	>50,000	41.7 ± 7.0	>1198	>1198	>10,000	>10,000	6.87 ± 0.73	>1455	>1455

10; (CAB02-140)[22, 27]		>10,000	>10,000	212 ± 62.9	>47	>47	3320 ± 450	6480 ± 972	1.89 ± 0.38	1757	3429
11; (CAB02-110)		6400 ± 3800	>10,000	318 ± 95.1	20	>31	2420 ± 219	5990 ± 2040	5.66 ± 0.42	428	1058
12; (CAB02-003HP)		>50,000	>50,000	95 ± 26	>526	>526	>10,000	>10,000	12.5 ± 1.85	>800	>800
13; (CAB02-011HP)		1489 ± 95	11,459 ± 3085	28.4 ± 8	52	402	200 ± 38.1	1246 ± 195	1.65 ± 0.21	121	755
15; (CAB02-120)		5940 ± 556	3040 ± 1350	>10,000	<0.6	<0.31	80.3 ± 28.6	510 ± 57.3	76.4 ± 7.09	1.1	6.7
16; (CAB02-142)		11,900 ± 2580	3790 ± 462	297 ± 34.2	40	1276	200 ± 18	781 ± 68.6	32.2 ± 8.28	6	24
17; (RNB01-007)		1850 ± 333	4530 ± 2010	526 ± 128	3.5	8.6	1490 ± 275	9350 ± 288	33 ± 2.52	45	2833

20; (CAB02-021HP)		1159 ± 241	496 ± 36	82.3 ± 36	14	6.0					
21; (CAB02-017HP)		>50,000	>50,000	67.9 ± 24	>736	>736	603 ± 220	1490 ± 275	2.23 ± 0.93	270	668
22; (CAB02-019HP)		46,260 ± 3740	>50,000	172.2 ± 28	269	>290					
25; (CAB02-033HP)		>50,000	>50,000	6407 ± 1678	>7.8	>7.8					
26; (CAB02-035HP)		>50,000	>50,000	5000 ± 296	>10	>10					
27; (CAB02-029HP)		>50,000	>50,000	39,290 ± 10,710	>1.2	>1.2					
28; (CAB02-031HP)		>50,000	>50,000	>50,000							

[a] K_i values determined by competitive inhibition of [^{3}H]*N*-methylspiperone or [^{3}H]-(*R*)-(+)-7-OH-DPAT binding in membranes harvested from HEK 293 cells stably expressing hD_2R, hD_3R, or hD_4R. All K_i values are presented as means ± SEM.

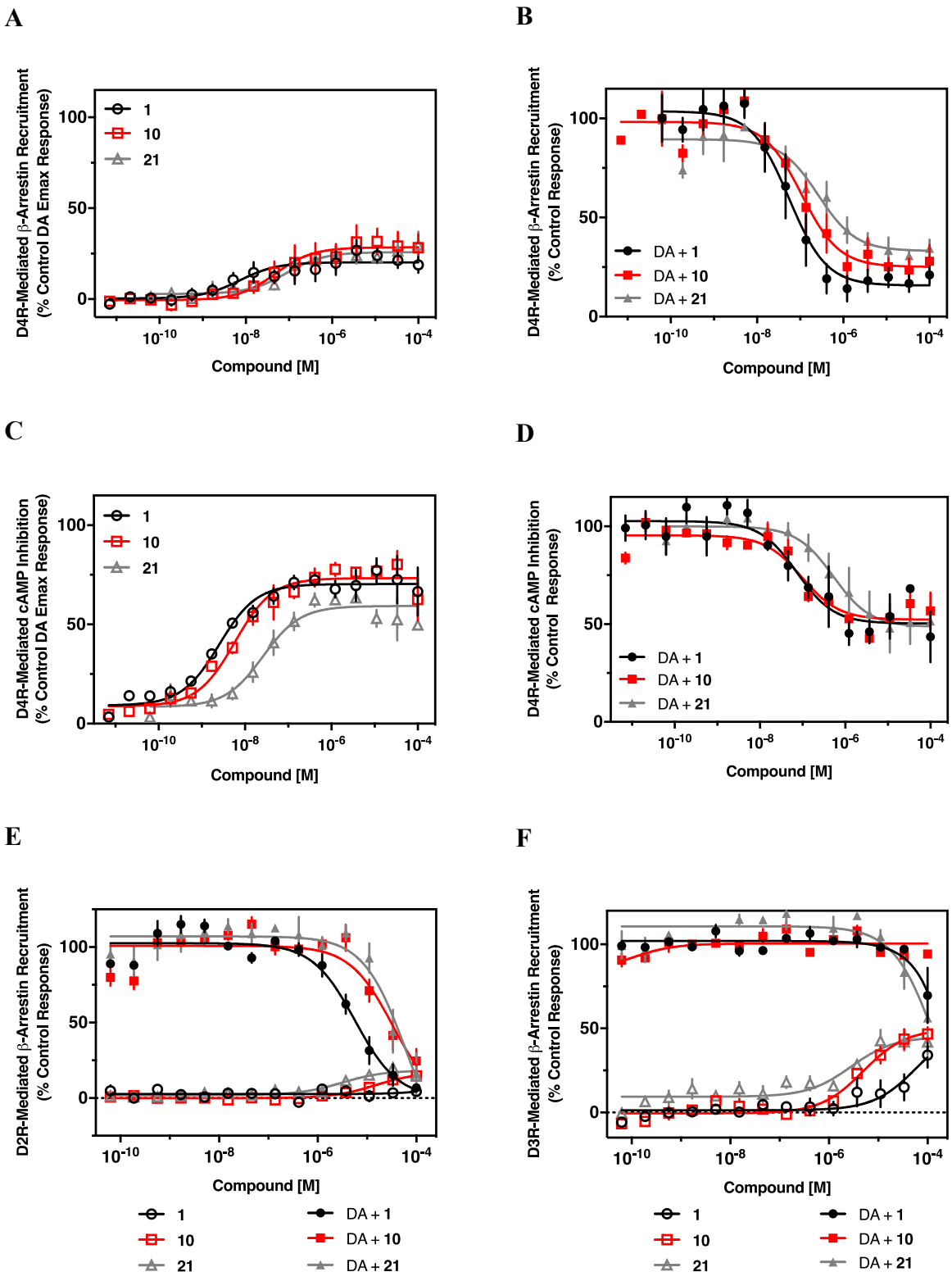

A
D4R-Mediated β-Arrestin Recruitment (% Control DA Emax Response)
1
10
21
Compound [M]
B
D4R-Mediated β-Arrestin Recruitment (% Control Response)
DA + 1
DA + 10
DA + 21
Compound [M]
C
D4R-Mediated cAMP Inhibition (% Control DA Emax Response)
1
10
21
Compound [M]
D
D4R-Mediated cAMP Inhibition (% Control Response)
DA + 1
DA + 10
DA + 21
Compound [M]
E
D2R-Mediated β-Arrestin Recruitment (% Control Response)
Compound [M]
1
10
21
DA + 1
DA + 10
DA + 21
F
D3R-Mediated β-Arrestin Recruitment (% Control Response)
Compound [M]
1
10
21
DA + 1
DA + 10
DA + 21

Figure 3. Compounds 10 (red) and 21 (gray) show similar pharmacology to parent compound 1 (black). D_4R-expressing stable cells lines were plated and compounds were assayed for agonist (**A**) and antagonist (**B**) activity on β-arrestin recruitment. Similarly, D_4R-mediated inhibition of cAMP accumulation was also examined in both agonist (**C**), and antagonist (**D**) modes, as indicated. Assays were conducted as described in the Experimental Procedures; briefly, agonist assays were conducted by incubating the cells with the indicated concentration of test compound and measuring luminescence. Antagonist assays were conducted by incubating the compound with an EC_{80} concentration of dopamine (1 μM for β-arrestin and 10 nM in cAMP) and the indicated concentration of test compound. For cAMP assays cells were first stimulated with 10 μM forskolin. Agonist mode assays are expressed as a percentage of the maximum dopamine response, whereas antagonist mode assays are expressed as a percentage of dopamine's EC_{80} response. E_{max} and EC_{50} values are shown in Table 2 and 3. Data were fit using nonlinear regression of individual experiments performed in triplicate and are shown as means ± SEM; n = 3. Dopamine and sulpiride were run during each assay as positive controls for a full agonist and full antagonist respectively (data not shown). Compounds were also tested for both agonist and antagonist activity on cells stably expressing the closely related D_2R (**E**) or D_3R (**F**). Assays were conducted as described in the Experimental Procedures. Agonist mode assays (open symbols) are expressed as a percentage of the maximum dopamine response observed for each receptor, whereas antagonist mode assays (solid symbols) are expressed as a percentage of dopamine's EC_{80} response. E_{max} and EC_{50} values are shown in Table 2 and 3. Data were fit using nonlinear regression of individual experiments performed in triplicate and are shown as means ± SEM; n = 3.

Replacing the piperidinyl ring of **1** with a piperazine (Figure 2, Class 1)—typified by **10** and **21**—resulted in similar binding and agonist efficacy profiles at D_4R, improved subtype selectivity (Tables 1 and 2), and a gain in efficacy at both D_2R and D_3R (Figure 3 and Table 2 and 3). Replacing the pyridinyl ring of **1** with a phenyl or napthyl moiety (Figure 2, Class 2),—typified by **6** and **13**—resulted in improved subtype selectivity, and importantly a diminished-efficacy partial agonist profile at D_4R. These compounds showed no measurable agonist efficacy at either D_2R or D_3Rs (Figure 4). A *para*- substitution on the pyridinyl ring of **1** (Figure 2, Class 3)—typified by **12** and **9**—resulted in compounds that lost all agonist efficacy but retained high-affinity binding at D_4R, with very minimal binding at D_2R or D_3R. The compounds showed potent antagonism of the D_4R response with minimal low potency D_2R blockade and no measurable affinity or efficacy at D_3R. Therefore, this class of compounds represents highly selective D_4R antagonists with no measurable agonist efficacy on any D_2-like receptor (Figure 5, Table 1-3).

Individual compounds within Classes 1-3 resulted in modest changes to overall efficacy and potency as overviewed in Tables 1-3. For this reason, we chose to focus on typified examples of a range of agonist efficacy (higher, medium, and none) at the D_4R. Using these classes, we performed molecular dynamic simulations to identify interaction sites on the receptor that may play a pivotal role in engendering agonist selectivity and efficacy.

Table 2. Efficacy as measured via modulation of cAMP accumulation.[a]

Compound	D_2R efficacy				D_4R efficacy				EC_{50}	IC_{50}
	cAMP E_{max} %[b]	cAMP EC_{50} (nM)	cAMP Ant. %[c]	cAMP IC_{50} (nM)	cAMP E_{max} %[b]	cAMP EC_{50} (nM)	cAMP Ant. %[c]	cAMP IC_{50} (nM)	D_2R/D_4R	D_2R/D_4R
1	Inactive	Inactive	ND	>50,000	61.9 ± 4.7	2.7 ± 0.9	53.8 ± 6.0	68.4 ± 32.8	ND	>735
6	Inactive	Inactive	100 ± 0.00	16,447 ± 3540	32.9 ± 3.9	15.4 ± 13.2	46.7 ± 6.0	2.0 ± 0.05	ND	8224
7	Inactive	Inactive	100 ± 0	44,834 ± 28,125	Inactive	Inactive	95.8 ± 2.2	3064 ± 1220	ND	15
8;	Inactive	Inactive	97.5 ± 2.5	71,437 ± 28,563	Inactive	Inactive	100 ± 0	70,157 ± 20,766	ND	1.0
9	Inactive	Inactive	100 ± 0	71065 ± 20585	Inactive	Inactive	100 ± 0	453 ± 15	ND	157
10	18.96 ± 5.2	763 ± 386	ND	>100,000	64.2 ± 5.7	3.6 ± 1.3	43.2 ±1.8	82.7 ± 37.9	214	>1210
11	54.4 ± 7.5	2092 ± 46	ND	>100,000	64.6 ± 4.2	3.4 ± 2.0	45.0 ± 7.7	463 ± 157	612	>216
15	83.1 ± 4.2	50.1 ± 25	ND	>100,000	28.1 ± 1.6	349 ± 75	77.6 ± 5.2	6343 ± 2524	0.14	>16
16	79.7 ± 8.4	154 ± 31	ND	>100,000	30.0 ± 2.1	612 ± 563	84.2 ± 6.0	1629 ± 255	0.25	>61
17	Inactive	Inactive	ND	>100,000	13.7 ± 1.2	568 ± 456	87.0 ± 3.4	2120 ± 534	ND	>47
12	Inactive	Inactive	98.3 ± 1.7	66,077 ± 18,646	Inactive	Inactive	93.4 ± 2.6	4701 ± 1466	ND	14
13	Inactive	Inactive	100 ± 0	68,329 ± 31,671	27.8 ± 8.4	108.5 ± 94.3	73.8 ± 13.6	2521 ± 1067	ND	27
20	Inactive	Inactive	96.6 ± 3.5	16,278 ± 11,601	25.6 ± 7.2	539 ± 151	70.8 ± 15	1908 ± 242	ND	9
21	18.80 ± 8.19	1600 ± 396	88 ± 6.1	40,466 ± 29,968	58.0 ± 1.8	28.7 ± 9.9	58.4 ± 9.7	1311 ± 814	56	31
22	Inactive	Inactive	100 ± 0	46,795 ± 27,644	Inactive	Inactive	100 ± 0	7059 ± 1136	ND	7
25	38.6 ± 3	1965 ± 44	100 ± 0	>100,000	47.3 ± 7.9	1075 ± 390	100 ± 0	86,493 ± 3130	2.0	>1.1
26	Inactive	Inactive	100 ± 0	86,617 ± 13,383	Inactive	Inactive	100 ± 0	40,000 ± 9421	ND	2
27	Inactive	Inactive	98.1 ± 1.5	94,255 ± 5745	Inactive	Inactive	100 ± 0	>100,000	ND	<1
28	Inactive	Inactive	76.2 ± 17.6	72,516 ± 18,052	Inactive	Inactive	100 ± 0	>100,000	ND	<1

[a] values determined by nonlinear regression of individual experiments run in triplicate as detailed in materials and methods under cAMP accumulation assays. All EC_{50}, IC_{50}, and E_{max} values are presented as means ± SEM; n = 3-4. ND indicates Not Determined due to an incomplete curve. Inactive indicates no measurable activity in indicated assay.

[b]A measure of agonism as defined by the maximum inhibition of cyclic AMP observed for each compound.

[c]A measure of antagonism as defined by the maximum blockade of dopamine mediated cAMP inhibition by each compound.

Table 3. Efficacy as measured via modulation of β-arrestin recruitment.[a]

Compound	D_2R efficacy				D_3R efficacy				D_4R efficacy				EC_{50}		IC_{50}	
	β-arr E_{max}	β-arr $EC_{50\ (nM)}$	β-arr Ant. %	β-arr IC_{50}	β-arr E_{max}	β-arr $EC_{50\ (nM)}$	β-arr Ant. %	β-arr IC_{50}	β-arr E_{max}	β-arr $EC_{50\ (nM)}$	β-arr Ant. %	β-arr IC_{50}	D_2R/D_4R	D_3R/D_4R	D_2R/D_4R	D_3R/D_4R
1	Inactive	Inactive	94.8 ± 2.8	5846 ± 1802	ND	>100,000	ND	>100,000	22.5 ± 3.98	473 ± 457	81.7 ± 2.7	191 ± 98	ND	>4	31	>524
6	Inactive	Inactive	99.7 ± 0.3	7692 ± 2301	Inactive	Inactive	ND	>50,000	14 ± 0.3	242 ± 89	93.3 ± 1.8	135 ± 65	ND	ND	57	>371
7	Inactive	Inactive	100 ± 0	89,153 ± 10,847	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	100 ± 0	7352 ± 1749	ND	ND	12	ND
8	Inactive	Inactive	100 ± 0	>100,000	Inactive	Inactive	Inactive	Inactive	Inactive	inactive	100 ± 0	42,357 ± 30,018	ND	ND	>2	ND
9	Inactive	Inactive	100 ± 0	>100,000	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	98.1 ± 2	394 ± 78	ND	ND	>254	ND
10	23.9 ± 5.1	26,175 ± 12,448	76.5 ± 6.9	16,010 ± 5174	49.4 ± 2.0	6354 ± 2617	Inactive	>100,000	30.7 ± 6.4	394 ± 294	78.9 ± 3.1	313 ± 215	66	>16	51	>320
11	39.6 ± 5.3	8321 ± 3455	78.9 ± 8.6	25,008 ± 5017	58.4 ± 6.6	5581 ± 1614	Inactive	>100,000	24.7± 5	278 ± 167	80.6 ± 3.0	197 ± 115	30	>20	127	>509
15	48.9 ± 6.8	2480 ± 1834	72.1 ± 7.9	7627 ± 1573	55.4 ± 1.57	970 ± 115	ND	>50,000	Inactive	Inactive	98.7 ± 1.0	3805 ± 2944	12	>5	2.0	>26
16	44.1 ± 6.3	1455 ± 572	77.7 ± 3.7	7067 ± 2290	41.4 ± 5.83	1601 ± 867	ND	>50,000	Inactive	Inactive	97.9 ± 1.2	1086 ± 597	ND	>1	7.0	>46
17	Inactive	Inactive	94.6 ± 5.4	11,847 ± 2000	Inactive	Inactive	ND	>50,000	Inactive	Inactive	97.1 ± 0.8	430 ± 195	ND	ND	28	>116
12	Inactive	Inactive	100 ± 0	>100,000	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	100 ± 0	7777 ± 2166	ND	ND	>13	ND
13	Inactive	Inactive	100 ± 0	>100,000	Inactive	Inactive	Inactive	Inactive	16.4 ± 3.9	9212 ± 6238	96.7 ± 2.7	4252 ± 1077	ND	ND	>24	ND
20	Inactive	Inactive	100 ± 0	67,613 ± 17,748	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	91.7 ± 6.8	2622 ± 678	ND	ND	26	ND
21	18.7 ± 0.4	3887 ± 1878	100 ± 0	88,447 ± 11,553	44.7 ± 5.9	2755 ± 472	100 ± 0	88205 ± 9631	26.2 ± 5.1	133 ± 60.3	59.7 ± 4.6	370 ± 105	29	21	239	238
22	Inactive	Inactive	100 ± 0	70,703 ± 29,297	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	80.4 ± 6.0	10,449 ± 2482	ND	ND	6.8	ND
25	21.3 ± 6.8	48,503 ± 27,571	Inactive	Inactive	18.6 ± 2.7	2802 ± 2507	Inactive	Inactive	19.0 ± 2.7	2657 ± 121	100 ± 0	25,780 ± 9773	18	1.0	ND	ND
26	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	93.1 ± 7	23,450 ± 11,959	ND	ND	ND	ND
27	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	ND	ND	ND	ND
28	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	Inactive	100 ± 0	>100,000	ND	ND	ND	ND

[a] values determined by nonlinear regression of individual experiments run in triplicate as detailed in materials and methods under β-arrestin assays. All EC_{50}, IC_{50}, and E_{max} values are presented as means ± SEM; n = 3-4. ND indicates Not Determined due to an incomplete curve. Inactive indicates no measurable activity in indicated assay.

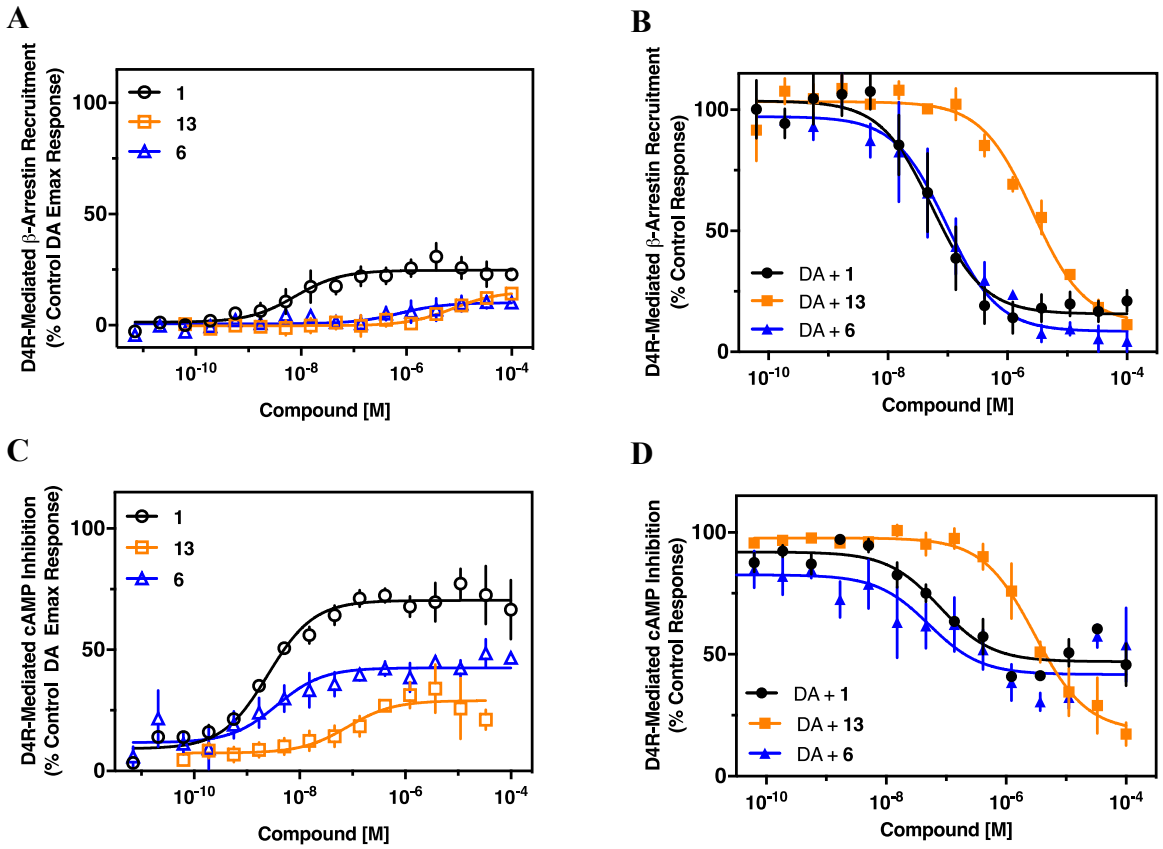


Figure 4. Compounds 13 (yellow) and 6 (blue) show diminished agonist activity at the D_4R compared to parent compound 1 (black). D_4R-expressing stable cells lines were plated and compounds were assayed for agonist (**A**) and antagonist (**B**) activity on β-arrestin recruitment. Similarly, D_4R-mediated inhibition of cAMP accumulation was also examined in both agonist (**C**), and antagonist (**D**) modes, as indicated. Assays were conducted as described in the Experimental Procedures; briefly, agonist assays were conducted by incubating the cells with the indicated concentration of test compound and measuring luminescence. Antagonist assays were conducted by incubating the compound with an EC_{80} concentration of dopamine (1 μM for β-arrestin and 10 nM in cAMP) and the indicated concentration of test compound. For cAMP assays cells were first stimulated with 10 μM forskolin. Agonist mode assays are expressed as a percentage of the maximum dopamine response, whereas antagonist mode assays are

expressed as a percentage of dopamine's EC_{80} response. E_{max} and EC_{50} values are shown in Table 2 and 3. Dopamine and sulpiride were run during each assay as positive controls for a full agonist and full antagonist respectively (data not shown). Data were fit using nonlinear regression of individual experiments performed in triplicate and are shown as means ± SEM; n = 3.

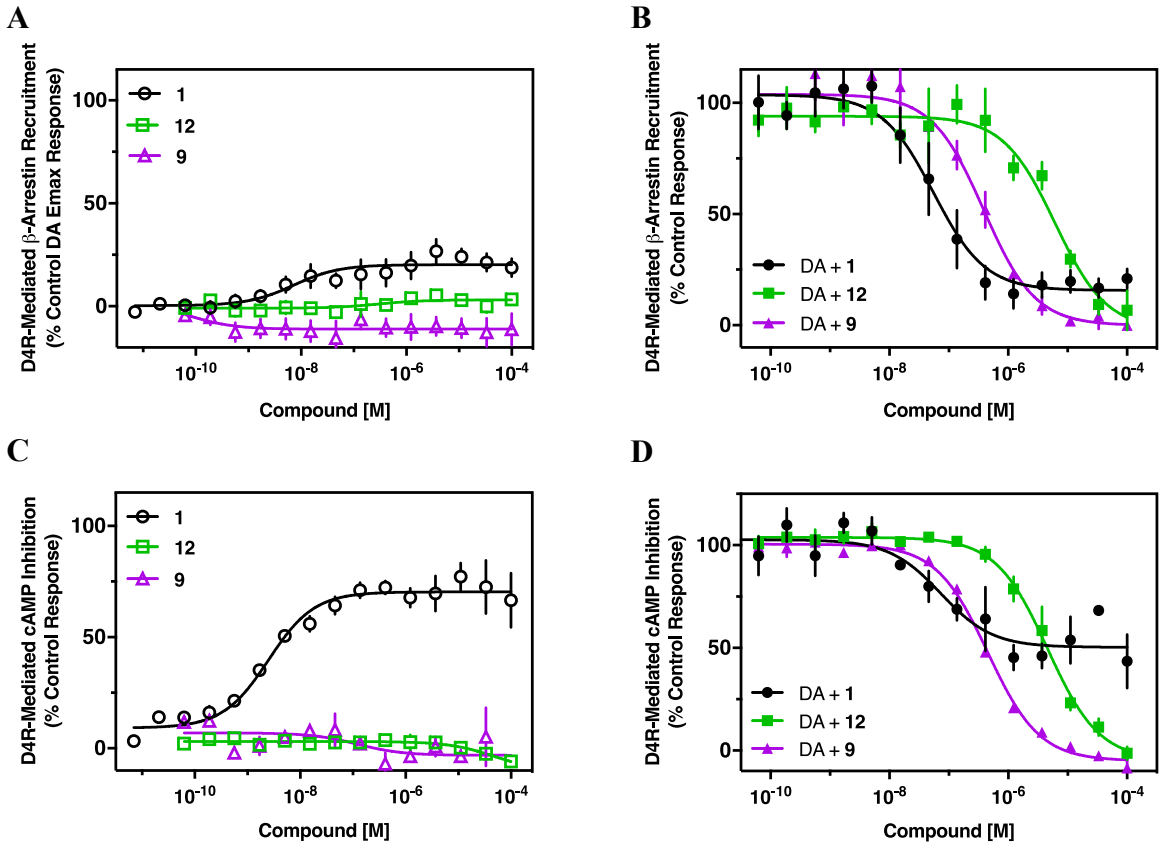


Figure 5. Compounds 12 (green) and 9 (purple) are full antagonists at the D_4R. D_4R-expressing stable cells lines were plated and compounds were assayed for agonist (**A**) and antagonist (**B**) activity on β-arrestin recruitment. Similarly, D_4R-mediated inhibition of cAMP accumulation was also examined in both agonist (**C**), and antagonist (**D**) modes, as indicated. Assays were conducted as described in the Experimental Procedures; briefly, agonist assays were conducted by incubating the cells with the indicated concentration of test compound and measuring luminescence. Antagonist assays were conducted by incubating the compound with an EC_{80} concentration of dopamine (1 μM for β-arrestin and 10 nM in cAMP) and the indicated concentration of test compound. For cAMP assays cells were first stimulated with 10 μM forskolin. Assays were conducted as described in the Experimental Procedures. Agonist mode assays are expressed as a percentage of the maximum dopamine response, whereas antagonist

mode assays are expressed as a percentage of dopamine's EC_{80} (1 μM in β-arrestin and 10 nM in cAMP) response. E_{max} and EC_{50} values are shown in Table 2 and 3. Dopamine and sulpiride were run during each assay as positive controls for a full agonist and full antagonist respectively (data not shown). Data were fit using nonlinear regression of individual experiments performed in triplicate and are shown as means ± SEM; n = 3.

Molecular Dynamics (MD) Studies.

To gain insights on probable ligand interactions at D_4R, a set of seven ligands from the parent compound and the three class of modifications (i.e., **1**, **6**, **9**, **10**, **12**, **13**, and **21**) were docked to the crystal structures of D_2R,[26] D_3R,[25] and D_4R.[24] Each receptor-ligand combination was subjected to 100 ns MD simulations, followed by the simulation interaction diagram and clustering analysis as described in the method section. The results are included in the supporting documents (Tables S2-S4 and Figures S2-S39). Comparisons of structural and dynamic properties of each ligand-receptor system, with reference to the parent compound **1** for each receptor system, are listed in Table S1. Although the same class modifications caused similar changes in the majority of the analyzed properties, some subtle differences are also identified. A representative ligand-receptor system from each class modification is presented here.

In order to explore Class 1 modifications that showed a gain of efficacy at D_2R and D_3R with minimal changes in D_4R binding or efficacy, **10** was selected to be presented here along with parent compound **1**. The comparative ligand binding at of **10** D_2R (Figure 6) and D_3R (Figure 7) revealed that the modest ligand change—the substitution of a piperazine for a piperidine—induced a dramatic shift in the binding orientation at D_2R and D_3R: compared to the parent compound **1**,

10 took on a rotated orientation in both receptors, in which the arylamide portion of the **10** occupies a region of the binding pocket that accommodates the 2-(piperidin-4-yl)pyridinyl portion of **1**. This pose allows **10** to better engage with the conserved transmembrane (TM) 3 aspartate residue ($D^{3.32}$) located within the orthosteric binding pocket of biogenic amine receptors like dopaminergic receptors.[32] Additionally, there was new engagement with conserved $V^{2.61}$, and additional TM5 and TM6 helix shifts in both receptors. In contrast, the binding orientation of **10** at D_4R is similar to that of **1** (Figure S7), although a shift in the orientation of the pyridinylpiperidine ring system deeper into the receptor was observed. **21** docked similarly to **10** at D_2R and at D_4R (i.e., rotated 180° in comparison to **1**), but differed at D_3R in which the pose was similar to that of **1**, possibly indicating a different activation mechanism for D_3R by this compound.

13 (Figure 8), representing Class 2 modifications that showed a partial loss of efficacy at D_4R, and **9** (Figure 9), representing Class 3 modifications that showed a complete loss of efficacy at D_4R, are shown in models of D_4R alongside the parent compound **1**. **13** uniquely engaged with $S^{2.64}$, $E^{2.65}$, $T^{7.39}$, and induced conformational shifts in several TM domains and intra/extracellular loops. **9** showed grater engagement with ECL2 and uniquely interacted with $C^{3.25}$ and $W^{6.48}$. Whereas **13** adopted pose similar to **1**, **9** adopted a rotated orientation in which the arylamide portion of the **9** occupies a region of the binding pocket that accommodates the 2-(piperidin-4-yl)pyridinyl portion of **1**. (Table S1). The results seen in these two comparisons are consistent with previous observations in which regiosubstitutions on an aryl ring of a terminal arylpiperazine can modulate efficacy at D_4R.[33-34] In particular, the inclusion of a *para* substitution on the terminal arylpiperazine has reliably produced D_4R antagonists for a wide variety of molecules with diverse substituents on the secondary pharmacophore.

CONCLUSIONS

Evidence from human genetic studies and animal models suggest D_4R signaling may mediate behavioral traits including impulsivity,[35] novelty-seeking,[35-38] fear and anxiety,[39-40] and sensitivity to drugs of abuse.[40-43] While modulation of postsynaptic D_4R expression in the prefrontal cortex is typically hypothesized to mediate the reported *in vivo* effects of D_4R agonists and antagonists, evidence suggests important roles of D_4R expression in the nucleus accumbens shell[44] and within the lateral habenula,[45] in which the receptor may be preferentially activated by norepinephrine rather than dopamine.[46-47] Furthermore, little is known about the physiological relevance of independent D_4R-mediated signaling pathways (e.g., cAMP and β-arrestin) in the manifestation of behavioral outputs. A recent report identified a D_4R-selective compound containing an unsubstituted phenylpiperazine that potently and partially activated $G\alpha_i$ but inhibited β-arrestin2 recruitment, and identified likely ligand-residue interactions that affect receptor activation states.[48] There remains much left to determine about the physiological role of D_4R signaling in modulating attention and cognitive processes and new selective agonists and antagonists of these receptors will be valuable tools for deduction of signaling importance by these receptors.

New highly selective D_4R partial agonists and antagonists will be useful to better characterize the role of D_4R signaling *in vivo*. While we have primarily focused on selectivity against the very closely related D_2R and D_3R, it will be important to establish global selectivity of these compounds for *in vivo* experimentation through a broader screen of biogenic amine receptors. To this end, we investigated a subset of these compounds on the related D_1-like DARs. None of the tested compounds showed any measurable agonist or antagonist effect at either the D_1R or D_5R (Figure S1). Comprehensive binding and functional studies, in concert with detailed molecular modeling analyses using newly published crystal structures, provides a platform for developing high-affinity

and highly subtype selective ligands of varying efficacies. This study aimed to identify key molecular interactions that dictate D_4R potency, efficacy and subtype selectivity.

The parent compound, **1**, was confirmed to be a high-affinity (low nM K_i value) partial agonist (E_{max} = 23-62%) at D_4R. Illustrative of broader trends from our library, the compound K_i values for all D_2-like receptors determined using [^{3}H]-(*R*)-(+)-7-OH-DPAT competition assays tended to be lower (more potent) than those obtained using [^{3}H]*N*-methylspiperone. As expected, the divergence between these values increased with agonist efficacy, consistent with previous experience regarding agonist versus antagonist radioligands.[30]

Key modifications to the **1** pharmacophore provided modest gains to D_4R affinity, but dramatic gains in selectivity over D_2R and D_3R, likely due to a substantial decrease in D_2R and D_3R engagement by the analogs. Interestingly, the manner of these substitutions produced three classes of lead compound: 1) those with binding and efficacy profiles similar to **1** at D_4R but gains in efficacy at D_2R and D_3R; 2) those with improved D_4R binding and subtype selectivity with lower partial agonist efficacy; and 3) those with improved D_4R binding and subtype selectivity with full antagonist characteristics. Molecular dynamics simulations suggest that the gain in D_2R and D_3R efficacy seen in compounds like **10** could be partially due to achieving a rotated ligand pose that more fully engages the conserved TM3 aspartate. Similarly, the complete shift to antagonism at D_4R seen in compounds like **9** could be partially due to inducing an alternate binding pose that either no longer allows full engagement of the orthosteric binding site and occupation of an alternative secondary binding pocket, or a ligand-dependent alteration of the receptor energy landscape leading to the stabilization of a different receptor conformation.

These molecular models provide testable predictions relative to the unique interaction sites of these diverse compounds within the D_4R. These interactions likely underlie agonist efficacy of a given compound. Interestingly, compounds can be 'rank ordered' by levels of agonist efficacy starting with **1** having the highest D_4R activation, followed by class 1 compounds (which show similar agonist efficacy), then class 2 compounds (which show less agonist efficacy) and class 3 compounds that lack any agonist efficacy. As expected, these compounds align the opposite way for antagonist efficacy, wherein a lower agonist efficacy correlates with a higher antagonist efficacy. Examined this way, one can see that it may be possible to 'dial-in' or 'dial-out' levels of D_4R stimulation via adjusting compound structure, and therefore interaction sites on the receptor, leading to divergent levels of partial agonism. Future studies will involve further SAR and receptor mutagenesis studies to verify these models. We are optimistic that some of the analogues may be developed into useful *in vivo* research tools and plan to examine ADME characteristics of selected analogues. It is interesting to speculate that a collection of partial agonists with varying efficacies may allow for the fine-tuning of D_4R activation, potentially leading to a fuller understanding of functional consequences of varying signaling levels for D_4R-targeted therapeutics for neuropsychiatric disorders.

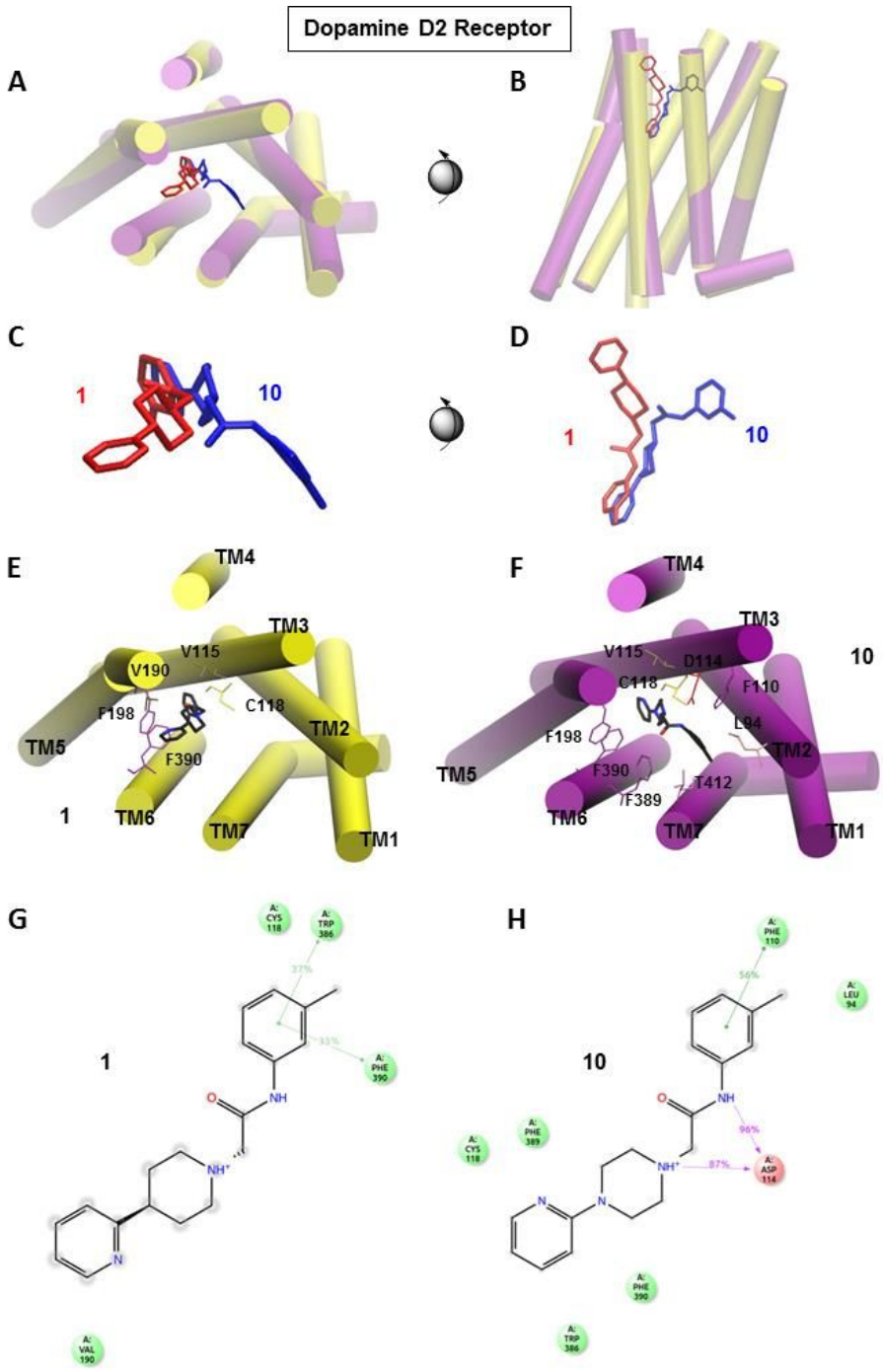


Figure 6. 1 and 10 docked at D_2R. (**A-D**) Comparative alignment of **1** (red ligand, yellow transmembrane domains) and **10** (blue ligand, purple transmembrane domains) following molecular dynamics simulations of the D_2R (PDB: 6CM4[26]). (**E-H**) Analysis of ligand interactions with specific side chains of **1** (**E**, **G**) and **10** (**F**, **H**). Although the structural

difference between **1** and **10** is only a piperidine versus a piperazine ring, this drives a dramatic shift in ligand orientation in which **10** is "flipped" and rotated by 180° about its longitudinal axis, with its pyridine ring deepest in the binding pocket. This allows the basic nitrogen of the neighboring piperazine ring to engage the conserved aspartate in TM3, a common feature of dopaminergic agonists.

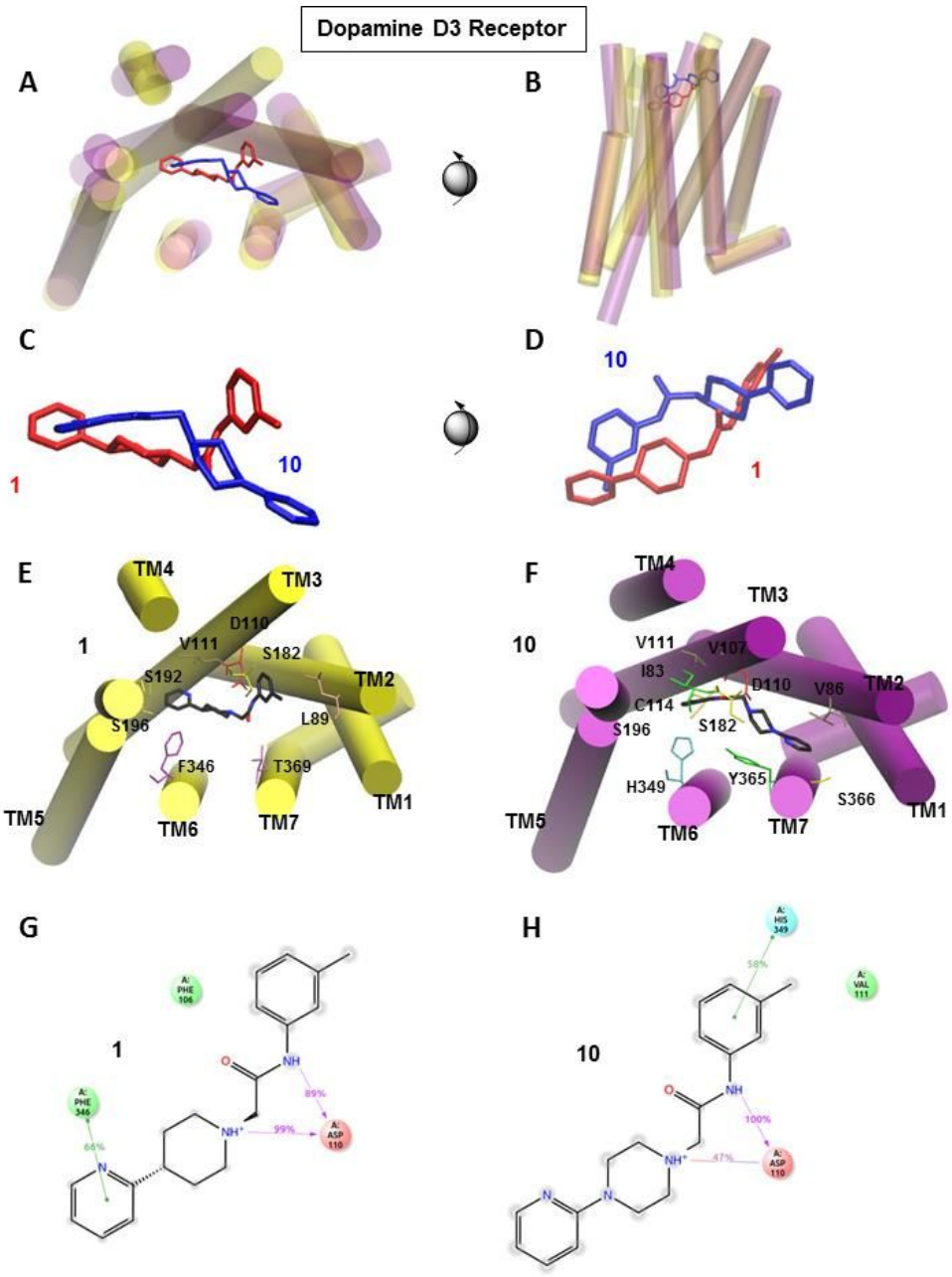


Figure 7. 1 and 10 docked at D_3R. (**A-D**) Comparative alignment of **1** (red ligand, yellow transmembrane domains) and **10** (blue ligand, purple transmembrane domains) following molecular dynamics simulations of the D_3R (PDB: 3PBL[25]). (**E-H**) Analysis of ligand interactions with specific side chains of **1** (**E**, **G**) and **10** (**F**, **H**). As seen in the D_2R model, **10** is also "flipped" and rotated by 180° about its longitudinal axis in the binding pocket at D_3R

compared to **1**. This allows for a different set of hydrophobic interactions and the engagement of the basic nitrogen of the piperazine ring to with the conserved aspartate in TM3.

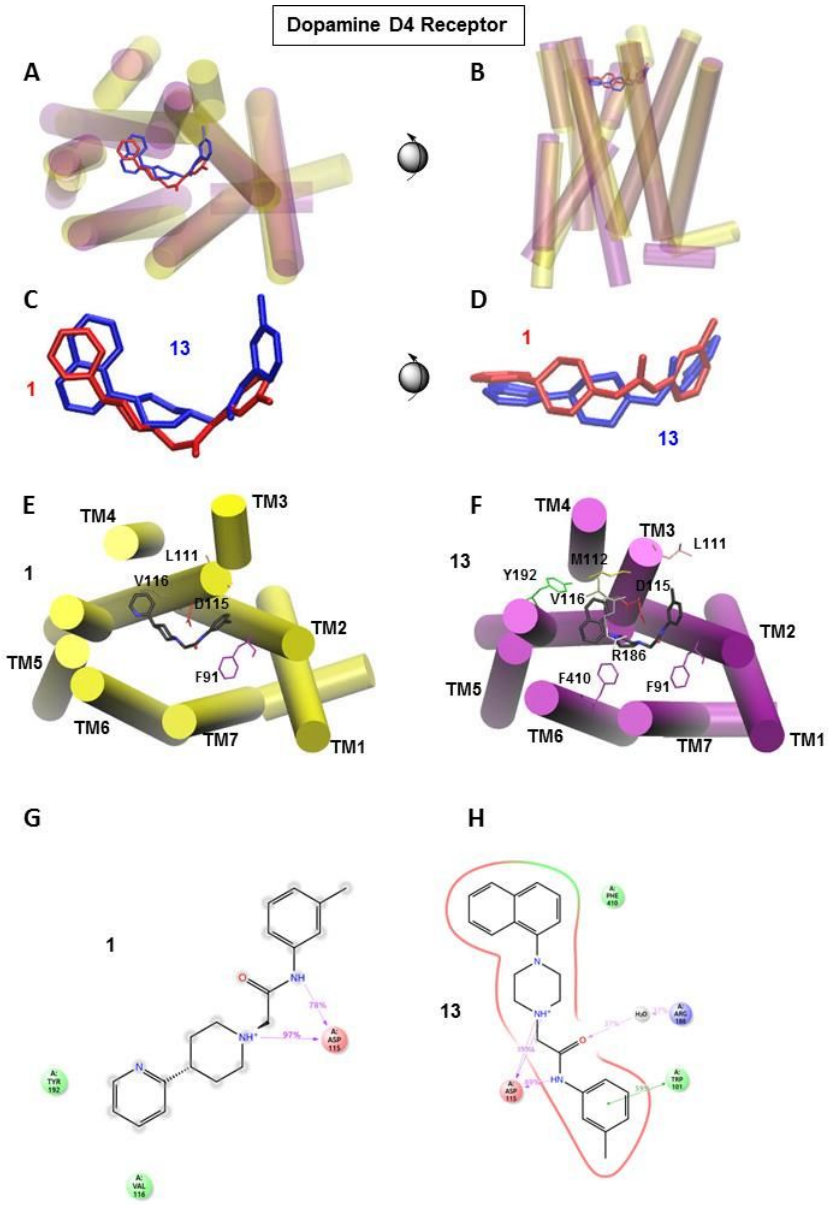


Figure 8. 1 and 13 docked at D_4R. (**A-D**) Comparative alignment of **1** (red ligand, yellow transmembrane domains) and **13** (blue ligand, purple transmembrane domains) following molecular dynamics simulations of the D_4R (PDB: 5WIU[24]). (**E-H**) Analysis of ligand

interactions with specific side chains of **1** (**E**, **G**) and **13** (**F**, **H**). The bulky napthyl ring of **13** shifts the overall fit within the extended binding pocket, partially disrupting the engagement of the basic nitrogen of the piperazine ring to with the conserved aspartate in TM3.

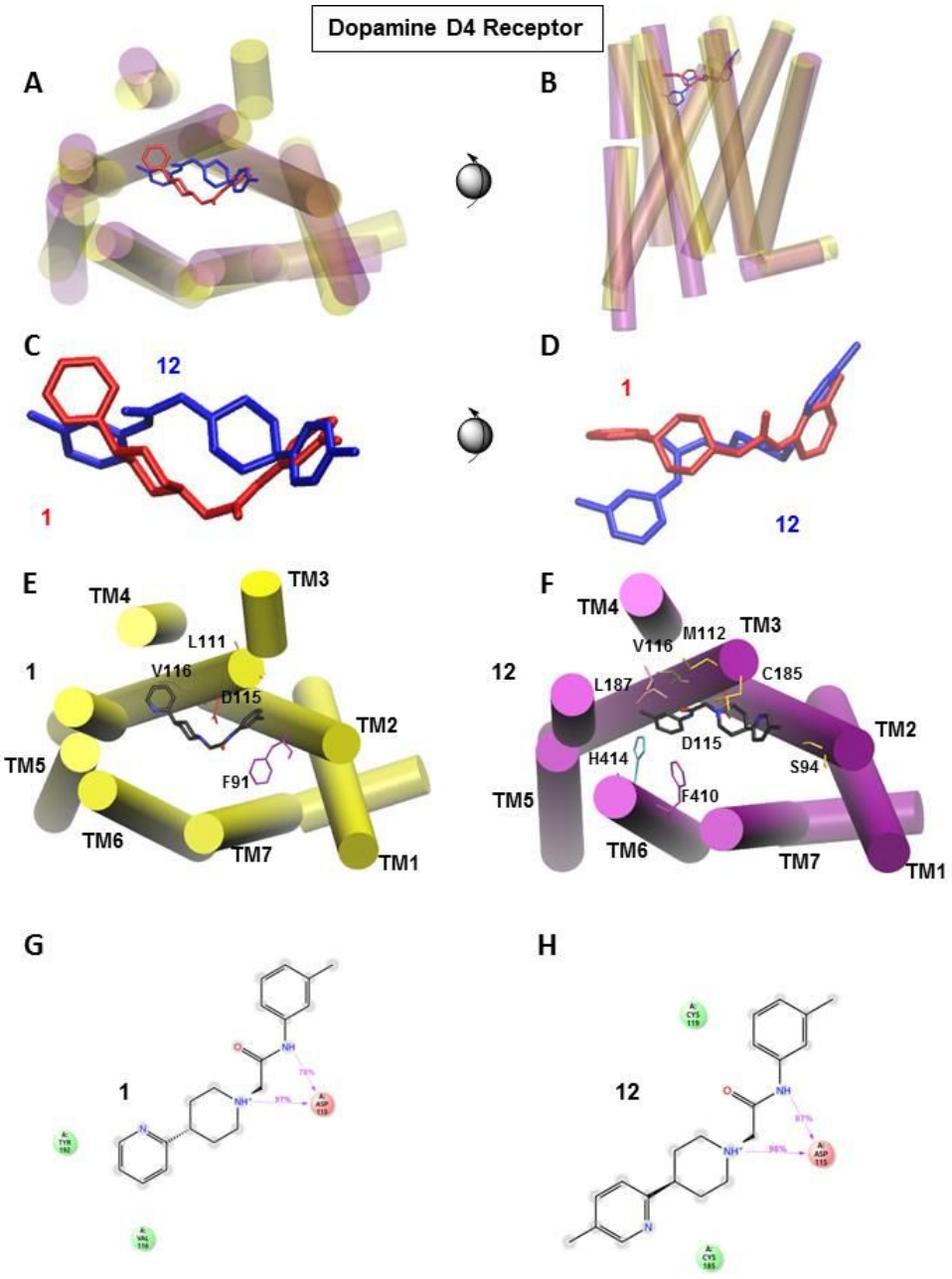


Figure 9. 1 and 9 docked at D_4R. (**A-D**) Comparative alignment of **1** (red ligand, yellow transmembrane domains) and **9** (blue ligand, purple transmembrane domains) following molecular dynamics simulations of the D_4R (PDB: 5WIU[24]). (**E-H**) Analysis of ligand interactions with specific side chains of **1** (**E**, **G**) and **9** (**F**, **H**). The inclusion of a single *para* substitution on the pyridine ring of **9** induces a "flipped" orientation of the ligand, in which the binding pose is rotated by 180° about its longitudinal axis, with its pyridine ring deepest in the binding pocket driving the arylamide into a deeper binding position.

EXPERIMENTAL METHODS

Synthesis. Reaction conditions and yields were not optimized. Anhydrous solvents were purchased from Aldrich and were used without further purification. All other chemicals and reagents were purchased from Sigma-Aldrich Co. LLC, Combi-Blocks, TCI America, OChem Incorporation, Acros Organics, and Alfa Aesar. All amine final products were converted into either the oxalate or hydrochloride salt. Spectroscopic data and yields refer to the free base form of compounds. Flash chromatography was performed using silica gel (EMD Chemicals, Inc.; 230-400 mesh, 60 Å) by using Teledyne ISCO CombiFlashRF system. ^{1}H NMR spectra were acquired using a Varian Mercury Plus 400 spectrometer at 400 MHz. Chemical shifts are reported in parts-per-million (ppm) and referenced according to deuterated solvent for ^{1}H spectra ($CDCl_3$, 7.26, CD_3OD, 3.31 or D_2O, 4.79). Combustion analysis was performed by Atlantic Microlab, Inc., (Norcross, GA) and the results agree within ± 0.4% of calculated values (Table S5). Melting point determination was conducted using a Stanford Research system Opti Melt Automated melting point apparatus and are uncorrected. On the basis of NMR and combustion data, all final compounds are >95% pure. All compounds within this series are covered under an existing patent,[49] but only **1**,[21-22] **6**,[22] and **10**[16, 21] have been previously described in the peer-reviewed literature.

General Method A. 2-Chloro-*N*-(*m*-tolyl)acetamide (5).[21, 27-28] 2-chloroacetyl chloride (1.16 g, 10.3 mmol) was added to a solution of *m*-toluidine (1.00 mL, 9.33 mmol) in ethyl acetate (30 mL) and triethylamine (1.43 mL, 10.3 mmol) at 0 °C. The reaction mixture was allowed to warm to room temperature and stirred overnight, under N_2 atmosphere. After the reaction was complete, the solvent was removed *in vacuo.* The crude mixture was diluted with water (100 mL) and EtOAc (100 mL), and then extracted with EtOAc (3 x 100 mL) and washed with brine (100 mL). The

combined organic layer was dried over MgSO4, filtered and concentrated. The product was purified by column chromatography (10-90% EtOAc:Hexanes gradient) to give **5** (1.30 g, 76% yield) as an off-white solid. ^{1}H NMR ($CDCl_3$) δ 8.19 (s, 1H), 7.38-7.33 (m, 1H), 7.26-7.22 (m, 1H), 6.99 (d, *J* = 7.6 Hz, 1H), 4.18 (s, 2H), 2.36 (s, 3H).

General Method B. 2-(4-Phenylpiperidin-1-yl)-*N*-(*m*-tolyl)acetamide (6; CAB03-015).[21-22, 27-28] K_2CO_3 (2.57 g, 18.6 mmol), NaI (50 mg) were added to a solution of 2-chloro-*N*-(m-tolyl)acetamide (570 mg, 3.10 mmol) and commercially available 4-phenylpiperidine (500 mg, 3.10 mmol) in an anhydrous acetonitrile (12 mL) solution. The reaction mixture was stirred at reflux (80 °C) for 20 h, under N_2 atmosphere. The reaction mixture was cooled to room temperature and the solvent was removed *in vacuo*. The residue was diluted with water (100 mL) and EtOAc (100 mL), and then extracted with EtOAc (3 x 100 mL) and washed with brine (100 mL). The combined organic layer was dried over $MgSO_4$, filtered and concentrated. The crude product was purified by column chromatography (10-90% EtOAc:Hexanes gradient) to give pure product **6** (710 mg, 74% yield) as an off-white solid. Mp 70-71 °C; ^{1}H NMR ($CDCl_3$) δ 9.15 (s, 1H), 7.42 – 7.40 (m, 2H), 7.38 – 7.31 (m, 2H), 7.24 – 7.20 (m, 4H), 6.93 (d, *J* = 7.2 Hz, 1H), 3.15 (s, 2H), 3.10 – 3.02 (m, 2H), 2.59 – 2.52 (m, 1H), 2.43 – 2.38 (m, 2H), 2.36 (s, 3H), 1.94 – 1.90 (m, 4H). Anal. ($C_{20}H_{24}N_2O$•HCl•$^1/_4H_2O$) C, H, N.

***N*-(*m*-tolyl)-2-(4-(*p*-tolyl)piperidin-1-yl)acetamide (7; CAB02-007HP)**. Compound **7** was synthesized as described for **6** using K_2CO_3 (1.18 g, 8.56 mmol), NaI (40.0 mg) 4-(*p*-tolyl)piperidine (250 mg, 1.43 mmol) and 2-chloro-*N*-(*m*-tolyl)acetamide (262 mg, 1.43 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (15-85% EtOAc:Hexanes gradient) to give pure product **7** (182 mg, 40% yield) as a white solid. Mp 63-65 °C; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.23 (s, 1H), 7.47 (d, *J* = 15.7 Hz,

2H), 7.31 (dd, *J* = 14.4, 5.5 Hz, 2H), 7.23 (d, *J* = 2.9 Hz, 3H), 7.00 (d, *J* = 7.5 Hz, 1H), 3.22 (s, 2H), 3.10 (d, *J* = 11.4 Hz, 2H), 2.58 (d, *J* = 12.5 Hz, 1H), 2.49-2.46 (m, 2H), 2.43 (s, 3H), 2.41 (s, 3H), 1.91 (dt, *J* = 37.8, 13.1 Hz, 4H). Anal. ($C_{21}H_{26}N_2O\bullet{}^1/_4H_2O\bullet{}^2/_5\ C_3H_8O$) C, H, N.

2-(4-(4-chlorophenyl)piperidin-1-yl)-*N*-(*m*-tolyl)acetamide (8; CAB02-009HP). Compound **8** was synthesized as described for **6** using K_2CO_3 (715 mg, 5.17 mmol), NaI (40.0 mg) 4-(4-chlorophenyl)piperidine (200 mg, 0.86 mmol) and 2-chloro-*N*-(*m*-tolyl)acetamide (158 mg, 0.86 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (40-60% EtOAc:Hexanes gradient) to give pure product **8** (120 mg, 41% yield) as a light brownish solid. Mp 114-116 °C; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.08 (s, 1H), 7.42 – 7.33 (m, 2H), 7.28 (d, *J* = 8.5 Hz, 1H), 7.24 (d, *J* = 2.4 Hz, 2H), 7.16 (d, *J* = 8.1 Hz, 2H), 6.95 – 6.88 (m, 1H), 3.13 (s, 2H), 3.01 (t, *J* = 7.1 Hz, 2H), 2.50 (d, *J* = 12.4 Hz, 1H), 2.35 (s, 2H), 2.34 (s, 3H), 1.88 (d, *J* = 13.1 Hz, 2H), 1.76 (q, *J* = 12.7 Hz, 2H). Anal. ($C_{20}H_{23}ClN_2O$) C, H, N.

2-(4-(5-methylpyridin-2-yl)piperidin-1-yl)-*N*-(*m*-tolyl)acetamide (9; CAB02-005HP). Compound **9** was synthesized as described for **6** using K_2CO_3 (1.64 g, 11.9 mmol), NaI (40.0 mg) 5-methyl-2-(piperidin-4-yl)pyridine (350 mg, 1.98 mmol) and 2-chloro-*N*-(*m*-tolyl)acetamide (363 mg, 1.98 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (50-50% EtOAc:Hexanes gradient) to give pure product **9** (420 mg, 66% yield) as a white solid. Mp 126-128 °C; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.09 (s, 1H), 8.03 (s, 1H), 7.43 – 7.30 (m, 3H), 7.20 (d, *J* = 8.2 Hz, 1H), 6.93 (s, 1H), 6.61 (d, *J* = 8.5 Hz, 1H), 3.62 - 3.49 (m, 3H), 3.18 (br s, 2H), 2.74 (d, *J* = 5.8 Hz, 4H), 2.34 (s, 3H), 2.20 (s, 3H), 1.58-1.52 (m, 2H).

2-(4-(pyridin-2-yl)piperazin-1-yl)-*N*-(*m*-tolyl)acetamide (10; CAB02-140).[22, 27] Compound **10** was synthesized as described for **6** using K_2CO_3 (1.13 g, 6.78 mmol), NaI (40.0 mg) 1-(pyridin-2-yl)piperazine (222 mg, 1.36 mmol) and 2-chloro-*N*-(*m*-tolyl)acetamide (250 mg, 1.36 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (20-80% EtOAc:Hexanes gradient) to give pure product **10** (330 mg, 78% yield) as a white solid. Mp 127-129 °C; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.09 (s, 1H), 8.21 (d, J = 4.6 Hz, 1H), 7.56 – 7.46 (m, 1H), 7.39 (d, J = 10.1 Hz, 2H), 7.24 – 7.19 (m, 1H), 6.94 (d, J = 7.4 Hz, 1H), 6.68 (q, J = 5.5, 4.4 Hz, 2H), 3.62 (t, J = 5.0 Hz, 4H), 3.19 (d, J = 3.2 Hz, 2H), 2.74 (d, J = 5.4 Hz, 4H), 2.35 (d, J = 3.2 Hz, 3H), 2.17 (br s, 4H). Anal. ($C_{18}H_{22}N_4O$•2HCl•H_2O) C, H, N.

2-(4-(pyrimidin-2-yl)piperazin-1-yl)-*N*-(*m*-tolyl)acetamide (11; CAB02-110). Compound **11** was synthesized as described for **6** using K_2CO_3 (1.13 g, 1.16 mmol), 2-(piperazin-1-yl)pyrimidine (223 mg, 1.36 mmol) and 2-chloro-*N*-(*m*-tolyl)acetamide (250 mg, 1.36 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (10-90% EtOAc:Hexanes gradient) to give pure product **11** (310 mg, 73% yield) as a cream solid. Mp 92-94 °C; ^{1}H NMR (400 MHz, $CDCl_3$) δ 9.16 – 9.01 (m, 1H), 8.37 – 8.27 (m, 2H), 7.39 (d, J = 14.2 Hz, 2H), 7.22 (d, J = 8.1 Hz, 1H), 6.94 (d, J = 8.4 Hz, 1H), 6.53 (d, J = 4.6 Hz, 1H), 3.91 (s, 4H), 3.18 (q, J = 2.1, 1.6 Hz, 2H), 2.69 (d, J = 5.6 Hz, 4H), 2.36 (s, 3H). Anal. ($C_{17}H_{21}N_5O$•2HCl•1$^3/_4$$H_2O$) C, H, N.

2-(4-(5-chloropyridin-2-yl)piperazin-1-yl)-*N*-(*m*-tolyl)acetamide (12; CAB02-003HP). Compound **12** was synthesized as described for **6** using K_2CO_3 (1.78 g, 12.86 mmol), NaI (40.0 mg), 1-(5-chloropyridin-2-yl)piperazine (422 mg, 2.14 mmol) and 2-chloro-*N*-(*m*-tolyl)acetamide (400 mg, 2.14 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (20-80% EtOAc:Hexanes gradient) to give pure product **12** (490 mg,

65% yield) as a white solid. Mp 107-109°C; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.02 (s, 1H), 8.11 (d, *J* = 3.3 Hz, 1H), 7.47 – 7.40 (m, 1H), 7.36 (d, *J* = 11.8 Hz, 2H), 7.19 (d, *J* = 8.5 Hz, 1H), 6.95 – 6.88 (m, 1H), 6.59 (d, *J* = 8.9 Hz, 1H), 3.58 (t, *J* = 5.2 Hz, 4H), 3.17 (d, *J* = 2.8 Hz, 2H), 2.71 (t, *J* = 5.0 Hz, 4H), 2.33 (s, 3H). Anal. ($C_{18}H_{21}ClN_4O$•2HCl•½H_2O) C, H, N.

2-(4-(naphthalen-1-yl)piperazin-1-yl)-*N*-(*m*-tolyl)acetamide (13; CAB02-011HP). Compound **13** was synthesized as described for **6** using K_2CO_3 (2.62 g, 18.9 mmol), NaI (50.0 mg), 1-(naphthalen-1-yl)piperazine[29] (670 mg, 3.16mmol) and 2-chloro-*N*-(*m*-tolyl)acetamide (580 mg, 3.16 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (40-60% EtOAc:Hexanes gradient) to give pure product **13** (546 mg, 48% yield) as a brown oil; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.17 (s, 1H), 8.20 (d, *J* = 7.5 Hz, 1H), 7.85 (s, 1H), 7.60 (d, *J* = 8.2 Hz, 1H), 7.55 – 7.47 (m, 2H), 7.43 (d, *J* = 11.4 Hz, 3H), 7.24 (d, *J* = 8.4 Hz, 1H), 7.15 (d, *J* = 7.3 Hz, 1H), 6.96 (d, *J* = 7.4 Hz, 1H), 3.34 – 3.27 (m, 2H), 3.23 (br s, 4H), 2.95 (br s, 4H), 2.38 (s, 3H). Anal. ($C_{23}H_{25}N_3O$•2HCl) C, H, N.

3-chloro-*N*-(*m*-tolyl)propanamide (14). Compound **14** was synthesized as described for **5** using 3-chloropropanoyl chloride (1.30 g, 10.3 mmol) was added to a solution of *m*-toluidine (1 mL, 9.33 mmol) in ethyl acetate (30 mL) and triethylamine (1.44 mL). The crude product was purified by column chromatography (20-80% EtOAc:Hexanes gradient) to give compound **14** (1.43 g, 78% yield) as a white solid. ^{1}H NMR ($CDCl_3$) δ 7.44 (s, 1H), 7.36 – 7.22 (m, 2H), 6.99 (d, *J* = 7.4 Hz, 1H), 3.96-3.92 (m, 2H), 2.85 (t, *J* = 6.3 Hz, 2H), 2.39 (s, 3H).

3-(4-(pyridin-2-yl)piperidin-1-yl)-*N*-(*m*-tolyl)propanamide (15; CAB02-120). Compound **15** was synthesized as described for **6** using K_2CO_3 (1.26 g, 7.56 mmol), NaI (50.0 mg), 2-(piperidin-4-yl)pyridine (246 mg, 1.52 mmol) and 3-chloro-*N*-(*m*-tolyl)propanamide (300 mg, 1.52 mmol) in

an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (50-50% EtOAc:Hexanes gradient) to give pure product **15** (325 mg, 66% yield) as a light brown oil; ^{1}H NMR (400 MHz, $CDCl_3$): δ 11.08 (s, 1H), 8.55 (d, *J* = 4.6 Hz, 1H), 7.69 – 7.61 (m, 1H), 7.45 (s, 1H), 7.29 (d, *J* = 7.5 Hz, 1H), 7.23 -7.12 (m, 3H), 6.88 (d, *J* = 7.5 Hz, 1H), 3.21 (d, *J* = 11.2 Hz, 2H), 2.87 – 2.70 (m, 3H), 2.53 (t, *J* = 5.7 Hz, 2H), 2.34 (s, 3H), 2.24 (t, *J* = 11.6 Hz, 2H), 2.09 (d, *J* = 13.2 Hz, 2H), 2.02 – 1.87 (m, 2H). Anal. ($C_{20}H_{25}N_3O$•2HCl•3½H_2O) C, H, N.

3-(4-(pyridin-2-yl)piperazin-1-yl)-*N*-(*m*-tolyl)propanamide (16; CAB02-142). Compound **16** was synthesized as described for **6** using K_2CO_3 (1.26 g, 9.12 mmol), 1-(pyridin-2-yl)piperazine (248 mg, 1.52 mmol) and 3-chloro-*N*-(*m*-tolyl)propanamide (300 mg, 1.52 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (50-50% EtOAc:Hexanes gradient) to give pure product **16** (350 mg, 71% yield) as a white solid. Mp 99-101 °C; ^{1}H NMR (400 MHz $CDCl_3$): δ 10.74 (s, 1H), 8.21 (br s, 1H), 7.51 (d, *J* = 8.0 Hz, 1H), 7.40 (s, 1H), 7.24 (d, *J* = 5.7 Hz, 1H), 7.15 (td, *J* = 8.2, 3.3 Hz, 1H), 6.86 (d, *J* = 7.3 Hz, 1H), 6.68 (q, *J* = 7.4, 5.6 Hz, 2H), 3.64 (d, *J* = 6.4 Hz, 4H), 2.81 – 2.65 (m, 6H), 2.55 (q, *J* = 4.7 Hz, 2H), 2.30 (s, 3H). Anal. ($C_{19}H_{24}N_4O$•3HCl) C, H, N.

3-(4-(pyrimidin-2-yl)piperazin-1-yl)-*N*-(*m*-tolyl)propanamide (17; RNB01-007). Compound **17** was synthesized as described for **6** using K_2CO_3 (1.26 g, 9.12 mmol), 2-(piperazin-1-yl)pyrimidine (249 mg, 1.52 mmol) and 3-chloro-*N*-(*m*-tolyl)propanamide (350 mg, 1.52 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (50-50% EtOAc:Hexanes gradient) to give pure product **17** (321 mg, 56% yield) as a cream solid. Mp 85-86 °C; ^{1}H NMR (400 MHz, $CDCl_3$): δ 10.76 (s, 1H), 8.33 (dt, *J* = 5.1, 2.4 Hz, 2H), 7.40 (s, 1H), 7.32 – 7.23 (m, 1H), 7.21 – 7.13 (m, 1H), 6.88 (d, *J* = 7.5 Hz, 1H), 6.54 (dp,

J = 5.0, 2.6, 2.1 Hz, 1H), 3.94 (t, *J* = 4.8 Hz, 4H), 2.77 (t, *J* = 5.7 Hz, 2H), 2.67 (t, *J* = 4.6 Hz, 4H), 2.57 (q, *J* = 5.7, 5.0 Hz, 2H), 2.32 (s, 3H). Anal. ($C_{18}H_{23}N_5O$•HCl) C, H, N.

2-chloro-*N*-(3-ethylphenyl)acetamide (19). Compound **19** was synthesized as described for **5** using 2-chloroacetyl chloride (3.62 mL, 45.4 mmol) was added to a solution of 3-ethylaniline (5.13 mL, 41.3 mmol) in ethyl acetate (30 mL) and triethylamine (1.44 mL). The crude product was purified by column chromatography (20-80% EtOAc:Hexanes gradient) to give compound **19** (8.00 g, 98% yield) as a cream solid. ^{1}H NMR (400 MHz, $CDCl_3$): δ 8.23 (s, 1H), 7.47-7.38 (m, 2H), 7.32-7.27 (m, 1H), 7.04 (d, *J* = 7.5 Hz, 1H), 4.20 (s, 2H), 2.75 – 2.58 (m, 2H), 1.28-1.22 (m, 3H).

***N*-(3-ethylphenyl)-2-(4-(pyridin-2-yl)piperidin-1-yl)acetamide (20; CAB02-021HP)**. Compound **20** was synthesized as described for **6** using K_2CO_3 (1.54 g, 11.17 mmol), 2-(piperidin-4-yl)pyridine (300 mg, 1.86 mmol) and 2-chloro-*N*-(3-ethylphenyl)acetamide (368 mg, 1.86 mmol) in an anhydrous acetonitrile (6 mL) solution The crude product was purified by column chromatography (40-60% EtOAc:Hexanes gradient) to give pure product **20** (435 mg, 73% yield) as a white solid. Mp 56-58 °C; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.16 (s, 1H), 7.48 – 7.38 (m, 2H), 7.33 (d, *J* = 7.4 Hz, 2H), 7.26 (br s, 4H), 6.97 (d, *J* = 7.5 Hz, 1H), 3.16 (d, *J* = 3.3 Hz, 2H), 3.05 (d, *J* = 11.5 Hz, 2H), 2.66 (d, *J* = 7.9 Hz, 2H), 2.60 – 2.54 (m, 1H), 2.40 (t, *J* = 12.0 Hz, 2H), 1.87 (dt, *J* = 38.0, 13.2 Hz, 4H), 1.25 (t, *J* = 7.3, 5.9 Hz, 3H). Anal. ($C_{20}H_{25}N_3O \cdot C_2H_2O_4$) C, H, N.

***N*-(3-ethylphenyl)-2-(4-(pyridin-2-yl)piperazin-1-yl)acetamide (21; CAB02-017HP)**. Compound **21**was synthesized as described for **6** using K_2CO_3 (2.74 g, 19.8 mmol), 1-(pyridin-2-yl)piperazine (539 mg, 3.30 mmol) and 2-chloro-*N*-(3-ethylphenyl)acetamide (650 mg, 3.30 mmol) in an anhydrous acetonitrile (8 mL) solution. The crude product was purified by column

chromatography (50-50% EtOAc:Hexanes gradient) to give pure product **21** (792 mg, 74% yield) as a white solid. Mp 109-111 °C; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.07 (s, 1H), 8.19 (s, 1H), 7.54 – 7.44 (m, 1H), 7.38 (d, *J* = 8.0 Hz, 2H), 7.27 – 7.20 (m, 1H), 6.95 (d, *J* = 7.6 Hz, 1H), 6.66 (d, *J* = 8.6 Hz, 2H), 3.60 (d, *J* = 6.0 Hz, 4H), 3.17 (t, *J* = 2.3 Hz, 2H), 2.73 (d, *J* = 5.0 Hz, 4H), 2.61 (t, *J* = 8.0 Hz, 2H), 1.26 – 1.15 (m, 3H). ($C_{19}H_{24}N_4O$•2HCl•$^3/_4H_2O$) C, H, N.

2-(4-(5-chloropyridin-2-yl)piperazin-1-yl)-*N*-(3-ethylphenyl)acetamide (22; CAB02-019HP). Compound **22** was synthesized as described for **6** using K_2CO_3 (1.26 g, 9.12 mmol), 1-(5-chloropyridin-2-yl)piperazine (300 mg, 1.52 mmol) and 2-chloro-*N*-(3-ethylphenyl)acetamide (300 mg, 1.52 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (20-80% EtOAc:Hexanes gradient) to give pure product **22** (480 mg, 88% yield) as a white solid. Mp 101-103°C; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.03 (s, 1H), 8.11 (s, 1H), 7.46 – 7.34 (m, 3H), 7.25 -7.23 (m, 1H), 6.95 (d, *J* = 7.5 Hz, 1H), 6.59 (d, *J* = 8.9 Hz, 1H), 3.57 (t, *J* = 4.9 Hz, 4H), 3.17 (d, *J* = 2.7 Hz, 2H), 2.71 (t, *J* = 4.7 Hz, 4H), 2.61 (t, *J* = 8.1 Hz, 2H), 1.32 – 1.13 (m, 3H). Anal. ($C_{19}H_{23}ClN_4O$•2HCl•$^3/_4H_2O$) C, H, N.

2-chloro-*N*-(pyridin-3-yl)acetamide (24a). Compound **24a** was synthesized as described for **5** using 2-chloroacetyl chloride (0.71 mL, 17.5 mmol) was added to a solution of pyridin-3-amine (1.50 g, 16.0 mmol) in ethyl acetate (25 mL) and triethylamine (0.4 mL). The crude product was purified by column chromatography (20-80% EtOAc:Hexanes gradient) to give **24a** (1.17 g, 43% yield) as a white solid. ^{1}H NMR (400 MHz, D_2O): δ 9.37 – 9.08 (m, 1H), 8.60 – 8.32 (m, 2H), 8.06 – 7.87 (m, 1H), 5.67 (s, 2H).

2-chloro-*N*-(pyrimidin-5-yl)acetamide (24b). Compound **24b** was synthesized as described for **5** using 2-chloroacetyl chloride (0.46 mL, 5.78 mmol) was added to a solution of pyrimidin-5-

amine (500 mg, 5.26 mmol) in ethyl acetate (10 mL) and triethylamine (0.4 mL). The crude product was purified by column chromatography (20-80% EtOAc:Hexanes gradient) to give **24b** (510 mg, 57% yield) as a brown solid. ^{1}H NMR (400 MHz, D_2O): δ 9.17 (s, 1H), 8.54 (s, 2H), 8.01 (s, 1H), 5.66 (s, 2H).

2-(4-(pyridin-2-yl)piperazin-1-yl)-*N*-(pyridin-3-yl)acetamide (25; CAB02-033HP). Compound **25** was synthesized as described for **6** using K_2CO_3 (1.27 g, 9.17 mmol), 1-(pyridin-2-yl)piperazine (249 mg, 1.52 mmol) and compound **24a** 2-chloro-*N*-(pyridin-3-yl)acetamide (260 mg, 1.52 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (20-80% EtOAc:Hexanes gradient) to give pure product **25** (287 mg, 63% yield) as a white solid. Mp 173-174 °C; ^{1}H NMR (400 MHz $CDCl_3$): δ 9.23 (s, 1H), 8.59 (s, 1H), 8.37 (s, 1H), 8.23 (d, J = 12.8 Hz, 2H), 7.51 (s, 1H), 6.68 (d, J = 8.1 Hz, 2H), 3.63 (br s, 4H), 3.23 (d, J = 2.9 Hz, 2H), 2.76 (br s, 4H). Anal. ($C_{16}H_{19}N_5O$• 4HCl•1$^1/_{10}$ H_2O•$^1/_4$ C_3H_8O) C, H, N.

2-(4-(5-chloropyridin-2-yl)piperazin-1-yl)-*N*-(pyridin-3-yl)acetamide (26; CAB02-035HP). Compound **26** was synthesized as described for **6** using K_2CO_3 (2.63 g, 19.0 mmol), 1-(5-chloropyridin-2-yl)piperazine (627 mg, 3.17 mmol) and compound **24a** 2-chloro-*N*-(pyridin-3-yl)acetamide (540 mg, 3.17 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (20-80% EtOAc:Hexanes gradient) to give pure product **26** (721 mg, 68% yield) as a white solid. Mp 155-156 °C; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.17 (s, 1H), 8.57 (s, 1H), 8.36 (br s, 1H), 8.22 (d, J = 8.2 Hz, 1H), 8.12 (s, 1H), 7.49 – 7.39 (m, 1H), 7.31 – 7.27 (m, 1H), 6.60 (d, J = 9.1 Hz, 1H), 3.59 (s, 4H), 3.25 – 3.15 (m, 2H), 2.74 (d, J = 5.0 Hz, 4H). Anal. ($C_{16}H_{18}ClN_5O$• 4HCl•H_2O•$^1/_2$ C_3H_8O) C, H, N.

2-(4-(pyridin-2-yl)piperazin-1-yl)-*N*-(pyrimidin-5-yl)acetamide (27; CAB02-029HP). Compound **27** was synthesized as described for **6** using K_2CO_3 (1.45 g, 10.5 mmol), 1-(pyridin-2-yl)piperazine (285 mg, 1.75 mmol) and compound **24b** 2-chloro-*N*-(pyrimidin-5-yl)acetamide (300 mg, 1.75 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (20-80% EtOAc:Hexanes gradient) to give pure product **27** (268 mg, 51% yield) as a white solid. Mp 144-146 °C; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.17 (s, 1H), 9.02 - 8.81 (m, 3H), 8.13 (br s, 1H), 7.43 (br s, 1H), 6.60 (br s, 2H), 3.56 (br s, 4H), 3.18 (br s, 2H), 2.69 (br s, 4H). Anal. ($C_{15}H_{18}N_6O•{}^3/_2C_2H_2O_4•{}^3/_4H_2O$) C, H, N.

2-(4-(5-chloropyridin-2-yl)piperazin-1-yl)-*N*-(pyrimidin-5-yl)acetamide (28; CAB02-031HP). Compound **28** was synthesized as described for **6** using K_2CO_3 (866 mg, 6.26 mmol), 1-(5-chloropyridin-2-yl)piperazine (207 mg, 1.04 mmol) and compound **24b** 2-chloro-*N*-(pyrimidin-5-yl)acetamide (180 mg, 1.04 mmol) in an anhydrous acetonitrile (6 mL) solution. The crude product was purified by column chromatography (20-80% EtOAc:Hexanes gradient) to give pure product **28** (157 mg, 45% yield) as a yellowish oil; ^{1}H NMR (400 MHz, $CDCl_3$): δ 9.21 (s, 1H), 9.08 – 8.98 (m, 3H), 8.15 (d, J = 3.7 Hz, 1H), 7.47 (d, J = 8.9 Hz, 1H), 6.63 (d, J = 9.2 Hz, 1H), 3.62 (br s, 4H), 3.30 – 3.23 (m, 2H), 2.77 (br s, 4H). Anal. ($C_{15}H_{17}ClN_6O•C_2H_2O_4•1{}^1/_2H_2O$) C, H, N.

Radioligand binding studies.

HEK293 cells stably expressing human $D_{2L}R$, D_3R, or $D_{4.4}R$ were grown in a 50:50 mix of Ham's F12 and DMEM culture media, supplemented with 2 mM L-glutamine, 20 mM HEPES, 0.1 mM non-essential amino acids, 1X antibiotic/antimycotic, 10% heat-inactivated fetal bovine serum,

and 200 μg/ml hygromycin (Life Technologies, Grand Island, NY) and grown in an incubator at 37 °C and 5% CO_2. Upon reaching 80-90% confluence, cells were harvested using pre-mixed Earle's Balanced Salt Solution (EBSS) with 5 mM EDTA (Life Technologies) and centrifuged at 3000 rpm for 10 min at 21 °C. The supernatant was removed and the cell pellet was resuspended in 10 ml hypotonic lysis buffer (5 mM Tris, 5 mM $MgCl_2$, pH 7.4 at 4 °C) then centrifuged at 20,000 rpm for 30 min at 4 °C. The membrane pellet was resuspended in fresh binding buffer for either [^{3}H]*N*-methylspiperone (Perkin Elmer, Waltham, MA) binding experiments (fresh EBSS buffer made from 8.7 g/L Earle's Balanced Salts without phenol red (US Biological, Salem, MA), 2.2 g/L sodium bicarbonate, pH 7.4) or [^{3}H]-(R)-(+)-7-OH-DPAT (ARC, Saint Louis, MO) binding experiments (50 mM Tris, 10 mM $MgCl_2$, 1 mM EDTA, pH 7.4). A Bradford protein assay (Bio-Rad, Hercules, CA) was used to determine the protein concentration. Membranes were used fresh for [^{3}H]-(R)-(+)-7-OH-DPAT binding experiments, or diluted to 500 μg/ml and stored in a -80 °C freezer for later use in [^{3}H]*N*-methylspiperone binding experiments.

All test compounds were freshly dissolved in 30% DMSO and 70% H_2O to a stock concentration of 100 μM. To assist the solubilization of free-base compounds, 10 μl of glacial acetic acid was added along with the DMSO. Each test compound was then diluted into half-log serial dilutions, tested in triplicate, using 30% DMSO vehicle. Competitive-inhibition experiments were conducted in 96-well plates containing 300 μL fresh binding buffer, 50 μL of diluted test compound, 100 μL of membrane suspension ([^{3}H]*N*-methylspiperone: 20 μg/well for D_2R and D_3R, 30 μg/well for D_4R; [^{3}H]-(R)-(+)-7-OH-DPAT: 80 μg/well for D_2R, 40 μg/well for D_3R, 60 μg/well for D_4R), and 50 μl of radioligand diluted in binding buffer ([^{3}H]*N*-methylspiperone: 0.4 nM final concentration for all receptors; [^{3}H]-(R)-(+)-7-OH-DPAT: 1.5 nM final concentration for D_2R, 0.5 nM final concentration for D_3R, 3 nM final concentration for D_4R). Aliquots of [^{3}H]*N*-

methylspiperone and [^{3}H]-(*R*)-(+)-7-OH-DPAT solution were also quantified accurately to determine how much radioactivity was added. Nonspecific binding was determined using 10 μM (+)-butaclamol (Sigma-Aldrich, St. Louis, MO) and total binding was determined with 30% DMSO vehicle. The reaction was incubated for 60 ([^{3}H]*N*-methylspiperone) or 90 minutes ([^{3}H]-(R)-(+)-7-OH-DPAT) at room temperature and terminated by filtration through Perkin Elmer Uni-Filter-96 GF/B plates, presoaked in 0.5% polyethylenimine, using a Brandel 96-Well Plate Harvester Manifold (Brandel Instruments, Gaithersburg, MD). Filters were washed 3 times (~1 mL/well) with ice cold binding buffer. After drying, 65 μL Perkin Elmer MicroScint 20 Scintillation Cocktail was added to each well and filters were counted after at least 18 hours of incubation using a Perkin Elmer MicroBeta Microplate Counter. IC_{50} values for each compound were determined from dose-response curves and K_i values were calculated using the Cheng-Prusoff equation in GraphPad Prism 6 (GraphPad Software, San Diego, CA).[50] K_d values for [^{3}H]*N*-methylspiperone and [^{3}H]-(*R*)-(+)-7-OH-DPAT were determined via separate homologous competitive binding experiments at each receptor. K_i values for each compound/receptor/radioligand combination were calculated from at least three independent experiments and are reported as means ± SEM.

Functional Assays.

β-Arrestin Recruitment Assay

Assays were conducted with minor modifications as previously published by our laboratory,[31, 51-54] using the DiscoverX PathHunter technology (DiscoverX, Inc., Fremont, CA). Briefly, CHO-K1 cells stably expressing the human D_2R long isoform, D_3R, or D_4R (DiscoverX, Inc.) were maintained in Ham's F12 media supplemented with 10% fetal bovine serum, 100 U/mL penicillin,

100 μg/mL streptomycin, 800 μg/mL G418 and 300 μg/mL hygromycin at 37 °C, 5% CO_2, and 90% humidity. The cells were seeded in this media at a density of 2,625 cells/well in 384-well black, clear-bottom plates. Compounds were diluted in PBS in the presence of 0.2 μM sodium metabisulfite. Following overnight incubation, the cells were treated with multiple concentrations of compound and incubated at 37 °C for 90 min. DiscoverX reagent was then added to cells according to the manufacturer's recommendations followed by 45-60 min incubation at room temperature. Luminescence was measured on a Hamamatsu FDSS μCell reader. Data were collected as RLUs and subsequently normalized to a percentage of the control luminescence seen with a maximum concentration of dopamine for agonist mode assays and the EC_{80} of dopamine for antagonist mode assays. The Hill coefficients of the concentration-response curves did not significantly differ from unity.

cAMP Inhibition Assay

D_4R and D_2R-mediated inhibition of forskolin-stimulated cAMP production was assayed using the PerkinElmer LANCE UltracAMP assay kit (PerkinElmer, Inc., Waltham, MA). CHO-K1 cells stably expressing the human D_2R long isoform or D_4R were maintained in Ham's F12 supplemented with 10% fetal bovine serum, 100 U/mL penicillin, 100 μg/mL streptomycin, 800 μg/mL G418 and 300 μg/mL hygromycin at 37°C, 5% CO_2, and 90% humidity. Cells were seeded in Hank's Balanced Salt Solution (with CaCl and $MgCl_2$) with 5mM HEPES buffer and 0.2 μM sodium metabisulfite at a density of 5000 cells/well in 384-well white plates. Compounds and forskolin were made in the same buffer. Immediately after plating, cells were treated with 2.5 μL of compound (at various concentrations) and 2.5 μL of forskolin and incubated at room temperature for 30 minutes. The final concentration of forskolin was 10 μM. When running assay in antagonist mode, the EC_{80} of dopamine (10 nM) was added with the Forskolin solution. Eu-

cAMP tracer and ULight-anti-cAMP solutions were added as directed by the manufacturer and cells were incubated for 2 h in the dark at room temperature, after which a TR-FRET signal was measured using a BMG Labtech PHERAstar Fs (BMG Labtech U.S.A, Cary, NC). Values were normalized to a percentage of the control TR-FRET signal seen with a maximum concentration of dopamine for agonist mode assays and the EC_{80} of dopamine for antagonist mode assays. The Hill coefficients of the concentration-response curves did not significantly differ from unity with the data fitting to a single site model.

Molecular Docking Studies:

Crystal structures of D_2R, D_3R, and D_4R. In this study, we used the crystal structure of the human dopamine D_2, D_3, and D_4 receptor in complex with antagonists risperidone (PDB: 6CM4[26]), eticlopride (PDB: 3PBL[25]), and nemonapride (PDB: 5WIU[24]), respectively. Each of the three crystal structures was prealigned in membrane using the OPM web server.[55]

Protein structure preparation. The structures of D_2R, D_3R, and D_4R were further prepared using Maestro Protein Preparation Wizard.[56] First, the hydrogens and missing side chains were added. Second, the protonation state of the receptor was optimized at pH = 7. Third, a restrained minimization was performed to relax the receptor structure using OPLS3 force field.[57]

Ligand preparation. The 2D structures of **1**, **6**, **9**, **10**, **12**, **13**, and **21** were first constructed in Chemdraw and then converted into a 3D structure using Maestro Elements. Next, the protonation state was generated at pH = 7 using the pK_a prediction program Epik that is based on the Hammett and Taft methodologies.[56] Lastly, the geometry of each ligand was optimized using an energy minimization.

Ligand docking. The orthosteric ligand pockets of D_2R, D_3R, and D_4R were specified by the crystal ligands risperidone, eticlopride, and nemonapride, respectively, and a 3D box was formed around each crystal ligand to enclose the orthosteric ligand binding pocket. Each ligand was first docked using the Glide XP scoring function with default procedures and parameters.[58-59] Reproductions of the crystal binding poses of risperidone, eticlopride, and nemonapride in D_2R, D_3R, and D_4R, respectively, provide a solid validation for our XP docking protocol (Figures S2-S4). To refine the docking poses of non-crystal ligands, Induced Fit Docking (IFD) was conducted on the complex from the Glide XP docking.

Molecular Dynamics (MD) simulation system setup. Seven MD simulation systems were built using the complexes from the IFD docking. Each pre-aligned complex was placed in a double lipid membrane formed by POPC lipids[60] and then solvated in an orthorhombic water box with a buffer distance of 10Å using the SPC water model.[61] Each system was neutralized using Na^+ ions, added with a salt concentration of 0.15 M NaCl. The OPLS3 force field[57] was used to represent the receptor-ligand-lipid system.

Relaxation and production runs. Using Desmond, each system was first relaxed using the default relaxation protocol for membrane proteins.[62] After the relaxation, a 100.0 ns production run was conducted under the NPT ensemble for each system using the default protocol. A temperature of 300 K was controlled using the Nosé-Hoover chain coupling scheme[63] with a coupling constant of 1.0 ps. A pressure of 1 atm was controlled using the Martyna-Tuckerman-Klein chain coupling scheme[63] with a coupling constant of 2.0 ps. M-SHAKE[64] was applied to constrain all bonds connecting hydrogen atoms, enabling a 2.0 fs time step in the simulations. The k-space Gaussian split Ewald method[65] was used to treat long-range electrostatic interactions under periodic boundary conditions (charge grid spacing of ~1.0 Å, and direct sum tolerance of 10^{-9}). The cutoff

distance for short-range non-bonded interactions was 9 Å, with the long-range van der Waals interactions based on a uniform density approximation. To reduce the computation, non-bonded forces were calculated using an r-RESPA integrator[66] where the short-range forces were updated every step and the long-range forces were updated every three steps. The trajectories were saved at 100.0 ps intervals for analysis.

Simulation interaction diagram (SID) analyses. The SID tool was used to generate graphical information about the behavior and interaction of the protein and ligand during simulation. The analysis gives us graphical representation of Root Mean Square Deviation (RMSD), Root Mean Square Fluctuation (RMSF), secondary structures changes, protein-ligand contacts, and ligand torsion profiles of rotatable bonds.

Convergence of simulations. To check the convergence of the simulations, we investigated the protein Cα and ligand RMSD plots for each system (Figures S34-S36). The relatively flat plots within last 20 ns indicate that the complex systems have reached a steady state.

Trajectory clustering analyses. The Desmond trajectory clustering tool[67] was used to group complex structures for each system. The Backbone RMSD matrix was used as structural similarity metric and hierarchical clustering with average linkage[67] was selected as the clustering method. The merging distance cutoff was set to be 2.5 Å. For all systems, a dominant cluster with was identified to have more than 80% of the trajectory population.

ASSOCIATED CONTENT

Supporting Information. Representation of compound effects on D_1-like dopamine receptors and comparison of ligand-residue contacts in the D_2-like receptors. List of MD simulations and the

examples of validation analysis. Elemental analysis for all final compounds results and LC/MS data for compound 9. SMILES data (CSV). The supporting information is available free of charge on the ACS website.

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Notes

The authors declare no competing financial interest.

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ABBREVIATIONS USED

TM, transmembrane; D_2R, dopamine D_2 receptor; D_3R, dopamine D_3 receptor; D_4R, dopamine D_4 receptor; $CDCl_3$, deuterated chloroform; D_2O, deuterium oxide; EtOAc, Ethyl acetate; PP, phenylpiperazine

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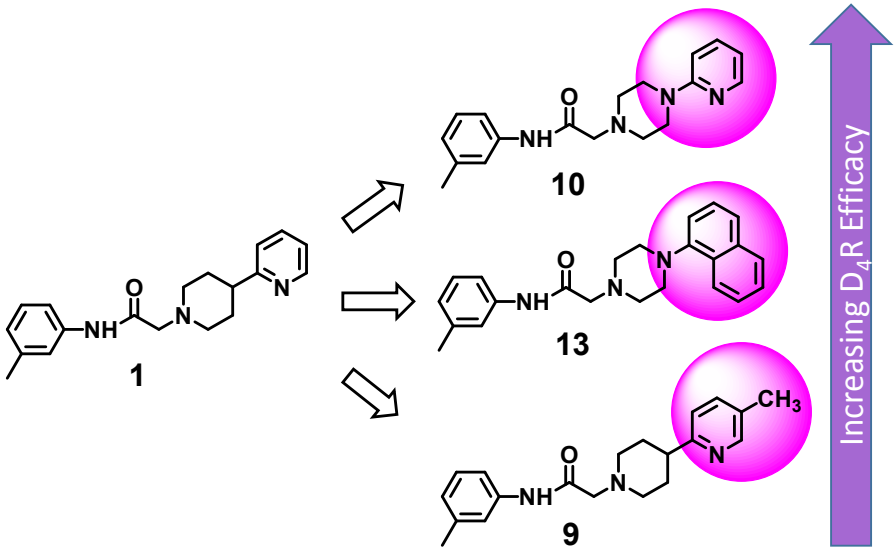

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