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Discovery of Potent and Selective Allosteric Inhibitors of Protein Arginine Methyltransferase 3 (PRMT3).

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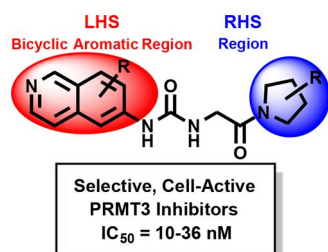
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PRMT3 catalyzes the asymmetric dimethylation of arginine residues of various proteins. It is crucial for maturation of ribosomes, and has been implicated in several diseases. We recently disclosed a highly potent, selective, and cell-active allosteric inhibitor of PRMT3, compound **4**. Here, we report comprehensive structure-activity relationship studies that target the allosteric binding site of PRMT3. We conducted design, synthesis, and evaluation of novel compounds in biochemical, selectivity, and cellular assays that culminated in the discovery of **4** and other highly potent (IC₅₀ values: ~10–36 nM), selective, and cell-active allosteric inhibitors of PRMT3 (compounds **29**, **30**, **36**, and **37**). In addition, we generated compounds that are very close analogs of these potent inhibitors, but displayed drastically reduced potency as negative controls (compounds **49–51**). These inhibitors and negative controls are valuable chemical tools for the biomedical community to further investigate biological functions and disease associations of PRMT3.

The following graphic will be used for the TOC:



Discovery of Potent and Selective Allosteric Inhibitors of Protein Arginine Methyltransferase 3 (PRMT3)

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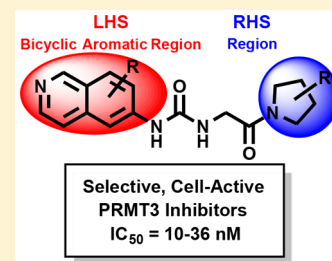
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Supporting Information

ABSTRACT: PRMT3 catalyzes the asymmetric dimethylation of arginine residues of various proteins. It is crucial for maturation of ribosomes and has been implicated in several diseases. We recently disclosed a highly potent, selective, and cell-active allosteric inhibitor of PRMT3, compound 4. Here, we report comprehensive structure–activity relationship studies that target the allosteric binding site of PRMT3. We conducted design, synthesis, and evaluation of novel compounds in biochemical, selectivity, and cellular assays that culminated in the discovery of 4 and other highly potent (IC_{50} values: ~ 10 – 36 nM), selective, and cell-active allosteric inhibitors of PRMT3 (compounds 29, 30, 36, and 37). In addition, we generated compounds that are very close analogs of these potent inhibitors but displayed drastically reduced potency as negative controls (compounds 49–51). These inhibitors and negative controls are valuable chemical tools for the biomedical community to further investigate biological functions and disease associations of PRMT3.



INTRODUCTION

Protein arginine methyltransferase 3 (PRMT3) is a type I PRMT that catalyzes mono- and asymmetric dimethylation of arginine residues.¹ Ribosomal protein S2 (rpS2) was identified as the major substrate of PRMT3 via its interaction with PRMT3 zinc finger domain in mammalian cells.^{2,3} PRMT3 plays a role in ribosome biosynthesis. However, the molecular mechanism by which PRMT3 influences ribosomal biosynthesis remains unclear.⁴ Very recently, an extraribosomal complex comprising PRMT3, rpS2, and human programmed cell-death 2-like (PDCD2L) protein was identified.⁵ While PRMT3 is localized exclusively in the cytoplasm,⁶ it has been shown that in cells treated with palmitic acid or T0901317 (a liver X receptor α (LXR α) agonist), PRMT3 colocalizes with LXR α in the cell nucleus, regulating hepatic lipogenesis.⁷ However, this effect appears to be independent of the PRMT3 methyltransferase activity. While rpS2 is the primary substrate

of PRMT3, it is not the sole substrate. PRMT3 along with PRMT1 methylates the recombinant mammalian nuclear poly(A)-binding protein (PABPN1) and has been implicated in oculopharyngeal muscular dystrophy, which is caused by polyalanine expansion in PABPN1.^{8,9} A protein complex comprising the von Hippel–Lindau (VHL) tumor suppressor protein, PRMT3, and ARF (alternative reading frame) methylates p53.¹⁰ Importantly, the tumor suppressor DAL-1 (differentially expressed in adenocarcinoma of the lung, also known as 4.1B) interacts with PRMT3 and consequently inhibits its methyltransferase activity, suggesting a possible role of PRMT3 regulation in tumor growth.¹¹ The interaction between DAL-1 and PRMT3 in the induction of apoptosis in MCF-7 cells suggests that this interaction is likely to be an

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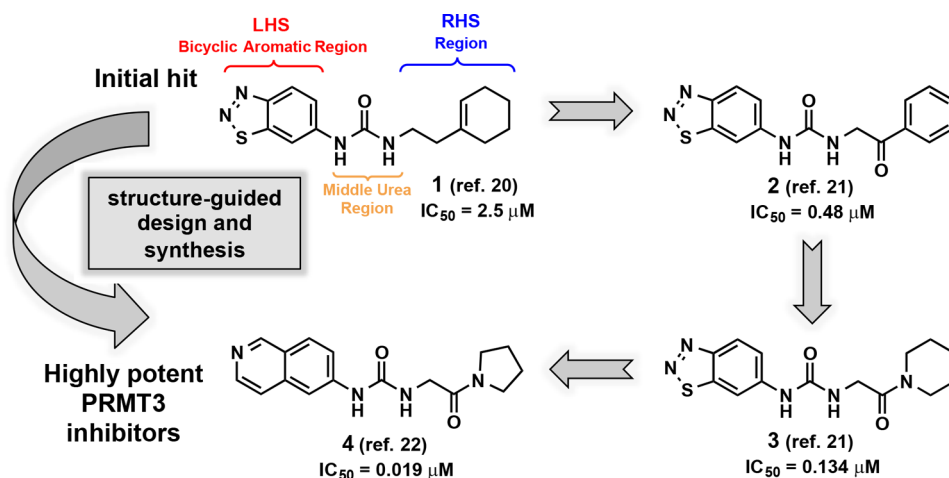


Figure 1. Design and synthesis of highly potent inhibitors of PRMT3.

62 important modulator of the apoptotic pathway and can be
 63 critical to controlling tumorigenesis in breast cancer cells.¹² It
 64 has also been shown that PRMT3 methylates a histone peptide
 65 (H4 1–24) *in vitro*.¹³ Modified histone H4R3 is associated
 66 with increased transcription of a number of genes, including
 67 those under control of estrogen and androgen receptors.^{14–16}
 68 Furthermore, PRMT3 expression levels are elevated in
 69 myocardial tissues from patients with atherosclerosis, poten-
 70 tially implicating the involvement of PRMT3.¹⁷ Additionally,
 71 PRMT3 function has been reported to be essential for
 72 dendritic spine maturation in rats.¹⁸ A recent study suggests
 73 that PRMT3 mediates the preventive effects of irisin against
 74 lipogenesis and oxidative stress.¹⁹

75 Our group embarked on research efforts to discover potent,
 76 selective, and cell-active inhibitors of PRMT3 as chemical tools
 77 for better understanding of biology and function of this
 78 understudied protein methyltransferase. We previously re-
 79 ported the discovery of a novel allosteric binding site of
 80 PRMT3 and the first selective, allosteric inhibitors of PRMT3
 81 (compounds 1–3, Figure 1) and subsequently disclosed the
 82 discovery of SGC707 (4) (Figure 1), a highly potent, selective,
 83 and cell-active allosteric inhibitor of PRMT3.^{20–22} Here, we
 84 describe the design and synthesis of a large set of novel analogs
 85 and evaluation of these compounds in biochemical, selectivity,
 86 and cellular assays. This comprehensive structure–activity
 87 relationship (SAR) study resulted in the identification of
 88 multiple highly potent, selective, and cell-active allosteric
 89 inhibitors of PRMT3 including compound 4.

90 ■ RESULTS AND DISCUSSION

91 Our earlier efforts resulted in the identification of selective
 92 small-molecule inhibitors of PRMT3 (compounds 2 and 3)
 93 starting from a hit, compound 1 (Figure 1).^{20,21} X-ray crystal
 94 structures of 1 and 2 in complex with PRMT3 were obtained
 95 and showed that these inhibitors occupied a novel allosteric
 96 binding site (PDB ID: 3SMQ and 4HSG). These cocrystal
 97 structures revealed that the left-hand side (LHS) bicyclic
 98 benzothiadiazole moiety fits tightly in the allosteric pocket and
 99 the middle nitrogen atom forms a hydrogen bond with T466
 100 (Figure 2). The urea linker is located at the entrance of the
 101 cavity and forms hydrogen bonds with the guanidine of R396
 102 and the carboxylate of E422 (Figure 2). In addition, the right-
 103 hand side (RHS) moiety extends out of the allosteric binding
 104 pocket and makes hydrophobic interactions with a surface

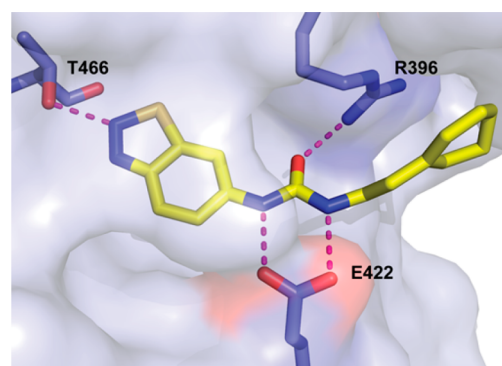
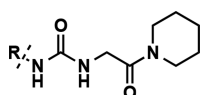


Figure 2. Reported cocrystal structure of compound 1 in complex with PRMT3 indicating key hydrogen bonding interactions (magenta dotted lines) (PDB ID: 3SMQ).²⁰

105 composed of the side chains from two different subunits of the
 106 PRMT3 homodimer. Both structural and SAR data clearly
 107 indicate that the middle urea region is essential for the affinity,
 108 and replacement of this group with its bioisosteres and more
 109 rigid analogs did not yield any inhibitors with improved
 110 potency.²¹ Therefore, in the current study the middle urea
 111 region of this scaffold was kept unmodified. However, further
 112 optimization of the RHS moiety led to the discovery of 3
 113 (Figure 1).²¹ Herein, we further optimized both the LHS and
 114 RHS moieties of this scaffold to achieve improved potency for
 115 inhibiting PRMT3. First, we conducted a scaffold hopping
 116 exercise by using the benzothiadiazole ring of 3 as a query for
 117 the allosteric pocket. A hydrogen-bond constraint was imposed
 118 in this scaffold hopping study to preserve the important
 119 hydrogen-bond interaction between the inhibitors and the
 120 hydroxyl group of T466. As a result of this exercise, 120
 121 isoquinoline (compound 5), isobenzofuran-1-one (compound
 122 6), and quinazoline (compound 7) groups were selected for
 123 experimental validation (Table 1).

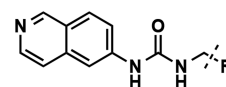
124 The RHS of compound 3, piperidineamide, was kept exactly
 125 the same in these newly synthesized analogs to accurately
 126 compare the effect of the different LHS bicyclic heteroaromatic
 127 rings on potency. The isoquinoline containing analog
 128 (compound 5) with IC_{50} of 84 ± 5 nM showed a small
 129 improvement over the parent compound, 3 ($IC_{50} = 134 \pm 5$
 130 nM). However, compounds 6 and 7 were around 6-fold less
 131 potent as compared to 3 (Table 1). Therefore, the isoquinoline

Table 1. Inhibitors with Different LHS Bicyclic Ring Systems



Compound	Structure (R)	IC ₅₀ (nM)
3		134 ± 5
5		84 ± 5
6		757 ± 1
7		967 ± 115
8		>2000

Table 2. Inhibitors with Saturated Aliphatic Groups as the RHS Moiety



Compound	Structure (R)	IC ₅₀ (nM)
9		421 ± 29
10		540 ± 54
11		295 ± 43
12		>8000
13		833 ± 66
14		291 ± 36

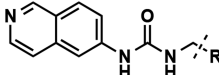
bicyclic ring system was taken forward as the LHS moiety for further optimization. Compound **8** (Table 1) was also prepared to confirm the importance of the positioning and hydrogen bonding of the isoquinoline nitrogen with T466. This bicyclic ring is still an isoquinoline but substituted at the 7-position instead of the 6-position (isoquinoline numbering) in effect walking the nitrogen to the adjacent position of compound **5**. As expected, this modification resulted in ablation of inhibitory activity.

As the 6-substituted isoquinoline is an optimal LHS bicycle, we then turned our attention to optimizing the RHS moiety of the scaffold. We first revisited saturated aliphatic groups as the RHS functionality inspired from our initial studies (Table 2).^{20,21} Compound **9**, a cyclohexylethyl group containing analog, corresponding to the RHS region of the original hit (compound **1**) was 5-fold less potent than **5**, displaying IC₅₀ of 421 ± 29 nM. As a logical extension of this compound, we also synthesized the fully saturated, cyclohexylethyl analog (**10**) as well as derivatives containing different ring sizes. Compound **10** (IC₅₀ = 540 ± 54 nM) was very similar to **9** in potency. The cyclopentane-bearing analog (**11**) showed slight improvement in potency with IC₅₀ of 295 ± 43 nM, while the cyclopropane-containing analog **12** was virtually inactive (IC₅₀ > 8000 nM). These results indicated that hydrophobicity of the RHS moiety plays an important role in potency, and cyclohexyl and cyclopentyl rings are preferred compared to the cyclopropyl group. Replacing the cyclohexyl group with a phenyl ring (compound **13**) resulted in a decreased potency (IC₅₀ = 833 ± 66 nM), underlying the importance of changes to the hydrophobicity of the RHS moiety. On the basis of these results, compound **10** was further investigated to improve the potency. A docking study with this compound hinted that a substituent at the C1 position of the cyclohexyl group would be a favorable position from which E422 might be

possibly reached for further interactions. Therefore, compound **14**, featuring a methyleneamino substituted cyclohexyl group, was synthesized. Interestingly, compound **14** displayed a modest improvement in potency with IC₅₀ of 291 ± 36 nM, compared to compound **10**. These compounds were synthesized following the previously published synthetic route.²¹

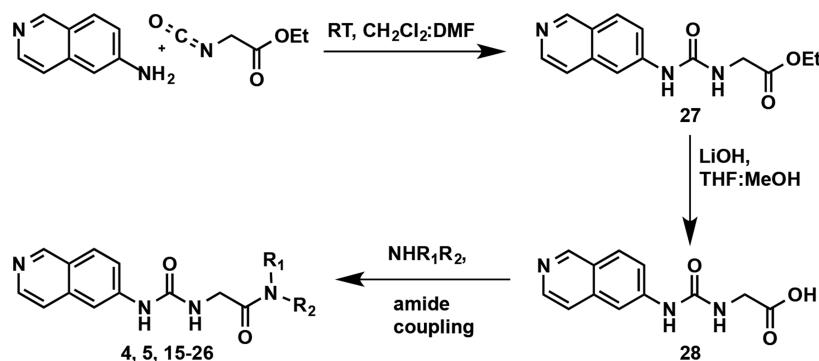
Since no significant improvement in potency was achieved with compounds **9–14** featuring aliphatic groups as the RHS moiety, we decided to keep the amide functionality as in compound **5** and further investigate the substituents on the nitrogen atom (Table 3) as the amide group could form direct or water-mediated contacts with the side chain of K392.²¹ We first synthesized new amide derivatives of compound **5**, by replacing the six-membered piperidine ring with the four-membered azetidine ring (compound **15**), five-membered pyrrolidine ring (compound **4**), and seven-membered azepane ring (compound **16**). While the azetidine amide analog **15** displayed only a slight improvement in potency (IC₅₀ = 61 ± 8 nM), the pyrrolidine amide **4** (IC₅₀ = 19 ± 1 nM) and azepane amide **16** (IC₅₀ = 17 ± 2 nM) were ~5-fold more potent than **5** in inhibiting PRMT3. The six-membered ring analogs of **5** such as 4,4-difluoro piperidine amide **17** (IC₅₀ = 35 ± 1 nM) showed a more than 2-fold improvement over the unsubstituted piperidine amide **5**. However, exchanging the piperidine ring with the 4-methylpiperazine ring (compound **18**), which alters the electronic nature and polarity of the ring system, resulted in the loss of the inhibitory activity. We also designed and synthesized noncyclic di- and monosubstituted amide derivatives (compounds **19–26**). The dimethyl and diethyl amide derivatives **19** and **20** displayed reduced potency with IC₅₀ of 150 ± 11 and 114 ± 3 nM, respectively. The *N*-cyclopentyl, *N*-methyl amide **21** (IC₅₀ = 87 ± 5 nM) was as

Table 3. Inhibitors Containing Different RHS Amide Moieties



Compound	Structure (R)	IC ₅₀ (nM)	Compound	Structure (R)	IC ₅₀ (nM)
5		84 ± 5	20		114 ± 3
15		61 ± 8	21		87 ± 5
4		19 ± 1	22		476 ± 34
16		17 ± 2	23		1938 ± 95
17		35 ± 1	24		158 ± 9
18		>1900	25		292 ± 23
19		150 ± 11	26		477 ± 5

Scheme 1. General Synthetic Route for the Preparation of Compounds Listed in Tables 3 and 4



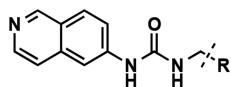
199 potent as compound 5. The Weinreb amide derivative 22,
 200 however, was around 6-fold less potent than compound 5. The
 201 monosubstituted amides were also investigated (compounds
 202 23–26). While *N*-methyl amide 23 displayed significantly
 203 weaker inhibitory effect, the cyclopropyl (24), cyclopentyl
 204 (25), and cyclohexyl (26) amide derivatives showed reduced
 205 potency as the ring size increased. Taken together, these results
 206 suggest that cyclic amides are preferred RHS moieties, which
 207 possess balanced steric and hydrophobic properties interacting
 208 with PRMT3. We, therefore, designated the pyrrolidine amide
 209 as the RHS moiety for the rest of the SAR study.

210 The compounds in Table 3 were synthesized via the general
 211 route shown in Scheme 1. The synthesis started with reacting
 212 commercially available 6-aminoisoquinoline and ethyl iso-
 213 cyanatoacetate to obtain the desired ethyl ester 27. The
 214 hydrolysis of the ethyl ester 27 resulted in the carboxylic acid

215 28, which was used as the key intermediate to perform amide
 216 coupling reactions with various amines to yield the desired
 217 amide analogs (4, 5, and 15–26). Detailed reaction conditions,
 218 yields, and characterization data for final compounds are
 219 reported in the Experimental Section.

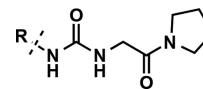
220 Next, we focused our attention on analogs of compound 4
 221 (Table 4), containing substituted pyrrolidine (compounds
 222 29–31) and fused bicyclic (compounds 32 and 33) and
 223 bridged bicyclic moieties (compounds 34 and 35). These
 224 compounds were again prepared according to the synthetic
 225 route outlined in Scheme 1. The 3,3,4,4-tetrafluoro pyrrolidine
 226 derivative (compound 29) as well as 2,5-dimethylpyrrolidine
 227 (a mixture of *cis* and *trans* isomers) (compound 30) analog
 228 showed very similar potency compared to compound 4.
 229 However, replacing pyrrolidine with *D*-proline (compound 31)
 230 resulted in around 9-fold drop in potency. The fused 5,5-

Table 4. Inhibitors with Modified Pyrrolidine Amide Moieties



Compound	Structure (R)	IC ₅₀ (nM)	Compound	Structure (R)	IC ₅₀ (nM)
4		19 ± 1	32		55 ± 5
29		24 ± 3	33		>5000
30		22 ± 2	34		46 ± 5
31		166 ± 11	35		22 ± 4

Table 5. Inhibitors with Substituted Isoquinolines



Compound	Structure (R)	IC ₅₀ (nM)
4		19 ± 1
36		19 ± 4
37		36 ± 6
38		194 ± 8
39		10 ± 1
40		19 ± 2

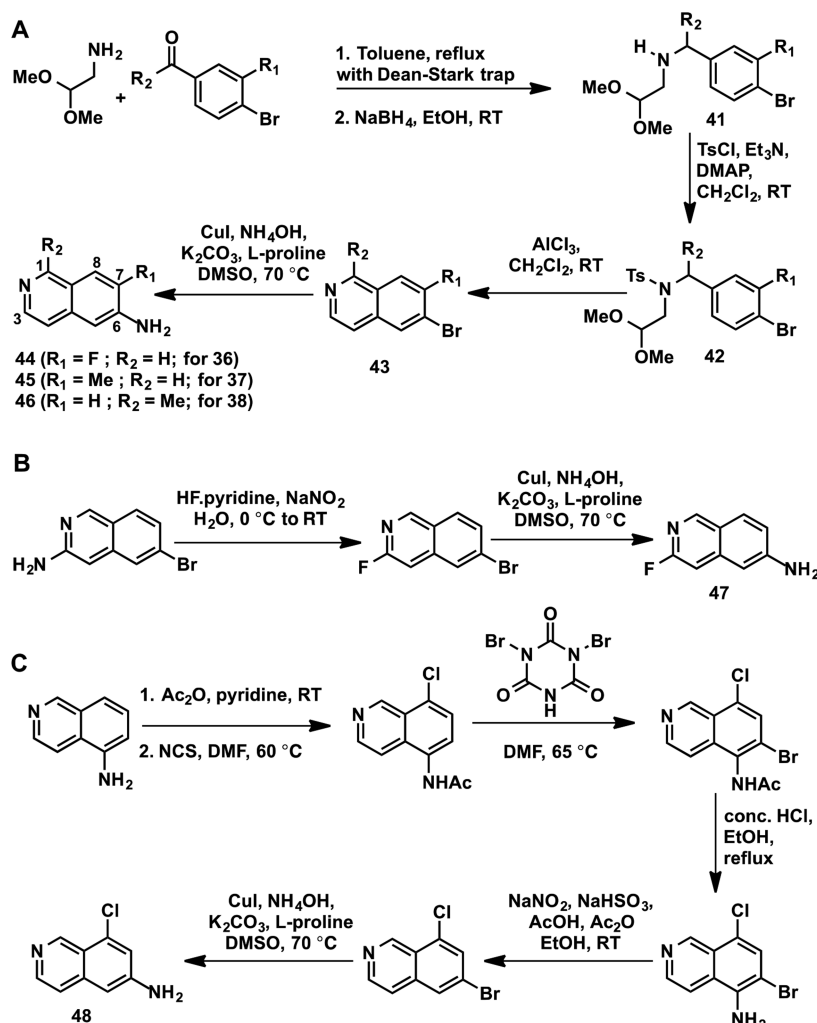
231 bicyclic ring system (compound 32) was also tolerated, albeit
 232 with reduced potency (IC₅₀ = 55 ± 5 nM). Interestingly, the
 233 benzene-fused pyrrolidine ring (isoindoline amide, compound
 234 33) led to a complete loss of the inhibitory effect. Finally, 7-
 235 azabicyclo[2.2.1]heptane (compound 34) and 8-
 236 azabicyclo[3.2.1]octane (compound 35), two bridged bicyclic
 237 pyrrolidine containing moieties, did not result in any
 238 improvement of potency compared to compound 4, with
 239 IC₅₀ of 46 ± 5 and 22 ± 4 nM, respectively. These results
 240 indicate that small substituents such as fluoro and methyl
 241 groups on the pyrrolidine ring as well as relatively flexible
 242 hydrophobic bicyclic ring systems are tolerated.

243 The results summarized in Table 4 and discussed above have
 244 shown that analogs of 4, namely, compounds 29, 30, 32, 34,
 245 and 35, potently inhibited PRMT3 with IC₅₀ values of around
 246 20–50 nM. Although these analogs did not display improved
 247 potency compared to compound 4, these substituted
 248 pyrrolidine groups are valuable alternatives to the unsub-
 249 stituted pyrrolidine group (compound 4). After completing
 250 optimization of the RHS moiety, we further investigated the
 251 LHS isoquinoline ring. Analysis of the crystal structure of
 252 PRMT3 in complex with compound 4 (PDB ID: 4RYL)²²
 253 suggested that there is room in the binding pocket to tolerate a
 254 relatively small substituent at the 1-, 3-, 7-, and 8-positions of
 255 the isoquinoline ring system. Our structural analysis also
 256 suggested that a substituent at the 4- and 5-positions of the
 257 isoquinoline ring would not be tolerated. Therefore, we
 258 designed and synthesized the corresponding substituted
 259 isoquinoline analogs (compounds 36–40) to determine
 260 whether potency could further be enhanced (Table 5). For
 261 example, compounds 36 and 37 featuring small 7-fluoro and 7-
 262 methyl substituents were prepared. Compound 36 showed
 263 similar potency as 4, while 37, which has a slightly larger
 264 methyl substituent, was around 2-fold less potent. Compound
 265 38, however, displayed significant potency loss (about 10-fold),
 266 indicating that the methyl group at the 1-position of the
 267 isoquinoline ring is not preferred. Interestingly, the 3-fluoro
 268 substituted analog 39 displayed almost 2-fold higher potency
 269 with IC₅₀ of 10 ± 1 nM. This result suggests that the electronic
 270 modulation of the isoquinoline ring by a fluoro group does not
 271 have significant impact on the hydrogen bonding ability of the

272 isoquinoline with T466 and a small substituent such as the
 273 fluoro group at the 3-position enhances potency, consistent
 274 with our structural analysis. In addition, we synthesized the 8-
 275 chloroisoquinoline derivative 40, which exhibited similar
 276 potency as compound 4. While the result obtained for
 277 compound 39 was consistent with our prediction based on
 278 the analysis of the crystal structure of the PRMT3–compound
 279 4 complex (PDB ID: 4RYL), it was surprising that a small
 280 substituent such as the fluoro group at the 7-position
 281 (compound 36) or the chloro group at the 8-position
 282 (compound 40) did not increase potency and a slightly larger
 283 substituent such as the methyl group at the 1- and 7-positions
 284 (compounds 37 and 38) reduced potency. More comprehen-
 285 sive structural analyses such as molecular dynamics simulation
 286 are needed to explain the SAR results. Nevertheless, the fluoro
 287 or chloro substituent could potentially improve metabolic
 288 stability of these compounds (36, 39, and 40), which are
 289 interesting alternative PRMT3 inhibitors to compound 4.
 290 Overall, these results have demonstrated that a small
 291 substituent at the isoquinoline ring can be tolerated but has
 292 limited impact on enhancing potency.

293 The substituted 6-amino isoquinoline derivatives used for
 294 the synthesis of compounds 36–40 (Table 5) were not
 295 commercially available. Therefore, we devised synthetic routes
 296 and prepared these substituted 6-amino isoquinolines as shown
 297 in Scheme 2. The synthesis of 6-amino-7-fluoroisoquinoline
 298 (43), 6-amino-7-methylisoquinoline (44), and 6-amino-1-
 299 methylisoquinoline (45) started with reductive amination
 300 reactions of amino acetaldehyde dimethyl acetal with the
 301 corresponding 4-bromo aryl aldehyde or methyl aryl ketone to
 302 give amino dimethyl acetals 41 (Scheme 2A). The
 303 intermediates 41 were converted to the sulfonamides 42, via
 304 tosylation, which were then treated with aluminum chloride to
 305 yield the desired 6-bromoisoquinolines (43). These sub-
 306 stituted 6-bromoisoquinolines were then converted to the
 307 desired 6-aminoisoquinolines (44–46) via aryl amination

Scheme 2. Synthetic Routes for Preparing Intermediates 44–48 for Synthesis of Compounds 36–40



308 reactions (Scheme 2A). The 3-fluoro-6-aminoisoquinoline
309 (47) was synthesized starting from the commercially available
310 3-amino-6-bromoisoquinoline in two steps via the Balz–
311 Schiemann reaction^{23,24} followed by an aryl amination
312 (Scheme 2B). As shown in Scheme 2C, 6-amino-8-
313 chloroisoquinoline (48) was prepared in six steps. The
314 commercially available 5-aminoisoquinoline was first acetylated
315 and then chlorinated to install a chloro group at the 8-position.
316 Bromination at the 6-position was achieved by using
317 dibromoisocyanuric acid. Deacetylation followed by reductive
318 diazotization resulted in 6-amino-8-chloroisoquinoline (48)
319 (Scheme 2C). Intermediates 44–48 were then used to prepare
320 compounds 36–40 according to the synthetic route outlined
321 in Scheme 1.

322 In addition, we designed and synthesized several close
323 analogs of compound 4 to serve as negative controls for
324 chemical biology studies. As described earlier, the middle urea
325 region of these PRMT3 inhibitors forms the key hydrogen-
326 bonding interactions with E422 of PRMT3. We therefore
327 predicted that taking either of these hydrogen-bonding
328 interactions away by methylating either nitrogen atom of the
329 urea would drastically decrease PRMT3 inhibition. Indeed, as
330 shown in Table 6, compound 49 displayed markedly
331 diminished inhibitory activity (IC₅₀ = 2594 ± 129 nM),
332 while compound 50 was completely inactive (IC₅₀ > 50 000

Table 6. Compounds Prepared as Negative Controls

Compound	Structure	IC ₅₀ (nM)
49		2594 ± 129
50		>50000
51		No Inhibition

nM). Furthermore, the nitrogen atom in the isoquinoline ring
333 of compound 4 forms a key hydrogen bond with T466 of
334 PRMT3 in the crystal structure of the PRMT3–compound 4
335 complex (PDB ID: 4RYL). Thus, we replaced the isoquinoline
336 ring of 4 with the naphthalene ring (compound 51 (XY1)),
337 effectively removing the critical hydrogen bond with T466. As
338 we reported previously,²² compound 51 displayed no
339 inhibition of the PRMT3 catalytic activity in biochemical
340 assays.

36

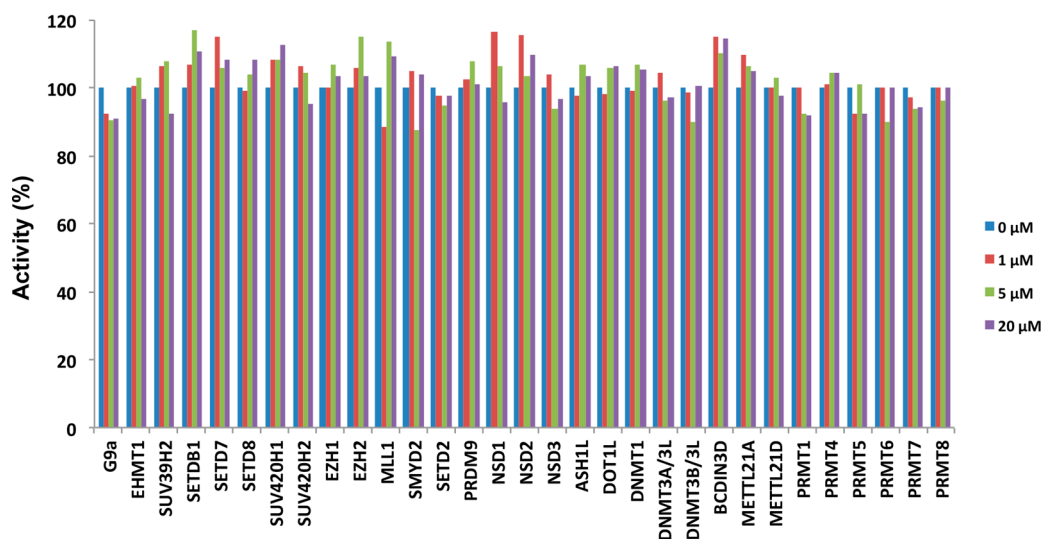


Figure 3. Inhibitor 36 is highly selective for PRMT3 over 31 other methyltransferases. The selectivity data for compounds 29 and 30 are shown in the Supporting Information.

342 We previously reported that compound 4 was more than
 343 200-fold selective for PRMT3 over 31 other methyltransferases
 344 and more than 250 kinases, GPCRs, ion channels, and
 345 transporters.²² Similarly, inhibitors 29, 30, and 36 were
 346 selective for PRMT3 over 31 other lysine methyltransferases,
 347 arginine methyltransferases, and DNA and RNA methyltrans-
 348 ferases (Figure 3 and Supporting Information). In addition, 29,
 349 30, and 36 were tested in a CEREP selectivity panel consisting
 350 of 55 protein targets (47 GPCRs, five ion channels, and three
 351 transporters) and did not show any significant off-target
 352 activities (% of inhibition <50% at 10 μ M). It is of note that
 353 the cocrystal structure of compound 4 in complex with
 354 PRMT3 reported recently (PDB ID: 4RYL)²² clearly shows
 355 that this inhibitor binds the same allosteric pocket as earlier
 356 inhibitors (compounds 1 and 2 (PDB ID: 3SMQ and 4HSG)).
 357 To establish the target engagement of PRMT3 inhibitors in
 358 cells (namely, inhibitors 4, 29, 36, and 37), we used an
 359 InCELL Hunter Assay, which measures intracellular binding of
 360 inhibitors to the methyltransferase domain of PRMT3 in cell
 361 lines expressing the methyltransferase domain of PRMT3
 362 tagged with a short fragment of β -galactosidase (ePL). Binding
 363 of a compound to ePL-PRMT3 increases the fusion protein
 364 half-life. Inhibitors 4, 29, 36, and 37 stabilized PRMT3 in
 365 A549 cells, a human lung carcinoma cell line, with EC_{50} values
 366 of 2.0, 2.7, 1.6, and 4.9 μ M, respectively (Figure 4, top). The
 367 same assay was performed in HEK293 cells and these
 368 compounds displayed EC_{50} values of 1.8, 3.1, 2.7, and 5.2
 369 μ M, respectively (Figure 4, bottom). Compound 51 was used
 370 as a negative control in these assays. As expected, no
 371 stabilization was observed with this compound.

372 Furthermore, to establish whether these PRMT3 inhibitors
 373 can inhibit the PRMT3 catalytic activity in cells, we examined
 374 their effects on H4R3 asymmetric dimethylation. Since
 375 methylated arginine residues have relatively slow turnover,
 376 we overexpressed human Flag-tagged PRMT3 and followed
 377 the methylation of both endogenous H4 and exogenously
 378 introduced GFP-tagged H4. As we previously reported,
 379 overexpressed PRMT3 increased the endogenous H4R3me2a
 380 from the baseline levels, and compound 4 effectively inhibited
 381 this increase with an IC_{50} of 225 nM.²² The asymmetric

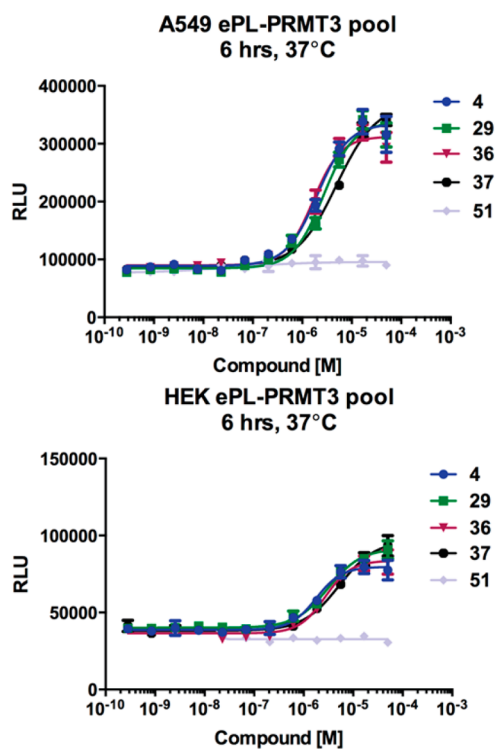


Figure 4. InCELL Hunter Assay results of compounds 4, 29, 36, 37, and 51 in A549 and HEK cells.

dimethylation of exogenous H4R3 was also inhibited by 382
 compound 4 (IC_{50} = 91 nM), indicating that this inhibitor has 383
 robust cellular effect.²² Similarly, as shown in Figure 5, 384
 compounds 29, 30, and 36 inhibited the exogenous 385
 asymmetric dimethylation of H4R3 (IC_{50} = 240, 184, and 386
 134 nM, respectively). The dependency on the transfected 387
 PRMT3 catalytic activity was determined by using the 388
 catalytically dead PRMT3 mutant (E335Q) that did not affect 389
 endogenous or exogenous H4R3me2a levels and therefore was 390
 used to establish the baseline levels of the mark. It is of note 391

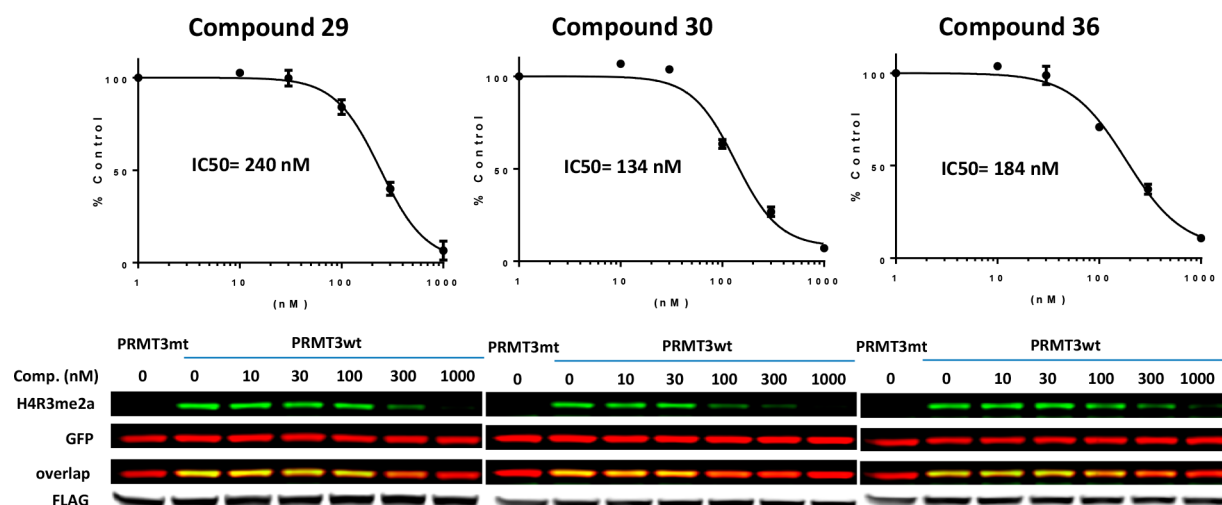


Figure 5. Cellular inhibitory activity of compounds 29, 30, and 36. HEK293 cells were cotransfected with FLAG tagged PRMT3 (wt) or its catalytic mutant (mt) and GFP-tagged histone H4 and treated with different concentrations of compounds, as indicated. Total cell lysates were collected 24 h post inhibitor treatment and analyzed for H4R3me2a, GFP, and FLAG levels by Western blotting. The graphs represent nonlinear fits of H4R3me2a fluorescence intensities normalized to GFP. The results are the averages of three replicates.

392 that effects of 1 μM compounds 29, 30, and 36 matched with
393 that of the catalytically dead PRMT3 mutant E335Q.

394 ■ CONCLUSION

395 In summary, we conducted comprehensive SAR studies,
396 starting from early inhibitors 1–3 and culminating in the
397 discovery of highly potent (IC_{50} values = ~ 10 –36 nM),
398 selective, and cell-active allosteric inhibitors of PRMT3
399 (inhibitors 4, 29, 30, 36, and 37). In addition, we generated
400 compounds that are very close analogs of these potent
401 inhibitors but that displayed drastically diminished potency
402 as negative controls (compounds 49–51). The new inhibitors
403 (compounds 29, 30, and 36) were highly selective for PRMT3
404 over 31 other methyltransferases and 55 other protein targets.
405 In cell-based assays, compounds 29, 30, and 36 engaged
406 PRMT3 and potently inhibited its methyltransferase activity
407 (Figures 4 and 5). These inhibitors and negative controls are
408 excellent chemical tools for the biomedical community to
409 further investigate biological functions and disease associations
410 of PRMT3.

411 ■ EXPERIMENTAL SECTION

412 **Chemistry General Procedures.** Analytical thin-layer chroma-
413 tography (TLC) was performed employing EMD Milipore 210–270
414 μm 60-F254 silica gel plates. The plates were visualized by exposure
415 to UV light. Flash column chromatography was performed on a
416 Teledyne ISCO CombiFlash Rf⁺ system equipped with a variable
417 wavelength UV detector and a fraction collector using RediSep Rf
418 normal phase silica columns. Nuclear magnetic resonance (NMR)
419 spectra were acquired on a Bruker DRX-600 spectrometer or on a
420 Varian Mercury spectrometer at 400 MHz. Chemical shifts are
421 reported in parts per million (ppm, δ) scale relative to solvent residual
422 peak (chloroform-*d*: ^1H , 7.26 ppm; ^{13}C , 77.16 ppm; methanol-*d*₄: ^1H ,
423 3.31 ppm; ^{13}C , 49.0 ppm). ^1H NMR data are reported as follows:
424 chemical shift, multiplicity (s = singlet, d = doublet, t = triplet, q =
425 quartet, p = pentet, m = multiplet, app = apparent), coupling
426 constant, and integration. HPLC spectra for all compounds were
427 acquired using an Agilent 6110 series system with a UV detector set
428 to 254 nm. Samples were injected (5 μL) onto an Agilent Eclipse
429 Plus, 4.6 \AA , ~ 50 mm, 1.8 μm , C18 column at room temperature,
430 either with a linear gradient from 50% to 100% B (MeOH + 0.1%
431 acetic acid) in 5.0 min followed by pumping 100% B for another 2

min with A being H_2O + 0.1% acetic acid, or by a linear gradient from 432
10% to 100% B (MeOH + 0.1% acetic acid) in 5.0 min followed by 433
pumping 100% B for another 2 min with A being H_2O + 0.1% acetic 434
acid. The flow rate was 1.0 mL/min. Mass spectrometry (MS) data 435
were acquired in positive ion mode using an Agilent 6110 single- 436
quadrupole mass spectrometer with an electrospray ionization (ESI) 437
source. HRMS analysis was conducted on an Agilent Technologies 438
G1969A high-resolution API-TOF mass spectrometer attached to an 439
Agilent Technologies 1200 HPLC system. Samples were ionized by 440
ESI in positive mode. All biologically evaluated compounds had >95% 441
purity using the HPLC methods described above. 442

1-(Benzo[d][1,2,3]thiadiazol-6-yl)-3-(2-oxo-2-(piperidin-1-yl)- 443
ethyl)urea (3). Compound 3 was prepared according to previously 444
published procedures.²¹ 445

1-(Isoquinolin-6-yl)-3-(2-oxo-2-(pyrrolidin-1-yl)ethyl)urea (4). 446
Compound 4 was prepared according to previously published 447
procedures.²² 448

1-(Isoquinolin-6-yl)-3-(2-oxo-2-(piperidin-1-yl)ethyl)urea (5). To 449
a solution of isoquinolin-6-amine (50 mg, 0.347 mmol) in *N,N*- 450
dimethylformamide (DMF) (1.6 mL) at room temperature was added 451
N,N'-carbonyldiimidazole (CDI) (84 mg, 0.520 mmol). The resulting 452
solution was stirred for 12 h prior to the addition of 2-amino-1- 453
(piperidin-1-yl)ethan-1-one (99 mg, 0.694 mmol) and stirred for a 454
further 6 h. Following dilution with water (20 mL), the aqueous layer 455
was extracted with ethyl acetate (EtOAc) (3×20 mL), and the 456
combined organic extracts were dried with anhydrous sodium sulfate. 457
After filtration, all solvents were removed under reduced pressure, and 458
the residue was purified by column chromatography on silica gel to 459
afford title compound (5) (31 mg, 29% yield). ^1H NMR (500 MHz, 460
DMSO-*d*₆) δ 9.08 (s, 1H), 8.35 (d, J = 5.7 Hz, 1H), 8.08 (br s, 1H), 461
7.98 (d, J = 8.9 Hz, 1H), 7.63 (d, J = 5.8 Hz, 1H), 7.02 (br s, 2H), 462
6.57 (t, J = 4.6 Hz, 1H), 4.02 (d, J = 4.7 Hz, 2H), 3.50–3.44 (m, 2H), 463
3.38–3.33 (m, 2H), 1.65–1.57 (m, 2H), 1.57–1.50 (m, 2H), 1.50– 464
1.40 (m, 2H). m/z (HRMS) [$M + \text{H}$]⁺ for $\text{C}_{17}\text{H}_{21}\text{N}_4\text{O}_2$: calculated 465
313.1659, found 313.1662. 466

1-(1-Oxo-1,3-dihydroisobenzofuran-5-yl)-3-(2-oxo-2-(piperidin- 467
1-yl)ethyl)urea (6). To a solution of 5-amino-3H-benzofuran-1-one 468
(75 mg, 0.5 mmol, 1.0 equiv) in DMF (1.5 mL) was added CDI (90 469
mg, 0.55 mmol, 1.1 equiv), and the resulting mixture was stirred for 8 470
h at rt. 2-Amino-1-piperidin-1-ylethanone hydrochloride salt (134 mg, 471
0.75 mmol, 1.5 equiv) was then added followed by Hunig's base (131 472
 μL , 0.75 mmol, 1.5 equiv). After being stirred for 18 h at rt, the 473
resulting mixture was diluted with water (25 mL) and extracted with 474
EtOAc (3×25 mL). Combined organic layers were dried over 475
sodium sulfate and concentrated under reduced pressure to give crude 476

477 product, which was then purified by flash column chromatography to
478 yield desired compound as white solid (39 mg, 25%). ¹H NMR (600
479 MHz, methanol-*d*₄) δ 7.85 (s, 1H), 7.73 (d, *J* = 8.5 Hz, 1H), 7.42 (dd,
480 *J* = 8.5, 1.8 Hz, 1H), 5.31 (s, 2H), 4.10 (s, 2H), 3.57 (t, *J* = 5.6 Hz,
481 2H), 3.45 (t, *J* = 5.5 Hz, 2H), 1.74–1.50 (m, 6H). MS (ESI) *m/z* [*M*
482 + *H*]⁺ for C₁₆H₂₀N₃O₄⁺: calculated 318.1, found 318.1.

483 **1-(2-Oxo-2-(piperidin-1-yl)ethyl)-3-(quinazolin-7-yl)urea (7)**. To
484 a solution of quinazolin-7-amine (73 mg, 0.5 mmol, 1.0 equiv) in
485 DMF (1.5 mL) was added CDI (90 mg, 0.55 mmol, 1.1 equiv), and
486 the resulting mixture was stirred for 8 h at rt. 2-Amino-1-piperidin-1-
487 ylethanone hydrochloride salt (134 mg, 0.75 mmol, 1.5 equiv) was
488 then added followed by Hunig's base (131 μL, 0.75 mmol, 1.5 equiv).
489 After being stirred for 18 h at rt, the resulting mixture was diluted with
490 water (25 mL) and extracted with EtOAc (3 × 25 mL). Combined
491 organic layers were dried over sodium sulfate and concentrated under
492 reduced pressure to give crude product, which was then purified by
493 flash column chromatography to yield desired compound (10 mg,
494 6%). ¹H NMR (600 MHz, methanol-*d*₄) δ 9.29 (s, 1H), 9.06 (s, 1H),
495 8.22 (d, *J* = 2.1 Hz, 1H), 8.00 (d, *J* = 8.9 Hz, 1H), 7.71 (dd, *J* = 8.9,
496 2.1 Hz, 1H), 4.14 (s, 2H), 3.58 (t, *J* = 5.6 Hz, 2H), 3.47 (t, *J* = 5.5 Hz,
497 2H), 1.75–1.53 (m, 6H). MS (ESI) *m/z* [*M* + *H*]⁺ for C₁₆H₂₀N₅O₂⁺:
498 calculated 314.2, found 314.2.

499 **1-(Isoquinolin-7-yl)-3-(2-oxo-2-(piperidin-1-yl)ethyl)urea (8)**. To
500 a solution of isoquinolin-7-amine (50 mg, 0.347 mmol) in DMF (1.6
501 mL) at room temperature was added CDI (84 mg, 0.520 mmol). The
502 resulting solution was stirred for 12 h prior to the addition of 2-
503 amino-1-(piperidin-1-yl)ethan-1-one (99 mg, 0.694 mmol) and
504 stirred for a further 6 h. Following dilution with water (20 mL),
505 the aqueous layer was extracted with EtOAc (3 × 20 mL), and the
506 combined organic extracts were dried with anhydrous sodium sulfate.
507 After filtration, all solvents were removed under reduced pressure, and
508 the residue was purified by column chromatography on silica gel to
509 afford title compound (8) (45 mg, 42% yield). ¹H NMR (500 MHz,
510 DMSO-*d*₆) δ 9.13 (s, 1H), 8.33 (d, *J* = 5.6 Hz, 1H), 8.22 (d, *J* = 1.9
511 Hz, 1H), 7.85 (d, *J* = 8.9 Hz, 1H), 7.69 (d, *J* = 5.6 Hz, 1H), 7.11 (br s,
512 1H), 6.92 (br s, 1H), 6.50 (t, *J* = 4.7 Hz, 1H), 4.03 (dd, *J* = 14.2, 5.9
513 Hz, 2H), 3.47–3.44 (m, 2H), 3.38–3.34 (m, 2H), 1.63–1.56 (m,
514 2H), 1.56–1.50 (m, 2H), 1.49–1.41 (m, 2H). *m/z* (HRMS) [*M* +
515 *H*]⁺ for C₁₇H₂₁N₄O₂⁺: calculated 313.1659, found 313.1664.

516 **General Procedures for the Preparation of Compounds 9–**
517 **14 in Table 2.** Compounds 9–14 shown in Table 2 were prepared
518 according general procedures described below. To a solution of
519 isoquinolin-6-amine (1.0 equiv) and triethylamine (TEA) (2 equiv) in
520 DMF (1 mL/0.347 mmol) was added CDI (1.5 equiv), and the
521 reaction mixture was allowed to stir at 25 °C for 4 h. To the reaction
522 mixture was then added the corresponding amine (2 equiv), and the
523 mixture was allowed to stir for additional 1 h. Then 50 mL of water
524 and 50 mL of EtOAc were added to the reaction mixture. After
525 extraction, the organic layer was washed with brine, dried over
526 anhydrous Na₂SO₄, filtered, and concentrated in vacuo. The residue
527 was purified by column chromatography on silica gel eluting with 0–
528 5% MeOH in DCM to give the product.

529 **1-(2-(Cyclohex-1-en-1-yl)ethyl)-3-(isoquinolin-6-yl)urea (9)**. Yel-
530 low oil (67 mg, 62% yield). ¹H NMR (chloroform-*d*) δ: 9.07 (s, 1H),
531 8.40 (d, *J* = 5.8 Hz, 1H), 8.04 (s, 1H), 7.81 (d, *J* = 8.8 Hz, 1H), 7.66
532 (s, 1H), 7.53 (d, *J* = 5.8 Hz, 1H), 7.44 (dd, *J* = 8.8, 2.0 Hz, 1H), 7.27
533 (s, 1H), 5.45 (s, 1H), 5.27–5.30 (m, 1H), 3.42–3.77 (m, 2H), 2.20–
534 2.17 (m, 6H), 1.97–1.92 (m, 4H), 1.627–1.47 (m, 4H). MS (ESI)
535 *m/z* [*M* + *H*]⁺ for C₁₈H₂₂N₃O⁺: calculated 296.2, found 296.1.

536 **1-(2-Cyclohexylethyl)-3-(isoquinolin-6-yl)urea (10)**. Yellow oil
537 (69 mg, 64% yield). ¹H NMR (DMSO-*d*₆) δ: 9.07 (s, 1H), 8.87 (s,
538 1H), 8.33 (d, *J* = 5.8 Hz, 1H), 8.06 (d, *J* = 1.8 Hz, 1H), 7.95 (d, *J* =
539 9.0 Hz, 1H), 7.60 (d, *J* = 6.0 Hz, 1H), 7.52 (dd, *J* = 8.8, 2.0 Hz, 1H),
540 6.28 (br t, *J* = 5.5 Hz, 1H), 3.11–3.24 (m, 2H), 1.58–1.76 (m, 5H),
541 1.11–1.39 (m, 6H), 0.83–0.98 (m, 2H). MS (ESI) *m/z* [*M* + *H*]⁺ for
542 C₁₈H₂₄N₃O⁺: calculated 298.2, found 298.1.

543 **1-(2-Cyclopentylethyl)-3-(isoquinolin-6-yl)urea (11)**. Light yellow
544 oil (30 mg, 29% yield). ¹H NMR (chloroform-*d*) δ: 9.04 (s, 1H), 8.36
545 (d, *J* = 5.8 Hz, 1H), 8.03 (s, 2H), 7.76 (d, *J* = 8.8 Hz, 1H), 7.34–7.56
546 (m, 2H), 7.27 (s, 1H), 3.19–3.40 (m, 2H), 1.64–1.82 (m, 3H),

1.40–1.64 (m, 6H), 0.95–1.16 (m, 2H), 0.01 (s, 1H). MS (ESI) *m/z* 547
[*M* + *H*]⁺ for C₁₇H₂₂N₃O⁺: calculated 284.2, found 284.1. 548

549 **1-(2-Cyclopropylethyl)-3-(isoquinolin-6-yl)urea (12)**. White solid
550 (27 mg, 29% yield). ¹H NMR (DMSO-*d*₆) δ: 9.59 (s, 1H), 9.46 (s, 550
1H), 8.34–8.51 (m, 2H), 8.28 (d, *J* = 9.0 Hz, 1H), 8.12 (d, *J* = 6.5 551
Hz, 1H), 7.77 (dd, *J* = 9.0, 2.0 Hz, 1H), 6.71 (br t, *J* = 5.4 Hz, 1H), 552
3.11–3.27 (m, 3H), 1.38 (q, *J* = 7.0 Hz, 2H), 0.61–0.80 (m, 1H), 553
0.35–0.49 (m, 2H). MS (ESI) *m/z* [*M* + *H*]⁺ for C₁₅H₁₈N₃O⁺: 554
calculated 256.1, found 256.1. 555

556 **1-(Isoquinolin-6-yl)-3-phenethylurea (13)**. Light yellow oil (23 556
mg, 22% yield). ¹H NMR (chloroform-*d*) δ: 8.95 (s, 1H), 7.89–8.47 557
(m, 3H), 7.74 (d, *J* = 8.8 Hz, 1H), 7.46 (d, *J* = 5.8 Hz, 1H), 7.37 (dd, 558
J = 8.9, 1.9 Hz, 1H), 7.20–7.30 (m, 2H), 7.09–7.20 (m, 3H), 5.63 559
(br s, 1H), 3.55 (q, *J* = 6.8 Hz, 2H), 2.84 (t, *J* = 6.9 Hz, 2H). MS 560
(ESI) *m/z* [*M* + *H*]⁺ for C₁₈H₁₈N₃O⁺: calculated 292.1, found 292.1. 561

562 **1-(2-(1-(Aminomethyl)cyclohexyl)ethyl)-3-(isoquinolin-6-yl)urea 562**
(14). The general procedure was applied using *tert*-butyl ((1-(2- 563
aminoethyl)cyclohexyl)methyl)carbamate as the amine (285 mg, 1.11 564
mmol) to give *tert*-butyl ((1-(2-(3-(isoquinolin-6-yl)ureido)ethyl)- 565
cyclohexyl)methyl)carbamate as a white solid. To the solution of *tert*- 566
butyl ((1-(2-(3-(isoquinolin-6-yl)ureido)ethyl)cyclohexyl)methyl)- 567
carbamate (130 mg, 0.305 mmol) in DCM (1 mL) was added TFA 568
(1.000 mL, 12.98 mmol). Then the reaction mixture was stirred at 25 569
°C for 0.5 h. To the mixture was added 5 mL of toluene, and it was 570
then concentrated in vacuo. The residue was purified by preparative- 571
HPLC to give the product as white solid (23 mg, 22% yield). ¹H 572
NMR (methanol-*d*₄) δ 8.94–9.07 (m, 1H), 8.28 (br d, *J* = 5.8 Hz, 573
1H), 8.07 (br s, 1H), 7.88–7.99 (m, 1H), 7.49–7.69 (m, 2H), 3.26– 574
3.44 (m, 2H), 3.02–3.26 (m, 2H), 2.65 (s, 2H), 1.14–1.78 (m, 13H). 575
MS (ESI) *m/z* [*M* + *H*]⁺ for C₁₉H₂₇N₄O⁺: calculated 327.2, found 576
327.2. 577

578 **General Procedures for the Synthesis of Amides 15–35 in 578**
Tables 3 and 4. Synthesis of (Isoquinolin-6-ylcarbamoyl)glycine 579
(28) (Scheme 1). To a stirring solution of 6-aminoisoquinoline (1.2 g, 580
8.32 mmol, 1 equiv) in a mixture of dichloromethane and DMF (30 581
and 10 mL) was added ethyl isocyanatoacetate (2.80 mL, 25 mmol, 582
3.0 equiv), and the resulting mixture was stirred overnight at room 583
temperature. After removal of volatiles, the crude mixture was purified 584
by flash column chromatography (gradient from 100% dichloro- 585
methane to 10% methanol in dichloromethane) to yield the desired 586
ethyl ester (27)²² as a pale yellow solid, which was resuspended in 587
methanol (48 mL) and water (16 mL) followed by the addition of 1 588
N solution of NaOH (24 mL). The resulting clear mixture was then 589
stirred at room temperature overnight. After concentration of the 590
mixture under reduced pressure, the crude mixture was purified by 591
reverse phase flash column chromatography (gradient from 100% 592
water to 10% methanol in dichloromethane) to yield the desired acid 593
28 as a TFA salt (2.04 g, 57% over two steps). 594

595 To a stirring mixture of the above acid 28 (1.0 equiv) in DMF (0.8 595
mL/0.1 mmol) was added *N*-(3-(dimethylamino)propyl)-*N'*-ethyl- 596
carbodiimide hydrochloride (EDC·HCl) (1.5 equiv), 1-hydroxy-7- 597
azabenzotriazole (HOAt) (1.5 equiv), and the corresponding amine 598
(1.5 equiv) followed by *N*-methylmorpholine (NMM) (2 equiv), and 599
the resulting mixture was stirred for 18 h at room temperature. The 600
reaction was purified by either flash column chromatography or 601
HPLC to give pure products. 602

603 **1-(2-(Azetidin-1-yl)-2-oxoethyl)-3-(isoquinolin-6-yl)urea (15).** 603
The reaction mixture was purified by HPLC to give pure product 604
as a white solid (mono-TFA salt, 8 mg, 10%). ¹H NMR (methanol- 605
*d*₄) δ 9.02 (d, *J* = 0.9 Hz, 1H), 8.29 (d, *J* = 5.9 Hz, 1H), 8.08 (d, *J* = 606
2.1 Hz, 1H), 7.97 (d, *J* = 9.0 Hz, 1H), 7.66–7.61 (m, 1H), 7.57 (dd, *J* 607
= 8.9, 2.1 Hz, 1H), 4.35–4.27 (m, 2H), 4.07 (t, *J* = 7.8 Hz, 2H), 3.87 608
(s, 2H), 2.43–2.32 (m, 2H). MS (ESI) *m/z* [*M* + *H*]⁺ for 609
C₁₅H₁₇N₄O₂⁺: calculated 285.1, found 285.2. 610

611 **1-(2-(Azepan-1-yl)-2-oxoethyl)-3-(isoquinolin-6-yl)urea (16).** The 611
title compound was obtained as a white solid (mono-TFA salt, 21 mg, 612
40%). ¹H NMR (600 MHz, methanol-*d*₄) δ 9.37 (s, 1H), 8.37 (d, *J* = 613
2.0 Hz, 1H), 8.31 (d, *J* = 6.6 Hz, 1H), 8.27 (d, *J* = 9.0 Hz, 1H), 8.07 614
(d, *J* = 6.6 Hz, 1H), 7.81 (dd, *J* = 9.0, 2.0 Hz, 1H), 4.17 (s, 2H), 615
3.61–3.56 (m, 2H), 3.56–3.51 (m, 2H), 1.86–1.82 (m, 2H), 1.78– 616

617 1.71 (m, 2H), 1.69–1.58 (m, 4H). ¹³C NMR (151 MHz, methanol-*d*₄) δ 170.5, 156.7, 149.3, 146.9, 145.6, 142.1, 133.3, 132.1, 125.4, 619 124.2, 112.4, 48.1, 47.4, 42.5, 29.7, 28.5, 28.3, 27.8. MS (ESI) *m/z* [M + H]⁺ for C₁₈H₂₃N₄O₂⁺: calculated 327.2, found 327.2.

621 **1-(2-(4,4-Difluoropiperidin-1-yl)-2-oxoethyl)-3-(isoquinolin-6-yl)-urea (17)**. The title compound was obtained as a white solid (mono-TFA salt, 51 mg, 66%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.39 (d, 624 *J* = 0.9 Hz, 1H), 8.45 (d, *J* = 2.1 Hz, 1H), 8.37–8.27 (m, 2H), 8.14 (d, *J* = 6.7 Hz, 1H), 7.86 (dd, *J* = 9.1, 2.1 Hz, 1H), 4.21 (s, 2H), 3.75 (t, *J* = 6.1 Hz, 2H), 3.65 (t, *J* = 6.0 Hz, 2H), 2.14–1.96 (m, 4H). ¹³C NMR (151 MHz, methanol-*d*₄) δ 169.5, 156.8, 149.3, 147.0, 145.7, 628 142.1, 132.2, 125.3, 124.3, 122.9, 112.5, 111.2, 42.6, 40.3, 35.1, 34.6. MS (ESI) *m/z* [M + H]⁺ for C₁₇H₁₉F₂N₄O₂⁺: calculated 349.2, found 630 349.2.

631 **1-(Isoquinolin-6-yl)-3-(2-(4-methylpiperazin-1-yl)-2-oxoethyl)-urea (18)**. The title compound was obtained as a light yellow solid (bis-TFA salt, 48 mg, 52%). ¹H NMR (400 MHz, DMSO-*d*₆) δ 9.96 (br s, 1H), 9.47 (s, 1H), 8.44 (d, *J* = 6.5 Hz, 1H), 8.32–8.28 (m, 2H), 635 8.10 (d, *J* = 6.5 Hz, 1H), 7.78 (dd, *J* = 9.0, 2.1 Hz, 1H), 6.90 (br s, 636 1H), 4.12 (br s, 2H), 3.40 (br s, 8H); these protons are obscured by residual water in DMSO, 2.83 (br s, 3H). MS (ESI) *m/z* [M + H]⁺ for C₁₇H₂₂N₅O₂⁺: calculated 328.2, found 638 328.2.

639 **2-(3-(Isoquinolin-6-yl)ureido)-N,N-dimethylacetamide (19)**. The title compound was obtained as a white solid (mono-TFA salt, 14.6 mg, 18%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.03 (s, 1H), 8.29 (d, 642 *J* = 5.9 Hz, 1H), 8.10 (d, *J* = 2.1 Hz, 1H), 7.98 (d, *J* = 8.9 Hz, 1H), 643 7.65 (d, *J* = 5.9 Hz, 1H), 7.59 (dd, *J* = 8.9, 2.1 Hz, 1H), 4.13 (s, 2H), 644 3.08 (s, 3H), 2.99 (s, 3H). MS (ESI) *m/z* [M + H]⁺ for C₁₄H₁₇N₄O₂⁺: calculated 273.1, found 273.2.

646 **N,N-Diethyl-2-(3-(isoquinolin-6-yl)ureido)acetamide (20)**. The title compound was obtained as a white solid (34.1 mg, 81%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.05 (s, 1H), 8.30 (d, *J* = 5.9 Hz, 649 1H), 8.11 (s, 1H), 8.00 (d, *J* = 9.0 Hz, 1H), 7.67 (d, *J* = 6.0 Hz, 1H), 650 7.60 (dd, *J* = 8.9, 2.1 Hz, 1H), 4.14 (s, 2H), 3.42 (apparent p, *J* = 7.0 651 Hz, 4H), 1.27 (t, *J* = 7.2 Hz, 3H), 1.16 (t, *J* = 7.1 Hz, 3H). MS (ESI) 652 *m/z* [M + H]⁺ for C₁₆H₂₁N₄O₂⁺: calculated 301.2, found 301.2.

653 **N-Cyclopentyl-2-(3-(isoquinolin-6-yl)ureido)-N-methylacetamide (21)**. The title compound was obtained as a white solid (18.2 mg, 40%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.03 (s, 1H), 8.29 (d, 656 *J* = 5.9 Hz, 1H), 8.10 (d, *J* = 2.1 Hz, 1H), 7.98 (d, *J* = 8.9 Hz, 1H), 657 7.65 (d, *J* = 5.9 Hz, 1H), 7.59 (dd, *J* = 8.9, 2.1 Hz, 1H), 4.92–4.90 658 (m, 1H), 4.27–4.25 (m, 1H), 4.21 (s, 1H), 4.11 (s, 1H), 2.93 (s, 1H), 659 2.86 (s, 1H), 1.94 (s, 1H), 1.86–1.55 (m, 7H). MS (ESI) *m/z* [M + 660 H]⁺ for C₁₈H₂₃N₄O₂⁺: calculated 327.2, found 327.2.

661 **2-(3-(Isoquinolin-6-yl)ureido)-N-methoxy-N-methylacetamide (22)**. The title compound was obtained as a white solid (mono-TFA salt, 34.9 mg, 63%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.37 (d, *J* = 664 1.1 Hz, 1H), 8.33–8.28 (m, 2H), 8.25 (d, *J* = 9.1 Hz, 1H), 8.05 (d, *J* = 665 = 6.7 Hz, 1H), 7.79 (dd, *J* = 9.1, 2.1 Hz, 1H), 4.24 (s, 2H), 3.82 (s, 666 3H), 3.25 (s, 3H). MS (ESI) *m/z* [M + H]⁺ for C₁₄H₁₇N₄O₃⁺: calculated 289.1, found 289.1.

668 **2-(3-(Isoquinolin-6-yl)ureido)-N-methylacetamide (23)**. The reaction mixture was then purified by HPLC to give pure product as a white mono-TFA salt (4 mg, 8%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.41 (d, *J* = 0.9 Hz, 1H), 8.46 (d, *J* = 2.1 Hz, 1H), 8.36–8.27 (m, 672 2H), 8.16 (d, *J* = 6.7 Hz, 1H), 7.87 (dd, *J* = 9.1, 2.1 Hz, 1H), 3.92 (s, 673 2H), 2.78 (s, 3H). MS (ESI) *m/z* [M + H]⁺ for C₁₃H₁₅N₄O₂⁺: calculated 259.1, found 259.1.

675 **N-Cyclopropyl-2-(3-(isoquinolin-6-yl)ureido)acetamide (24)**. The title compound was obtained as a white solid (58 mg, 78%). ¹H NMR (400 MHz, DMSO-*d*₆) δ 9.91 (s, 1H), 9.52 (s, 1H), 8.45 (d, *J* = 6.6 678 Hz, 1H), 8.44–8.28 (m, 2H), 8.18 (d, *J* = 6.6 Hz, 1H), 8.10 (d, *J* = 679 4.1 Hz, 1H), 7.79 (dd, *J* = 9.0, 2.0 Hz, 1H), 6.83 (t, *J* = 5.3 Hz, 1H), 680 3.74 (d, *J* = 5.2 Hz, 2H), 2.69–2.62 (m, 1H), 0.65–0.61 (m, 2H), 681 0.48–0.37 (m, 2H). MS (ESI) *m/z* [M + H]⁺ for C₁₅H₁₇N₄O₂⁺: calculated 285.1, found 285.1.

683 **N-Cyclopentyl-2-(3-(isoquinolin-6-yl)ureido)acetamide (25)**. The title compound was obtained as a white solid (15 mg, 38%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.04 (s, 1H), 8.30 (d, *J* = 5.9 Hz, 1H), 686 8.09 (d, *J* = 2.1 Hz, 1H), 7.99 (d, *J* = 8.9 Hz, 1H), 7.66 (d, *J* = 6.0 Hz,

1H), 7.59 (dd, *J* = 8.9, 2.1 Hz, 1H), 4.15 (p, *J* = 6.7 Hz, 1H), 3.88 (s, 687 2H), 2.00–1.89 (m, 2H), 1.73 (s, 2H), 1.68–1.56 (m, 2H), 1.49 (dq, 688 *J* = 14.4, 8.3, 7.5 Hz, 2H). MS (ESI) *m/z* [M + H]⁺ for C₁₇H₂₁N₄O₂⁺: calculated 313.2, found 313.2.

N-Cyclohexyl-2-(3-(isoquinolin-6-yl)ureido)acetamide (26). The title compound was obtained as a white solid (mono-TFA salt, 48.3 mg, 53%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.40 (s, 1H), 8.45 (d, 693 *J* = 2.1 Hz, 1H), 8.34–8.31 (m, 2H), 8.14 (d, *J* = 6.7 Hz, 1H), 7.86 (dd, *J* = 9.0, 2.1 Hz, 1H), 3.91 (s, 2H), 3.73–3.69 (m, 1H), 1.90–1.87 (m, 2H), 1.78–1.75 (m, 2H), 1.66–1.63 (m, 1H), 1.42–1.19 (m, 5H). MS (ESI) *m/z* [M + H]⁺ for C₁₅H₂₃N₄O₂⁺: calculated 327.2, found 327.2.

1-(Isoquinolin-6-yl)-3-(2-oxo-2-(3,3,4,4-tetrafluoropyrrolidin-1-yl)ethyl)urea (29). The title compound was obtained as a white solid (48.3 mg, 53%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.04 (s, 1H), 8.30 (d, *J* = 5.9 Hz, 1H), 8.11–8.07 (m, 1H), 7.98 (d, *J* = 8.9 Hz, 702 1H), 7.65 (d, *J* = 5.9 Hz, 1H), 7.59 (dd, *J* = 8.9, 2.1 Hz, 1H), 4.28 (t, *J* = 13.5 Hz, 2H), 4.08–4.01 (m, 4H). MS *m/z* (HRMS) [M + H]⁺ for C₁₆H₁₅F₄N₄O₂⁺: calculated 371.1126, found 371.1153.

1-(2-(2,5-Dimethylpyrrolidin-1-yl)-2-oxoethyl)-3-(isoquinolin-6-yl)urea (30). The title compound was obtained as a white solid (48.2 mg, 88%). The amine, 2,5-dimethylpyrrolidine, is used as mixture of cis and trans for the coupling reaction, and only the major product is reported below. ¹H NMR (400 MHz, methanol-*d*₄) δ 9.03 (br s, 1H), 8.29 (d, *J* = 5.9 Hz, 1H), 8.09 (d, *J* = 2.1 Hz, 1H), 7.98 (d, *J* = 8.9 Hz, 711 1H), 7.65 (d, *J* = 5.9 Hz, 1H), 7.59 (dd, *J* = 8.9, 2.2 Hz, 1H), 4.19–4.01 (m, 4H), 2.17–1.97 (m, 2H), 1.79–1.71 (m, 2H), 1.34 (d, *J* = 713 6.4 Hz, 3H), 1.33 (d, *J* = 6.4 Hz, 3H). MS *m/z* (HRMS) [M + H]⁺ for C₁₈H₂₃N₄O₂⁺: calculated 327.1816, found 371.1819.

Methyl(isoquinolin-6-ylcarbamoyl)glycyl-L-prolinate (31). The title compound was obtained as a yellow solid (mono-TFA salt, 51 mg, 65%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.40 (s, 1H), 8.39 (s, 718 1H), 8.32 (br s, 2H), 8.13 (s, 1H), 7.84 (s, 1H), 4.52 (dd, *J* = 8.7, 3.9 719 Hz, 1H), 4.23–4.08 (m, 2H), 3.81 (s, 1H), 3.75–3.57 (m, 4H), 2.32–720 2.23 (m, 1H), 2.14–1.97 (m, 3H). MS (ESI) *m/z* [M + H]⁺ for C₁₈H₂₁N₄O₄⁺: calculated 357.2, found 357.2. [α]_D²⁰ = –70 (c 1.6, 722 CH₃OH).

1-(2-(Hexahydrocyclopenta[c]pyrrol-2(1H)-yl)-2-oxoethyl)-3-(isoquinolin-6-yl)urea (32). The title compound was obtained as a white solid (mono-TFA salt, 33 mg, 44%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.41 (s, 1H), 8.46 (s, 1H), 8.33 (d, *J* = 7.4 Hz, 2H), 8.15 (s, 727 1H), 7.87 (d, *J* = 9.1 Hz, 1H), 4.07 (s, 2H), 3.73–3.65 (m, 2H), 728 3.31–3.30 (m, 2H), 2.87–2.79 (m, 1H), 2.75–2.66 (m, 1H), 1.97–729 1.77 (m, 3H), 1.73–1.63 (m, 1H), 1.59–1.46 (m, 2H). MS (ESI) *m/z* [M + H]⁺ for C₁₉H₂₃N₄O₂⁺: calculated 339.2, found 339.2.

1-(2-(Isoindolin-2-yl)-2-oxoethyl)-3-(isoquinolin-6-yl)urea (33). The title compound was obtained as a white solid (42 mg, 73%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.04 (s, 1H), 8.30 (d, *J* = 5.9 Hz, 734 1H), 8.12 (d, *J* = 2.1 Hz, 1H), 7.99 (d, *J* = 8.9 Hz, 1H), 7.63 (d, *J* = 735 5.8 Hz, 1H), 7.56 (dd, *J* = 8.9, 2.1 Hz, 1H), 7.36–7.31 (m, 3H), 6.65 736 (t, *J* = 4.8 Hz, 1H), 4.88 (s, 2H), 4.71 (s, 2H), 4.09 (d, *J* = 4.7 Hz, 737 2H). MS (ESI) *m/z* [M + H]⁺ for C₂₀H₁₉N₄O₂⁺: calculated 347.2, found 347.2.

1-(2-(7-Azabicyclo[2.2.1]heptan-7-yl)-2-oxoethyl)-3-(isoquinolin-6-yl)urea (34). The title compound was obtained as a white solid (mono-TFA salt, 33 mg, 45%). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.40 (br s, 1H), 8.43 (d, *J* = 2.1 Hz, 1H), 8.35–8.28 (m, 2H), 8.13 (d, 742 *J* = 6.7 Hz, 1H), 7.85 (dd, *J* = 9.1, 2.1 Hz, 1H), 4.60 (t, *J* = 4.8 Hz, 744 1H), 4.41 (t, *J* = 4.8 Hz, 1H), 4.10 (s, 2H), 1.90 (q, *J* = 9.1, 7.0 Hz, 745 2H), 1.77 (s, 2H), 1.68–1.59 (m, 2H), 1.58–1.50 (m, 2H). MS (ESI) 746 *m/z* [M + H]⁺ for C₁₈H₂₁N₄O₂⁺: calculated 325.2, found 325.2.

1-(2-(8-Azabicyclo[3.2.1]octan-8-yl)-2-oxoethyl)-3-(isoquinolin-6-yl)urea (35). The title compound was obtained as a white solid (22 mg, 38%). ¹H NMR (400 MHz, methanol-*d*₄) δ 8.99 (s, 1H), 8.26 (d, 750 *J* = 5.9 Hz, 1H), 8.05 (s, 1H), 7.93 (d, *J* = 9.0 Hz, 1H), 7.62–7.52 (m, 751 2H), 4.62–4.55 (m, 1H), 4.27 (d, *J* = 6.7 Hz, 1H), 4.18–4.02 (m, 752 2H), 2.15–2.03 (m, 1H), 1.97–1.70 (m, 6H), 1.62 (dd, *J* = 13.2, 5.4 753 Hz, 2H), 1.53 (d, *J* = 12.8 Hz, 1H). MS (ESI) *m/z* [M + H]⁺ for C₁₉H₂₃N₄O₂⁺: calculated 339.2, found 339.2.

756 1-(7-Fluoroisoquinolin-6-yl)-3-(2-oxo-2-(pyrrolidin-1-yl)ethyl)-
757 urea (36) (Scheme 2A; Table 5). A mixture of aminoacetaldehyde
758 dimethyl acetal (0.5 g, 2.46 mmol, 1.0 equiv) and 4-bromo-3-
759 fluorobenzaldehyde (0.4 mL, 3.70 mmol, 1.5 equiv) in toluene (40
760 mL) in a round-bottom flask equipped with a reflux condenser and
761 Dean–Stark trap was heated to reflux for 6 h. Then the reaction
762 mixture was quenched with water (20 mL) and extracted with DCM
763 (40 mL). After concentration of volatiles, crude mixture was dissolved
764 in EtOH (20 mL), and NaBH₄ (0.19 g, 4.92 mmol, 2 equiv) was
765 added at room temperature and stirred overnight. The reaction was
766 then quenched with water (50 mL) and extracted with EtOAc (50 mL
767 × 3). Combined organic layers were washed with brine (50 mL × 2)
768 and dried over Na₂SO₄ and concentrated under reduced pressure to
769 give the desired amino acetal (41 (R₁ = F, R₂ = H) in Scheme 2A)
770 (0.65 g, 90%). The amino acetal (0.35 g, 1.19 mmol) was
771 resuspended in DCM (20 mL), and TEA (0.5 mL, 3.57 mmol, 3
772 equiv), TsCl (0.27 g, 1.43 mmol, 1.2 equiv), and DMAP (15 mg, 10
773 mol %) were added to give a clear solution, which was stirred at room
774 temperature overnight. The reaction mixture was then suspended in
775 water (20 mL) and extracted with DCM (50 mL × 3). Combined
776 organic layers were washed with brine, dried over Na₂SO₄, and
777 concentrated down. The crude mixture was purified by flash column
778 chromatography to give the desired tosyl amine (0.51 g, 90%) (42 (R₁
779 = F, R₂ = H) in Scheme 2A).

780 To a flame-dried flask equipped with Teflon stir bar was added
781 AlCl₃ (0.27 g, 2.02 mmol, 4.5 equiv) under nitrogen atmosphere
782 followed by the addition of the above solution of tosyl amine (0.2 g,
783 0.45 mmol, 1.0 equiv) in DCM (6 mL). The resulting solution was
784 stirred under nitrogen at room temperature overnight. The reaction
785 mixture was then cooled down to 0 °C, quenched with NaHCO₃ (10
786 mL), and extracted with DCM (20 mL × 3). Combined organic layers
787 were washed with brine (10 mL), dried over Na₂SO₄, and
788 concentrated. The crude oil was then purified by flash column
789 chromatography to yield desired 6-bromo-7-fluoroisouinoline (58 mg,
790 58%) (43 (R₁ = F, R₂ = H) in Scheme 2A).

791 To a flame-dried pressure vessel equipped with Teflon stirring bar
792 was added CuI (10 mg, 0.05 mmol, 20 mol %), L-proline (12 mg, 0.10
793 mmol, 40 mol %), and K₂CO₃ (104 mg, 0.75 mmol, 3 equiv) as solid,
794 and the vessel was flame-dried again under vacuum. Then DMSO (1
795 mL) solution of 6-bromo-7-fluoroisouinoline (58 mg, 0.25 mmol, 1
796 equiv) was added to the pressure vessel under nitrogen atmosphere
797 followed by the addition of NH₄OH (0.5 mL). The resulting
798 suspension in a sealed vessel was then heated to 70 °C overnight. The
799 reaction mixture was then cooled down to rt, suspended in water (5
800 mL) and EtOAc (10 mL), and further extracted with EtOAc (10 mL
801 × 3). Combined organic layers were washed with brine (10 mL),
802 dried over Na₂SO₄, and concentrated. The crude oil was then purified
803 by flash column chromatography to yield desired 7-fluoroisouinoline-
804 6-amine (44 (R₁ = F, R₂ = H) in Scheme 2A). This amine was then
805 immediately dissolved in DCM/DMF (1 mL/0.3 mL), and ethyl
806 isocyanato acetate (96 mg, 0.75 mmol, 3 equiv) was added. The
807 resulting mixture was stirred at room temperature overnight, and after
808 removal of volatiles, it was purified by flash column chromatography
809 and immediately hydrolyzed to acid with 1 N NaOH (1 mL) in
810 MeOH (1.5 mL) and water (0.5 mL) overnight. After purification by
811 reverse phase chromatography, the desired acid was obtained as a
812 white solid. To a stirring mixture of the acid (27 mg, 0.072 mmol) in
813 THF (1.0 mL) was added pyrrolidine (10 μL, 0.122 mmol, 1.70
814 equiv) followed by EDC-HCl (23.4 mg, 0.122 mmol, 1.70 equiv), and
815 the resulting mixture was stirred overnight at room temperature. Flash
816 column chromatography yielded 1-(7-fluoroisoquinolin-6-yl)-3-(2-
817 oxo-2-(pyrrolidin-1-yl)ethyl)urea (36) as a white solid (16.2 mg,
818 20% yield over four steps, starting from 6-bromo-7-fluoroisouinoline
819 43 (R₁ = F, R₂ = H)). ¹H NMR (400 MHz, methanol-*d*₄) δ 9.03 (s,
820 1H), 8.65 (d, *J* = 7.8 Hz, 1H), 8.31 (d, *J* = 5.8 Hz, 1H), 7.80 (d, *J* =
821 11.5 Hz, 1H), 7.67 (d, *J* = 5.9 Hz, 1H), 4.08 (br s, 2H), 3.53 (t, *J* =
822 6.8 Hz, 2H), 3.48 (t, *J* = 6.9 Hz, 2H), 2.07–2.00 (m, 2H), 1.95–1.88
823 (m, 2H). MS *m/z* (HRMS) [*M* + *H*]⁺ for C₁₆H₁₈FN₄O₂⁺: calculated
824 317.1408, found 317.1418.

1-(7-Methylisoquinolin-6-yl)-3-(2-oxo-2-(pyrrolidin-1-yl)ethyl)-
urea (37) (Scheme 2A; Table 5). The same procedures as above were
used for the synthesis of 1-(7-methylisoquinolin-6-yl)-3-(2-oxo-2-
(pyrrolidin-1-yl)ethyl)urea starting from 4-bromo-3-methylbenzalde-
hyde. 6-Bromo-7-methylisouinoline (43 (R₁ = Me, R₂ = H); 50%,
over the first four steps). Compound 37 was obtained in 20% (24 mg)
over the last four steps as described above. ¹H NMR (400 MHz,
methanol-*d*₄) δ 8.98 (s, 1H), 8.41 (s, 1H), 8.26 (d, *J* = 5.9 Hz, 1H),
7.86 (s, 1H), 7.63 (d, *J* = 5.9 Hz, 1H), 4.07 (s, 2H), 3.53 (t, *J* = 6.8
Hz, 2H), 3.48 (t, *J* = 6.9 Hz, 2H), 2.50 (s, 3H), 2.03 (p, *J* = 6.7 Hz,
2H), 1.91 (p, *J* = 6.6 Hz, 2H). MS *m/z* (HRMS) [*M* + *H*]⁺ for
C₁₇H₂₁N₄O₂⁺: calculated 313.1659, found 313.1662.

1-(1-Methylisoquinolin-6-yl)-3-(2-oxo-2-(pyrrolidin-1-yl)ethyl)-
urea (38) (Scheme 2A; Table 5). The same procedures as above were
used for the synthesis of 1-(7-methylisoquinolin-6-yl)-3-(2-oxo-2-
(pyrrolidin-1-yl)ethyl)urea (36) starting from 4'-bromoacetophe-
none. 6-Bromo-7-methylisouinoline (43 (R₁ = Me, R₂ = H)) was
obtained in 27%, over the first four steps. Compound 38 was then
obtained (2 mg, 2%) over the last four steps as described above. ¹H
NMR (400 MHz, methanol-*d*₄) δ 8.17–8.09 (m, 2H), 8.05 (d, *J* = 2.2
Hz, 1H), 7.59 (dd, *J* = 9.1, 2.2 Hz, 1H), 7.50 (d, *J* = 6.0 Hz, 1H), 4.05
(s, 2H), 3.52–3.45 (m, 4H), 2.87 (s, 3H), 2.03 (p, *J* = 6.8 Hz, 2H),
1.91 (p, *J* = 7.1 Hz, 2H). MS (ESI) *m/z* [*M* + *H*]⁺ for C₁₇H₂₁N₄O₂⁺:
calculated 313.2, found 313.2.

1-(3-Fluoroisoquinolin-6-yl)-3-(2-oxo-2-(pyrrolidin-1-yl)ethyl)-
urea (39) (Scheme 2B; Table 5). To the mixture of 6-
bromoisouinolin-3-amine (158 mg, 0.71 mmol, 1.0 equiv) and
HF-pyridine (10 mL) at 0 °C was added dropwise a solution of
NaNO₂ (243 mg, 3.54 mmol, 5 equiv) in water (5 mL). Upon
completion of the addition, the cold bath was removed and the
reaction was allowed to warm up to room temperature for 1.5 h at
which point saturated NaHCO₃ solution (45 mL) was added. The
reaction mixture was diluted with DCM (20 mL) and saturated
NH₄Cl (10 mL) solution, and phases were separated and aqueous
phase further extracted with DCM (20 mL × 3). Combined organic
layers were dried over Na₂SO₄ and concentrated under reduced
pressure. Crude material was purified by flash column chromatog-
raphy to yield 6-bromo-3-fluoroisouinoline as a white solid (128 mg,
80%). The same procedure that was used for the synthesis of 36 (last
four steps) was repeated to obtain the title compound 39 (6 mg, 5%).
¹H NMR (400 MHz, methanol-*d*₄) δ 8.79 (s, 1H), 8.10 (s, 1H), 7.99
(d, *J* = 8.9 Hz, 1H), 7.50 (dt, *J* = 8.9, 2.3 Hz, 1H), 7.23 (s, 1H), 4.05
(s, 2H), 3.53 (t, *J* = 6.8 Hz, 2H), 3.48 (t, *J* = 6.9 Hz, 2H), 2.02 (q, *J* =
6.8 Hz, 2H), 1.91 (p, *J* = 6.8 Hz, 2H). MS (ESI) *m/z* [*M* + *H*]⁺ for
C₁₆H₁₈FN₄O₂⁺: calculated 317.1, found 317.2.

1-(8-Chloroisoquinolin-6-yl)-3-(2-oxo-2-(pyrrolidin-1-yl)ethyl)-
urea (40) (Scheme 2C; Table 5). To a stirring mixture of 5-
aminoisouinoline (5.76 g, 40 mmol, 1 equiv) in pyridine (40 mL)
was added acetic anhydride (5.7 mL, 60 mmol, 1.5 equiv), and the
resulting reaction mixture was stirred at room temperature overnight.
The precipitate formed was filtered and washed with cold hexanes
(400 mL) in portions to give acetylated product (6.98 g, 94%). To a
stirring mixture of 5-acetyl aminoisouinoline (3.36 g, 18 mmol, 1
equiv) in DMF (30 mL) was added NCS (2.40 mL, 18 mmol, 1.0
equiv), and the resulting mixture was heated to 65 °C for 3 days. The
reaction mixture was then diluted with EtOAc (50 mL), and water
(50 mL) was added. After separation, the aqueous phase was
extracted with EtOAc (50 mL × 3), and combined organic layers were
then dried over Na₂SO₄ and concentrated under reduced pressure.
Crude material was purified by flash column chromatography to yield
desired compound (3.53 g, 88%).

To a solution of 5-acetyl-amino-8-chloroisoquinoline (1.0 g, 4.53
mmol, 1.0 equiv) in DMF (10 mL) was added dibromocyanuric acid
(1.3 g, 4.53 mmol, 1 equiv), and the reaction mixture was heated to
65 °C for 3 h. After concentration, the obtained crude product
resuspended in EtOH (45 mL), conc. HCl (9 mL) was added, and
reaction mixture was heated to reflux for 3 h. The reaction mixture
was then cooled down to rt and neutralized with 1 N NaOH to pH 7
and extracted with EtOAc (100 mL × 3). Combined organic layers
were then dried over Na₂SO₄ and concentrated under reduced

895 pressure. Crude material (300 mg, 26% over two steps) was used for
896 the next step without further purification. Crude material (300 mg,
897 1.2 mmol, 1.0 equiv) was dissolved in EtOH (45 mL) followed by the
898 addition of Ac₂O (7.5 mL) and a solution of NaNO₂ (in 15 mL
899 water) and NaHSO₃ (in 18 mL water). The resulting mixture was
900 stirred at rt for 10 min, AcOH (7.5 mL) was added, and the reaction
901 was allowed to stir at rt overnight. The reaction mixture was
902 neutralized with 1 N NaOH (~350 mL) to pH 8–9 and extracted
903 with EtOAc (250 mL × 3). Combined organic layers were then dried
904 over Na₂SO₄ and concentrated under reduced pressure. Crude
905 material was purified by flash column chromatography to yield the
906 desired compound (100 mg, 34%). The same procedures that were
907 used for the synthesis of **36** (last four steps) were repeated to obtain
908 the title compound **40** (51 mg, 30%). ¹H NMR (400 MHz, methanol-
909 *d*₄) δ 9.60 (br s, 1H), 8.40 (d, *J* = 6.7 Hz, 1H), 8.29 (d, *J* = 2.0 Hz,
910 1H), 8.21 (d, *J* = 6.7 Hz, 1H), 8.12 (d, *J* = 1.9 Hz, 1H), 4.08 (s, 2H),
911 3.54–3.46 (m, 4H), 2.07–2.00 (m, 2H), 1.95–1.89 (m, 2H). MS
912 (ESI) *m/z* [M + H]⁺ for C₁₆H₁₈ClN₄O₂⁺: calculated 333.1 and 335.1;
913 found 333.1 and 335.1.

914 *1-(Naphthalen-2-yl)-3-(2-oxo-2-(pyrrolidin-1-yl)ethyl)urea (51)*.
915 Compound **51** was prepared according to a previously published
916 procedure.²²

917 Synthesis and characterization data for compounds **49** and **50** are
918 detailed in the [Supporting Information](#).

919 **PRMT3 Biochemical Assay**. The radiometric scintillation
920 proximity assays to evaluate the potency of the compounds were
921 performed as described previously.²² The reactions were done under
922 balanced conditions using the biotinylated histone H4 peptide (Tufts
923 University Peptide Synthesis Core Facility, Boston, MA) with the
924 sequence of SGRGKGGKGLGKGGAKRHRKVLDRDK-biotin) as
925 substrate and [³H]S-adenosylmethionine (Waltham, MA, Cat#
926 NET155 V001MC, specific activity range 12–18 Ci/mmol) as the
927 methyl donor.

928 **Selectivity Assays**. The methyltransferase selectivity of **29**, **30**,
929 and **36** was assessed at compound concentrations of 1, 5, and 20 μM
930 as described previously.^{22,25–27}

931 **Cellular PRMT3 Assay**. Compound effects in cells were
932 determined as described previously (PMID: 27423858, 25728001).
933 Briefly, HEK293 cells were grown in DMEM supplemented with 10%
934 FBS, penicillin (100 units/mL), and streptomycin (100 μg/mL). The
935 cells were cotransfected with FLAG-tagged PRMT3/mutantPRMT3
936 and GFP-tagged histone H4 (constructs described in PMID
937 25728001) using 293fectin Transfection Reagent (Invitrogen),
938 following manufacturer instructions. Cells were lysed in lysis buffer
939 (in mM: 20 Tris-HCl pH = 8, 150 NaCl, 1 EDTA, 10 MgCl₂, 0.5%
940 Triton-X100, 12.5 U/mL benzonase) (Sigma), complete EDTA-free
941 protease inhibitor cocktail (Roche). After 3 min incubation at rt,
942 SDS was added to a final 1% concentration. Lysates were separated on
943 SDS PAGE, blotted, and probed with indicated antibodies: mouse
944 anti-GFP (1:5000, Clontech #632381), mouse anti-H4 (1:1000,
945 Abcam #174628), rabbit anti-H4R3me2a (1:1000 Active Motif
946 #39705), and mouse anti-FLAG (1:5000, Sigma #F1804). The signal
947 was read on an Odyssey scanner (LiCor) at 800 and 700 nm.
948 Fluorescence intensity of H4R3me2a was quantified and normalized
949 to GFP and H4 signals for exogenous and endogenous histones,
950 respectively.

951 **PRMT3 In-Cell Hunter Assay**. This cellular assay was performed
952 as described previously.²²

953 ■ ASSOCIATED CONTENT

954 ● Supporting Information

955 The Supporting Information is available free of charge on the
956 [ACS Publications website](#) at DOI: [10.1021/acs.jmedchem.7b01674](https://doi.org/10.1021/acs.jmedchem.7b01674).

958 Synthesis and characterization data for compounds **49**
959 and **50**, ¹H NMR spectra of compounds **29**, **30**, **36**, and **37**,
960 and selectivity data for compounds **29** and **30** (PDF)
961 Molecular formula strings (CSV)

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Notes

The authors declare the following competing financial
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■ ABBREVIATIONS

PRMT3, protein arginine methyltransferase 3; rpS2, ribosomal
protein S2; PABPN1, recombinant mammalian nuclear
poly(A)-binding protein; LXRA, liver X receptor α; DAL-1,
differentially expressed in adenocarcinoma of the lung, also
known as 4.1B; SAR, structure–activity relationship; LHS, left-
hand side; RHS, right-hand side; GPCRs, G-protein coupled
receptors

■ REFERENCES

- (1) Bedford, M. T.; Clarke, S. G. Protein Arginine Methylation in Mammals: Who, What, and Why. *Mol. Cell* **2009**, *33*, 1–13.
- (2) Swiercz, R.; Person, M. D.; Bedford, M. T. Ribosomal Protein S2 is A Substrate for Mammalian PRMT3 (Protein Arginine Methyltransferase 3). *Biochem. J.* **2005**, *386*, 85–91.

- (3) Swiercz, R.; Cheng, D.; Kim, D.; Bedford, M. T. Ribosomal Protein rpS2 Is Hypomethylated in PRMT3-Deficient Mice. *J. Biol. Chem.* **2007**, *282*, 16917–16923.
- (4) Bachand, F.; Silver, P. A. PRMT3 is A Ribosomal Protein Methyltransferase that Affects the Cellular Levels of Ribosomal Subunits. *EMBO J.* **2004**, *23*, 2641–2650.
- (5) Landry-Voyer, A. M.; Bilodeau, S.; Bergeron, D.; Dionne, K. L.; Port, S. A.; Rouleau, C.; Boisvert, F. M.; Kehlenbach, R. H.; Bachand, F. Human PDCD2L Is an Export Substrate of CRM1 That Associates with 40S Ribosomal Subunit Precursors. *Mol. Cell. Biol.* **2016**, *36*, 3019–3032.
- (6) Tang, J.; Gary, J. D.; Clarke, S.; Herschman, H. R. Prmt 3, A Type I Protein Arginine N-Methyltransferase that Differs From PRMT1 in its Oligomerization, Subcellular Localization, Substrate Specificity, and Regulation. *J. Biol. Chem.* **1998**, *273*, 16935–16945.
- (7) Kim, D. I.; Park, M. J.; Lim, S. K.; Park, J. I.; Yoon, K. C.; Han, H. J.; Gustafsson, J. A.; Lim, J. H.; Park, S. H. PRMT3 Regulates Hepatic Lipogenesis Through Direct Interaction with LXRalpha. *Diabetes* **2015**, *64*, 60–71.
- (8) Fronz, K.; Otto, S.; Kolbel, K.; Kuhn, U.; Friedrich, H.; Schierhorn, A.; Beck-Sickinger, A. G.; Ostareck-Lederer, A.; Wahle, E. Promiscuous Modification of the Nuclear Poly(A)-Binding Protein by Multiple Protein-Arginine Methyltransferases Does Not Affect The Aggregation Behavior. *J. Biol. Chem.* **2008**, *283*, 20408–20420.
- (9) Tavanez, J. P.; Bengoechea, R.; Berciano, M. T.; Lafarga, M.; Carmo-Fonseca, M.; Enguita, F. J. Hsp70 Chaperones and Type I PRMTs are Sequestered at Intracellular Inclusions Caused by Polyalanine Expansions in PABPN1. *PLoS One* **2009**, *4*, e6418.
- (10) Lai, Y.; Song, M.; Hakala, K.; Weintraub, S. T.; Shiiio, Y. Proteomic Dissection of the von Hippel-Lindau (VHL) Interactome. *J. Proteome Res.* **2011**, *10*, 5175–5182.
- (11) Singh, V.; Miranda, T. B.; Jiang, W.; Frankel, A.; Roemer, M. E.; Robb, V. A.; Gutmann, D. H.; Herschman, H. R.; Clarke, S.; Newsham, I. F. DAL-1/4.1B Tumor Suppressor Interacts with Protein Arginine N-Methyltransferase 3 (PRMT3) and Inhibits its Ability to Methylate Substrates In Vitro and In Vivo. *Oncogene* **2004**, *23*, 7761–7771.
- (12) Jiang, W.; Newsham, I. F. The Tumor Suppressor DAL-1/4.1B and Protein Methylation Cooperate in Inducing Apoptosis in MCF-7 Breast Cancer Cells. *Mol. Cancer* **2006**, *5*, 4.
- (13) Allali-Hassani, A.; Wasney, G. A.; Siarheyeva, A.; Hajian, T.; Arrowsmith, C. H.; Vedadi, M. Fluorescence-Based Methods For Screening Writers And Readers Of Histone Methyl Marks. *J. Biomol. Screening* **2012**, *17*, 71–84.
- (14) Herrmann, F.; Pably, P.; Eckerich, C.; Bedford, M. T.; Fackelmayer, F. O. Human Protein Arginine Methyltransferases in Vivo-Distinct Properties of Eight Canonical Members of the PRMT Family. *J. Cell Sci.* **2009**, *122*, 667–677.
- (15) Wagner, S.; Weber, S.; Kleinschmidt, M. A.; Nagata, K.; Bauer, U. M. SET-Mediated Promoter Hypoacetylation is A Prerequisite for Coactivation of the Estrogen-Responsive pS2 Gene by PRMT1. *J. Biol. Chem.* **2006**, *281*, 27242–27250.
- (16) Obianyo, O.; Causey, C. P.; Jones, J. E.; Thompson, P. R. Activity-Based Protein Profiling of Protein Arginine Methyltransferase 1. *ACS Chem. Biol.* **2011**, *6*, 1127–1135.
- (17) Chen, X.; Niroomand, F.; Liu, Z.; Zankl, A.; Katus, H. A.; Jahn, L.; Tiefenbacher, C. P. Expression of Nitric Oxide Related Enzymes in Coronary Heart Disease. *Basic Res. Cardiol.* **2006**, *101*, 346–353.
- (18) Miyata, S.; Mori, Y.; Tohyama, M. PRMT3 is Essential for Dendritic Spine Maturation in Rat Hippocampal Neurons. *Brain Res.* **2010**, *1352*, 11–20.
- (19) Park, M. J.; Kim, D. I.; Choi, J. H.; Heo, Y. R.; Park, S. H. New Role of Irisin in Hepatocytes: The Protective Effect of Hepatic Steatosis In Vitro. *Cell. Signalling* **2015**, *27*, 1831–1839.
- (20) Siarheyeva, A.; Senisterra, G.; Allali-Hassani, A.; Dong, A.; Dobrovetsky, E.; Wasney, G. A.; Chau, I.; Marcellus, R.; Hajian, T.; Liu, F.; Korboukh, I.; Smil, D.; Bolshan, Y.; Min, J.; Wu, H.; Zeng, H.; Loppnau, P.; Poda, G.; Griffin, C.; Aman, A.; Brown, P. J.; Jin, J.; Al-awar, R.; Arrowsmith, C. H.; Schapira, M.; Vedadi, M. An Allosteric Inhibitor of Protein Arginine Methyltransferase 3. *Structure* **2012**, *20*, 1425–1435.
- (21) Liu, F.; Li, F.; Ma, A.; Dobrovetsky, E.; Dong, A.; Gao, C.; Korboukh, I.; Liu, J.; Smil, D.; Brown, P. J.; Frye, S. V.; Arrowsmith, C. H.; Schapira, M.; Vedadi, M.; Jin, J. Exploiting An Allosteric Binding Site of PRMT3 Yields Potent and Selective Inhibitors. *J. Med. Chem.* **2013**, *56*, 2110–2124.
- (22) Kaniskan, H. Ü.; Szewczyk, M. M.; Yu, Z.; Eram, M. S.; Yang, X.; Schmidt, K.; Luo, X.; Dai, M.; He, F.; Zang, I.; Lin, Y.; Kennedy, S.; Li, F.; Dobrovetsky, E.; Dong, A.; Smil, D.; Min, S. J.; Landon, M.; Lin-Jones, J.; Huang, X. P.; Roth, B. L.; Schapira, M.; Atadja, P.; Baryshte-Lovejoy, D.; Arrowsmith, C. H.; Brown, P. J.; Zhao, K.; Jin, J.; Vedadi, M. A Potent, Selective and Cell-Active Allosteric Inhibitor of Protein Arginine Methyltransferase 3 (PRMT3). *Angew. Chem., Int. Ed.* **2015**, *54*, 5166–5170.
- (23) Balz, G.; Schiemann, G. On Aromatic Fluoric Compounds, I.: A New Method for its Representation. *Ber. Dtsch. Chem. Ges. B* **1927**, *60*, 1186–1190.
- (24) Zhu, G. D.; Gong, J.; Claiborne, A.; Woods, K. W.; Gandhi, V. B.; Thomas, S.; Luo, Y.; Liu, X.; Shi, Y.; Guan, R.; Magnone, S. R.; Klinghofer, V.; Johnson, E. F.; Bouska, J.; Shoemaker, A.; Oleksijew, A.; Stoll, V. S.; De Jong, R.; Oltersdorf, T.; Li, Q.; Rosenberg, S. H.; Giranda, V. L. Isoquinoline-Pyridine-Based Protein Kinase B/Akt Antagonists: SAR and In Vivo Antitumor Activity. *Bioorg. Med. Chem. Lett.* **2006**, *16*, 3150–3155.
- (25) Baryshte-Lovejoy, D.; Li, F.; Oudhoff, M. J.; Tatlock, J. H.; Dong, A.; Zeng, H.; Wu, H.; Freeman, S. A.; Schapira, M.; Senisterra, G. A.; Kuznetsova, E.; Marcellus, R.; Allali-Hassani, A.; Kennedy, S.; Lambert, J. P.; Couzens, A. L.; Aman, A.; Gingras, A. C.; Al-Awar, R.; Fish, P. V.; Gerstenberger, B. S.; Roberts, L.; Benn, C. L.; Grimley, R. L.; Braam, M. J.; Rossi, F. M.; Sudol, M.; Brown, P. J.; Bunnage, M. E.; Owen, D. R.; Zaph, C.; Vedadi, M.; Arrowsmith, C. H. (R)-PFI-2 is a Potent and Selective Inhibitor of SETD7Methyltransferase Activity in Cells. *Proc. Natl. Acad. Sci. U. S. A.* **2014**, *111*, 12853–12858.
- (26) Eram, M. S.; Kuznetsova, E.; Li, F.; Lima-Fernandes, E.; Kennedy, S.; Chau, I.; Arrowsmith, C. H.; Schapira, M.; Vedadi, M. Kinetic Characterization of Human Histone H3 Lysine 36 Methyltransferases, ASH1L and SETD2. *Biochim. Biophys. Acta, Gen. Subj.* **2015**, *1850*, 1842–1848.
- (27) Eram, M. S.; Bustos, S. P.; Lima-Fernandes, E.; Siarheyeva, A.; Senisterra, G.; Hajian, T.; Chau, I.; Duan, S.; Wu, H.; Dombrowski, L.; Schapira, M.; Arrowsmith, C. H.; Vedadi, M. Trimethylation of Histone H3 Lysine 36 by Human Methyltransferase PRDM9 Protein. *J. Biol. Chem.* **2014**, *289*, 12177–12188.