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A Broad Anti-influenza Hybrid Small Molecule That Potently Disrupts the Interaction of Polymerase Acidic Protein–Basic Protein 1 (PA-PB1) Subunits

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ABSTRACT

In continuing our efforts to identify small molecules able to disrupt PA-PB1 subunits interaction of influenza virus (Flu) RNA-dependent RNA polymerase, this paper was devoted to the optimization of a dihydrotriazolopyrimidine derivative, previously identified through a structure-based drug discovery. The structure modifications performed around the bicyclic core led to the identification of compounds endowed with both the ability to disrupt PA-PB1 subunits interaction and anti-Flu activity with no cytotoxicity. Very interesting results were obtained with the hybrid molecules 36 and 37, designed by merging some peculiar structural features known to impart PA-PB1 interaction inhibition, with compound 36 that emerged as the most potent PA-PB1 interaction inhibitor (IC$_{50}$ of 1.1 µM) among all the small molecules reported so far. Calculations showed a very favored H-bonding between the 2-amidic carbonyl of 36 and Q408, which seems to justify its potent ability to interfere with the polymerase subunits interaction.

INTRODUCTION

Influenza is a highly contagious, acute, febrile, respiratory illness. Only two classes of drugs are currently available to treat influenza infections, i.e., M2 ion channel inhibitors and neuraminidase inhibitors. Unfortunately, their clinical use is limited by serious side effects, low efficacy, and the emergence of resistant virus variants.\textsuperscript{1–3} Because of these issues, the M2 ion channel inhibitors are no longer even recommended;\textsuperscript{4} thus, the neuraminidase inhibitors, such as oseltamivir, represent the firstline therapy, although their widespread use has been reported to favor the emergence of resistant viral strains.\textsuperscript{5} Clearly, new anti-influenza virus (Flu) strategies based on alternative mechanisms of action are strongly needed. Along this line, we have chosen the viral RNA-dependent RNA polymerase (RdRP) as a valid antiviral target since it is essential for virus replication and plays an important role in the viral pathogenesis by contributing to the host-adaptation process. In addition, it is highly conserved among FluA, -B, and -C, and its mechanism of action significantly differs from that of the human RNA polymerases.\textsuperscript{6} Flu RdRP is a complex of
three subunits, polymerase acidic protein (PA), polymerase basic protein 1 (PB1), and polymerase basic protein 2 (PB2), whose correct assembly into functional RdRP is an essential step for Flu RNA synthesis and replication. The inhibition of protein–protein interactions (PPIs) between the subunits of the viral RNA polymerase represents an attractive as well as challenging strategy that could expand the narrow target spectrum of anti-Flu drugs.\textsuperscript{7–9} Previous studies have revealed that the N-terminal and the C-terminal regions of PB1 interact with the C-terminus of PA\textsuperscript{10–14} and the N-terminus of PB2,\textsuperscript{11,15} respectively. While no small molecule targeting the PB1–PB2 interaction is known, with only a few short peptides reported for this activity,\textsuperscript{16,17} various small molecules that are able to disrupt the interactions between the PA and PB1 subunits have emerged during the past 3 years.\textsuperscript{18–25} Their PPI inhibitory activity correlated to the inhibition of viral RdRP activity and of virus replication in a cellular context, thus validating this antiviral strategy. Different approaches led to identification of the PA–PB1 small molecule inhibitors reported so far (Figure 1). Nitrobenzofurazan derivatives have emerged from a biochemical ELISA-based screening,\textsuperscript{21} which was followed by an optimization study that gave compound 123 as one of the most active. drug discovery (SBDD) strategy. In particular, compounds 3 (benzbromarone)\textsuperscript{19} and 4 (diclazuril)\textsuperscript{19} came from an in silico screening performed on a database of 4000 drugs, while by screening 3 million small molecules we have discovered the promising hit compounds 5–8.\textsuperscript{18} A successive round of optimization performed on compounds 6 and 7 led to the improved derivatives 9\textsuperscript{22} and 10\textsuperscript{22} (Figure 1), whose anti-Flu activity also encompassed a panel of clinical isolates of FluA, including an oseltamivir-resistant strain, and of FluB, without showing appreciable cytotoxicity. In this study, with the aim of broadening the class of PA–PB1 interaction inhibitors as alternative anti-Flu agents, the optimization of the dihydrotriazolopyrimidine derivative 8 is reported. On the other hand, anthracene derivative 220 was discovered by serendipity. However, the largest number of PA–PB1 interaction inhibitors was identified through a structure-based.

**DESIGN OF TRIAZOLOPYRIMIDINE DERIVATIVES**
Among the hit compounds previously identified, the dihydrotriazolopyrimidine derivative 8 showed a weak PA-PB1 interaction inhibitory activity (IC$_{50}$ = 170.6 µM) and no antiviral activity up to 100 µM, but the lack of any cytotoxic effect (CC$_{50}$ > 250 µM in MDCK cells)$^9$ made it worthy of further investigation. The structural modifications were initially focused on the benzamide moiety at the C-2 position (Table 1). The methoxy group was run into ortho and meta positions (compounds 11 and 12) and an analogous set of derivatives was synthesized having a fluorine atom (compounds 13-15). Since in these two series of compounds the para derivatives were slightly more active than the other isomers, the successive substituents were placed only at the para position, synthesizing compounds 16-24. Additional derivatives were 25, characterized by a bicyclic aromatic ring, 26, devoid of any substituent on the phenyl ring, and 27, where an ethyl chain was inserted between the phenyl ring and the amide moiety. Since some difficulties were encountered with the purification of this first series of derivatives, the 4,7-dihydro-[1,2,4]triazolo[1,5-a]pyrimidine nucleus was oxidized leading to more manageable aromatic compounds. Derivatives 28-30 were synthesized using the phenyl, the p-methoxyphenyl, and p-propoxyphenyl rings, respectively, as C-2 substituents.

Previous computational studies indicated that a more linear shape of the compounds could increase the inhibitory effect.$^{15}$ Moreover, the alignment of the 1,2,4-triazolo[1,5-a]pyrimidine derivative 28 to the recently published pharmacophore for PA-PB1 inhibitors$^{15}$ (Figure 2, A and B), indicated that the 7-phenyl ring was not fitting any hydrophobic pharmacophoric point (green spheres in Figure 2) but, on the contrary, it was pointing towards polar atomic coordinates (red and blue spheres in Figure 2). In the light of the above considerations, we decided to further modify the central core by interchanging the methyl and the phenyl ring, synthesizing compounds 31-33. Figure 2C reports the alignment of 31 to the pharmacophore.

Since the H-bond acceptor and H-bond donor pharmacophoric points underneath the amide group proved to be essential for pharmacophore definition,$^{15}$ the presence of an inverse amide group linking the triazolopyrimidine core and the phenyl ring was studied by synthesizing the couple of positional isomers 34 and 35.
Finally, as additional analogues of 8, hybrid molecules were designed by combining some of the structural features shown to confer PA-PB1 inhibitory activity. Among the planned molecules, the positional isomers 36 and 37 (Table 1) were synthesized by merging the 1,2,4-triazolopyrimidine nucleus with the cycloheptathiophene-3-carboxamide core that characterizes the previous hit 7 (Figure 1). The two hybrid molecules were aligned to the pharmacophore, obtaining a good similarity both for polar and hydrophobic regions (Figure 3), with the 1,2,4-triazolopyrimidine nucleus being oriented in the lower hydrophobic region of the pharmacophore, in an opposite way to compounds 28 and 31 (Figure 2), to gain the better alignment of the polar regions.

**CHEMISTRY**

The synthesis of all the target compounds was accomplished through a carbodiimide-mediated coupling reaction by reacting the 2-amino and 2-carboxylic acid 1,2,4-triazolo[1,5-a]pyrimidine synthones with the appropriate benzoyl chlorides and amines, respectively. Although the triazolopyrimidines chemistry has been widely explored, very few reports were focused on the synthesis of 2-amino and 2-carboxylic acid 1,2,4-triazolo[1,5-a]-pyrimidine derivatives. Thus, the synthesis of the synthones 38, 41, 42, 45, and 47 required an in-depth study aimed to determine the best synthetic pathway and conditions to obtain the desired positional isomers in high yield. In Schemes 1 and 2, selected procedures among those reported in the literature or appositely setup are shown, while a thorough comparative study will be reported in due course. Synthone 38 was prepared as reported in the literature, by reacting 3,5-diamino-1,2,4-triazole with benzylideneacetone in DMF at reflux (Scheme 1). The same reaction was applied to prepare synthone 41 (Scheme 1), but adding Ac₂O to the reaction mixture after the condensation completion, in order to protect the amino group in the successive oxidation step. The oxidation of compound 39 performed with N-bromosuccinimide (NBS) gave intermediate 40, which after acid hydrolysis gave the desired synthone 41. An analogous three-step procedure was planned to synthesize the unknown synthone 42 by reacting 3,5-diamino-1,2,4-triazole with phenyl 1-propenyl
ketone in DMF at reflux (Scheme 1). Fortunately, the reaction furnished directly the aromatic compound 42. The reaction of synthones 38, 41, and 42 with the appropriate benzyol chloride, performed in pyridine, furnished the target compounds 8 and 11–33. All the 4,7-dihydrotriazolopyrimidine derivatives were purified by crystallization from EtOH, since the compounds underwent an extensive transformation to a main unidentified product when column chromatography was used as purification method.

Similarly to the preparation of synthones 41 and 42, the synthesis of triazolopyrimidine-2-carboxylic acids 45 and 47 was accomplished by reacting ethyl 5-amino-1,2,4-triazole-3-carboxylate 29 with benzylideneacetone and phenyl 1-propenyl ketone, respectively, in DMF at reflux (Scheme 2). Using 3-amino-1,2,4-triazole-5-carboxylic acid as starting material, the reaction furnished only decarboxylated triazolopyrimidine scaffolds. In agreement with what has been described above, the reaction with benzylideneacetone gave the saturated compound 43, which was then oxidized with NBS in EtOH at reflux in the presence of AcONa, to give 44. On the other hand, the reaction with phenyl 1-propenyl ketone provided directly the aromatic intermediate 46. Ethyl triazolopyrimidine esters 44 and 46 were then hydrolyzed under basic conditions, furnishing the key acids 45 and 47. The carbodiimide-mediated coupling reaction was then carried out by reacting the 1,2,4-triazolopyrimidine-2-carbonyl chloride, prepared from the acids 45 and 47 by reaction with oxalyl chloride in CH₂Cl₂, with 2-amino-5,6,7,8-tetrahydro-4H-cyclohepta[b]thiophene-3-carboxamide or aniline, in CH₂Cl₂ in the presence of DIPEA, to give the target compounds 34–37.

RESULTS AND DISCUSSION

Hit compound 8 (compound 31 in ref 18), previously tested as provided from the vendor, was synthesized and retested, giving comparable results in terms of PA–PB1 interaction inhibitory activity (IC₅₀ = 153 μM) and maintaining the same profile of antiviral activity and cytotoxicity. The in-house synthesized 8 was then used as comparative compound in all successive studies.
The whole set of derivatives was evaluated for the ability to inhibit the physical interaction between PA and PB1 subunits by ELISA, including the PB1(1−15)−Tat peptide as a positive control. In parallel, for all the synthesized compounds, the antiviral activity was tested by plaque reduction assay (PRA) in Mardin–Darby canine kidney (MDCK) cells infected with a reference FluA virus, the A/PR/8/34 strain. Ribavirin (RBV), a known broad-spectrum inhibitor of RNA viruses polymerase, was included as a positive control of inhibition, exhibiting EC$_{50}$ = 10 μM. To exclude that the observed antiviral activities could be due to toxic effects in the target cells, all the synthesized compounds were tested by MTT assays in two cell lines, i.e., MDCK and human embryonic kidney (HEK) 293T. The antiviral activity and toxicity data for the tested compounds are reported in Table 1.

As to what impacts the modifications made on the phenyl ring at the C-2 position of the dihydrotriazolopyrimidine core, the shifting of the methoxy group from para (compound 8) to meta (compound 12) and ortho (compound 11) positions decreased the PA–PB1 interaction inhibitory activity. The same behavior was observed for the fluoro analogues 13–15. Among the various para-substituted derivatives, compounds 16–18 were more active than hit 8, but only for p-propoxy derivative 16 did the ability to inhibit the PA–PB1 interaction perfectly translate to anti-Flu activity in a cellular context, with EC$_{50}$ = 47 μM. On the other hand, compounds 19, 21, and 25 inhibited the viral growth but did not interfere with the PA–PB1 complex formation. For these compounds, all characterized by a bulky substituent at the C-2 position, an alternative mechanism of action might be postulated, or simply the antiviral activity could be due to a certain toxicity.

The aromatic triazolopyrimidine compounds 28–30 were all devoid of activity against the PA–PB1 interaction, thus making them less suitable than their 4,7-dihydrotriazolopyrimidine counterparts (compounds 26, 8, and 16). The Fingerprints for Ligands and Proteins (FLAP) binding poses evaluated in silico for compound 26 and its aromatic analogue 28 were very similar, with the heterocyclic and heteroaromatic cores interacting with W706 (Figure 4). However, compound 28,
due to its more linear shape, appears to match the hydrophobic field generated by W706 less efficiently than 26, and this difference might be responsible for the lower activity of the aromatic analogues.

When in the aromatic scaffold the methyl and phenyl groups were interchanged (compounds 31–33), the PA–PB1 inhibitory activity was restored, with compound 31 exhibiting a good IC$_{50}$ value of 26 μM, perfectly comparable to that obtained in inhibiting the vral replication (EC$_{50}$ = 25 μM). The ability of compound 31 to interfere with PA–PB1 complex markedly decreased when the C-2 amide linker was inverted, as in compound 35, which however maintained the antiviral activity.

Definitely, the most exciting result in this study was achieved with the hybrid molecules 36 and 37, designed by merging some peculiar structural features of the PA–PB1 interaction inhibitors developed by us. With an IC$_{50}$ = 1.1 μM, compound 36 emerged as the most potent PA–PB1 inhibitor within this series of compounds as well as among all the small molecules published so far. The other hybrid molecule 37, although endowed with a lower ability to interfere with PA–PB1 complex formation (IC$_{50}$ = 28 μM), emerged as the best in inhibiting the viral growth (EC$_{50}$ = 8.0 μM). Structurally, the two molecules differ only in opposite positions of the substituents on the triazolopyrimidine core, with the 5-methyl group and 7-phenyl ring being the most suitable substitution pattern for PA–PB1 inhibition. To evaluate possible differences in the binding mode of compounds 36 and 37, their FLAP binding poses were analyzed (Figure 5). Both compounds orient the triazolopyrimidine ring toward the W706 residue of PA that defines the first hydrophobic pocket, to give an efficient π–π stacking. In addition, compound 37, due to its elongated shape, seems to be able to locate the phenyl ring into the second hydrophobic pocket of PA, defined by P710 and L666, and the cycloheptathiophene ring into the third hydrophobic pocket defined by L640, V636, and W619, according to the cavity description by Liu and co-workers33 (Figure 5A). This binding mode is comparable to that previously observed for compound 9$^{34}$ (data not shown). On the other hand, compound 36 seems to be shifted toward the opposite side of the cavity, thus
matching only the first hydrophobic region (Figure 5B). Changing the perspective (Figure 5C,D), we can notice that, based on this model, the shift for compound 36 is due to a favored H-bonding between its 2-amidic carbonyl group and Q408, according to the FLAP GRID fields analysis. In our previous studies, the interactions with W706 and with the second hydrophobic pocket in proximity of P710 were usually detected for the most active compounds; the achievement of more active derivatives designed to optimize these hydrophobic interactions validated the hypothesis about this favorable binding mode. On the contrary, compound 36 emerges as the first compound within our series of derivatives for which an interaction with Q408 seems to occur. Although these findings need to be further investigated, it is known that Q408 is a key residue for PB1 binding through H-bonding, and this might be the reason for the surprisingly potent activity. The interaction with Q408 has been recently hypothesized also for other PA–PB1 inhibitors, although their inhibitory effect was lower than that of compound 36. From the comparison of the spatial dispositions of the two amidic carbonyl groups in compounds 36 and 37 in Figures 5 with the ones in Figure 3, minor differences emerge. These differences are induced by the interaction with the protein structure, and this is a demonstration that combining a pharmacophore approach with a structure-based approach, when possible, represents a suitable strategy for pharmacophore refinement.

Compounds 16, 31, 36, and 37, endowed with the best ability to inhibit both PA–PB1 interaction and viral growth, were further characterized. First, we investigated their ability to interfere with the catalytic activity of FluA RdRP in a cellular context by minireplicon assays performed in transfected HEK 293T cells. As shown in Table 2, for all the compounds the ability to disrupt the PA–PB1 interaction in vitro correlated well with the polymerase inhibitory activity, with the best compounds 36 and 37 showing EC₅₀ values of 12 and 16 μM, respectively, comparable to that of the reference compound RBV (EC₅₀ = 18 μM). We then tested the ability of the best compound 36 to interfere with the physical interaction between PA and PB1 in a cellular context. To this end, we investigated whether the compound could affect PA–PB1 binding in the cell cytoplasm and consequently block the intranuclear translocation of PA, which requires formation of
a PA−PB1 complex, while PB2 enters the cell nucleus independently. Thus, we transfected HEK 293T cells with plasmids expressing PB1, PB2, and a PA−GFP fusion protein and analyzed the intracellular localization of PA−GFP in the presence or absence of compound 36 (or DMSO as a control). As previously shown, individually expressed PA−GFP was largely cytoplasmic, while coexpression of PA−GFP with PB1 and PB2 resulted in marked nuclear accumulation of PA (Figure 6). Treatment of PA−PB1−PB2-coexpressing cells with compound 36 reduced PA nuclear localization, while DMSO had no effect (Figure 6).

Finally, the antiviral effects of compounds 16, 31, 36, and 37 against a number of strains of FluA of both H1N1 and H3N2 subtypes, including an oseltamivir-resistant clinical isolate (A/Parma/24/09), and three strains of FluB were also evaluated (Table 3). All the compounds showed an interesting antiviral activity against the whole panel of Flu strains, perfectly comparable to that measured against the A/PR/8/34 strain. Compound 37 confirmed its anti-Flu potency by exhibiting the best antiviral activity, with EC$_{50}$ = 5 μM against both the FluA oseltamivir-resistant clinical isolate and Flu B/Lee/40 strain. At this stage, the absorption, distribution, metabolism, and excretion (ADME) profile was preliminarily determined to assess the drug-like properties of these new small molecules. Toward this end, for the same set of compounds, 16, 31, 36, and 37, along with the hit 8, the solubility (equilibrium solubility in phosphate buffer at pH 7.4), permeability (parallel artificial membrane permeation assay (PAMPA)), and human liver microsome (HLM) metabolic stability were experimentally determined. Concerning the solubility, compound 8 showed the highest equilibrium solubility (13 μg/mL), followed by compounds 16 and 31 (5 μg/mL) and then by compounds 36 and 37, which showed very low solubility (<1 μg/mL). Because of this issue, we could not clearly estimate the cell permeability of compound 37. Based on the PAMPA, all the tested compounds showed a medium/high permeability (data are reported in the Experimental Section) and a percentage of compound trapped into the membrane ranging from 41 to 57%, with the exception of 31, the sole compound not retained by the lipid membrane. Notably, all the studied PA−PB1 inhibitors were metabolically stable in HLM, since no metabolites were detected after 30
min exposure to cytochrome metabolism. Altogether, these studies suggested that the triazolopyrimidine-based compounds are endowed with an adequate ADME profile for a drug-discovery phase, even though the most promising antiviral derivatives 36 and 37 suffered from low solubility. Since these hybrid molecules are made of a triazolopyrimidine core merged to a cycloheptathiophene scaffold, we hypothesize that the latter may be responsible for the low solubility. Indeed, ADME studies performed on the previous cycloheptathiophene derivatives 7 and 10 showed the same poor equilibrium solubility (<1 μg/mL) and a medium/high permeability, although they interacted almost entirely with the lipid membrane, hampering the enrichment of the acceptor phase. Thus, although compound 36 is characterized by a promising ADME profile, further modifications of the cycloheptathiophene moiety will be required to achieve the best compromise between solubility and cell permeability.

CONCLUSIONS

The limited therapeutic options against Flu infection along with the drug resistance issue make imperative the search for next generation agents. Although the inhibition of viral polymerases is a common approach in the identification of antiviral drugs, the development of compounds able to interfere with the correct assembly of viral polymerase complexes is an innovative strategy.35-38

In this context, we have been recently interested in the inhibition of the interaction of Flu polymerase PA–PB1 subunits by small molecules. In the present work, starting from the dihydrotriazolopyrimidine hit 8, a weak PA–PB1 interaction inhibitor with no significant anti-Flu activity, and through a hit-to-lead optimization, novel potent inhibitors endowed with a broad anti-Flu activity have been discovered. The best results were achieved with the hybrid molecules 36 and 37, obtained by combining the herein developed triazolopyrimidine and the previously explored cycloheptathiophene scaffolds. With an IC$_{50}$ = 1.1 μM, compound 36 exhibits a 150-fold higher
activity than hit compound 8, definitely emerging as the most potent in the scenario of the PA–PB1 small molecule inhibitors developed so far. This ability translates in a broad anti-Flu activity with no cytotoxicity. From this study, the triazolopyrimidine core emerges as very suitable to inhibit the physical interaction between PA and PB1 subunits, probably thanks to an efficient π–π staking interaction with W706 of the first hydrophobic pocket, as suggested by the FLAP poses. The computational studies also showed that the different binding mode of the various triazolopyrimidine derivatives is markedly influenced by the substituents at the C-5 and C-7 positions but mainly by the group placed at the C-2 position. While the 2-cycloheptanethiophene moiety is definitely able to ensure potent activity, a wider exploration of the C-2 position is strongly required, also to meet the need for compounds with an improved ADME profile. The design of new drug-like analogues, also based on hydrophilic interactions while decreasing unnecessary hydrophobic moieties, is also supported by the peculiar ability of the potent compound 36 to establish a very favored H-bonding with Q408.

During the final drafting of this manuscript, novel crystal structures of the influenza virus polymerase were published, thus opening new opportunities to refine the SBDD.

**EXPERIMENTAL SECTION**

**Computational methods.** The binding poses in the PA cavity were generated using the FLAP software (Molecular Discovery Ltd., UK; [www.moldiscovery.com](http://www.moldiscovery.com)). Indeed, the FLAP approach was previously used to identify inhibitors of the PA-PB1 complex by virtual screening and proved also to be useful to design more active compounds. The procedure has been extensively described elsewhere. As in the previous studies, the main cavity of the crystallographic structure of a large C-terminal fragment of PA (aa 257-716) (pdb code: 3CM8) was used as a template. A total of 50 conformers for each ligand were generated to mimic the compound flexibility, and the most abundant protonation state predicted of each molecule was used, as predicted by MoKa. The
probes used to generate the GRID Molecular Interaction Fields were H (shape), DRY (hydrophobic interactions), N1 (H-bond donor) and O (H-bond acceptor) interactions. The FLAP software was also used to align the selected compounds into the pharmacophore model. The pharmacophore generation using FLAPpharm algorithm was recently described. Here, the pharmacophore was used as a template to run the FLAP virtual screening module.

Chemistry. All reactions were routinely checked by TLC on silica gel 60F254 (Merck) and visualized by using UV or iodine. Flash column chromatography separations were carried out on Merck silica gel 60 (mesh 230-400). Melting points were determined in capillary tubes (Büchi Electrothermal Mod. 9100) and are uncorrected. HRMS spectra were registered on Agilent Technologies 6540 UHD Accurate Mass Q-TOF LC/MS, HPLC 1290 Infinity. Purities of the compounds were determined by elemental analyses and the data for C, H, and N are within ± 0.4% of the theoretical values (purity of ≥95%). Elemental analyses were performed on a Fisons elemental analyzer, Model EA1108CHN. \(^1\)H NMR and \(^{13}\)C NMR spectra were recorded at 200 MHz (Bruker Avance DPX-200) and 400 MHz (Bruker Avance DRX-400) using residual solvents such as chloroform (\(\delta = 7.26\)) or dimethylsulfoxide (\(\delta = 2.48\)) as an internal standard. Chemical shifts are given in ppm (\(\delta\)) and the spectral data are consistent with the assigned structures. Reagents and solvents were purchased from common commercial suppliers and were used as such. After extraction, organic solutions were dried over anhydrous Na₂SO₄, filtered, and concentrated with a Büchi rotary evaporator at reduced pressure. Yields are of purified product and were not optimized. All starting materials were commercially available unless otherwise indicated.

General procedure for carbodiimide formation (Method A). A solution of the appropriate synthones (1.0 equiv) in pyridine was added of the suitable benzoyl chloride (2.0 equiv). The reaction mixture was maintained at room temperature until no starting material was detected by TCL. After cooling, the reaction mixture was poured into ice/water, obtaining a precipitate which was filtered and purified as described below.
Compounds 8 and 11-27 were prepared starting from synthone 38 through Method A and purified by crystallization by EtOH.

4-Methoxy-N-(5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (8). Yield, 100%. Light yellow crystals, mp 228-230 °C; \(^1\)H NMR (DMSO-\(d_6\)) \(\delta\) 1.95 (s, 3H, CH\(_3\)), 3.75 (s, 3H, OCH\(_3\)), 4.50 and 6.00 (s, each 1H, CH), 6.95 (d, \(J = 7.9\) Hz, 2H, aromatic CH), 7.20-7.35 (m, 5 H, aromatic CH), 7.85 (d, \(J = 7.9\) Hz, 2H, aromatic CH), 9.50 (s, 1H, NH), 10.25 (s, 1H, NHCO); \(^13\)C NMR (DMSO-\(d_6\)) \(\delta\) 18.7, 55.8, 59.8, 96.1, 113.9, 126.3, 127.2, 128.2, 128.9, 130.1, 131.9, 143.0, 148.9, 154.3, 162.4, 164.9. HRMS: \(m/z\) calcld for C\(_{20}\)H\(_{19}\)N\(_5\)O\(_2\) 362.1572 and C\(_{20}\)H\(_{19}\)N\(_5\)O\(_2\)·0.2 H\(_2\)O 380.1678 (M+H\(^+\)), found 362.1619 and 380.1724. Anal. (C\(_{20}\)H\(_{19}\)N\(_5\)O\(_2\)·0.2 H\(_2\)O) C, H, N.

2-Methoxy-N-(5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (11). Yield, 94%. Light yellow crystals, mp 154-156 °C; \(^1\)H NMR (DMSO-\(d_6\)) \(\delta\) 1.95 (s, 3H, CH\(_3\)), 3.75 (s, 3H, OCH\(_3\)), 4.50 and 5.90 (s, each 1H, CH), 6.95 (t, \(J = 7.4\) Hz, 1H, aromatic CH), 7.10 (d, \(J = 8.2\) Hz, 1H, aromatic CH), 7.20-7.35 (m, 5H, aromatic CH), 7.45 (t, \(J = 7.4\) Hz, 1H, aromatic CH), 7.55-7.65 (m, 1H, aromatic CH), 9.50 (s, 1H, NH), 10.00 (s, 1H, NHCO). Anal. (C\(_{20}\)H\(_{19}\)N\(_5\)O\(_2\)·0.3 H\(_2\)O) C, H, N.

3-Methoxy-N-(5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (12). Yield, 75%. Light yellow crystals, mp 159-161 °C; \(^1\)H NMR (DMSO-\(d_6\)) \(\delta\) 1.95 (s, 3H, CH\(_3\)), 3.75 (s, 3H, OCH\(_3\)), 4.50 and 5.90 (s, each 1H, CH), 7.00-7.45 (m, 9H, aromatic CH), 9.50 (s, 1H, NH), 10.45 (s, 1H, NHCO). Anal. (C\(_{20}\)H\(_{19}\)N\(_5\)O\(_2\)·0.2 H\(_2\)O) C, H, N.

4-Fluoro-N-(5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (13). Yield, 100%. Light yellow crystals, mp 253-255 °C; \(^1\)H NMR (DMSO-\(d_6\)) \(\delta\) 1.95 (s, 3H, CH\(_3\)), 4.50 and 6.00 (s, each 1H, CH), 7.20-7.35 (m, 7H, aromatic CH), 7.90-7.95 (m, 2H, aromatic CH), 9.50 (s, 1H, NH), 10.50 (s, 1H, NHCO). Anal. (C\(_{19}\)H\(_{16}\)FN\(_3\)O·0.4 H\(_2\)O) C, H, N.

3-Fluoro-N-(5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (14). Yield, 100%. Light yellow crystals, mp 248-250 °C; \(^1\)H NMR (DMSO-\(d_6\)) \(\delta\) 1.95 (s, 3H,
CH(CH₃), 4.50 and 6.00 (s, each 1H, CH), 7.20-7.35 (m, 7H, aromatic CH), 7.45-7.55 (m, 2H, aromatic CH), 9.50 (s, 1H, NH), 10.60 (s, 1H, NHCO). Anal. (C₁₉H₁₆F₅N₅O · 0.5 H₂O) C, H, N.

**2-Fluoro-N-(5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (15).** Yield, 100%. Light yellow crystals, mp 139-141 °C; ^1^H NMR (DMSO-δ₆) δ 1.95 (s, 3H, CH₃), 4.50 and 5.90 (s, each 1H, CH), 7.15-7.35 (m, 7H, aromatic CH), 7.45-7.55 (m, 2H, aromatic CH), 9.50 (s, 1H, NH), 10.50 (s, 1H, NHCO). Anal. (C₁₉H₁₆F₅N₅O · 0.3 H₂O) C, H, N.

**N-(5-Methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)-4-propoxybenzamide (16).** Yield, 100%. Light yellow crystals, mp 235-237 °C; ^1^H NMR (DMSO-δ₆) δ 0.95 (t, J = 7.0 Hz, 3H, CH₂CH₃), 1.70 (sex, J = 7.0 Hz, 2H, CH₂CH₃), 1.90 (s, 3H, CH₃), 3.95 (t, J = 7.0 Hz, 2H, OCH₂), 4.50 and 5.95 (s, each 1H, CH), 6.90 (d, J = 8.7 Hz, 2H, aromatic CH), 7.20-7.35 (m, 5H, aromatic CH), 7.80 (d, J = 8.7 Hz, 2H, aromatic CH), 9.50 (s, 1H, NH), 10.25 (s, 1H, NHCO). Anal. (C₂₂H₂₃N₅O₂ · 0.2 H₂O) C, H, N.

**4-Butoxy-N-(5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (17).** Yield, 45%. White crystals, mp 249-251 °C; ^1^H NMR (DMSO-δ₆) δ 0.90 (t, J = 7.4 Hz, 3H, CH₂CH₃), 1.40 (sex, J = 7.0 Hz, 2H, CH₂CH₃), 1.70 (quin, J = 6.5 Hz, 2H, CH₂CH₂CH₃), 1.85 (s, 3H, CH₃), 4.00 (t, J = 6.5 Hz, 2H, OCH₂), 4.50 and 5.95 (s, each 1H, CH), 6.90 (d, J = 8.5 Hz, 2H, aromatic CH), 7.20-7.35 (m, 5H, aromatic CH), 7.80 (d, J = 8.5 Hz, 2H, aromatic CH), 9.50 (s, 1H, NH), 10.25 (s, 1H, NHCO). Anal. (C₂₃H₂₅N₅O₂ · 0.2 H₂O) C, H, N.

**4-Butyl-N-(5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (18).** Yield, 51%. White crystals, mp 261-263 °C; ^1^H NMR (DMSO-δ₆) δ 0.90 (t, J = 7.4 Hz, 3H, CH₂CH₃), 1.40 (sex, J = 7.4 Hz, 2H, CH₂CH₃), 1.70 (quin, J = 7.4 Hz, 2H, CH₂CH₂CH₃), 1.85 (s, 3H, CH₃), 2.55 (t, J = 7.4 Hz, 2H, CCH₂), 4.50 and 5.95 (s, each 1H, CH), 7.20-7.25 (m, 5H, aromatic CH), 7.30-7.35 (m, 2H, aromatic CH), 7.80 (d, J = 8.1 Hz, 2H, aromatic CH), 9.50 (s, 1H, NH), 10.25 (s, 1H, NHCO). Anal. (C₂₃H₂₅N₅O · 0.4 H₂O) C, H, N.

**N-(5-Methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)-4-phenoxybenzamide (19).** Yield, 84%. White crystals, mp 217-219 °C; ^1^H NMR (DMSO-δ₆) δ 1.95 (s, 3H, CH₃), 4.50
and 5.90 (s, each 1H, CH), 6.90-7.40 (m, 12 H, aromatic CH), 7.90 (d, \( J = 8.4 \) Hz, 2H, aromatic CH), 9.55 (s, 1H, NH), 10.40 (s, 1H, NHCO). Anal. (C_{25}H_{21}N_{5}O \cdot 0.3 H_{2}O) C, H, N.

4-Isopropoxy-N-(5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (20). Yield, 20%. White crystals, mp 229-231 °C; \(^1\)H NMR (DMSO-d\(_6\)) \( \delta \) 1.20 (d, \( J = 6.0 \) Hz, 6H, CH(CH\(_3\))\(_2\)), 1.80 (s, 3H, CH\(_3\)), 4.50 (s, 1H, CH), 4.60 (quin, \( J = 6.0 \) Hz, 1H, CH(CH\(_3\))\(_2\)), 5.85 (s, 1H, CH), 6.90 (d, \( J = 8.7 \) Hz, 2H, aromatic CH), 7.20-7.35 (m, 5H, aromatic CH), 7.80 (d, \( J = 8.7 \) Hz, 2H, aromatic CH), 9.55 (s, 1H, NH), 10.25 (s, 1H, NHCO). Anal. (C\(_{22}\)H\(_{23}\)N\(_5\)O \cdot 0.2 H\(_2\)O) C, H, N.

N-(5-Methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)biphenyl-4-carboxamide (21). Yield, 56%. Light brown crystals, mp 257-259 °C; \(^1\)H NMR (DMSO-d\(_6\)) \( \delta \) 1.85 (s, 3H, CH\(_3\)), 4.50 and 5.90 (s, each 1H, CH), 7.20-7.45 (m, 8H, aromatic CH), 7.60-7.70 (m, 4H, aromatic CH), 7.90 (d, \( J = 8.4 \) Hz, 2H, aromatic CH), 9.55 (s, 1H, NH), 10.50 (s, 1H, NHCO). Anal. (C\(_{25}\)H\(_{21}\)N\(_5\)O \cdot 0.3 H\(_2\)O) C, H, N.

4-Ethoxy-N-(5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (22). Yield, 36%. Pink crystals, mp 227 °C (dec.); \(^1\)H NMR (DMSO-d\(_6\)) \( \delta \) 1.25 (t, \( J = 7.0 \) Hz, 3H, CH\(_2\)CH\(_3\)), 1.80 (s, 3H, CH\(_3\)), 4.00 (q, \( J = 7.0 \) Hz, 2H, CH\(_2\)CH\(_3\)), 4.50 and 5.90 (s, each 1H, CH), 6.90 (d, \( J = 8.8 \) Hz, 2H, aromatic CH), 7.20-7.30 (m, 5H, aromatic CH), 7.80 (d, \( J = 8.8 \) Hz, 2H, aromatic CH), 9.55 (s, 1H, NH), 10.25 (s, 1H, NHCO). Anal. (C\(_{21}\)H\(_{21}\)N\(_5\)O \cdot 0.5 H\(_2\)O) C, H, N.

N-(5-Methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)-4-nitrobenzamide (23). Yield, 60%. Light yellow crystals, mp 272-274 °C; \(^1\)H NMR (DMSO-d\(_6\)) \( \delta \) 1.80 (s, 3H, CH\(_3\)), 4.50 and 5.90 (s, each 1H, CH), 7.15-7.30 (m, 5H, aromatic CH), 8.05 and 8.25 (d, \( J = 8.8 \) Hz, each 2H, aromatic CH), 9.55 (s, 1H, NH), 10.85 (s, 1H, NHCO). Anal. (C\(_{19}\)H\(_{16}\)N\(_6\)O\(_3\) \cdot 0.4 H\(_2\)O) C, H, N.

4-Chloro-N-(5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (24). Yield, 31%. White crystals, mp 254-256 °C; \(^1\)H NMR (DMSO-d\(_6\)) \( \delta \) 1.80 (s, 3H, CH\(_3\)), 4.50 and 5.90 (s, each 1H, CH), 7.10-7.30 (m, 5H, aromatic CH), 7.45 and 7.80 (d, \( J = 8.8 \) Hz, each 2H, aromatic CH), 9.55 (s, 1H, NH), 10.55 (s, 1H, NHCO). Anal. (C\(_{19}\)H\(_{16}\)ClN\(_5\)O \cdot 0.2 H\(_2\)O) C, H, N.
N-(5-Methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)-2-naphthamide (25). Yield, 42%. Pink crystals, mp 230 °C (dec.); $^1$H NMR (DMSO-$d_6$) $\delta$ 1.80 (s, 3H, CH$_3$), 4.50 and 5.90 (s, each 1H, CH), 7.20-7.30 (m, 5H, aromatic CH), 7.50-7.55 (m, 2H, aromatic CH), 7.90-8.00 (m, 4H, aromatic CH), 8.45-8.50 (m, 1H, aromatic CH), 9.55 (s, 1H, NH), 10.50 (s, 1H, NHCO). Anal. (C$_{23}$H$_{19}$N$_5$O · 0.3 H$_2$O) C, H, N.

N-(5-Methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (26). Yield, 18%. Light brown crystals, mp 257 °C (dec.); $^1$H NMR (DMSO-$d_6$) $\delta$ 1.80 (s, 3H, CH$_3$), 4.50 and 5.90 (s, each 1H, CH), 7.20-7.50 (m, 8H, aromatic CH), 7.75 and 7.80 (m, 2H aromatic CH), 9.55 (s, 1H, NH), 10.50 (s, 1H, NHCO). Anal. (C$_{19}$H$_{17}$N$_5$O · 0.2 H$_2$O) C, H, N.

N-(5-Methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)-3-phenylpropanamide (27). Yield, 9%. White crystals, mp 169-171 °C; $^1$H NMR (DMSO-$d_6$) $\delta$ 1.80 (s, 3H, CH$_3$), 2.50 and 2.75 (t, $J$ = 7.2 Hz, each 2H, CH$_2$), 4.50 and 5.90 (s, each 1H, CH), 7.00-7.25 (m, 10H, aromatic CH), 9.55 (s, 1H, NH), 10.00 (s, 1H, NHCO). Anal. (C$_{21}$H$_{21}$N$_5$O · 0.3 H$_2$O) C, H, N.

Compounds 28-30 were prepared starting from synthone 41 through Method A and purified by flash chromatography eluting with CHCl$_3$/MeOH (98:2).

N-(5-Methyl-7-phenyl[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (28). Yield, 19%. White crystals, mp 183-185 °C; $^1$H NMR (DMSO-$d_6$) $\delta$ 2.75 (s, 3H, CH$_3$), 7.05 (s, 1H, H-6), 7.40-7.55 (m, 6H, aromatic CH), 8.00 (d, $J$ = 7.0 Hz, 2H, aromatic CH), 8.15-8.20 (m, 2H, aromatic CH), 9.75 (s, 1H, NHCO); $^{13}$C NMR (CDCl$_3$) $\delta$ 25.1, 109.4, 127.9, 128.6, 128.9, 129.3, 129.6, 131.8, 132.2, 133.7, 146.8, 154.9, 160.0, 164.7, 165.0. HRMS: m/z calcd for C$_{19}$H$_{15}$N$_5$O 330.1310 (M + H$^+$), found 330.1359.

4-Methoxy-N-(5-methyl-7-phenyl[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (29). Yield, 68%. White crystals, mp 190-192 °C; $^1$H NMR (DMSO-$d_6$) $\delta$ 2.75 (s, 3H, CH$_3$), 3.80 (s, 3H, OCH$_3$), 6.90 (d, $J$ = 8.8 Hz, 2H, aromatic CH) 7.05 (s, 1H, H-6), 7.50-7.55 (m, 3H, aromatic CH),
7.95 (d, $J = 8.8$ Hz, 2H, aromatic CH), 8.15-8.20 (m, 2H, aromatic CH), 9.25 (s, 1H, NHCO). Anal. (C$_{20}$H$_{17}$N$_{5}$O$_{2}$) C, H, N.

$N$-(5-Methyl-7-phenyl[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)-4-propoxybenzamide (30). Yield, 27%. White crystals, mp 180-182 °C; $^1$H NMR (DMSO-$d_6$) $\delta$ 1.05 (t, $J = 7.0$ Hz, 3H, CH$_2$CH$_3$), 1.90 (sex, $J = 7.0$ Hz, 2H, CH$_2$CH$_3$), 2.75 (s, 3H, CH$_3$), 4.00 (t, $J = 7.0$ Hz, 2H, OCH$_2$), 6.90 (d, $J = 8.8$ Hz, 2H, aromatic CH) 7.05 (s, 1H, H-6), 7.55-7.65 (m, 3H, aromatic CH), 8.00 (d, $J = 8.8$ Hz, 2H, aromatic CH), 8.20-8.25 (m, 2H, aromatic CH), 9.30 (bs, 1H, NHCO). Anal. (C$_{22}$H$_{21}$N$_{5}$O$_{2}$) C, H, N.

Compounds 31-33 were prepared starting from synthone 42 through Method A and purified by flash chromatography eluting with CHCl$_3$/MeOH (98:2).

$N$-(7-Methyl-5-phenyl[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (31). Yield, 23%. Light brown crystals, mp 217 °C (dec.); $^1$H NMR (DMSO-$d_6$) $\delta$ 2.75 (s, 3H, CH$_3$), 7.50-7.65 (m, 6H, aromatic CH), 7.90 (s, 1H, H-6), 8.05 (d, $J = 7.0$ Hz, 2H, aromatic CH), 8.25-8.30 (m, 2H, aromatic CH), 11.50 (s, 1H, NHCO); $^{13}$C NMR (DMSO-$d_6$) $\delta$ 17.5, 107.3, 127.8, 128.5, 128.8, 129.5, 131.5, 132.6, 134.1, 136.6, 148.2, 154.5, 159.8, 160.8, 165.3. HRMS: $m/z$ calcd for C$_{19}$H$_{15}$N$_{5}$O 330.1310 (M + H$^+$), found 330.1355.

4-Methoxy-$N$-(7-methyl-5-phenyl[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)benzamide (32). Yield, 42%. White crystals, mp 210-213 °C; $^1$H NMR (DMSO-$d_6$) $\delta$ 2.80 (s, 3H, CH$_3$), 3.85 (s, 3H, OCH$_3$), 7.05 (d, $J = 8.4$ Hz, 2H, aromatic CH) 7.55-7.60 (m, 3H, aromatic CH), 7.90 (s, 1H, H-6), 8.05 (d, $J = 8.4$ Hz, 2H, aromatic CH), 8.25-8.30 (m, 2H, aromatic CH), 11.25 (s, 1H, NHCO). Anal. (C$_{20}$H$_{17}$N$_{5}$O$_{2}$) C, H, N.

$N$-(7-Methyl-5-phenyl[1,2,4]triazolo[1,5-a]pyrimidin-2-yl)-4-propoxybenzamide (33). Yield, 35%. White crystals, mp 184-186 °C; $^1$H NMR (DMSO-$d_6$) $\delta$ 1.00 (t, $J = 7.0$ Hz, 3H, CH$_2$CH$_3$), 1.75 (sex, $J = 7.0$ Hz, 2H, CH$_2$CH$_3$), 2.85 (s, 3H, CH$_3$), 4.00 (t, $J = 7.0$ Hz, 2H, OCH$_2$), 7.05 (d, $J = 8.8$ Hz, 2H, aromatic CH) 7.55-7.60 (m, 3H, aromatic CH), 7.90 (s, 1H, H-6), 8.05 (d, $J = 8.8$ Hz,
2H, aromatic CH), 8.25-8.30 (m, 2H, aromatic CH), 11.25 (s, 1H, NHCO). Anal. (C_{22}H_{21}N_{5}O_{2}) C, H, N.

**General procedure for carbodiimide formation (Method B).** To a solution of the suitable carboxylic acid (1.0 equiv) in well dry CH\(_2\)Cl\(_2\), oxalyl chloride (3 equiv) was added and after 30 min DMF (2 drops) was added. After 2 h, the reaction mixture was evaporated to dryness to give a residue that was dissolved in well dry CH\(_2\)Cl\(_2\) and added of the appropriate aniline (1.0 equiv) and DIPEA (1.0 equiv). After 1 h, the reaction mixture was evaporated to dryness to give a residue that was treated with ice/water to give a solid that was filtered and purified as described below.

Compounds 34 and 36 were prepared starting from synthone 45 through Method B and purified by flash chromatography eluting with CHCl\(_3\)/MeOH (98:2) and then by crystallization by EtOH/DMF mixture.

**7-Methyl-N,5-diphenyl[1,2,4]triazolo[1,5-a]pyrimidine-2-carboxamide (34).** Yield, 42%. Yellow crystals, mp 186-188 °C; \(^1\)H NMR (CDCl\(_3\)) \(\delta\) 2.85 (s, 3H, CH\(_3\)), 7.15-7.20 (m, 2H, H-6 and aromatic CH), 7.40 (t, \(J = 7.9\) Hz, 2H, aromatic CH), 7.60-7.65 (m, 3H, aromatic CH), 7.80 (d, \(J = 7.9\) Hz, 2H, aromatic CH), 8.15-8.20 (m, 2H, aromatic CH), 9.00 (s, 1H, NHCO). HRMS: \(m/z\) calcld for C\(_{19}\)H\(_{15}\)N\(_5\)O 330.1310 (M + H\(^+\)), found 330.1358. Anal. (C\(_{19}\)H\(_{15}\)N\(_5\)O) C, H, N.

**5-Methyl-N,7-diphenyl[1,2,4]triazolo[1,5-a]pyrimidine-2-carboxamide (35).** Yield, 39%. White crystals, mp 242-245 °C; \(^1\)H NMR (CDCl\(_3\)) \(\delta\) 3.00 (s, 3H, CH\(_3\)), 7.20 (t, \(J = 7.3\) Hz, 1H, aromatic CH), 7.40 (t, \(J = 7.9\) Hz, 2H, aromatic CH), 7.60-7.65 (m, 3H, aromatic CH), 7.80 (d, \(J = 7.9\) Hz, 2H, aromatic CH), 8.25-8.30 (m, 2H, aromatic CH), 9.50 (s, 1H, NHCO). HRMS: \(m/z\) calcld for C\(_{19}\)H\(_{15}\)N\(_5\)O 330.1310 (M + H\(^+\)), found 330.1360. Anal. (C\(_{19}\)H\(_{15}\)N\(_5\)O) C, H, N.

**N-[3-(aminocarbonyl)-5,6,7,8-tetrahydro-4H-cyclohepta[b]thien-2-yl]-7-methyl-5-phenyl[1,2,4]triazolo[1,5-a]pyrimidine-2-carboxamide (36).** Yield, 30%. Yellow crystals, mp 288 °C (dec.); \(^1\)H NMR (DMSO-\(d_6\)) \(\delta\) 1.50-1.65 (m, 4H, cycloheptane CH\(_2\)), 1.75-1.80, (m, 2H, cycloheptane CH\(_2\)), 2.60-2.70 (m, 5H, cycloheptane CH\(_2\) and CH\(_3\)), 2.75-2.80 (m, 2H, cycloheptane CH\(_2\)), 7.45-7.60 (m, 6H, aromatic CH, NH\(_2\), and H-6), 8.20-8.25 (m, 2H, aromatic CH), 12.00 (s,
N-[(Aminocarbonyl)-5,6,7,8-tetrahydro-4H-cyclohepta[b]thien-2-yl]-5-methyl-7-phenyl[1,2,4]triazolo[1,5-a]pyrimidine-2-carboxamide (37). Yield, 25%. Orange crystals, mp 313 °C (dec.); \(^1\)H NMR (DMSO-\(d_6\)) \(\delta\) 1.50-1.65 (m, 4H, cycloheptane CH\(_2\)), 1.75-1.80, 2.70-2.75, and 2.80-2.85 (m, each 2H, cycloheptane CH\(_2\)), 2.90 (s, 3H, CH\(_3\)), 7.45-7.60 (m, 5H, aromatic CH and NH\(_2\)), 8.05 (s, 1H, H-6), 8.25-8.30 (m, 2H, aromatic CH), 12.00 (s, 1H, NHCO); \(^{13}\)C NMR (DMSO-\(d_6\)) \(\delta\) 17.4, 27.5, 27.9, 28.6, 28.7, 31.9, 112.3, 122.2, 129.1, 129.7, 130.0, 131.7, 132.2, 135.6, 136.7, 147.1, 155.5, 155.9, 157.5, 167.4, 167.7. HRMS: \(m/z\) calcd for C\(_{23}\)H\(_{22}\)N\(_6\)O\(_2\)S 447.1558 (M + H\(^+\)), found 447.1611. Anal. (C\(_{23}\)H\(_{22}\)N\(_6\)O\(_2\)S) C, H, N.

7-Methyl-5-phenyl[1,2,4]triazolo[1,5-a]pyrimidin-2-amine (42). To a solution of 3,5-diamino-1,2,4-triazole (0.1 g, 0.001 mmol) in DMF (5 mL) at reflux, phenyl 1-propenyl ketone (0.14 mL, 0.001 mmol) was added and the reaction mixture was maintained at reflux for 30 min. After cooling, the mixture was evaporated to dryness, obtaining a residue that was purified by flash chromatography eluting with CH\(_2\)Cl\(_2\)/MeOH (98:2), to give 42 (0.1 g, 44%); mp 225-227 °C; \(^1\)H NMR (DMSO-\(d_6\)) \(\delta\) 2.60 (s, 3H, CH\(_3\)), 6.35 (s, 2H, NH\(_2\)), 7.45-7.50 (m, 3H, aromatic CH), 7.05 (s, 1H, H-6), 8.05-8.15 (m, 2H, aromatic CH); \(^{13}\)C NMR (DMSO-\(d_6\)) \(\delta\) 17.4, 27.5, 27.9, 28.6, 28.7, 32.0, 109.2, 122.1, 128.1, 129.6, 131.8, 132.1, 135.6, 136.2, 136.7, 149.7, 155.2, 155.5, 157.9, 161.9, 167.7. HRMS: \(m/z\) calcd for C\(_{23}\)H\(_{22}\)N\(_6\)O\(_2\)S 447.1558 (M + H\(^+\)), found 447.1601. Anal. (C\(_{23}\)H\(_{22}\)N\(_6\)O\(_2\)S) C, H, N.

Ethyl 5-methyl-7-phenyl-4,7-dihydro[1,2,4]triazolo[1,5-a]pyrimidine-2-carboxylate (43). The title compound was prepared starting from ethyl 5-amino-1,2,4-triazole-3-carboxylate\(^{29}\) and following the same procedure as used for the synthesis of 42 (2 h) using benzylideneacetone. After cooling, the reaction mixture was poured into ice/water obtaining a precipitate that was filtered and washed with Et\(_2\)O, to give 43 in 29% yield, which was used without further purification; \(^1\)H NMR
(DMSO-$d_6$) $\delta$ 1.20 (t, $J = 7.1$ Hz, 3H, CH$_2$CH$_3$), 1.80 (s, 3H, CH$_3$), 4.20 (q, $J = 7.1$ Hz, 2H, CH$_2$CH$_3$), 4.55 and 6.00 (bs, each 1H, CH), 7.20-7.30 (m, 5H, aromatic CH), 9.75 (s, 1H, NH).

**Ethyl 5-methyl-7-phenyl[1,2,4]triazolo[1,5-a]pyrimidine-2-carboxylate (44).** To a suspension of 43 (1.4 g, 4.92 mmol) in EtOH (30 mL), NaOAc (0.59 g, 7.18 mmol) was added and the reaction mixture was heated at 40-50 °C. Then, NBS (0.87 g, 4.88 mmol) was added and the reaction mixture was refluxed for 30 min. After cooling, the reaction mixture was poured into ice/water obtaining a precipitate that was filtered and purified by flash chromatography eluting with CH$_2$Cl$_2$/MeOH (98:2), to give 44 (0.45 g, 33%); mp 174-176 °C; $^1$H NMR (CDCl$_3$) $\delta$ 1.45 (t, $J = 7.1$ Hz, 3H, CH$_2$CH$_3$), 2.75 (s, 3H, CH$_3$), 4.50 (q, $J = 7.1$ Hz, 2H, CH$_2$CH$_3$), 7.15 (s, 1H, H-6), 7.55-7.65 (m, 3H, aromatic CH), 8.05-8.10 (m, 2H, aromatic CH).

**5-Methyl-7-phenyl[1,2,4]triazolo[1,5-a]pyrimidine-2-carboxylic acid (45).** A mixture of 44 (0.45 g, 1.59 mmol) and NaOH (0.079 g, 1.99 mmol) in MeOH (10 mL) was refluxed for 30 min. After cooling, the reaction mixture was poured into ice/water and acidified with 2N HCl obtaining a precipitate that was filtered. The filtrate was extracted with EtOAc and the organic layers were evaporated to dryness obtaining a residue that was treated with Et$_2$O and filtered, to give 45 (0.13 g, 32%); mp 172-174 °C; $^1$H NMR (DMSO-$d_6$) $\delta$ 2.70 (s, 3H, CH$_3$), 7.55-7.60 (m, 4H, H-6 and aromatic CH), 8.05-8.10 (m, 2H, aromatic CH).

**Ethyl 7-methyl-5-phenyl[1,2,4]triazolo[1,5-a]pyrimidine-2-carboxylate (46).** The title compound was prepared starting from ethyl 5-amino-1,2,4-triazole-3-carboxylate$^{20}$ following the same procedure as used for the synthesis of 42 (1 h). After cooling, the reaction mixture was poured into ice/water and extracted with EtOAc. The organic layers were evaporated to dryness obtaining a residue that was treated with Et$_2$O, to give 46 in 11% yield; mp 170-172 °C; $^1$H NMR (DMSO-$d_6$) $\delta$ 1.30 (t, $J = 7.1$ Hz, 3H, CH$_2$CH$_3$), 2.80 (s, 3H, CH$_3$), 4.50 (q, $J = 7.1$ Hz, 2H, CH$_2$CH$_3$), 7.50-7.65 (m, 3H, aromatic CH), 8.05 (s, 1H, H-6), 8.15-8.25 (m, 2H, aromatic CH).

**7-Methyl-5-phenyl[1,2,4]triazolo[1,5-a]pyrimidine-2-carboxylic acid (47).** The title compound was prepared from 46 following the same procedure as used for the synthesis of 45 (2 h). After
cooling, the reaction mixture was evaporated to dryness obtaining a residue that was treated with ice/water and acidified with 2N HCl obtaining a precipitate that was filtered and washed with Et₂O, to give 47 in 87% yield; mp 168-169 °C; ¹H NMR (DMSO-d₆) δ 2.90 (s, 3H, CH₃), 7.50-7.60 (m, 3H, aromatic CH), 8.05 (s, 1H, H-6), 8.20-8.25 (m, 2H, aromatic CH).

Compounds 35 and 37 were prepared starting from synthone 47 through Method B and purified by flash chromatography eluting with CHCl₃/MeOH (98:2) and then by crystallization by EtOH/DMF mixture.

**Biology**

**Compounds and peptide.** RBV (1-D-ribofuranosyl-1,2,4-triazole-3-carboxamide) was obtained from Roche. Each test compound was dissolved in DMSO 100%. The PB1₁₁₅–Tat peptide was synthesized and purified by the Peptide Facility of CRIBI Biotechnology Center (University of Padua, Padua, Italy). This peptide contains the first 15 N-terminal amino acids of PB1 protein conjugated to the C-terminal sequence of HIV Tat protein (amino acids 47–59), which allows intracellular delivery.⁴⁴

**Plasmids.** Plasmids pcDNA-PB1, pcDNA-PB2, pcDNA-PA, and pcDNA-NP, containing cDNA copies of the influenza A/PR/8/34 virus PB1, PB2, PA, and NP genes, respectively, were created as described elsewhere³⁴ and kindly provided by P. Digard (Roslin Institute, University of Edinburgh, United Kingdom). Plasmid pPolI-Flu-ffLuc, which contains an influenza virus-based luciferase minireplicon vRNA under the control of the human RNA polymerase I promoter, was provided by L. Tiley (University of Cambridge, United Kingdom). Plasmid pRL-SV40 expressing the *Renilla* luciferase was purchased from Promega. The pcDNA-PA-GFP plasmid, which encodes a PA-GFP fusion protein was kindly provided by E. Fodor (University of Oxford, United Kingdom).

**Cells and Virus.** Human Embryonic Kidney (HEK) 293T and Mardin-Darby canine kidney (MDCK) cells were grown in Dulbecco’s modified Eagle’s medium (DMEM, Life Biotechnologies) supplemented with 10% (v/v) fetal bovine serum (FBS, Life Technologies) and antibiotics (100 U/mL penicillin and 100 µg/mL streptomycin, Life Technologies). The cells were maintained at 37
°C in a humidified atmosphere with 5% CO₂. Influenza A/PR/8/34 virus (H1N1, Cambridge lineage) was obtained from P. Digard (Roslin Institute, University of Edinburgh, United Kingdom). The FluA strains A/Wisconsin/67/05 and A/Solomon Island/3/06 and the FluB strains B/Malaysia/2506/4 and B/Bangladesh/333/07 were provided by R. Cusinato (Clinical Microbiology and Virology Unit, Padua University Hospital, Padua, Italy). The clinical isolate A/Parma/24/09 was kindly provided by I. Donatelli (Istituto Superiore di Sanità, Rome, Italy). Influenza B/Lee/40 virus was obtained from W. S. Barclay (Imperial College, London, United Kingdom). All influenza viruses were propagated in MDCK cells.

**PA-PB1 interaction enzyme-linked immunosorbent assay (ELISA).** The PA–PB1 interaction was detected by a procedure already described. Briefly, microtiter plates (Nuova Aptca) were coated with 400 ng of 6His-PA(239−716) for 3 h at 37 °C and then blocked with 2% BSA (Sigma) in PBS for 1 h at 37 °C. The 6His-PA(239−716) protein was expressed in *Escherichia coli* strain BL21(DE3)pLysS and purified as described. After washing, 200 ng of GST-PB1(1−25), or of GST alone as a control, in the absence or the presence of test compounds at various concentrations (10, 50, 100, 200 μM), were added and incubated O/N at room temperature. *Escherichia coli*-expressed, purified GST and GST-PB1(1−25) proteins were obtained as previously described. After washing, the interaction between 6His-PA(239−716) and GST-PB1(1−25) was detected with an anti-GST monoclonal antibody conjugated to horseradish peroxidase (HRP) (GenScript). Following washes, the substrate 3,3′,5,5′tetramethylbenzidine (TMB, KPL) was added and absorbance was measured at 450 nm by an ELISA plate reader (Tecan Sunrise™). Values obtained from the samples treated with only DMSO were used to set as 100% of PA–PB1 interaction.

**Cytotoxicity assay.** Cytotoxicity of compounds was tested in MDCK and HEK 293T cells by the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide (MTT) method, as previously reported.

**Plaque reduction assay (PRA).** The experiments were carried out as previously described. Briefly, confluent monolayers of MDCK cells were infected with FluA or FluB virus at 40
PFU/well in DMEM supplemented with 1 μg/mL of TPCK-treated trypsin (Worthington Biochemical Corporation) and 0.14% BSA and incubated for 1 h at 37°C. The influenza viruses infection was performed in the presence of different concentrations of test compounds or solvent (DMSO) as a control. Serum-free medium containing 1 μg/mL of TPCK-treated trypsin, 0.14% BSA, 1.2% Avicel, and DMSO or test compounds at the indicated concentrations was added after 1 h of virus adsorption. After 48 h of incubation, cells were fixed with 4% formaldehyde and stained with 0.1% toluidine blue. Viral plaques were counted, and the mean plaque number in the DMSO-treated control was set at 100%.

**Minireplicon assay.** HEK 293T cells were seeded at 10^5 per well on 24-well plates. After 24 h, cells were transfected, in the presence of test compounds at different concentrations or DMSO, with pcDNA-PB1, pcDNA-PB2, pcDNA-PA, pcDNA-NP plasmids (100 ng/well of each) along with pPolI-Flu-ffLuc plasmid (50 ng/well) as described elsewhere. In addition, a plasmid constitutively expressing *Renilla* luciferase, pRL-SV40 (50 ng/well), was included in the transfection mixture to normalize variations in transfection efficiency. After 4 h, the medium was replaced with fresh DMEM containing DMSO or test compounds. At 24 h post-transfection, cells were lysed, and the relative firefly and *Renilla* luciferase activities were determined using the Dual Luciferase Assay Kit from Promega and a luminescence counter (Victor X2, PerkinElmer). The luciferase activities of the samples treated with DMSO were set as 100%.

**Analysis of nuclear accumulation of the PA-PB1 complex in the presence of compound 36.** HEK 293T cells were transiently transfected using the Arrest-IN™ (Biosystems) with pcDNA-PA-GFP, pcDNA-PB1, and pcDNA-PB2 in the absence or the presence of compound 36 (50 μM) or DMSO as a control. At 24 hr post-transfection, cells were fixed for 20 min with 4% formaldehyde in PBS. After permeabilization with 0.2 % Triton X-100 in PBS for 5 min at RT, cells were incubated for 20 min with TOTO-3 iodide (Molecular Probes) in PBS and 4% FBS, mounted using mounting fluid (70% glycerol in PBS), and imaged using a Leica TCS-NT/SP2 confocal
microscope equipped with a 63X oil immersion objective. Images were digitally analyzed with Leica software.

**Preliminary ADME studies**

**Metabolic stability.** The selected substrates were incubated with human liver microsomes (HLM, 0.5 mg protein/ml) (BD Biosciences) according to manufacturer’s recommendations with minor modification. In summary, substrates at 5 µM final concentration were pre-incubated in a shaking water bath for 5 min at 37 °C in 100 mM potassium phosphate buffer (pH 7.4) in a total volume of 250 µL. Thus, 10 µL of a 1 mM NADPH aqueous solution were added to activate the enzymatic process. After incubation for 0 and 30 min, the addition of 250 µL of cold acetonitrile (containing 0.6 µM labetalol as internal standard) was used to terminate the reaction. Proteins were precipitated by centrifugation at 12,000 x g for 5 min at 4 °C, and aliquots of supernatants were analyzed by HPLC-MS/MS, on an Agilent 6550 UHD accurate mass Q-TOF LC/MSMS system (Agilent Technologies, Palo Alto, CA) governed by Agilent MassHunter software (B.05.01 version). The system consists of a binary pump, autosampler, thermostated column compartment, DAD detector, source and Q-TOF spectrometer. Chromatographic separation of the metabolites (Agilent 1290 UHPLC system) was performed with Agilent RRHD 1.7 µ-C18, 100 x 2.1 mm (Phenomenex USA) at a constant temperature of 40 °C. The mobile phases consisted of A: H2O/0.1% formic acid and B: acetonitrile/0.1% formic acid at the flow of 0.45 mL/min with the following gradient: Time 0 min, B 10%; Time 6 min, B 100%. The DAD Detector stored all the acquired spectra in the 190-640 nm range (2 nm spectrum step). The ion source was an Agilent Dual JetStream operating under positive ionization mode (4000 V), with as nitrogen the desolvating gas (290 °C, 12 L/min, 35 psig). The fragmentor was set to 375 V, the skimmer to 65 V, and the octrapole RF to 750 V. The spectrometric data were collected in AutoMS/MS mode in the 100-1000 mass range, with 3 scans/sec at Collision Energy of 30 V. The TOF operated at 2 GHz.

**Permeability assay.** The PAMPA (Parallel Artificial Membrane Permeation Assay) method was used to study permeability of compounds 8, 16, 31, 36, and 37. In a PAMPA assay drugs permeate
by passive diffusion from the donor compartment (320 µL, Roche Teflon plate), to the acceptor compartment (280 µL, Millipore MAIPN4550), where the acceptor and the donor compartments are separated by a phospholipid coated filter (4.5 µL, Millipore MAIPN4550). Donor buffer: 0.05 M MOPSO at pH 6.5 + 0.5% (w/v) Glycocholic acid. Acceptor buffer: 0.05 M MOPSO at pH 6.5. Membrane: 10% (w/v) Egg Lecithin in Dodecane + 0.5% (w/v) Cholesterol. Permeation time was 18 h. The permeation constant, $P_{\text{eff}} \times 10^{-6} \text{cm/s}$, and the sample distribution can be retrieved by UV analytics (SpectraMax Plus 384 Absorbance Microplate Reader, Molecular Devices) of donor ($t_{\text{start}}$), donor ($t_{\text{end}}$) and acceptor ($t_{\text{end}}$) using the pION PAMPA Evolution software. According to this method, low permeability is expected when $P_{\text{eff}} < 0.2 \times 10^{-6} \text{cm/s}$ and Membrane% < 20%, where $P_{\text{eff}}$ represents the effective permeability and Membrane% represents the percentage of compounds trapped into the membrane. When one or both parameters are above the cut-off then a medium to high permeability is expected (compound 8: $P_{\text{eff}} = 3.52 \times 10^{-6} \text{cm/s}$ and Membrane% = 57%; compound 16: $P_{\text{eff}} = 2.93 \times 10^{-6} \text{cm/s}$ and Membrane% = 41%; compound 31: $P_{\text{eff}} = 5.49 \times 10^{-6} \text{cm/s}$ and Membrane% = 2%; compound 36: $P_{\text{eff}} = 0.61 \times 10^{-6} \text{cm/s}$ and Membrane% = 45%; compound 37: undetected; compound 7: $P_{\text{eff}} = 0.00 \times 10^{-6} \text{cm/s}$ and Membrane% = 99%; compound 10: $P_{\text{eff}} = 0.00 \times 10^{-6} \text{cm/s}$ and Membrane% = 98%).

**Equilibrium solubility in aqueous media.** An accurately weighted amount of compound (about 1 mg) as dry powder was placed in a glass tube and 330 µL of 0.15 M Phosphate buffer at pH 7.4 were added. Thus, the sample was ultrasonicated for 1 hour, shaken at room temperature for 2 hours (Branson 1210, Branson Ultrasonics, Danbury, CT) and let stand to equilibrate overnight. The next day, the pH of the sample was checked and the solution was filtered using a MultiScreenHTS-PCF filter (Millipore, Darmstadt, Germany). Aliquots of the filtrate were used to generate three different samples (undiluted, diluted as 1:10 and as 1:100) by dilution with the same buffer. Compound calibration curves were generated from standard 1 mg/mL DMSO solutions diluted in buffer. Calibration standards and samples were then analyzed by LC-UV.MS using an Agilent 1260 Infinity HPLC-MS system (Agilent Technologies, Santa Clara, CA) equipped with a DAD detector.
and an API single quadrupole mass spectrometer (Agilent 6140, Santa Clara, CA). A Kinetex XB 2.6 µm, 2.1 x 50 mm analytical column (Phenomenex, Torrance, CA) operating at 60 °C was used. The mobile phase consisted of A (water) and B (acetonitrile), both containing 0.1 %/vol formic acid. The gradient elution was performed with a flow rate of 1.5 mL/min using a generic fast gradient. After detection with DAD, the eluent entered the electrospray system using the following source settings: capillary voltage + 3.5 kV, drying gas flow (N2) 13 L/min, nebulizer pressure 60 sig, drying gas temperature 350 °C. The integral of the pseudo molecular ion intensity, [M+H]+, was acquired in single reaction monitoring mode (SRM).

ASSOCIATED CONTENT

Supporting information

Table containing Elemental Analysis data for target compounds 8 and 11-37. This material is available free of charge via the Internet at http://pubs.acs.org.

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Author contributions

⊥There are two sets of equal contributions: (1) S.M. and G.N. contributed equally to this work; (2) A.L. and O.T. contributed equally to this work.

Notes

The authors declare no competing financial interest.
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ABBREVIATIONS USED

ADME, absorption, distribution, metabolism and excretion; CC_{50}, concentration that causes a decrease of cell viability by 50%; Flu, influenza virus; FluA, influenza A virus; FluB, influenza B virus; HEK, human embryonic kidney; HLM, human liver microsomes; MDCK, Mardin-Darby canine kidney; PA, polymerase acidic protein; PAMPA, parallel artificial membrane permeability assay; PB1, polymerase basic protein 1; PB2, polymerase basic protein 2; PPI, protein-protein interaction; PRA, plaque reduction assays; RBV, Ribavirin; RdRP, RNA-dependent RNA polymerase.

REFERENCES


Table 1. Structure and Biological Activity of the Compounds Synthesized in This Study.
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<th>Compd</th>
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<th>PRA in MDCK cells EC_{50}, µM (^b)</th>
<th>Cytotoxicity (MTT Assay)</th>
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<td>HEK 293T cells CC_{50}, µM (^c)</td>
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Table 2. Activity of Selected Compounds Against FluA RNA Polymerase Activity.

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36 12 ± 1
37 16 ± 5
RBV 18 ± 4

* The EC\textsubscript{50} value represents the compound concentration that reduces by 50\% the activity of FluA virus RNA polymerase in 293T cells. All data shown represent the means ± SD of data derived from at least three independent experiments in duplicate.

Table 3. Activity of Selected Compounds Against a Panel of FluA and FluB Strains.

<table>
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<td>B/Lee/40</td>
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\textsuperscript{a} The EC\textsubscript{50} value represents the compound concentration that inhibits 50\% of plaque formation. All data shown represent the means ± SD of data derived from at least three independent experiments.

Figure legends

**Figure 1.** Small molecules RNA-dependent RNA polymerase PA-PB1 interaction inhibitors. For the definition of IC\textsubscript{50}, EC\textsubscript{50}, and CC\textsubscript{50} values, see Table 1.

**Figure 2.** Pharmacophore model for PA-PB1 inhibitors (A) and alignment of 28 (B) and 31 (C) on it using FLAP. Color code for the pharmacophore points: green = hydrophobic; red = H-bond acceptor; blue = H-bond donor.

**Figure 3.** Alignment of 36 (A) and 37 (B) to the pharmacophore model.
**Figure 4.** FLAP binding poses for compounds 26 (A) and 28 (B). A detail of the interaction of the two compounds with W706 is also reported (C). The GRID hydrophobic regions (green) generated using the FLAP software are displayed, together with some of the PA key residues located in the cavity.

**Figure 5.** FLAP binding poses for compounds 36 (B, D) and 37 (A, C). Two different orientations in the PA cavity are reported for each compound, to better visualize the hypothesized interactions.

**Figure 6.** Effects of compound 36 on PA-PB1 interaction in cells. HEK 293T cells were transfected with plasmids expressing PB1, PB2, and a PA-GFP fusion protein in the absence or the presence of compound 36 or DMSO as a control. Non-transfected cells (None) and cells transfected with the PA-GFP-expressing plasmid alone served as negative controls. At 24 hr post-transfection, cells were examined by confocal laser scanning microscopy. Individual blue (TOTO-3 iodide) and green (GFP) channels are shown, with merged images on the right.

**Scheme Footnotes**

**Scheme 1**

Reagents and conditions: (i) DMF, reflux; (ii) pyridine; (iii) DMF, Ac₂O, reflux; (iv) AcONa, NBS, EtOH, reflux; (v) 12N HCl, EtOH, reflux.

**Scheme 2**

Reagents and conditions: (i) DMF, reflux; (ii) AcONa, NBS, EtOH, reflux; (iii) NaOH, MeOH, reflux; (iv) 1) oxalyl chloride, CH₂Cl₂, DMF; 2) R’NH₂, CH₂Cl₂, DIPEA.
Figure 1.

**HTS**

1. 
   - IC\textsubscript{50} = 35 µM
   - EC\textsubscript{50} = 1 µM
   - CC\textsubscript{50} = 40 µM

**Serendipity**

2. 
   - IC\textsubscript{50} = 20.3 µM
   - EC\textsubscript{50} = 14.5 µM
   - CC\textsubscript{50} > 250 µM

   (benzbramarone)

3. 
   - IC\textsubscript{50} = 25.4 µM
   - EC\textsubscript{50} > 1000 µM
   - CC\textsubscript{50} > 250 µM

   (diclazuril)

**SBDD**

4. 
   - IC\textsubscript{50} = 30.4 µM
   - EC\textsubscript{50} = 12.2 µM
   - CC\textsubscript{50} > 250 µM

5. 
   - IC\textsubscript{50} = 32 µM
   - EC\textsubscript{50} = 18 µM
   - CC\textsubscript{50} > 250 µM

   First Round of Optimization

9. 
   - IC\textsubscript{50} = 7.5 µM
   - EC\textsubscript{50} = 23.7 µM
   - CC\textsubscript{50} > 250 µM

10. 
    - IC\textsubscript{50} = 170.6 µM
    - EC\textsubscript{50} > 100 µM
    - CC\textsubscript{50} > 250 µM
Figure 4.

Figure 5.
Figure 6.
Scheme 1

Scheme 2