

Syntheses of triazole-modified zanamivir analogues via click chemistry and anti-AIV activities

Jian Li,^a Mingyue Zheng,^a Wei Tang,^b Pei-Lan He,^b Weiliang Zhu,^a Tianxian Li,^c Jian-Ping Zuo,^{b,*} Hong Liu^{a,*} and Hualiang Jiang^{a,d,*}

^aDrug Discovery and Design Centre, State Key Laboratory of Drug Research, Shanghai Institute of Materia Medica, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai 201203, China

^bLaboratory of Immunopharmacology, State Key Laboratory of Drug Research, Shanghai Institute of Materia Medica, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai 201203, China

^cWuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China

^dSchool of Pharmacy, East China University of Science and Technology, Shanghai 200237, China

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Abstract—Sixteen novel 4-triazole-modified zanamivir (**1**) analogues were synthesized using the click reactions, and their inhibitory activities against avian influenza virus (AIV, H5N1) were determined. Compound **3b** exerts promising inhibitory activity with EC₅₀ of 6.4 μM, which is very close to that of zanamivir (EC₅₀ = 2.8 μM). Molecular modeling provided the information about the binding model between inhibitors and neuraminidase, which are in good agreement with inhibitory activities.

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Recently, the H5N1 subtype of avian influenza virus (AIV) has been spreading in Southern China, Africa, and European Union mainly imputing to migratory birds.¹ More than 200 human cases of AIV infection mainly as a result of poultry-to-human transmission have been reported with a >50% case fatality rate for H5N1 infections.² A mutant virus capable of efficient human-to-human transmission could trigger another influenza pandemic.^{2,3} Whereas H5N1 vaccines have been significantly hampered by the high mutability of the virus.⁴ Accordingly, discovering effective drugs, which are not susceptible to mutation, is an urgent need.

There are currently only a few drugs available for AIV treatment. The licensed existing drugs are the zanamivir⁵ (**1**) and oseltamivir phosphate⁶ (**2**) (Fig. 1) as specific neuraminidase (NA) inhibitors. However, these drugs are not effectively used owing to the rapid emergence of resistant virus during treatment. Many groups have designed and synthesized some zanamivir analogues

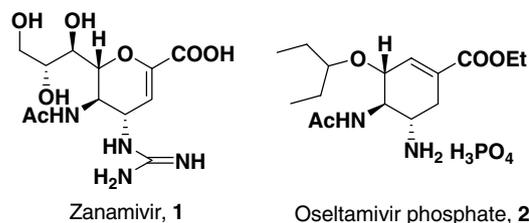


Figure 1. The structures of zanamivir (**1**) and oseltamivir phosphate (**2**).

aimed at developing more potent, long-lasting therapeutic drugs for anti-AIV infection.⁷ For example, Woodhall et al.⁸ have synthesized a series of zanamivir mimetics based on sialic acid aldolase.

Click chemistry, coined by Barry K. Sharpless,⁹ is experiencing a growing popularity.¹⁰ The process of click chemistry is modular, wide in scope, high yielding, and requires only simple reaction and purification conditions. Such kind of chemistry is possible to generate a plethora of new compounds reliably and thereby has been applied in lead discovery and optimization. The Huisgen 1,3-dipolar cycloaddition of azides and alkynes¹¹ is regarded as the ‘cream of the crop’ of concerted

Keywords: Zanamivir analogues; Avian influenza virus; Click chemistry; Molecular modeling.

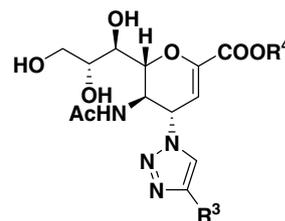
* Corresponding authors. Tel.: +86 21 50806600x1210; fax: +86 21 50807088; e-mail addresses: jpzuo@mail.shnc.ac.cn; hliu@mail.shnc.ac.cn; hljiang@mail.shnc.ac.cn

reactions, therefore it has been a general and standard reaction of click chemistry.^{9,10}

Compound **9**, a key intermediate for synthesizing zanamivir (Scheme 1), contains an azide group. Accordingly, this compound is a good starting material to synthesize zanamivir analogues by using click reactions. Thus, we designed and synthesized a series of zanamivir analogues (**3a–p**) with different substituted triazoles and tested their preliminary anti-AIV activities. This reaction produces a unique substituted position for R³. To increase the structural diversity of the analogues, we selected R³ with different size. Scheme 1 depicts the sequence of reactions that led to the preparation of compounds **3a–p** using *N*-acetylneuraminic acid (NANA, **4**) as the starting material. Meanwhile, taking compounds **3b** and **3i** as examples, the interaction models between inhibitors and neuraminidase were studied.

As shown in Scheme 1, compound **4** was esterified with methanol in the presence of an acidic ion exchange resin.¹² Oxazoline **7** was prepared using a modification of the procedure described by Chandler et al.¹³ Compound **6** was obtained using acetic anhydride in pyridine with 4-(dimethylamino)pyridine (DMAP) catalysis, then was treated with trimethylsilyl trifluoromethanesulfonate (TMSOTf) in ethyl acetate at 52 °C to give **7** in high yield. Compound **7** was hydrolyzed without purification. Reacted with diphenylphosphoryl azide (DPPA) and 1,8-diazabicyclo[5,4,0]undecen-7-ene (DBU), the alcohol **8** was converted to the inverted azide **9**, the key intermediate, applying Scheigetz methods.¹⁴ Compound **10** was obtained by a click reaction between azide **9** and

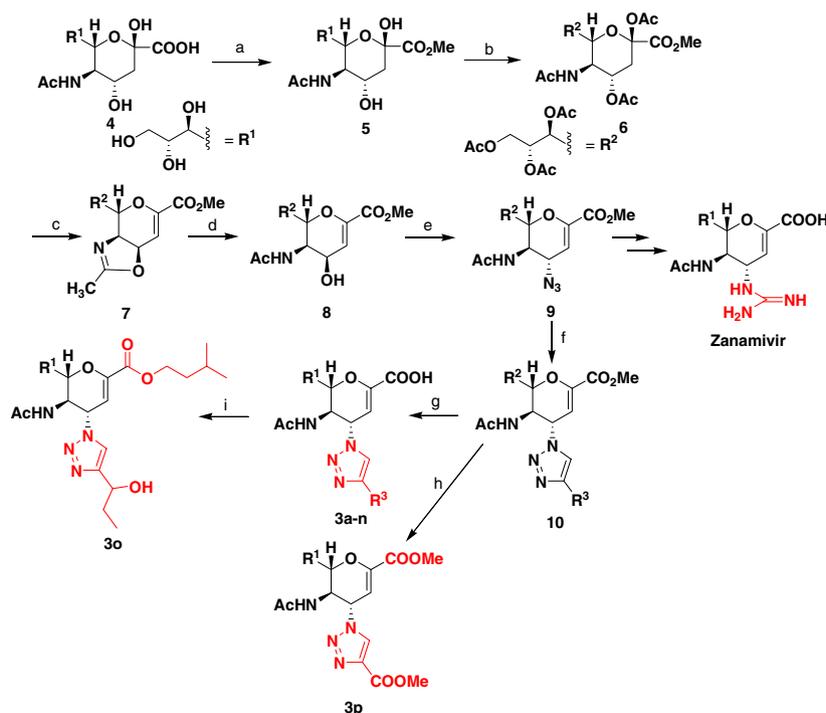
Table 1. Chemical Structures of Compounds **3a–p** and their anti-AIV activities



Compound	R ³	R ⁴	Protective rate ^a at 50 μM
3a	C ₆ H ₅	H	18.7
3b	CH(OH)C ₂ H ₅	H	> 61.4
3c	Cyclopropyl	H	8.9
3d	CH ₂ CH ₂ OH	H	14.5
3e	(CH ₂) ₃ OH	H	6.3
3f	Pyridin-2-yl	H	NA ^b
3g	C ₆ H ₄ -4-F	H	NA ^b
3h	C ₆ H ₄ -4-C ₂ H ₅	H	34.4
3i	C ₆ H ₄ -4-OC ₃ H ₇	H	40.2
3j	C ₆ H ₄ -4-C ₃ H ₇	H	22.1
3k	C ₆ H ₄ -4-C ₆ H ₅	H	19.1
3l	CH ₂ OC ₆ H ₅	H	34.8
3m	CH ₂ N(C ₂ H ₄) ₂ O	H	17.3
3n	CH ₂ NH ₂	H	NA ^b
3o	CH(OH)C ₂ H ₅	(CH ₂) ₂ CH(CH ₃) ₂	8.9
3p	COOCH ₃	CH ₃	9.9

^a Antiviral efficacy of test compounds was assessed in vitro by Neutral Red (NR) uptake assay and expressed as percent protective rate against virus infection.¹⁵ Data are means of three independent experiments. The protective rate for zanamivir at 50 μM is 86.1%.

^b No activity at 50 μM.



Scheme 1. Reagents and conditions: (a) H⁺ Resin, CH₃OH, 25 °C (91%); (b) Ac₂O, pyridine, DMAP (85%); (c) TMSOTf, EtOAc, N₂ (84%); (d) AcOH, EtOAc, H₂O (42%); (e) DPPA, DBU, benzene (85%); (f) R³C≡CH, sodium ascorbate, CuSO₄, C₂H₅OH/H₂O = 1:1, 25 °C (60–80%); (g) (1) NaOH, CH₃OH, 25 °C, (2) H⁺ Resin (95%); (h) (1) NaOCH₃, CH₃OH, 25 °C, (2) H⁺ Resin (90%); (i) 3-methyl-1-butanol, H⁺ Resin, THF (50%).

alkyne in 60–80% yield, and then hydrolyzed with NaOH/methanol and NaOCH₃/methanol to give **3a–n** and **3p**, respectively. **3o** was synthesized by the corresponding acid reacting with 3-methyl-1-butanol in the presence of an acidic ion exchange resin.

Protective rates¹⁵ of compounds **3a–p** against infected cell (MDCK cell) at 50 μM are summarized in Table 1. EC₅₀ values (the concentration of a compound in the media which reduced virus-infected cell numbers by 50% of the untreated control value) of compound **3b** and zanamivir (**1**) were determined as 6.4 and 2.8 μM, respectively. Although general structure–activity relationship of those compounds is not evident, the bioassay results still provide some information for further structural modification. Replacement of carboxylic acid group with esters cannot be tolerated (compounds **3b** and **3o**), leading to a remarkable loss of activity.

Comparing compound **3a** with compounds **3g–k**, the substitutions on the phenyl ring substantially play an important role in the potency activity of compounds. Generally, alkyl (**3h** and **3j**) and alkoxy (**3i**) substituents are favorable to the activities of these compounds, however, introductions of large aromatic (**3k**) or halogen (**3g**) substituents are improper. Among non-aromatic substituents of R³, propyl alcohol of **3b** is favorable to increase activity.

To better understand the activity discrepancy of compounds **3a–h** with zanamivir, we compare the 3D binding models of zanamivir¹⁶ to NA (Fig. 2A) obtained from the crystal structure with that of inhibitors **3b** and **3i** to NA derived from docking simulation. Molecular docking was performed by using the AutoDock3.05 program.¹⁷ The crystal structure of a wild-type NA in complex with zanamivir was retrieved from Protein

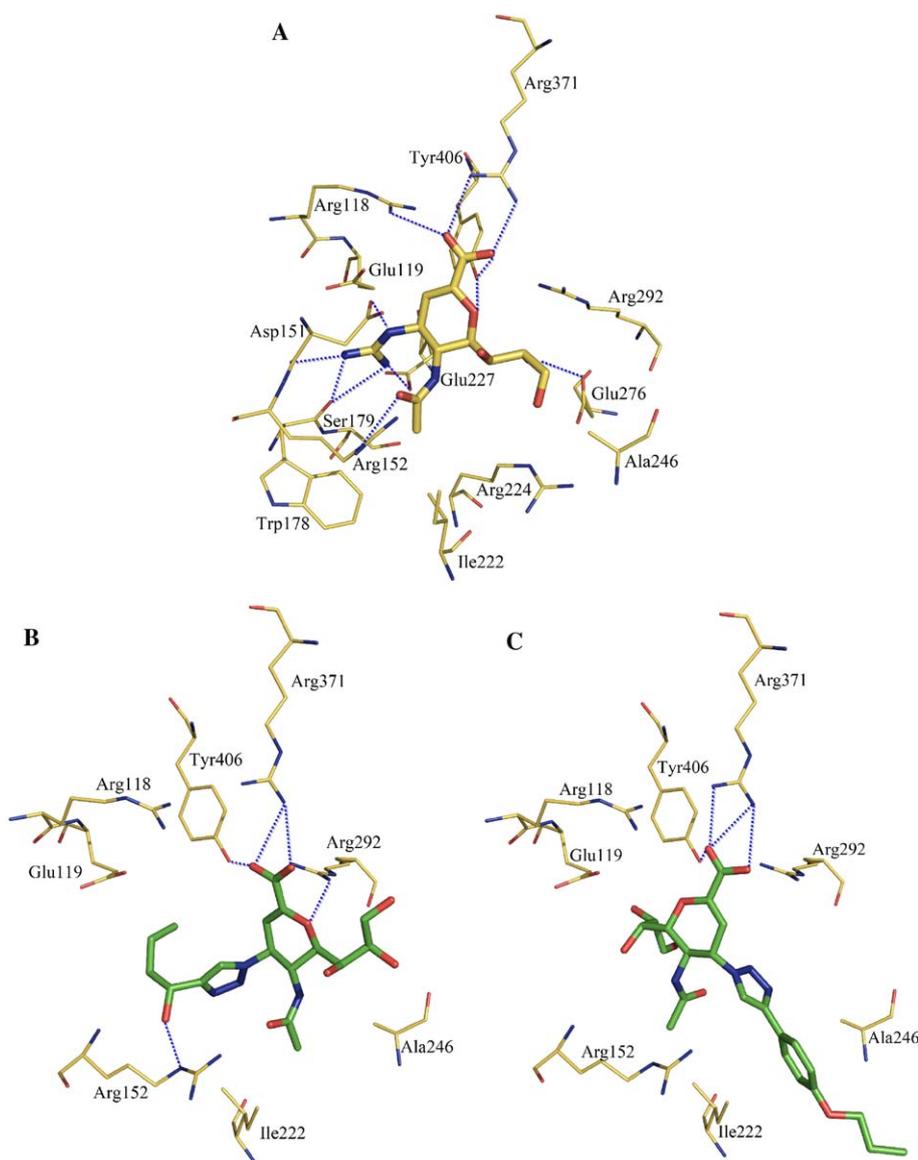


Figure 2. Detailed interactions of zanamivir (A), **3b** (B), and **3i** (C) to the binding sites of NA. Hydrogen-bonds are represented by blue dotted lines; Docking models of **3b** (D) and **3i** (E) overlaid with the binding conformation of zanamivir (**1**) into the active sites of NA. The NA surface was colored by electrostatic potential. These images were generated using the PyMol program (<http://www.pymol.org/>). Compounds **3b**, **3i**, and zanamivir (**1**) are indicated by green, green, and yellow thick sticks, respectively.

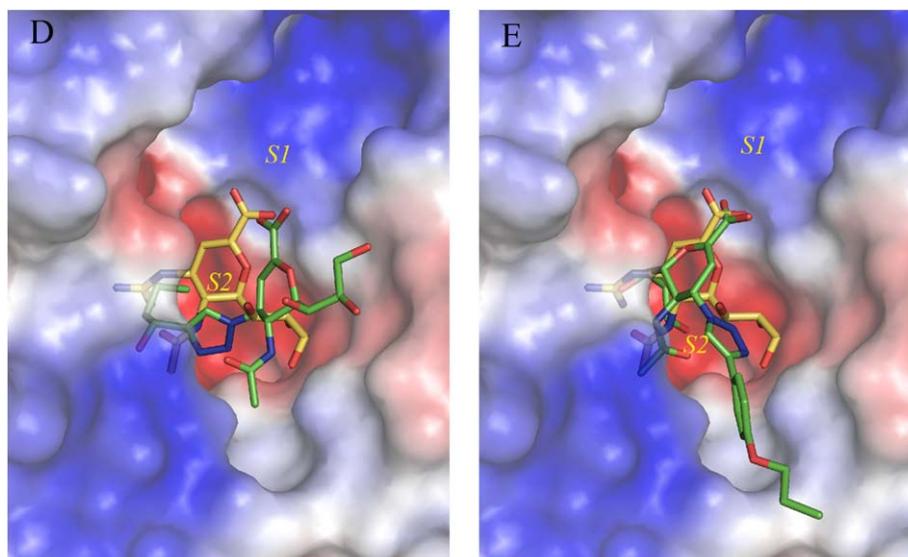


Figure 2. (continued)

Data Bank (PDB entry 1NNC).¹⁶ During the docking simulation, the protonation states of the residues of NA at pH 7.0 were used, and the docking parameters in our previous study¹⁸ were adopted. For each inhibitor, conformation with the lowest predicted binding free energy to NA was selected for further analysis. Figures 2B–E show the binding models of compounds **3b** and **3i** with NA.

The binding site of NA has been characterized as highly polar by virtue of the 10 charged (Arg 118, 152, 224, 292, 371, Glu 119, 227, 276, 277, and Asp 151) and only four hydrophobic (Trp 178, Ile 222, Ala 246, and Tyr 406) constitutional amino acids.¹⁹ Figure 2A indicates that the carboxylic acid of zanamivir (**1**) forms strong hydrogen-bonds with two arginine residues (Arg118 and Arg371) in the S1 region (Fig. 2D). Around the guanidinyll moiety of zanamivir, there is a specially restricted region (S2, Fig. 2D) with negatively charged electrostatic environment caused by three acidic residues, Glu119, Asp151, and Glu227 (Fig. 2A). Actually, two different orientations of R³ group are observed when the guanidinyll is replaced by a bulky and less polar triazole ring, which more or less decreased the interaction between inhibitors and NA, and hence resulted in a drop of inhibitory activity. In Figures 2B and D, the binding conformation of compound **3b**, which has a smaller propyl alcohol group at R³ moiety, moves up and only forms a hydrogen-bond with residue Arg152 in the S2 region (guanidinyll moiety of zanamivir forms five hydrogen-bonds in S2 region, Fig. 2A). The R³ of **3i** is too large to be accommodated in the subsite S2, and hence the six-membered ring flips over and takes a reversed orientation of zanamivir (Figs. 2C and E). Accordingly, being devoid of hydrogen-bond interaction with S2 (Fig. 2C), this series of compounds are generally less potent than **3b** and zanamivir. This alternative binding model (Fig. 2E) can also be seen in the X-ray crystal structures of the complexes of NA with some inhibitors discovered by Stoll et al.²⁰

In summary, 16 novel 4-triazole-modified zanamivir analogues were designed and synthesized by using the click reactions. Some compounds exert moderate inhibition against AIV (H5N1), compound **3b** is almost as active as zanamivir (**1**). Molecular modeling result provides the information about the binding model between inhibitors and neuraminidase, and is helpful for future inhibitors' design.

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