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P₂ pyridine N-oxide thrombin inhibitors: a novel peptidomimetic scaffold

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Abstract—In this study, we have demonstrated that the critical hydrogen bonding motif of the established 3-aminopyrazinone thrombin inhibitors can be effectively mimicked by a 2-aminopyridine N-oxide. As this peptidomimetic core is more resistant toward oxidative metabolism, it also overcomes the metabolic liability associated with the pyrazinones. An optimization study of the P₁ benzylamide delivered the potent thrombin inhibitor **21** ($K_i = 3.2 \text{ nM}$, 2xaPTT = 360 nM), which exhibited good plasma levels and half-life after oral dosing in the dog ($C_{\text{max}} = 2.6 \,\mu\text{M}$, $t_{1/2} = 4.5 \,\text{h}$). © 2005 Elsevier Ltd. All rights reserved.

Thrombosis-related disorders such as deep vein thrombosis, pulmonary embolism, and thromboembolic stroke remain a major cause of morbidity worldwide.¹ The limitations associated with current therapies² have driven the search for small-molecule direct inhibitors of specific enzymes involved in the coagulation cascade.³ In this regard, inhibitors of both thrombin and factor Xa have attracted considerable recent attention.⁴ In our laboratories, the search for potent and orally bioavailable direct thrombin inhibitors has led to the evaluation of pyrazinone based small molecule peptidomimetics (**1**, Fig. 1).⁵ Detailed metabolic studies indicated a significant degree of oxidative metabolism around the pyrazinone core.⁶ As a result, we sought to

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Figure 1. From pyrazinone to pyridine N-oxide.

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identify alternative P_2 peptidomimetic cores that would retain the classical H-bond network with glycine-216 of the enzyme (Fig. 1); one such alternative envisioned was a pyridine N-oxide scaffold.⁷

Preparation of pyridine N-oxide derivative 2, the direct analog of pyrazinone 1, afforded a 6 nM thrombin inhibitor and provided support for this strategy. A cyano group at the 5-position provided a further potency enhancement (Fig. 1, 3). As anticipated, the corresponding neutral pyridine derivatives are significantly less potent against thrombin than their parent compounds (pyridine of 2: $K_i = 620$ nM; pyridine of 3: $K_i = 103$ nM; structures not shown), consistent with the N-oxide oxygen serving as an H-bond acceptor. Additionally, X-ray crystallographic analysis of a related inhibitor 4 bound in the active site of thrombin (Fig. 2, PDB Code: 1Z71) clearly demonstrates the H-bond network with glycine-216.

An initial study focused on incorporating the optimized P_1 groups recently discovered in our laboratories into the P_2 pyridine N-oxide template (Table 1).⁸ Compounds were evaluated for their thrombin inhibitory potency and their functional ability to double the activated partial thromboplastin time (2xaPTT) in human plasma.⁹ The unsubstituted P_1 benzyl amide **5** ($K_i = 150$ nM) functions as the benchmark compound. Installation of the N-linked triazole at the *ortho*-position of the P_1 benzyl or pyridyl group^{8a} yields inhibitors (**6–8**) with both good intrinsic and functional potency. Introduction of a 2-aminomethyl substituent^{8b} also results in a significant potency improvement, as illustrated by compounds **9** and **10**. Incorporation of a meta-chloro substituent affords a significant improvement in intrinsic potency





Figure 2. X-ray crystal structure of 4 bound in the thrombin active site.



	IN	F F H O	Ĥ						
Compd	Х	P ₁	$\frac{K_{i}}{(nM)^{a}}$	2xaPTT (µM)					
5	CN	"N	150	_					
6	Cl	N N N N	2.60	0.46					
7 8	Cl CN		2.50 0.23	0.40 0.15					
9 10	Cl CN	NH2	0.40 <0.01	0.13 0.09					
11 12	Cl CN	Survey CI	0.42 0.08	0.73 0.20					
13 14	Cl H		0.05 1.50	0.23 0.43					
15 16	H CN	N-N NN N CI	0.14 0.002	0.20 0.10					
17 18 19	Cl CN H	NH2	<0.01 0.001 0.04	0.15 0.07 0.10					

 ${}^{a}K_{i}$ values are the average of at least two determinations, standard error of the mean <10%.

(e.g., **12** vs **5**), but, as noted in earlier studies, the concomitant increase in lipophilicity is detrimental to functional activity.¹⁰ The combination of the *ortho*-azole and the *meta*-chloro substituents affords exquisitely potent thrombin inhibitors (**13–16**); for example, compound **16** displays a 2 pM K_i against thrombin, with a 2xaPTT of 100 nM. Similarly, the potency-enhancing aminomethyl and chlorine substituents can be merged

in an additive fashion to yield extremely potent thrombin inhibitors (17–19). The most potent compound produced from this study is 18 ($K_i = 1 \text{ pM}$), displaying a 2xaPTT of 70 nM.

Having completed an investigation of the P₁ SAR, we turned our attention to the evaluation of the pharmacokinetic profile of members of this series (Table 2). Upon oral dosing of aminomethyl derivative 9 (0.65 mpk) to dogs, a 0.82 μ M maximum plasma concentration (C_{max}) and a 1.5 h plasma half-life ($t_{1/2}$) were achieved. The *meta*-chloro analog 17 similarly displayed a promising pharmacokinetic profile ($C_{max} = 0.70 \ \mu$ M, $t_{1/2} = 1.3$ h). As the tri- and tetrazole analogs (13–16) had inferior pharmacokinetic profiles, our efforts focused on the optimization of the P₁ aminomethyl series.

Metabolism studies involving human and dog microsomal incubations revealed that the desired objective of minimizing the extent of P2 metabolism had been achieved; however, P_1 benzylic site oxidation and subsequent N-dealkylation now arose as the primary metabolic pathway. In an attempt to attenuate this metabolism, a study to substitute the benzylic sites was initiated (Table 2). Methylation of the benzylic position alpha to the P_1 amide group (Table 2, Y = Me) and resolution gave access to inhibitors 20 and 21. The more active enantiomer 21 displays an 8-fold loss in binding potency (vs 9) yet maintains good anticoagulant activity ($K_i = 3.2 \text{ nM}$, 2xaPTT = 360 nM); notably, this modification resulted in a significant improvement in the pharmacokinetic profile (21, $C_{\text{max}} = 2.6 \,\mu\text{M}$, $t_{1/2}$ = 4.5 h). Methylation at the other benzylic site was also tolerated, but did not lead to improved dog pharmacokinetics (22-23). Inspection of the X-ray crystal structure of the related inhibitor 4 bound in the active site of thrombin (Fig. 2) suggested that strategic placement of a hydrogen bonding group at the P_1 benzylic position could potentially gain access to an additional interaction with residues contained within the active site (e.g., Ser-195). This analysis is supported by the 5-fold

potency increase (vs 21) attained with the hydroxymethyl analog 24.

The high levels of potency demonstrated by the *ortho*aminomethyl and tetrazole analogs (Table 1, **15–19**) offered the possibility that significant truncation of these molecules could still deliver potent thrombin inhibitors. Accordingly, complete excision of the P₃ binding element afforded inhibitors in the low to mid nanomolar range (Table 3, **25–28**); most notable is compound **28** with a $K_i = 10$ nM and a 2xaPTT = 560 nM (MW = 346). Unfortunately, removal of the P₃ group afforded no significant advantage regarding pharmacokinetic profile.

The synthesis of these P₂ pyridine N-oxide inhibitors is outlined in Scheme 1.¹¹ Protection of 2-amino-6-methyl-



 $^{a}K_{i}$ values are the average of at least two determinations, standard error of the mean <10%.

Compd	Y	Z	$K_{\rm i} ({\rm nM})^{\rm a}$	2xaPTT (μM)	C _{max} (µM)	$t_{1/2}$ (h)		
9	Н	Н	0.40	0.13	0.82^{d}	1.5		
20	Me ^b	Н	260	_	_	_		
21	Me ^b	Н	3.2	0.36	2.6 ^e	4.5		
22	Н	Me ^b	20	5.9		_		
23	Н	Me ^b	0.45	0.27	0.1^{f}	2.0		
24	CH ₂ OH ^c	Н	0.48	0.23	0.34 ^g	1.5		

Table 2. P_1 benzylic substitution

^a K_i values are the average of at least two determinations, standard error of the mean <10%.

^b 20/21 and 22/23 are enantiomeric pairs.

^cSingle enantiomer, absolute configuration not established.

^d po dose = 0.65 mpk.

^e po dose = 0.95 mpk.

^f po dose = 0.7 mpk.

^g po dose = 0.85 mpk.



Scheme 1. Reagents and conditions: (a) Boc_2O ; (b) NCS, DCE; (c) LDA, diethyl carbonate, THF; (d) NaH, DMF, 32;⁵ (e) 1 N LiOH, THF; (f) P₁-NH₂, EDC, HOAt, DMF; (g) TFA, DCM; (h) mCPBA, DCE.

pyridine with di-tert-butyl dicarbonate, followed by regioselective chlorination affords **30**. The pyridylacetate **31** is produced via benzylic metalation of **30** with LDA and subsequent quenching with diethyl carbonate. Alkylation of **31** with the P₃ 2,2-difluoro-2-(2-pyr-idyl)ethyl-trifluoromethanesulfonate **32**⁵ completes the assembly of the key P₃–P₂ subunit **33**. Ester hydrolysis and P₁ amide coupling are followed by deprotection and then pyridine oxidation¹² with mCPBA to afford the final products **34**. The cyano pyridines are prepared via an analogous route starting from 2-amino-5-cyano-6-methylpyridine.

The des- P_3 analogs can be assembled in a similar manner from key intermediate **31**. Base hydrolysis is followed by EDC mediated amide formation. Amine deprotection and final pyridine N-oxidation deliver the des- P_3 thrombin inhibitors.

In conclusion, we have demonstrated that the critical hydrogen bonding motif of the established 3-aminopyrazinone thrombin inhibitors can be effectively mimicked by a 2-aminopyridine N-oxide. As this peptidomimetic core is more resistant toward oxidative metabolism, it also overcomes the metabolic liability associated with the pyrazinones. An optimization study of the P₁ benzyl-amide delivered the potent thrombin inhibitor, **21** which exhibited good plasma levels and half-life after oral dosing in the dog. Studies to explore the generality of 2-aminopyridine N-oxides as peptidomimetics are underway.

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