



The 7th International Electronic Conference on Medicinal Chemistry (ECMC 2021)

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Cyclic and pseudocyclic thrombin binding aptamer analogues as improved anticoagulant agents

C. Riccardi^{1,*}, A. Meyer², J.J. Vasseur², I. Russo Krauss¹, L. Paduano¹, F. Morvan²,
D. Montesarchio¹

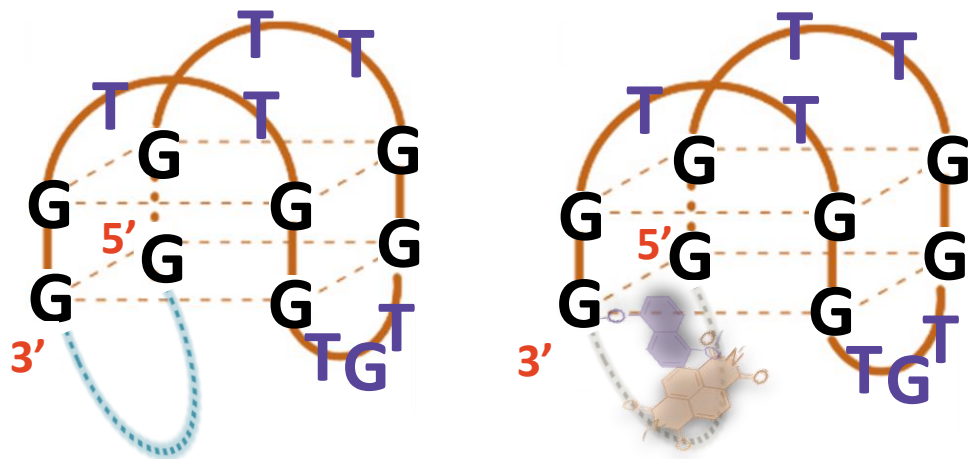
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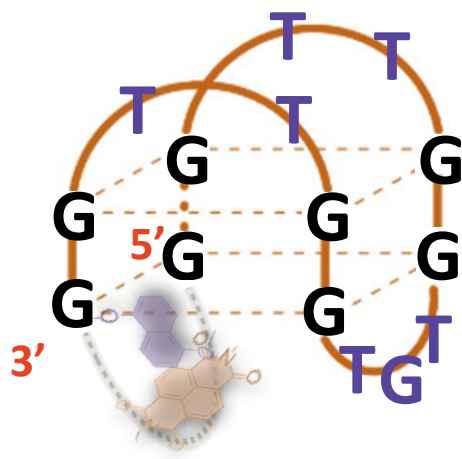
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Cyclic and pseudocyclic thrombin binding aptamer analogues as improved anticoagulant agents



Cyclic TBA analogues realized via *covalent* connection of the oligonucleotide ends with flexible linkers



End-modified TBA analogues stabilized by π/π or *charge-transfer interactions* providing a pseudocyclic structure

Improved anticoagulant activity

Higher G4 thermal stability

Enhanced nuclease resistance

vs. unmodified TBA



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Abstract:

The Thrombin Binding Aptamer or TBA (5'-GGTTGGTGTGGTTGG-3') is a 15-mer G-rich oligonucleotide able to **inhibit the thrombin-catalysed fibrinogen-fibrin conversion** after specific binding to its exosite I. TBA entered clinical trials but its evaluation was halted after phase I studies due to suboptimal dosing profiles. Aiming at obtaining TBA analogues better performing in vivo, a large number of chemically modified TBA variants have been proposed.

In this frame, **we prepared a series of cyclic TBA analogues** by linking its 5' and 3'-ends with a variety of flexible linkers. The first derivative was realized introducing a 20-atom long linker. Compared to native TBA, it exhibited a G-quadruplex (**G4**) **structure with exceptionally improved stability and nuclease resistance**. However, these favourable properties were associated with reduced biological activity, suggesting that higher flexibility in the linker structure was necessary. Therefore, a mini-library of second generation cyclic TBAs (cycTBA I-IV) was prepared, carrying circularizing linkers overall spanning from 22 to 48 atoms. Among these derivatives, cycTBA II showed **improved anticoagulant activity**, associated with a dramatically stabilized G4 structure and enhanced enzymatic resistance in serum compared to the native TBA. Current studies are focused on **pseudocyclic TBA analogues**, where the cyclic structure is obtained not through covalent bonds but via π - π stacking or charge-transfer interactions of different aromatic probes inserted at the termini of the oligonucleotide. Among ten different TBA derivatives, we identified a promising candidate in this pseudocyclic series showing improved anticoagulant activity compared to native TBA, also having higher nuclease resistance and G4 thermal stability.

Keywords: anticoagulant activity; biophysical characterization; G-quadruplex; thrombin; thrombin binding aptamer.



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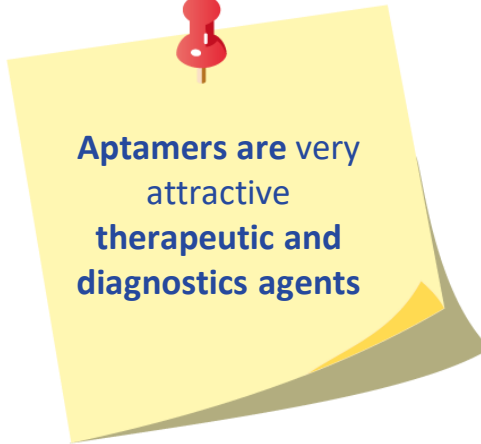
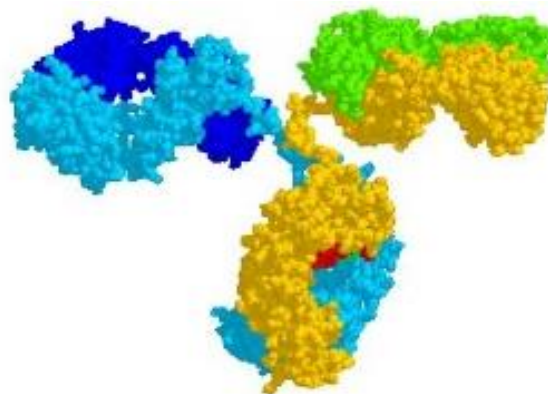
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- ❖ Short synthetic DNA or RNA sequences able to recognize with **high affinity and specificity** a wide range of molecular targets;
- ❖ Generally identified from combinatorial libraries by an in vitro selection procedure called **SELEX** (*Systematic Evolution of Ligands by EXponential enrichment*);
- ❖ Many aptamers are G-rich sequences and fold in **G-quadruplex (G4)** architectures.

Aptamers: promising alternatives to antibodies



VS



Aptamers are very attractive therapeutic and diagnostics agents

- ✓ **Smaller size**
- ✓ **Lower immunogenicity**
- ✓ **Stability in a wide range of pH and temperature**
- ✓ **Easy modification to increase their stability and affinity**

For recent reviews on aptamers, see for example:

Platella, C., **Riccardi**, C., Montesarchio, D., Roviello, G.N., Musumeci, D. *Biochim. Biophys. Acta - Gen. Subj.*, **2017**, 1861, 1429–1447;

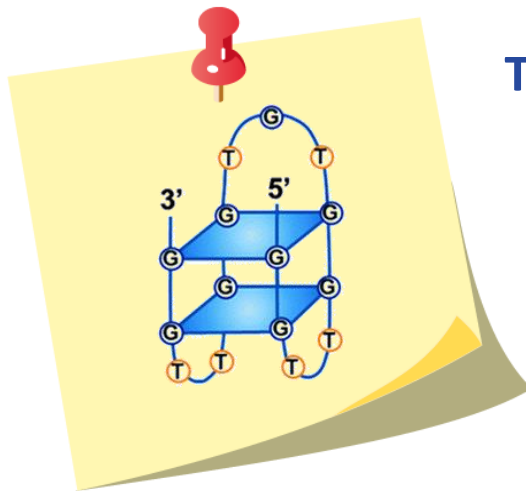
Musumeci, D., Platella, C., **Riccardi**, C., Moccia, F., Montesarchio, D. *Cancers*, **2017**, 9, 174-217.



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The Thrombin Binding Aptamer



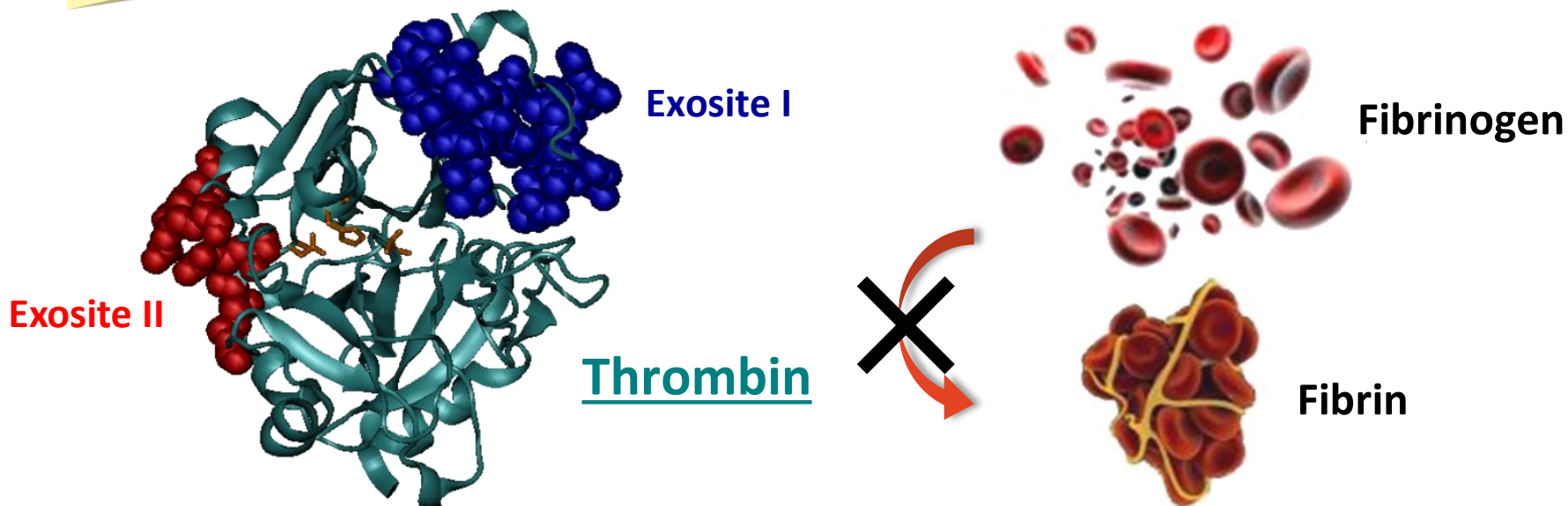
Thrombin binding aptamer or TBA₁₅ d(5'GGTTGGTGTGGTTGG3')

✓ Identified by SELEX against Thrombin in 1992

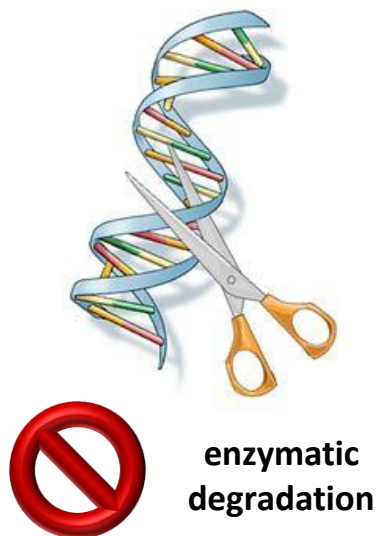
Bock L.C., et al. *Nature*, 1992, 355, 564–566.

✓ Structure solved in 1993

Macaya R.F., et al. *PNAS*, 1993, 90, 3745-3749.



The general approaches so far exploited to overcome the disadvantages of aptamers, in general, and of TBA, in particular, were based on:



modifications

on the nucleobase

on the sugar

on the phosphodiester linkages

conjugations

with PEG

with lipids

with nanoparticles

For recent reviews on chemically modified TBA analogues, see for example:

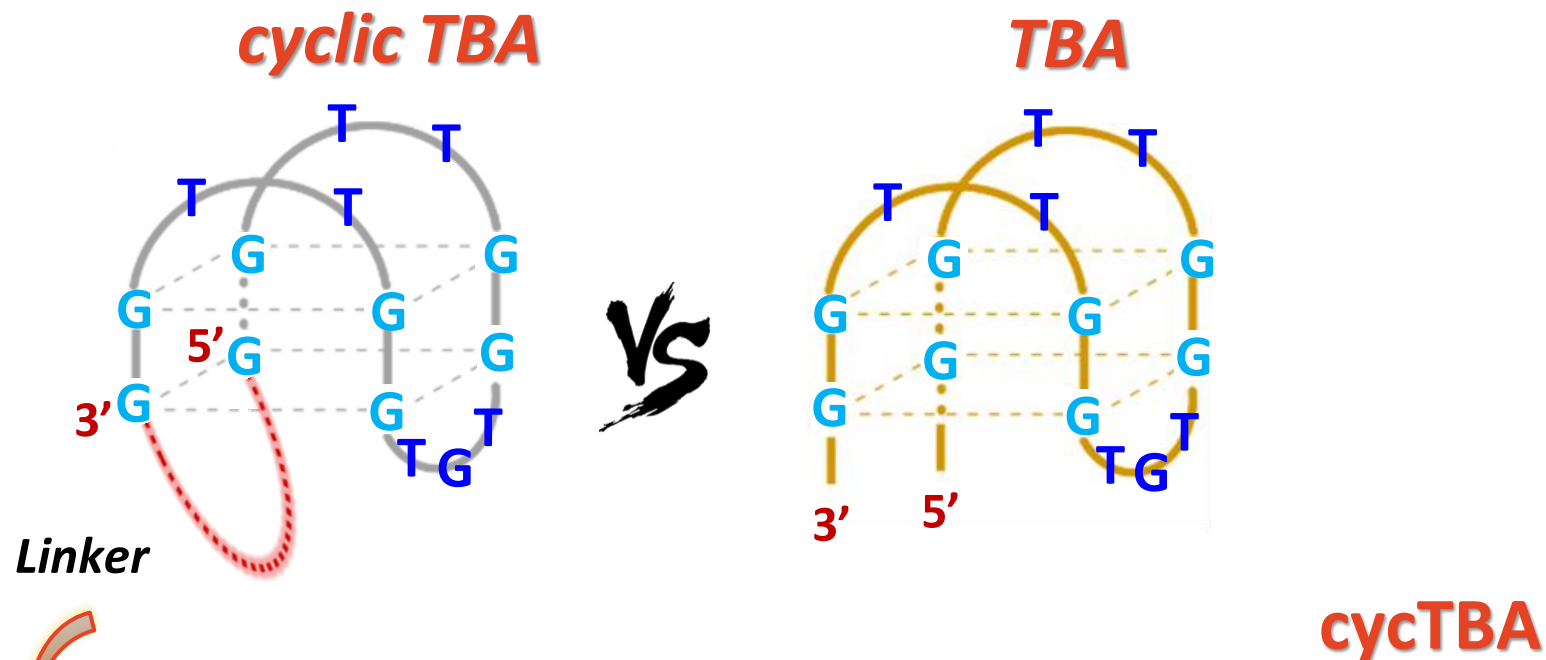
Riccardi C., et al. *Pharmacol Ther.*, **2021**, 217, 107649;

Musumeci D., Montesarchio D. *Pharmacol Ther.*, **2012**, 136, 202-215.

For a recent article on nanoparticle decoration, see for example:

Riccardi C., et al. *ACS Appl. Mater. Interfaces*, **2017**, 9, 35574–35587.





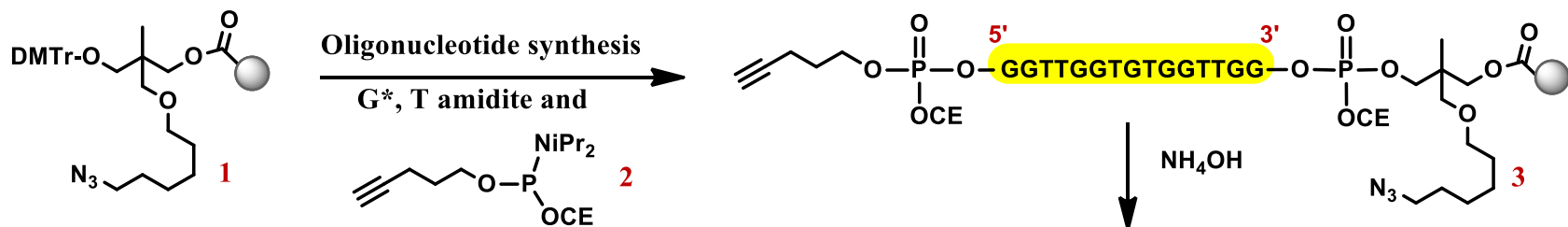
✓ **Two major benefits are expected upon TBA cyclization:**

- ✓ the absence of the 3' and 5' termini should protect the oligonucleotide from nuclease degradation
- ✓ the cyclization should impose a **structural pre-organization** favouring the G4 formation

20 atoms

Riccardi C., et al. *ChemBioChem*. 2019, 20(14), 1789-1794. doi: 10.1002/cbic.201900045.



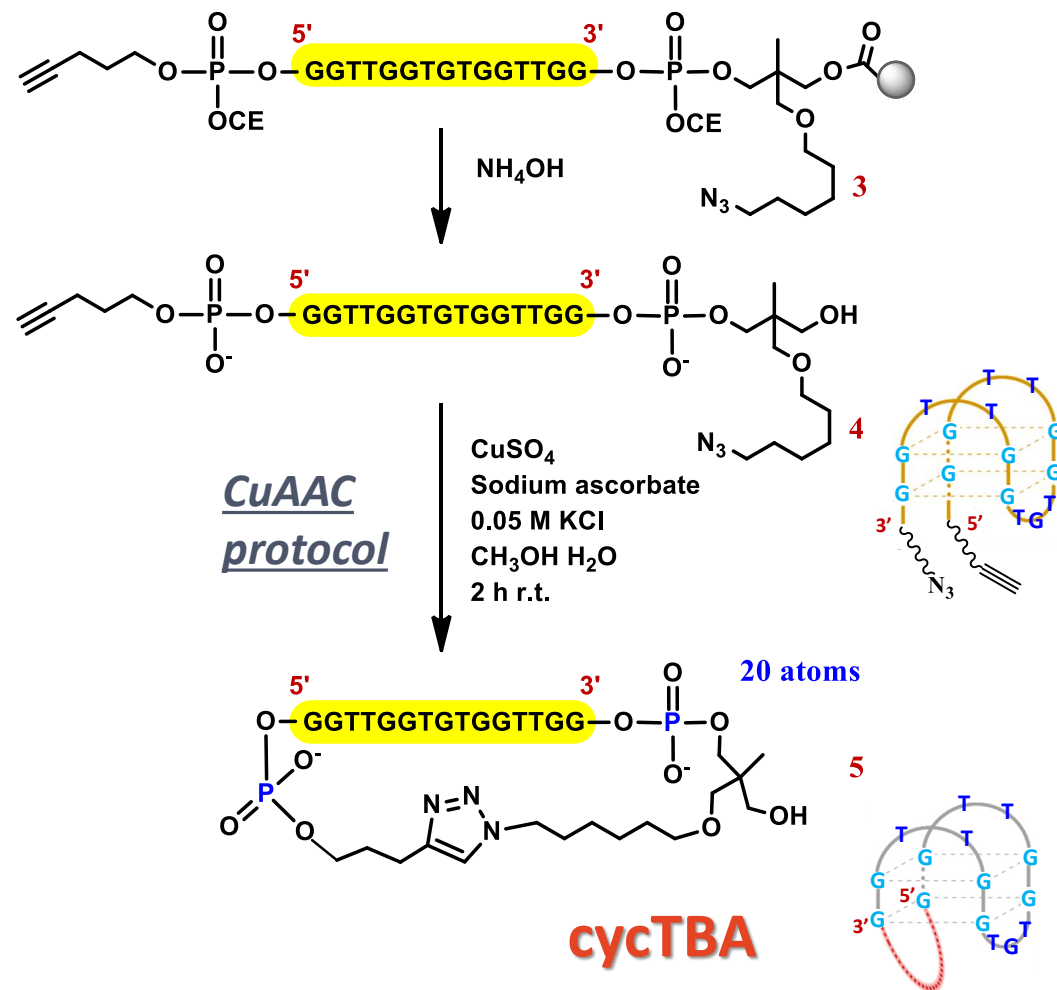


● = CPG solid support

DMTr = 4,4'-dimethoxytriphenylmethyl

G* = N²-isobutyroyl deoxyguanosine

CE = 2-cyanoethyl



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Jean-Jacques
Vasseur

François
Morvan

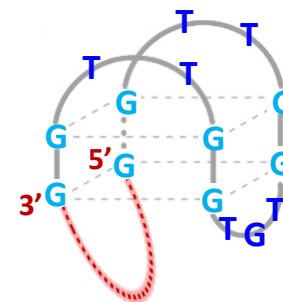
Albert
Meyer

Riccardi C., et al. *ChemBioChem*. 2019, 20(14), 1789-1794. doi: 10.1002/cbic.201900045.

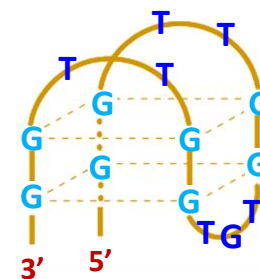


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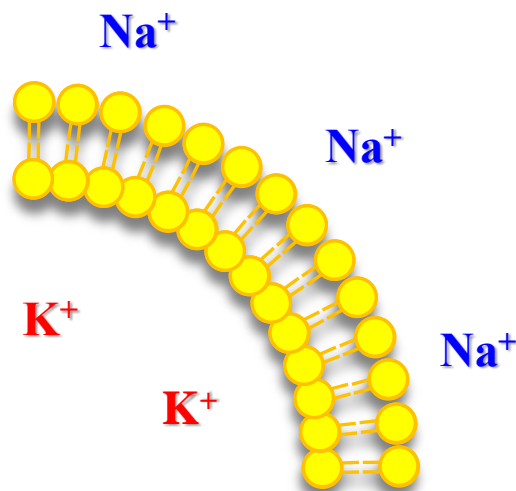


cycTBA



unmodified TBA

Anticoagulant activity vs. thrombin determined by Dynamic Light Scattering (DLS) analysis

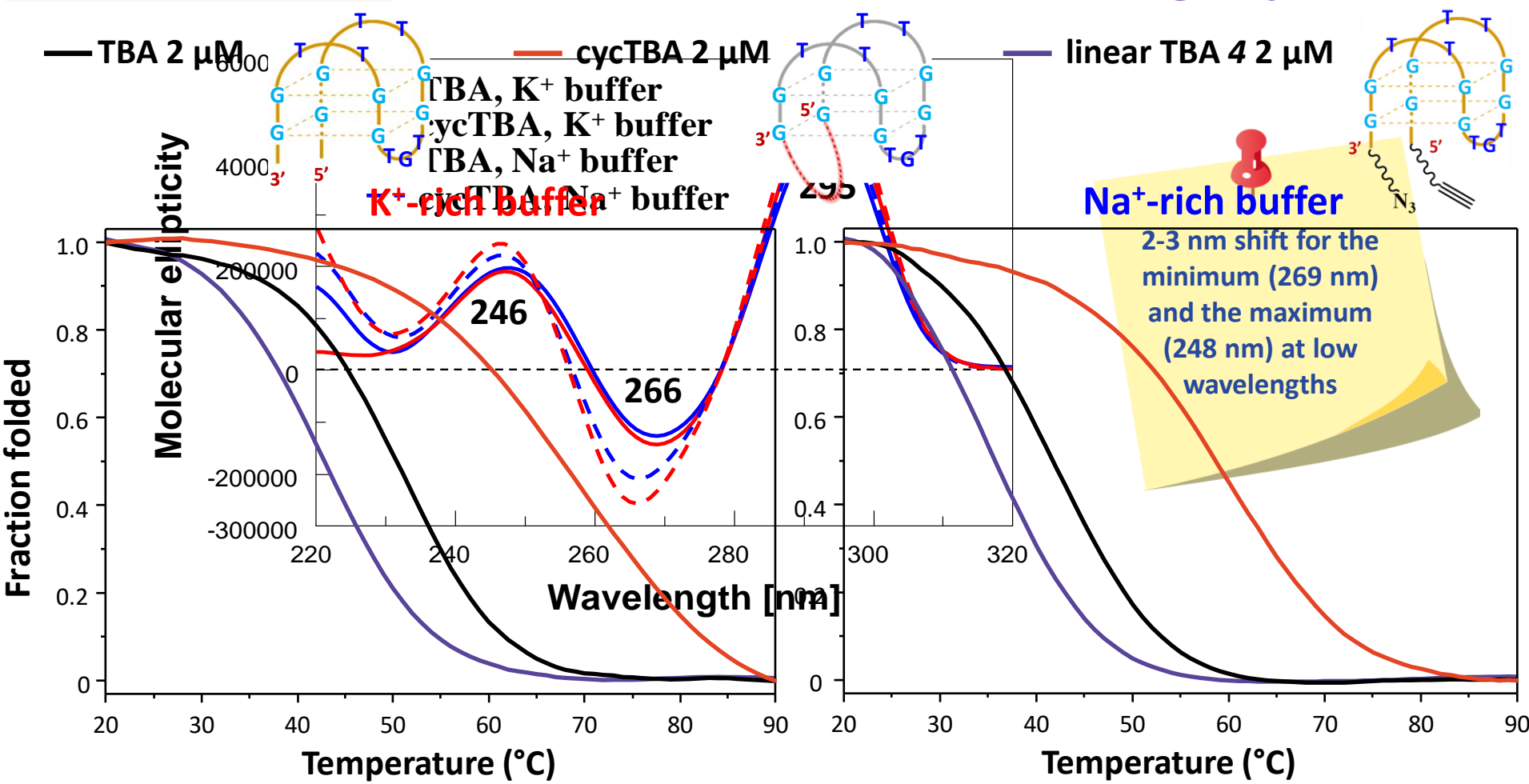


K⁺ buffer: 10 mM KH₂PO₄/K₂HPO₄, 70 mM KCl, 0.2 mM EDTA, pH = 7.0

Na⁺ buffer *i.e.* **PBS:** 137 mM NaCl, 2.7 mM KCl, 10 mM Na₂HPO₄, 1.8 mM KH₂PO₄, pH = 7.2

Riccardi C., et al. *ChemBioChem.* **2019**, 20(14), 1789-1794. doi: 10.1002/cbic.201900045.





T_m values (°C): 69 Vs 51 Vs 42

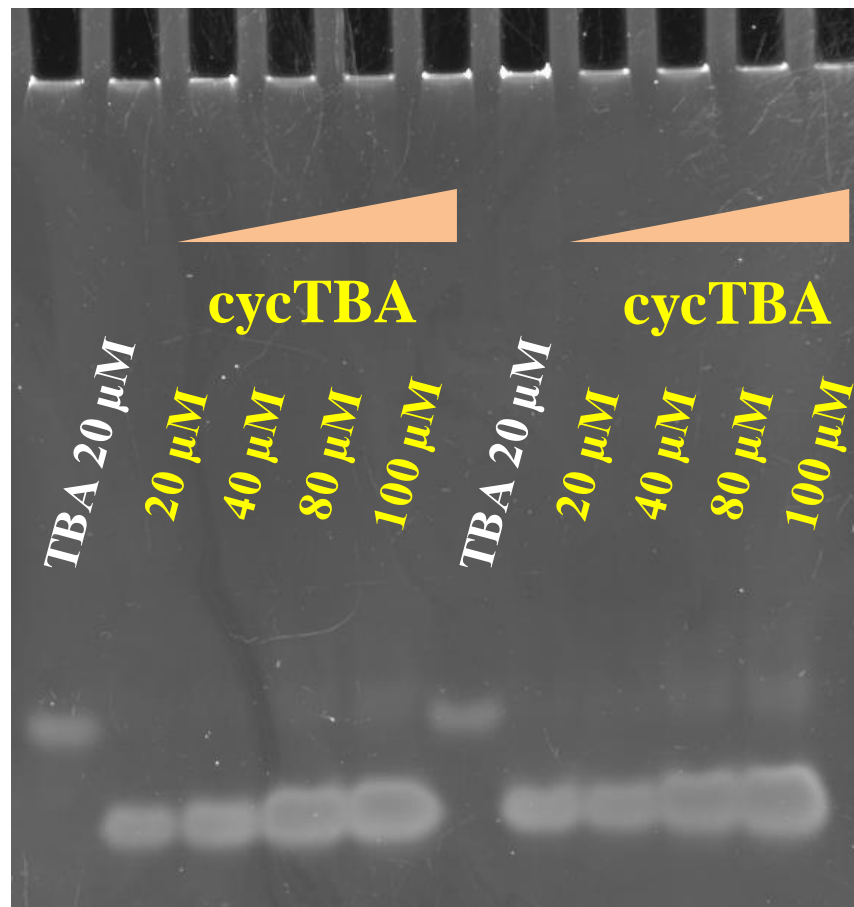
60 Vs 42 Vs 35

Riccardi C., et al. *ChemBioChem*. 2019, 20(14), 1789-1794. doi: 10.1002/cbic.201900045.



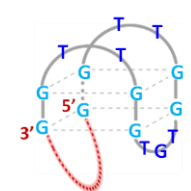


K⁺ buffer Na⁺ buffer



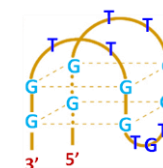
K⁺ buffer

Na⁺ buffer



cycTBA

VS



TBA

Riccardi C., et al. *ChemBioChem*. 2019, 20(14), 1789-1794. doi: 10.1002/cbic.201900045.

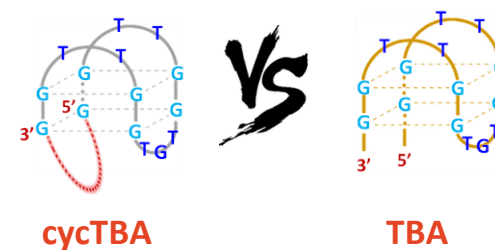
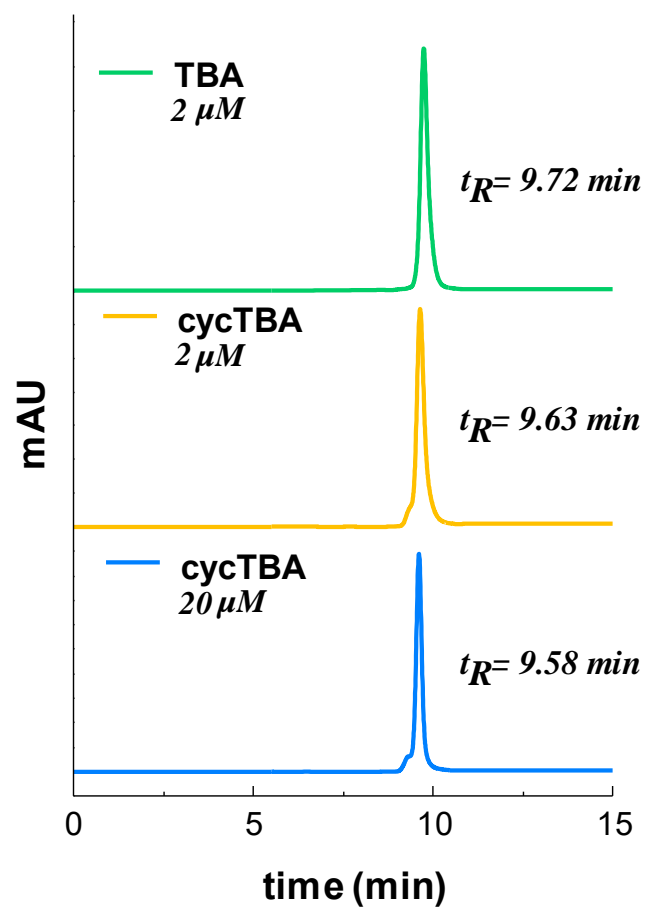
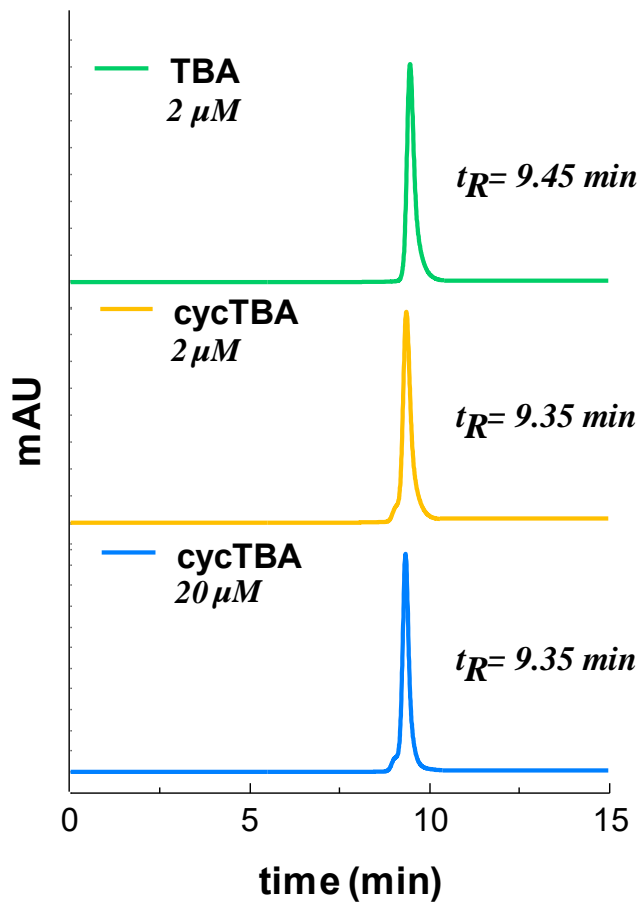


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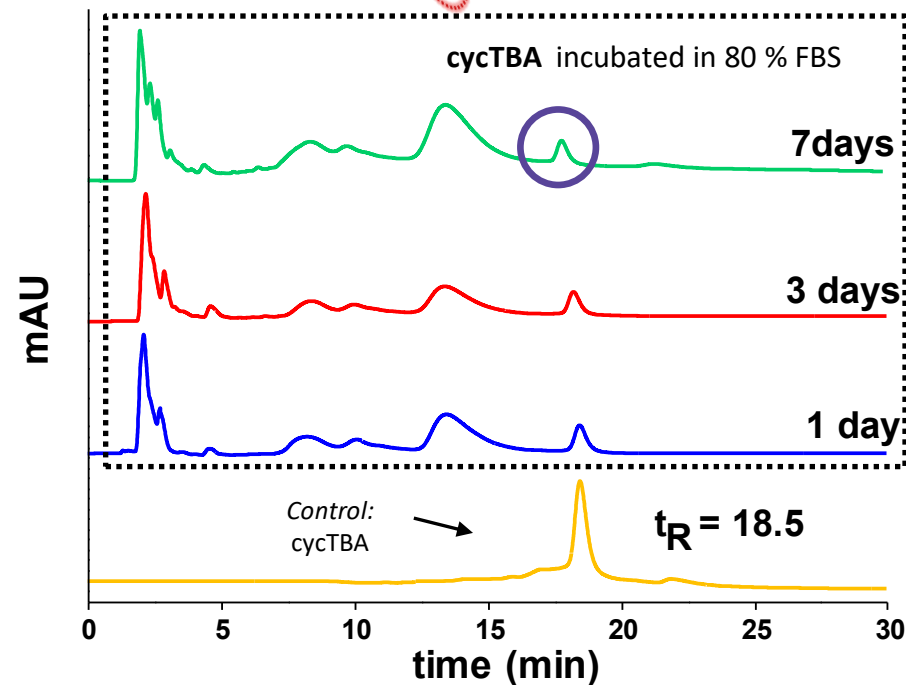
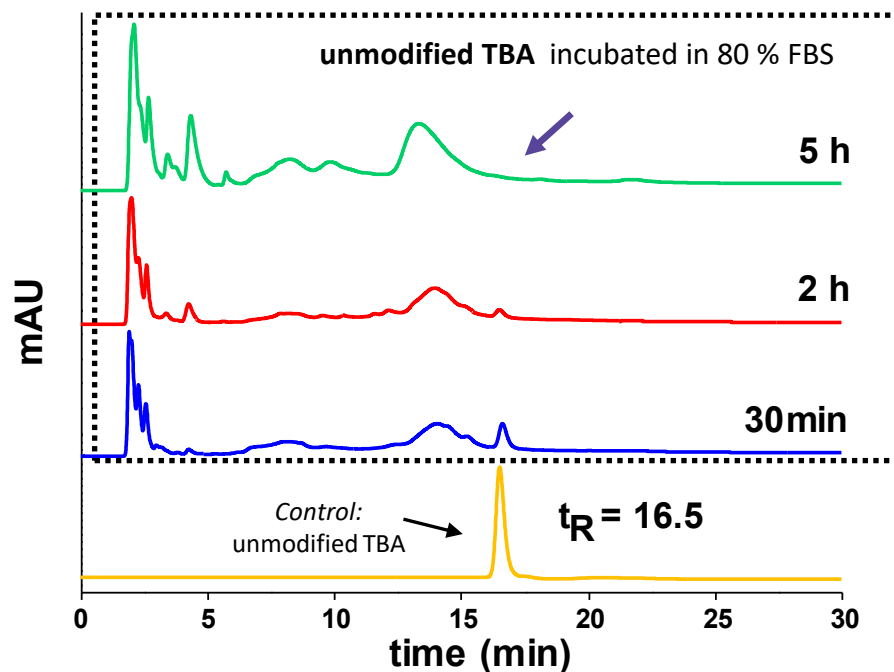
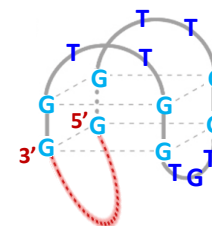
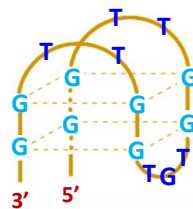
K⁺ buffer

Na⁺ buffer



Riccardi C., et al. *ChemBioChem*. 2019, 20(14), 1789-1794. doi: 10.1002/cbic.201900045.





Nucleogen DEAE 60-7 column 7 μm , 125 x 4 mm, $\lambda = 254$ nm; Linear gradient of B (0 to 100 %) in A in 30 min

Solution A: 20 mM $\text{KH}_2\text{PO}_4/\text{K}_2\text{HPO}_4$ aq. solution, pH 7.0, containing 20 % (v/v) CH_3CN ;

Solution B: 1 M KCl, 20 mM $\text{KH}_2\text{PO}_4/\text{K}_2\text{HPO}_4$ aq. solution, pH 7.0, containing 20 % (v/v) CH_3CN .

Riccardi C., et al. *ChemBioChem*. 2019, 20(14), 1789-1794. doi: 10.1002/cbic.201900045.

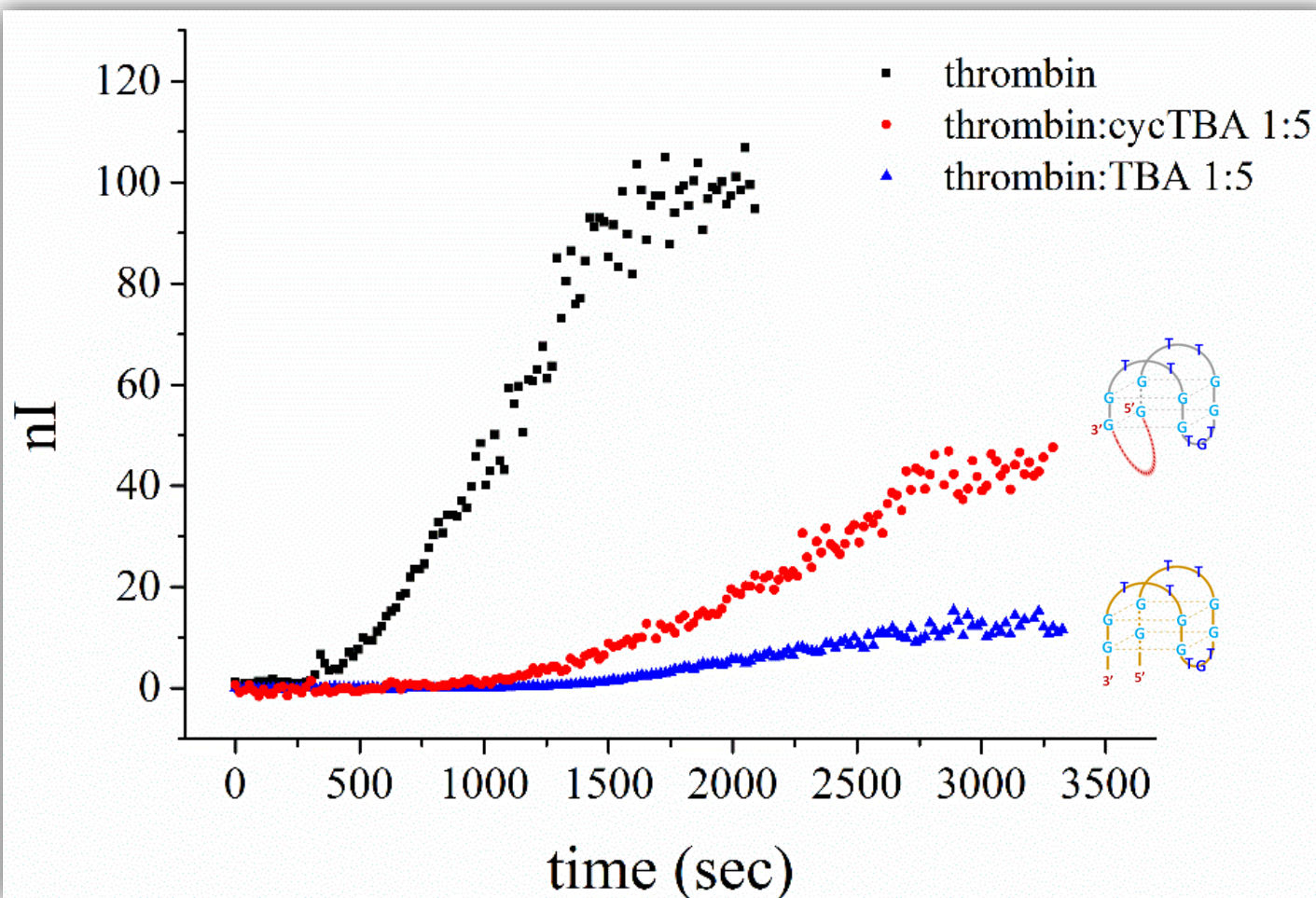




prof. Luigi Paduano Dr. Irene Russo Krauss



Dept. of Chemical Sciences, Naples



Fibrinogen: 1.2 μ M

Thrombin: 5 nM

Riccardi C., et al. *ChemBioChem*. 2019, 20(14), 1789-1794. doi: 10.1002/cbic.201900045.



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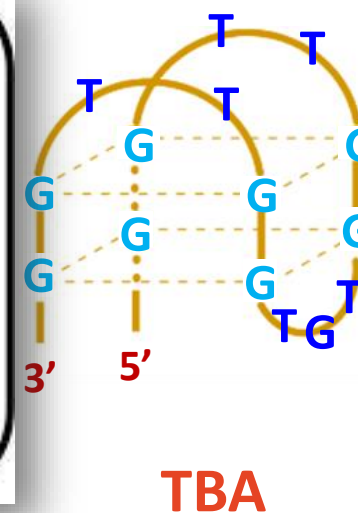
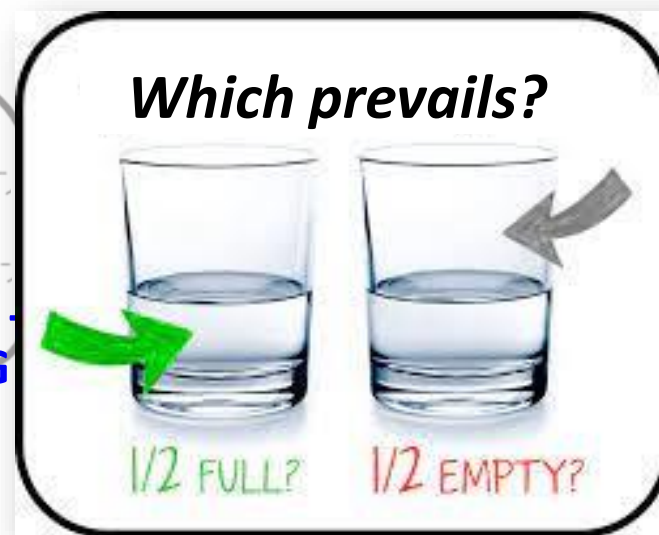
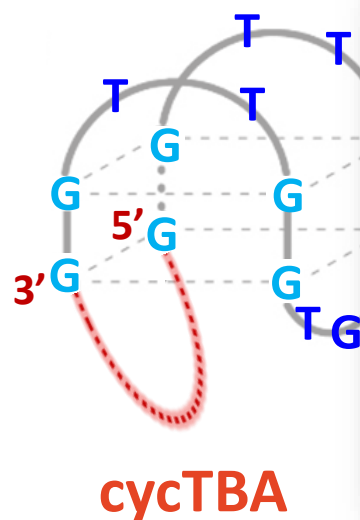
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- ❖ Remarkable increase in the thermal stability of the G-quadruplex structure;
- ❖ Noteworthy higher resistance to nuclease degradation;




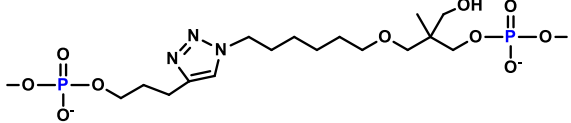
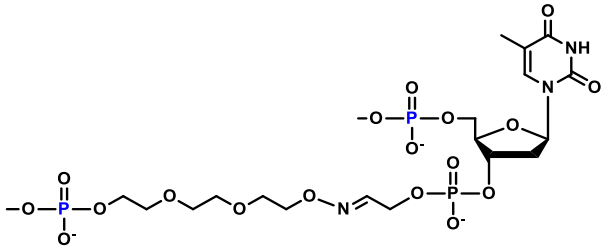
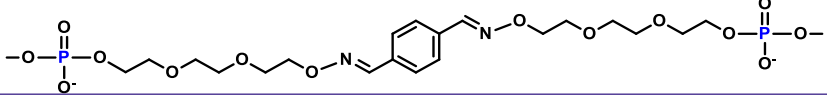
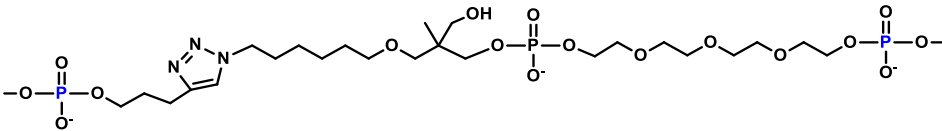
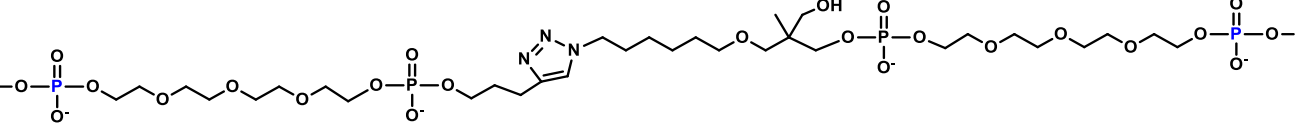
- ❖ Anticoagulant activity reduced by about 50 %;
- ❖ Binding affinity reduced by about 50 %.



Riccardi C., et al. *ChemBioChem*. 2019, 20(14), 1789-1794. doi: 10.1002/cbic.201900045.



 good balance between the compactness of the G-quadruplex core and its structural flexibility

Name	Linker connecting sequence (5'-3')	Linker connecting length
<u>cycTBA</u>		20 atoms
cycTBA I		22 atoms
cycTBA II		30 atoms
cycTBA III		34 atoms
cycTBA IV		48 atoms

oxime ligation method

CuAAC protocol

Riccardi C., et al. *Bioorg. Chem.* **2020**, *94*, 103379. doi: 10.1016/j.bioorg.2019.103379.



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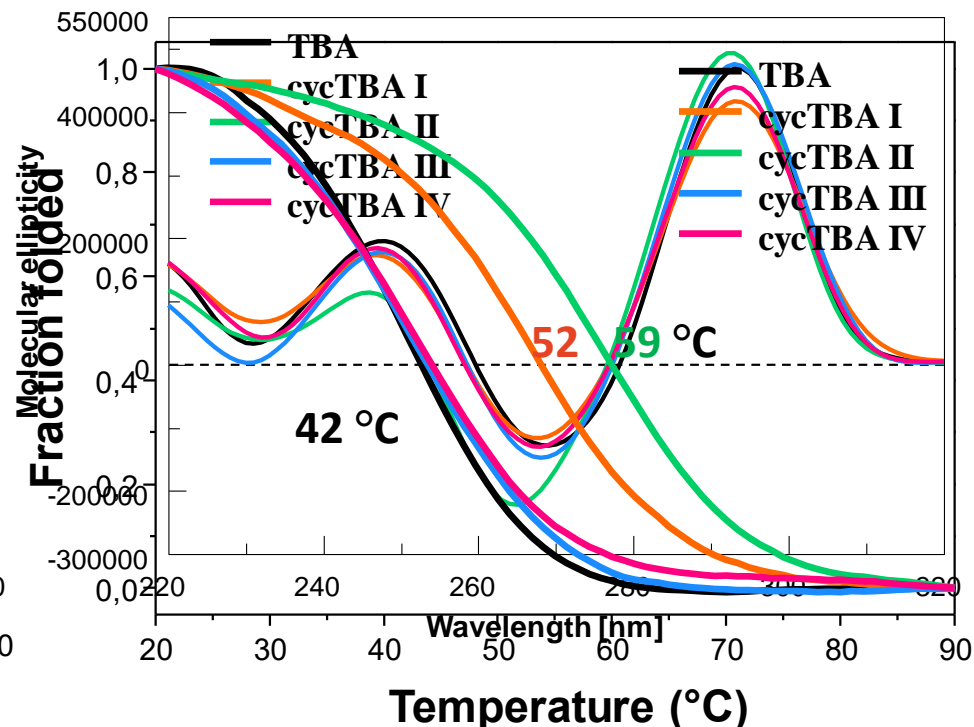
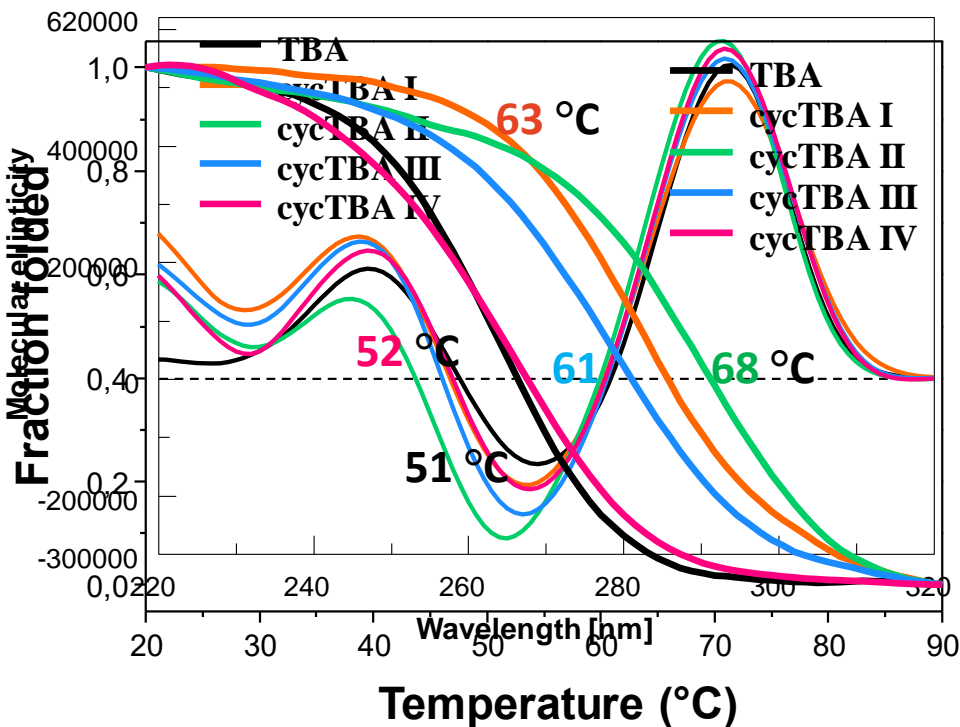
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❖ **UV and TDS analysis:** in both saline solutions, TDS profiles confirmed the formation of G-quadruplex structures, providing the typical “fingerprint” of these architectures;

❖ **CD analysis:**

K⁺-rich buffer

Na⁺-rich buffer



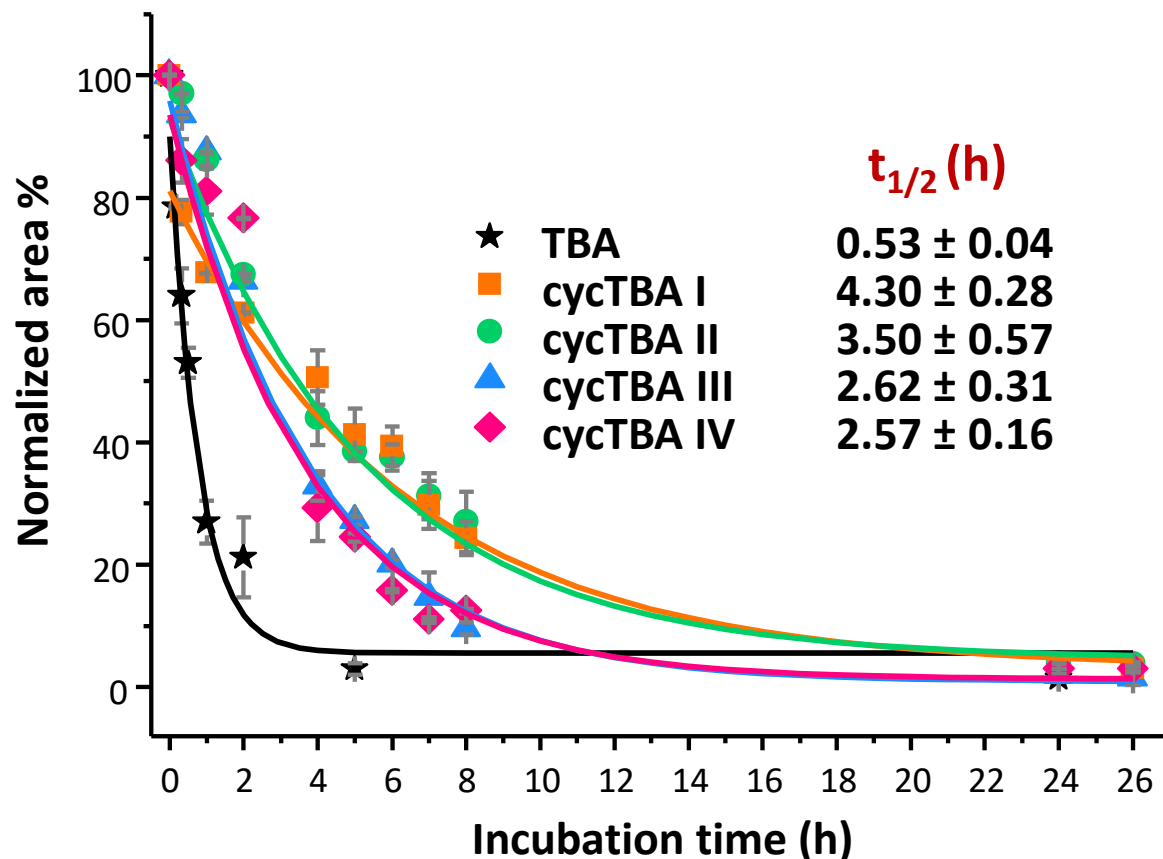
✓ In both saline conditions, **cycTBA I** and **cycTBA II** are the most stable derivatives

Riccardi C., et al. *Bioorg. Chem.* **2020**, *94*, 103379. doi: 10.1016/j.bioorg.2019.103379.



❖ Native gel electrophoresis and SE-HPLC investigations confirmed the presence of a single unimolecular G4 structure;

❖ Nuclease resistance experiments:



✓ **cycTBA I** and **cycTBA II** are the most resistant analogues in serum

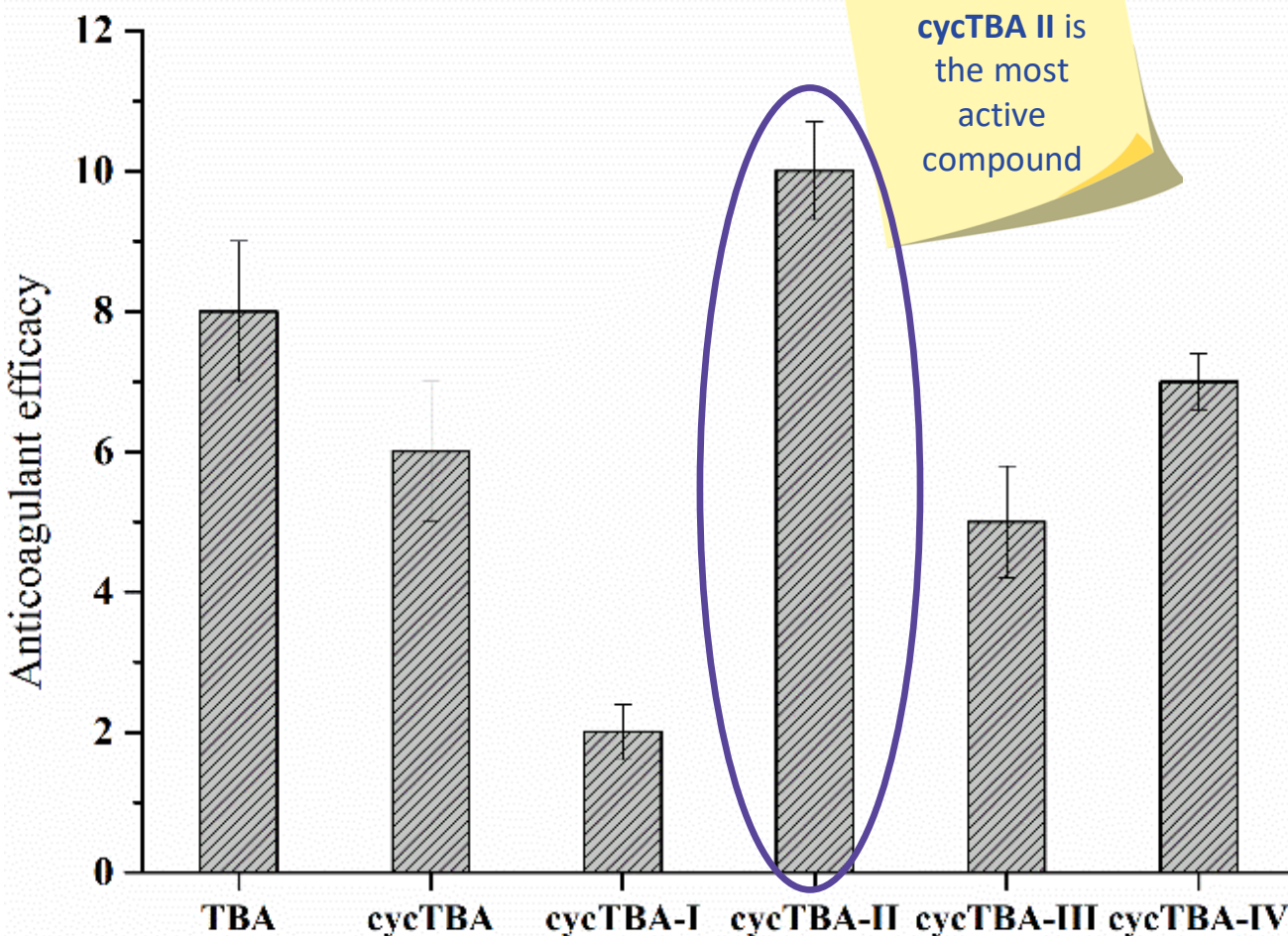
Nucleogen DEAE 60-7 column 7 μ m, 125 x 4 mm, λ = 254 nm;
 Linear gradient of B (0 to 100 %) in A in 30 min
 Solution A: 20 mM $\text{KH}_2\text{PO}_4/\text{K}_2\text{HPO}_4$ aq. solution, pH 7.0, containing 20 % (v/v) CH_3CN ;
 Solution B: 1 M KCl, 20 mM $\text{KH}_2\text{PO}_4/\text{K}_2\text{HPO}_4$ aq. solution, pH 7.0, containing 20 % (v/v) CH_3CN .

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cycTBA II is
the most
active
compound



prof. Luigi
Paduano



Dr. Irene
Russo Krauss



*Dept. of Chemical
Sciences, Naples*

Coagulation efficacy (defined as the ratio between the coagulation rate in the presence of thrombin and in the presence of both thrombin and each aptamer) of cycTBAs I-IV

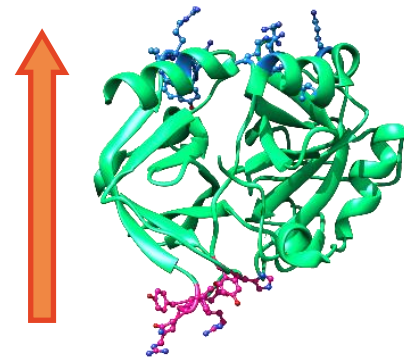
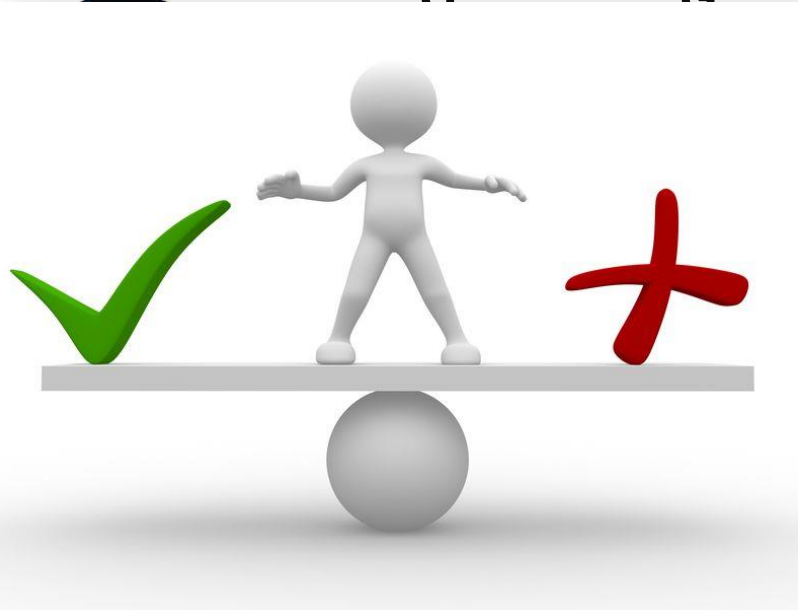
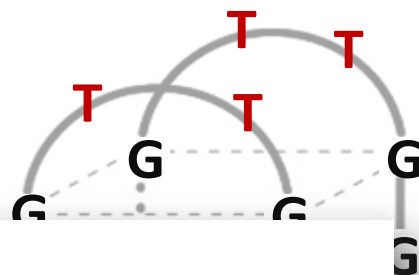
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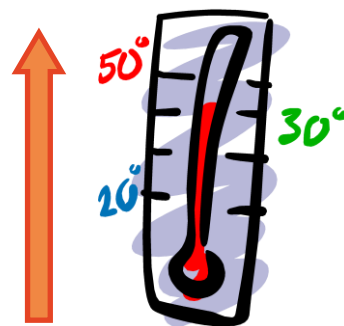
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A first improved TBA analogue



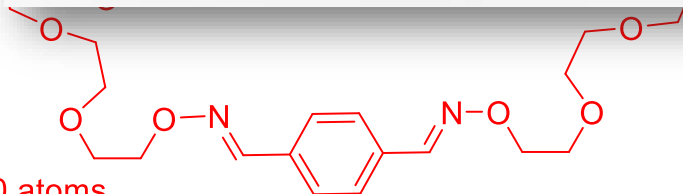
Improved inhibition of thrombin activity



Increased G4 stability
($\Delta T_m = +17^\circ\text{C}$)



6.6-fold higher nuclease resistance



Riccardi C., et al. *Bioorg. Chem.* **2020**, 94, 103379. doi: 10.1016/j.bioorg.2019.103379.

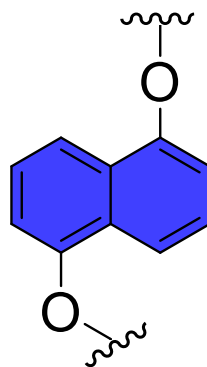


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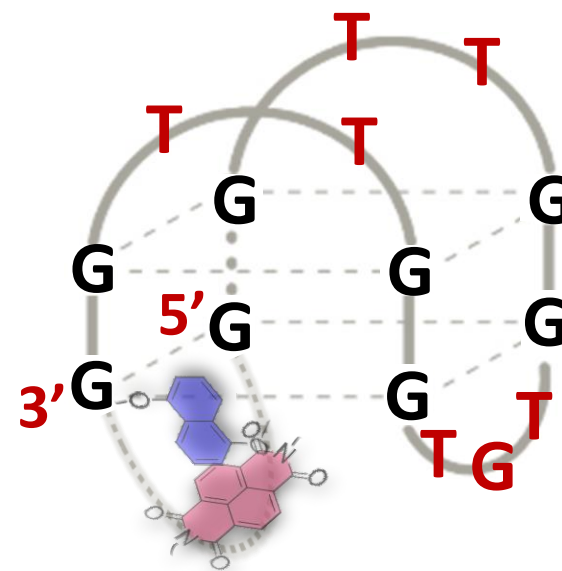
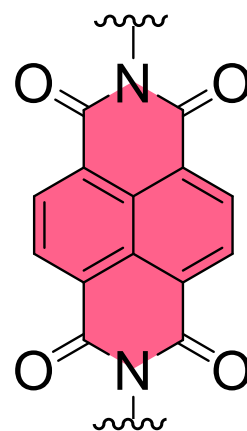
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End-modified thrombin binding aptamers stabilized by π/π or charge-transfer interactions

DAN



NDI



DAN: 1,5-dialkoxy naphthalene

NDI: 1,8,4,5-naphthalenetetra-carboxylic diimide



G-quadruplex structural flexibility necessary for thrombin recognition combined with the intriguing advantages found for the previously investigated cyclic TBA analogues

Pérez de Carvasal K., Riccardi C., et al. *Int. J. Mol. Sci.* **2021**, 22(17), 9510. doi: 10.3390/ijms22179510.



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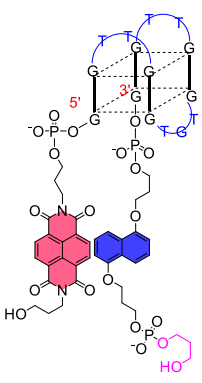
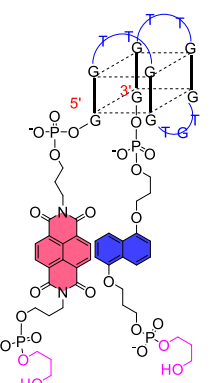
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TBA-Np/Dp

TBA-N/Dp

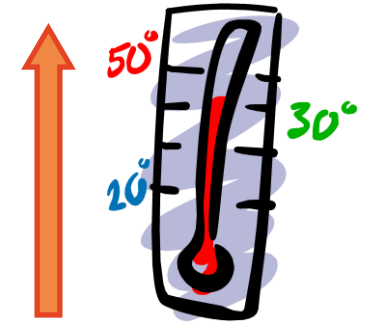
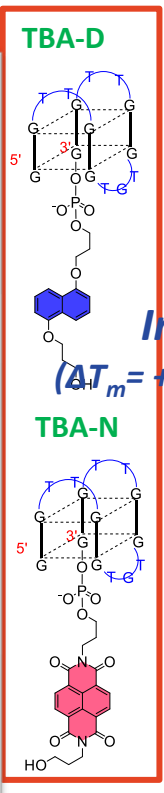
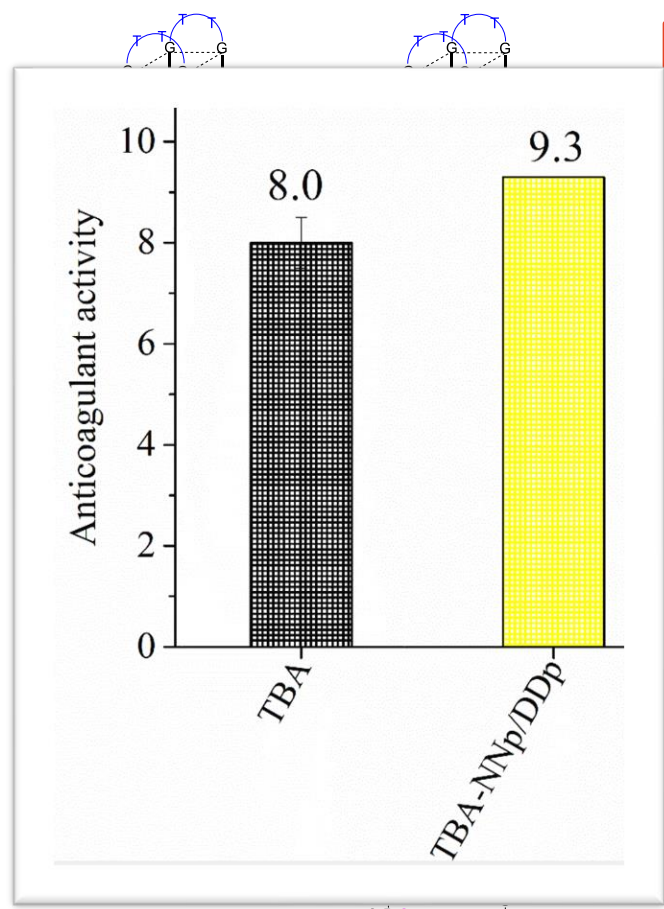
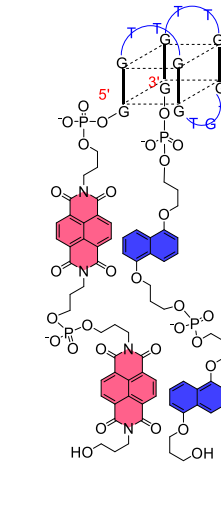
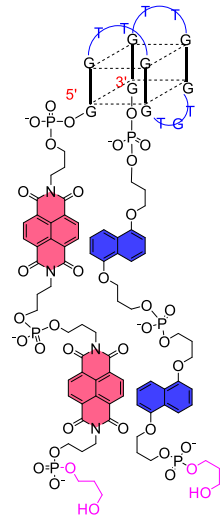
TBA-Np/D

TBA-N/D



TBA-NNp/DDp

TBA-NN/DD



Increased G4 stability
 ($\Delta T_m = +11$ and $+8^\circ\text{C}$, respectively in K^+ - and Na^+ -rich buffers)

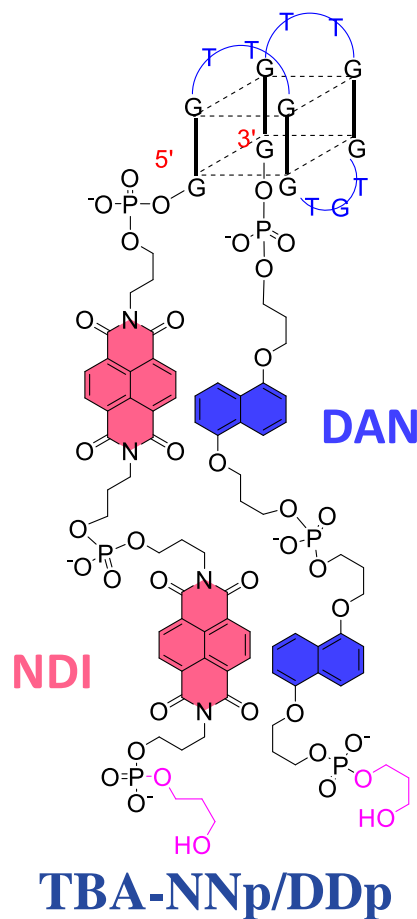
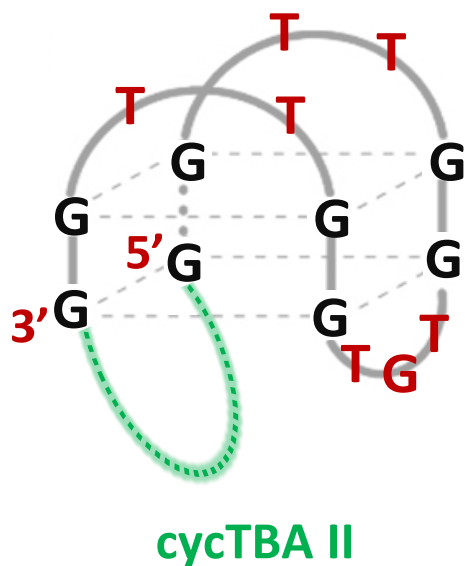


4.5-fold higher nuclease resistance

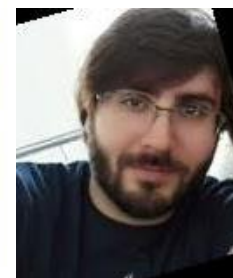
Pérez de Carvasal K., Riccardi C., et al. *Int. J. Mol. Sci.* **2021**, 22(17), 9510. doi: 10.3390/ijms22179510.



Analysis of the crystal structures obtained for thrombin with the most promising TBA derivatives



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...to be continued!!!

Pérez de Carvasal K., Riccardi C., et al. *Int. J. Mol. Sci.* **2021**, 22(17), 9510. doi: 10.3390/ijms22179510.



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Thank you for your kind attention



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