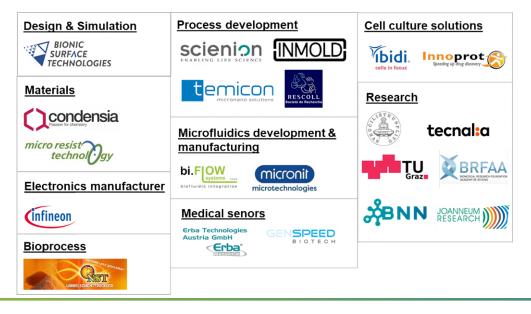
Microfluidics InnovationHub

We get Microfluidics rolling

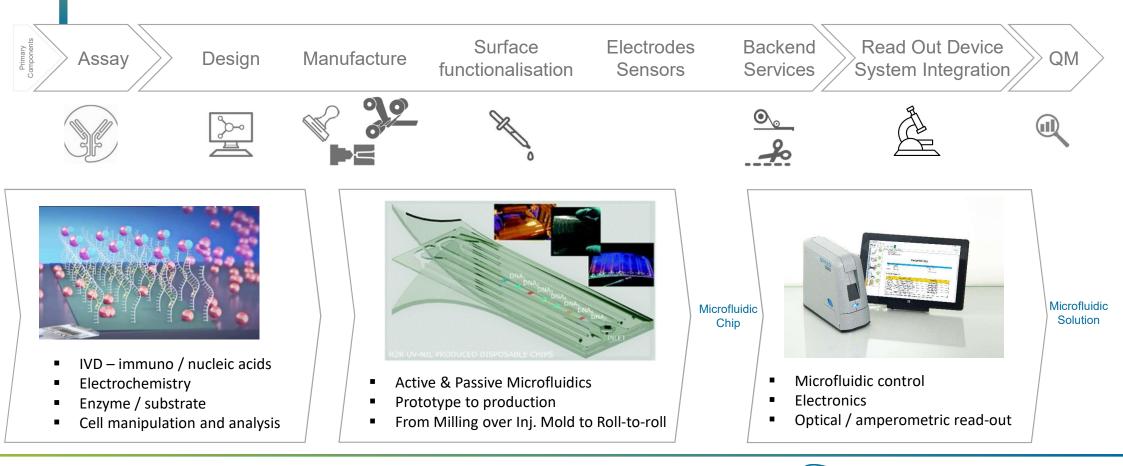
NextGenMicrofluidics (NGM)

- NGM is an Open Innovation Test Bed 21 companies
- MIH acts as a single-entry point towards their combined technologies and expertise
- worldwide biggest platform for upscaling and testing of microfluidic devices

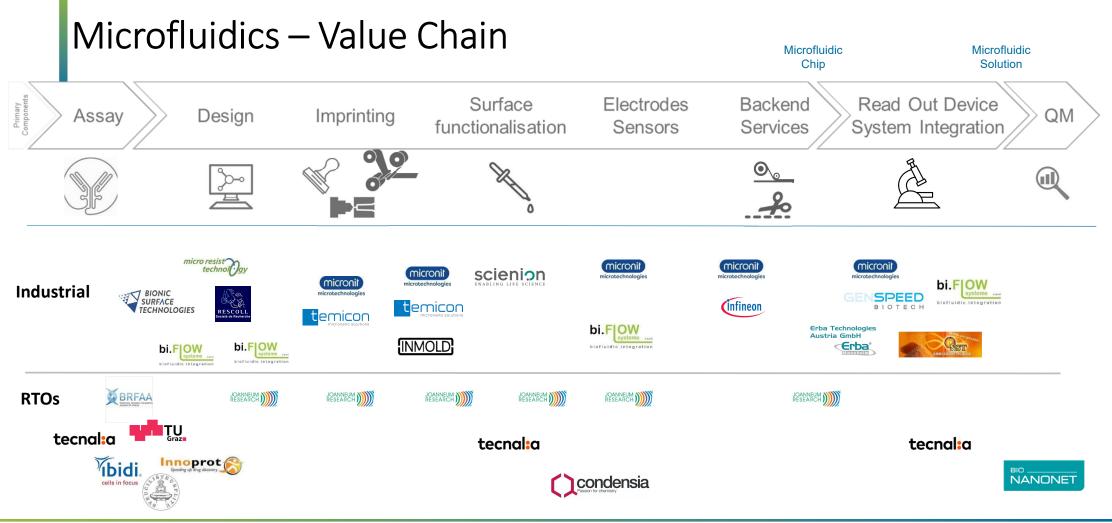




MIH Service Portfolio



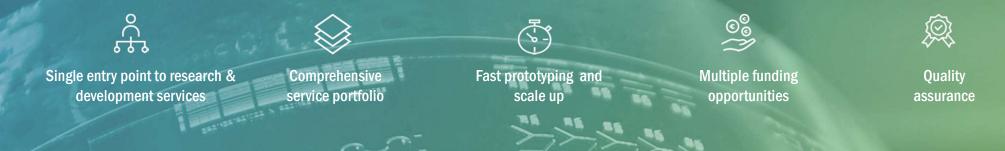




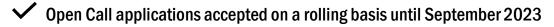




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Microfluidics Innovation Hub is the single entry point of the European project NextGenMicrofluidcs (www.nextgenmicrofluidics.eu). NextGenMicrofluidics has received funding from the European Union's HORIZON 2020 research & innovation programme under grant agreement no. 862092.





Functional nucleic acids: unleashing their untapped potential in a diverse set of applications

7 FEB 2023, 15:00 CET

Presented by George Tsekenis, PhD Head of the Applied Biophysics and Surface Science Group, BRFAA



www.microfluidicshub.eu

Content

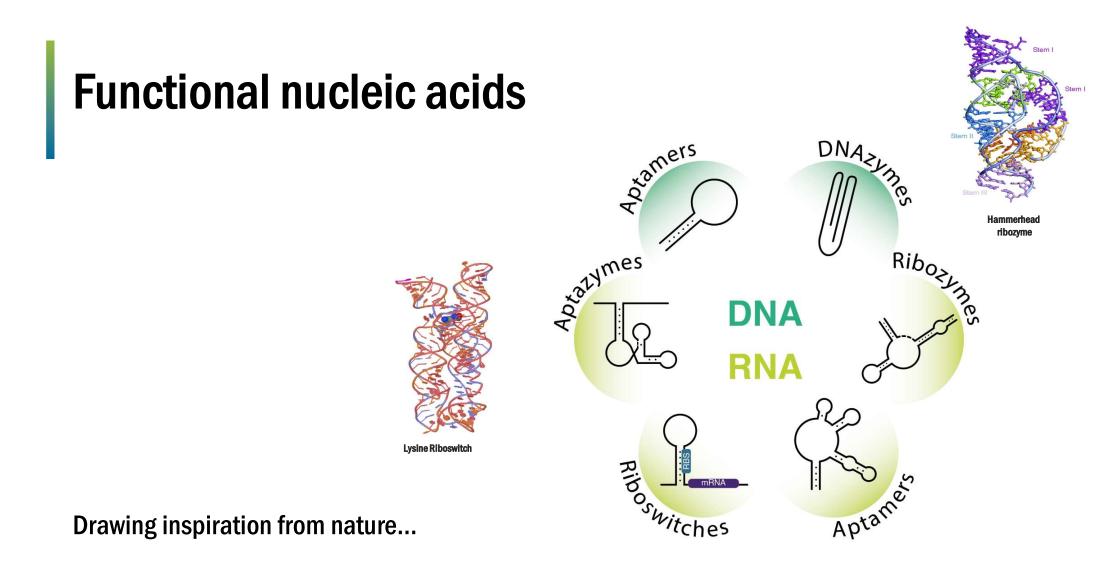
- Functional nucleic acids
 - Categories and selection strategies
 - Advantages over antibodies
 - Current challenges and ways forward
- Applications of functional nucleic acids
- Applied Biophysics and Surface Science (ABISS) Group





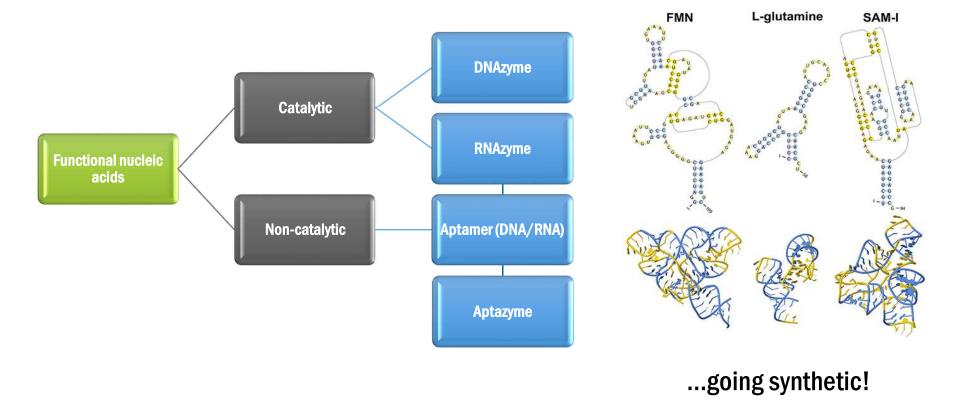
Functional nucleic acids Categories and selection strategies



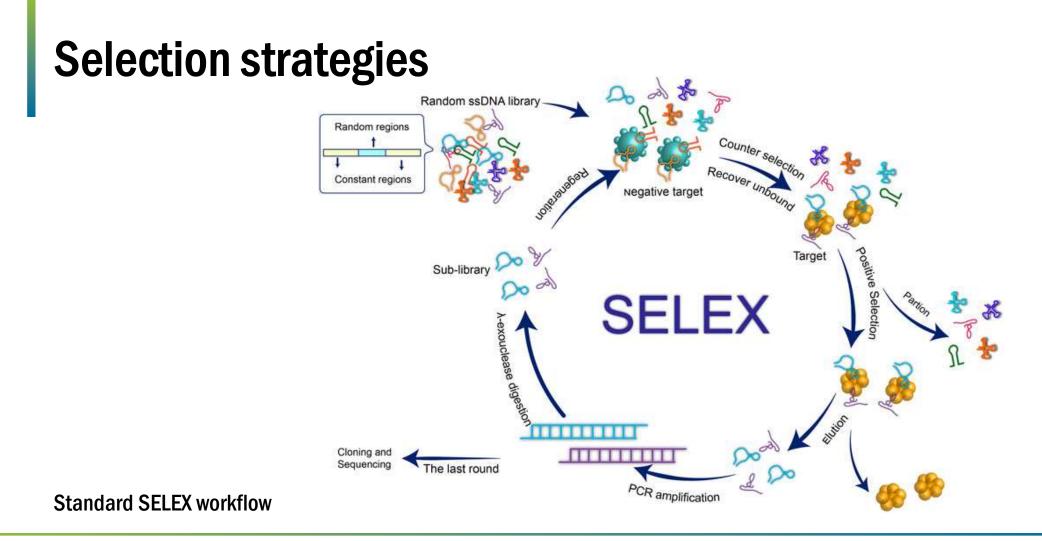




Functional nucleic acids





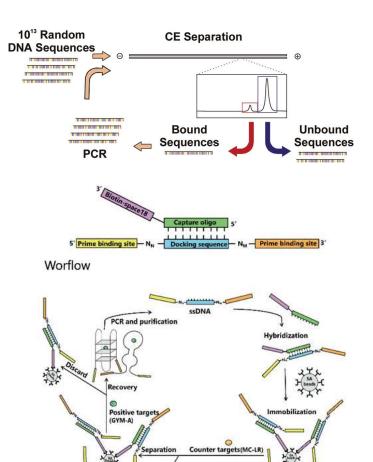




Selection strategies

Some of the countless SELEX variants

| SELEX variant | Description | | | | |
|----------------------------------|--------------------------------------------------------------------------|--|--|--|--|
| Magnetic bead-based SELEX | Accelerate SELEX process by immobilizing targets on magnetic beads | | | | |
| Capillary electrophoresis SELEX | Neither the ligand nor the oligo library are immobilized | | | | |
| Cell-SELEX | Whole cells employed as targets | | | | |
| Capture-SELEX | Immobilize oligonucleotide library, while the ligand is in solution | | | | |
| Next generation sequencing SELEX | Sequencing across all the selection rounds rather than just the last one | | | | |





Discard

 (\circ)

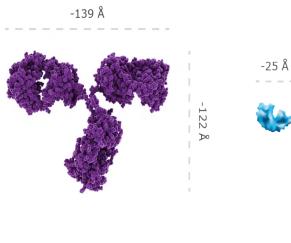


Functional nucleic acids Advantages over antibodies



Advantages

| | Antibodies | Aptamers | |
|--------------------------|----------------|----------------------------|--|
| Affinity for ligand | High | High | |
| Selectivity for ligand | High | High (?) | |
| Range of target analytes | Limited | Wide | |
| Cost | Expensive | Cheap | |
| Stability | Low | High | |
| Modification | Not controlled | Easy and highly controlled | |





14



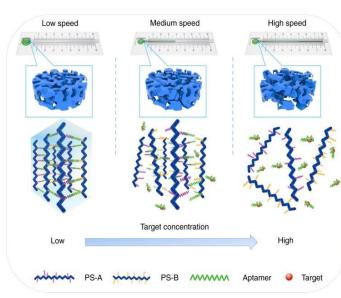
Are aptamers on a par to antibodies?



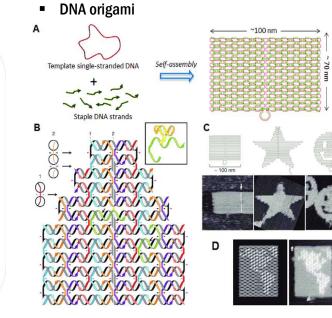
Advantages (I)

Base complementarity allows self-organized networks to be formed

Target-responsive hydrogels



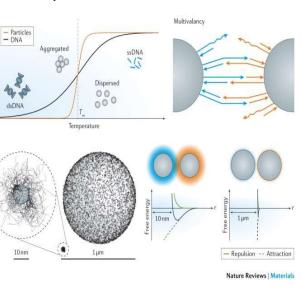
Nat Commun. 2019 Mar 8;10(1):1036. doi: 10.1038/s41467-019-08952-1

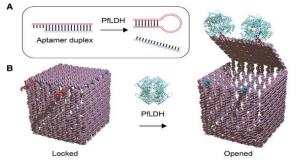


Nat Rev Methods Primers 1, 13 (2021). https://doi.org/10.1038/s43586-020-00009-8

Nat Rev Mater 1, 16008 (2016). https://doi.org/10.1038/natrevmats.2016.8







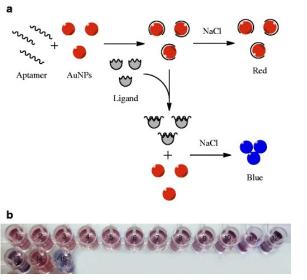
Nanomedicine: Nanotechnology, Biology and Medicine, 14, 2018,1161-1168, https://doi.org/10.1016/j.nano.2018.01.018.

Microparticles

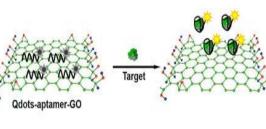
Advantages (II)

Interactions with 2D and 3D nanomaterials, organic molecules

Unique interactions endowed by the vary nature of nucleic acids

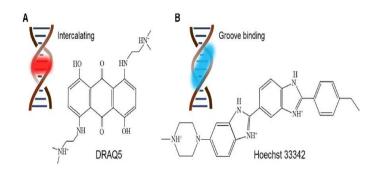


Microchim Acta 183, 1687-1697 (2016). https://doi.org/10.1007/s00604-016-1798-3

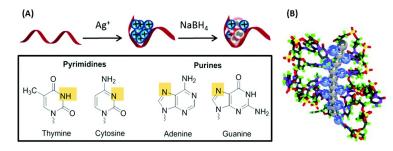




Biosensors and Bioelectronics, 85, 2016, 649-656, https://doi.org/10.1016/j.bios.2016.05.072.



Biochemical Society Transactions (2018) https://doi.org/10.1042/BST20170301

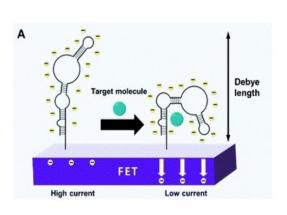


https://doi.org/10.1039/C6NR05872H



Advantages (III)

Signal generation or amplification made simple



10.1039/D0MA00639D (Review Article) Mater. Adv., 2020, 1, 2663-2687

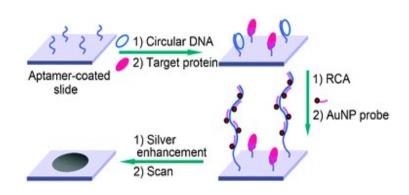
Aptamer

Polysulfone

membrane

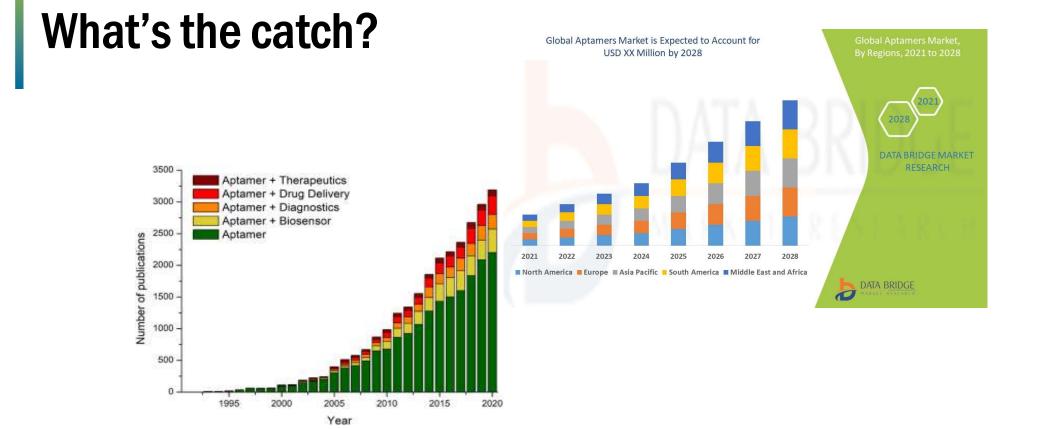
Reference electrode (coated silver wire

Sensor (insulated gold wire)



Chem. Commun., 2010, 46, 6720-6722 https://doi.org/10.1039/C002078H





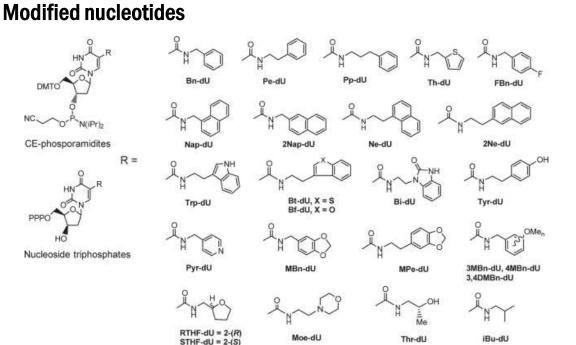


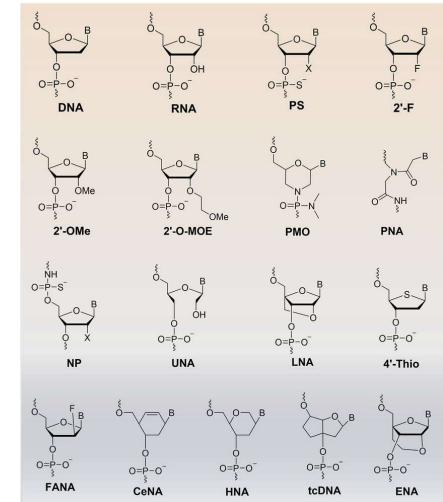


Functional nucleic acids Current challenges and ways forward



Limited possibilities in a 4 letter language





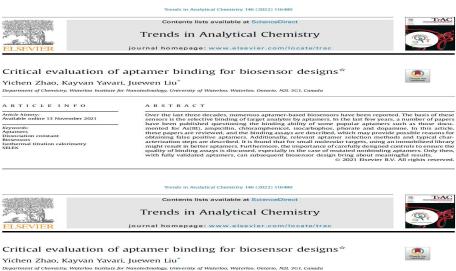


Issues with SELEX

| SELEX: choosing a library design | | | | | |
|----------------------------------|------------------|-------------------|----------------|----|--|
| Chemical nature | DNA | $\mathbf{\nabla}$ | RNA | | |
| Modification | Natural | | Modified | (V | |
| Modification site | Backbone | $\mathbf{\nabla}$ | Base | | |
| Primer binding sites | Present | $\mathbf{\nabla}$ | Primer-free | | |
| Source Che | emical synthesis | $\mathbf{\nabla}$ | Genome | | |
| Random region | Continuous | | Segmented | (7 | |
| Randomization | Uniform | $\mathbf{\nabla}$ | Doped | | |
| Secondary structure | No constraint | | Pre-structured | Ì | |



Validation of selected sequences



ABSTRACT

ARTICLE INFO

Article history: Available online 13 November 2021

s al titration calorin

Over the last three decades, numerous aptamer-based biosensors have been reported. The basis of these sensors is the selective binding of target analytes by aptamers. In the last few years, a number of papers have been published questioning the binding ability of some popular aptamers publish as those decubers are reviewed, and the binding ability of some popular aptamers such as those decubers are reviewed, and the binding abary are described, which may provide possible reasons for obtaining fails positive aptamers, Additionally, relevant aptamer selection methods and typical charming the sulfit in batter aptamers. Additionally, relevant aptamer selection methods and typical charming threshold in a subsect of the sepacities of the sepacities of the second of the second second to the second secon

JACS

Do Aptamers Always Bind? The Need for a Multifaceted Analytical Approach When Demonstrating Binding Affinity between Aptamer and Low Molecular Weight Compounds

Fabio Bottari, ▼ Elise Daems, ▼ Anne-Mare de Vries, ▼ Pieter Van Wielendaele, Stanislav Trashin, Ronny Blust, Frank Sobott, Annemieke Madder, José C. Martins,* and Karolien De Wael*



ABSTRACT: In this manuscript, we compare different analytical methodologies to validate or disprove the binding capabilities of aptamer sequences. This was prompted by the lack of a universally accepted and robust quality control protocol for the characterization of aptamer performances coupled with the observation of independent yet inconsistent data sets in the literature. As an example, we chose three aptamers with a reported affinity in the nanomolar range for ampicillin, a β -lactam antibiotic, used as biorecognition elements in several detection strategies described in the literature. Application of a well-known colorimetric assay based on aggregation of gold nanoparticles (AuNPs) yielded conflicting results with respect to the original report. Therefore, ampicillin binding was evaluated in solution using isothermal titration calorimetry (ITC), native nano-electrospray ionization mass spectrometry (native nESI-MS), and ¹H-nuclear magnetic resonance spectroscopy (¹H NMR). By coupling the thermodynamic data obtained with ITC with the structural information on the binding event given by native nESI-MS and ¹H NMR we could verify that none of the ampicillin aptamers



Article

show any specific binding with their intended target. The effect of AuNPs on the binding event was studied by both ITC and ¹H NMR, again without providing positive evidence of ampicillin binding. To validate the performance of our analytical approach, we investigated two well-characterized aptamers for cocaine/quinine (MN4), chosen for its nanomolar range affinity, and 1argininamide (IOLD) to show the versatility of our approach. The results clearly indicate the need for a multifaceted analytical approach, to unequivocally establish the actual detection potential and performance of aptamers aimed at small organic molecules.

■ INTRODUCTION

Aptamers are short single strands of DNA or RNA that recognize with high affinity a given target against which they are selected. Aptamers were first obtained in the 1990s1 following a procedure called SELEX (systematic evolution of ligands by exponential enrichment). From the beginning, they were considered a leap forward in many analytical and biomedical applications. Indeed, aptamers offer considerable advantages over traditional molecular biorecognition elements such as antibodies or enzymes, including stability over a wider

remain to be faced before this can be achieved. A variety of factors have been put forward to explain why aptamers have not yet penetrated the market:16 one of the main reasons can be identified as the so-called "thrombin problem". Indeed, rather than developing assays for more clinically relevant targets, hundreds of investigators continue to focus their attention on perfecting thrombin-binding aptamers or designing clever detection strategies for this target. The same can be said to a lesser extent for cocaine-binding aptamers in the field

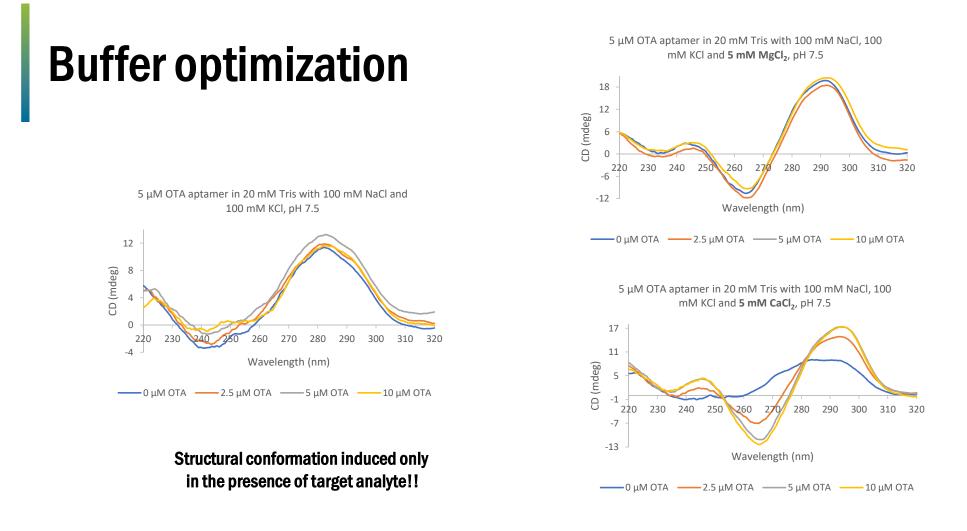


Validation of selected sequences

| | | | | | | 1. Candidate screening | 2. Truncation & optimization | 3. Characterization | 4. Functional validation |
|------------------------------|-------|-------|------------------|-------------------|------------------------------------|----------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|-----------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------|
| | Costs | Speed | Amount of sample | User-friendliness | Method milestones | Reduce the number of putative aptamer sequences from SELEX from hundreds to ~3 candidates | Determine minimal binding sequence | Determine the K _D , selectivity and other parameters | Assess the robustness of the aptamer for use in different application platforms |
| ITC | €€€ | チチ | 4444 | | - | | | | |
| Native (IM-)MS | €€€€€ | チデチデチ | 44 | | Important | 1. High-throughput 2. Cost-effective | 1. High-throughput 2. Cost-effective | 1. Quantitative 2. Precise | Validate function with at least two separate methods |
| Electrochemical techniques | € | チオチオチ | ۵ | | assay considerations | | 3. Provides insight about structure or important binding residues | 3. Measurement of multiple parameters in parallel | Determine functionality in solution and immobilized Does not need to be quantitative |
| Fluorescent-based techniques | €€ | オオオ | 44 | 2 | | | | | |
| MST | €€€ | チチチチ | ۵ | | | 1. Fluorescence | 1. DNase Assay | 1. SPR | Choose at least 1 assay from group not used |
| SPR | €€€€ | オオオ | ۵ | | Assay options (ascending order) | Polarization (FP) 2. SYBR Green (SG) 3. AuNP Assay 4. Affinity Chrom. (beads) 5. SPR | 2. FP 3. SG 4. Affinity Chrom. (beads) 5. SPR | 2. FP 3. Equil. dialysis 4. SG 5. Affinity Chrom. (beads) | in step 3 In solution |
| SERS | €€€ | オオオオオ | 444 | | | | | | FP, Equil. Dialysis, SG, Affinity Chrom. (either), Ultrafiltration, DNase |
| QCM | €€€€ | オオオオ | 66 | | | | | | DNA immobilized/constrained SPR. AuNPs |
| NMR spectroscopy | €€€€€ | オオオ | 44444 | | 8 | | | | and "opposited on a |
| X-ray crystallography | €€€€€ | 3 | 4444 | | | | | | DOI: 10.1021 /acc. analaham 5602102 |
| CD | €€ | チオチオキ | 4444 | 1 | | | | | DOI: 10.1021/acs.analchem.5b02102 Anal. Chem. 2015, 87, 8608-8612 |
| SAXS | •••• | デデ | 4444 | | | | | | |

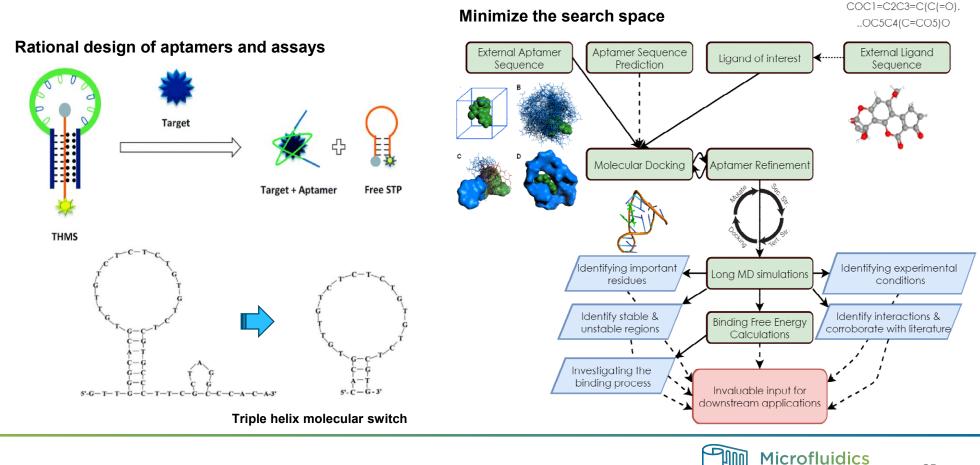
Trends in Analytical Chemistry 142 (2021) 116311 https://doi.org/10.1016/j.trac.2021.116311







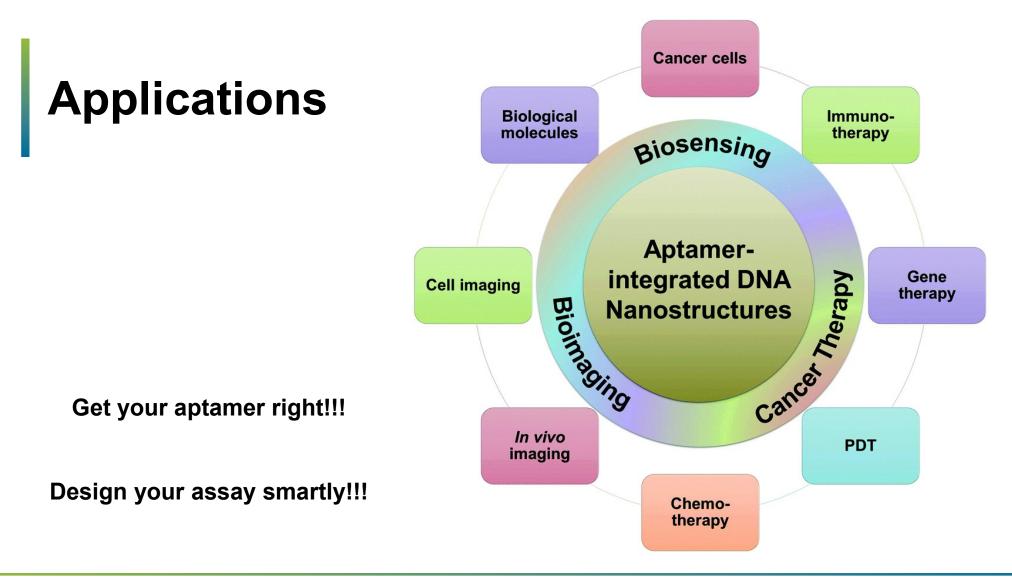
Post-SELEX sequence optimization





Functional nucleic acids Applications of functional nucleic acids









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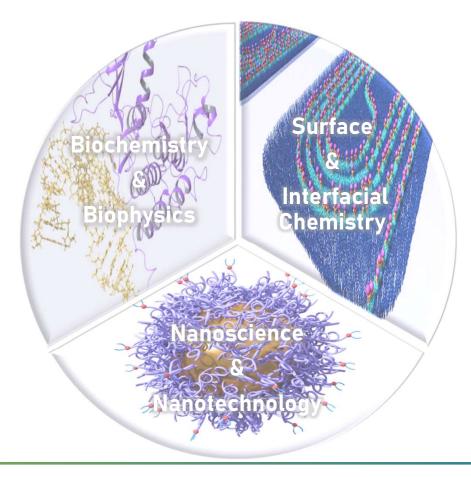


Biomedical Research Foundation Academy of Athens





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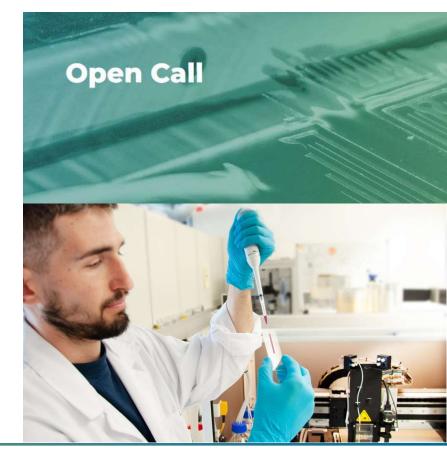


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