

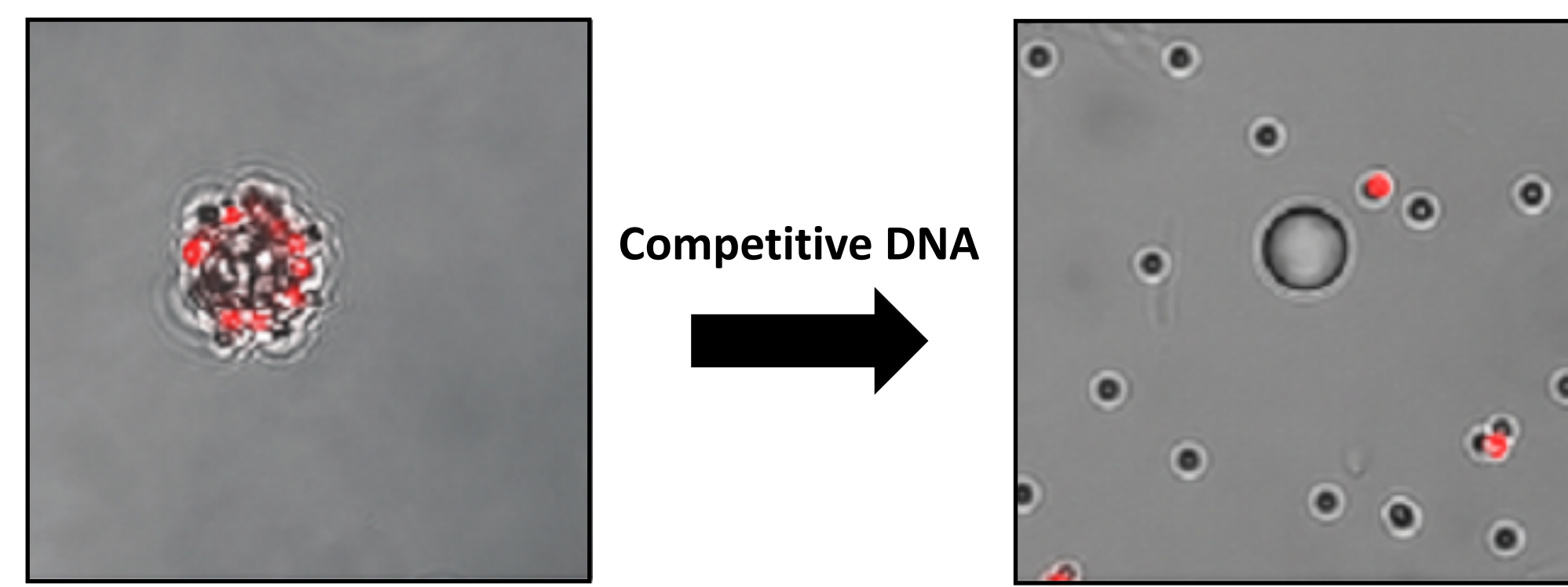
Programming Recognition-based Binding and Release with DNA, RNA, and LNA

We employ oligonucleotide-functionalized colloidal particles in the following scenarios:

- 1) for programmable, isothermal assembly and disassembly of multifunctional therapeutic agents
- 2) as nucleic acid detection platforms.

Isothermal Disassembly of DNA-linked particles

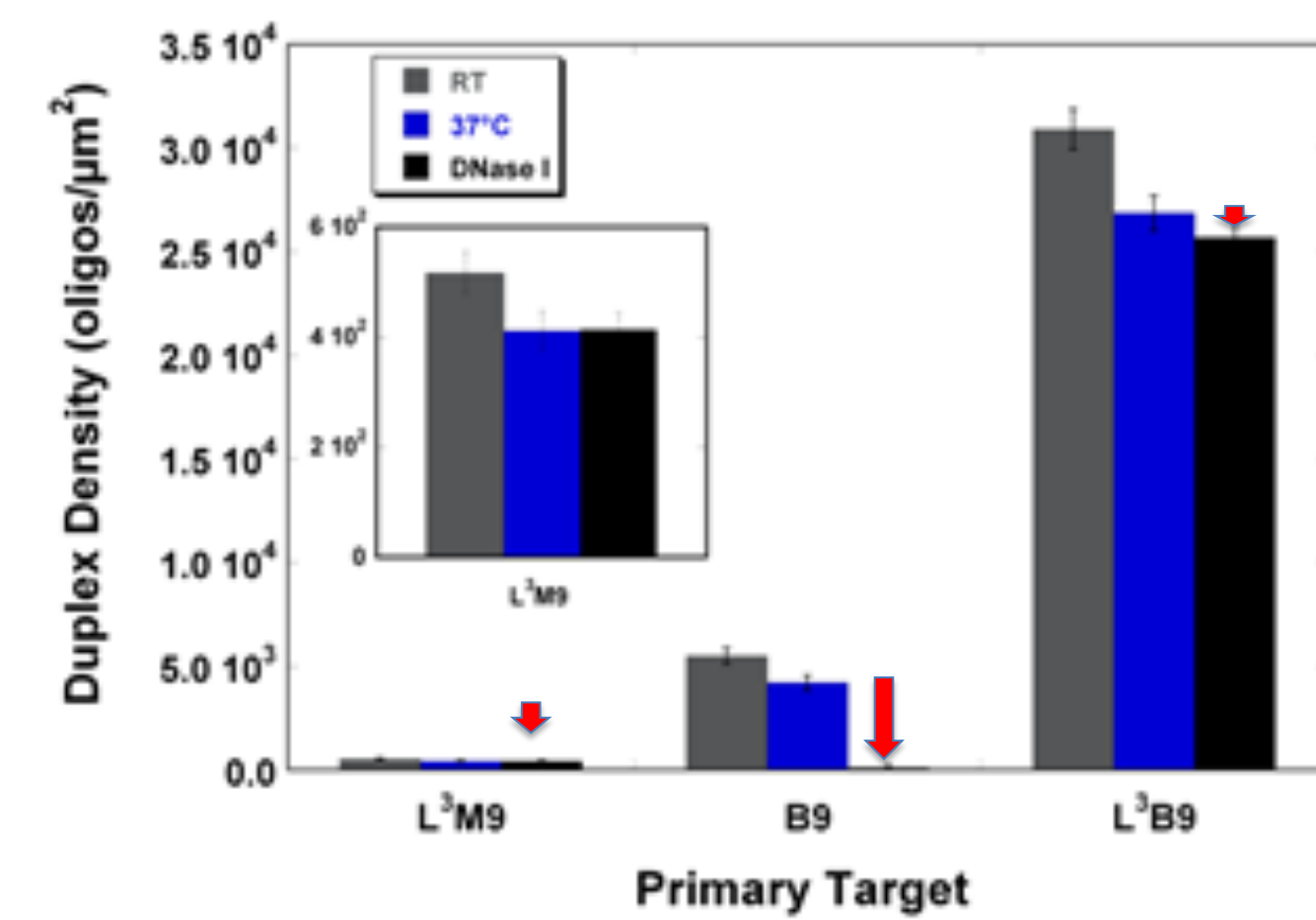
DNA-linked colloidal satellite as model multifunctional assembly Programmed Disassembly to release therapeutic agents



Tison & Milam *Langmuir* 2007

Locked Nucleic Acid (LNA) Confers Nuclease Resistance for Physiological Environment

Comparison of Duplex DNA & LNA Nuclease Stability



The red arrows indicates degradation-based loss of DNA (96% for DNA duplexes in middle) compared to LNA duplexes (<4% on left and right)

Eze & Milam *Soft Matter* 2013

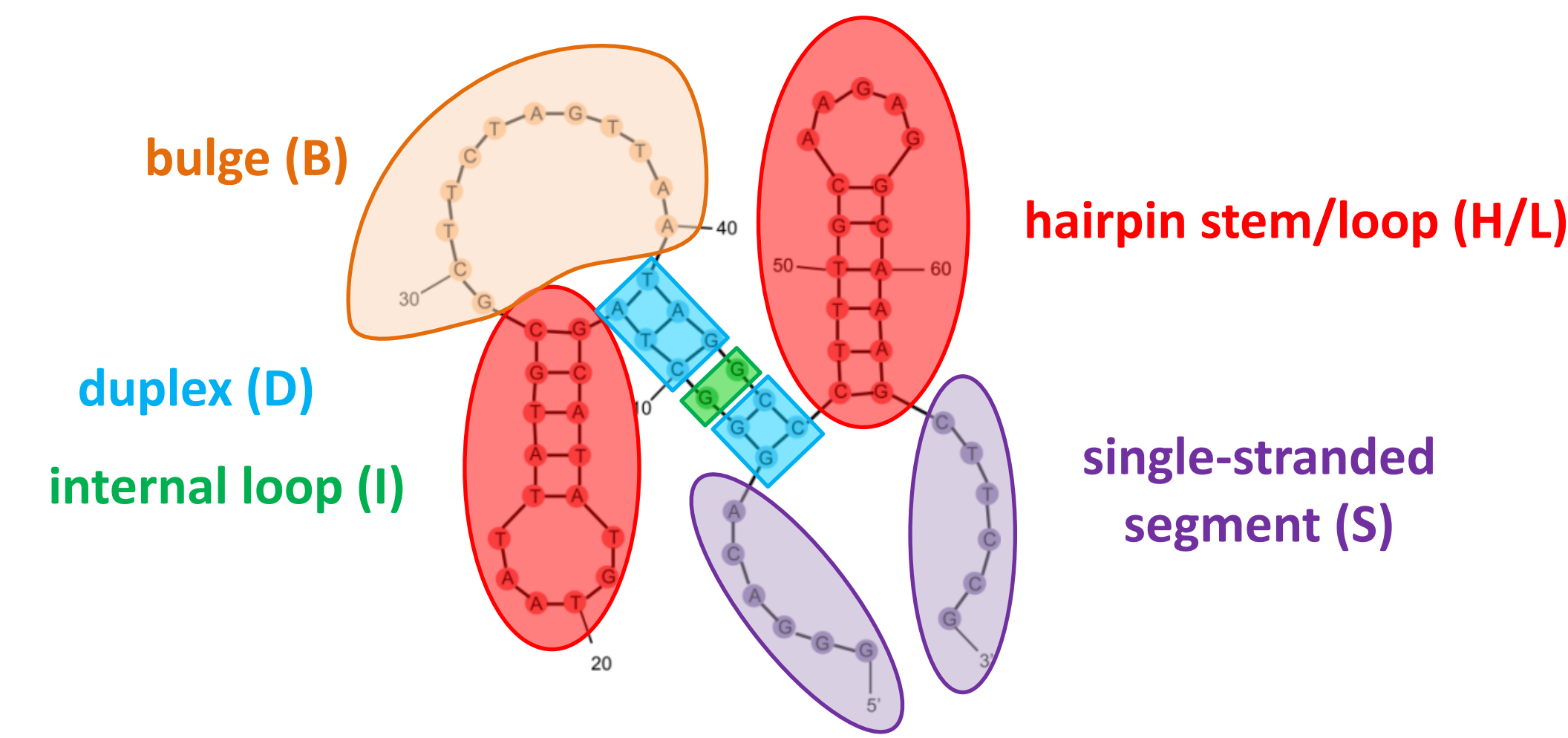
Key Advantages

- 1) Label-free targets can be detected
- 2) Enables isothermal assembly and disassembly conditions
- 3) Distinct displacement behavior allows for target discrimination

Evaluating Structural Patterns in DNA Aptamers

By adapting sequence (or primary structure) analysis tools used for DNA, we can find patterns in self-hybridized (or secondary structures) of oligonucleotide aptamers identified via CompELS to find the following:

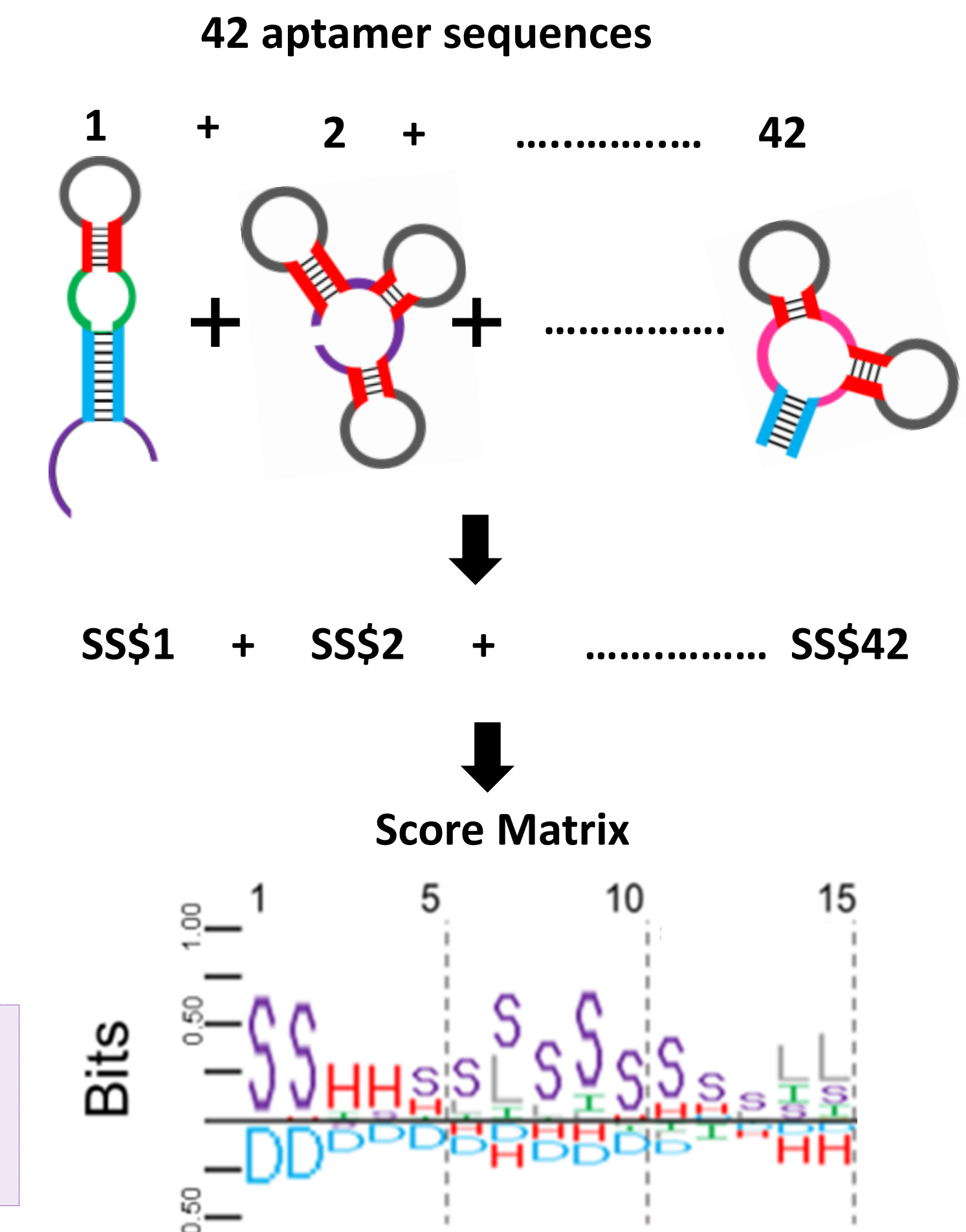
Identifying secondary structure elements in an aptamer sequence



Convert above information into a secondary structure string (SS\$)

5' -SSSSSSDDIDDHHLHLLLLHLLHHHBBBBDIIDDHHLHLLLLHLLHHHSSSSSS-3'

Identifying patterns in secondary structure among groups of aptamer sequences



Sullivan, Adams, Naik, Milam *Molecules*. 2020

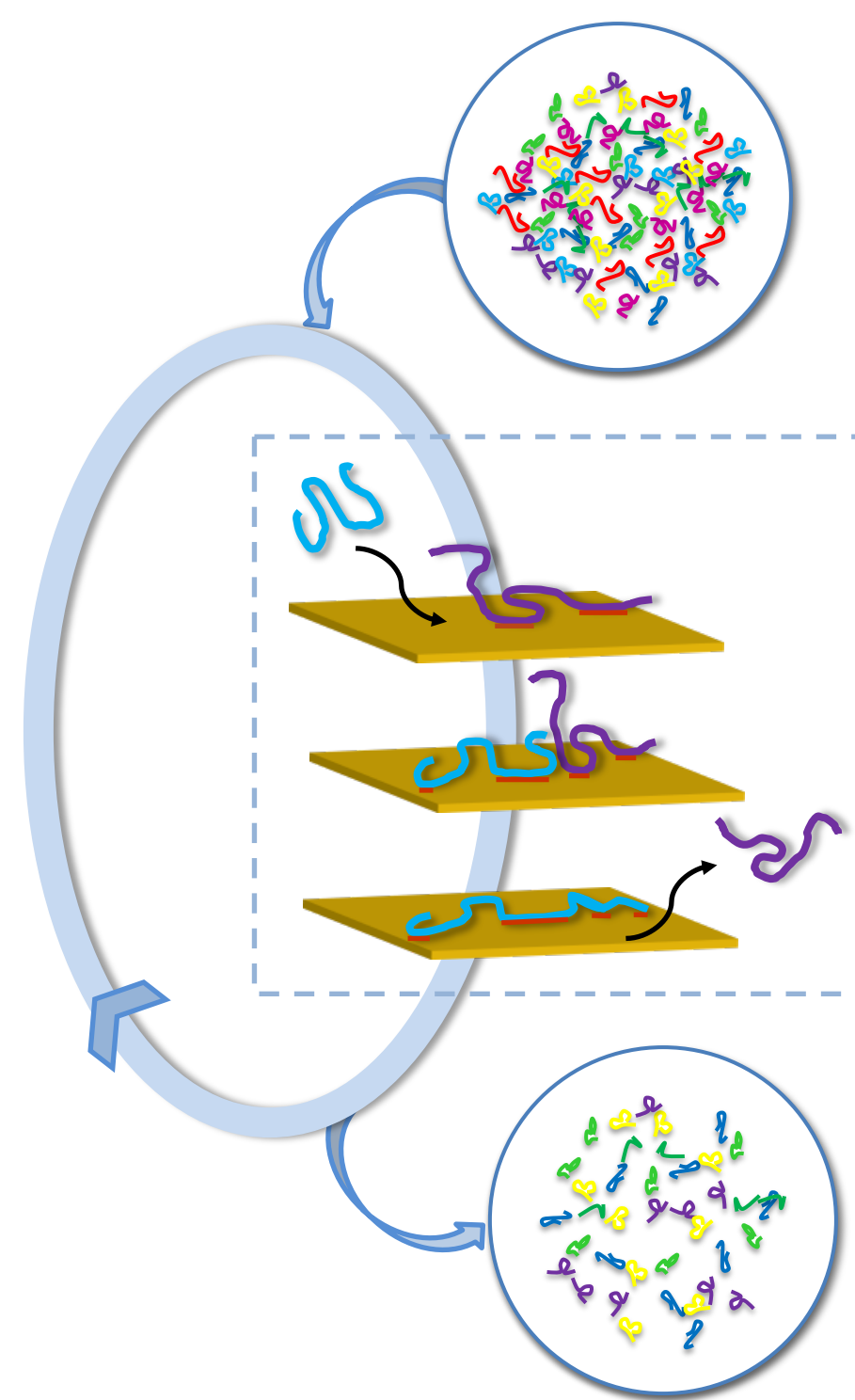
Key Advantages

- 1) Secondary structure element patterns may identify binding motif
- 2) Enables future screening library design

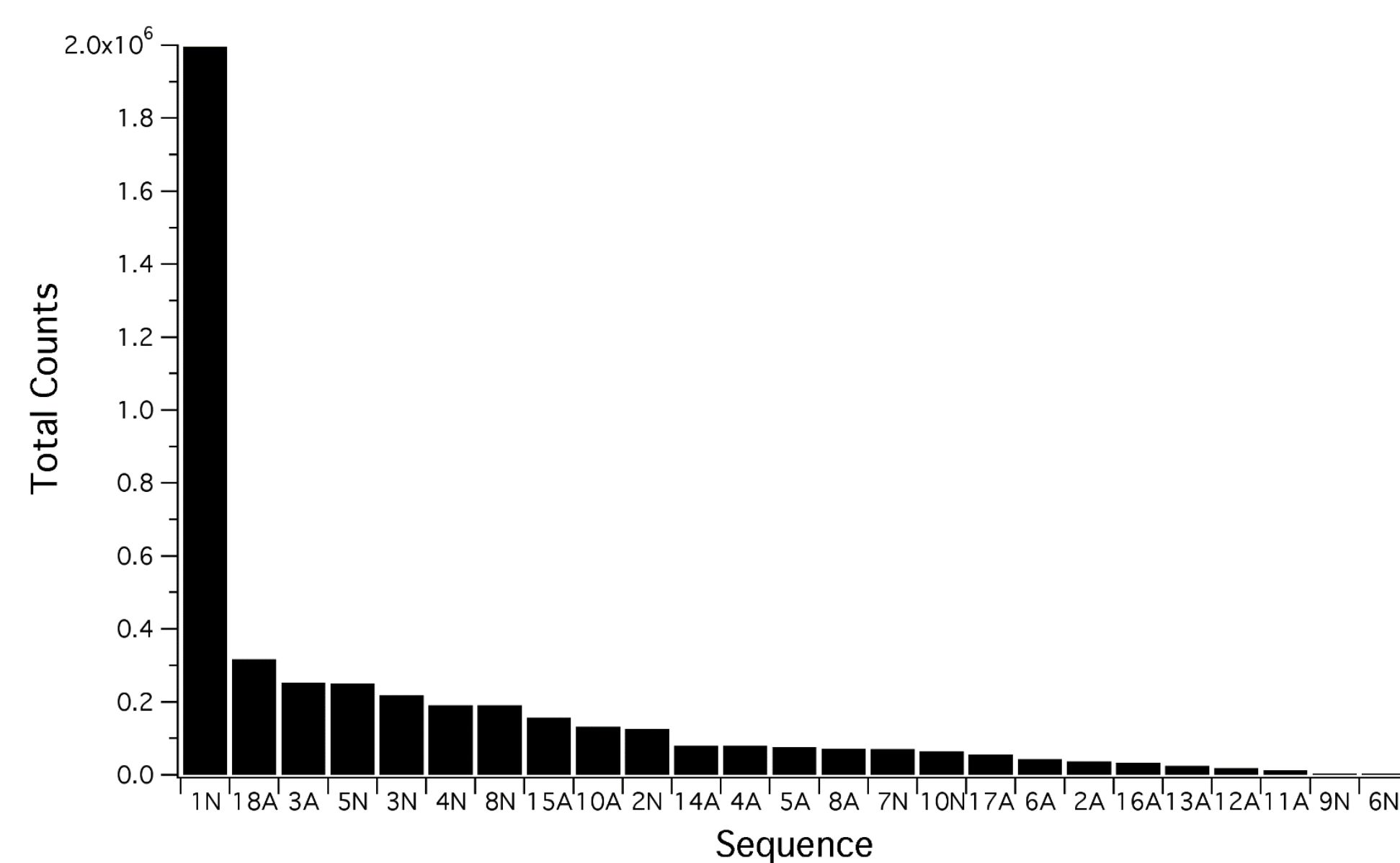
Selection of DNA Aptamers for Material & Biological Targets

As an alternative to laborious, error-prone evolutionary screening platform called SELEX, we developed an *in vitro* competition-based selection process called CompELS (competition-enhanced ligand selection) to identify DNA sequences from large (~10¹²) random sequence libraries called aptamers that selectively bind to a specific target with high affinity.

CompELS is a fast, versatile aptamer screening platform



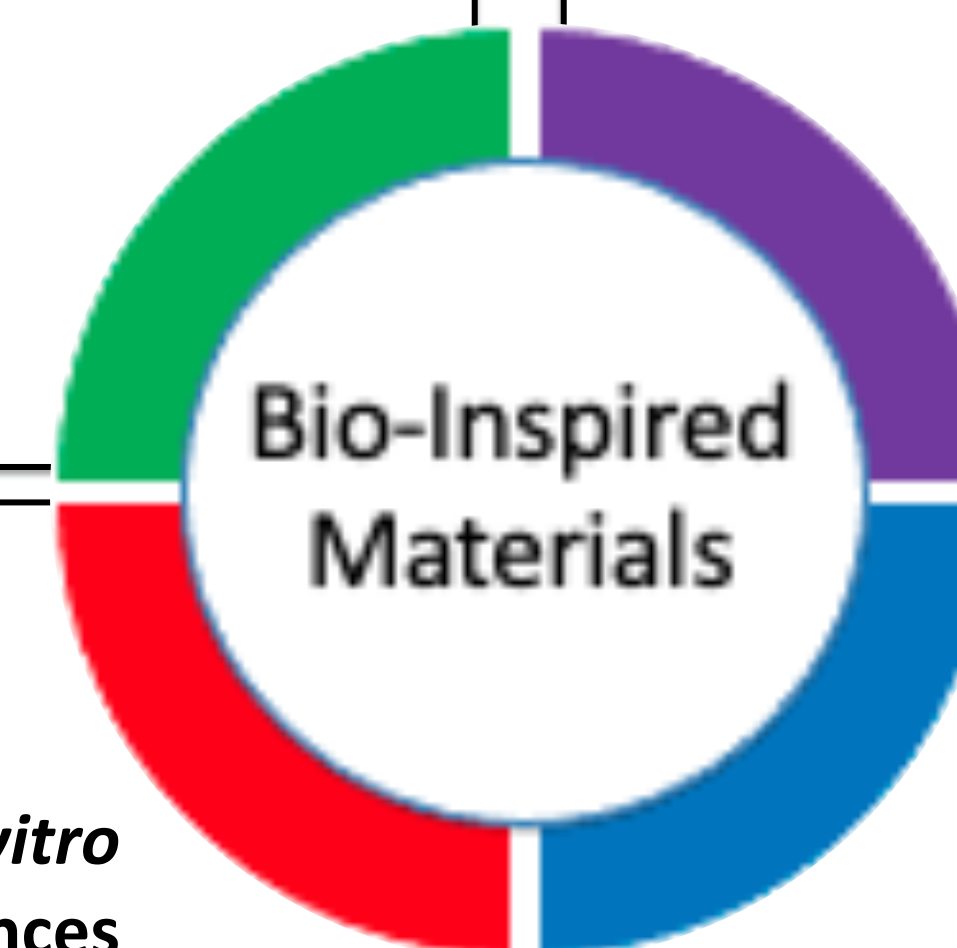
Ranking multiple aptamer sequences as high affinity ligands using Next Generation Sequencing (NGS) analysis



Tapp, Slocik, Dennis, Naik, Milam *ACS Combinatorial Sci.* 2018

Key Advantages

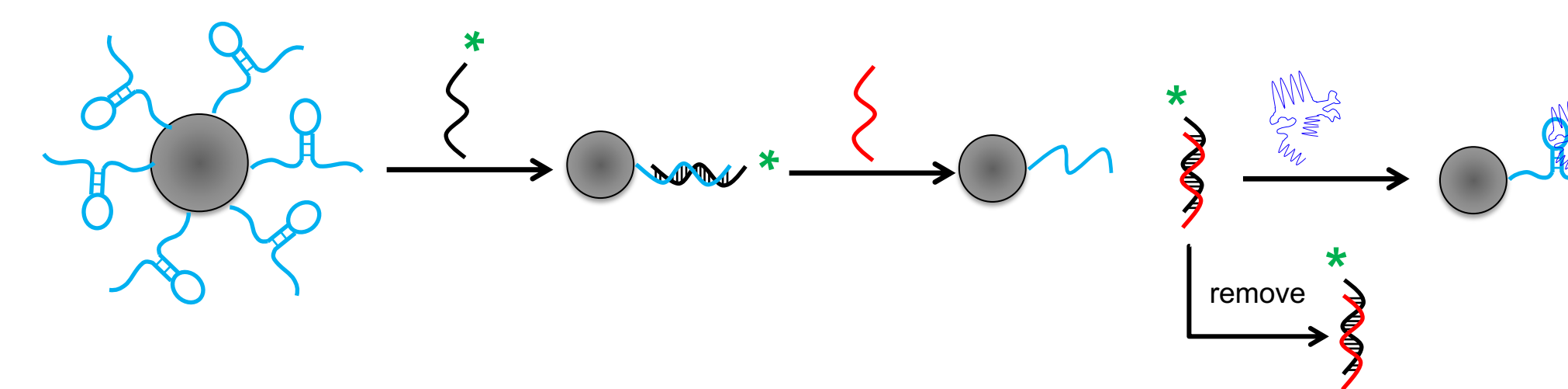
- 1) CompELS is faster and less error-prone than conventional evolutionary screening approach called SELEX
- 2) CompELS is versatile and adaptable to different target chemistries, sizes, etc.
- 3) Aptamers can serve as agents for therapeutics, diagnostics and materials surface functionalization



Employing DNA Aptamers to Program Release of Therapeutic Proteins

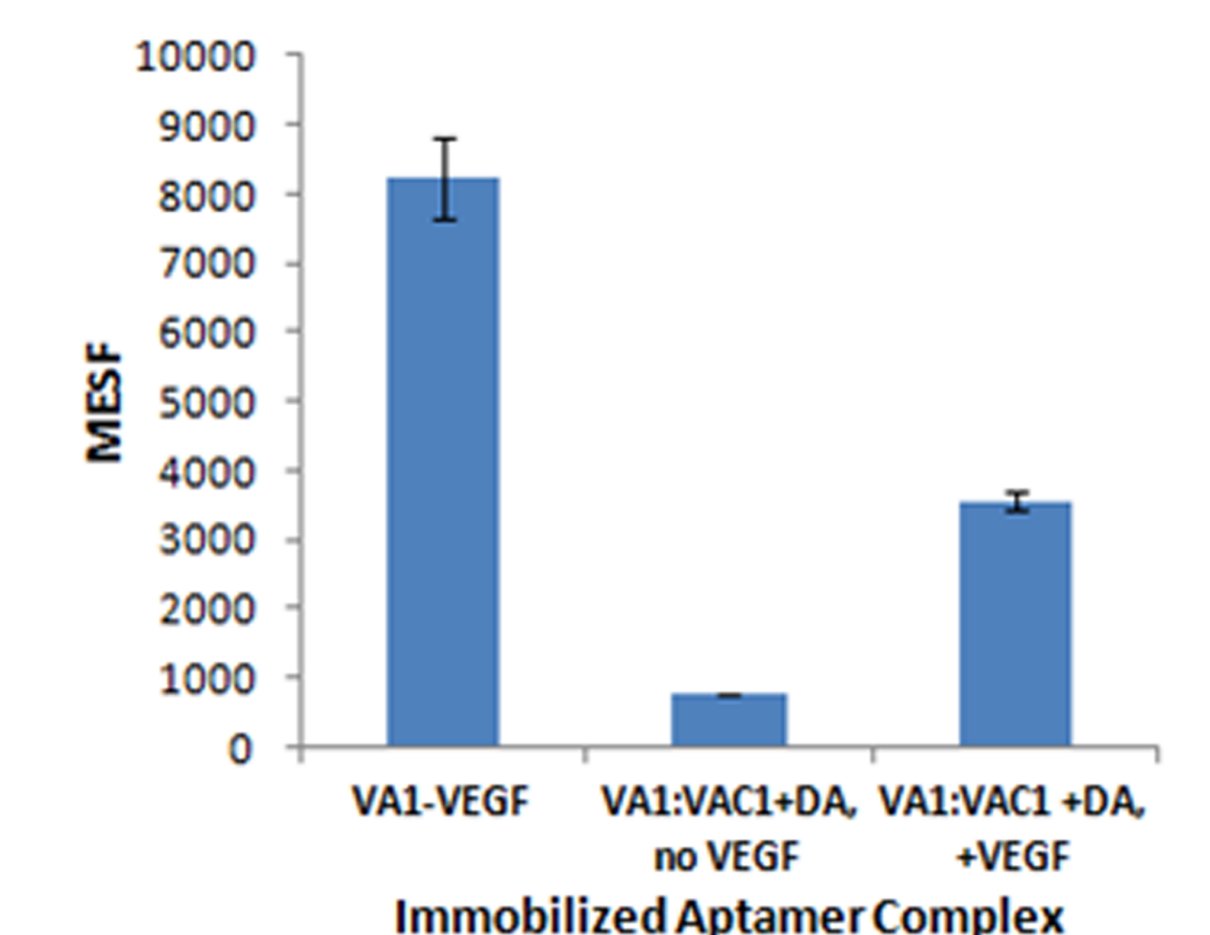
Aptamers have the ability to bind specifically to either a nucleotide or non-nucleotide target. Here, we explore the ability to regenerate aptamer binding activity for its various targets following a series of binding and release events.

Schematic of particle-immobilized aptamers that undergo serial binding, release, and binding events to various nucleotide and protein targets.



Dunaway, Sullivan, Siegel, & Milam, *Biointerphases* 2015

Partial Recovery of Aptamer Binding to VEGF Protein



Comparisons of VEGF binding to particle-immobilized aptamers (VA1) with no binding history (*far left*) and previously bound to oligonucleotide targets (*far right*) indicate that aptamer binding capabilities for its nonnucleotide target can be partially regenerated.

Key Advantages:

- 1) Potential to regenerate aptamer binding under biologically relevant conditions.
- 2) Programmable isothermal release or uptake of the non-nucleotide target by the aptamer sequences.
- 3) Method is potentially adaptable to other aptamer-target systems for therapeutic and diagnostic use.