New tools for Biology and Medicine

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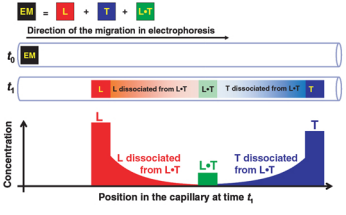
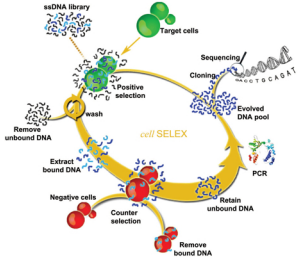
Modern biology and medicine require sensitive and informative tools for studies of molecular mechanisms of cellular processes, diagnosis of diseases at the molecular level and creation of mechanisms-based drugs. The research program at the Krylov lab is directed towards the creation of such tools. Our research can be subdivided into six general streams:

Kinetic studies of affinity interactions: Kinetic capillary electrophoresis (KCE) is a collection of separation-based methods that quantify binding parameters between interacting molecules.

Aptamer development: Aptamers are oligonucleotide-based affinity ligands that display strong binding capabilities and specificities towards their molecular targets. We employ a capillary electrophoresis-based partitioning approach to select aptamers from combinatorial libraries.



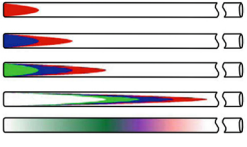


Smart drug candidates: Combining KCE methods for kinetic rate measurements with aptamer selection enables the isolation of aptamers with pre-defined binding parameters. Such "smart" aptamers can be fine tuned for use in pharmaceutical applications.

Aptamer-based biomarker discovery: Aptamer pools can be developed for targets on the surface of live cells. Such aptamer pools can differentiate between closely related cell types, including their healthy and diseased states. We use such pools to isolate and identify the molecular features that make cells different, thus identifying novel biomarkers without any prior knowledge of their identity.

Capillary microreactors: Capillaries can serve as nanoliter-volume microreactors. Our "Inject-Mix-React-Separate-and-Quantitate" (IMReSQ) approach allows for unwasteful and high-throughput studies of reaction kinetics.

Chemical analyses of single cells: Chemical cytometry, allows us to study highly heterogeneous tissues on a single-cell level. It involves the injection of a single cell into a capillary, separation of its individual components, their identification and quantification.



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