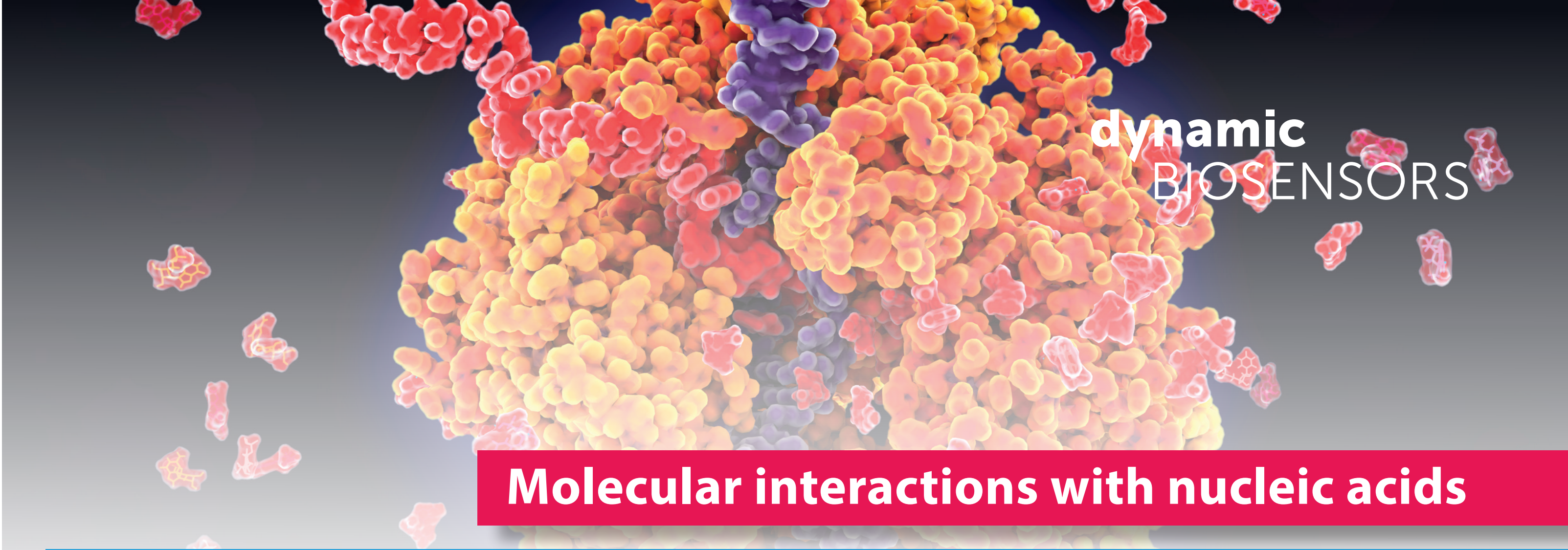
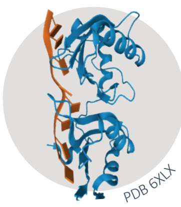


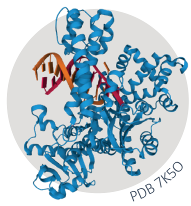
dynamic BIOSENSORS

Molecular interactions with nucleic acids

Studying nucleic acid binding molecules with switchSENSE®

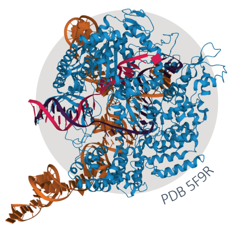


RNA Processing

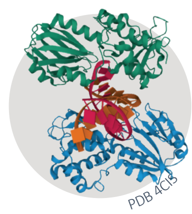


Enzymatic Activity and Inhibitor Screening

Nucleic Acids and Small Molecules



CRISPR-Cas9



Damage Recognition and Repair Mechanisms

Biosensors for real-time analysis of nucleic acid binding molecules

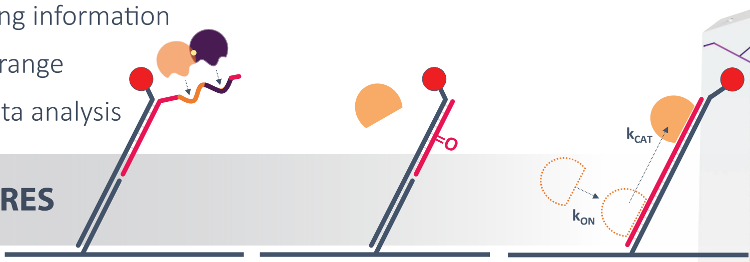
Easy biosensor modification with specific nucleic acid sequences

Real-time off-target binding information

High sensitivity up to fM range

Automated assays and data analysis

switchSENSE® FEATURES

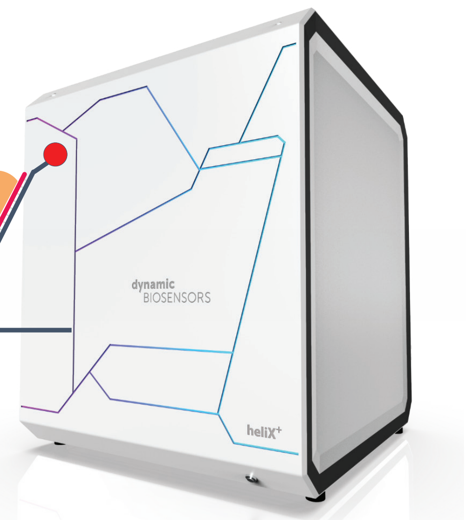


Determination of **cooperativity/avidity effects** of complex binders

Characterization of **kinetics and catalytic rates** of enzymes

Screening of inhibitors (IC50)

Small molecule interactions with nucleic acids



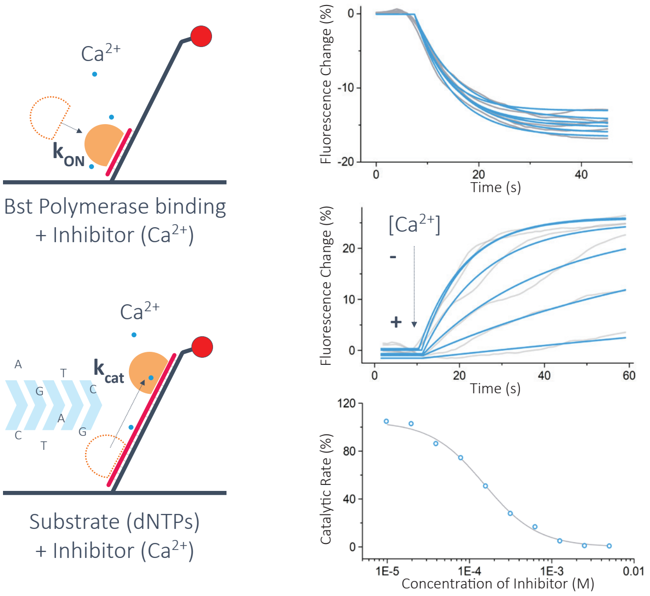
heliX® line of biosensor instruments

Contact **info@dynamic-biosensors.com** to speak to our application team about methodologies or to arrange a demonstration.

dynamic BIOSENSORS

www.dynamic-biosensors.com

Enzymatic Activity & Inhibitor Screening

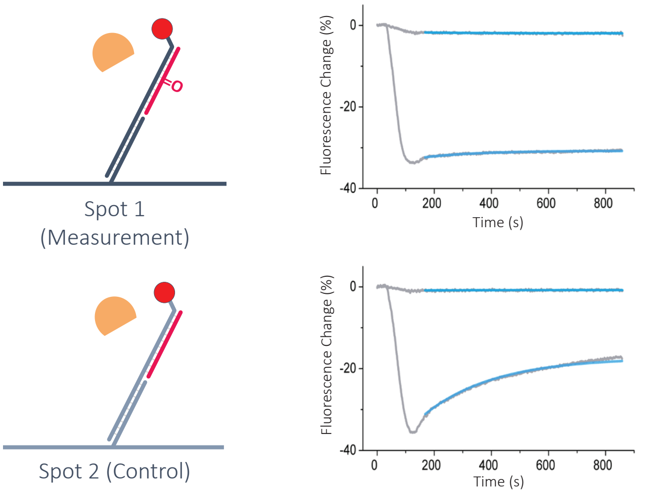


Characterizing kinetic and activity rates of enzymes (such as DNA/RNA polymerases and helicases) is of great importance for the development of drugs targeting those molecules.

switchSENSE® offers an easy inhibitor screening assay to study the compound´s mode of action and IC50 value. It has the unique capability to separately distinguish the inhibitor's effect on the protein-nucleic acid interaction and on the activity.

Inhibitor screening assay for Bst DNA polymerase activity in presence of increasing Ca^{2+} concentration. The Ca^{2+} ions don´t affect the binding (top graph), only inhibit the enzyme activity (middle graph). This yields an activity IC50 = 388 µM (bottom graph).

DNA Damage Recognition & Repair Mechanism

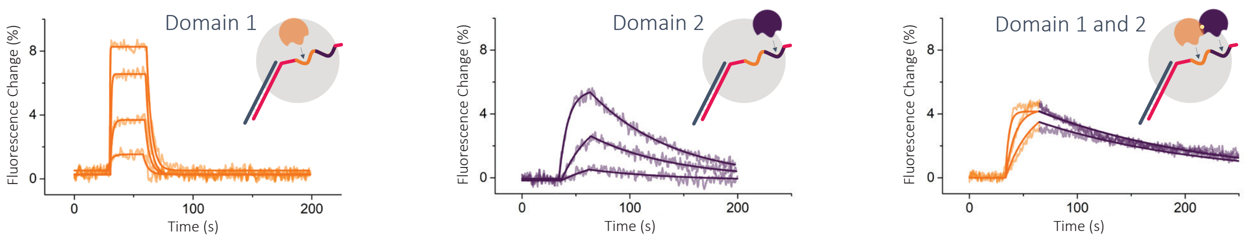


The **switch**SENSE® sensor surface carries a target DNA sequence (Spot 1) and a control DNA sequence (Spot 2) allowing the study of the kinetics of sequence specific binding and chemical modifications. Different modifications can be screened easily by changing the DNA sequence on the sensor surface.

The DNA repair enzyme hOGG1 binds 8-oxoguanine (8-oxoG), a common genomic base modification. This binding process is a crucial step in the base excision repair (BER) mechanism. In presence of the 8-oxoG modification (top graph), hOGG1 binding is stabilized, resulting in a slower dissociation rate than in the absence of this modification (bottom graph).

RNA Processing & Regulation

Splicing and post-transcriptional gene regulation often require complex protein-RNA binding mechanisms involving multidomain interactions. Impaired RNA binding results in defective RNA processing and is linked to human disease. **switch**SENSE® can determine the cooperativity/avidity, affinity and kinetic rates of such complex RBPs.



This RNA binding protein comprises two binding domains and modulates pre-mRNA splicing. To unravel the binding mechanism, RNA interactions of the individual and tandem domains are studied. Domain 1 has fast on- and off-rates, whereas domain 2 shows significantly slower rates. In the tandem protein, domain 1 drives the binding with its very fast on-rate, while domain 2 stabilizes the protein-RNA complex with its slower off-rate.

Publications & Further Information

Nemoz, C., et al. XLF and APLF bind Ku80 at two remote sites to ensure DNA repair by non-homologous end joining. *Nat Struct Mol Biol* **25**, 971–980 (2018).
Ponzo, I., et al. A DNA-Based Biosensor Assay for the Kinetic Characterization of Ion-Dependent Aptamer Folding and Protein Binding. *Molecules* (Basel, Switzerland), **24**(16), 2877 (2019).
Rueda, F.O., et al. Mapping the sugar dependency for rational generation of a DNA-RNA hybrid-guided Cas9 endonuclease. *Nat Commun* **8**, 1610 (2017).
Hyun-Seo, K., et al. An autoinhibitory intramolecular interaction proof-reads RNA recognition by the essential splicing factor U2AF2. *PNAS* **117**, 13, 7140-7149 (2020).
D. Ploschik, et al. DNA Primer Extension with Cyclopropenylated 7-Deaza-2′-deoxyadenosine and Efficient Bioorthogonal Labeling in Vitro and in Living Cells. *ChemBioChem* **19**, 18, 1949-1953 (2018).