

switchSENSE®

**Comprehensive biophysical information,
in one measurement**

Multi-parameter analysis

Binding parameters:

k_{on} , k_{off} , K_d , avidity
protein-protein interactions, nucleic acid binders,
small molecules, riboswitches, and more.



Multi-specific binders:

ternary complexes, affinity, avidity, stability,
 $t_{1/2}$, multispecific antibodies, PROTACs, ...



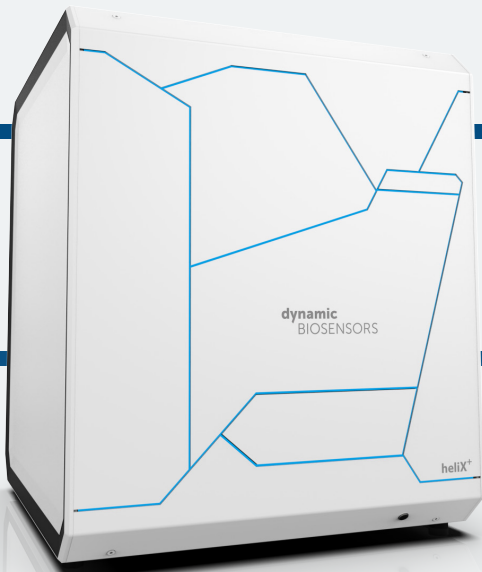
Enzymatic activity:

k_{on} , k_{off} , K_d , k_{cat} , K_M , IC_{50}
transcriptases, polymerases, helicases, ...



Conformational changes

Binding-induced protein conformational changes,
nucleic acid structural rearrangements (e.g. apta-
mers, RNA folding)

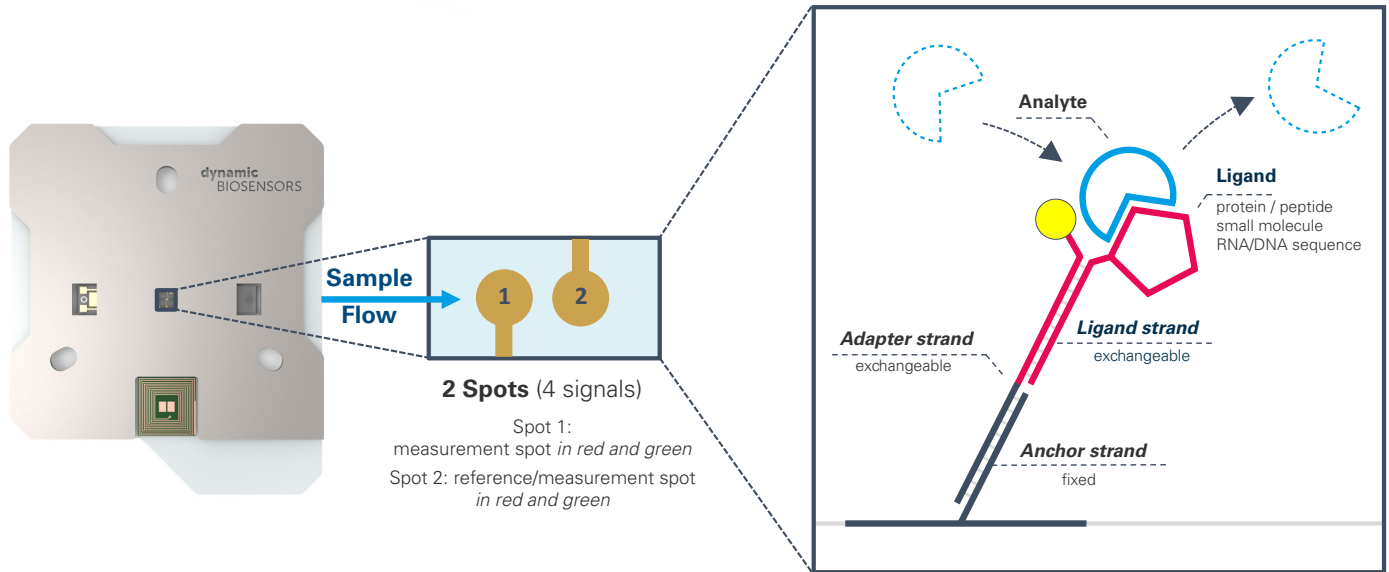


heliX®
instrument

The heliX[®] chip

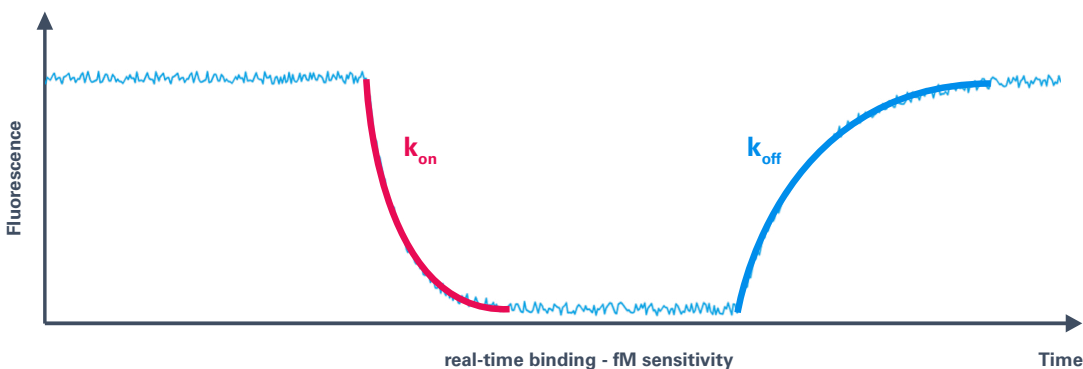
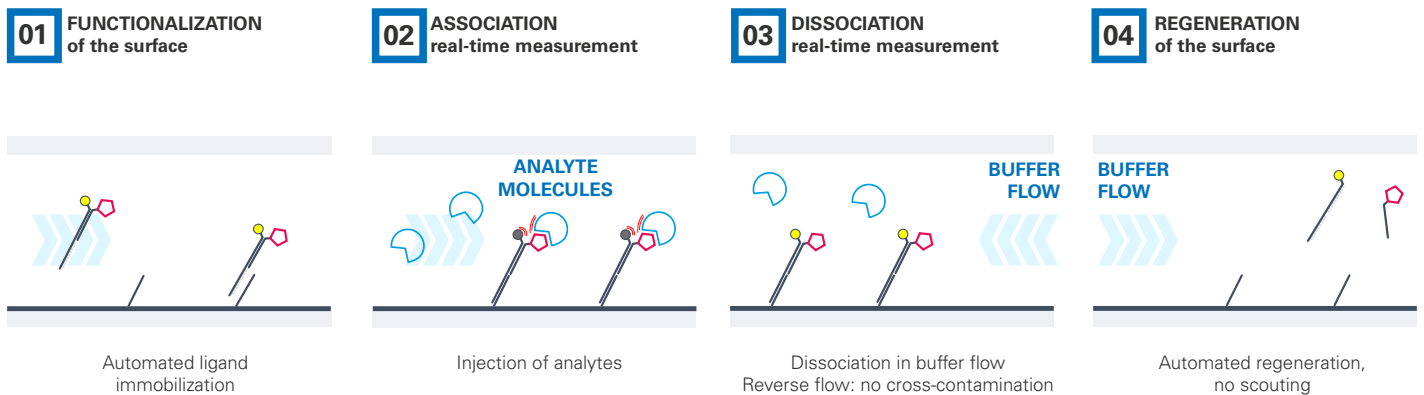
DNA nanolevers for limitless versatility

switchSENSE[®] is based on customizable DNA nanolevers on a chip surface. Each chip contains two electrodes ("Spots") with 2 different anchor strand sequences. The anchor strands remain fixed on the surface – the rest is up to you. It's like molecular lego!



Understanding interactions in unrivaled detail with Fluorescence Proximity Sensing

The dye fluorescence is quenched in the presence of analyte molecules. Changes in fluorescence directly report on association and dissociation.



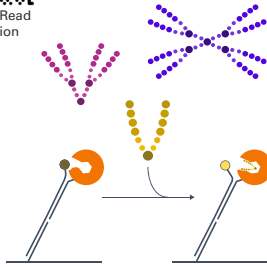
Multivalent multispecific binders

Fluorescence Proximity Sensing – Screening of multivalent peptides

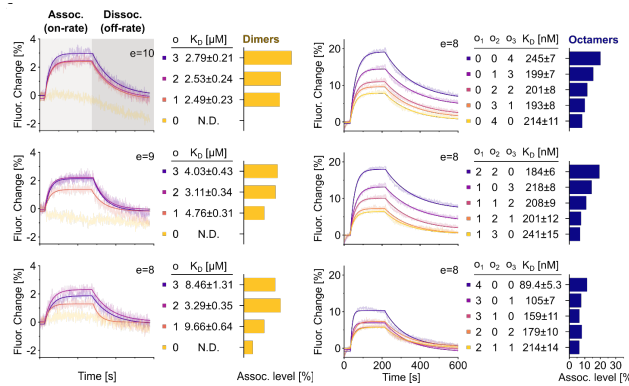
Screening of
> 100 multivalent peptides



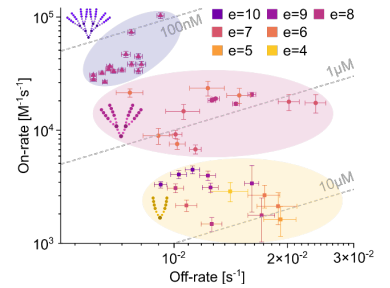
Scan and Read
Publication



switchSENSE® enables measurement of challenging dissociations:
multivalent peptides with complex rebinding effects



Kinetic analysis of multivalent peptide-protein interactions reveals structure-activity relationship

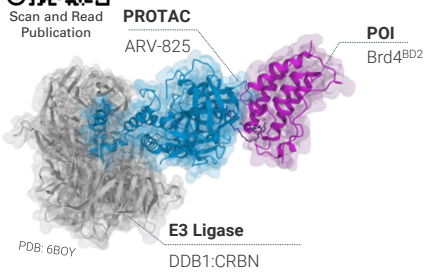


Schulte et al., *Communications Biology*, 2022

Targeted protein degradation and ternary interaction analysis



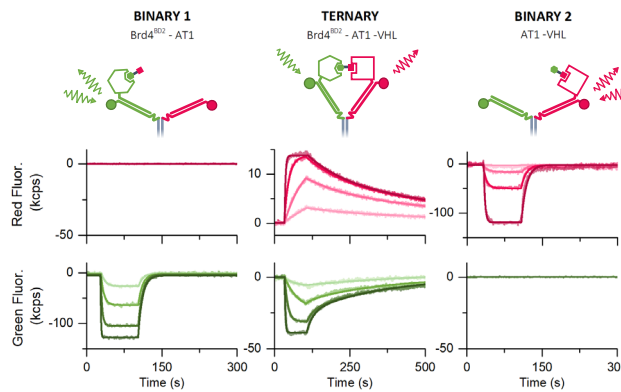
Scan and Read
Publication



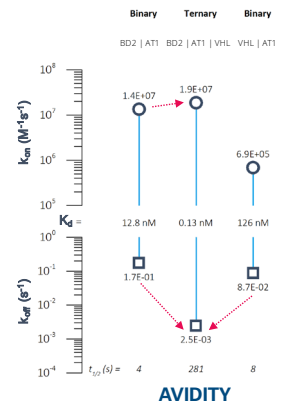
The insights into **proximity-mediated binding kinetics** can enable the development of PROTACs and molecular glues with improved properties for **targeted protein degradation**.

THE DNA Y-STRUCTURE

Analyte binary binding vs ternary complex formation using FRET



KINETIC ANALYSIS



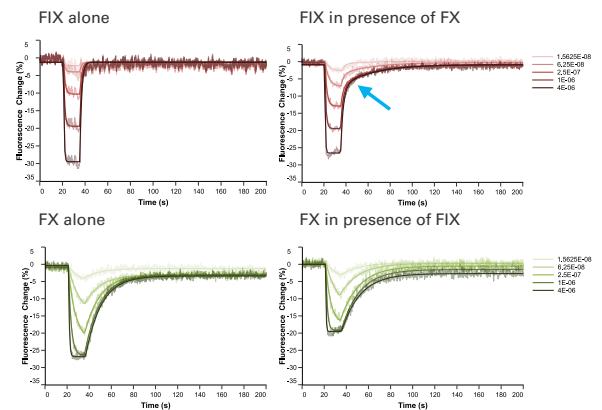
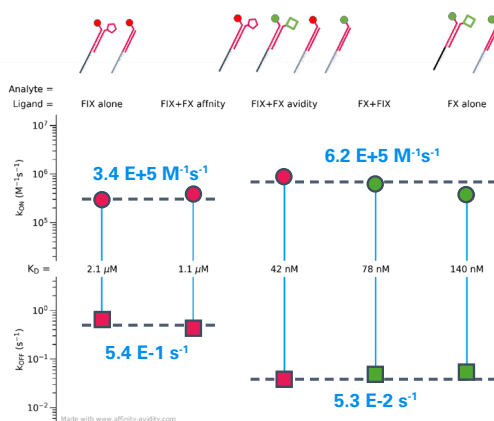
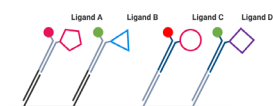
Ponzo et al., *ChemRxiv*, 2024

Affinity and avidity of bispecific antibodies

Binding of Hemlibra® to factor IX is stabilized by factor X, indicated by the additional slower off-rate in presence of factor X.

switchSENSE®

dual-color assays and ligand density control allow specific functionalisations of the surface and investigation of affinity and avidity of bispecific antibodies.



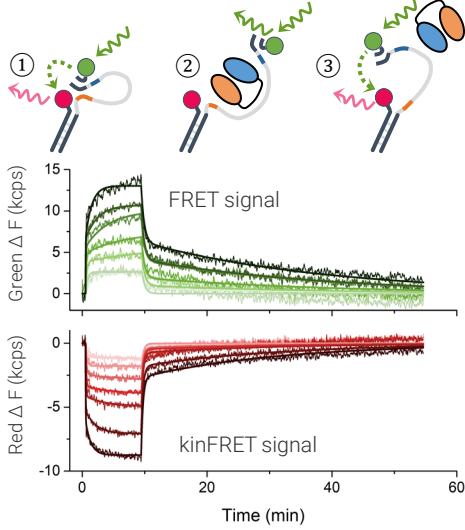
DNA/RNA binders

Detection of RNA folding and aptamer structural changes



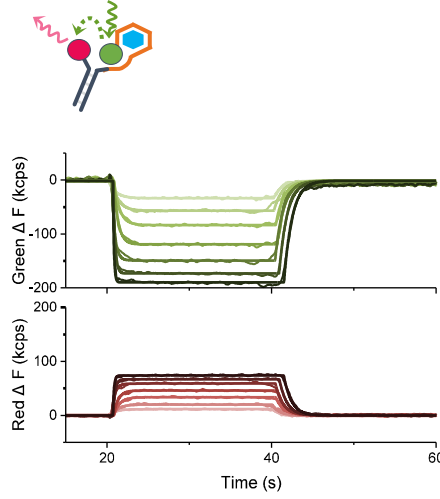
RNA LOOPING

Detection of RNA remodelling upon protein binding

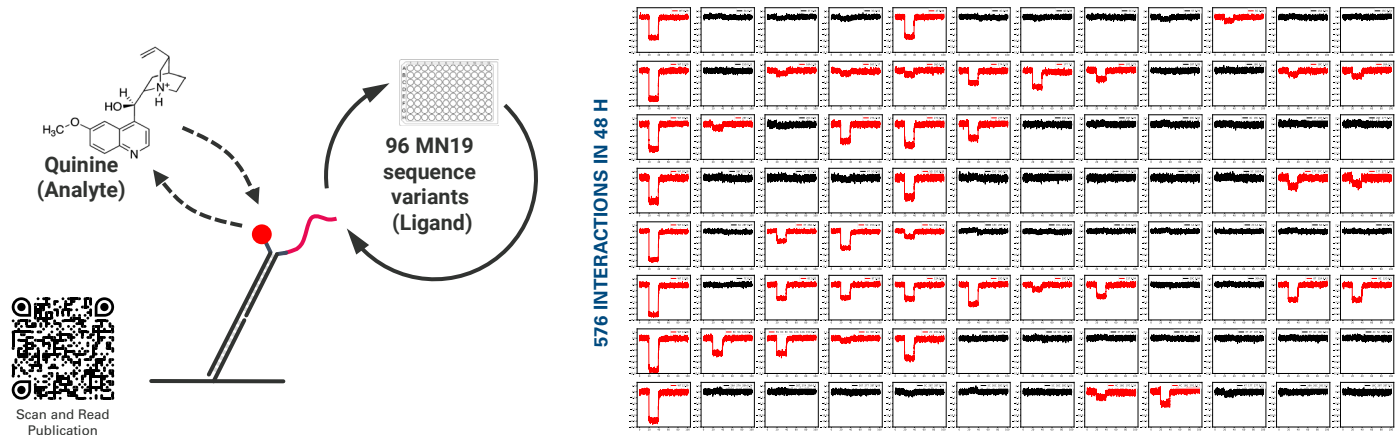


APTAMER FOLDING

Small molecule-induced structural changes

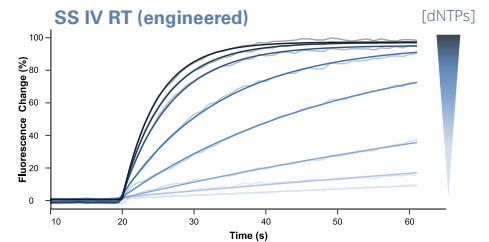
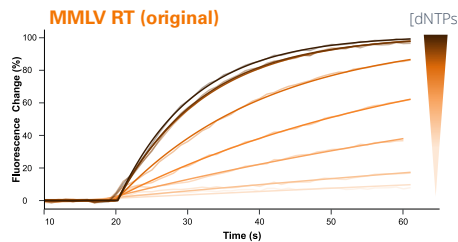
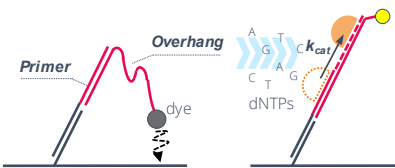


Aptamer sequence screening for high affinity and specificity engineering

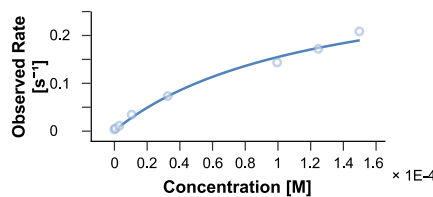
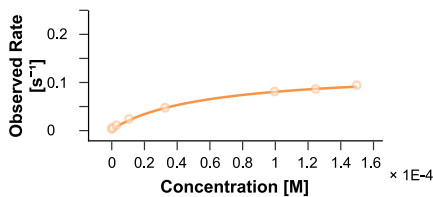


Real-time monitoring of reverse transcriptase enzymatic activity

Reverse transcriptase (RT) is the key enzyme for synthesizing cDNA from RNA templates



Catalytic rate plots based on real-time elongation show enhanced activity of the engineered variant compared to the original RT

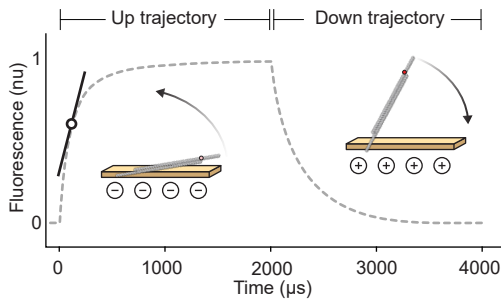


	k_{cat}
MMLV	0.088 ± 0.008
SS IV	0.247 ± 0.018

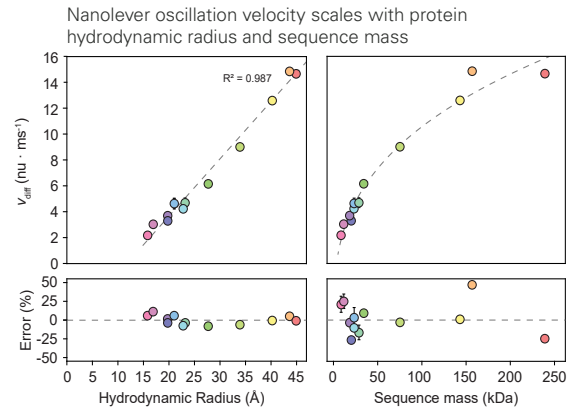


Protein conformational changes

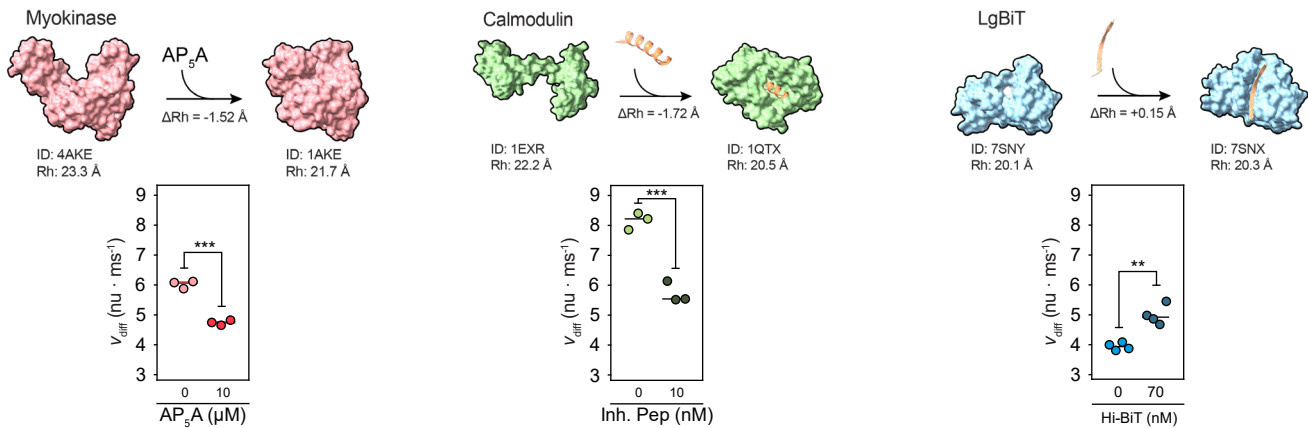
Molecular friction sensing using DNA origami nanolevers



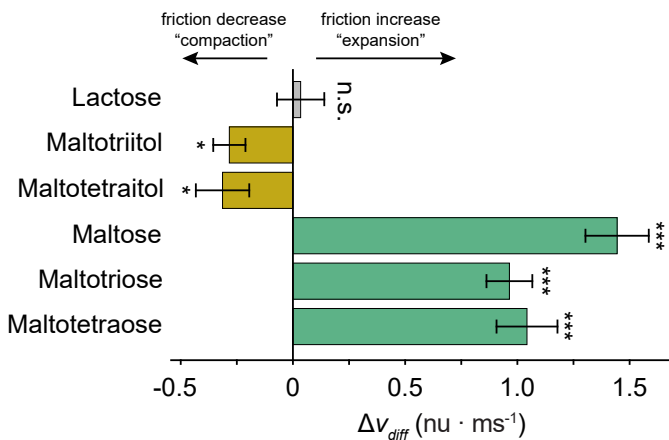
DNA origami-based nanolevers are electrically actuated to oscillate, and oscillation dynamics are monitored in real time using electrically triggered time-correlated single photon counting.



Binding-induced conformational changes can be detected by changes in switching velocity



Functionally relevant conformational states of the maltodextrin-binding protein MaIE



MaIE interacts with a broad range of (hydrogenated) oligosaccharides, yet only maltodextrin ligands induce a conformation that is compatible with docking to the ABC transporter MalFGK2. Conformational change analysis reveals these distinct conformational changes of hydrogenated maltodextrins and cognate maltodextrins.

Additional application examples

Explore publications utilizing **switchSENSE**® for a multitude of molecular interaction challenges



Bibliography



Automatic chip loader

Automatic exchange of **5 chips**

RFID tags for **seamless traceability**

Sample temperature adjustable between 15 °C and 40 °C



Autosampler

Fully **automated throughput** using 96 or 384 well plates

Additional space for different glass vials

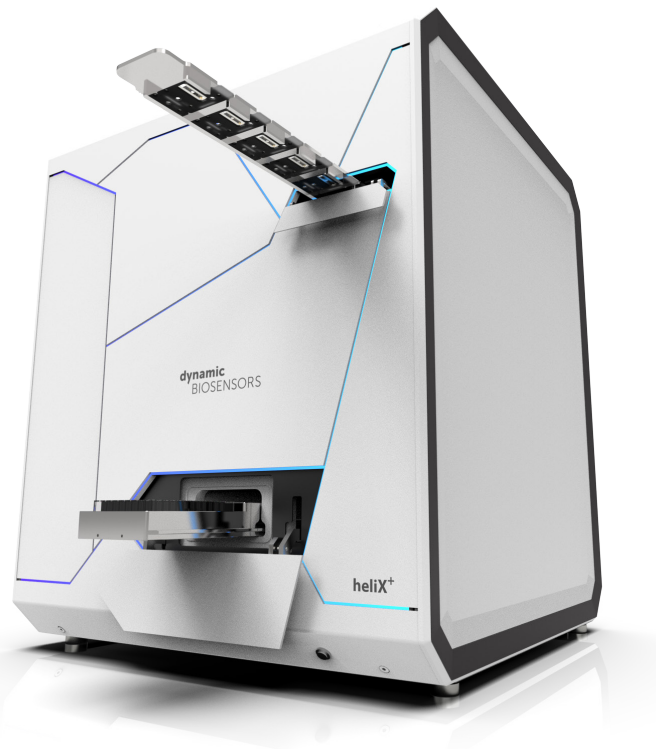
Temperature controlled sample compartment (4 - 40 °C)



Modular connection to heliOS network

Control of several **heliX**® units at the same time

Autonomous device operation with embedded control system



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Bruker Switzerland AG

Fällanden · Switzerland
Phone +41 44 825 91 11

Bruker Scientific LLC

Billerica, MA · USA
Phone +1 (978) 663-3660

Scan the QR-Code
for more details



info.biosensors@bruker.com
bruker.com