英柏 Inter-Bio

Surface Plasmon Resonance System

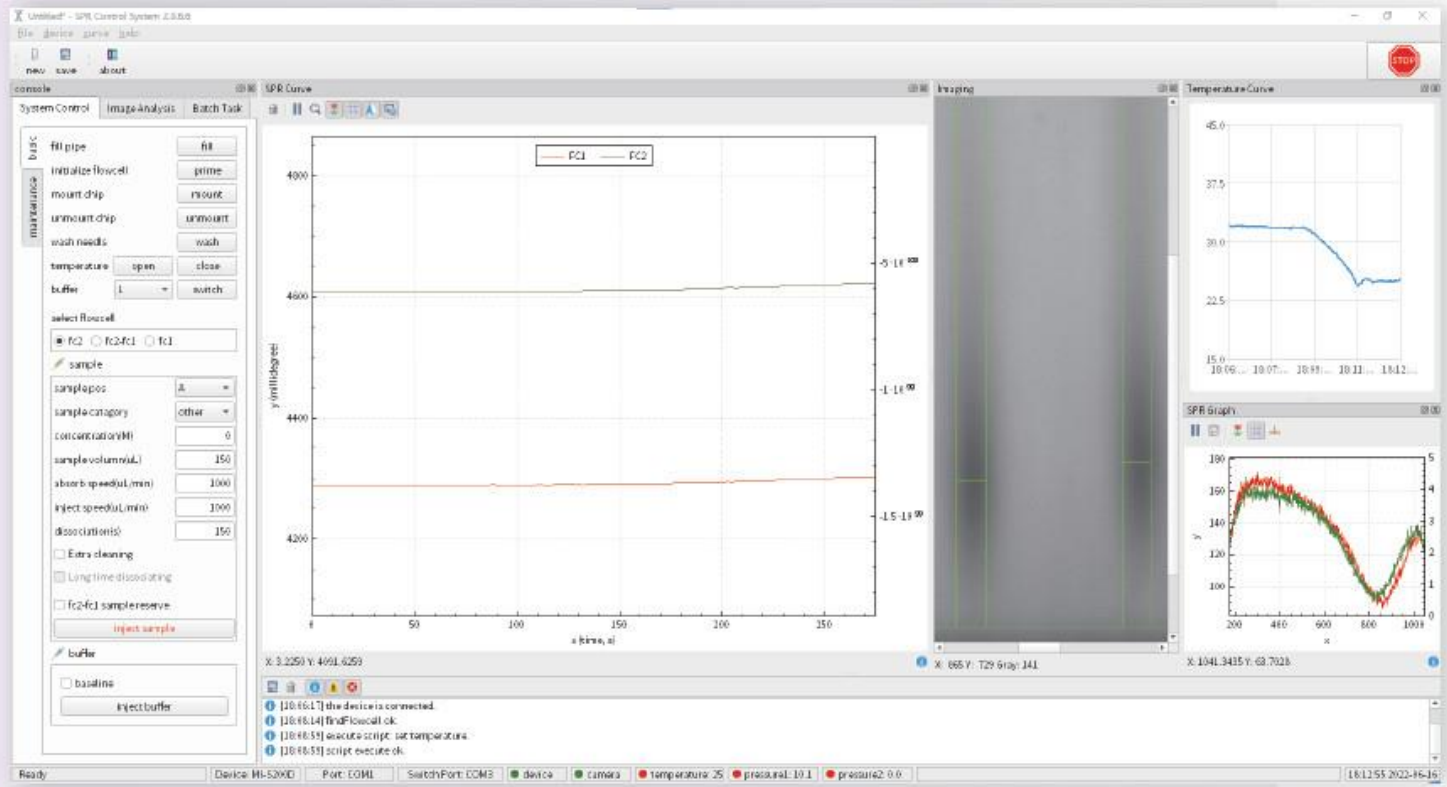
MI-S200D

Features

- Fully independent-developed designs and productions of core parts
- Real-time monitoring of response curve
- Stable and robust microfluidic system with accurate flow path control
- Wide dynamic range of refractive index
- Automatic sample injection, flow path cleaning and maintenance
- Unattended working time up to 60 hours
- Independently developed control system and data analysis software
- Reserving flow paths and system control interfaces to easily connect to chromatography, mass spectrometry and other instruments

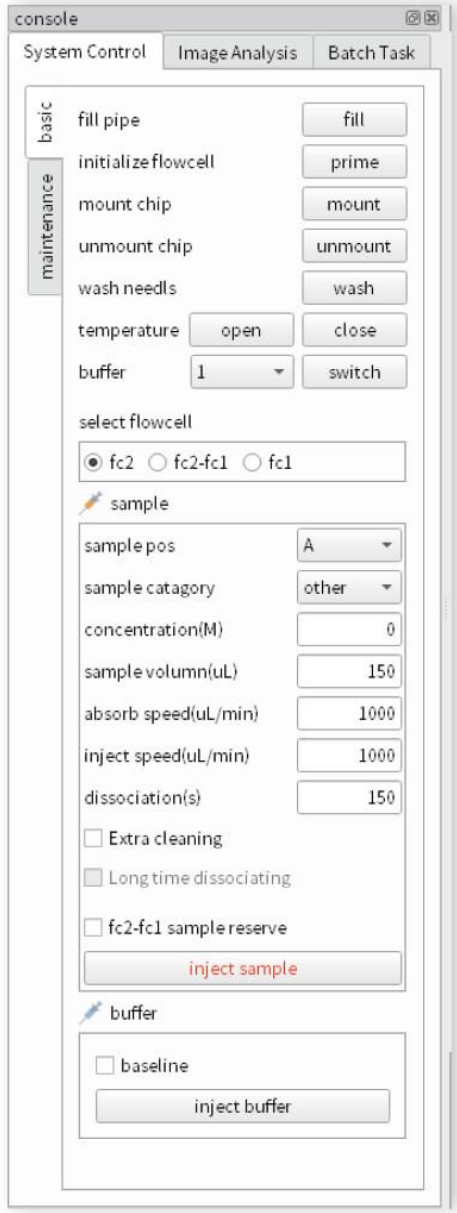
Fully self-developed control and analysis software

- Real-time monitoring of multi-parameter process
- Flexible command control provides convenience to the user
- Real-time SPR dip monitoring
- Convenient and quick report point setting
- Intelligent data quality assessment

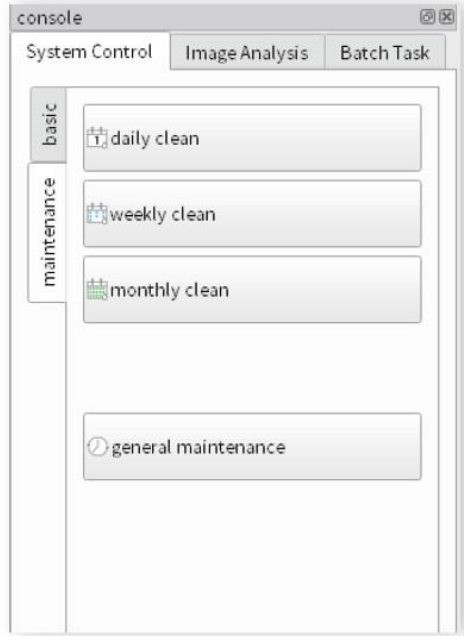


英柏 Inter-Bio

Intuitive Interface Concise Controls



- Intuitive and clear SPR operation control interface
- Flow path selection and prime, buffer switching and concentration setting are clear and concise
- Regular maintenance alarm to keep the system at top performance throughout time

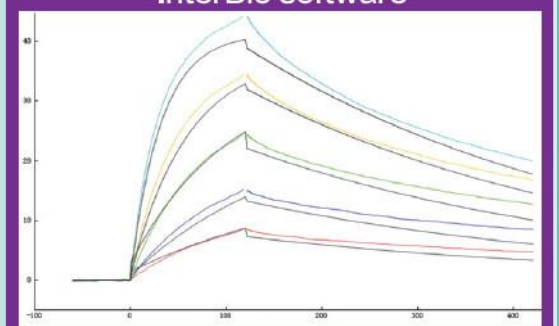


Fully self-developed core algorithm for kinetics analysis

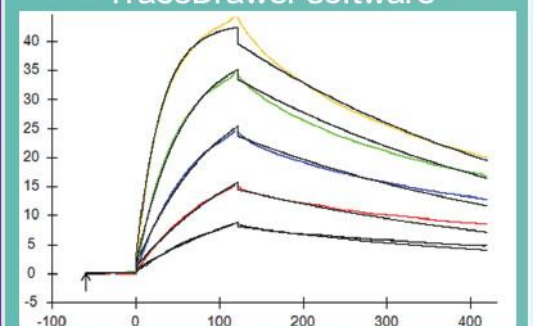
The analysis software independently developed by Inter-Bio is used to process SPR data from a variety of sources, the kinetics results acquired are well matched with the ones from TraceDrawer™ – an authoritative third-party kinetics analysis software as well as from Biacore T200 evaluation software.

	k_a(1/Ms)	k_d(1/s)	K_D(M)
InterBio	8.95E+05	2.63E-03	2.93E-09
TraceDrawer	9.84E+05	2.39E-03	2.43E-09
Biacore	9.57E+05	2.79E-03	2.92E-09

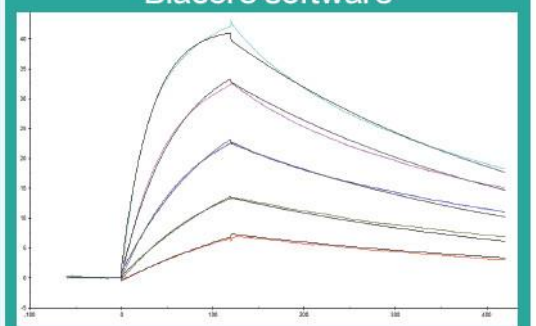
InterBio software



TraceDrawer software



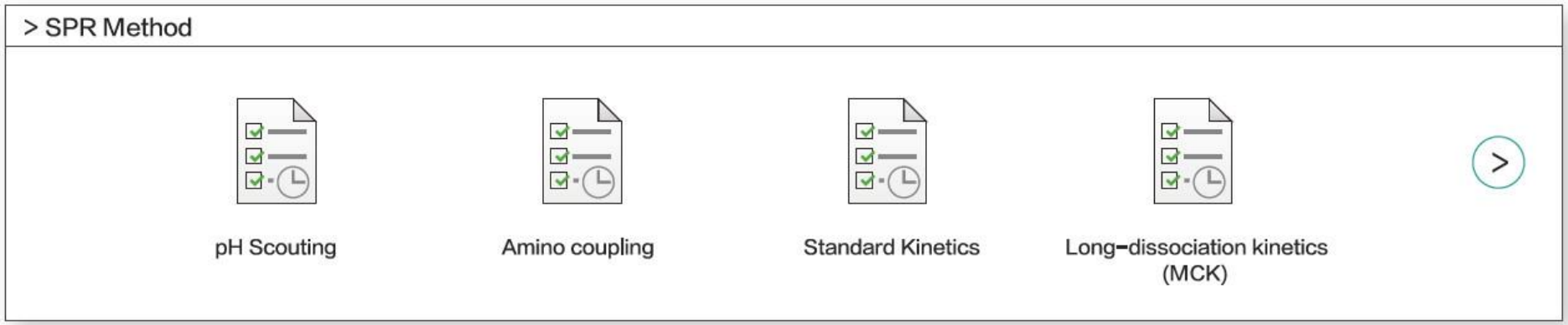
Biacore software



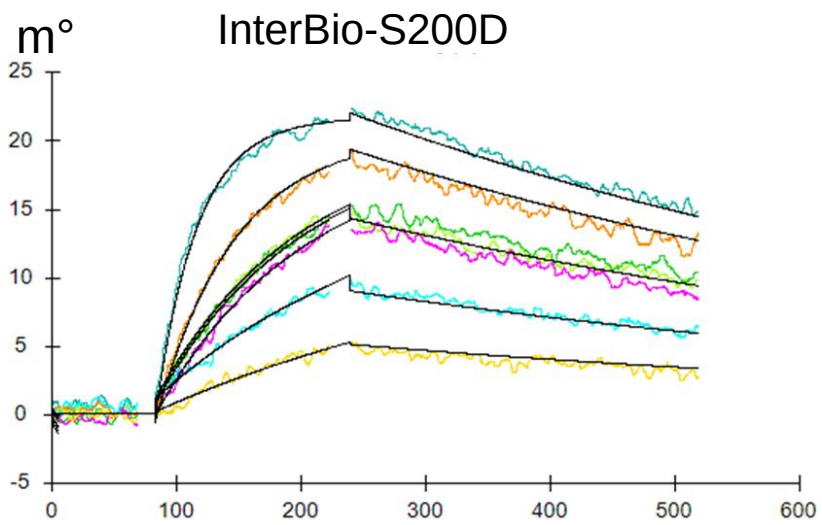
Features of Softwares

- Global fitting algorithm
- Local Rmax fitting (for capture method)
- Intelligent data quality assessment
- Both kinetics and steady-state fitting models
- Fully independent intellectual property rights

A variety of method templates for a quick start of SPR experiment

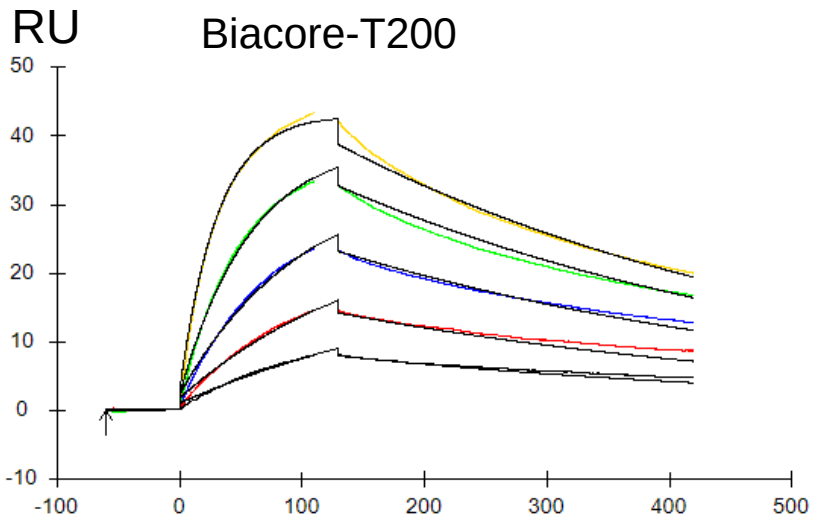


Monoclonal mouse-anti-human β2-microglobulin and human β2-microglobulin kinetic result



ka (1/(M*s))	kd (1/s)	KD (M)
8.88E+05	1.51E-03	1.70E-09

Ligand: Monoclonal mouse-anti-human β2-microglobulin
Analyte: microglobulin, 2-32nM
Assication time: 120s
Dissociation time: 300s
Analysis: TraceDrawer, 1:1 model

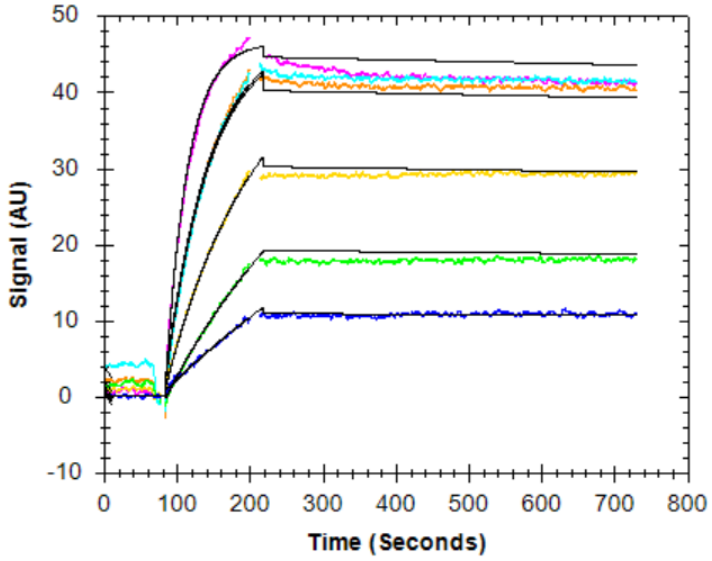


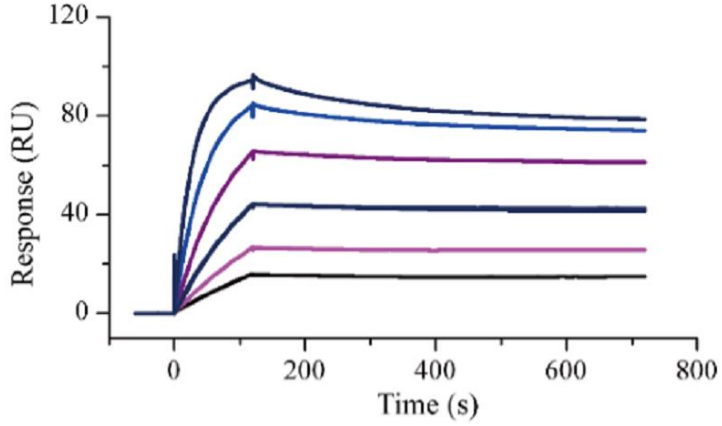
ka (1/(M*s))	kd (1/s)	KD (M)
9.40E+05	2.38E-03	2.54E-09

Ligand: Monoclonal mouse-anti-human β2-microglobulin
Analyte: microglobulin, 2-32nM
Assication time: 120s
Dissociation time: 300s
Analysis: TraceDrawer, 1:1 model

Case 1： Research of molecular mechanism of coronavirus infection

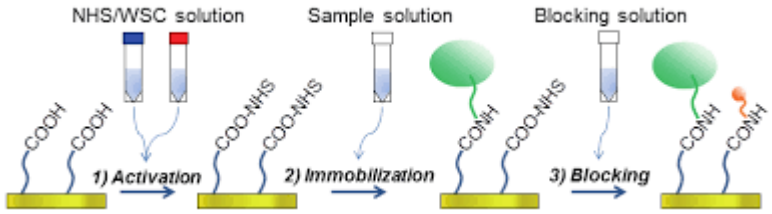
Coronavirus spike protein plays a key role in viral infection by recognizing host cell receptor ACE2. Understanding the binding mechanism between RBD (Receptor Binding Domain) of coronavirus spike protein and ACE2 receptor in cells is of great significance for elucidating the infection mechanism of coronavirus as well as developing specific drugs. Using Inter-Bio MI-S200D SPR Instrument and IB-CM5 sensorchip, researchers measured the binding affinity Ko between virus RBD and cell ACE2 receptor, which was about 200 pM and very similar to the results obtained on Biacore S200 (right).

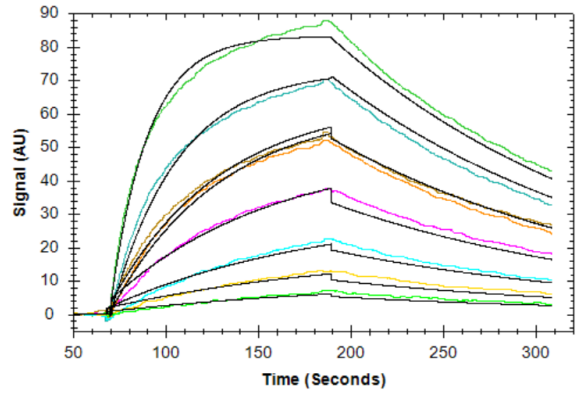




source：*Molecules* 2021, *26*(1), 57; https://doi.org/10.3390/molecules26010057

Case 2： drug development（antigen – antibody)

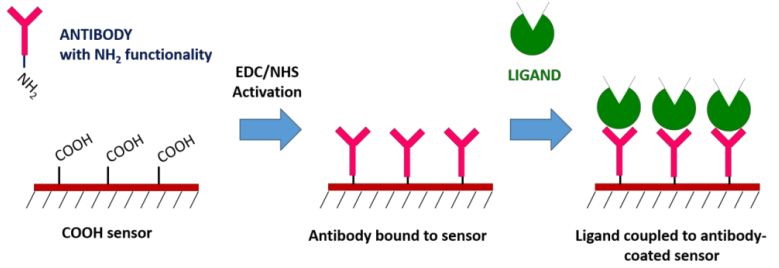


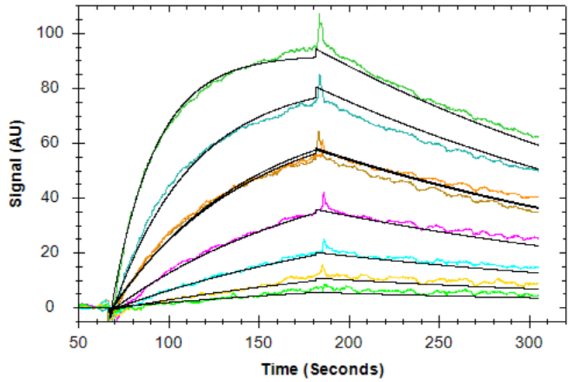


S200D-amino coupling

Researchers have used amino coupling method and antibody capture method to determine the interaction between the N-terminal domain (NTD) on subunit of virus spike protein and the neutralizing antibody on InterBio MI-S200D SPR Instrument. Almost same affinity results (affinity about 150 nM) were obtained using two different ligand immobilization strategies.

	ka (1/Ms)	kd (1/s)	KD (M)
Amino coupling	4.34E+04	5.97E-03	1.38E-07
Capture method	2.94E+04	5.21E-03	1.77E-07





S200D-capture method

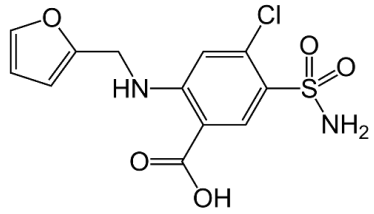
Case 3： Binding specificity （protein – LMW compound）

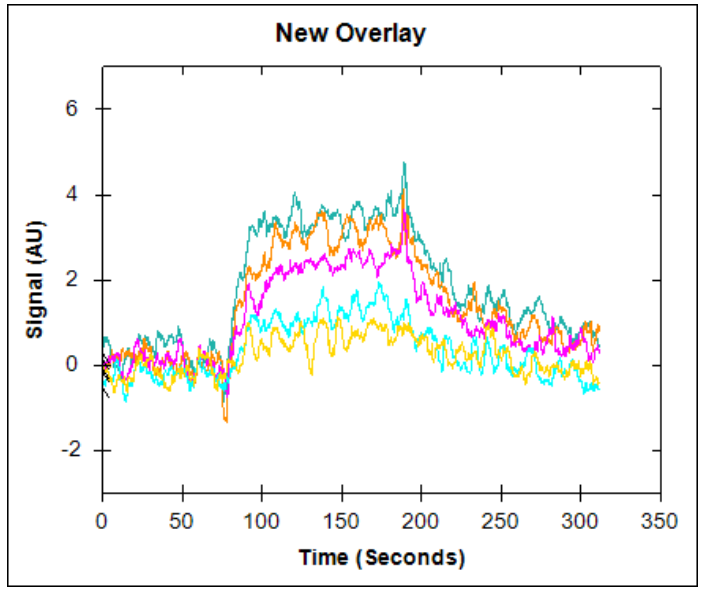
Screening small molecule compound with specific binding characteristics is an important task in drug development.

Intebio MI-S200D SPR system can well distinguish small molecular compounds with specific binding.

The results on the right show specific binding of Carbonic Anhydrase II (CA II) to Furosemide (left), while CA II could not bind to Warfarin, a negative control compound (right)

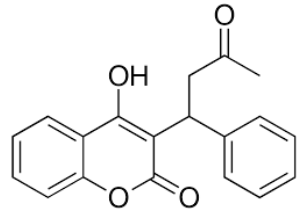
CA II – Furosemide

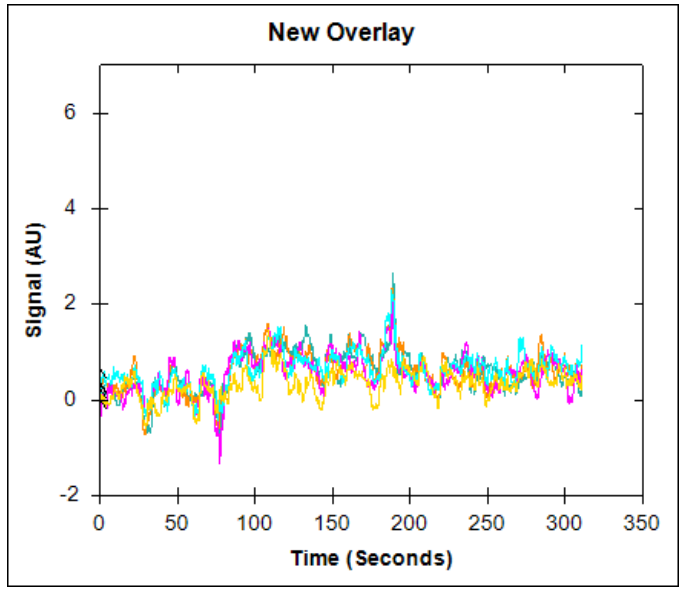




(0.469 µM - 7.5 µM)

CA II – Warfarin



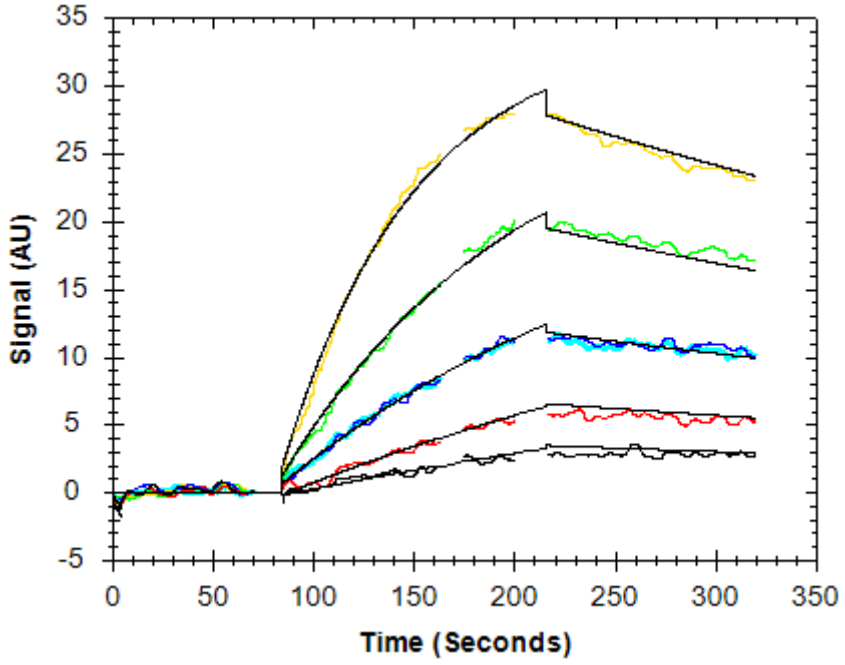


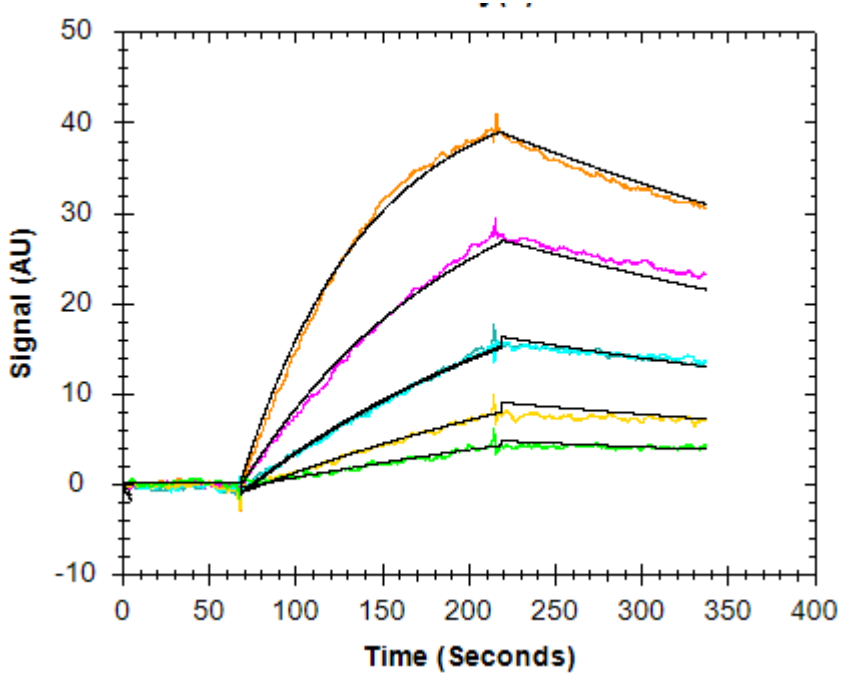
(0.469 µM - 7.5 µM)

Case 4： Validation of data reproducibility (antigen-antibody）

Excellent Repeatiblity of MI-S200D

Repeatability is very important for a high-end analytical instrument. In the left figure, the SPR sensorgram of the interaction between microglobin and its antibody is analyzed by Inter-Bio MI-S200D. The antibody is immobilized by amino coupling and 2-32 nm analyte (2 fold diluted) microglobin was injected(8 nm as repeated experiment). Among them, the colored line represents raw data, and the black solid line represents the fitted curve using 1:1 fitting model from Inter-Bio. It can be seen that the consistency and repeatability of the data are very good. The affinity was ~3 nm.

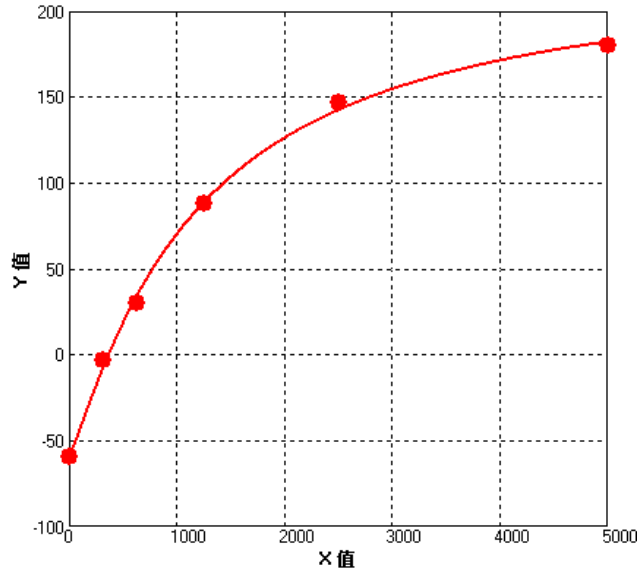




Case 5： Analysis of active concentration

Measurement of active concentration of protein drugs

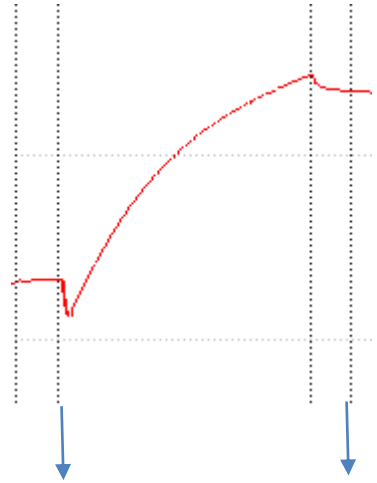
Researchers used Interbio MI-S200D SPR system and IB-CM5 sensorchip to measure the active concentration of monoclonal antibody cetuximab. The standard curve of concentration of cetuximab was acquired by using four-parameter fitting equation provided in the SPR analysis software independently developed by Interbio. The method's recovery rate of the positive control was 95%-105%.



方程: y = (A - D) / [1 + (x/C)^B] + D

A	=	228.34529
B	=	-1.14951
C	=	1188.56933
D	=	-58.33015
r^2	=	0.99871

Con(ng/ml)	Recovery(%)		Average	RSD%
	Repeat 1	Repeat 2		
875	96.48	102.95	99.72	4.59



Baseline report point

Dissociation report point