Antibody Analytics

BCMA: An off the shelf, SPR assay for the assessment of the binding of BCMA-targeted antibody-based therapeutics. Determine full binding kinetics in a single run.

B-cell maturation antigen (BCMA) / TNFRSF17 / CD269, is a cell surface receptor of the TNF receptor superfamily expressed on the surface of mature B cells. Engagement of this receptor by its respective ligands (TNFSF13B / BLys / BAFF and TNFSF13 / APRIL) promotes B cell survival and plays a role in the regulation of humoral immunity. It is also over-expressed in multiple myeloma and is a prime therapeutic target for the development of antibody-based therapies, including immune cell engagers, antibody drug conjugates and cell therapies.

- ✓ **Assay is pre-developed** on the Biacore 8K; simply plug and play
- ✓ **Expedited turnaround time** to obtain a **full kinetic profile** for your BCMA-targeted molecule
- ✓ Your molecule will be **analysed alongside an anti-BCMA positive control,** validated to bind to soluble and membrane bound BCMA.

Method	Ligand	Analyte	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	Chi2 (RU2)	Fit Model
Human Antibody Capture	Anti-BCMA human IgG1	Human BCMA	2.92E+05	7.31E-04	2.52E-09	111	0.26	Langmuir 1:1 binding

Kinetic data reported are calculated from the **average of four runs.**

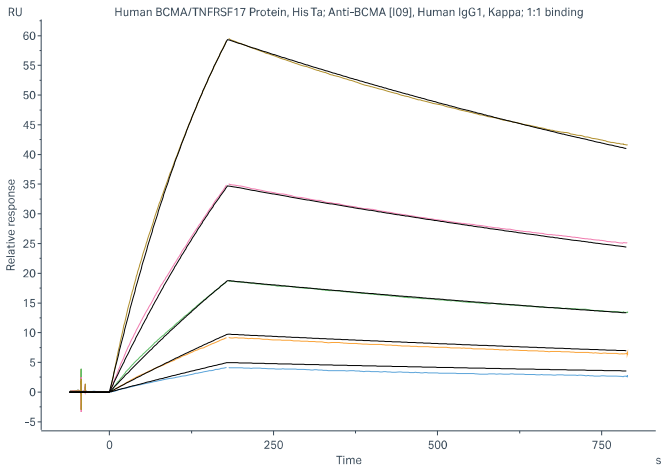

Figure 1: Human anti-BCMA [I09] IgG1, captured on a CM5 chip *via* its CH1 light chain domain, binds human BCMA.

Binding responses are shown as a plot of relative response *vs* time.

A 1:2, 5-point dilution series of human BCMA was injected over anti-BCMA human IgG1 using a **Biacore 8K** instrument.

A **Langmuir 1:1 model** was used to determine the kinetic parameters for the interaction (sensorgrams represent one of four independent runs).

Antibody Analytics

CD19: An off the shelf, SPR assay for the assessment of the binding of CD19-targeted therapeutics. Determine full binding kinetics in a single run.

CD19 / B-Lymphocyte Surface Antigen B4 / T-Cell Surface Antigen Leu-12 / CVID3 is a transmembrane protein expressed in all B lineage cells. Most B cell malignancies express normal to high levels of CD19 where it plays an active role in driving the growth of these cancers by stabilising concentrations of the MYC oncoprotein.

- ✓ **Assay is pre-developed** on the Biacore 8K; simply plug and play
- ✓ **Expedited turnaround time** to obtain a **full kinetic profile** for your CD19-targeted molecule
- ✓ Your molecule will be **analysed alongside an anti-CD19 positive control,** validated to bind to CD19.

Method	Ligand	Analyte	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	Chi2 (RU2)	Fit Model
Fc-Capture	Human CD19	Blinatumomab	1.22E+05	1.77E-05	1.07E-10	12.3	0.10	Langmuir 1:1 binding

Kinetic data reported are calculated from the **average of three runs.**

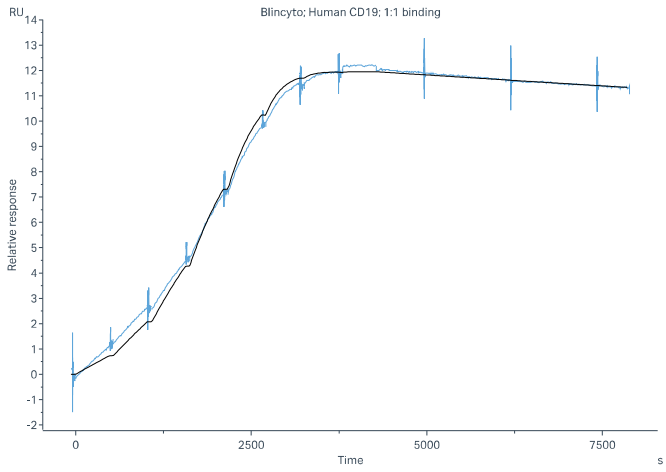

Figure 1: Human CD19 captured on a CM5 chip *via* an Anti-Fc antibody binds Blinatumomab.

Binding responses are shown as a plot of relative response *vs* time.

A 1:2, 8-point sequential dilution series of Blinatumomab was injected over the CD19 surface followed by an extended dissociation using a **Biacore 8K** instrument.

A **Langmuir 1:1 model** was used to determine the kinetic parameters for the interaction (sensorgram represents one of three independent runs).

Antibody Analytics

HER2: An off the shelf, SPR assay for the assessment of the binding of HER2-targeted antibody-based therapeutics. Determine full binding kinetics in a single run.

Human Epidermal growth factor Receptor 2 (HER2) / ERBB2 / HER-2/neu / NEU / NGL / TKR1 / c-erb B2 is a membrane surface bound receptor tyrosine kinase that shows gene amplification and protein overexpression in approximately 30% of aggressive breast cancers.

- ✓ **Assay is pre-developed** on the Biacore 8K; simply plug and play
- ✓ **Expedited turnaround time** to obtain a **full kinetic profile** for your **HER2**-targeted molecule
- ✓ Your molecule will be **analysed alongside an anti-HER2 positive control,** validated to bind to HER2.

Method	Ligand	Analyte	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	Chi2 (RU2)	Fit Model
Biotin-Capture	Human HER2	Herceptin	2.85E+06	4.04E-05	1.42E-11	32.3	0.11	Langmuir 1:1 binding

Kinetic data reported are calculated from the **average of three runs.**

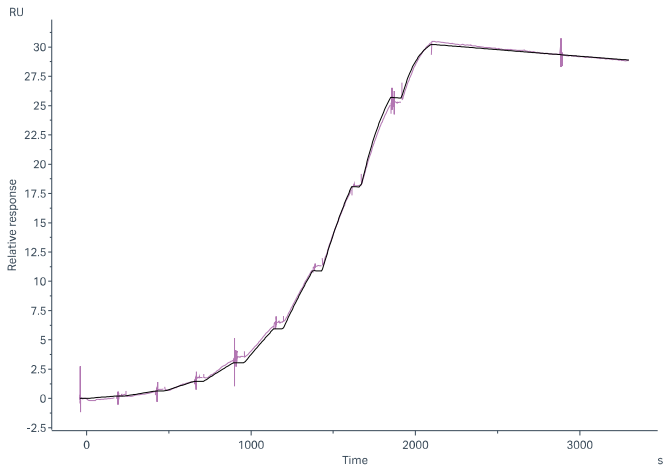

Figure 1: Human HER2 captured on a CM5 chip *via* streptavidin, binds Herceptin.

Binding responses are shown as a plot of relative response *vs* time.

A 1:2, 9-point sequential dilution series of Herceptin was injected over the HER2 surface followed by an extended dissociation using a **Biacore 8K** instrument.

A **Langmuir 1:1 model** was used to determine the kinetic parameters for the interaction (sensorgram represents one of three independent runs).

Antibody Analytics

LAG3: An off the shelf, SPR assay for the assessment of the binding of LAG3-targeted antibody-based therapeutics. Determine full binding kinetics in a single run.

LAG3 / CD223 / Lymphocyte activation gene 3 / protein FDC is a member of the immunoglobulin superfamily that is selectively expressed in activated T, NK cells, B cells and plasmacytoid dendritic cells. LAG3 binds MHC class II and negatively regulates cellular proliferation, activation and homeostasis of T cells. The protein has also been reported to play a role in Treg suppressive function, to maintain CD8+ T cells in a tolerogenic state and, together with PD-1, maintain CD8 exhaustion during chronic viral infection.

- ✓ **Assay is pre-developed** on the Biacore 8K; simply plug and play
- ✓ **Expedited turnaround time** to obtain a **full kinetic profile** for your **LAG3**-targeted molecule
- ✓ Your molecule will be **analysed alongside an anti-LAG3 positive control,** validated to bind to LAG3.

Method	Ligand	Analyte	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	Chi2 (RU2)	Fit Model
Human Antibody Capture	Human HER2	Herceptin	1.62E+06	8.76E-04	5.43E-10	51.3	0.92	Langmuir 1:1 binding

Kinetic data reported are calculated from the **average of four runs.**

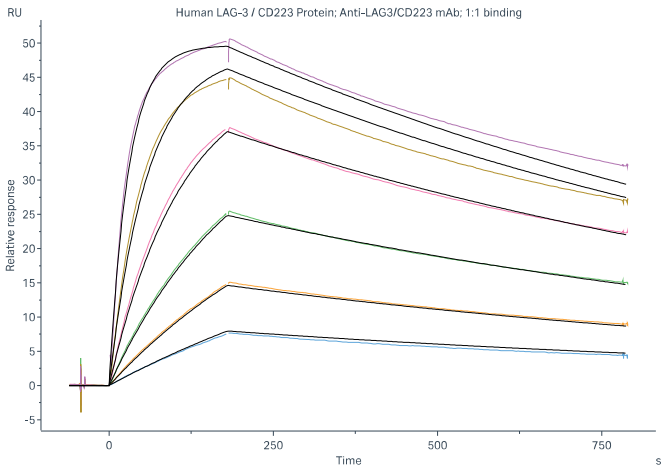

Figure 1: Human Anti-LAG3 IgG4 captured on a CM5 chip *via* its CH1 light chain domain, binds LAG3.

Binding responses are shown as a plot of relative response *vs* time.

A 1:2, 6-point dilution series of human LAG3 was injected over an anti-LAG3 IgG4 surface using a **Biacore 8K** instrument.

A **Langmuir 1:1 model** was used to determine the kinetic parameters for the interaction (sensorgrams represent one of four independent runs).

Antibody Analytics

PD-1: An off the shelf, SPR assay for the assessment of the binding of PD-1-targeted antibody-based therapeutics. Determine full binding kinetics in a single run.

Programmed cell death protein 1 / PD-1 / CD279 / PDCD1 is a member of the extended CD28 / CTLA-4 family of T cell regulators expressed on the surface of activated T cells, B cells, macrophages, myeloid cells and a subset of thymocytes. PD-1 is bound by either PD-L1 or PD-L2 (both members of the B7 family), leading to the inhibition of T-cell proliferation and the production of cytokines and subsequent suppression of the PI3K/AKT pathway. Monoclonal antibodies targeting PD-1 that boost the immune system are under development for the treatment of cancer.

- ✓ **Assay is pre-developed** on the Biacore 8K; simply plug and play
- ✓ **Expedited turnaround time** to obtain a **full kinetic profile** for your **PD-1**-targeted molecule
- ✓ Your molecule will be **analysed alongside an anti-PD-1 positive control,** validated to bind to PD-1.

Method	Ligand	Analyte	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	Chi2 (RU2)	Fit Model
Human Antibody Capture	Nivolumab	Human PD-1	2.56E+05	1.11E-03	4.35E-09	86.1	0.07	Langmuir 1:1 binding

Kinetic data reported are calculated from the **average of two runs.**

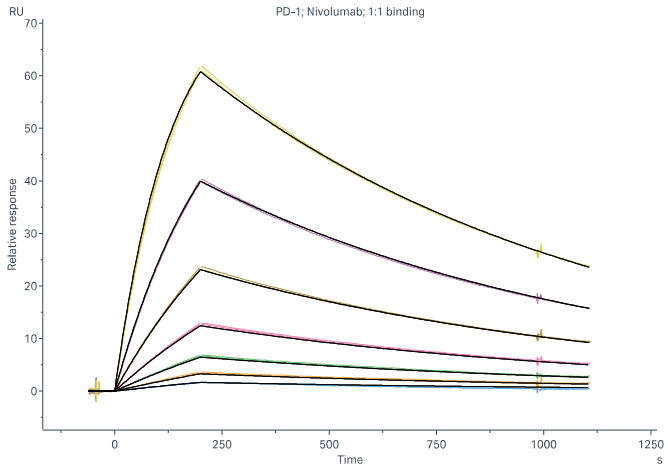

Figure 1: Nivolumab captured on a CM5 chip *via* its CH1 light chain domain, binds human PD-1.

Binding responses are shown as a plot of relative response *vs* time.

A 1:2, 7-point dilution series of human PD-1 was injected over Nivolumab captured on a CM5 surface using a **Biacore 8K** instrument.

A **Langmuir 1:1 model** was used to determine the kinetic parameters for the interaction (sensorgrams represent one of 2 independent runs).

Antibody Analytics

PSMA: An off the shelf, SPR assay for the assessment of the binding of PSMA-targeted antibody-based therapeutics. Determine full binding kinetics in a single run.

Prostate-specific membrane antigen (PSMA) / Folate hydrolase 1 / FOLH1 / Glutamate carboxypeptidase 2 / GCP2 / N-acetylated-alpha-linked acidic dipeptidase I / NAALAD 1is a type II transmembrane zinc metallopeptidase expressed at the highest levels in the nervous system, prostate, kidney and small intestine. This enzyme catalyses the hydrolysis of N-acetyl aspartylglutamate to glutamate and N-acetylaspartate. In some prostate cancers, PSMA is the second-most upregulated gene product showing significant increase in levels as compared to noncancerous prostate cells. Targeting this enzyme has been studied as a treatment against prostate cancer, ALS and other neurodegenerative diseases such as Parkinson's and Huntington's disease.

- ✓ **Assay is pre-developed** on the Biacore 8K; simply plug and play
- ✓ **Expedited turnaround time** to obtain a **full kinetic profile** for your **PSMA**-targeted molecule
- ✓ Your molecule will be **analysed alongside an anti-PSMA positive control,** validated to bind to PSMA.

Method	Ligand	Analyte	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	Chi2 (RU2)	Fit Model
Human Antibody Capture	Anti-human PSMA	Human PSMA	1.04E+05	3.43E-04	2.44E-09	24.7	0.02	Langmuir 1:1 binding

Kinetic data reported are calculated from the **average of three runs.**

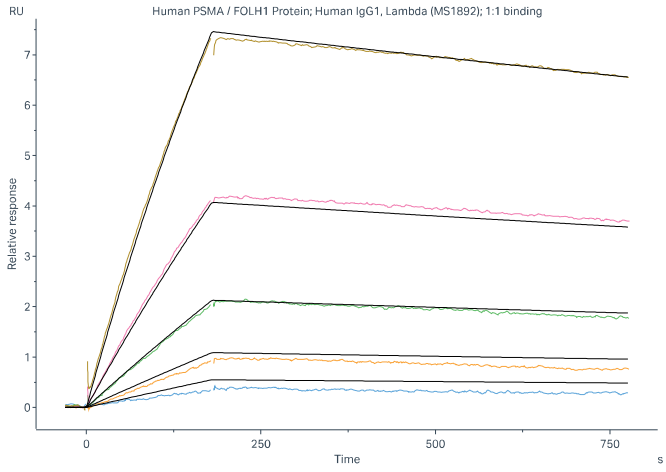

Figure 1: Anti-human PSMA antibody captured on a CM5 chip *via* its CH1 light chain domain, binds human PSMA.

Binding responses are shown as a plot of relative response *vs* time.

A 1:2, 5-point dilution series of human PSMA was injected over anti-PSMA antibody captured on a CM5 surface using a **Biacore 8K** instrument.

A **Langmuir 1:1 model** was used to determine the kinetic parameters for the interaction (sensorgrams represent one of 3 independent runs).

Antibody Analytics

TIGIT: An off the shelf, SPR assay for the assessment of the binding of TIGIT-targeted antibody-based therapeutics. Determine full binding kinetics in a single run.

T-cell immunoreceptor with Ig and ITIM domains / TIGIT / V-set and immunoglobulin domain-containing protein 9 / VSIG9 / V-set and transmembrane domain-containing protein 3 / VSTM3 is a single-pass type I membrane protein containing an immunoglobulin variable domain, a transmembrane domain and an immunoreceptor tyrosine-based inhibitory motif (ITIM). TIGIT is expressed at low levels on peripheral memory and regulatory CD4+ T cells and NK cells and expression is up-regulated following activation. TIGIT binds the poliovirus receptor with high affinity, and this causes an increase in IL-10 secretion, a decrease in IL-12B secretion and subsequent suppression of T-cell activation by promoting the generation of dendritic cells.

- ✓ **Assay is pre-developed** on the Biacore 8K; simply plug and play
- ✓ **Expedited turnaround time** to obtain a **full kinetic profile** for your **TIGIT**-targeted molecule
- ✓ Your molecule will be **analysed alongside an anti-TIGIT positive control,** validated to bind to TIGIT

Method	Ligand	Analyte	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	Chi2 (RU2)	Fit Model
Human Antibody Capture	Anti-human TIGIT	Human TIGIT	1.24E+06	7.98E-05	6.42E-11	34.7	0.08	Langmuir 1:1 binding

Kinetic data reported are calculated from the **average of four runs.**

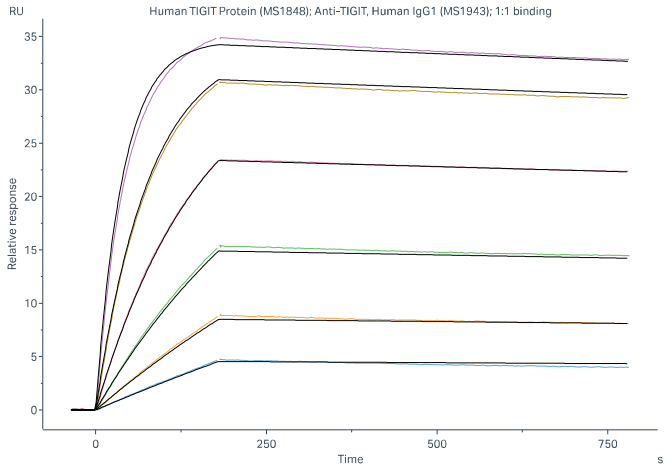

Figure 1: Anti-human TIGIT antibody captured on a CM5 chip *via* its CH1 light chain domain, binds human TIGIT.

Binding responses are shown as a plot of relative response *vs* time.

A 1:2, 6-point dilution series of human TIGIT was injected over anti-TIGIT antibody captured on a CM5 surface using a **Biacore 8K** instrument.

A **Langmuir 1:1 model** was used to determine the kinetic parameters for the interaction (sensorgrams represent one of 4 independent runs).

Antibody Analytics

TIM3: An off the shelf, SPR assay for the assessment of the binding of TIM3-targeted antibody-based therapeutics. Determine full binding kinetics in a single run.

T-cell immunoglobulin and mucin-domain containing-3 / TIM3 / Hepatitis A virus cellular receptor 2 / HAVCR2 / FLJ14428 / KIM3 / TIMD3 is a member of the TIM family of immune regulating molecules with one Ig-like V-type domain and a Ser/Thr-rich mucin stalk. TIM3 is a Th1-specific cell surface protein that regulates macrophage activation, inhibits T-helper type 1 lymphocyte-mediated auto- and alloimmune responses and promotes immunological tolerance.

- ✓ **Assay is pre-developed** on the Biacore 8K; simply plug and play
- ✓ **Expedited turnaround time** to obtain a **full kinetic profile** for your **TIM3**-targeted molecule
- ✓ Your molecule will be **analysed alongside an anti-TIM3 positive control,** validated to bind to TIM3

Method	Ligand	Analyte	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	Chi2 (RU2)	Fit Model
Human Antibody Capture	Anti-human TIM3	Human TIM3	3.48E+05	9.52E-03	2.76E-08	46.3	0.11	Langmuir 1:1 binding

Kinetic data reported are calculated from the **average of four runs.**

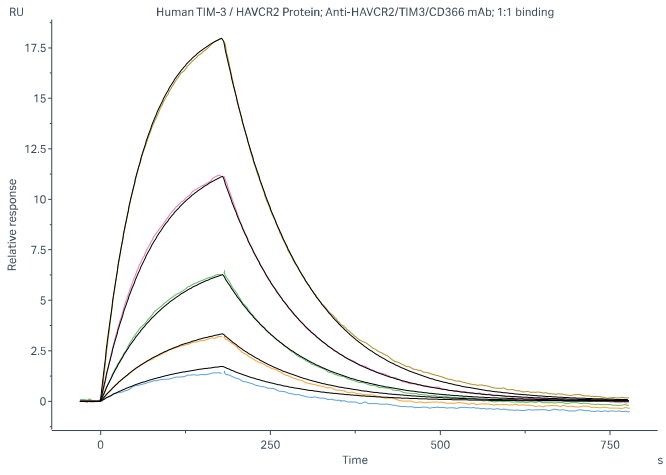

Figure 1: Anti-human TIM3 antibody captured on a CM5 chip *via* its CH1 light chain domain, binds human TIM3.

Binding responses are shown as a plot of relative response *vs* time.

A 1:2, 5-point dilution series of human TIM3 was injected over anti-TIM3 antibody captured on a CM5 surface using a **Biacore 8K** instrument.

A **Langmuir 1:1 model** was used to determine the kinetic parameters for the interaction (sensorgrams represent one of 4 independent runs).