Resource Summary Report

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Thermo Fisher: Sartorius: Octet BLI systems

RRID:SCR_023267
Type: Tool

Proper Citation

Thermo Fisher: Sartorius: Octet BLI systems (RRID:SCR_023267)

Resource Information

URL: https://www.sartorius.com/en/products/protein-analysis/octet-bli-detection/octet-systems-software

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Description: Octet BLI systems enable real-time, label-free analysis for determination of kinetics, affinity and antibody/protein quantitation. Includes Octet Analysis Studio for analysis of assays measuring kinetics and affinity values for drug-target binding and high-throughput kinetic screening for lead identification. Typical applications include kinetic analysis of protein-protein, protein-small molecules, antibody-antigen, antibody-VLP, antibody-Fc gamma receptors, including antibody-neonatal receptor (FcRn) interactions. Additional applications supported include lot release and stability analysis of drug molecules based on binding kinetics and affinity.

Synonyms: Octet BLI systems, Octet BLI systems with Octet Analysis Studio

Resource Type: instrument resource

Keywords: Sartorius, Octet Analysis Studio, Bio-Layer Interferometry, protein quantitation, assays measuring kinetics analysis, affinity values analysis, instrument, equipment, USEDit

Availability: Restricted

Resource Name: Thermo Fisher: Sartorius: Octet BLI systems

Resource ID: SCR_023267

Record Creation Time: 20230210T050214+0000

Record Last Update: 20260725T191029+0000

Ratings and Alerts

No rating or validation information has been found for Thermo Fisher: Sartorius: Octet BLI systems.

No alerts have been found for Thermo Fisher: Sartorius: Octet BLI systems.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Schleich FA, et al. (2025) Vaccination of nonhuman primates elicits a broadly neutralizing antibody lineage targeting a quaternary epitope on the HIV-1 Env trimer. Immunity, 58(6), 1598.

Chen H, et al. (2024) BRAIDing receptors for cell-specific targeting. eLife, 12.

Zhou X, et al. (2024) Antibody discovery identifies regulatory mechanisms of protein arginine deiminase 4. Nature chemical biology, 20(6), 742.

Dederer V, et al. (2024) A designed ankyrin-repeat protein that targets Parkinson's disease-associated LRRK2. The Journal of biological chemistry, 300(7), 107469.

Sampathkumar P, et al. (2024) Targeted protein degradation systems to enhance Wnt signaling. eLife, 13.

Pandey A, et al. (2024) Therapeutic Targeting and Structural Characterization of a Sotorasib-Modified KRAS G12C-MHC I complex Demonstrates the Antitumor Efficacy of Hapten-Based Strategies. Cancer research.

Cervantes Rincón T, et al. (2024) Human antibodies in Mexico and Brazil neutralizing tick-borne flaviviruses. Cell reports, 43(6), 114298.

Ray R, et al. (2024) Eliciting a single amino acid change by vaccination generates antibody protection against group 1 and group 2 influenza A viruses. Immunity, 57(5), 1141.

Shin OS, et al. (2024) Crimean-Congo hemorrhagic fever survivors elicit protective non-neutralizing antibodies that target 11 overlapping regions on glycoprotein GP38. Cell reports, 43(7), 114502.

Huet S, et al. (2023) Targeted Nanofitin-drug Conjugates Achieve Efficient Tumor Delivery and Therapeutic Effect in an EGFRpos Mouse Xenograft Model. Molecular cancer therapeutics, 22(11), 1343.

Bian X, et al. (2023) IgG Fc-binding protein positively regulates the assembly of pore-forming protein complex ??-CAT evolved to drive cell vesicular delivery and transport. The Journal of biological chemistry, 299(6), 104717.

Patel A, et al. (2023) Molecular basis of SARS-CoV-2 Omicron variant evasion from shared neutralizing antibody response. Structure (London, England : 1993), 31(7), 801.

Svoboda P, et al. (2023) A combination of two resistance mechanisms is critical for tick-borne encephalitis virus escape from a broadly neutralizing human antibody. Cell reports, 42(9), 113149.

Pan W, et al. (2023) Structures of NF-?B p52 homodimer-DNA complexes rationalize binding mechanisms and transcription activation. eLife, 12.