

Resource Summary Report

Generated by PRECISE-TBI on Aug 27, 2026

Cytiva: Biacore X100

RRID:SCR_025586

Type: Tool

Proper Citation

Cytiva: Biacore X100 (RRID:SCR_025586)

Resource Information

URL: <https://www.cytivalifesciences.com/en/us/shop/protein-analysis/spr-label-free-analysis/spr-systems/biacore-x100-p-05730>

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Description: Automated system for comprehensive, label-free analysis and characterization of biomolecular interactions in real-time. Can be used for applications, including structure function studies, pathway analysis, biomarker discovery and validation, drug target identification and validation, and assay development.

Synonyms: Biacore X100

Resource Type: instrument resource

Keywords: analysis and characterization of biomolecular interactions in real-time, structure function studies, pathway analysis, biomarker discovery and validation, drug target identification and validation, assay development,

Specification URL: <https://cdn.cytivalifesciences.com.cn/api/public/content/digi-15563-pdf>, <https://cdn.cytivalifesciences.com/api/public/content/digi-14524-original>,

Resource Name: Cytiva: Biacore X100

Resource ID: SCR_025586

Alternate IDs: Model_Number_Biacore_X100

Record Creation Time: 20240806T053245+0000

Record Last Update: 20260815T183216+0000

Ratings and Alerts

No rating or validation information has been found for Cytiva: Biacore X100.

No alerts have been found for Cytiva: Biacore X100.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Ravazza D, et al. (2026) Quantitative Mass Spectrometry-Based Biodistribution of Monoclonal Antibodies: An Alternative to Radio-Biodistribution. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(38), e20265.

Osman ST, et al. (2026) Repurposing SGLT2 and DPP-4 inhibitors for mild cognitive impairment in type 2 diabetes mellitus: Insights from proteomics, target prediction and molecular docking. British journal of pharmacology, 183(10), 2533.