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Specification Sheet

SP200 Automation Instrument
Product Specifications

The **SP200 Automation Instrument** powers the Proteograph® line of assay kits for large-scale, unbiased proteomics with reproducible and finely tuned automation methods. Its compact footprint and intuitive design ensure seamless integration into most laboratories.

SP200 Automation Instrument product specifications	
Instrument Control Computer	Processor: Intel Core i9 processor 14900 vPro (36 MB cache, 24 cores, 32 threads, up to 5.4 GHz Turbo, 65W) Memory: 16GB DDR5 Drive Storage: 512 GB Solid State Drive Operating System: Windows 11 Pro
Instrument Control Software	Version: 6 and later
Operating Environment	Temperature: 15-30°C Humidity: 15-85% relative humidity Altitude: 0-6562 ft (0-2000 m) above sea level
Dimensions (L x W x H)	139 cm x 102 cm x 91 cm (55in x 40 in x 36 in)
Weight	150 kg (331 lb)
Power Requirements	115 or 230 VAC (50 or 60 Hz)

Table / Bench Requirements	
The SP200 Automation Instrument must be installed on an appropriate surface such a table or laboratory bench. Below are the specifications required for such a surface.	
Minimum Surface Area (L x W)	107 cm x 91 cm (42 in x 36 in)
Surface Height	76-86 cm (30 – 34 in)
Other Requirements	The surface must support a total weight of 220 kg (485 lbs). Table legs should have cross support to resist lateral motion.

Ordering Information[a]	
Product	Code
SP200 Automation Instrument	S55R5000

[a] Additional consumables and peripheral equipment are required to use the Proteograph assay kits.

Please contact us at **1-844-ASK-SEER** or by email at **support@seer.bio**, if you have any questions.

Visit our website at **Seer.bio** for more information.

Proteograph Product Suite

The **Proteograph® Product Suite** includes the **SP200 Automation Instrument**, the Proteograph line of assay kits, and the Proteograph Analysis Suite software. The Proteograph Product Suite integrates seamlessly with existing liquid chromatography-mass spectrometry (LC-MS) proteomic analysis workflows to enable unbiased, deep, and rapid proteomics at scale, supporting high-throughput analysis of biofluid samples in large cohort studies.

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