Digest Buffer, Mass Spec Grade

Cat. No. Digest Buffer-52 **Lot. No.** (See product label)

SPECIFICATION

Product Overview	
Description	Digest Buffer is a BT surfactant-based buffer optimized for proteomics and biopharmaceutical research. It facilitates protein denaturation, reduction, and alkylation, followed by enzymatic hydrolysis to convert proteins into peptides with high efficiency and recovery. The surfactant is then degraded by formic acid, allowing direct peptide analysis via mass spectrometry without the need for desalting, minimizing peptide loss. Ideal for proteomics, biopharmaceuticals, and single-cell research.
Form	Lyophilized powder with 5 mg BT Surfactant and 48 mg ammonium bicarbonate
Molecular Mass	393.28 Da
Purity	> 99.9 % BT Surfactant peak area, analyzed by Thermo QE HF mass spectrometry coupled with positive ion mode ESI.
Storage	Powder at -20 centigrade, reconstituted solution at 4 centigrade for 6 months
CAS No.	881640-19-3
Usage Notes	Reference Protocol: Add 100 µL Digest Buffer to 10 µL (50 µg) protein sample and mix well. Add 1 µg MS-grade protease and incubate at 42 centigrade for 40 minutes. Then, add 3 µL formic acid and incubate at 42 centigrade for 20 minutes.

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Resuspension Buffer	Dissolve in 12 mL MS Grade water
pH Range	pH 7-9 is used for proteolysis experiments, will degrade and precipitate in solution at pH 2-4
Degradation	0.1 % BT Surfactant peak area after incubation with 0.2 % (v/v) formic acid at 42 centigrade for 30 minutes, analyzed by QE HF mass spectrometry using negative ion mode ESI.

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