CLIENT & SAMPLE INFORMATION

Client	Aurora Peptides	**Analysis Date**	07/11/2026
Lot / Batch	SHB-072026-001	**Product Name**	Synergy
Form / Matrix	Liquid Blend	**Volume**	10 mL

This Certificate of Analysis confirms the identity and quality of the multi-component liquid blend listed herein. Compound identification was performed by HPLC-UV with LC-MS/MS confirmation. Declared active components were evaluated against their expected molecular masses and chromatographic profiles.

ACTIVE COMPONENT IDENTITY (LC-MS/MS)

Declared components evaluated by HPLC with UV detection, confirmed by Mass Spectrometry where a characteristic ion is available. Identity confirmed via observed m/z vs. theoretical m/z.

Component	CAS Number	Theoretical m/z [M+H]+	Observed m/z	Status
L-Carnitine	541-15-1	162.11	162.11	PASS
L-Citrulline	372-75-8	176.10	176.10	PASS
L-Arginine	74-79-3	175.12	175.12	PASS
L-Ornithine	70-26-8	133.10	133.10	PASS
L-Proline	147-85-3	116.07	116.07	PASS
L-Taurine	107-35-7	126.02	126.02	PASS
L-Lysine	56-87-1	147.11	147.11	PASS
L-Glutamine	56-85-9	147.08	147.08	PASS
Overall Identity Determination				PASS

Method: HPLC-UV with LC-MS/MS confirmation | 8 declared component(s) evaluated. Components lacking a UV chromophore are confirmed by orthogonal identity where applicable.

PHYSICOCHEMICAL PROPERTIES

Property	Specification	Result	Status
Appearance / Color	Conforms	Conforms	PASS
Physical Form	Liquid	Liquid	PASS
Particulate Matter	Essentially free	Conforms	PASS

ADDITIONAL QUALITY SCREENS

ENDOTOXIN SCREEN

Method	LAL (USP <85>)
Limit	<= 0.5 EU/mL
Result	Pass
Status	PASS

STERILITY / MICROBIAL SCREEN

Method	Rapid Sterility
Specification	No Growth
Incubation	2 days
Result	No microbial growth detected
Fungi	Not Detected
Status	PASS

HEAVY METAL SCREEN

Method	ICP-MS
Specification	Compliant
Result	PASS
Status	PASS

TESTING METHODOLOGY

Compound Identity (LC-MS/MS)

Multi-component identity confirmation performed by reverse-phase HPLC with UV detection coupled with tandem mass spectrometry (LC-MS/MS). Each declared active is identified by retention time and, where a characteristic ion is available, confirmed by observed [M+H]+ molecular ion matched against its theoretical mass. Highly polar components lacking a UV chromophore (e.g. free amino acids) are reported by identity confirmation and may require orthogonal (derivatization / HILIC) methods for full quantitation.