Certificate of Analysis for NR-53823

Peptide Array, SARS Coronavirus Envelope (E) Protein

Catalog No. NR-53823

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Product Description:

The 9-peptide array spans the envelope (E) protein of the Urbani strain of severe acute respiratory syndrome coronavirus (SARS-CoV; GenPept: AAP13443). Peptides are 15 to 18-mers, with 10 amino acid overlaps.

Lot: A5091-1 to A5091-9 **Manufacturing Date: 08OCT2020**

The following information applies to all peptides:

• Appearance	White lyophilized powder
• Mass spectral analysis	Correct MW by MALDI
• Counter Ion	Trifluoroacetate
• Solubility	1 mg/mL in 70% acetonitrile in water

Peptide-specific information is shown in the tables and figures below.

Table 1: Peptide Analysis

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC[1]	Peptide Content[2]
1 of 10	18	1-MYSFVSEETGTLIVNSVL-18	1989.28	50.0	Crude	93.8%
2 of 10	18	9-TGTLIVNSVLLFLAFVVF-26	1953.41	72.2	Crude	93.7%
3 of 10	18	17-VLLFLAFVVFLLVTLAIL-34	2004.63	94.4	Crude	93.9%
4 of 10	18	25-VFLLVTLAILTALRLCAY-42	1993.53	83.3	87.5%	88.4%
5 of 10	17	33-ILTALRLCAYCCNIVNV-49	1882.35	76.5	94.7%	87.8%
6 of 10	18	40-CAYCCNIVNVSLVKPTVY-57	1989.41	66.7	96.1%	88.3%
7 of 10	18	48-NVSLVKPTVYVYSRVKNL-65	2079.47	50.0	86.9%	79.9%
8 of 10	16	56-VYVYSRVKNLNSSEGV-71	1814.02	43.8	96.7%	82.2%
9 of 10	15	62-VKNLNSSEGVPDLLV-76	1583.81	40.0	93.2%	85.8%

[1]Percent full length; the first 3 peptides were difficult to purify and therefore percent purity results are not available.
[2]Remainder is salt and water

Figure 1: Amino Acid Analysis[3,4]

Peptide		Ala (A)	Arg (R)	Asx (N,D)	Cys (C)	Glx (Q,E)	Gly (G)	His (H)	Ile (I)	Leu (L)	Lys (K)	Met (M)	Phe (F)	Pro (P)	Ser (S)	Thr (T)	Trp (W)	Tyr (Y)	Val (V)
1 of 9	Expected			1.0		2.0	1.0		1.0	2.0		1.0	1.0		3.0	2.0		1.0	3.0
	Actual			1.0		2.1	1.0		0.7	2.0		1.0	1.0		3.0	2.2		1.0	2.4
2 of 9	Expected	1.0		1.0			1.0		1.0	4.0			3.0		1.0	2.0			4.0
	Actual	0.9		1.2			0.9		0.7	3.9			3.2		1.0	2.1			2.8
3 of 9	Expected	2.0							1.0	7.0			3.0			1.0			4.0
	Actual	2.1							1.0	7.1			2.9			1.1			2.6
4 of 9	Expected	3.0	1.0		1.0				1.0	6.0			1.0			2.0		1.0	2.0
	Actual	3.1	1.1		0.0				0.9	6.1			0.9			2.0		1.0	1.9
5 of 9	Expected	2.0	1.0	2.0	3.0				2.0	3.0						1.0		1.0	2.0
	Actual	1.9	1.0	2.1	0.0				1.6	2.9						0.9		1.0	1.6
6 of 9	Expected	1.0		2.0	3.0				1.0	1.0	1.0			1.0	1.0	1.0		2.0	4.0
	Actual	0.9		1.8	0.0				0.7	1.1	1.1			1.1	0.9	1.1		2.0	4.0
7 of 9	Expected		1.0	2.0						2.0	2.0			1.0	2.0	1.0		2.0	5.0
	Actual		1.0	1.9						1.9	2.1			1.0	2.0	1.0		2.0	4.9

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Figure 1: Amino Acid Analysis (continued)[3,4]

Peptide		Ala (A)	Arg (R)	Asx (N,D)	Cys (C)	Glx (Q,E)	Gly (G)	His (H)	Ile (I)	Leu (L)	Lys (K)	Met (M)	Phe (F)	Pro (P)	Ser (S)	Thr (T)	Trp (W)	Tyr (Y)	Val (V)
8 of 9	Expected		1.0	2.0		1.0	1.0			1.0	1.0				3.0			2.0	4.0
	Actual		1.0	2.0		1.0	1.1			1.0	1.0				2.9			2.0	3.9
9 of 9	Expected			3.0		1.0	1.0			3.0	1.0			1.0	2.0				3.0
	Actual			3.0		1.0	1.0			3.1	0.9			1.0	2.0				3.1

[3]Cysteine (C) was completely destroyed during hydrolysis.
[4]Val-Ile, Val-Val, Ile-Ile and/or Ile-Val bonds were only partially destroyed during hydrolysis.

/Heather Couch/
Heather Couch 14 DEC 2020
Program Manager or designee, ATCC Federal Solutions

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