

Peptide Array, SARS Coronavirus Membrane (M) Protein

Catalog No. NR-53822

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Product Description:

The 30-peptide array spans the membrane (M) glycoprotein of the Urbani strain of severe acute respiratory syndrome coronavirus (SARS-CoV; GenPept: [AAP13444](#)). Peptides are 13 to 18-mers, with 10 amino acid overlaps.

Lot: A5090-1 to A5090-30

Manufacturing Date: 21SEP2020

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 30	16	1-MADNGTITVEELKQLL-16	1775.06	43.8%	93.1%	87.1%
2 of 30	17	7-ITVEELKQLLEQWNLVI-23	2068.45	52.9%	84.3%	88.7%
3 of 30	18	14-QLLEQWNLVIGFLFLAWI-31	2203.67	72.2%	90.5%	94.4%
4 of 30	17	22-VIGFLFLAWIMLLQFAY-38	2045.57	88.2%	95.4%	94.0%
5 of 30	18	29-AWIMLLQFAYSNRNRFLY-46	2306.72	66.7%	93.5%	85.5%
6 of 30	18	37-AYSNRNRFLYIIKLVFLW-54	2316.78	66.7%	87.2%	81.6%
7 of 30	18	45-LYIIKLVFLWLLWPVTLA-62	2201.81	83.3%	93.1%	89.4%
8 of 30	18	53-LWLLWPVTLACFVLAAVY-70	2078.60	88.9%	93.6%	94.1%
9 of 30	15	61-LACFVLAAVYRINWV-75	1738.13	86.7%	82.5%	86.9%
10 of 30	18	66-LAAVYRINWVTGGIAIAM-83	1919.32	72.2%	87.8%	88.0%
11 of 30	18	74-WVTGGIAIAMACIVGLMW-91	1892.39	77.8%	92.0%	93.6%
12 of 30	18	82-AMACIVGLMWLSYFVASF-99	2009.49	83.3%	95.0%	93.9%
13 of 30	17	90-MWLSYFVASFRLFARTR-106	2151.57	64.7%	80.3%	80.4%
14 of 30	15	97-ASFRLFARTRSMWSF-111	1863.18	53.3%	92.1%	78.1%
15 of 30	18	102-FARTRSMWSFNPETNILL-119	2183.53	44.4%	89.1%	84.8%
16 of 30	18	110-SFNPETNILLNVPLRGTI-127	1998.32	38.9%	87.7%	88.4%
17 of 30	16	118-LLNVPLRGTIVTRPLM-133	1793.26	50.0%	92.8%	82.0%
18 of 30	18	124-RGTIVTRPLMESELVIGA-141	1942.32	44.4%	89.1%	83.2%
19 of 30	18	132-LMESELVIGAVIIRGHLR-149	2006.46	55.6%	91.3%	79.3%
20 of 30	18	140-GAVIIRGHLRMAGHPLGR-157	1911.32	44.4%	81.1%	70.9%
21 of 30	18	148-LRMAGHPLGRCDIKDLPK-165	2020.46	38.9%	92.3%	72.0%
22 of 30	18	156-GRCDIKDLPKEITVATSR-173	2002.33	33.3%	88.0%	75.4%
23 of 30	17	164-PKEITVATSRTLSYYKL-180	1970.29	41.2%	89.2%	79.0%
24 of 30	16	171-TSRTLSYYKLGASQRV-186	1830.07	37.5%	96.5%	77.8%
25 of 30	18	177-YYKLGASQRVGTDSGFAA-194	1891.07	44.4%	88.0%	82.8%
26 of 30	16	185-RVGTDSGFAAYNRYRI-200	1846.03	43.8%	92.3%	77.9%
27 of 30	15	191-GFAAYNRYRIGNYKL-205	1806.05	53.3%	84.3%	77.5%

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
28 of 30	15	194-NRYRIGNYKLNTDHA-208	1835.01	33.3%	84.7%	73.7%
29 of 30	18	201-GNYKLNTDHAGSNDNIAL-218	1917.03	33.3%	81.1%	83.0%
30 of 30	13	209-HAGSNDNIALLVQ-221	1351.49	46.2%	96.1%	83.8%

¹Percent full length

²Remainder 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 30	Expected	1.0		2.0		3.0	1.0		1.0	3.0	1.0	1.0				2.0			1.0
	Actual	0.9		2.2		3.0	0.9		1.0	3.1	1.1	0.8				2.1			1.1
2 of 30	Expected			1.0		5.0			2.0	4.0	1.0					1.0	1.0		2.0
	Actual			1.1		4.9			2.2	4.0	1.0					0.9	0.0		2.0
3 of 30	Expected	1.0		1.0		3.0	1.0		2.0	5.0			2.0					2.0	1.0
	Actual	0.9		1.0		3.0	1.0		1.7	5.0			2.2					0.0	0.8
4 of 30	Expected	2.0				1.0	1.0		2.0	4.0		1.0	3.0					1.0	1.0
	Actual	2.0				1.0	1.1		1.5	3.9		0.9	2.9					0.0	1.0
5 of 30	Expected	2.0	2.0	2.0		1.0			1.0	3.0		1.0	2.0		1.0		1.0	2.0	
	Actual	2.1	2.2	1.8		1.0			1.0	2.9		1.0	2.0		0.9		0.0	2.1	
6 of 30	Expected	1.0	2.0	2.0					2.0	3.0	1.0		2.0		1.0		1.0	2.0	1.0
	Actual	1.0	2.1	1.9					1.2	3.0	0.9		2.1		0.9		0.0	2.2	1.0
7 of 30	Expected	1.0							2.0	6.0	1.0		1.0	1.0		1.0	2.0	1.0	2.0
	Actual	1.0							1.1	6.1	0.9		1.0	1.0		0.9	0.0	1.0	2.1
8 of 30	Expected	3.0			1.0					5.0			1.0	1.0		1.0	2.0	1.0	3.0
	Actual	2.9			0.0					4.8			1.1	1.0		0.9	0.0	1.1	3.1
9 of 30	Expected	3.0	1.0	1.0	1.0				1.0	2.0			1.0				1.0	1.0	3.0
	Actual	2.9	1.0	1.0	0.0				1.0	1.9			1.0				0.0	1.0	3.2
10 of 30	Expected	4.0	1.0	1.0			2.0		3.0	1.0		1.0				1.0	1.0	1.0	2.0
	Actual	3.9	1.0	1.0			1.9		3.1	1.1		0.9				0.9	0.0	1.1	1.9
11 of 30	Expected	3.0			1.0		3.0		3.0	1.0		2.0				1.0	2.0		2.0
	Actual	2.9			0.0		3.2		2.6	1.1		2.0				0.9	0.0		2.1
12 of 30	Expected	3.0			1.0		1.0		1.0	2.0		2.0	2.0		2.0		1.0	1.0	2.0
	Actual	3.0			0.0		1.0		0.7	1.9		2.0	2.1		1.9		0.0	1.1	1.5
13 of 30	Expected	2.0	3.0							2.0	1.0	3.0			2.0	1.0	1.0	1.0	1.0
	Actual	2.1	3.2							2.1	0.9	2.9			2.0	0.9	0.0	0.9	1.1
14 of 30	Expected	2.0	3.0							1.0	1.0	3.0			3.0	1.0	1.0		
	Actual	2.1	3.1							1.0	1.0	3.0			3.0	1.0	0.0		
15 of 30	Expected	1.0	2.0	2.0		1.0			1.0	2.0		1.0	2.0	1.0	2.0	2.0	1.0		
	Actual	1.1	2.0	2.0		1.0			1.1	2.1		0.9	2.0	1.1	1.8	2.0	0.0		
16 of 30	Expected		1.0	3.0		1.0	1.0		2.0	3.0			1.0	2.0	1.0	2.0			1.0
	Actual		1.1	3.0		1.0	1.0		2.0	2.9			0.9	2.0	1.0	2.0			1.1
17 of 30	Expected		2.0	1.0			1.0		1.0	4.0		1.0		2.0		2.0			2.0
	Actual		2.1	0.9			1.0		0.9	4.1		1.1		2.0		1.9			2.0
18 of 30	Expected	1.0	2.0			2.0	2.0		2.0	2.0		1.0		1.0	1.0	2.0			2.0
	Actual	1.0	2.2			2.0	2.1		1.3	1.9		0.9		1.1	1.0	1.9			1.4

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)
19 of 30	Expected	1.0	2.0			2.0	2.0	1.0	3.0	3.0		1.0			1.0				2.0
	Actual	1.1	2.1			2.0	2.1	1.1	2.1	3.0		0.9			0.9				1.3
20 of 30	Expected	2.0	3.0				4.0	2.0	2.0	2.0		1.0		1.0					1.0
	Actual	2.1	3.0				4.1	2.0	1.6	1.8		1.0		1.1					0.8
21 of 30	Expected	1.0	2.0	2.0	1.0		2.0	1.0	1.0	3.0	2.0	1.0		2.0					
	Actual	0.9	2.1	2.1	0.0		2.0	0.8	1.1	3.0	2.2	1.0		2.1					
22 of 30	Expected	1.0	2.0	2.0	1.0	1.0	1.0		2.0	1.0	2.0			1.0	1.0	2.0			1.0
	Actual	0.9	2.1	2.0	0.0	0.8	1.1		2.0	1.1	2.0			1.1	1.0	2.0			1.0
23 of 30	Expected	1.0	1.0			1.0			1.0	2.0	2.0			1.0	2.0	3.0		2.0	1.0
	Actual	1.0	1.1			0.9			0.9	2.2	2.1			1.0	1.8	2.8		2.2	1.0
24 of 30	Expected	1.0	2.0			1.0	1.0			2.0	1.0				3.0	2.0		2.0	1.0
	Actual	1.0	1.9			1.0	1.0			2.1	1.0				2.9	2.0		2.0	1.0
25 of 30	Expected	3.0	1.0	1.0		1.0	3.0			1.0	1.0		1.0		2.0	1.0		2.0	1.0
	Actual	3.1	1.0	0.9		1.1	3.0			1.1	1.0		1.0		1.9	0.9		1.9	1.0
26 of 30	Expected	2.0	3.0	2.0			2.0		1.0				1.0		1.0	1.0		2.0	1.0
	Actual	2.0	3.1	2.0			2.0		1.1				1.1		0.8	0.9		2.2	1.0
27 of 30	Expected	2.0	2.0	2.0			2.0		1.0	1.0	1.0		1.0					3.0	
	Actual	1.9	2.0	1.9			2.0		1.0	1.1	1.1		0.9					3.0	
28 of 30	Expected	1.0	2.0	4.0			1.0	1.0	1.0	1.0	1.0					1.0		2.0	
	Actual	0.9	2.2	4.0			1.1	0.8	1.1	1.0	1.1					0.8		2.2	
29 of 30	Expected	2.0		6.0			2.0	1.0	1.0	2.0	1.0				1.0	1.0		1.0	
	Actual	2.0		5.8			2.1	1.1	1.1	2.1	1.0				0.8	0.9		1.0	
30 of 30	Expected	2.0		3.0		1.0	1.0	1.0	1.0	2.0					1.0				1.0
	Actual	2.0		2.8		0.9	1.1	1.1	1.1	2.0					1.0				1.1

³Cysteine (C) and tryptophan (W) were completely destroyed during hydrolysis.

⁴Val-Ile, Val-Val, Ile-Ile and/or Ile-Val bonds were only partially destroyed during hydrolysis.

/Heather Couch/

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