

Peptide Array, SARS-Related Coronavirus 2 Nucleocapsid (N) Protein

Catalog No. NR-52404

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Product Description:

The 59-peptide array spans the nucleocapsid (N) protein of the USA-WA1/2020 strain of severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2; GenPept: [QHO60601](#)). Peptides are 17- or 13-mers, with 10 amino acid overlaps.

Lot: A5739-1 to A5739-59

Manufacturing Date: 04MAY2021

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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 59	17	1-MSDNGPQNQRNAPRITF-17	1946.14	23.53	99.84%	75%
2 of 59	17	8-NQRNAPRITFGGSDST-24	1817.94	17.65	99.48%	74%
3 of 59	17	15-ITFGGSDSTGSNQNGE-31	1667.67	11.76	96.72%	81%
4 of 59	17	22-DSTGSNQNGERSGARSK-38	1750.77	5.88	98.75%	69%
5 of 59	17	29-NGERSGARSKQRRPQGL-45	1897.10	11.76	99.32%	64%
6 of 59	17	36-RSKQRRPQGLPNNTASW-52	1996.23	17.65	98.62%	69%
7 of 59	17	43-QGLPNNTASWFTALTQH-59	1886.06	35.29	91.43%	78%
8 of 59	17	50-ASWFTALTQHGKEDLKF-66	1979.23	41.18	98.67%	72%
9 of 59	17	57-TQHGKEDLKFPRGQGV-73	1894.13	17.65	97.19%	67%
10 of 59	17	64-LKFPRGQGVPIINTNSSP-80	1812.07	23.53	98.17%	73%
11 of 59	17	71-GVPIINTNSSPDDQIGYY-87	1839.93	29.41	95.83%	82%
12 of 59	17	78-SSPDDQIGYYRRATRR-94	2054.25	29.41	81.18%	69%
13 of 59	17	85-GYYRRATRRIRGGDGKM-101	2013.31	29.41	88.80%	63%
14 of 59	17	92-RRIRGGDGKMKDLSRW-108	2028.38	23.53	98.01%	63%
15 of 59	17	99-GKMKDLSRWYFYLLGT-115	2125.47	47.06	99.26%	73%
16 of 59	17	106-PRWYFYLLGTGPEAGLP-122	1987.24	47.06	98.56%	79%
17 of 59	17	113-LGTGPEAGLPYGANKDG-129	1616.75	29.41	99.46%	76%
18 of 59	17	120-GLPYGANKDGIWVATE-136	1804.04	47.06	98.87%	78%
19 of 59	17	127-KDGIWVATEGALNTPK-143	1813.09	41.18	84.22%	73%
20 of 59	17	134-ATEGALNTPKDHIGTRN-150	1794.95	23.53	96.64%	70%
21 of 59	17	141-TPKDHIGTRNPANNAI-157	1789.98	29.41	92.07%	69%
22 of 59	17	148-TRNPANNAIIVLQLPQG-164	1777.02	41.18	98.14%	77%
23 of 59	17	155-AAIVLQLPQGTTLPKGF-171	1754.11	47.06	98.36%	77%
24 of 59	17	162-PQGTTLPKGFYAEGSRG-178	1765.95	23.53	82.56%	73%
25 of 59	17	169-KGFYAEGSRGGSQASSR-185	1744.84	23.53	99.60%	69%
26 of 59	17	176-SRGGSQASSRSSRSRN-192	1766.81	5.88	85.05%	66%

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
27 of 59	17	183-SSRSSSRSRNSSRNSTP-199	1852.90	0.00	84.60%	67%
28 of 59	17	190-SRNSSRNSTPGSSRGTS-206	1737.77	0.00	94.44%	69%
29 of 59	17	197-STPGSSRGTS-213	1633.77	17.65	85.15%	71%
30 of 59	17	204-GTSPARMAGNGGDAALA-220	1516.66	41.18	80.25%	74%
31 of 59	17	211-AGNGGDAALALLLDRL-227	1652.92	58.82	98.45%	76%
32 of 59	17	218-ALALLLDRLNQLLESKM-234	1941.38	58.82	91.83%	75%
33 of 59	17	225-DRLNQLLESKMSGKQQQ-241	1947.17	17.65	94.26%	71%
34 of 59	17	232-SKMSGKQQQQGQTVTK-248	1821.05	11.76	96.55%	70%
35 of 59	17	239-QQQQQGQTVTKKSAEAS-255	1789.93	23.53	96.29%	73%
36 of 59	17	246-VTKKSAEASKKPRQKR-262	1913.26	23.53	98.84%	59%
37 of 59	17	253-EASKKPRQKRTATKAYN-269	1977.26	23.53	93.62%	63%
38 of 59	17	260-QKRTATKAYNVTQAFGR-276	1940.19	35.29	95.30%	68%
39 of 59	17	267-AYNVTQAFRRGPEQTQ-283	1923.08	29.41	99.17%	75%
40 of 59	17	274-FGRRGPEQTQGNFGDQE-290	1923.00	11.76	84.54%	75%
41 of 59	17	281-QTQGNFGDQELIRQGT-297	1906.99	17.65	84.08%	78%
42 of 59	17	288-DQELIRQGTQDYKHWPQI-304	2127.35	29.41	97.85%	73%
43 of 59	17	295-GTDYKHWPQIAQFAPSA-311	1917.11	41.18	98.73%	75%
44 of 59	17	302-PQIAQFAPSASAFFGMS-318	1757.01	52.94	88.95%	82%
45 of 59	17	309-PSASAFFGMSRIGMEVT-325	1788.09	47.06	82.34%	77%
46 of 59	17	316-GMSRIGMEVTPSGTWLT-332	1823.13	35.29	81.43%	78%
47 of 59	17	323-EVTPSGTWLTYTGAIKL-339	1837.10	41.18	92.40%	78%
48 of 59	17	330-WLTYTGAIKLDDKDPNF-346	1997.24	41.18	97.32%	75%
49 of 59	17	337-IKLDKDPNFKDQVILL-353	2014.36	41.18	97.20%	72%
50 of 59	17	344-PNFKDQVILLNKHIDAY-360	2028.34	47.06	93.38%	72%
51 of 59	17	351-ILLNKHIDAYKTFPTE-367	2000.33	41.18	84.12%	72%
52 of 59	17	358-DAYKTFPTEPKKDKK-374	2021.35	17.65	87.38%	63%
53 of 59	17	365-PTEPKKDKKKADETQA-381	1942.21	11.76	98.57%	62%
54 of 59	17	372-KKKADETQALPQRQKK-388	2025.39	17.65	94.10%	61%
55 of 59	17	379-TQALPQRQKKQQTVLL-395	1981.34	29.41	98.93%	72%
56 of 59	17	386-QKKQQTVLLPAADLDD-402	1884.13	35.29	93.68%	74%
57 of 59	17	393-TLLPAADLDDFSKQLQQ-409	1903.13	41.18	96.98%	78%
58 of 59	17	400-LDDFSKQLQQSMSSADS-416	1887.02	29.41	87.23%	78%
59 of 59	13	407-LQQSMSSADSTQA-419	1353.44	30.77	88.82%	78%

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 59	Expected	1.0	2.0	4.0		2.0	1.0		1.0			1.0	1.0	2.0	1.0	1.0			
	Actual	1.0	2.1	3.8		1.9	0.9		1.0			1.0	1.1	2.1	0.8	0.9			
2 of 59	Expected	1.0	2.0	3.0		1.0	2.0		1.0				1.0	2.0	2.0	2.0			
	Actual	1.0	2.1	3.0		0.8	2.1		1.0				1.1	2.1	1.9	1.8			
3 of 59	Expected			3.0		2.0	4.0		1.0				1.0	1.0	3.0	2.0			
	Actual			2.9		1.7	4.0		1.1				1.0	1.1	2.8	1.7			
4 of 59	Expected	1.0	2.0	3.0		2.0	3.0				1.0				4.0	1.0			
	Actual	1.1	2.0	2.7		1.9	3.1				1.1				3.7	1.0			
5 of 59	Expected	1.0	4.0	1.0		3.0	3.0			1.0	1.0			1.0	2.0				
	Actual	1.0	3.9	0.9		2.9	3.0			1.0	1.0			1.1	2.0				

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)
6 of 59	Expected	1.0	3.0	2.0		2.0	1.0			1.0	1.0			2.0	2.0	1.0	1.0		
	Actual	1.0	3.0	2.0		1.8	1.0			1.0	1.1			2.0	2.0	0.9	0.0		
7 of 59	Expected	2.0		2.0		2.0	1.0	1.0		2.0			1.0	1.0	1.0	3.0	1.0		
	Actual	2.0		2.0		1.7	1.0	1.0		2.0			1.0	1.0	0.9	2.7	0.0		
8 of 59	Expected	2.0		1.0		2.0	1.0	1.0		2.0	2.0		2.0		1.0	2.0	1.0		
	Actual	1.9		1.0		2.0	1.1	1.1		2.1	1.9		2.0		0.9	1.8	0.0		
9 of 59	Expected		1.0	1.0		3.0	3.0	1.0		1.0	2.0		1.0	2.0		1.0			1.0
	Actual		1.0	1.0		2.7	3.0	1.0		1.0	2.0		1.0	2.1		0.8			1.1
10 of 59	Expected		1.0	2.0		1.0	2.0		1.0	1.0	1.0		1.0	3.0	2.0	1.0			1.0
	Actual		1.1	1.9		0.8	2.1		1.0	1.0	1.1		1.0	3.0	1.9	0.9			1.1
11 of 59	Expected			4.0		1.0	2.0		2.0					2.0	2.0	1.0		2.0	1.0
	Actual			3.8		1.0	2.0		2.0					2.1	1.9	1.0		2.0	1.0
12 of 59	Expected	1.0	4.0	2.0		1.0	1.0		2.0					1.0	2.0	1.0		2.0	
	Actual	1.1	4.1	2.0		0.8	1.0		2.0					1.1	2.0	0.9		2.0	
13 of 59	Expected	1.0	5.0	1.0			4.0		1.0		1.0	1.0				1.0		2.0	
	Actual	0.9	5.1	1.0			4.1		1.0		1.0	1.0				0.9		2.1	
14 of 59	Expected		4.0	2.0			3.0		1.0	1.0	2.0	1.0		1.0	1.0		1.0		
	Actual		4.0	2.0			3.0		1.0	1.0	2.1	0.9		1.1	0.8		0.0		
15 of 59	Expected		1.0	1.0			2.0			2.0	2.0	1.0	1.0	1.0	1.0	1.0	1.0	3.0	
	Actual		1.1	1.0			2.0			2.0	2.1	1.0	1.0	1.0	0.7	0.9	0.0	2.9	
16 of 59	Expected	1.0	1.0			1.0	3.0			2.0			1.0	3.0		1.0	1.0	3.0	
	Actual	1.0	1.0			0.9	3.1			2.0			1.0	3.1		0.9	0.0	3.1	
17 of 59	Expected	2.0		2.0		1.0	5.0			2.0	1.0			2.0		1.0		1.0	
	Actual	2.0		2.0		0.9	5.0			2.0	1.1			2.1		0.9		1.1	
18 of 59	Expected	2.0		2.0		1.0	3.0		2.0	1.0	1.0			1.0		1.0	1.0	1.0	1.0
	Actual	2.0		2.0		1.1	3.1		1.7	0.9	1.0			1.0		1.0	0.0	1.0	0.9
19 of 59	Expected	2.0		2.0		1.0	2.0		2.0	1.0	2.0			1.0		2.0	1.0		1.0
	Actual	1.9		1.8		1.0	1.9		2.0	1.1	1.7			1.1		2.0	1.0		1.1
20 of 59	Expected	2.0	1.0	3.0		1.0	2.0	1.0	1.0	1.0	1.0			1.0		3.0			
	Actual	1.8	1.1	2.9		0.9	2.2	1.0	1.0	1.0	1.0			1.0		2.9			
21 of 59	Expected	3.0	1.0	4.0			1.0	1.0	2.0		1.0			2.0		2.0			
	Actual	2.9	1.0	4.0			1.0	1.0	2.0		1.0			2.0		1.9			
22 of 59	Expected	3.0	1.0	3.0		2.0	1.0		1.0	2.0				2.0		1.0			1.0
	Actual	2.8	1.0	2.8		2.0	1.1		0.7	2.0				2.0		0.9			0.8
23 of 59	Expected	2.0				2.0	2.0		1.0	3.0	1.0		1.0	2.0		2.0			1.0
	Actual	1.9				2.0	2.0		0.7	3.0	1.0		1.0	2.0		1.9			0.7
24 of 59	Expected	1.0	1.0			2.0	4.0			1.0	1.0		1.0	2.0	1.0	2.0		1.0	
	Actual	0.9	1.0			1.8	3.9			1.1	1.1		1.1	1.8	1.0	1.7		1.0	
25 of 59	Expected	2.0	2.0			2.0	4.0				1.0		1.0		4.0			1.0	
	Actual	1.9	2.0			1.9	4.1				1.1		1.1		4.0			1.0	
26 of 59	Expected	1.0	4.0	1.0		1.0	2.0								8.0				
	Actual	1.1	4.0	1.0		1.0	1.8								7.8				
27 of 59	Expected		4.0	2.0										1.0	9.0	1.0			
	Actual		3.8	1.9										1.1	8.9	0.8			
28 of 59	Expected		3.0	2.0			2.0							1.0	7.0	2.0			
	Actual		3.0	1.8			2.1							1.0	6.8	2.1			
29 of 59	Expected	2.0	2.0	1.0			3.0					1.0		2.0	4.0	2.0			
	Actual	1.8	2.1	0.9			3.2					1.1		2.0	4.0	2.1			
30 of 59	Expected	5.0	1.0	2.0			4.0			1.0				1.0	1.0	1.0			
	Actual	5.0	1.1	1.8			4.0			1.0				1.0	0.8	1.0			
31 of 59	Expected	4.0	1.0	3.0			3.0			6.0									
	Actual	3.7	1.1	3.0			3.0			6.1									
32 of 59	Expected	2.0	1.0	2.0		2.0				7.0	1.0	1.0			1.0				
	Actual	2.2	1.1	2.1		1.8				7.0	0.8	1.1			0.9				
33 of 59	Expected		1.0	2.0		5.0	2.0			2.0	2.0	1.0			2.0				
	Actual		1.1	1.8		4.6	2.1			2.0	1.9	1.1			1.9				
34 of 59	Expected					5.0	3.0				3.0	1.0			2.0	2.0			1.0
	Actual					4.8	3.0				3.1	0.9			2.0	1.8			1.1
35 of 59	Expected	3.0				6.0	1.0				2.0				2.0	2.0			1.0
	Actual	2.8				5.9	1.0				1.9				1.9	1.8			1.1
36 of 59	Expected	3.0	2.0			2.0					5.0			1.0	2.0	1.0			1.0
	Actual	2.9	2.0			1.9					4.8			1.0	2.0	0.9			1.1

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)
37 of 59	Expected	3.0	2.0	1.0		2.0					4.0			1.0	1.0	2.0		1.0	
	Actual	2.9	2.1	1.0		1.9					3.9			1.0	0.9	1.9		1.0	
38 of 59	Expected	3.0	2.0	1.0		2.0	1.0				2.0		1.0			3.0		1.0	1.0
	Actual	2.9	2.0	0.9		2.0	1.1				1.7		1.0			3.0		1.2	1.1
39 of 59	Expected	2.0	2.0	1.0		4.0	2.0						1.0	1.0		2.0		1.0	1.0
	Actual	1.9	2.0	1.1		4.0	2.0						1.0	1.0		1.8		1.0	1.0
40 of 59	Expected		2.0	2.0		5.0	4.0						2.0	1.0		1.0			
	Actual		2.1	2.0		4.8	4.1						2.0	1.0		0.9			
41 of 59	Expected		1.0	3.0		5.0	3.0		1.0	1.0			1.0			2.0			
	Actual		1.0	3.0		4.8	3.1		1.0	1.0			1.0			1.8			
42 of 59	Expected		1.0	2.0		4.0	1.0	1.0	2.0	1.0	1.0			1.0		1.0	1.0	1.0	1.0
	Actual		0.9	2.1		3.9	1.0	1.0	1.8	1.0	1.1			1.0		0.9	0.0	1.1	
43 of 59	Expected	3.0		1.0		2.0	1.0	1.0	1.0		1.0		1.0	2.0	1.0	1.0	1.0	1.0	1.0
	Actual	2.9		1.0		1.9	1.0	1.1	1.0		1.0		1.1	2.1	0.7	0.9	0.7	1.1	
44 of 59	Expected	4.0				2.0	1.0		1.0			1.0	3.0	2.0	3.0				
	Actual	3.8				1.8	1.1		1.0			1.0	3.0	2.0	3.0				
45 of 59	Expected	2.0	1.0			1.0	2.0		1.0			2.0	2.0	1.0	3.0	1.0			1.0
	Actual	1.9	1.0			0.9	2.0		1.0			2.0	2.1	1.0	2.4	1.0			1.1
46 of 59	Expected		1.0			1.0	3.0		1.0	1.0		2.0		1.0	2.0	3.0	1.0		1.0
	Actual		0.8			0.9	3.0		1.0	1.1		2.0		1.1	1.8	2.9	0.0		1.2
47 of 59	Expected	1.0				1.0	2.0		1.0	2.0	1.0			1.0	1.0	4.0	1.0	1.0	1.0
	Actual	0.9				0.9	2.0		1.0	2.1	1.0			1.0	0.8	4.0	0.0	1.1	1.1
48 of 59	Expected	1.0		4.0			1.0		1.0	2.0	2.0		1.0	1.0		2.0	1.0	1.0	1.0
	Actual	0.9		3.9			1.0		0.9	2.0	1.8		1.1	1.0		1.8	0.0	1.1	
49 of 59	Expected			5.0		1.0			2.0	3.0	3.0		1.0	1.0					1.0
	Actual			4.8		1.0			1.9	3.1	2.8		1.1	1.0					0.8
50 of 59	Expected	1.0		4.0		1.0		1.0	2.0	2.0	2.0		1.0	1.0				1.0	1.0
	Actual	0.9		3.9		0.9		1.1	1.8	2.0	1.8		1.1	1.0				1.1	0.9
51 of 59	Expected	1.0		2.0		1.0		1.0	2.0	2.0	2.0		1.0	2.0		2.0			1.0
	Actual	1.0		2.1		1.0		1.0	1.7	2.0	1.7		1.1	2.1		2.1			1.1
52 of 59	Expected	1.0		2.0		1.0					6.0		1.0	3.0		2.0		1.0	1.0
	Actual	1.0		2.1		0.9					6.0		1.0	3.0		2.1		1.0	1.0
53 of 59	Expected	2.0		2.0		3.0					6.0			2.0		2.0			
	Actual	2.0		2.0		2.9					6.1			2.1		1.8			
54 of 59	Expected	2.0	1.0	1.0		4.0				1.0	6.0			1.0		1.0			
	Actual	1.9	1.0	0.9		4.1				1.1	6.0			1.1		0.9			
55 of 59	Expected	1.0	1.0			5.0				3.0	2.0			1.0		3.0			1.0
	Actual	1.0	1.1			5.0				2.9	2.0			1.0		3.0			1.1
56 of 59	Expected	2.0		3.0		3.0				3.0	2.0			1.0		2.0			1.0
	Actual	1.9		3.0		2.9				3.0	2.1			1.0		1.8			1.1
57 of 59	Expected	2.0		3.0		3.0				4.0	1.0		1.0	1.0	1.0	1.0			
	Actual	2.0		3.0		3.0				3.9	1.1		1.0	1.0	0.9	0.9			
58 of 59	Expected	1.0		3.0		3.0				2.0	1.0	1.0	1.0		5.0				
	Actual	1.0		2.8		3.0				2.1	1.0	1.0	1.1		4.9				
59 of 59	Expected	2.0		1.0		3.0				1.0		1.0			4.0	1.0			
	Actual	2.0		1.0		3.0				1.0		1.0			3.9	1.0			

³Tryptophan (W) was partially or 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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