

**Peptide Array, SARS Coronavirus Spike (S) Protein**

**Catalog No. NR-52418**

This reagent is the tangible property of the U.S. Government.

**Product Description:**

The 169-peptide array spans the spike (S) protein of the Urbani strain of severe acute respiratory syndrome coronavirus (SARS-CoV; GenBank: [AAP13441](#)). Peptides are typically 15- to 20-mers, with approximately 10 amino acid overlaps.

Note: due to difficulty in synthesis and isolation, seven designed peptides were split into two shorter peptides to give 8- to 11-mers; therefore, there are 176 total peptides in the NR-52418 array.

**Lot: U5567FC110**

The following information applies to all peptides:

- Appearance White lyophilized powder
- Mass spectral analysis Correct MW by MALDI or Electrospray

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

**Table 1: Peptide Analysis**

Peptide	Mfg. Date	Length	Sequence	Molecular Weight (amu)	Purity by HPLC <sup>1</sup>	Peptide Content <sup>2</sup>	Counter Ion(s)
1 of 169	12/1/2020	16	1-MFIFLLFLTLTSGSDL-16	1817.6	85.3%	63.33%	TFA-
2 of 169	6/26/2020	17	9-TLTSGSGLDRCTTFDDV-25	1845.2	92.7%	60.23%	TFA-
3 of 169	5/3/2020	18	16-LDRCTTFDDVQAPNYTQH-33	2124.0	85.4%	85.22%	TFA-
4 of 169	5/6/2020	18	24-DVQAPNYTQHTSSMRGVY-41	2053.6	86.0%	82.21%	TFA-
5 of 169	4/30/2020	17	32-QHTSSMRGVYYPDEIFR-48	2085.9	89.4%	64.74%	TFA-
6 of 169	5/2/2020	16	39-GVYYPDEIFRSDTLYL-54	1950.6	93.5%	68.63%	TFA-
7 of 169	7/4/2020	18	45-EIFRSDTLYLQDLFLPF-62	2218.0	93.8%	55.39%	CH <sub>3</sub> COO-+TFA-
8 of 169	5/5/2020	18	53-YLTQDLFLPFYSNVTGFH-70	2161.8	96.1%	89.59%	TFA-
9 of 169	5/2/2020	16	61-PFYSNVTGFHTINHTF-76	1881.6	90.9%	71.86%	TFA-
10 of 169	5/1/2020	18	67-TGFHTINHTFGNPVVPFK-84	2026.8	94.3%	74.88%	TFA-
11 of 169	5/1/2020	17	75-TFGNPVVPFKDGIYFAA-91	1856.4	90.8%	72.28%	TFA-
12 of 169	5/26/2020	18	82-PFKDGIYFAATEKSNVVR-99	2041.8	93.8%	52.68%	TFA-
13 of 169	5/7/2020	18	90-AATEKSNVVRGWVFGSTM-107	1939.8	94.4%	60.91%	TFA-
14 of 169	5/2/2020	18	98-VRGWVFGSTMNKSQSVI-115	2009.7	94.0%	73.04%	TFA-
15 of 169	11/25/2020	16	106-TMNNKSQSVIINNST-121	1764.8	88.7%	75.45%	TFA-
16.1 of 169	11/17/2020	10	114-VIINNSTNV-123	1086.0	90.4%	70.94%	TFA-
16.2 of 169	11/17/2020	10	121-TNVVIRACNF-130	1136.0	89.7%	76.60%	TFA-
17 of 169	9/1/2020	18	121-TNVVIRACNFELCDNPFF-138	2101.6	88.3%	50.23%	TFA-
18 of 169	5/5/2020	16	129-NFELCDNPFFAVSKPM-144	1858.6	89.0%	74.71%	TFA-
19 of 169	5/4/2020	18	135-NPFFAVSKPMGTQHTMI-152	2006.7	89.4%	84.31%	TFA-
20 of 169	5/1/2020	15	143-PMGTQHTMIFDNAF-157	1710.4	93.9%	86.15%	TFA-
21 of 169	9/1/2020	17	148-THTMIFDNAFNCTFEYI-164	2066.8	86.3%	64.68%	CH <sub>3</sub> COO-+TFA-
22 of 169	8/25/2020	18	155-NAFNCTFEYISDAFSLDV-172	2055.6	85.6%	89.82%	CH <sub>3</sub> COO-+TFA-
23 of 169	5/2/2020	18	163-YISDAFSLDVSEKSGNFK-180	2006.8	85.5%	80.28%	TFA-
24 of 169	4/30/2020	18	171-DVSEKSGNFKHLREFVFK-188	2166.6	98.3%	77.04%	TFA-
25 of 169	5/16/2020	18	179-FKHLREFVFKKDGFLYV-196	2287.6	89.2%	61.64%	TFA-
26 of 169	4/25/2020	17	187-FKNKDGFLYVYKGYQPI-203	2079.9	88.4%	80.89%	TFA-

Table 1: Peptide Analysis (continued)

Peptide	Mfg. Date	Length	Sequence	Molecular Weight (amu)	Purity by HPLC <sup>1</sup>	Peptide Content <sup>2</sup>	Counter Ion(s)
27 of 169	5/5/2020	16	194-LYVYKGYQPIDVVRDL-209	1940.7	97.6%	84.69%	TFA-
28 of 169	4/26/2020	18	200-YQPIDVVRDLPSGFNTLK-217	2061.9	93.5%	85.33%	TFA-
29 of 169	5/5/2020	17	208-DLPSGFNTLKPIFKLPL-224	1899.8	93.3%	82.20%	TFA-
30 of 169	5/2/2020	18	215-TLKPIFKLPLGINITNFR-232	2085.0	96.3%	59.73%	TFA-
31 of 169	6/23/2020	16	223-PLGINITNFRILTA-238	1760.6	90.5%	52.91%	TFA-
32 of 169	5/2/2020	17	229-TNFRILTA-245	1950.8	94.6%	88.00%	TFA-
33 of 169	4/26/2020	18	236-TAFSPAQDIWGTSAAYF-253	1903.2	86.2%	70.81%	TFA-
34 of 169	4/26/2020	15	244-IWGTSAAYFVGYLK-258	1646.2	86.1%	87.08%	TFA-
35 of 169	5/13/2020	18	249-AAAYFVGYLKPTTFMLKY-266	2084.0	94.7%	71.57%	TFA-
36 of 169	5/4/2020	16	257-LKPTTFMLKYDENGTI-272	1870.5	93.4%	77.53%	TFA-
37 of 169	5/15/2020	18	263-MLKYDENGITDAVDCSQ-280	2002.6	85.4%	83.56%	TFA-
38 of 169	4/30/2020	17	271-TITDAVDCSQNPLAELK-287	1817.4	86.3%	65.99%	TFA-
39 of 169	6/8/2020	18	278-CSQNPLAELKCSVKSFEI-295	1995.9	86.6%	57.89%	TFA-
40 of 169	5/7/2020	15	286-LKCSVKSFEIDKGIY-300	1729.8	93.1%	70.45%	TFA-
41 of 169	4/26/2020	18	291-KSFEIDKGIYQTSNFRV-308	2130.6	92.5%	80.44%	TFA-
42 of 169	4/24/2020	18	299-IYQTSNFRVPSGDVVR-316	2083.8	94.1%	71.50%	TFA-
43 of 169	5/1/2020	16	307-VVPSGDVVRFPNITNL-322	1726.4	93.2%	57.14%	TFA-
44 of 169	5/16/2020	17	313-VVRFNITNLCPFGEVF-329	1951.4	87.2%	57.00%	TFA-
45 of 169	4/26/2020	18	320-TNLCPFGEVFNATKFP-337	1970.6	92.1%	84.21%	TFA-
46 of 169	4/24/2020	18	328-VFNATKFPVYAWERKKI-345	2184.0	95.1%	53.95%	TFA-
47 of 169	5/7/2020	17	336-SVYAWERKKISNCVADY-352	2031.6	93.4%	56.94%	TFA-
48 of 169	4/23/2020	18	343-KKISNCVADYSVLYNSTF-360	2051.8	87.1%	64.68%	TFA-
49 of 169	8/8/2020	15	351-DYSVLYNSTFFSTFK-365	1818.6	85.2%	60.58%	TFA-
50 of 169	5/13/2020	17	358-STFFSTFKCYGVSATKL-374	1886.7	86.8%	72.00%	TFA-
51 of 169	4/27/2020	18	365-KCYGVSATKLNLCFSNV-382	1961.4	89.9%	84.73%	TFA-
52 of 169	5/1/2020	18	373-KLNLCFSNVYADSFVVK-390	2061.9	90.7%	65.02%	TFA-
53 of 169	5/31/2020	18	381-NVYADSFVVKGDVVRQIA-398	1995.6	87.4%	64.88%	TFA-
54 of 169	4/25/2020	18	389-VKGDVVRQIAPGQTGVIA-406	1823.7	85.3%	73.30%	TFA-
55 of 169	5/2/2020	16	397-IAPGQTGVIAADYNYKL-412	1722.6	93.1%	86.84%	TFA-
56 of 169	4/25/2020	18	403-GVIADYNYKLPPDFMGCV-420	2019.6	85.6%	78.47%	TFA-
57 of 169	4/24/2020	18	411-KLPDFMGCVLAWNTRNI-428	2093.1	85.9%	77.72%	TFA-
58 of 169	4/26/2020	18	419-CVLAWNTRNIDATSTGNY-436	1998.8	86.9%	89.50%	TFA-
59 of 169	4/27/2020	18	427-NIDATSTGNYNYKYRYLR-444	2211.9	91.5%	77.27%	TFA-
60 of 169	5/1/2020	17	435-NYNYKYRYLRHGKLRPF-451	2288.0	93.1%	71.78%	TFA-
61 of 169	4/23/2020	17	442-YLRHGKLRPFERDISNV-458	2100.0	90.6%	73.98%	TFA-
62 of 169	5/2/2020	17	449-RPFERDISNVFSPDGK-465	1960.8	92.9%	70.81%	TFA-
63 of 169	5/2/2020	17	456-SNVFSPDGKPPAL-472	1726.4	86.5%	77.83%	TFA-
64 of 169	5/4/2020	16	463-DGKPPALNCYWPL-478	1774.4	89.3%	80.00%	TFA-
65 of 169	5/4/2020	16	469-PPALNCYWPLNDYGFY-484	1932.4	85.5%	89.42%	TFA-
66 of 169	5/2/2020	17	475-YWPLNDYGFYTTTGIGY-491	2030.6	98.4%	91.95%	TFA-
67 of 169	4/29/2020	18	482-GFYTTTGIGYQPYRVVVL-499	2033.8	90.7%	70.68%	TFA-
68 of 169	7/20/2020	17	490-GYQPYRVVLSFELLNA-506	1968.0	92.5%	77.08%	TFA-
69 of 169	4/25/2020	18	497-VVLSFELLNAPATVCGPK-514	1857.6	89.0%	72.50%	TFA-
70 of 169	4/30/2020	17	505-NAPATVCGPKLSTDLIK-521	1727.4	96.8%	63.35%	TFA-
71 of 169	4/24/2020	18	512-GPKLSTDLIKQCVNFN-529	2037.9	89.1%	62.11%	TFA-

Table 1: Peptide Analysis (continued)

Peptide	Mfg. Date	Length	Sequence	Molecular Weight (amu)	Purity by HPLC <sup>1</sup>	Peptide Content <sup>2</sup>	Counter Ion(s)
72 of 169	5/1/2020	18	520-IKNQCVNFNFNGLTGTGV-537	1925.6	85.9%	76.19%	TFA-
73 of 169	5/7/2020	18	528-NFNGLTGTGVLTPSSKRF-545	1895.6	85.8%	57.14%	TFA-
74 of 169	4/23/2020	18	536-GVLTPSSKRFQPFQFGR-553	2079.9	92.7%	67.28%	TFA-
75 of 169	4/29/2020	15	544-RFQPFQFGRDVSD-558	1873.6	94.1%	79.41%	TFA-
76 of 169	4/27/2020	18	549-QQFGRDVSDFTDSVRDPK-566	2097.7	87.8%	81.90%	TFA-
77 of 169	5/3/2020	17	557-DFTDSVRDPKTSEILDI-573	1950.6	89.3%	51.78%	CH <sub>3</sub> COO-+TFA-
78 of 169	4/27/2020	18	564-DPKTSEILDISPCSFQGGV-581	1864.8	92.2%	78.46%	TFA-
79 of 169	5/2/2020	19	572-DISPCSFQGGVSVITPGTNA-590	1821.6	92.6%	61.11%	TFA-
80 of 169	8/28/2020	16	583-VITPGTNASSEVAVLY-598	1620.4	88.0%	51.61%	CH <sub>3</sub> COO-+TFA-
81 of 169	11/25/2020	16	590-ASSEVAVLYQDVNCTD-605	1713.2	89.2%	52.46%	TFA-
82 of 169	6/7/2020	16	597-LYQDVNCTDVSTAIHA-612	1749.3	89.8%	78.69%	TFA-
83 of 169	5/2/2020	18	603-CTDVSTAIHADQLTPAWR-620	1984.6	88.7%	76.50%	TFA-
84 of 169	4/26/2020	18	611-HADQLTPAWRIYSTGNV-628	2042.7	85.1%	85.59%	TFA-
85 of 169	6/23/2020	18	619-WRIYSTGNVVFQTAGCL-636	2057.8	89.3%	74.26%	TFA-
86 of 169	9/8/2020	16	627-NVFQTAGCLIGAEHV-642	1686.4	86.0%	61.46%	TFA-
87.1 of 169	11/10/2020	11	633-AGCLIGAEHVD-643	1084.0	86.2%	64.91%	TFA-
87.2 of 169	11/10/2020	10	641-HVDTSYECEDI-650	1180.8	90.1%	68.42%	TFA-
88 of 169	4/25/2020	18	641-HVDTSYECIDIPIGAGICA-658	1863.6	85.9%	76.81%	TFA-
89 of 169	4/25/2020	18	649-DIPIGAGICASYHTVSL-666	1830.6	88.7%	88.36%	TFA-
90 of 169	7/5/2020	18	657-CASYHTVSLLRSTSQKSI-674	1980.9	95.5%	70.85%	TFA-
91 of 169	6/20/2020	17	665-LLRSTSQKSIVAYTMSL-681	1897.8	89.5%	69.41%	TFA-
92 of 169	8/4/2020	16	672-KSIVAYTMSLGADSSI-687	1642.4	87.7%	57.05%	TFA-
93 of 169	7/25/2020	17	680-SLGADSSIIAYSNNTIAI-696	1696.6	85.8%	67.65%	TFA-
94 of 169	8/8/2020	16	688-AYSNTIAIPTNFSIS-703	1712.6	86.2%	88.38%	TFA-
95 of 169	7/21/2020	17	695-AIPTNFSISITTEVMPV-711	1819.6	92.0%	51.55%	TFA-
96 of 169	6/11/2020	17	702-ISITTEVMPVSMAKTSV-718	1793.6	94.2%	57.14%	TFA-
97 of 169	6/8/2020	16	709-MPVSMAKTSVDCNMYI-724	1789.6	88.4%	73.96%	TFA-
98 of 169	9/7/2020	18	715-KTSVDCNMYICGDSTECA-732	1939.6	94.2%	63.83%	TFA-
99 of 169	5/25/2020	16	723-YICGDSTECANLLQY-738	1805.4	92.9%	69.47%	TFA-
100 of 169	6/13/2020	17	729-TECANLLQYGSFCTQL-745	1903.4	85.4%	53.69%	TFA-
101 of 169	4/24/2020	18	736-LQYGSFCTQLNRALSGIA-753	1941.6	85.0%	65.43%	TFA-
102 of 169	4/24/2020	18	744-QLNRALSGIAEQDRNTR-761	2012.7	86.8%	72.06%	TFA-
103 of 169	4/29/2020	17	752-IAAEQDRNTREVFQVK-768	1974.6	89.2%	74.10%	TFA-
104 of 169	4/26/2020	18	759-NTREVFQVKQMYKPTL-776	2153.7	95.0%	82.67%	TFA-
105 of 169	4/26/2020	18	767-VKQMYKPTLKYFGGFNF-784	2169.0	94.6%	80.15%	TFA-
106 of 169	4/24/2020	18	775-TLKYFGGFNFSQILPDPL-792	2057.0	85.2%	86.96%	TFA-
107 of 169	5/3/2020	18	783-NFSQILPDPLKPTKRSFI-800	2100.9	92.6%	81.69%	TFA-
108 of 169	4/25/2020	18	791-PLKPTKRSFIEDLLFNKV-808	2145.0	85.0%	78.63%	TFA-
109 of 169	5/3/2020	18	799-FIEDLLFNKVTLADAGFM-816	2043.6	85.8%	88.46%	CH <sub>3</sub> COO-+TFA-
110 of 169	5/16/2020	17	807-KVTLADAGFMKQYGECL-823	1873.4	90.6%	83.16%	TFA-
111 of 169	4/26/2020	18	814-GFMKQYGECLGDINARDL-831	2029.8	85.2%	84.89%	TFA-
112 of 169	4/28/2020	16	822-CLGDINARDLICAQKF-837	1779.6	87.9%	82.22%	TFA-
113 of 169	5/23/2020	16	828-ARDLICAQKFNGLTVL-843	1761.2	86.8%	72.33%	TFA-
114 of 169	4/26/2020	18	834-AQKFNGLTVLPLLTDMM-851	1972.6	90.0%	88.61%	TFA-
115 of 169	6/10/2020	18	842-VLPLLTDMMIAAYTAAL-859	1887.6	96.4%	89.76%	TFA-

Table 1: Peptide Analysis (continued)

Peptide	Mfg. Date	Length	Sequence	Molecular Weight (amu)	Purity by HPLC <sup>1</sup>	Peptide Content <sup>2</sup>	Counter Ion(s)
116 of 169	8/3/2020	17	850-DMIAAYTAALVSGTATA-866	1626.4	93.1%	64.97%	TFA-
117 of 169	7/22/2020	18	857-AALVSGTATAGWTFGAGA-874	1608.4	85.2%	52.63%	TFA-
118 of 169	7/20/2020	18	865-TAGWTFGAGAALQIPFAM-882	1809.8	85.8%	87.06%	TFA-
119 of 169	5/2/2020	16	873-GAALQIPFAMQMAYRF-888	1815.0	90.5%	88.27%	TFA-
120 of 169	5/2/2020	15	879-PFAMQMAYRFNGIGV-893	1701.4	90.8%	69.51%	TFA-
121 of 169	6/25/2020	16	884-MAYRFNGIGVTQNVLY-899	1845.8	95.8%	84.74%	TFA-
122 of 169	4/29/2020	17	890-GIGVTQNVLYENQKQIA-906	1874.6	85.8%	82.89%	TFA-
123 of 169	4/29/2020	17	897-VLYENQKQIANQFNKAI-913	2020.8	93.7%	77.01%	TFA-
124 of 169	4/29/2020	17	904-QIANQFNKAISQIQESL-920	1931.6	85.1%	75.84%	TFA-
125 of 169	6/10/2020	17	911-KAISQIQESLTTTSTAL-927	1791.8	85.1%	77.54%	TFA-
126 of 169	6/8/2020	17	918-ESLTTTSTALGKLQDVV-934	1762.4	86.1%	51.32%	TFA-
127 of 169	4/27/2020	17	925-TALGKLQDVVNQNAQAL-941	1782.2	90.3%	86.93%	TFA-
128 of 169	4/29/2020	17	932-DVVNQNAQALNTLVKQL-948	1867.6	85.9%	61.62%	TFA-
129 of 169	4/25/2020	17	939-QALNTLVKQLSSNFGAI-955	1803.4	87.5%	88.10%	TFA-
130 of 169	6/13/2020	18	946-KQLSSNFGAISSVLNDIL-963	1905.8	85.6%	65.61%	TFA-
131 of 169	4/26/2020	18	954-AISSVLNDILSRDKVEA-971	1942.6	88.8%	84.62%	TFA-
132 of 169	4/27/2020	18	962-ILSRDKVEAEVQIDRLI-979	2109.9	86.3%	73.81%	TFA-
133 of 169	4/29/2020	17	970-EAEVQIDRLITGRLQSL-986	1941.0	85.1%	71.57%	TFA-
134 of 169	5/26/2020	18	977-RLITGRLQSLQTYVTQQL-994	2117.7	86.8%	86.40%	TFA-
135 of 169	4/26/2020	18	985-SLQTYVTQQLIRAAEIRA-1002	2061.0	90.2%	81.03%	TFA-
136 of 169	6/7/2020	18	993-QLIRAAEIRASANLAATK-1010	1896.9	85.1%	69.49%	TFA-
137 of 169	7/17/2020	15	1001-RASANLAATKMSECV-1015	1551.4	86.3%	72.37%	TFA-
138 of 169	5/23/2020	18	1007-AATKMSECVLGQSKRVDF-1024	1969.8	90.1%	54.67%	TFA-
139 of 169	5/18/2020	18	1015-VLGQSKRVDFCGKGYHLM-1032	2038.0	93.0%	74.06%	TFA-
140 of 169	4/26/2020	18	1023-DFCGKGYHLMSPQAAPH-1040	2005.5	87.8%	81.35%	TFA-
141 of 169	4/26/2020	17	1031-LMSFPQAAPHGVVFLHV-1047	1849.8	95.6%	58.65%	TFA-
142 of 169	4/24/2020	18	1038-APHGVVFLHVTVPSQER-1055	2036.0	96.7%	70.48%	TFA-
143 of 169	4/25/2020	18	1046-HVTYVPSQERNFTTAPAI-1063	2030.4	86.1%	83.56%	TFA-
144 of 169	4/24/2020	18	1054-ERNFTTAPAICHEGKAYF-1071	2054.7	89.0%	72.73%	TFA-
145 of 169	4/24/2020	18	1062-AICHEGKAYFPREGVVFV-1079	2069.4	88.0%	67.17%	TFA-
146 of 169	5/2/2020	17	1070-YFPREGVVFVNGTSWFI-1086	2065.8	85.6%	89.71%	TFA-
147 of 169	5/7/2020	16	1077-FVFNGTSWFITQRNFF-1092	2010.8	89.0%	71.71%	TFA-
148 of 169	6/6/2020	15	1083-SWFITQRNFFSPQII-1097	1883.8	94.5%	61.15%	TFA-
149 of 169	5/2/2020	17	1088-QRNFFSPQIITDNTFV-1104	2027.6	92.1%	77.73%	TFA-
150.1 of 169	11/17/2020	10	1095-QIITDNTFV-1104	1152.0	85.0%	51.79%	TFA-
150.2 of 169	11/17/2020	8	1103-FVSGNCDV-1110	839.2	89.6%	51.11%	TFA-
151 of 169	10/20/2020	10	1111-VIGIINNTVY-1120	1105.8	94.4%	88.00%	TFA-
152 of 169	5/1/2020	17	1111-VIGIINNTVYDPLQPEL-1127	1897.4	91.1%	70.97%	TFA-
153 of 169	4/29/2020	17	1118-TVYDPLQPELDSFKEEL-1134	2022.8	89.2%	87.50%	TFA-
154 of 169	4/23/2020	17	1125-PELDSFKEELDKYFKNH-1141	2139.2	94.2%	64.68%	TFA-
155 of 169	4/25/2020	17	1132-EELDKYFKNHTSPDVL-1148	2049.6	89.7%	75.71%	TFA-
156 of 169	4/24/2020	18	1139-KNHTSPDVLGDISGINA-1156	1852.4	89.3%	63.68%	TFA-
157 of 169	6/13/2020	17	1147-DLGDISGINASVVNIQK-1163	1742.4	85.2%	73.63%	HCOO-+TFA-
158 of 169	4/21/2020	18	1154-INASVVNIQKEIDRLNEV-1171	2053.8	86.3%	67.78%	CH <sub>3</sub> COO-+TFA-
159 of 169	5/14/2020	18	1162-QKEIDRLNEVAKNLNESL-1179	2112.9	85.2%	70.48%	TFA-

Table 1: Peptide Analysis (continued)

Peptide	Mfg. Date	Length	Sequence	Molecular Weight (amu)	Purity by HPLC <sup>1</sup>	Peptide Content <sup>2</sup>	Counter Ion(s)
160 of 169	4/19/2020	18	1170-EVAKNLNESLIDLQELGK-1187	2013.0	91.0%	65.52%	TFA-
161 of 169	5/2/2020	17	1178-SLIDLQELGKYEQYIKW-1194	2125.8	96.4%	86.13%	TFA-
162 of 169	4/27/2020	18	1185-LGKYEQYIKWPWYVWLGF-1202	2376.3	88.1%	87.11%	TFA-
163.1 of 169	11/25/2020	11	1193-KWPWYVWLGF-1203	1494.4	90.2%	58.90%	TFA-
163.2 of 169	11/25/2020	9	1202-FIAGLIAIV-1210	915.4	85.2%	86.03%	TFA-
164.1 of 169	9/15/2020	8	1201-GFIAGLIA-1208	760.4	93.9%	70.73%	TFA-
164.2 of 169	9/15/2020	8	1209-IVMVTILL-1216	900.5	86.4%	58.56%	TFA-
165.1 of 169	12/1/2020	10	1207-IAIVMVTILL-1216	1085.2	85.0%	54.17%	TFA-
165.2 of 169	12/1/2020	10	1217-CCMTSCCSCL-1226	1053.0	93.5%	80.98%	TFA-
166.1 of 169	9/22/2020	8	1217-CCMTSCCS-1224	836.1	86.4%	69.77%	TFA-
166.2 of 169	9/22/2020	10	1225-CLKGACSCGS-1234	927.2	90.3%	77.27%	TFA-
167 of 169	10/10/2020	10	1233-GSCCKFDEDD-1242	1117.8	96.3%	80.65%	TFA-
168 of 169	4/23/2020	18	1233-GSCCKFDEDDSEPVKGV-1250	1927.8	85.1%	65.52%	TFA-
169 of 169	4/24/2020	15	1241-DDSEPVKGVKLHYT-1255	1700.7	90.6%	63.37%	TFA-

<sup>1</sup>Percent full length

<sup>2</sup>Remainder is salt and water

Figure 1: Amino Acid Analysis<sup>3</sup>

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 169	Expected			1.0			1.0		1.0	5.0		1.0	3.0		2.0	2.0			
	Actual			1.4			1.2		1.2	4.4		0.8	2.0		2.1	2.3			
2 of 169	Expected		1.0	4.0	1.0		1.0			2.0			1.0		2.0	4.0			1.0
	Actual		1.1	3.9	0.0		1.0			2.1			1.2		1.8	3.5			1.1
3 of 169	Expected	1.0	1.0	4.0	1.0	2.0		1.0		1.0			1.0	1.0		3.0		1.0	1.0
	Actual	1.0	1.0	3.9	0.0	2.1		1.2		1.0			1.0	1.0		2.5		1.0	1.0
4 of 169	Expected	1.0	1.0	2.0		2.0	1.0	1.0				1.0		1.0	2.0	2.0		2.0	2.0
	Actual	0.9	1.0	2.0		2.1	1.0	1.0				1.0		1.0	1.8	1.8		1.7	1.6
5 of 169	Expected		2.0	1.0		2.0	1.0	1.0	1.0			1.0	1.0	1.0	2.0	1.0		2.0	1.0
	Actual		2.0	1.1		2.2	1.1	1.0	0.7			0.9	1.0	1.0	1.9	1.0		1.6	0.7
6 of 169	Expected		1.0	2.0		1.0	1.0		1.0	2.0			1.0	1.0	1.0	1.0		3.0	1.0
	Actual		1.0	2.0		1.1	1.0		0.9	2.0			0.9	1.1	0.9	0.9		2.9	0.9
7 of 169	Expected		1.0	2.0		2.0			1.0	4.0			3.0	1.0	1.0	2.0		1.0	
	Actual		1.0	2.0		2.1			1.0	3.9			3.0	1.1	0.9	1.6		1.1	
8 of 169	Expected			2.0		1.0	1.0	1.0		3.0			3.0	1.0	1.0	2.0		2.0	1.0
	Actual			2.0		1.1	1.0	1.2		2.9			3.0	1.0	0.9	1.7		2.0	1.0
9 of 169	Expected			2.0			1.0	2.0	1.0				3.0	1.0	1.0	3.0		1.0	1.0
	Actual			2.0			1.1	2.2	1.0				3.2	1.1	0.9	2.7		1.1	1.0
10 of 169	Expected			2.0			2.0	2.0	2.0		1.0		3.0	2.0		3.0			1.0
	Actual			2.1			2.1	2.2	1.9		1.0		3.2	2.2		2.6			1.0
11 of 169	Expected	2.0		2.0			2.0		2.0		1.0		3.0	2.0		1.0		1.0	1.0
	Actual	2.0		2.0			2.0		1.9		1.0		3.1	2.1		0.9		0.9	1.1
12 of 169	Expected	2.0	1.0	2.0		1.0	1.0		1.0		2.0		2.0	1.0	1.0	1.0		1.0	2.0
	Actual	2.1	1.1	1.9		1.0	1.2		1.2		1.8		2.4	1.1	0.7	0.8		1.2	2.2
13 of 169	Expected	2.0	1.0	1.0		1.0	2.0				1.0	1.0	1.0		2.0	2.0	1.0		3.0
	Actual	1.6	1.1	1.1		1.2	2.2				1.1	1.1	1.0		1.9	2.0	0.0		2.1
14 of 169	Expected		1.0	2.0		1.0	2.0		1.0		1.0	1.0	1.0		3.0	1.0	1.0		3.0
	Actual		0.8	2.0		1.0	2.2		1.0		1.0	1.1	1.0		2.8	1.0	0.0		2.6

Figure 1: Amino Acid Analysis (continued)<sup>3</sup>

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)
15 of 169	Expected			4.0		1.0			3.0		1.0	1.0			3.0	2.0			1.0
	Actual			4.4		1.2			2.3		1.1	1.0			2.7	2.0			0.7
16.1 of 169	Expected			3.0					3.0						1.0	1.0			2.0
	Actual			3.2					2.8						0.7	1.0			1.9
16.2 of 169	Expected	1.0	1.0	2.0	1.0				1.0				1.0			1.0			2.0
	Actual	1.1	1.0	2.0	0.0				1.0				1.1			0.9			1.5
17 of 169	Expected	1.0	1.0	4.0	2.0	1.0			1.0	1.0			3.0	1.0		1.0			2.0
	Actual	1.1	1.1	3.8	0.0	1.1			0.9	1.1			3.6	1.1		0.8			1.5
18 of 169	Expected	1.0		3.0	1.0	1.0				1.0	1.0	1.0	3.0	2.0	1.0				1.0
	Actual	1.0		3.0	0.0	1.1				1.0	1.0	0.9	2.8	2.0	0.9				1.0
19 of 169	Expected	1.0		1.0		1.0	1.0	1.0	1.0		1.0	2.0	2.0	2.0	1.0	3.0			1.0
	Actual	1.0		1.0		1.1	1.0	1.1	1.0		0.9	1.9	2.0	2.0	0.9	2.7			1.0
20 of 169	Expected	1.0		2.0		1.0	1.0	1.0	1.0				2.0	2.0	1.0		3.0		
	Actual	1.0		2.1		1.1	1.0	1.1	0.9				2.1	2.0	1.1		3.3		
21 of 169	Expected	1.0		3.0	1.0	1.0		1.0	2.0				1.0	3.0			3.0	1.0	
	Actual	1.1		3.0	0.0	1.1		1.0	1.8				1.0	3.1			2.7	1.0	
22 of 169	Expected	2.0		4.0	1.0	1.0			1.0	1.0			3.0		2.0	1.0		1.0	1.0
	Actual	2.0		3.8	0.0	1.1			1.0	1.1			3.5		1.6	0.8		1.1	1.1
23 of 169	Expected	1.0		3.0		1.0	1.0		1.0	1.0	2.0		2.0		4.0			1.0	1.0
	Actual	0.9		3.1		0.9	1.1		0.9	1.1	2.1		2.1		3.6			0.9	1.1
24 of 169	Expected		1.0	2.0		2.0	1.0	1.0		1.0	3.0		3.0		2.0				2.0
	Actual		1.0	1.9		2.1	1.0	1.0		1.0	2.9		2.6		1.9				1.7
25 of 169	Expected		1.0	2.0		1.0	1.0	1.0		2.0	3.0		4.0					1.0	2.0
	Actual		1.0	2.0		1.1	1.1	1.2		2.0	2.9		4.0					1.1	1.9
26 of 169	Expected			2.0		1.0	2.0		1.0	1.0	3.0		2.0	1.0				3.0	1.0
	Actual			1.9		1.1	1.9		1.0	1.0	2.9		1.9	1.0				2.8	0.8
27 of 169	Expected		1.0	2.0		1.0	1.0		1.0	2.0	1.0			1.0				3.0	3.0
	Actual		0.9	2.0		1.1	1.0		1.0	2.0	1.0			1.0				2.8	2.3
28 of 169	Expected		1.0	3.0		1.0	1.0		1.0	2.0	1.0		1.0	2.0	1.0	1.0		1.0	2.0
	Actual		0.9	3.0		1.1	1.0		1.0	2.0	0.9		1.1	2.0	1.0	0.9		1.0	1.5
29 of 169	Expected			2.0			1.0		1.0	4.0	2.0		2.0	3.0	1.0	1.0			
	Actual			2.0			1.0		1.0	4.0	2.0		2.0	3.1	0.8	0.9			
30 of 169	Expected		1.0	2.0			1.0		3.0	3.0	2.0		2.0	2.0		2.0			
	Actual		1.0	2.0			1.0		3.1	2.9	2.0		1.9	2.0		1.7			
31 of 169	Expected	2.0	1.0	2.0			1.0		3.0	2.0			2.0	1.0		2.0			
	Actual	2.2	1.0	2.0			0.9		2.8	1.9			2.2	0.9		1.8			
32 of 169	Expected	3.0	1.0	2.0		1.0			2.0	1.0			2.0	1.0	1.0	2.0	1.0		
	Actual	3.1	1.1	2.0		1.0			1.9	1.0			2.1	1.1	1.0	2.0	0.0		
33 of 169	Expected	5.0		1.0		1.0	1.0		1.0				2.0	1.0	2.0	2.0	1.0	1.0	
	Actual	4.8		1.2		1.2	1.2		0.8				2.3	1.1	1.8	1.9	0.0	1.1	
34 of 169	Expected	3.0					2.0		1.0	1.0	1.0		1.0		1.0	1.0	1.0	2.0	1.0
	Actual	3.1					2.1		0.8	1.1	1.1		1.0		1.0	1.0	0.0	2.2	1.0
35 of 169	Expected	3.0					1.0			2.0	2.0	1.0	2.0	1.0		2.0		3.0	1.0
	Actual	3.0					1.2			2.0	2.0	1.0	2.0	1.1		2.0		3.0	1.0
36 of 169	Expected			2.0		1.0	1.0		1.0	2.0	2.0	1.0	1.0	1.0		3.0		1.0	
	Actual			2.1		1.1	1.0		1.0	2.0	1.8	1.0	1.0	1.0		2.5		1.0	

Figure 1: Amino Acid Analysis (continued)<sup>3</sup>

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 169	Expected	1.0		4.0	1.0	2.0	1.0		1.0	1.0	1.0	1.0			1.0	2.0		1.0	1.0
	Actual	1.1		4.1	0.0	2.1	1.1		0.9	1.0	0.9	1.0			0.9	1.7		1.0	1.0
38 of 169	Expected	2.0		3.0	1.0	2.0			1.0	2.0	1.0			1.0	1.0	2.0			1.0
	Actual	2.0		3.0	0.0	2.3			0.7	2.0	1.1			1.0	0.9	1.5			1.0
39 of 169	Expected	1.0		1.0	2.0	3.0			1.0	2.0	2.0		1.0	1.0	3.0				1.0
	Actual	1.0		1.1	0.0	3.3			1.0	1.8	1.8		1.0	0.9	2.3				0.9
40 of 169	Expected			1.0	1.0	1.0	1.0		2.0	1.0	3.0		1.0		2.0			1.0	1.0
	Actual			1.0	0.0	1.0	1.0		2.0	1.1	2.9		1.1		1.7			0.9	0.9
41 of 169	Expected		1.0	2.0		2.0	1.0		2.0		2.0		2.0		2.0	1.0		1.0	2.0
	Actual		1.0	2.1		2.2	1.1		1.7		1.9		2.1		1.8	1.0		0.8	1.6
42 of 169	Expected		2.0	2.0		1.0	1.0		1.0				2.0	1.0	2.0	1.0		1.0	4.0
	Actual		2.0	2.1		1.1	1.0		0.9				2.0	1.0	1.8	0.9		0.8	3.0
43 of 169	Expected		1.0	3.0			1.0		1.0	1.0			1.0	2.0	1.0	1.0			4.0
	Actual		0.9	3.0			1.0		0.9	1.0			1.0	2.0	0.9	0.8			2.4
44 of 169	Expected		1.0	2.0	1.0	1.0	1.0		1.0	1.0			3.0	2.0		1.0			3.0
	Actual		0.9	1.8	0.0	1.2	1.2		1.0	1.1			3.3	2.2		0.8			1.9
45 of 169	Expected	1.0		2.0	1.0	1.0	1.0			1.0	1.0		3.0	2.0	1.0	2.0			2.0
	Actual	1.0		1.9	0.0	1.1	1.0			1.0	1.0		3.1	2.1	0.8	1.7			2.0
46 of 169	Expected	2.0	1.0	1.0		1.0			1.0		3.0		2.0	1.0	1.0	1.0	1.0	1.0	2.0
	Actual	2.0	1.1	1.0		1.1			1.0		2.8		2.0	1.2	1.0	0.9	0.0	1.1	1.7
47 of 169	Expected	2.0	1.0	2.0	1.0	1.0			1.0		2.0				2.0		1.0	2.0	2.0
	Actual	1.9	1.0	2.0	0.0	1.1			1.0		1.9				1.6		0.0	2.0	2.0
48 of 169	Expected	1.0		3.0	1.0				1.0	1.0	2.0		1.0		3.0	1.0		2.0	2.0
	Actual	1.0		3.1	0.0				1.0	1.0	1.8		1.2		2.7	1.0		2.3	1.9
49 of 169	Expected			2.0						1.0	1.0		3.0		3.0	2.0		2.0	1.0
	Actual			2.1						1.2	0.8		3.8		3.0	2.0		2.6	1.2
50 of 169	Expected	1.0			1.0		1.0			1.0	2.0		3.0		3.0	3.0		1.0	1.0
	Actual	1.1			0.0		1.0			1.0	1.9		2.8		2.4	2.6		1.0	1.0
51 of 169	Expected	1.0		3.0	2.0		1.0			2.0	2.0		1.0		2.0	1.0		1.0	2.0
	Actual	1.0		3.0	0.0		1.2			2.1	1.9		1.1		1.8	0.9		1.1	2.1
52 of 169	Expected	1.0		4.0	1.0					2.0	2.0		2.0		2.0			1.0	3.0
	Actual	1.1		4.0	0.0					1.9	1.9		2.0		1.8			0.9	2.3
53 of 169	Expected	2.0	1.0	4.0		1.0	1.0		1.0		1.0		1.0		1.0			1.0	4.0
	Actual	2.0	0.8	4.0		1.1	1.0		1.0		0.9		0.9		0.9			0.8	2.9
54 of 169	Expected	2.0	1.0	2.0		2.0	3.0		2.0		1.0			1.0		1.0			3.0
	Actual	2.2	0.8	2.0		2.3	3.1		1.7		0.8			1.1		1.0			2.3
55 of 169	Expected	2.0		2.0		1.0	2.0		2.0	1.0	1.0			1.0		1.0		2.0	1.0
	Actual	2.1		2.0		0.9	2.1		1.8	1.1	1.0			1.1		1.0		2.3	0.9
56 of 169	Expected	1.0		4.0	1.0		2.0		1.0	1.0	1.0	1.0	1.0	1.0				2.0	2.0
	Actual	1.0		3.9	0.0		1.9		1.1	1.0	1.0	0.9	1.0	1.0				2.0	1.8
57 of 169	Expected	1.0	1.0	4.0	1.0		1.0		1.0	2.0	1.0	1.0	1.0	1.0		1.0	1.0		1.0
	Actual	1.1	1.0	4.0	0.0		1.0		1.0	2.0	0.9	0.9	0.9	1.0		0.9	0.0		1.0
58 of 169	Expected	2.0	1.0	4.0	1.0		1.0		1.0	1.0					1.0	3.0	1.0	1.0	1.0
	Actual	2.0	1.1	4.0	0.0		1.1		1.0	1.0					0.9	2.7	0.0	1.1	0.8
59 of 169	Expected	1.0	2.0	4.0			1.0		1.0	1.0	1.0				1.0	2.0		4.0	
	Actual	1.1	2.0	4.0			1.0		1.0	1.0	0.9				1.1	1.8		4.0	
60 of 169	Expected		3.0	2.0			1.0	1.0		2.0	2.0		1.0	1.0				4.0	
	Actual		3.0	2.1			1.1	1.1		2.0	1.9		1.1	1.1				4.0	

Figure 1: Amino Acid Analysis (continued)<sup>3</sup>

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)
61 of 169	Expected		3.0	2.0		1.0	1.0	1.0	1.0	2.0	1.0		1.0	1.0	1.0			1.0	1.0
	Actual		3.0	2.0		1.2	1.1	1.0	1.1	1.9	0.8		1.2	1.1	1.0			1.0	1.2
62 of 169	Expected		2.0	3.0		1.0	1.0		1.0		1.0		2.0	3.0	2.0				1.0
	Actual		2.0	3.0		1.1	1.0		1.0		1.0		2.2	3.1	1.8				1.0
63 of 169	Expected	1.0		2.0	1.0		1.0			1.0	1.0		1.0	5.0	2.0	1.0			1.0
	Actual	1.0		1.9	0.0		1.0			1.1	1.0		1.0	5.3	1.7	0.9			1.0
64 of 169	Expected	1.0		2.0	2.0		1.0			2.0	1.0			4.0		1.0	1.0	1.0	
	Actual	1.0		2.0	0.0		1.0			2.0	1.0			4.0		0.9	0.0	1.0	
65 of 169	Expected	1.0		3.0	1.0		1.0			2.0			1.0	3.0			1.0	3.0	
	Actual	1.0		3.0	0.0		1.0			2.0			1.0	3.1			0.0	3.0	
66 of 169	Expected			2.0			3.0		1.0	1.0			1.0	1.0		3.0	1.0	4.0	
	Actual			2.0			3.3		1.0	1.0			1.0	1.1		2.9	0.0	4.6	
67 of 169	Expected		1.0			1.0	3.0		1.0	1.0			1.0	1.0		3.0		3.0	3.0
	Actual		1.0			1.1	2.7		0.9	1.0			0.9	1.0		2.3		2.7	2.5
68 of 169	Expected	1.0	1.0	1.0		2.0	1.0			3.0			1.0	1.0	1.0			2.0	3.0
	Actual	1.2	0.8	0.9		2.0	1.2			2.8			1.1	1.0	0.8			1.7	2.1
69 of 169	Expected	2.0		1.0	1.0	1.0	1.0			3.0	1.0		1.0	2.0	1.0	1.0			3.0
	Actual	2.0		1.0	0.0	1.1	1.0			2.9	1.0		1.0	2.0	0.9	0.9			2.1
70 of 169	Expected	2.0		2.0	1.0		1.0		1.0	2.0	2.0			2.0	1.0	2.0			1.0
	Actual	2.1		2.1	0.0		1.0		0.9	2.0	1.9			2.1	1.0	1.8			0.9
71 of 169	Expected			4.0	1.0	1.0	1.0		1.0	2.0	2.0		2.0	1.0	1.0	1.0			1.0
	Actual			4.2	0.0	1.2	1.0		0.9	1.9	1.8		2.2	1.0	0.9	1.0			0.9
72 of 169	Expected			4.0	1.0	1.0	3.0		1.0	1.0	1.0		2.0			2.0			2.0
	Actual			4.3	0.0	1.1	3.3		0.7	1.1	0.8		2.2			2.1			2.1
73 of 169	Expected		1.0	2.0			3.0			2.0	1.0		2.0	1.0	2.0	3.0			1.0
	Actual		1.1	2.1			3.0			1.9	1.0		2.0	1.0	1.9	2.9			0.9
74 of 169	Expected		2.0			3.0	2.0			1.0	1.0		3.0	2.0	2.0	1.0			1.0
	Actual		1.9			3.2	2.0			0.9	0.9		3.1	2.0	1.7	0.9			0.9
75 of 169	Expected		2.0	2.0		3.0	1.0						4.0	1.0	1.0				1.0
	Actual		1.8	1.9		3.1	1.0						3.7	0.9	0.8				0.9
76 of 169	Expected		2.0	4.0		2.0	1.0				1.0		2.0	1.0	2.0	1.0			2.0
	Actual		1.8	4.1		1.9	1.0				1.0		1.9	1.0	1.8	1.0			1.8
77 of 169	Expected		1.0	4.0		1.0			2.0	1.0	1.0		1.0	1.0	2.0	2.0			1.0
	Actual		0.8	4.0		1.1			2.1	0.8	1.0		0.9	1.0	1.7	1.8			1.1
78 of 169	Expected			2.0	1.0	1.0	2.0		2.0	1.0	1.0		1.0	2.0	3.0	1.0			1.0
	Actual			2.0	0.0	1.1	2.2		1.9	0.9	1.0		1.1	2.3	2.7	0.9			1.1
79 of 169	Expected	1.0		2.0	1.0		3.0		2.0				1.0	2.0	3.0	2.0			2.0
	Actual	1.0		2.0	0.0		3.2		2.0				1.1	2.2	2.5	1.8			1.7
80 of 169	Expected	2.0		1.0		1.0	1.0		1.0	1.0				1.0	2.0	2.0		1.0	3.0
	Actual	2.0		0.9		1.1	1.0		0.9	1.1				1.1	1.7	1.5		1.0	3.0
81 of 169	Expected	2.0		3.0	1.0	2.0				1.0					2.0	1.0		1.0	3.0
	Actual	1.9		3.0	0.0	2.1				1.0					1.4	0.8		1.0	2.9
82 of 169	Expected	2.0		3.0	1.0	1.0		1.0	1.0	1.0					1.0	2.0		1.0	2.0
	Actual	2.0		3.1	0.0	1.1		0.9	0.8	1.0					0.8	1.9		1.0	2.0
83 of 169	Expected	3.0	1.0	2.0	1.0	1.0		1.0	1.0	1.0				1.0	1.0	3.0	1.0		1.0
	Actual	3.0	1.0	2.0	0.0	0.9		0.8	1.0	1.1				1.1	0.9	2.8	0.0		1.0
84 of 169	Expected	2.0	1.0	3.0		1.0	1.0	1.0	1.0	1.0				1.0	1.0	2.0	1.0	1.0	1.0
	Actual	1.9	0.9	3.1		1.1	1.0	1.0	0.8	1.0				1.0	0.9	1.9	0.0	0.9	1.0



Figure 1: Amino Acid Analysis (continued)<sup>3</sup>

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)
85 of 169	Expected	1.0	1.0	2.0	1.0	2.0	2.0		1.0	1.0			1.0		1.0	2.0	1.0	1.0	1.0
	Actual	1.0	0.8	1.9	0.0	2.0	1.9		1.0	1.0			0.9		1.0	1.9	0.0	0.9	0.9
86 of 169	Expected	2.0		1.0	1.0	3.0	2.0	1.0	1.0	1.0			1.0			1.0			2.0
	Actual	1.9		1.0	0.0	3.2	1.9	0.9	1.0	1.0			0.9			0.8			1.8
87.1 of 169	Expected	2.0		1.0	1.0	1.0	2.0	1.0	1.0	1.0									1.0
	Actual	1.9		1.1	0.0	1.1	2.1	1.1	1.0	1.1									0.9
87.2 of 169	Expected			2.0	1.0	1.0		1.0	1.0						1.0	1.0		1.0	1.0
	Actual			1.9	0.0	1.1		1.0	1.0						0.7	0.8		1.0	0.9
88 of 169	Expected	2.0		2.0	2.0	1.0	2.0	1.0	3.0					1.0	1.0	1.0		1.0	1.0
	Actual	2.0		2.0	0.0	1.1	2.0	0.8	3.0					1.0	0.8	0.9		1.0	1.1
89 of 169	Expected	2.0		1.0	1.0		2.0	1.0	3.0	2.0				1.0	2.0	1.0		1.0	1.0
	Actual	2.0		1.0	0.0		1.9	1.1	2.9	2.1				1.0	1.9	0.9		1.0	1.0
90 of 169	Expected	1.0	1.0		1.0	1.0		1.0	1.0	2.0	1.0				5.0	2.0		1.0	1.0
	Actual	0.9	1.0		0.0	1.1		0.9	1.0	2.0	1.0				4.1	1.6		1.0	0.9
91 of 169	Expected	2.0	4.0				1.0		1.0	1.0		1.0	3.0	1.0		1.0		1.0	1.0
	Actual	1.6	3.4				1.0		0.8	0.8		1.3	3.5	1.0		0.9		0.9	1.2
92 of 169	Expected	2.0		1.0			1.0		2.0	1.0	1.0	1.0			4.0	1.0		1.0	1.0
	Actual	2.1		1.1			1.0		1.8	1.1	0.9	1.0			3.6	1.0		1.1	0.7
93 of 169	Expected	3.0		3.0			1.0		3.0	1.0					4.0	1.0		1.0	
	Actual	3.0		3.1			1.0		3.0	1.0					3.5	0.9		1.0	
94 of 169	Expected	2.0		3.0					3.0				1.0	1.0	3.0	2.0		1.0	
	Actual	1.9		2.9					3.2				1.0	0.9	2.4	1.6		0.8	
95 of 169	Expected	1.0		1.0		1.0			3.0			1.0	1.0	2.0	2.0	3.0			2.0
	Actual	1.0		1.1		1.1			2.9			0.9	0.9	1.7	1.4	2.1			1.7
96 of 169	Expected	1.0				1.0			2.0		1.0	2.0		1.0	3.0	3.0			3.0
	Actual	1.0				1.0			2.1		0.9	2.1		1.2	2.7	2.3			3.1
97 of 169	Expected	1.0		2.0	1.0				1.0		1.0	3.0		1.0	2.0	1.0		1.0	2.0
	Actual	1.0		2.1	0.0				0.9		1.0	2.6		0.9	1.6	1.1		0.9	1.8
98 of 169	Expected	1.0		3.0	3.0	1.0	1.0		1.0		1.0	1.0			2.0	2.0		1.0	1.0
	Actual	1.2		2.7	0.0	1.0	1.2		1.2		0.9	1.0			1.0	1.3		1.1	0.9
99 of 169	Expected	1.0		2.0	2.0	2.0	1.0		1.0	3.0					1.0	1.0		2.0	
	Actual	1.0		2.0	0.0	2.1	1.0		1.0	2.9					0.8	0.9		2.0	
100 of 169	Expected	1.0		1.0	2.0	3.0	1.0			4.0			1.0		1.0	2.0		1.0	
	Actual	0.9		1.1	0.0	3.3	0.9			3.6			0.8		0.9	1.7		0.8	
101 of 169	Expected	2.0	1.0	1.0	1.0	2.0	2.0		1.0	3.0			1.0		2.0	1.0		1.0	
	Actual	2.0	1.0	1.0	0.0	2.1	1.9		1.0	2.9			1.0		1.8	0.9		1.0	
102 of 169	Expected	3.0	3.0	3.0		3.0	1.0		1.0	2.0					1.0	1.0			
	Actual	2.9	2.9	3.0		3.2	1.0		1.0	1.9					0.9	0.9			
103 of 169	Expected	3.0	2.0	2.0		4.0			1.0		1.0		1.0			1.0			2.0
	Actual	2.9	1.9	2.0		4.3			0.9		0.9		0.8			0.9			1.7
104 of 169	Expected	1.0	1.0	1.0		3.0				1.0	2.0	1.0	1.0	1.0		3.0		1.0	2.0
	Actual	1.0	1.0	1.0		3.2				1.0	1.9	1.0	0.9	1.0		2.7		1.0	1.8
105 of 169	Expected			1.0		1.0	2.0			1.0	3.0	1.0	3.0	1.0		2.0		2.0	1.0
	Actual			1.1		1.1	2.0			1.0	2.8	1.0	3.1	1.0		1.9		2.1	0.9
106 of 169	Expected			2.0		1.0	2.0		1.0	3.0	1.0		3.0	2.0	1.0	1.0		1.0	
	Actual			2.1		1.1	2.0		0.9	2.9	0.9		3.0	2.1	0.9	0.7		0.9	
107 of 169	Expected		1.0	2.0		1.0			2.0	2.0	2.0		2.0	3.0	2.0	1.0			
	Actual		1.1	2.0		1.0			2.0	2.1	2.0		2.1	3.1	1.6	0.9			

Figure 1: Amino Acid Analysis (continued)<sup>3</sup>

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)
108 of 169	Expected		1.0	2.0		1.0			1.0	3.0	3.0		2.0	2.0	1.0	1.0			1.0
	Actual		1.0	2.1		1.1			0.9	3.0	2.8		2.0	2.0	0.9	0.9			1.0
109 of 169	Expected	2.0		3.0		1.0	1.0		1.0	3.0	1.0	1.0	3.0			1.0			1.0
	Actual	2.0		3.1		1.1	1.0		1.0	3.0	0.9	0.9	2.8			0.9			0.9
110 of 169	Expected	2.0		1.0	1.0	2.0	2.0			2.0	2.0	1.0	1.0			1.0		1.0	1.0
	Actual	1.9		1.1	0.0	2.3	2.1			2.1	1.7	1.0	1.1			0.7		1.1	0.8
111 of 169	Expected	1.0	1.0	3.0	1.0	2.0	3.0		1.0	2.0	1.0	1.0	1.0					1.0	
	Actual	1.0	1.0	3.0	0.0	2.1	3.0		1.0	2.0	0.9	0.9	1.0					1.0	
112 of 169	Expected	2.0	1.0	3.0	2.0	1.0	1.0		2.0	2.0	1.0		1.0						
	Actual	2.0	1.0	3.0	0.0	1.0	1.0		2.0	2.0	1.0		1.0						
113 of 169	Expected	2.0	1.0	2.0	1.0	1.0	1.0		1.0	3.0	1.0		1.0			1.0			1.0
	Actual	2.1	1.1	2.3	0.0	1.0	1.1		0.9	2.9	0.9		1.0			0.8			1.0
114 of 169	Expected	1.0		3.0		1.0	1.0			4.0	1.0	1.0	1.0	2.0		2.0			1.0
	Actual	1.0		2.9		1.1	1.0			4.1	0.9	1.0	1.1	2.1		1.6			0.8
115 of 169	Expected	4.0		2.0					1.0	4.0		1.0		2.0		2.0		1.0	1.0
	Actual	3.9		2.0					1.0	4.1		1.0		2.2		1.9		1.1	0.9
116 of 169	Expected	6.0		1.0			1.0		1.0	1.0		1.0			1.0	3.0		1.0	1.0
	Actual	5.8		1.2			1.0		1.0	1.1		1.0			0.9	2.8		1.0	1.1
117 of 169	Expected	6.0					4.0			1.0			1.0		1.0	3.0	1.0		1.0
	Actual	5.8					3.7			1.2			1.0		0.8	2.5	0.0		0.9
118 of 169	Expected	5.0				1.0	3.0		1.0	1.0		1.0	2.0	1.0		2.0	1.0		
	Actual	4.7				1.2	2.8		1.0	1.1		1.1	2.1	1.0		1.8	0.0		
119 of 169	Expected	4.0	1.0			2.0	1.0		1.0	1.0		2.0	2.0	1.0				1.0	
	Actual	3.8	1.0			2.1	1.0		1.0	1.0		2.0	2.1	1.1				1.1	
120 of 169	Expected	2.0	1.0	1.0		1.0	2.0		1.0			2.0	2.0	1.0				1.0	1.0
	Actual	1.9	0.9	1.0		1.1	2.0		1.0			1.9	2.1	1.0				1.0	1.0
121 of 169	Expected	1.0	1.0	2.0		1.0	2.0		1.0	1.0		1.0	1.0			1.0		2.0	2.0
	Actual	1.0	1.0	2.1		1.1	1.9		0.9	0.8		1.0	1.1			0.9		2.1	1.9
122 of 169	Expected	1.0		2.0		4.0	2.0		2.0	1.0	1.0					1.0		1.0	2.0
	Actual	1.1		2.0		4.3	1.9		1.9	0.8	1.0					0.9		1.0	1.8
123 of 169	Expected	2.0		3.0		4.0			2.0	1.0	2.0		1.0					1.0	1.0
	Actual	2.0		3.1		4.3			2.0	0.7	1.9		1.0					1.0	0.8
124 of 169	Expected	2.0		2.0		5.0			3.0	1.0	1.0		1.0		2.0				
	Actual	1.9		2.0		5.4			2.8	1.0	1.0		1.0		1.8				
125 of 169	Expected	2.0				3.0			2.0	2.0	1.0				3.0	4.0			
	Actual	2.1				3.0			1.9	2.1	0.9				2.3	3.5			
126 of 169	Expected	1.0		1.0		2.0	1.0			3.0	1.0				2.0	4.0			2.0
	Actual	1.0		1.0		2.2	1.0			2.9	0.9				1.5	3.2			1.4
127 of 169	Expected	3.0		3.0		3.0	1.0			3.0	1.0					1.0			2.0
	Actual	2.9		3.0		3.3	1.0			3.0	0.9					0.9			1.9
128 of 169	Expected	2.0		4.0		3.0				3.0	1.0					1.0			3.0
	Actual	1.9		4.0		3.3				2.9	0.9					1.0			1.9
129 of 169	Expected	2.0		2.0		2.0	1.0		1.0	3.0	1.0		1.0		2.0	1.0			1.0
	Actual	2.0		2.1		2.0	1.0		1.0	3.0	0.9		1.0		1.9	0.9			0.9
130 of 169	Expected	1.0		3.0		1.0	1.0		2.0	3.0	1.0		1.0		4.0				1.0
	Actual	1.0		3.3		1.1	1.0		2.0	2.4	1.1		1.0		3.9				0.9
131 of 169	Expected	2.0	1.0	3.0		1.0			2.0	3.0	1.0				3.0				2.0
	Actual	2.0	1.1	3.1		1.2			1.9	2.9	0.9				2.6				1.8

Figure 1: Amino Acid Analysis (continued)<sup>3</sup>

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)
132 of 169	Expected	1.0	2.0	2.0		3.0			3.0	3.0	1.0				1.0				2.0
	Actual	1.1	1.9	2.1		3.3			2.8	2.8	0.9				0.9				1.8
133 of 169	Expected	1.0	2.0	1.0		4.0	1.0		2.0	3.0					1.0	1.0			1.0
	Actual	1.0	1.9	1.1		4.2	1.0		1.9	2.9					0.9	0.9			0.9
134 of 169	Expected		2.0			4.0	1.0		1.0	4.0					1.0	3.0		1.0	1.0
	Actual		1.8			4.3	1.0		0.9	3.8					0.8	2.5		1.0	1.0
135 of 169	Expected	3.0	2.0			4.0			2.0	2.0					1.0	2.0		1.0	1.0
	Actual	3.0	1.7			4.3			1.9	1.9					0.9	1.7		0.9	0.9
136 of 169	Expected	6.0	2.0	1.0		2.0			2.0	2.0	1.0				1.0	1.0			
	Actual	5.9	1.8	1.1		2.3			1.7	2.0	1.0				1.0	1.0			
137 of 169	Expected	4.0	1.0	1.0	1.0	1.0				1.0	1.0	1.0			2.0	1.0			1.0
	Actual	3.9	1.0	1.0	0.0	1.1				1.0	1.0	1.0			1.7	0.9			1.1
138 of 169	Expected	2.0	1.0	1.0	1.0	2.0	1.0			1.0	2.0	1.0	1.0		2.0	1.0			2.0
	Actual	1.8	1.0	1.1	0.0	2.2	1.2			1.0	1.9	1.0	1.1		1.8	0.8			1.9
139 of 169	Expected		1.0	1.0	1.0	1.0	3.0	1.0		2.0	2.0	1.0	1.0		1.0			1.0	2.0
	Actual		1.0	1.0	0.0	1.1	3.0	0.7		1.9	2.0	1.0	1.0		0.9			1.0	1.9
140 of 169	Expected	2.0		1.0	1.0	1.0	2.0	2.0		1.0	1.0	1.0	2.0	2.0	1.0			1.0	
	Actual	2.0		1.1	0.0	1.0	2.0	2.1		1.0	1.0	1.0	2.0	2.1	0.9			1.0	
141 of 169	Expected	2.0				1.0	1.0	2.0		2.0		1.0	2.0	2.0	1.0				3.0
	Actual	1.9				1.1	1.0	2.0		2.0		1.0	2.0	2.0	0.9				2.6
142 of 169	Expected	1.0	1.0			2.0	1.0	2.0		1.0			1.0	2.0	1.0	1.0		1.0	4.0
	Actual	1.0	1.0			2.0	1.0	1.6		0.9			0.9	2.0	0.9	0.8		1.0	3.1
143 of 169	Expected	2.0	1.0	1.0		2.0		1.0	1.0				1.0	2.0	1.0	3.0		1.0	2.0
	Actual	1.9	1.0	1.0		2.1		0.8	1.0				1.0	1.9	0.9	2.6		0.9	1.6
144 of 169	Expected	3.0	1.0	1.0	1.0	2.0	1.0	1.0	1.0		1.0		2.0	1.0		2.0		1.0	
	Actual	3.0	1.0	1.0	0.0	2.1	1.0	1.1	0.9		1.0		2.2	1.1		1.7		1.1	
145 of 169	Expected	2.0	1.0		1.0	2.0	2.0	1.0	1.0		1.0		3.0	1.0				1.0	2.0
	Actual	2.0	1.0		0.0	2.2	2.1	1.1	0.9		1.0		2.5	1.1				1.0	1.6
146 of 169	Expected		1.0	1.0		1.0	2.0		1.0				4.0	1.0	1.0	1.0	1.0	1.0	2.0
	Actual		0.9	1.0		1.0	2.0		1.1				4.1	1.0	0.9	1.0	0.0	1.0	2.0
147 of 169	Expected		1.0	2.0		1.0	1.0		1.0				5.0		1.0	2.0	1.0		1.0
	Actual		1.0	2.1		1.1	1.0		0.8				4.5		1.0	1.8	0.0		0.8
148 of 169	Expected		1.0	1.0		2.0			3.0				3.0	1.0	2.0	1.0	1.0		
	Actual		1.1	1.2		2.2			2.6				3.2	1.2	1.9	1.0	0.0		
149 of 169	Expected		1.0	3.0		2.0			2.0				3.0	1.0	1.0	3.0			1.0
	Actual		1.1	3.2		2.1			1.7				3.2	1.1	1.1	2.8			1.2
150.1 of 169	Expected			2.0		1.0			2.0				1.0			3.0			1.0
	Actual			2.1		1.2			1.8				1.4			2.7			1.2
150.2 of 169	Expected			2.0	1.0		1.0						1.0		1.0				2.0
	Actual			2.0	0.0		1.1						0.9		0.8				1.6
151 of 169	Expected			2.0			1.0		3.0							1.0		1.0	2.0
	Actual			2.2			1.1		2.8							0.9		1.2	1.9
152 of 169	Expected			3.0		2.0	1.0		3.0	2.0				2.0		1.0		1.0	2.0
	Actual			3.2		2.1	1.1		2.5	2.2				2.3		0.9		1.1	1.7
153 of 169	Expected			2.0		4.0				3.0	1.0		1.0	2.0	1.0	1.0		1.0	1.0
	Actual			1.9		4.0				3.0	1.0		1.0	2.0	1.0	0.8		0.9	0.9
154 of 169	Expected			3.0		3.0		1.0		2.0	3.0		2.0	1.0	1.0			1.0	
	Actual			3.1		3.0		1.1		2.1	2.8		2.1	1.0	0.8			1.1	

Figure 1: Amino Acid Analysis (continued)<sup>3</sup>

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)	
155 of 169	Expected			4.0		2.0		1.0		2.0	2.0		1.0	1.0	1.0	1.0		1.0	1.0	
	Actual			4.0		2.1		1.0		2.0	1.9		1.0	1.0	0.9	0.9		1.0	1.0	
156 of 169	Expected	1.0		5.0			2.0	1.0	2.0	1.0	1.0			1.0	2.0	1.0			1.0	
	Actual	1.1		4.9			2.1	1.1	2.0	1.0	1.0			1.1	1.7	0.9			1.0	
157 of 169	Expected	1.0		4.0		1.0	2.0		3.0	1.0	1.0				2.0				2.0	
	Actual	1.0		3.9		0.9	2.1		3.0	1.1	1.0				1.7				1.3	
158 of 169	Expected	1.0	1.0	4.0		3.0			3.0	1.0	1.0				1.0				3.0	
	Actual	1.1	1.0	3.9		3.0			3.0	1.1	0.9				0.8				2.5	
159 of 169	Expected	1.0	1.0	4.0		4.0			1.0	3.0	2.0				1.0				1.0	
	Actual	1.0	1.0	3.9		4.4			1.0	2.9	1.8				0.8				1.0	
160 of 169	Expected	1.0		3.0		4.0	1.0		1.0	4.0	2.0				1.0				1.0	
	Actual	1.1		2.9		4.0	1.0		1.0	4.1	1.9				0.9				0.9	
161 of 169	Expected			1.0		4.0	1.0		2.0	3.0	2.0				1.0		1.0	2.0		
	Actual			0.9		4.3	1.1		1.8	3.1	1.9				1.0		0.0	2.0		
162 of 169	Expected					2.0	2.0		1.0	2.0	2.0		1.0	1.0				3.0	3.0	1.0
	Actual					2.1	2.2		1.0	2.1	1.8		1.1	1.1				0.0	3.1	0.9
163.1 of 169	Expected						1.0		1.0	1.0	1.0		1.0	1.0				3.0	1.0	1.0
	Actual						1.0		1.0	1.0	1.0		1.0	1.0				0.0	1.0	1.0
163.2 of 169	Expected	2.0					1.0		3.0	1.0			1.0							1.0
	Actual	2.1					1.0		2.9	1.0			1.0							0.9
164.1 of 169	Expected	2.0					2.0		2.0	1.0			1.0							
	Actual	2.0					2.0		2.0	1.0			1.0							
164.2 of 169	Expected								2.0	2.0		1.0					1.0			2.0
	Actual								1.6	2.4		1.1					1.0			1.5
165.1 of 169	Expected	1.0							3.0	2.0		1.0						1.0		2.0
	Actual	1.0							2.7	2.3		1.1						0.8		1.6
165.2 of 169	Expected				5.0					1.0		1.0			2.0	1.0				
	Actual				0.0					1.0		1.0			1.4	0.9				
166.1 of 169	Expected				4.0							1.0			2.0	1.0				
	Actual				0.0							1.2			1.8	1.0				
166.2 of 169	Expected	1.0			3.0		2.0			1.0	1.0				2.0					
	Actual	1.1			0.0		2.0			1.0	1.0				1.4					
167 of 169	Expected			3.0	2.0	1.0	1.0						1.0		1.0					
	Actual			2.9	0.0	1.1	0.9						1.0		0.7					
168 of 169	Expected			3.0	2.0	2.0	2.0			1.0	2.0		1.0	1.0	2.0					2.0
	Actual			3.0	0.0	2.2	2.0			0.9	2.0		1.0	1.1	1.4					1.9
169 of 169	Expected			2.0		1.0	1.0	1.0		2.0	2.0			1.0	1.0	1.0			1.0	2.0
	Actual			2.0		1.2	1.1	1.1		2.0	1.8			1.1	1.0	1.0			1.1	1.8

<sup>3</sup>Cysteine (C) and tryptophan (W) were completely destroyed and serine (S) and threonine (T) were partially destroyed during hydrolysis.

Table 2: Peptide Solubility<sup>4,5,6</sup>

Peptide	Sequence	Water Solubility, mg/mL	DPBS Solubility, mg/mL	DMSO Solubility, mg/mL
1 of 169	1-MFIFLLFLTTLTSGSDL-16	N/A	N/A	5
2 of 169	9-TLTSGSDLDRCTTFDDV-25	N/A	5	10
3 of 169	16-LDRCTTFDDVQAPNYTQH-33	5	5	5
4 of 169	24-DVQAPNYTQHTSSMRGVY-41	5	5	5
5 of 169	32-QHTSSMRGVYYPDEIFR-48	5	5	10

Table 2: Peptide Solubility (continued)<sup>4,5,6</sup>

Peptide	Sequence	Water Solubility, mg/mL	DPBS Solubility, mg/mL	DMSO Solubility, mg/mL
6 of 169	39-GVYYYPDEIFRSDTLYL-54	N/A	N/A	10
7 of 169	45-EIFRSDTLYLTQDLFLPF-62	N/A	N/A	10
8 of 169	53-YLTQDLFLPFYSNVTGFH-70	N/A	N/A	5
9 of 169	61-PFYSNVTGFHTINHTE-76	5	N/A	10
10 of 169	67-TGFHTINHTEGPNVIPFK-84	5	5	10
11 of 169	75-TFGNPVIPFKDGIYFAA-91	5	5	10
12 of 169	82-PFKDGIYFAATEKSNVVR-99	5	5	10
13 of 169	90-AATEKSNVVRGWVFGSTM-107	5	2	10
14 of 169	98-VRGWVFGSTMNNKSQSVI-115	5	5	10
15 of 169	106-TMNNKSQSVIINNST-121	N/A	N/A	10
16.1 of 169	114-VIIINNSTNV-123	N/A	N/A	10
16.2 of 169	121-TNVVIRACNF-130	5	N/A	10
17 of 169	121-TNVVIRACNFECDNPFF-138	N/A	N/A	2
18 of 169	129-NFELCDNPFFAVSKPM-144	5	N/A	10
19 of 169	135-NPFFAVSKPMGTQHTMI-152	5	5	10
20 of 169	143-PMGTQHTMIFDNAF-157	5	N/A	10
21 of 169	148-THTMIFDNAFNCTFEYI-164	N/A	N/A	10
22 of 169	155-NAFNCTFEYISDAFSLDV-172	N/A	N/A	N/A
23 of 169	163-YISDAFSLDVSEKSGNFK-180	2	N/A	5
24 of 169	171-DVSEKSGNFKHLREFVFK-188	N/A	N/A	10
25 of 169	179-FKHLREFVFKNKDGFLYV-196	5	N/A	10
26 of 169	187-FKNKDGFLYVYKGYQPI-203	10	5	10
27 of 169	194-LYVYKGYQPIDVVRDL-209	2	N/A	5
28 of 169	200-YQPIDVVRDLPSGFNTLK-217	5	5	10
29 of 169	208-DLPSGFNTLKPIFKLPL-224	5	5	5
30 of 169	215-TLKPIFKLPLGINITNFR-232	5	N/A	10
31 of 169	223-PLGINITNFRAILTAF-238	N/A	N/A	5
32 of 169	229-TNFRAILTAFSPAQDIW-245	N/A	N/A	5
33 of 169	236-TAFSPAQDIWGTSAAYF-253	2	N/A	5
34 of 169	244-IWGTSAAYFVGYLK-258	N/A	N/A	10
35 of 169	249-AAAYFVGYLKPTTFMLKY-266	N/A	N/A	5
36 of 169	257-LKPTTFMLKYDENGTI-272	5	5	10
37 of 169	263-MLKYDENGITITDAVDCSQ-280	N/A	N/A	10
38 of 169	271-TITDAVDCSQNPLAELK-287	5	5	10
39 of 169	278-CSQNPLAELKCSVKSFEI-295	N/A	N/A	5
40 of 169	286-LKCSVKSFEIDKGIY-300	N/A	N/A	5
41 of 169	291-KSFEIDKGIYQTSNFRVV-308	2	N/A	5
42 of 169	299-IYQTSNFRVVPSGDVVRV-316	10	10	10
43 of 169	307-VVPSGDVVRFPNITNL-322	5	5	10
44 of 169	313-VVRFNITNLCPFGEVF-329	N/A	N/A	10
45 of 169	320-TNLCPFGEVFNATKFPSV-337	5	5	10
46 of 169	328-VFNATKFPSVYAWERKKI-345	5	5	5
47 of 169	336-SVYAWERKKISNCVADY-352	N/A	N/A	5
48 of 169	343-KKISNCVADYSVLYNSTF-360	N/A	N/A	10
49 of 169	351-DYSVLYNSTFFSTFK-365	N/A	N/A	15
50 of 169	358-STFFSTFKCYGVSATKL-374	N/A	N/A	5

Table 2: Peptide Solubility (continued)<sup>4,5,6</sup>

Peptide	Sequence	Water Solubility, mg/mL	DPBS Solubility, mg/mL	DMSO Solubility, mg/mL
51 of 169	365-KCYGVSATKLNLCFSNV-382	5	5	10
52 of 169	373-KLNLCFSNVYADSFVVK-390	N/A	N/A	10
53 of 169	381-NVYADSFVVKGDDVRQIA-398	N/A	N/A	10
54 of 169	389-VKGDDVRQIAPGQTVIA-406	10	5	10
55 of 169	397-IAPGQTVIADYNYKL-412	5	5	10
56 of 169	403-GVIADYNYKLPDDFMGCV-420	N/A	N/A	10
57 of 169	411-KLPDDFMGCVLAWNTRNI-428	N/A	N/A	10
58 of 169	419-CVLAWNTRNIDATSTGNY-436	2	N/A	5
59 of 169	427-NIDATSTGNYNYKYRYLR-444	5	N/A	10
60 of 169	435-NYNYKYRYLRHGKLRPF-451	5	5	10
61 of 169	442-YLRHGKLRPFERDISNV-458	5	5	5
62 of 169	449-RPFERDISNVPFSPDGK-465	5	5	10
63 of 169	456-SNVPFSPDGKPCPPAL-472	5	5	10
64 of 169	463-DGKPCPPALNCYWPL-478	2	5	5
65 of 169	469-PPALNCYWPLNDYGFY-484	N/A	N/A	5
66 of 169	475-YWPLNDYGFYTTTGIGY-491	N/A	N/A	10
67 of 169	482-GFYTTTGIGYQPYRVVVL-499	5	N/A	10
68 of 169	490-GYQPYRVVLSFELLNA-506	N/A	N/A	5
69 of 169	497-VVLSFELLNAPATVCGPK-514	N/A	N/A	10
70 of 169	505-NAPATVCGPKLSTDLIK-521	5	5	10
71 of 169	512-GPKLSTDLIKNCVNFNF-529	N/A	N/A	10
72 of 169	520-IKNQCVNFNFNGLTGTGV-537	N/A	N/A	10
73 of 169	528-NFNGLTGTGVLTPSSKRF-545	5	5	10
74 of 169	536-GVLTPSSKRFQPFQFGR-553	5	5	10
75 of 169	544-RFQPFQFGRDVSDF-558	5	5	10
76 of 169	549-QQFGRDVSDFTDSVRDPK-566	5	5	10
77 of 169	557-DFTDSVRDPKTSEILDI-573	N/A	N/A	10
78 of 169	564-DPKTSEILDISPCFSGGV-581	5	5	10
79 of 169	572-DISPCFSGGVSVITPGTNA-590	N/A	N/A	2
80 of 169	583-VITPGTNASSEVAVLY-598	N/A	N/A	10
81 of 169	590-ASSEVAVLYQDVNCTD-605	N/A	N/A	5
82 of 169	597-LYQDVNCTDVSTAIHA-612	N/A	N/A	10
83 of 169	603-CTDVSTAIHADQLTPAWR-620	2	5	10
84 of 169	611-HADQLTPAWRIYSTGNNV-628	5	5	5
85 of 169	619-WRIYSTGNNVFQTQAGCL-636	N/A	N/A	10
86 of 169	627-NVFQTQAGCLIGAEHV-642	N/A	N/A	10
87.1 of 169	633-AGCLIGAEHVD-643	2	N/A	10
87.2 of 169	641-HVDTSYECEDI-650	N/A	N/A	10
88 of 169	641-HVDTSYECDIPIGAGICA-658	N/A	N/A	10
89 of 169	649-DIPIGAGICASYHTVSL-666	N/A	N/A	10
90 of 169	657-CASYHTVSLLRSTSQKSI-674	N/A	N/A	10
91 of 169	665-LLRSTSQKSIVAYTMSL-681	5	N/A	10
92 of 169	672-KSIVAYTMSLGADSSI-687	2	N/A	10
93 of 169	680-SLGADSSIAYSNNTIAI-696	N/A	N/A	N/A
94 of 169	688-AYSNNTIAIPTNFSIS-703	N/A	N/A	10
95 of 169	695-AIPTNFSISITTEVMPV-711	N/A	N/A	10

Table 2: Peptide Solubility (continued)<sup>4,5,6</sup>

Peptide	Sequence	Water Solubility, mg/mL	DPBS Solubility, mg/mL	DMSO Solubility, mg/mL
96 of 169	702-ISITTEVMPVSMAKTSV-718	N/A	N/A	10
97 of 169	709-MPVSMAKTSVDCNMYI-724	N/A	N/A	5
98 of 169	715-KTSVDCNMYICGDSTECA-732	N/A	N/A	N/A
99 of 169	723-YICGDSTECANLLLQY-738	N/A	N/A	2
100 of 169	729-TECANLLLQYGSFCTQL-745	N/A	N/A	10
101 of 169	736-LQYGSFCTQLNRALSGIA-753	N/A	N/A	10
102 of 169	744-QLNRALSGIAAEQDRNTR-761	5	5	5
103 of 169	752-IAAEQDRNTREVFAQVK-768	5	5	10
104 of 169	759-NTREVFAQVKQMYKTPTL-776	N/A	5	10
105 of 169	767-VKQMYKTPTLKYFGGFNF-784	5	5	5
106 of 169	775-TLKYFGGFNFSQILPDPL-792	N/A	N/A	10
107 of 169	783-NFSQILPDPLKPTKRSFI-800	5	5	5
108 of 169	791-PLKPTKRSFIEDLLFNKV-808	5	2	10
109 of 169	799-FIEDLLFNKVTLADAGFM-816	N/A	N/A	N/A
110 of 169	807-KVTLADAGFMKQYGECL-823	5	N/A	10
111 of 169	814-GFMKQYGECLGDINARDL-831	2	N/A	5
112 of 169	822-CLGDINARDLICAQKF-837	N/A	N/A	10
113 of 169	828-ARDLICAQKFNGLTVL-843	N/A	N/A	5
114 of 169	834-AQKFNGLTVLPPLTDDM-851	5	2	5
115 of 169	842-VLPPLTDDMIAAYTAAL-859	N/A	N/A	5
116 of 169	850-DMIAAYTAALVSGTATA-866	N/A	N/A	N/A
117 of 169	857-AALVSGTATAGWTFGAGA-874	N/A	N/A	10
118 of 169	865-TAGWTFGAGAALQIPFAM-882	N/A	N/A	10
119 of 169	873-GAALQIPFAMQMAYRF-888	5	N/A	10
120 of 169	879-PFAMQMAYRFNGIGV-893	N/A	N/A	10
121 of 169	884-MAYRFNGIGVTQNVLY-899	N/A	N/A	5
122 of 169	890-GIGVTQNVLYENQKQIA-906	N/A	N/A	N/A
123 of 169	897-VLYENQKQIANQFNKAI-913	5	N/A	10
124 of 169	904-QIANQFNKAISQIQESL-920	5	N/A	10
125 of 169	911-KAISQIQESLTTTSTAL-927	N/A	N/A	5
126 of 169	918-ESLTTTSTALGKLQDVV-934	2	N/A	5
127 of 169	925-TALGKLQDVVNQNAQAL-941	5	N/A	10
128 of 169	932-DVVNQNQAALNTLVKQL-948	N/A	N/A	10
129 of 169	939-QALNTLVKQLSSNFGAI-955	N/A	N/A	10
130 of 169	946-KQLSSNFGAISSVLNDIL-963	N/A	N/A	10
131 of 169	954-AISSVLNDILSRDKVEA-971	2	2	5
132 of 169	962-ILSRDKVEAEVQIDRLI-979	2	N/A	10
133 of 169	970-EAEVQIDRLITGRLQSL-986	5	N/A	10
134 of 169	977-RLITGRLQSLQTYVTQQL-994	N/A	5	10
135 of 169	985-SLQTYVTQQLIRAAEIRA-1002	N/A	N/A	10
136 of 169	993-QLIRAAEIRASANLAATK-1010	5	5	5
137 of 169	1001-RASANLAATKMSECV-1015	5	N/A	10
138 of 169	1007-AATKMSECVLGQSKRVDF-1024	5	5	10
139 of 169	1015-VLGQSKRVDFCGKGYHLM-1032	N/A	2	5
140 of 169	1023-DFCGKGYHLMSFPQAAPH-1040	10	10	10
141 of 169	1031-LMSFPQAAPHGVVFLHV-1047	N/A	N/A	10

Table 2: Peptide Solubility (continued)<sup>4,5,6</sup>

Peptide	Sequence	Water Solubility, mg/mL	DPBS Solubility, mg/mL	DMSO Solubility, mg/mL
142 of 169	1038-APHGVVFLHVITYVPSQER-1055	5	5	5
143 of 169	1046-HVTYVPSQERNFTTAPAI-1063	10	5	10
144 of 169	1054-ERNFTTAPAICHEGKAYF-1071	5	5	5
145 of 169	1062-AICHEGKAYFPREGVVFV-1079	N/A	N/A	5
146 of 169	1070-YFPREGVVFVFNQTSWFI-1086	N/A	N/A	10
147 of 169	1077-FVFNQTSWFITQRNFF-1092	N/A	N/A	10
148 of 169	1083-SWFITQRNFFSPQII-1097	N/A	N/A	10
149 of 169	1088-QRNFFSPQIITDNTFV-1104	N/A	5	10
150.1 of 169	1095-QIITDNTFV-1104	N/A	N/A	5
150.2 of 169	1103-FVSGNCDV-1110	5	2	10
151 of 169	1111-VIGIINNTVY-1120	N/A	N/A	5
152 of 169	1111-VIGIINNTVYDPLQPEL-1127	N/A	5	10
153 of 169	1118-TVYDPLQPELDSFKEEL-1134	5	N/A	10
154 of 169	1125-PELDSFKEELDKYFKNH-1141	5	5	10
155 of 169	1132-EELDKYFKNHTSPDVL-1148	5	5	10
156 of 169	1139-KNHTSPDVLGDISGINA-1156	N/A	N/A	10
157 of 169	1147-DLGDISGINASVVNIQK-1163	N/A	N/A	10
158 of 169	1154-INASVVNIQKEIDRLNEV-1171	N/A	N/A	N/A
159 of 169	1162-QKEIDRLNEVAKNLNESL-1179	5	5	10
160 of 169	1170-EVAKNLNESLIDLQELGK-1187	N/A	N/A	10
161 of 169	1178-SLIDLQELGKYEQYIKW-1194	N/A	N/A	5
162 of 169	1185-LGKYEQYIKWPWYVWLGFI-1202	N/A	N/A	10
163.1 of 169	1193-KWPWYVWLGFI-1203	N/A	N/A	10
163.2 of 169	1202-FIAGLIAIV-1210	N/A	N/A	10
164.1 of 169	1201-GFIAGLIA-1208	N/A	N/A	10
164.2 of 169	1209-IVMVTILL-1216	N/A	N/A	10
165.1 of 169	1207-IAIVMVTILL-1216	N/A	N/A	10
165.2 of 169	1217-CCMTSCCSCL-1226	N/A	N/A	N/A
166.1 of 169	1217-CCMTSCCS-1224	N/A	N/A	10
166.2 of 169	1225-CLKGACSCGS-1234	5	5	5
167 of 169	1233-GSCCKFDEDD-1242	5	5	10
168 of 169	1233-GSCCKFDEDDSEPVKGV-1250	5	5	5
169 of 169	1241-DDSEPVKGVKLHYT-1255	10	10	10

<sup>4</sup>N/A signifies solubility less than 0.1 mg/mL.

<sup>5</sup>Peptides 22, 98, 122 and 165.2 were soluble in formic acid (HCOOH) at 2 mg/mL.

<sup>6</sup>Peptides 93, 109, 116 and 158 were soluble in 3% ammonia in water at 2 mg/mL.

/Heather Couch/

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