

Peptide Array, Human Coronavirus NL63 Spike (S) Glycoprotein

Catalog No. NR-53729

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Product Description:

The 226-peptide array spans the spike (S) glycoprotein of the NL63 strain of human coronavirus (HCoV-NL63; GenPept: [Q6Q1S2](#)). Peptides are 14- or 17-mers, with 11 to 13 amino acid overlaps.

Lot: A4635-1 to A4635-226

Manufacturing Date: 16JUL2020

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 226	17	1-MKLFLLLVLPASCFF-17	1968.59	82.4%	90.47%	88.3%
2 of 226	17	7-LLVLPASCFFTCNSNA-23	1813.18	64.7%	87.87%	93.3%
3 of 226	17	13-ASCFFTCNSNANLSMLQ-29	1851.12	52.9%	96.99%	93.4%
4 of 226	17	19-CNSNANLSMLQLGVPDN-35	1790.02	41.2%	90.17%	93.2%
5 of 226	17	25-LSMLQLGVPDNSSTIVT-41	1775.06	41.2%	82.15%	93.1%
6 of 226	17	31-GVPDNSSTIVTGLLPTH-47	1707.91	29.4%	88.39%	86.7%
7 of 226	17	37-STIVTGLLPTHWF CANQ-53	1888.19	47.1%	96.26%	87.8%
8 of 226	17	43-LLPTHWF CANQSTSVYS-59	1954.19	47.1%	96.09%	88.2%
9 of 226	17	49-F CANQSTSVYSANGFFY-65	1906.06	52.9%	95.29%	93.6%
10 of 226	17	55-TSVYSANGFFYIDVGNH-71	1891.02	47.1%	90.15%	87.8%
11 of 226	17	61-NGFFYIDVGNHRSAFAL-77	1928.14	52.9%	94.34%	83.1%
12 of 226	17	67-DVGNHRSAFALHTGYYD-83	1923.03	41.2%	88.16%	78.6%
13 of 226	17	73-SAFALHTGYYDANQYYI-89	1997.14	58.8%	96.64%	88.4%
14 of 226	17	79-TGYYDANQYYIYVTNEI-95	2090.21	52.9%	93.37%	94.1%
15 of 226	17	85-NQYYIYVTNEI GLNASV-101	1961.15	52.9%	84.34%	93.7%
16 of 226	17	91-VTNEI GLNASVTLKICK-107	1803.16	47.1%	80.75%	82.1%
17 of 226	17	97-LNASVTLKICKFSRNTT-113	1896.25	41.2%	80.32%	78.4%
18 of 226	17	103-LKICKFSRNTTFDFLSN-119	2034.37	41.2%	82.42%	79.5%
19 of 226	17	109-SRNTTFDFLSNASSSFD-125	1895.96	29.4%	93.91%	87.9%
20 of 226	17	115-DFLSNASSSFD CIVNLL-131	1845.07	52.9%	80.34%	93.4%
21 of 226	17	121-SSSFD CIVNLLFTEQLG-137	1873.12	47.1%	86.73%	93.5%
22 of 226	17	127-IVNLLFTEQLGAPLGIT-143	1799.15	52.9%	84.11%	93.2%
23 of 226	17	133-TEQLGAPLGITISGETV-149	1685.90	35.3%	90.43%	92.8%
24 of 226	17	139-PLGITISGETVRLHLYN-155	1883.18	41.2%	91.09%	82.7%
25 of 226	17	145-SGETVRLHLYNVTRTFY-161	2056.31	41.2%	81.42%	79.7%
26 of 226	17	151-LHLYNVTRTFYVPAAYK-167	2056.39	58.8%	97.15%	79.7%

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
27 of 226	17	157-TRTFYVPAAYKLTKLSV-173	1958.33	52.9%	95.35%	78.9%
28 of 226	17	163-PAAYKLTKLSVKCYFNY-179	2009.39	58.8%	80.25%	79.3%
29 of 226	17	169-TKLSVKCYFNYSVFSV-185	1988.35	58.8%	87.19%	83.5%
30 of 226	17	175-CYFNYSVFSVNVATVT-191	1917.19	64.7%	88.73%	93.6%
31 of 226	17	181-CVFSVNVATVTVNVTT-197	1791.07	52.9%	82.50%	87.3%
32 of 226	17	187-NATVTVNVTTHNGRVVN-203	1795.98	35.3%	94.92%	82.0%
33 of 226	17	193-NVTTHNGRVVNYTVCCD-209	1907.05	35.3%	86.61%	82.9%
34 of 226	17	199-GRVVNYTVCCDCNGYTD-215	1894.02	41.2%	88.54%	87.9%
35 of 226	17	205-TVCCDCNGYTDNIFSVQ-221	1894.03	41.2%	87.68%	93.6%
36 of 226	17	211-NGYTDNIFSVQQDGRIP-227	1924.06	29.4%	98.02%	88.0%
37 of 226	17	217-IFSVQQDGRIPNGPFN-233	1936.17	35.3%	96.82%	88.1%
38 of 226	17	223-DGRIPNGPFNFWLLT-239	2008.28	41.2%	86.03%	88.5%
39 of 226	17	229-GPFNFWLLTNGSTLV-245	1927.20	47.1%	87.42%	93.6%
40 of 226	17	235-WFLLTNGSTLVGDVSR-251	1878.17	47.1%	96.09%	87.8%
41 of 226	17	241-GSTLVGDVSRLYQPLRL-257	1874.17	41.2%	90.68%	82.6%
42 of 226	17	247-GVSRLYQPLRLTCLWPV-263	2001.43	52.9%	92.44%	83.6%
43 of 226	17	253-YQPLRLTCLWPVPLK-269	1971.40	47.1%	90.13%	83.4%
44 of 226	17	259-TCLWPVPLKSSSTGFVY-275	1855.19	47.1%	83.63%	87.6%
45 of 226	17	265-PGLKSSSTGFVYFNATGS-281	1732.91	35.3%	84.35%	86.9%
46 of 226	17	271-TGFVYFNATGSDVNCNG-287	1765.88	41.2%	96.07%	93.1%
47 of 226	17	277-NATGSDVNCNGYQHNSV-293	1779.82	29.4%	94.58%	87.2%
48 of 226	17	283-VNCNGYQHNSVVDVMRY-299	1998.23	47.1%	98.09%	83.5%
49 of 226	17	289-YQHNSVVDVMRYNLFNS-305	2086.31	47.1%	84.45%	84.2%
50 of 226	17	295-VDMRYNLFNSANSLDN-311	1972.17	47.1%	96.58%	88.3%
51 of 226	17	301-NLNFNSANSLDNKSGVI-317	1806.01	41.2%	95.84%	87.3%
52 of 226	17	307-NSLDNLKSGVIVFKTLQ-323	1876.19	41.2%	90.55%	82.7%
53 of 226	17	313-KSGVIVFKTLQYDVLFY-329	2020.40	58.8%	91.83%	83.7%
54 of 226	17	319-FKTLQYDVLFYCSNSSS-335	2002.23	47.1%	80.02%	88.4%
55 of 226	17	325-DVLFYCSNSSSGVLDTT-341	1807.95	41.2%	91.10%	93.3%
56 of 226	17	331-SNSSSGVLDTTIPFGPS-347	1665.78	23.5%	84.58%	92.7%
57 of 226	17	337-VLDTTIPFGPSSQPYC-353	1888.12	41.2%	91.70%	93.6%
58 of 226	17	343-PFGPSSQPYCFINSTI-359	1921.16	41.2%	82.81%	93.6%
59 of 226	17	349-SQPYCFINSTINTTHV-365	1988.20	41.2%	95.81%	88.3%
60 of 226	17	355-FINSTINTTHVSTFVGI-371	1851.10	41.2%	82.48%	87.6%
61 of 226	17	361-NTTHVSTFVGIPLPPTVR-377	1839.13	35.3%	93.76%	82.4%
62 of 226	17	367-TFVGIPLPPTVREIVVAR-383	1867.28	52.9%	91.34%	82.6%
63 of 226	17	373-PPTVREIVVARTGQFYI-389	1946.28	47.1%	97.90%	83.2%
64 of 226	17	379-IVVARTGQFYINGFKYF-395	2023.36	58.8%	81.42%	83.8%
65 of 226	17	385-GQFYINGFKYFDLGFIE-401	2058.32	52.9%	93.55%	88.7%
66 of 226	17	391-GFKYFDLGFIEAVNFNV-407	1980.25	58.8%	89.95%	88.3%
67 of 226	17	397-LGFIEAVNFNVTTASAT-413	1754.97	52.9%	84.30%	93.0%
68 of 226	17	403-VNFNVTTASATDFWTV-419	1844.02	52.9%	92.11%	93.4%
69 of 226	17	409-TASATDFWTVAFATFVD-425	1850.02	58.8%	86.60%	93.4%
70 of 226	17	415-FWTVAFATFVDVLVNV-431	1915.23	70.6%	85.72%	93.6%
71 of 226	17	421-ATFVDVLVNVSATNIQN-437	1805.03	52.9%	91.76%	93.2%

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
72 of 226	17	427-LVNVSATNIQNLLYCD5-443	1867.11	52.9%	90.84%	93.5%
73 of 226	17	433-TNIQNLLYCDSPFEKLQ-449	2026.30	41.2%	93.64%	88.6%
74 of 226	17	439-LYCDSPFEKLQCEHLQF-455	2100.41	47.1%	96.80%	84.3%
75 of 226	17	445-FEKLQCEHLQFGLQDGF-461	2039.31	41.2%	92.02%	83.8%
76 of 226	17	451-EHLQFGLQDGFYSANFL-467	1986.18	47.1%	90.97%	88.3%
77 of 226	17	457-LQDGFYSANFLDDNVLP-473	1928.09	47.1%	92.04%	93.6%
78 of 226	17	463-SANFLDDNVLPETYVAL-479	1881.07	52.9%	86.92%	93.5%
79 of 226	17	469-DNVLPETYVALPIYYQH-485	2035.28	52.9%	91.91%	88.6%
80 of 226	17	475-TYVALPIYYQHTDINFT-491	2059.30	52.9%	88.53%	88.7%
81 of 226	17	481-IYYQHTDINFTATASFG-497	1949.10	47.1%	89.70%	88.2%
82 of 226	17	487-DINFTATASFGGSCYVC-503	1755.95	52.9%	83.78%	93.0%
83 of 226	17	493-TASFGGSCYVCKPHQVN-509	1798.03	41.2%	83.05%	82.0%
84 of 226	17	499-SCYVCKPHQVNISLNGN-515	1876.15	41.2%	94.41%	82.7%
85 of 226	17	505-PHQVNISLNGNTSVCVR-521	1838.09	35.3%	96.81%	82.4%
86 of 226	17	511-SLNGNTSVCVRTSHFSI-527	1822.04	35.3%	97.35%	82.2%
87 of 226	17	517-SVCVRTSHFSIRIYINR-533	2101.42	47.1%	98.71%	76.2%
88 of 226	17	523-SHFSIRIYINRVKSGSP-539	2011.27	35.3%	91.04%	75.4%
89 of 226	17	529-YIYNRVKSGSPGDSSWH-545	1953.10	29.4%	89.94%	78.9%
90 of 226	17	535-KSGSPGDSSWHIYLKSG-551	1805.97	23.5%	93.99%	77.5%
91 of 226	17	541-DSSWHIYLKSGTCPFSF-557	1975.21	41.2%	95.83%	83.4%
92 of 226	17	547-YLKSGTCPFSFKLNNF-563	1953.25	41.2%	91.21%	83.3%
93 of 226	17	553-CPFSFKLNNFQKFKTI-569	2049.43	41.2%	87.97%	79.6%
94 of 226	17	559-KLNNFQKFKTICFSTVE-575	2047.41	41.2%	88.48%	79.6%
95 of 226	17	564-KFKTICFSTVEVPGSCN-580	1860.19	41.2%	86.03%	82.6%
96 of 226	17	570-FSTVEVPGSCNFPLEAT-586	1798.01	41.2%	93.82%	93.2%
97 of 226	17	576-PGSCNFPLEATWHYTSY-592	1973.15	41.2%	88.80%	88.3%
98 of 226	17	582-PLEATWHYTSYTIVGAL-598	1922.16	52.9%	93.20%	88.0%
99 of 226	17	588-HYTSYTIVGALYVTWSE-604	1990.19	52.9%	94.99%	88.3%
100 of 226	17	594-IVGALYVTWSEGNSITG-610	1766.97	47.1%	93.43%	93.1%
101 of 226	17	600-VTWSEGNSITGVYPVPS-616	1792.96	35.3%	89.03%	93.2%
102 of 226	17	606-NSITGVYPVSGIREFS-622	1823.04	35.3%	95.82%	87.4%
103 of 226	17	612-PYPVSGIREFSNLVLNN-628	1919.17	41.2%	81.81%	88.0%
104 of 226	17	618-IREFSNLVLNNCTKYNI-634	2041.36	47.1%	92.83%	83.8%
105 of 226	17	624-LVLNNCTKYNIYDYVGT-640	1993.26	52.9%	96.52%	88.4%
106 of 226	17	630-TKYNIYDYVGTGIIRSS-646	1950.17	41.2%	80.07%	83.2%
107 of 226	17	636-DYVGTGIIRSSNQLAG-652	1737.89	35.3%	84.99%	86.9%
108 of 226	17	642-IIRSSNQLAGGITYVS-658	1765.99	41.2%	86.49%	87.1%
109 of 226	17	648-NQLAGGITYVSNSGNL-664	1694.82	35.3%	91.27%	92.9%
110 of 226	17	654-GITYVSNSGNLLGFKNV-670	1783.02	41.2%	92.60%	87.2%
111 of 226	17	660-NSGNLLGFKNVSTGNIF-676	1781.99	35.3%	89.42%	87.2%
112 of 226	17	666-GFKNVSTGNIFIVTPCN-682	1811.10	41.2%	84.82%	87.3%
113 of 226	17	672-TGNIFIVTPCNQPDQVA-688	1817.06	41.2%	82.96%	93.3%
114 of 226	17	678-VTPCNQPDQVAVYQQSI-694	1890.11	41.2%	94.45%	93.6%
115 of 226	17	684-PDQVAVYQQSIIGAMTA-700	1792.05	52.9%	89.19%	93.2%
116 of 226	17	690-YQQSIIGAMTAVNESRY-706	1931.15	47.1%	87.11%	88.0%

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
117 of 226	17	696-GAMTAVNESRYGLQNLL-712	1837.09	47.1%	93.21%	87.5%
118 of 226	17	702-NESRYGLQNLLQLPNFY-718	2069.30	41.2%	89.97%	88.7%
119 of 226	17	708-LQNLLQLPNFYYSNGG-724	1940.18	47.1%	93.99%	93.6%
120 of 226	17	714-LPNFYYSNGGNCTTA-730	1834.98	41.2%	91.42%	93.4%
121 of 226	17	720-VSNGGNCTTAVMTYSN-736	1732.87	35.3%	93.29%	92.9%
122 of 226	17	726-NCTTAVMTYSNFGICAD-742	1811.05	52.9%	97.13%	93.3%
123 of 226	17	732-MTYSNFGICADGSLIPV-748	1788.08	52.9%	96.29%	93.2%
124 of 226	17	738-GICADGSLIPVRPRNSS-754	1742.00	35.3%	94.59%	81.6%
125 of 226	17	744-SLIPVRPRNSSDNGISA-760	1782.98	29.4%	94.53%	82.0%
126 of 226	17	750-PRNSSDNGISAITANL-766	1742.92	35.3%	97.66%	87.0%
127 of 226	17	756-NGISAITANLSIPSNW-772	1771.01	47.1%	90.21%	93.1%
128 of 226	17	762-ITANLSIPSNWTTSVQV-778	1831.06	41.2%	82.86%	93.3%
129 of 226	17	768-IPSNWTTSVQVEYLQIT-784	1979.22	41.2%	88.76%	93.8%
130 of 226	17	773-TSVQVEYLQITSTPIVV-789	1877.17	47.1%	92.12%	93.5%
131 of 226	17	779-YLQITSTPIVVDCATYV-795	1886.19	58.8%	93.40%	93.6%
132 of 226	17	785-TPIVVDCATYVCNGNPR-801	1822.10	47.1%	92.93%	87.4%
133 of 226	17	790-CATYVCNGNPRCKNLLK-806	1897.28	47.1%	83.40%	78.4%
134 of 226	17	796-NGNPRCKNLLKQYTSAC-812	1910.21	35.3%	80.17%	78.5%
135 of 226	17	802-KNLLKQYTSACKTIEDA-818	1926.22	41.2%	96.14%	78.6%
136 of 226	17	808-YTSACKTIEDALRLSAH-824	1879.13	47.1%	93.98%	78.2%
137 of 226	17	814-TIEDALRLSAHLETNDV-830	1897.08	41.2%	83.59%	82.9%
138 of 226	17	820-RLSAHLETNDVSSMLTF-836	1921.17	41.2%	92.74%	83.0%
139 of 226	17	826-ETNDVSSMLTFDSNAFS-842	1864.97	35.3%	92.19%	93.5%
140 of 226	17	832-SMLTFDSNAFSLANVTS-848	1805.00	47.1%	91.05%	93.2%
141 of 226	17	838-SNAFSLANVTSFGDYNL-854	1819.95	47.1%	97.10%	93.3%
142 of 226	17	844-ANVTSFGDYNLSSVLPQ-860	1811.97	41.2%	80.27%	93.3%
143 of 226	17	849-GDYNLSSVLPQRNIRSS-865	1906.09	29.4%	81.00%	82.9%
144 of 226	17	855-SVLPQRNIRSSRIAGRS-871	1897.18	29.4%	80.13%	74.4%
145 of 226	17	861-NIRSSRIAGRSALEDLL-877	1871.14	41.2%	93.85%	78.1%
146 of 226	17	867-IAGRSALEDLLFSKVVT-883	1819.14	52.9%	81.79%	82.2%
147 of 226	17	872-LEDLLFSKVVTSGLGTV-888	1778.09	47.1%	85.18%	87.2%
148 of 226	17	878-SKVVTSGLGTVDVDYKS-894	1754.96	35.3%	83.51%	81.7%
149 of 226	17	884-GLGTVDVDYKCTKGLS-900	1742.97	35.3%	81.28%	81.6%
150 of 226	17	890-VDYKCTKGLSIADLAC-906	1787.09	52.9%	85.39%	82.0%
151 of 226	17	896-TKGLSIADLACAQYNG-912	1788.01	52.9%	94.93%	87.2%
152 of 226	17	902-ADLACAQYNGIMVLPQ-918	1799.10	64.7%	83.58%	93.2%
153 of 226	17	907-AQYNGIMVLPGVADAE-923	1811.04	58.8%	95.59%	93.3%
154 of 226	17	913-IMVLPGVADAERMAMYT-929	1868.27	64.7%	80.10%	87.7%
155 of 226	17	919-VADAERMAMYTGSLIGG-935	1742.01	52.9%	80.92%	87.0%
156 of 226	17	925-MAMYTGSLIGGMVLGGL-941	1671.08	58.8%	80.40%	92.8%
157 of 226	17	931-SLIGGMVLGGLTSAAAI-947	1530.86	58.8%	93.14%	92.1%
158 of 226	17	937-VLGGLTSAAAIPFSLAL-953	1600.93	64.7%	92.65%	92.4%
159 of 226	17	943-SAAAIIPFSLALQARLNY-959	1806.10	64.7%	80.52%	87.3%
160 of 226	17	949-FSLALQARLNYVALQTD-965	1923.20	58.8%	90.56%	88.0%
161 of 226	17	955-ARLNYVALQTDVLQENQ-971	1975.19	47.1%	80.69%	88.3%

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
162 of 226	17	961-ALQTDVLQENQKILAAS-977	1842.09	47.1%	90.28%	87.6%
163 of 226	17	967-LQENQKILAASFNKAIN-983	1902.19	47.1%	96.27%	82.9%
164 of 226	17	973-ILAASFNKAINNIVASF-989	1793.11	64.7%	92.92%	87.3%
165 of 226	17	979-NKAINNIVASFSSVND-995	1763.93	47.1%	81.70%	87.0%
166 of 226	17	985-IVASFSSVNDAITQTAE-1001	1752.90	47.1%	93.76%	93.0%
167 of 226	17	991-SVNDAITQTAEIHTVT-1007	1770.92	41.2%	94.10%	87.1%
168 of 226	17	997-TQTAEIHTVTIALNKI-1013	1824.12	47.1%	95.92%	82.3%
169 of 226	17	1003-IHTVTIALNKIQDVVNQ-1019	1906.22	47.1%	80.28%	82.9%
170 of 226	17	1009-ALNKIQDVVNQQGSALN-1025	1812.02	41.2%	96.91%	87.3%
171 of 226	17	1015-DVVNQQGSALNHLTSQL-1031	1823.99	35.3%	90.80%	87.4%
172 of 226	17	1021-GSALNHLTSQLRHNFA-1037	1894.09	35.3%	87.90%	78.3%
173 of 226	17	1026-LTSQLRHNFAISNSIQ-1042	1957.19	35.3%	92.23%	83.3%
174 of 226	17	1032-HNFAISNSIQAIYDRL-1048	1990.21	47.1%	80.32%	83.5%
175 of 226	17	1038-SNSIQAIYDRLDSIQAD-1054	1909.04	41.2%	80.28%	88.0%
176 of 226	17	1044-IYDRLDSIQADQQVDRL-1060	2048.25	41.2%	90.10%	83.9%
177 of 226	17	1050-SIQADQQVDRLITGRLA-1066	1884.13	41.2%	92.04%	82.7%
178 of 226	17	1056-DQQVDRLITGRLAALNA-1072	1854.11	47.1%	89.61%	82.5%
179 of 226	17	1061-LITGRLAALNAFVSQVL-1077	1786.16	64.7%	80.17%	87.2%
180 of 226	17	1067-AALNAFVSQVLNKEYTEV-1083	1867.14	58.8%	95.07%	87.7%
181 of 226	17	1073-VSQVLNKEYTEVRGSRRL-1089	2005.31	35.3%	80.08%	75.4%
182 of 226	17	1079-KYTEVRGSRRLAQKIN-1095	2047.35	29.4%	80.01%	72.3%
183 of 226	17	1085-GSRRLAQKINECVKSQ-1101	1945.24	29.4%	83.29%	74.8%
184 of 226	17	1091-AQQKINECVKSQSNRYG-1107	1953.17	29.4%	96.32%	78.9%
185 of 226	17	1097-ECVKSQSNRYGFCGNGT-1113	1850.02	29.4%	82.78%	82.5%
186 of 226	17	1103-SNRYGFCGNGTHIFSIV-1119	1872.10	41.2%	80.01%	82.6%
187 of 226	17	1109-CGNGTHIFSIVNSAPDG-1125	1688.85	35.3%	88.80%	86.6%
188 of 226	17	1115-IFSIVNSAPDGLLFLHT-1131	1844.15	52.9%	94.88%	87.6%
189 of 226	17	1121-SAPDGLLFLHTVLLPTD-1137	1809.10	47.1%	81.96%	87.3%
190 of 226	17	1127-LFLHTVLLPTDYKNVKA-1143	1972.36	52.9%	83.90%	79.0%
191 of 226	17	1133-LLPTDYKNVKAWSGICV-1149	1907.27	52.9%	81.04%	82.9%
192 of 226	17	1139-KNVKAWSGICVDGIYGY-1155	1873.16	52.9%	89.81%	82.6%
193 of 226	17	1145-SGICVDGIYGYVLRQPN-1161	1854.11	47.1%	91.42%	87.6%
194 of 226	17	1151-GIYGYVLRQPNLVLYSD-1167	1970.25	52.9%	84.64%	88.3%
195 of 226	17	1157-LRQPNLVLYSDNGVFRV-1173	1990.30	47.1%	87.10%	83.5%
196 of 226	17	1163-VLYSDNGVFRVTSRVMF-1179	1990.32	52.9%	87.58%	83.5%
197 of 226	17	1169-GVFRVTSRVMFQRLPV-1185	1989.43	47.1%	80.19%	79.2%
198 of 226	17	1175-SRVMFQRLPVLSDVQ-1191	2019.41	47.1%	94.64%	83.7%
199 of 226	17	1181-PRLPVLSDVQIYNCNV-1197	1977.32	52.9%	83.42%	88.3%
200 of 226	17	1187-SDFVQIYNCNVTFVNIS-1203	1963.20	52.9%	85.60%	93.7%
201 of 226	17	1193-YNCNVTFVNISRVELHT-1209	2009.28	47.1%	94.39%	83.6%
202 of 226	17	1199-FVNISRVELHTVIPDYV-1215	2001.32	52.9%	87.50%	83.6%
203 of 226	17	1205-VELHTVIPDYVDVNKTL-1221	1955.24	47.1%	81.69%	83.3%
204 of 226	17	1211-IPDYVDVNKTLQEFAQN-1227	1994.19	41.2%	80.49%	88.4%
205 of 226	17	1217-VNKTLQEFAQNLPKYVK-1233	2020.36	41.2%	80.22%	79.4%
206 of 226	17	1223-EFAQNLPKYVKPNFDLT-1239	2024.31	41.2%	90.20%	83.8%

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
207 of 226	17	1229-PKYVKPNFDLTPFNLT-1245	2057.37	41.2%	89.63%	84.0%
208 of 226	17	1235-NFDLTPFNLTYNLSSE-1251	1988.18	41.2%	85.83%	93.8%
209 of 226	17	1241-FNLTYLNLSSSELKQLEA-1257	1983.25	47.1%	83.45%	88.3%
210 of 226	17	1247-NLSELKQLEAKTASLF-1263	1879.15	41.2%	82.68%	82.7%
211 of 226	17	1253-KQLEAKTASLFQTTVEL-1269	1907.20	41.2%	88.87%	82.9%
212 of 226	17	1259-TASLFQTTVELQGLIDQ-1275	1864.09	41.2%	80.56%	93.5%
213 of 226	17	1265-TTVELQGLIDQINSTYV-1281	1894.11	41.2%	81.09%	93.6%
214 of 226	17	1271-GLIDQINSTYVDLKLLN-1287	1919.21	47.1%	83.90%	88.0%
215 of 226	17	1277-NSTYVDLKLLNRFENYI-1293	2102.37	47.1%	90.70%	84.3%
216 of 226	17	1283-LKLLNRFENYIKWPWWV-1299	2305.76	58.8%	80.64%	81.5%
217 of 226	17	1289-FENYIKWPWWVWLIISV-1305	2279.71	70.6%	93.28%	89.7%
218 of 226	17	1295-WPWWVWLIISVVFVLL-1311	2155.71	88.2%	90.76%	84.3%
219 of 226	17	1301-LIISVVFVLLSLLVFC-1317	1877.46	88.2%	83.92%	93.5%
220 of 226	17	1307-FVLLSLLVFCCLSTGC-1323	1817.32	76.5%	86.91%	93.3%
221 of 226	17	1313-LLVFCCLSTGCCGCCNC-1329	1742.21	70.6%	94.88%	93.0%
222 of 226	17	1319-LSTGCCGCCNCLTSSMR-1335	1739.10	47.1%	92.64%	86.9%
223 of 226	17	1325-GCCNCLTSSMRGCCDCG-1341	1713.04	47.1%	90.65%	86.8%
224 of 226	17	1331-TSSMRGCCDCGSKLPY-1347	1809.10	35.3%	93.28%	82.2%
225 of 226	17	1337-CCDCGSKLPYYEFK-1353	1985.28	47.1%	98.22%	83.5%
226 of 226	14	1343-TKLPYYEFKVVHVQ-1356	1781.04	42.9%	93.87%	77.3%

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 226	Expected	1.0			1.0				1.0	6.0	1.0	1.0	3.0	1.0	1.0				1.0
	Actual	1.0			0.0				1.0	6.1	1.0	1.1	2.9	1.1	0.9				0.9
2 of 226	Expected	2.0		2.0	2.0					4.0			2.0	1.0	2.0	1.0			1.0
	Actual	1.9		1.8	0.0					4.1			2.0	1.1	2.0	1.0			1.1
3 of 226	Expected	2.0		3.0	2.0	1.0				2.0		1.0	2.0		3.0	1.0			
	Actual	2.0		2.9	0.0	0.9				2.1		1.0	2.1		2.8	1.0			
4 of 226	Expected	1.0		5.0	1.0	1.0	1.0			3.0		1.0		1.0	2.0				1.0
	Actual	1.0		4.8	0.0	0.9	1.1			3.1		1.0		1.1	1.8				1.1
5 of 226	Expected			2.0		1.0	1.0		1.0	3.0		1.0		1.0	3.0	2.0			2.0
	Actual			1.9		0.9	1.1		0.9	3.0		1.0		1.1	2.9	2.1			2.1
6 of 226	Expected			2.0			2.0	1.0	1.0	2.0				2.0	2.0	3.0			2.0
	Actual			1.8			2.1	1.1	1.0	2.0				2.0	1.8	3.2			2.0
7 of 226	Expected	1.0		1.0	1.0	1.0	1.0	1.0	1.0	2.0			1.0	1.0	1.0	3.0	1.0		1.0
	Actual	1.0		1.0	0.0	0.9	1.1	1.1	0.9	2.1			1.1	1.0	0.8	2.8	0.0		1.1
8 of 226	Expected	1.0		1.0	1.0	1.0		1.0		2.0			1.0	1.0	3.0	2.0	1.0	1.0	1.0
	Actual	1.0		1.0	0.0	0.8		1.0		2.0			1.0	1.0	2.8	1.9	0.0	1.1	1.2
9 of 226	Expected	2.0		2.0	1.0	1.0	1.0						3.0		3.0	1.0			2.0
	Actual	1.9		1.8	0.0	0.9	1.1						3.1		2.8	1.0			2.2
10 of 226	Expected	1.0		3.0			2.0	1.0	1.0				2.0		2.0	1.0			2.0
	Actual	0.9		2.8			2.1	1.1	1.0				2.1		1.9	1.0			1.9
11 of 226	Expected	2.0	1.0	3.0			2.0	1.0	1.0	1.0			3.0		1.0				1.0
	Actual	2.0	1.0	2.9			2.0	1.0	1.0	1.1			3.0		0.9				1.1
12 of 226	Expected	2.0	1.0	3.0			2.0	2.0		1.0			1.0		1.0	1.0			2.0
	Actual	1.9	1.0	2.8			2.0	2.1		1.0			1.1		0.8	1.0			2.2
13 of 226	Expected	3.0		2.0		1.0	1.0	1.0	1.0	1.0			1.0		1.0	1.0			4.0
	Actual	2.8		2.0		1.0	1.0	1.0	1.1	1.0			1.0		1.0	0.9			4.2

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)
14 of 226	Expected	1.0		3.0		2.0	1.0		2.0							2.0		5.0	1.0
	Actual	1.0		2.9		2.0	1.0		2.2							1.9		5.0	1.0
15 of 226	Expected	1.0		3.0		2.0	1.0		2.0	1.0					1.0	1.0		3.0	2.0
	Actual	1.1		2.9		1.8	1.1		1.9	1.2					0.9	1.0		2.8	2.2
16 of 226	Expected	1.0		2.0	1.0	1.0	1.0		2.0	2.0	2.0				1.0	2.0			2.0
	Actual	1.0		2.0	0.0	0.9	1.0		1.9	2.1	2.1				1.0	1.9			2.1
17 of 226	Expected	1.0	1.0	2.0	1.0				1.0	2.0	2.0		1.0		2.0	3.0			1.0
	Actual	0.9	1.0	1.9	0.0				0.8	2.1	2.2		1.0		2.0	3.1			1.1
18 of 226	Expected		1.0	3.0	1.0				1.0	2.0	2.0		3.0		2.0	2.0			
	Actual		1.1	3.1	0.0				1.0	2.1	1.8		3.1		1.9	2.0			
19 of 226	Expected	1.0	1.0	4.0						1.0			3.0		5.0	2.0			
	Actual	1.1	1.0	3.8						1.0			3.1		4.9	2.0			
20 of 226	Expected	1.0		4.0	1.0				1.0	3.0			2.0		4.0				1.0
	Actual	1.1		3.9	0.0				0.8	3.0			2.0		4.0				1.0
21 of 226	Expected			2.0	1.0	2.0	1.0		1.0	3.0			2.0		3.0	1.0			1.0
	Actual			2.0	0.0	1.9	1.0		0.8	3.0			2.0		2.8	1.2			0.9
22 of 226	Expected	1.0		1.0		2.0	2.0		2.0	4.0			1.0	1.0		2.0			1.0
	Actual	1.0		0.9		1.9	2.1		1.6	4.0			1.1	1.1		1.9			0.7
23 of 226	Expected	1.0				3.0	3.0		2.0	2.0				1.0	1.0	3.0			1.0
	Actual	1.0				2.9	3.1		2.1	2.2				1.0	0.9	2.8			1.0
24 of 226	Expected		1.0	1.0		1.0	2.0	1.0	2.0	3.0				1.0	1.0	2.0		1.0	1.0
	Actual		1.1	1.1		1.0	2.0	1.1	1.8	3.0				0.9	1.0	1.9		1.0	1.1
25 of 226	Expected		2.0	1.0		1.0	1.0	1.0		2.0			1.0		1.0	3.0		2.0	2.0
	Actual		2.1	1.0		0.9	1.0	1.1		2.1			1.1		0.8	2.8		2.1	2.2
26 of 226	Expected	2.0	1.0	1.0				1.0		2.0	1.0		1.0	1.0		2.0		3.0	2.0
	Actual	2.0	1.0	1.0				1.0		2.0	1.0		1.0	1.0		1.9		3.0	2.1
27 of 226	Expected	2.0	1.0							2.0	2.0		1.0	1.0	1.0	3.0		2.0	2.0
	Actual	1.9	1.0							2.2	2.0		1.1	1.0	0.8	2.8		2.1	2.1
28 of 226	Expected	2.0		1.0	1.0					2.0	3.0		1.0	1.0	1.0	1.0		3.0	1.0
	Actual	1.9		1.0	0.0					2.0	2.9		1.2	0.9	0.8	1.0		3.2	1.1
29 of 226	Expected			1.0	2.0					1.0	2.0		2.0		3.0	1.0		2.0	3.0
	Actual			1.0	0.0					1.0	1.9		2.2		2.9	0.9		2.1	3.1
30 of 226	Expected	1.0		2.0	2.0								2.0		2.0	2.0		2.0	4.0
	Actual	1.2		1.8	0.0								1.9		1.9	2.2		1.8	3.6
31 of 226	Expected	1.0		2.0	1.0			1.0					1.0		1.0	4.0			6.0
	Actual	1.0		1.9	0.0			1.2					0.9		1.0	4.0			5.7
32 of 226	Expected	1.0	1.0	4.0			1.0	1.0								4.0			5.0
	Actual	0.9	1.0	4.0			1.1	1.0								3.8			4.6
33 of 226	Expected		1.0	5.0	1.0		1.0	1.0								3.0		1.0	4.0
	Actual		1.0	4.8	0.0		1.0	1.0								2.9		1.0	3.8
34 of 226	Expected		1.0	5.0	2.0		2.0									2.0		2.0	3.0
	Actual		1.0	4.8	0.0		2.0									1.9		2.1	3.0
35 of 226	Expected			5.0	2.0	1.0	1.0		1.0				1.0		1.0	2.0		1.0	2.0
	Actual			5.1	0.0	1.0	1.1		1.0				1.1		0.9	1.9		1.1	1.8
36 of 226	Expected		1.0	4.0		2.0	2.0		2.0				1.0	1.0	1.0	1.0		1.0	1.0
	Actual		1.2	3.9		1.9	2.0		2.0				1.0	1.1	0.9	0.9		1.0	1.1
37 of 226	Expected		1.0	3.0		2.0	2.0		2.0				3.0	2.0	1.0				1.0
	Actual		1.1	2.8		2.0	2.0		2.0				3.1	2.1	0.8				1.1
38 of 226	Expected	1.0	1.0	4.0			2.0		1.0	2.0			3.0	2.0		1.0	1.0		
	Actual		1.1	3.9			1.9		0.9	2.1			3.2	2.1		1.0	0.0		
39 of 226	Expected			3.0			2.0			3.0			3.0	1.0	1.0	2.0	1.0		1.0
	Actual			3.1			1.9			3.2			2.9	1.0	0.9	2.0	0.0		1.1
40 of 226	Expected		1.0	2.0			2.0			4.0			1.0		2.0	2.0	1.0		2.0
	Actual		1.2	2.0			2.0			3.9			1.0		1.8	2.0	0.0		1.9
41 of 226	Expected	2.0	1.0			1.0	2.0			4.0				1.0	2.0	1.0		1.0	2.0
	Actual	2.0	0.9			1.0	1.9			4.1				1.2	1.8	0.8		1.1	2.2
42 of 226	Expected		2.0		1.0	1.0	1.0			4.0				2.0	1.0	1.0	1.0	1.0	2.0
	Actual		2.1		0.0	1.0	1.0			4.0				2.2	0.8	1.1	0.0	1.0	2.2
43 of 226	Expected		1.0		1.0	1.0	1.0			4.0	1.0			3.0	1.0	1.0	1.0	1.0	1.0
	Actual		1.0		0.0	1.0	1.0			3.9	1.0			3.0	1.0	0.9	0.0	1.0	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)
44 of 226	Expected				1.0		2.0			2.0	1.0		1.0	2.0	2.0	2.0	1.0	1.0	2.0
	Actual				0.0		2.0			1.9	1.0		1.0	2.0	1.8	1.9	0.0	1.1	2.2
45 of 226	Expected	1.0		1.0			3.0			1.0	1.0		2.0	1.0	3.0	2.0		1.0	1.0
	Actual	1.1		0.9			2.9			1.1	1.1		2.0	1.1	2.8	1.9		0.9	1.0
46 of 226	Expected	1.0		4.0	1.0		3.0						2.0		1.0	2.0		1.0	2.0
	Actual	1.1		3.9	0.0		2.9						2.1		0.8	2.0		1.0	2.2
47 of 226	Expected	1.0		5.0	1.0	1.0	2.0	1.0							2.0	1.0		1.0	2.0
	Actual	1.0		4.8	0.0	1.0	1.9	1.0							2.0	1.0		1.0	2.1
48 of 226	Expected		1.0	4.0	1.0	1.0	1.0	1.0				1.0			1.0			2.0	4.0
	Actual		1.2	4.1	0.0	1.1	0.9	1.0				1.0			0.8			2.1	3.7
49 of 226	Expected		1.0	4.0		1.0		1.0		1.0		1.0	1.0		2.0			2.0	3.0
	Actual		1.1	3.9		1.0		1.0		1.1		0.9	1.1		1.8			2.0	2.6
50 of 226	Expected	1.0	1.0	6.0						2.0		1.0	1.0		2.0			1.0	2.0
	Actual	1.1	0.9	5.9						2.0		0.8	1.2		1.8			1.1	2.2
51 of 226	Expected	1.0		5.0			1.0		1.0	3.0	1.0		1.0		3.0				1.0
	Actual	1.2		4.9			1.0		0.6	2.9	1.0		0.9		2.8				0.7
52 of 226	Expected			3.0		1.0	1.0		1.0	3.0	2.0		1.0		2.0	1.0			2.0
	Actual			2.9		0.8	1.0		0.5	3.0	2.2		1.2		1.8	1.0			1.5
53 of 226	Expected			1.0		1.0	1.0		1.0	2.0	2.0		2.0		1.0	1.0		2.0	3.0
	Actual			1.0		0.9	1.0		0.5	2.1	2.0		2.1		0.8	1.0		2.2	2.7
54 of 226	Expected			2.0	1.0	1.0				2.0	1.0		2.0		4.0	1.0		2.0	1.0
	Actual			2.0	0.0	0.8				2.1	1.0		2.1		3.9	0.9		2.1	1.2
55 of 226	Expected			3.0	1.0		1.0			2.0			1.0		4.0	2.0		1.0	2.0
	Actual			2.8	0.0		1.1			1.9			0.8		4.0	2.1		1.1	2.0
56 of 226	Expected			2.0			2.0		1.0	1.0			1.0	2.0	5.0	2.0			1.0
	Actual			1.9			1.9		1.0	1.0			1.0	2.1	4.8	1.8			1.2
57 of 226	Expected			1.0	1.0	1.0	1.0		1.0	1.0			1.0	3.0	2.0	2.0		2.0	1.0
	Actual			0.9	0.0	0.8	1.1		1.0	1.0			1.1	3.3	1.8	1.9		2.2	1.1
58 of 226	Expected			1.0	1.0	1.0	1.0		2.0				2.0	3.0	3.0	1.0		2.0	
	Actual			1.1	0.0	0.8	1.0		2.2				2.1	3.0	2.9	1.1		2.1	
59 of 226	Expected			2.0	1.0	1.0		1.0	2.0				1.0	1.0	2.0	3.0		2.0	1.0
	Actual			2.0	0.0	0.8		1.0	2.2				1.1	1.1	1.8	2.9		2.1	1.0
60 of 226	Expected			2.0			1.0	1.0	3.0				2.0		2.0	4.0			2.0
	Actual			2.0			1.1	1.0	3.0				2.0		1.8	3.8			2.1
61 of 226	Expected		1.0	1.0			1.0	1.0	1.0	1.0			1.0	2.0	1.0	4.0			3.0
	Actual		1.1	1.0			1.1	0.8	1.1	1.1			1.1	2.1	0.8	3.8			3.1
62 of 226	Expected	1.0	2.0			1.0	1.0		2.0	1.0			1.0	2.0		2.0			4.0
	Actual	1.0	2.2			0.9	1.0		1.8	1.0			1.0	2.1		1.8			4.0
63 of 226	Expected	1.0	2.0			2.0	1.0		2.0				1.0	2.0		2.0		1.0	3.0
	Actual	1.1	2.1			1.9	1.1		2.0				1.0	1.9		1.9		0.9	3.1
64 of 226	Expected	1.0	1.0	1.0		1.0	2.0		2.0		1.0		3.0			1.0		2.0	2.0
	Actual	1.0	1.0	1.0		1.0	2.1		1.7		1.1		3.2			0.8		2.1	1.7
65 of 226	Expected			2.0		2.0	3.0		2.0	1.0	1.0		4.0					2.0	
	Actual			2.0		1.8	3.0		1.9	1.1	1.1		4.0					2.0	
66 of 226	Expected	1.0		3.0		1.0	2.0		1.0	1.0	1.0		4.0					1.0	2.0
	Actual	1.1		3.0		1.0	2.0		1.0	1.1	0.9		3.9					0.9	2.3
67 of 226	Expected	3.0		2.0		1.0	1.0		1.0	1.0			2.0		1.0	3.0			2.0
	Actual	3.2		2.0		0.9	1.0		1.0	1.0			2.1		0.8	3.1			2.1
68 of 226	Expected	3.0		3.0									2.0		1.0	4.0	1.0		3.0
	Actual	3.1		3.0									2.1		0.8	4.0	0.0		3.3
69 of 226	Expected	4.0		2.0									3.0		1.0	4.0	1.0		2.0
	Actual	3.9		2.0									2.9		1.0	3.9	0.0		2.2
70 of 226	Expected	2.0		2.0						1.0			3.0		1.0	2.0	1.0		5.0
	Actual	1.9		2.0						1.1			2.9		1.0	2.1	0.0		5.0
71 of 226	Expected	2.0		4.0		1.0			1.0	1.0			1.0		1.0	2.0			4.0
	Actual	2.0		3.9		1.1			1.1	1.1			0.9		0.9	2.0			4.0
72 of 226	Expected	1.0		4.0	1.0	1.0			1.0	3.0					2.0	1.0		1.0	2.0
	Actual	1.0		4.1	0.0	1.0			1.0	3.1					1.8	1.0		1.0	2.1
73 of 226	Expected			3.0	1.0	3.0			1.0	3.0	1.0		1.0	1.0	1.0	1.0		1.0	
	Actual			3.0	0.0	3.0			1.0	3.0	1.1		1.0	1.0	1.0	0.9		1.0	

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)
74 of 226	Expected			1.0	2.0	4.0		1.0		3.0	1.0		2.0	1.0	1.0			1.0	
	Actual			1.1	0.0	4.1		1.0		3.0	1.1		1.9	1.0	0.9			1.0	
75 of 226	Expected			1.0	1.0	5.0	2.0	1.0		3.0	1.0		3.0						
	Actual			0.8	0.0	4.8	2.0	1.1		3.0	1.1		3.1						
76 of 226	Expected	1.0		2.0		3.0	2.0	1.0		3.0			3.0		1.0			1.0	
	Actual	1.1		2.1		2.9	2.0	1.0		3.0			3.1		0.8			1.1	
77 of 226	Expected	1.0		5.0		1.0	1.0			3.0			2.0	1.0	1.0			1.0	1.0
	Actual	1.0		5.0		1.0	1.0			2.9			2.0	1.1	1.0			1.0	1.1
78 of 226	Expected	2.0		4.0		1.0				3.0			1.0	1.0	1.0	1.0		1.0	2.0
	Actual	2.0		4.0		1.0				3.0			1.0	1.0	0.9	1.0		1.0	2.2
79 of 226	Expected	1.0		2.0		2.0		1.0	1.0	2.0				2.0		1.0		3.0	2.0
	Actual	1.0		2.0		2.0		1.1	1.0	1.9				2.0		1.0		3.0	2.0
80 of 226	Expected	1.0		2.0		1.0		1.0	2.0	1.0			1.0	1.0		3.0		3.0	1.0
	Actual	0.9		2.2		1.0		1.0	2.0	1.0			1.1	1.0		2.8		2.9	1.0
81 of 226	Expected	2.0		2.0		1.0	1.0	1.0	2.0				2.0		1.0	3.0		2.0	
	Actual	2.1		2.1		1.0	1.1	1.0	1.8				2.2		0.8	2.9		2.0	
82 of 226	Expected	2.0		2.0	2.0		2.0		1.0				2.0		2.0	2.0		1.0	1.0
	Actual	1.9		1.9	0.0		2.0		1.0				1.9		1.9	1.9		1.1	1.2
83 of 226	Expected	1.0		1.0	2.0	1.0	2.0	1.0			1.0		1.0	1.0	2.0	1.0		1.0	2.0
	Actual	0.9		1.2	0.0	1.0	1.9	1.0			1.1		0.9	1.0	1.9	1.0		1.0	2.2
84 of 226	Expected			3.0	2.0	1.0	1.0	1.0	1.0	1.0				1.0	2.0			1.0	2.0
	Actual			2.8	0.0	0.8	1.1	1.0	1.1	1.0	1.0			1.1	1.8			0.9	2.3
85 of 226	Expected		1.0	3.0	1.0	1.0	1.0	1.0	1.0	1.0				1.0	2.0	1.0			3.0
	Actual		1.1	3.1	0.0	0.9	1.0	1.0	1.0	1.1				1.0	1.8	1.0			3.2
86 of 226	Expected		1.0	2.0	1.0		1.0	1.0	1.0	1.0			1.0		4.0	2.0			2.0
	Actual		1.0	1.9	0.0		0.9	1.1	1.1	1.0			1.1		3.8	1.9			2.2
87 of 226	Expected		3.0	1.0	1.0			1.0	2.0				1.0		3.0	1.0		2.0	2.0
	Actual		3.0	1.1	0.0			1.0	2.0				1.0		2.8	1.0		2.0	2.1
88 of 226	Expected		2.0	1.0			1.0	1.0	2.0		1.0		1.0	1.0	4.0			2.0	1.0
	Actual		2.0	1.1			1.0	0.9	1.9		1.0		1.0	1.1	3.9			1.9	1.1
89 of 226	Expected		1.0	2.0			2.0	1.0	1.0		1.0			1.0	4.0		1.0	2.0	1.0
	Actual		1.0	2.0			1.9	1.1	1.0		1.0			1.0	4.1		0.0	1.9	1.1
90 of 226	Expected			1.0			3.0	1.0	1.0	1.0	2.0			1.0	5.0		1.0	1.0	
	Actual			1.0			2.8	1.0	1.0	1.1	2.0			0.9	5.1		0.0	1.0	
91 of 226	Expected			1.0	1.0		1.0	1.0	1.0	1.0	1.0		2.0	1.0	4.0	1.0	1.0	1.0	
	Actual			1.1	0.0		1.0	1.0	1.0	1.1	1.1		2.0	1.0	3.8	0.9	0.0	1.0	
92 of 226	Expected			2.0	1.0		1.0			2.0	2.0		3.0	1.0	3.0	1.0		1.0	
	Actual			2.0	0.0		1.0			2.0	2.0		3.1	1.0	3.0	0.9		1.1	
93 of 226	Expected			2.0	1.0	1.0			1.0	1.0	3.0		4.0	1.0	2.0	1.0			
	Actual			1.9	0.0	1.0			1.1	1.0	3.1		4.1	1.0	2.1	1.0			
94 of 226	Expected			2.0	1.0	2.0			1.0	1.0	3.0		3.0		1.0	2.0			1.0
	Actual			1.9	0.0	2.0			0.9	1.0	3.2		3.2		0.9	2.0			1.2
95 of 226	Expected			1.0	2.0	1.0	1.0		1.0		2.0		2.0	1.0	2.0	2.0			2.0
	Actual			1.2	0.0	0.9	1.0		1.0		2.0		2.0	1.0	1.8	1.8			2.2
96 of 226	Expected	1.0		1.0	1.0	2.0	1.0			1.0			2.0	2.0	2.0	2.0			2.0
	Actual	1.0		1.1	0.0	1.8	1.0			1.1			2.0	2.0	1.8	1.8			2.1
97 of 226	Expected	1.0		1.0	1.0	1.0	1.0	1.0		1.0			1.0	2.0	2.0	2.0	1.0	2.0	
	Actual	1.0		1.0	0.0	0.9	1.0	1.0		1.0			1.1	2.0	2.1	1.9	0.0	2.0	
98 of 226	Expected	2.0				1.0	1.0	1.0	1.0	2.0				1.0	1.0	3.0	1.0	2.0	1.0
	Actual	2.1				1.0	1.1	1.0	1.1	1.9				1.0	1.0	3.0	0.0	2.1	1.0
99 of 226	Expected	1.0				1.0	1.0	1.0	1.0	1.0					2.0	3.0	1.0	3.0	2.0
	Actual	1.1				1.1	0.9	1.0	1.1	1.1					1.8	2.9	0.0	2.8	2.1
100 of 226	Expected	1.0		1.0		1.0	3.0		2.0	1.0					2.0	2.0	1.0	1.0	2.0
	Actual	1.0		1.1		0.9	2.8		1.8	1.1					1.9	2.2	0.0	1.0	2.2
101 of 226	Expected			1.0		1.0	2.0		1.0					2.0	3.0	2.0	1.0	1.0	3.0
	Actual			0.9		1.0	1.9		1.0					2.0	3.1	2.0	0.0	1.1	3.1
102 of 226	Expected		1.0	1.0		1.0	2.0		2.0				1.0	2.0	3.0	1.0		1.0	2.0
	Actual		1.0	1.0		1.0	2.0		2.0				1.1	2.0	2.9	1.0		1.0	2.1
103 of 226	Expected		1.0	3.0		1.0	1.0		1.0	2.0			1.0	2.0	2.0			1.0	2.0
	Actual		1.0	3.1		1.0	1.0		1.0	2.1			1.0	1.8	2.0			1.0	2.1

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)
104 of 226	Expected		1.0	4.0	1.0	1.0			2.0	2.0	1.0		1.0		1.0	1.0		1.0	1.0
	Actual		1.0	4.0	0.0	0.9			2.0	2.0	1.0		1.1		0.8	1.0		1.2	1.1
105 of 226	Expected			4.0	1.0		1.0		1.0	2.0	1.0					2.0		3.0	2.0
	Actual			3.8	0.0		1.1		1.0	1.9	1.0					1.9		3.1	2.1
106 of 226	Expected		1.0	2.0			2.0		3.0		1.0				2.0	2.0		3.0	1.0
	Actual		1.1	1.9			2.1		2.5		0.9				1.9	1.8		3.0	1.2
107 of 226	Expected	1.0	1.0	2.0		1.0	3.0		2.0	1.0					3.0	1.0		1.0	1.0
	Actual	1.0	1.0	2.0		1.0	3.0		1.4	1.0					2.8	1.0		1.0	1.1
108 of 226	Expected	1.0	1.0	1.0		1.0	2.0		3.0	1.0					4.0	1.0		1.0	1.0
	Actual	1.0	0.9	0.9		0.8	2.1		2.0	1.1					3.8	1.0		1.1	1.2
109 of 226	Expected	1.0		3.0		1.0	3.0		1.0	2.0					3.0	1.0		1.0	1.0
	Actual	1.0		3.0		0.8	3.1		1.0	1.9					3.1	1.0		1.0	1.2
110 of 226	Expected			3.0			3.0		1.0	2.0	1.0		1.0		2.0	1.0		1.0	2.0
	Actual			2.9			3.0		0.9	2.0	1.0		1.1		2.0	0.9		1.0	2.2
111 of 226	Expected			4.0			3.0		1.0	2.0	1.0		2.0		2.0	1.0			1.0
	Actual			3.9			2.8		1.1	2.0	1.0		2.0		1.8	1.0			1.2
112 of 226	Expected			3.0	1.0		2.0		2.0		1.0		2.0	1.0	1.0	2.0			2.0
	Actual			3.2	0.0		2.1		1.9		1.0		2.1	1.1	0.9	1.9			2.0
113 of 226	Expected	1.0		3.0	1.0	2.0	1.0		2.0				1.0	2.0		2.0			2.0
	Actual	1.0		3.0	0.0	2.0	1.0		1.8				1.1	2.0		1.8			1.9
114 of 226	Expected	1.0		2.0	1.0	4.0			1.0					2.0	1.0	1.0		1.0	3.0
	Actual	1.0		2.0	0.0	4.0			1.1					1.9	0.9	0.8		1.1	3.3
115 of 226	Expected	3.0		1.0		3.0	1.0		2.0			1.0		1.0	1.0	1.0		1.0	2.0
	Actual	3.0		1.1		3.0	1.1		1.7			1.0		1.0	0.9	0.9		1.0	2.2
116 of 226	Expected	2.0	1.0	1.0		3.0	1.0		2.0			1.0			2.0	1.0		2.0	1.0
	Actual	1.9	1.1	1.2		2.8	1.0		1.5			0.9			2.0	0.9		1.9	1.2
117 of 226	Expected	2.0	1.0	2.0		2.0	2.0			3.0		1.0			1.0	1.0		1.0	1.0
	Actual	1.9	1.1	1.9		1.9	2.1			3.1		1.0			0.9	0.9		1.1	1.1
118 of 226	Expected		1.0	3.0		3.0	1.0			4.0			1.0	1.0	1.0				2.0
	Actual		0.9	3.0		2.9	1.0			3.8			1.2	1.0	1.0				2.1
119 of 226	Expected			3.0		2.0	2.0			4.0			1.0	1.0	1.0				2.0
	Actual			3.1		2.1	2.1			4.0			1.0	1.0	0.9				2.1
120 of 226	Expected	1.0		4.0	1.0		2.0			1.0			1.0	1.0	1.0	2.0		2.0	1.0
	Actual	1.0		3.8	0.0		2.1			1.0			1.1	1.0	0.8	2.1		2.0	1.1
121 of 226	Expected	1.0		4.0	1.0		2.0					1.0			2.0	3.0		1.0	2.0
	Actual	1.0		4.3	0.0		2.1					1.0			1.8	2.9		1.0	2.1
122 of 226	Expected	2.0		3.0	2.0		1.0		1.0			1.0	1.0		1.0	3.0		1.0	1.0
	Actual	1.9		3.1	0.0		1.2		0.8			1.0	1.2		0.9	2.8		1.1	1.1
123 of 226	Expected	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	1.1		1.9	0.0		2.1		1.8	1.1		0.8	1.0	1.1	2.0	0.8		0.9	1.2
124 of 226	Expected	1.0	2.0	2.0	1.0		2.0		2.0	1.0				2.0	3.0				1.0
	Actual	1.0	2.2	1.9	0.0		1.9		1.8	1.0				2.1	2.8				1.1
125 of 226	Expected	1.0	2.0	3.0			1.0		2.0	1.0				2.0	4.0				1.0
	Actual	1.0	2.1	2.9			1.0		2.0	1.0				2.0	3.8				1.1
126 of 226	Expected	2.0	1.0	4.0			1.0		3.0	1.0				1.0	3.0	1.0			
	Actual	2.1	1.0	3.9			1.1		2.4	1.1				1.0	2.8	1.0			
127 of 226	Expected	2.0		3.0			1.0		4.0	1.0				1.0	3.0	1.0	1.0		
	Actual	1.9		3.0			1.1		3.2	1.1				1.0	2.9	1.0	0.0		
128 of 226	Expected	1.0		2.0		1.0			2.0	1.0				1.0	3.0	3.0	1.0		2.0
	Actual	1.0		2.0		1.0			2.0	1.1				1.0	2.9	2.9	0.0		2.0
129 of 226	Expected			1.0		3.0			2.0	1.0				1.0	2.0	3.0	1.0	1.0	2.0
	Actual			1.1		3.0			1.8	1.1				0.8	1.8	2.8	0.0	1.2	2.2
130 of 226	Expected					3.0			2.0	1.0				1.0	2.0	3.0		1.0	4.0
	Actual					2.8			1.9	1.0				1.1	1.9	2.9		1.0	3.9
131 of 226	Expected	1.0		1.0	1.0	1.0			2.0	1.0				1.0	1.0	3.0		2.0	3.0
	Actual	1.1		1.1	0.0	1.0			1.8	1.0				1.0	0.8	3.1		2.1	3.1
132 of 226	Expected	1.0	1.0	3.0	2.0		1.0		1.0					2.0		2.0		1.0	3.0
	Actual	1.0	1.1	2.9	0.0		1.0		0.5					1.8		1.8		1.1	2.7
133 of 226	Expected	1.0	1.0	3.0	3.0		1.0			2.0	2.0			1.0		1.0		1.0	1.0
	Actual	0.9	1.1	2.8	0.0		1.0			2.1	2.1			1.1		0.9		1.0	1.0

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)
134 of 226	Expected	1.0	1.0	3.0	2.0	1.0	1.0			2.0	2.0			1.0	1.0	1.0		1.0	
	Actual	1.1	1.0	2.8	0.0	1.0	1.0			2.0	2.0			1.0	0.9	1.0		1.1	
135 of 226	Expected	2.0		2.0	1.0	2.0			1.0	2.0	3.0				1.0	2.0		1.0	
	Actual	1.9		2.0	0.0	2.0			1.0	2.2	3.3				0.9	1.8		1.1	
136 of 226	Expected	3.0	1.0	1.0	1.0	1.0		1.0	1.0	2.0	1.0				2.0	2.0		1.0	
	Actual	2.9	1.1	1.0	0.0	1.0		1.1	1.0	2.1	0.9				2.0	2.0		0.9	
137 of 226	Expected	2.0	1.0	3.0		2.0		1.0	1.0	3.0					1.0	2.0			1.0
	Actual	2.1	1.0	3.1		1.9		1.1	0.9	3.0					0.9	1.8			1.2
138 of 226	Expected	1.0	1.0	2.0		1.0		1.0		3.0		1.0	1.0		3.0	2.0			1.0
	Actual	1.0	0.9	1.9		1.0		0.9		3.0		1.1	1.2		2.8	2.0			1.2
139 of 226	Expected	1.0		4.0		1.0				1.0	1.0	2.0			4.0	2.0			1.0
	Actual	1.0		3.8		1.1				1.0	0.9	2.1			3.9	1.9			1.0
140 of 226	Expected	2.0		3.0						2.0	1.0	2.0			4.0	2.0			1.0
	Actual	2.1		3.1						2.0		1.1	2.0		4.0	1.8			1.0
141 of 226	Expected	2.0		4.0			1.0			2.0			2.0		3.0	1.0		1.0	1.0
	Actual	1.8		4.0			1.0			2.0			2.0		2.8	1.0		1.1	1.1
142 of 226	Expected	1.0		3.0		1.0	1.0			2.0			1.0	1.0	3.0	1.0		1.0	2.0
	Actual	0.8		2.9		1.0	1.0			2.1			1.1	1.1	2.8	0.9		1.0	2.2
143 of 226	Expected		2.0	3.0		1.0	1.0		1.0	2.0				1.0	4.0			1.0	1.0
	Actual		2.1	3.0		1.0	1.0		1.0	1.9				1.0	4.0			1.0	1.1
144 of 226	Expected	1.0	4.0	1.0		1.0	1.0		2.0	1.0				1.0	4.0				1.0
	Actual	1.2	4.1	1.0		0.9	1.1		1.9	0.9				1.0	4.0				1.0
145 of 226	Expected	2.0	3.0	2.0		1.0	1.0		2.0	3.0					3.0				
	Actual	1.9	3.0	2.1		1.0	1.0		1.9	3.2					3.0				
146 of 226	Expected	2.0	1.0	1.0		1.0	1.0		1.0	3.0	1.0		1.0		2.0	1.0			2.0
	Actual	2.0	0.8	1.1		1.0	1.0		1.0	3.1	1.1		1.1		1.8	1.1			2.0
147 of 226	Expected			1.0		1.0	2.0			4.0	1.0		1.0		2.0	2.0			3.0
	Actual			1.1		1.0	2.1			4.0	1.0		1.0		1.8	2.0			2.9
148 of 226	Expected			2.0			2.0			1.0	2.0				3.0	2.0		1.0	4.0
	Actual			2.1			2.0			1.0	2.0				2.8	1.9		1.0	3.6
149 of 226	Expected			2.0	1.0		3.0			2.0	2.0				2.0	2.0		1.0	2.0
	Actual			2.0	0.0		3.0			2.1	2.1				1.8	1.9		1.0	2.1
150 of 226	Expected	2.0		2.0	2.0		1.0		1.0	2.0	2.0				2.0	1.0		1.0	1.0
	Actual	2.2		1.8	0.0		1.1		1.1	2.2	1.8				1.8	1.0		1.0	1.0
151 of 226	Expected	3.0		2.0	1.0	1.0	2.0		1.0	2.0	1.0				1.0	1.0		2.0	
	Actual	3.0		2.1	0.0	1.0	2.3		1.1	2.0	0.9				0.9	0.9		2.1	
152 of 226	Expected	3.0		2.0	1.0	1.0	2.0		1.0	2.0		1.0		1.0				2.0	1.0
	Actual	2.8		2.0	0.0	1.0	2.1		1.0	2.0		1.0		1.0				2.0	1.1
153 of 226	Expected	3.0		2.0		2.0	2.0		1.0	1.0	1.0		1.0					2.0	2.0
	Actual	3.0		2.0		2.0	2.0		1.0	1.0	0.9		1.0					2.0	2.1
154 of 226	Expected	3.0	1.0	1.0		1.0	1.0		1.0	1.0	3.0		1.0			1.0		1.0	2.0
	Actual	3.0	1.1	1.0		1.0	1.0		0.9	0.9	3.0		1.0			1.0		1.1	2.0
155 of 226	Expected	3.0	1.0	1.0		1.0	3.0		1.0	1.0	2.0				1.0	1.0		1.0	1.0
	Actual	2.9	1.0	1.1		1.1	2.9		1.0	1.0	1.9				0.9	0.9		1.0	1.1
156 of 226	Expected	1.0					5.0		1.0	3.0	3.0				1.0	1.0		1.0	1.0
	Actual	1.1					4.8		1.1	2.9	2.8				1.0	1.0		1.0	1.0
157 of 226	Expected	3.0					4.0		2.0	3.0	1.0				2.0	1.0			1.0
	Actual	3.0					3.9		2.0	2.9	1.0				1.9	1.1			1.1
158 of 226	Expected	4.0					2.0		1.0	4.0			1.0	1.0	2.0	1.0			1.0
	Actual	4.0					2.0		1.0	4.0			1.0	1.0	1.8	1.0			1.1
159 of 226	Expected	5.0	1.0	1.0		1.0			1.0	3.0			1.0	1.0	2.0			1.0	
	Actual	4.8	1.0	1.1		1.0			1.0	3.0			1.0	1.0	1.9			1.1	
160 of 226	Expected	3.0	1.0	2.0		2.0				4.0			1.0		1.0	1.0		1.0	1.0
	Actual	2.9	1.0	2.1		2.0				4.0			1.0		0.8	1.0		1.1	1.1
161 of 226	Expected	2.0	1.0	3.0		4.0				3.0						1.0		1.0	2.0
	Actual	1.8	1.0	3.0		4.2				2.9						1.0		1.0	2.1
162 of 226	Expected	3.0		2.0		4.0			1.0	3.0	1.0				1.0	1.0			1.0
	Actual	3.0		2.1		3.9			1.0	3.1	1.0				0.9	1.0			1.1
163 of 226	Expected	3.0		3.0		3.0			2.0	2.0	2.0		1.0		1.0				
	Actual	3.0		3.0		3.1			2.0	1.9	1.8		1.1		1.0				

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)
164 of 226	Expected	4.0		3.0					3.0	1.0	1.0		2.0		2.0				1.0
	Actual	4.0		3.1					2.6	1.0	1.0		2.1		1.9				0.8
165 of 226	Expected	3.0		5.0					2.0		1.0		1.0		3.0				2.0
	Actual	2.8		4.8					1.7		1.1		1.1		2.9				1.7
166 of 226	Expected	3.0		2.0		2.0			2.0				1.0		3.0	2.0			2.0
	Actual	3.1		2.1		1.9			1.7				1.1		2.8	1.9			1.8
167 of 226	Expected	3.0		2.0		2.0		1.0	2.0						1.0	4.0			2.0
	Actual	3.2		1.8		1.9		1.1	2.0						0.9	4.2			2.1
168 of 226	Expected	3.0		1.0		2.0		1.0	3.0	1.0	1.0					4.0			1.0
	Actual	2.8		1.0		2.0		0.9	2.9	1.1	1.0					3.9			1.1
169 of 226	Expected	1.0		3.0		2.0		1.0	3.0	1.0	1.0					2.0			3.0
	Actual	1.1		2.9		1.9		1.1	3.0	1.0	0.9					2.1			2.2
170 of 226	Expected	2.0		4.0		3.0	1.0		1.0	2.0	1.0				1.0				2.0
	Actual	2.1		4.0		2.8	1.1		1.0	2.1	1.0				0.9				1.5
171 of 226	Expected	1.0		3.0		3.0	1.0	1.0		3.0					2.0	1.0			2.0
	Actual	1.0		2.9		3.0	1.0	1.0		3.1					2.0	1.0			1.6
172 of 226	Expected	2.0	1.0	2.0		2.0	1.0	2.0		3.0			1.0		2.0	1.0			
	Actual	2.0	1.1	1.9		1.8	1.1	2.2		3.2			1.0		1.8	1.0			
173 of 226	Expected	1.0	1.0	2.0		3.0		1.0	2.0	2.0			1.0		3.0	1.0			
	Actual	1.0	1.0	1.9		2.9		1.0	2.2	2.1			1.1		2.9	1.0			
174 of 226	Expected	2.0	1.0	3.0		2.0		1.0	3.0	1.0			1.0		2.0			1.0	
	Actual	1.0	1.2	3.1		2.0		1.1	3.2	1.2			1.0		1.8			1.1	
175 of 226	Expected	2.0	1.0	4.0		2.0			3.0	1.0					3.0			1.0	
	Actual	2.2	1.0	4.1		1.8			3.0	1.1					2.9			1.0	
176 of 226	Expected	1.0	2.0	4.0		3.0			2.0	2.0					1.0			1.0	1.0
	Actual	0.9	2.1	3.9		3.0			2.0	2.1					1.0			0.9	1.1
177 of 226	Expected	2.0	2.0	2.0		3.0	1.0		2.0	2.0					1.0	1.0			1.0
	Actual	2.1	2.1	2.0		2.8	1.0		2.0	2.1					0.8	0.9			1.1
178 of 226	Expected	3.0	2.0	3.0		2.0	1.0		1.0	3.0						1.0			1.0
	Actual	3.0	2.0	3.0		2.0	1.0		1.0	3.0						0.9			1.1
179 of 226	Expected	3.0	1.0	1.0		1.0	1.0		1.0	4.0			1.0		1.0	1.0			2.0
	Actual	3.0	0.9	1.1		1.0	1.0		0.9	4.0			1.1		0.9	0.9			2.2
180 of 226	Expected	3.0		2.0		2.0				2.0	1.0		1.0		1.0	1.0		1.0	3.0
	Actual	2.9		2.0		2.0				2.0	1.1		1.0		0.9	1.0		1.0	3.2
181 of 226	Expected		3.0	1.0		2.0	1.0			2.0	1.0				2.0	1.0		1.0	3.0
	Actual		3.1	1.0		1.8	1.1			2.1	1.0				2.0	1.0		1.0	3.0
182 of 226	Expected	1.0	3.0	1.0		3.0	1.0		1.0	1.0	2.0				1.0	1.0		1.0	1.0
	Actual	1.0	3.0	1.2		2.9	1.0		1.1	1.1	2.1				0.9	0.9		0.9	1.0
183 of 226	Expected	1.0	2.0	1.0	1.0	4.0	1.0		1.0	1.0	2.0				2.0				1.0
	Actual	1.0	1.9	1.1	0.0	3.9	0.9		1.1	1.0	2.0				2.0				1.1
184 of 226	Expected	1.0	1.0	2.0	1.0	4.0	1.0		1.0		2.0				2.0			1.0	1.0
	Actual	0.9	1.1	1.9	0.0	4.1	1.1		0.9		2.0				1.9			1.0	1.0
185 of 226	Expected		1.0	2.0	2.0	2.0	3.0				1.0		1.0		2.0	1.0		1.0	1.0
	Actual		1.0	2.0	0.0	2.0	3.1				1.0		1.0		1.9	0.9		1.0	1.0
186 of 226	Expected		1.0	2.0	1.0		3.0	1.0	2.0				2.0		2.0	1.0		1.0	1.0
	Actual		0.9	2.0	0.0		2.9	1.1	1.7				2.0		1.9	1.1		1.0	0.9
187 of 226	Expected	1.0		3.0	1.0		3.0	1.0	2.0				1.0	1.0	2.0	1.0			1.0
	Actual	1.0		2.9	0.0		3.3	1.0	1.7				1.0	1.0	1.8	1.0			0.8
188 of 226	Expected	1.0		2.0			1.0	1.0	2.0	3.0			2.0	1.0	2.0	1.0			1.0
	Actual	1.0		1.9			1.1	1.1	1.6	3.1			2.0	1.0	1.8	1.0			0.8
189 of 226	Expected	1.0		2.0			1.0	1.0		5.0			1.0	2.0	1.0	2.0			1.0
	Actual	1.1		2.0			1.0	1.1		4.9			1.1	1.9	0.8	1.9			1.1
190 of 226	Expected	1.0		2.0				1.0		4.0	2.0		1.0	1.0		2.0		1.0	2.0
	Actual	1.0		1.9				1.1		4.1	1.9		1.1	1.0		1.9		1.0	2.0
191 of 226	Expected	1.0		2.0	1.0		1.0		1.0	2.0	2.0			1.0	1.0	1.0	1.0	1.0	2.0
	Actual	1.1		2.1	0.0		1.2		0.8	2.0	2.0			1.0	0.9	0.9	0.0	1.0	2.0
192 of 226	Expected	1.0		2.0	1.0		3.0		2.0		2.0				1.0		1.0	2.0	2.0
	Actual	0.9		2.1	0.0		3.2		1.8		2.2				0.9		0.0	2.1	2.0
193 of 226	Expected		1.0	2.0	1.0	1.0	3.0		2.0	1.0				1.0	1.0			2.0	2.0
	Actual		1.0	2.1	0.0	1.0	3.0		1.9	1.0				1.0	0.8			2.2	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)
194 of 226	Expected		1.0	2.0		1.0	2.0		1.0	3.0				1.0	1.0			3.0	2.0
	Actual		0.9	2.0		1.1	1.9		1.1	2.9				0.9	1.0			3.0	2.2
195 of 226	Expected		2.0	3.0		1.0	1.0			3.0			1.0	1.0	1.0			1.0	3.0
	Actual		2.0	3.2		0.9	1.1			2.8			1.1	0.9	1.0			1.0	2.9
196 of 226	Expected		2.0	2.0			1.0			1.0		1.0	2.0		2.0	1.0		1.0	4.0
	Actual		1.9	2.0			1.1			1.0		1.0	2.1		1.8	1.0		0.9	4.2
197 of 226	Expected		3.0			1.0	1.0			1.0		1.0	2.0	2.0	1.0	1.0			4.0
	Actual		3.1			1.0	1.1			1.1		0.9	1.9	2.1	1.0	0.9			4.2
198 of 226	Expected		2.0	1.0		2.0				2.0		1.0	2.0	2.0	2.0				3.0
	Actual		2.0	1.1		2.0				2.1		0.9	2.0	2.0	1.9				3.2
199 of 226	Expected		1.0	3.0	1.0	1.0			1.0	2.0			1.0	2.0	1.0			1.0	3.0
	Actual		1.0	3.2	0.0	1.0			1.0	2.0			1.0	1.9	0.9			1.0	3.1
200 of 226	Expected			4.0	1.0	1.0			2.0				2.0		2.0	1.0		1.0	3.0
	Actual			4.1	0.0	0.9			2.1				2.0		2.0	0.9		1.0	3.3
201 of 226	Expected		1.0	3.0	1.0	1.0		1.0	1.0	1.0			1.0		1.0	2.0		1.0	3.0
	Actual		1.0	2.9	0.0	1.0		1.1	1.0	1.1			1.0		0.9	1.8		1.0	3.0
202 of 226	Expected		1.0	2.0		1.0		1.0	2.0	1.0			1.0	1.0	1.0	1.0		1.0	4.0
	Actual		1.0	2.0		1.1		1.0	1.8	1.1			0.9	1.0	1.0	0.9		1.1	3.9
203 of 226	Expected			3.0		1.0		1.0	1.0	2.0	1.0			1.0		2.0		1.0	4.0
	Actual			3.1		1.0		1.0	0.9	2.1	1.1			1.0		1.8		1.0	4.0
204 of 226	Expected	1.0		4.0		3.0			1.0	1.0	1.0		1.0	1.0		1.0		1.0	2.0
	Actual	1.1		4.0		3.0			0.9	1.1	1.0		1.0	1.0		0.9		1.0	2.1
205 of 226	Expected	1.0		2.0		3.0				2.0	3.0		1.0	1.0		1.0		1.0	2.0
	Actual	1.1		1.9		2.8				2.0	3.0		1.0	1.1		0.9		1.0	2.1
206 of 226	Expected	1.0		3.0		2.0				2.0	2.0		2.0	2.0		1.0		1.0	1.0
	Actual	1.0		3.1		1.9				2.1	2.1		1.9	2.0		1.0		1.0	1.1
207 of 226	Expected									2.0	2.0		2.0	3.0		2.0		2.0	1.0
	Actual									2.1	1.9		2.0	2.9		2.0		2.0	1.0
208 of 226	Expected			4.0		1.0				4.0			2.0	1.0	2.0	2.0		1.0	
	Actual			4.1		1.1				4.1			2.0	1.0	1.8	2.0		1.0	
209 of 226	Expected	1.0		2.0		3.0				5.0	1.0		1.0		2.0	1.0		1.0	
	Actual	1.1		2.1		2.8				5.2	1.0		1.0		2.1	0.9		1.0	
210 of 226	Expected	2.0		1.0		3.0				4.0	2.0		1.0		3.0	1.0			
	Actual	2.1		0.9		2.9				4.1	2.1		1.1		2.9	1.0			
211 of 226	Expected	2.0				4.0				3.0	2.0		1.0		1.0	3.0			1.0
	Actual	2.0				3.8				3.2	2.1		1.1		1.0	2.8			1.0
212 of 226	Expected	1.0		1.0		4.0	1.0		1.0	3.0			1.0		1.0	3.0			1.0
	Actual	0.9		1.1		4.1	1.1		1.1	2.9			0.9		0.9	2.9			1.1
213 of 226	Expected			2.0		3.0	1.0			2.0	2.0				1.0	3.0		1.0	2.0
	Actual			2.1		2.9	1.0			2.1	2.0				0.9	2.8		1.1	2.2
214 of 226	Expected			4.0		1.0	1.0			2.0	4.0	1.0			1.0	1.0		1.0	1.0
	Actual			4.1		1.1	1.0			1.9	4.1	1.1			0.8	1.0		1.0	1.1
215 of 226	Expected		1.0	4.0		1.0			1.0	3.0	1.0		1.0		1.0	1.0		2.0	1.0
	Actual		1.0	4.0		1.1			1.1	3.0	1.0		1.0		0.9	0.9		1.9	1.0
216 of 226	Expected		1.0	2.0		1.0			1.0	3.0	2.0		1.0	1.0			3.0	1.0	1.0
	Actual		1.0	2.0		1.0			1.0	2.8	2.0		1.0	1.0			0.0	1.0	1.2
217 of 226	Expected			1.0		1.0				3.0	1.0	1.0		1.0	1.0	1.0		4.0	1.0
	Actual			1.0		1.0				2.7	1.1	1.0		1.0	1.0	0.9		0.0	1.0
218 of 226	Expected									2.0	3.0			1.0	1.0	1.0		4.0	5.0
	Actual									1.4	3.2			0.9	1.1	1.0		0.0	3.3
219 of 226	Expected				1.0					2.0	5.0			2.0		2.0			5.0
	Actual				0.0					1.1	5.0			2.1		1.9			4.3
220 of 226	Expected				3.0		1.0			5.0			2.0		2.0	1.0			3.0
	Actual				0.0		1.1			4.7			1.8		1.8	1.2			2.2
221 of 226	Expected			1.0	7.0		2.0			3.0			1.0		1.0	1.0			1.0
	Actual			1.0	0.0		2.1			3.0			1.0		0.9	1.0			1.1
222 of 226	Expected		1.0	1.0	5.0		2.0			2.0		1.0			3.0	2.0			
	Actual		1.1	1.1	0.0		2.1			2.1		0.9			2.8	1.9			
223 of 226	Expected		1.0	2.0	6.0		3.0			1.0		1.0			2.0	1.0			
	Actual		1.1	2.2	0.0		3.2			0.9		0.9			2.1	1.0			

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)
224 of 226	Expected		1.0	1.0	3.0		2.0			1.0	1.0	1.0		1.0	3.0	2.0		1.0	
	Actual		1.0	1.1	0.0		1.9			1.1	1.0	1.0		1.0	2.8	2.0		1.0	
225 of 226	Expected			1.0	3.0	2.0	1.0			1.0	2.0		1.0	1.0	1.0	1.0		2.0	1.0
	Actual			0.9	0.0	2.0	1.0			1.0	2.1		1.0	1.0	1.0	0.9		2.0	1.1
226 of 226	Expected					3.0		1.0		1.0	2.0		1.0	1.0		1.0		2.0	2.0
	Actual					2.8		1.1		1.0	1.8		1.0	1.0		1.0		1.9	2.2

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

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

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