

Peptide Array, Human Coronavirus OC43 Spike (S) Glycoprotein

Catalog No. NR-53728

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Product Description:

The 226-peptide array spans the spike (S) glycoprotein of the OC43 strain of human coronavirus (HCoV-OC43; GenPept: [AAR01015](#)). Peptides are 17- or 18-mers, with 11 or 12 amino acid overlaps.

Lot: A4634-1 to A4634-226

Manufacturing Date: 11JUL2020

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-MFLILLISLPTAFVIG-17	1819.34	76.47	98.92%	93.3
2 of 226	17	7-ISLPTAFVIGDLKCTS-23	1736.07	52.94	80.26%	86.9
3 of 226	17	13-FAVIGDLKCTSDTSYIN-29	1847.08	47.06	86.41%	87.6
4 of 226	17	19-LKCTSDTSYINDKDTGP-35	1858.01	23.53	86.12%	82.5
5 of 226	17	25-TSYINDKDTGPPPISTD-41	1820.93	17.65	87.16%	87.4
6 of 226	17	31-KDTGPPPISTDVDVTN-47	1756.89	17.65	81.28%	87.0
7 of 226	17	37-PISTDVDVTNGLGTY-53	1815.95	35.29	80.03%	93.3
8 of 226	17	43-VDVTNGLGTYVLDREVY-59	1947.17	52.94	89.48%	88.1
9 of 226	17	49-LGTYVLDREVYLNNTLF-65	2051.36	58.82	80.64%	88.7
10 of 226	17	55-LDRVYLNNTLFLNGYYP-71	2062.34	52.94	80.16%	88.7
11 of 226	17	61-NTLFLNGYYPSTSGSTY-77	1899.03	35.29	80.33%	93.5
12 of 226	17	67-NGYYPSTSGSTYRNMALK-83	1923.12	35.29	92.74%	83.1
13 of 226	17	73-SGSTYRNMALKGSVLLS-89	1784.07	41.18	93.69%	82.0
14 of 226	17	79-NMALKGSVLLSRLWFKP-95	1960.43	52.94	97.33%	78.9
15 of 226	17	85-SVLLSRLWFKPPFLSDF-101	2052.46	52.94	91.99%	84.0
16 of 226	17	91-LWFKPPFLSDFINGIFA-107	2012.39	58.82	87.01%	88.5
17 of 226	17	97-FLSDFINGIFAKVKNTK-113	1942.30	47.06	96.95%	78.7
18 of 226	17	103-NGIFAKVKNTKVIKDRV-119	1930.33	41.18	98.96%	71.1
19 of 226	17	109-VKNTKVIKDRVMYSEFP-125	2054.44	41.18	96.99%	75.8
20 of 226	17	115-IKDRVMYSEFPAITIGS-131	1927.25	47.06	82.26%	83.1
21 of 226	17	121-YSEFPAITIGSTFVNTS-137	1834.01	41.18	96.31%	93.4
22 of 226	17	127-ITIGSTFVNTSYSVVVQ-143	1815.06	47.06	92.86%	93.3
23 of 226	17	133-FVNTSYSVVVQPRITNS-149	1911.15	41.18	94.19%	88.0
24 of 226	17	139-SVVVQPRITINSTQDGYN-155	1878.03	29.41	80.53%	87.7
25 of 226	17	145-RTINSTQDGYNKLGQLL-161	1921.14	29.41	80.12%	83.0
26 of 226	17	150-TQDGYNKLGQLLEVSV-166	1867.11	41.18	84.89%	87.7

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
27 of 226	17	156-KLQGLLEVSVCQYNMCE-172	1957.32	52.94	80.36%	88.2
28 of 226	17	162-EVSVCQYNMCEYPQTIC-178	2010.31	52.94	90.58%	93.9
29 of 226	17	168-YNMCEYPQTICHPNLGN-184	1997.26	41.18	92.09%	88.4
30 of 226	17	174-PQTICHPNLGNHRKELW-190	2043.35	29.41	93.18%	75.7
31 of 226	17	180-PNLGNHRKELWHLDTGV-196	1986.23	29.41	88.81%	75.2
32 of 226	17	186-RKELWHLDTGVVSCLYK-202	2047.41	47.06	98.47%	75.8
33 of 226	17	192-LDTGVVSCLYKRNFYD-208	1994.25	47.06	83.32%	83.5
34 of 226	17	198-SCLYKRNFYDVNADYL-214	2085.31	52.94	94.11%	84.2
35 of 226	17	204-NFTYDVNADYLYFHFYQ-220	2220.37	58.82	83.42%	89.4
36 of 226	17	210-NADYLYFHFYQEGGTFY-226	2135.26	52.94	92.51%	89.0
37 of 226	17	216-FHFYQEGGTFYAYFTDT-232	2094.21	47.06	81.01%	88.9
38 of 226	17	222-GGTFYAYFTDTGVVTKF-238	1874.08	47.06	92.59%	87.7
39 of 226	17	228-YFTDTGVVTKFLFNVYL-244	2027.34	58.82	89.64%	88.6
40 of 226	17	234-VVTKFLFNVYLGMAISH-250	1939.36	64.71	88.89%	83.1
41 of 226	17	240-FNVYLGMAISHYYVMPL-256	2018.42	70.59	84.46%	88.5
42 of 226	17	246-MALSHYYVMPLTCNSKV-262	1957.36	58.82	92.31%	83.3
43 of 226	17	252-YVMPLTCNSKVKNNGFTL-268	1915.31	47.06	95.51%	83.0
44 of 226	17	258-CNSKVKNNGFTLEYWVTP-274	1986.28	41.18	93.72%	83.5
45 of 226	17	264-NGFTLEYWVTPLSRQY-280	2075.30	41.18	93.46%	88.8
46 of 226	17	270-YWVTPLSRQYLLAFNQ-286	2100.40	52.94	91.74%	88.9
47 of 226	17	276-TSRQYLLAFNQDGIIFN-292	2000.25	47.06	81.46%	88.4
48 of 226	17	282-LAFNQDGIIFNAVDCMS-298	1858.13	58.82	97.37%	93.4
49 of 226	17	288-GIIFNAVDCMSDFMSEI-304	1892.21	58.82	89.02%	93.5
50 of 226	17	294-VDCMSDFMSEIKCKTQS-310	1952.29	41.18	93.55%	83.3
51 of 226	17	300-FMSEIKCKTQSIAPPTG-316	1838.19	35.29	97.48%	82.4
52 of 226	17	306-CKTQSIAPPTGVYELNG-322	1778.02	35.29	84.19%	87.2
53 of 226	17	312-APPTGVYELNGYTVQPI-328	1819.04	41.18	80.05%	93.3
54 of 226	17	318-YELNGYTVQPIADVYRR-334	2057.29	47.06	96.20%	84.0
55 of 226	17	324-TVQPIADVYRRKLNLPN-340	1997.33	41.18	83.48%	79.2
56 of 226	17	330-DVYRRKLNLPNCNIEAW-346	2104.42	47.06	80.10%	80.1
57 of 226	17	336-LNLPNCNIEAWLNDKSV-352	1943.22	47.06	81.52%	88.1
58 of 226	17	342-NIEAWLNDKSVSPLNW-358	1983.22	41.18	95.20%	88.3
59 of 226	17	348-NDKSVSPLNWERKTF-364	2005.23	23.53	87.41%	79.3
60 of 226	17	354-SPLNWERKTFSNCFNM-370	2088.36	35.29	88.38%	84.2
61 of 226	17	360-RKTFSNCFNMSSLMSF-376	2014.34	41.18	92.20%	83.7
62 of 226	17	366-CNFMSSLMSFIQADSF-382	1942.23	52.94	95.58%	93.7
63 of 226	17	372-SLMSFIQADSFTCNNID-388	1906.13	47.06	82.61%	93.5
64 of 226	17	377-IQADSFTCNNIDAANKIY-393	1887.10	52.94	87.61%	87.8
65 of 226	17	383-TCNNIDAANKIYGMCFS-399	1838.12	52.94	91.81%	87.5
66 of 226	17	389-AAKIYGMCFSITIDKF-405	1895.27	58.82	87.61%	82.9
67 of 226	17	395-MCFSSITIDKFAIPNGR-411	1900.26	47.06	80.06%	82.9
68 of 226	17	401-TIDKFAIPNGRKVDLQL-417	1928.27	41.18	89.69%	78.6
69 of 226	17	407-IPNGRKVDLQLGNLGYL-423	1870.19	41.18	93.77%	82.6
70 of 226	17	413-VDLQLGNLGYLQSFNYR-429	2000.24	47.06	96.97%	88.4
71 of 226	17	419-NLGYLQSFNYRIDTTAT-435	1977.16	41.18	80.87%	88.3

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
72 of 226	17	425-SFNRYRIDTTATSCQLYY-441	2046.23	47.06	97.67%	88.7
73 of 226	17	431-DTTATSCQLYYNLPAAAN-447	1846.00	47.06	80.62%	93.4
74 of 226	17	437-CQLYYNLPAAANVSVSRLF-453	1945.23	58.82	85.03%	88.1
75 of 226	17	443-LPAAANVSVSRLFNPSTWN-459	1860.07	41.18	89.19%	87.6
76 of 226	17	449-SVSRLFNPSTWNKRFGLFI-465	2043.32	35.29	88.10%	79.6
77 of 226	17	455-PSTWNKRFGLFIEDSVFK-471	2058.33	35.29	80.15%	79.7
78 of 226	17	461-RFGLFIEDSVFKPRPAGV-477	1922.23	41.18	92.20%	78.6
79 of 226	17	467-DSVFKPRPAGVLTNHDV-483	1852.09	35.29	92.58%	77.9
80 of 226	17	473-RPAGVLTNHDVVYAQHC-489	1880.12	47.06	80.12%	78.2
81 of 226	17	479-TNHDVVYAQHCFKAPKN-495	1972.22	41.18	80.09%	75.1
82 of 226	17	485-YAQHCFKAPKNFCPCKL-501	1998.43	52.94	81.40%	75.3
83 of 226	17	491-KAPKNFCPCKLNGSCVG-507	1766.15	41.18	94.88%	77.1
84 of 226	17	497-CPCKLNGSCVGSVGGPKN-513	1620.90	29.41	93.83%	80.5
85 of 226	17	503-GSCVGSVGGPKNNGIGTC-519	1507.67	23.53	81.98%	85.2
86 of 226	17	509-GPGKNNIGITCPAGTNY-525	1620.76	23.53	80.81%	86.1
87 of 226	17	515-GITCPAGTNYLTCDNL-531	1712.92	41.18	82.05%	92.9
88 of 226	17	521-AGTNYLTCDNLCTPDI-537	1811.02	41.18	81.78%	93.3
89 of 226	17	527-TCDNLCTPDPITFKATG-543	1797.05	35.29	84.41%	87.3
90 of 226	17	533-TPDPITFKATGTYKCPQ-549	1868.14	29.41	87.13%	82.6
91 of 226	17	539-FKATGTYKCPQTKSLVG-555	1829.15	35.29	86.44%	77.8
92 of 226	17	545-YKCPQTKSLVGIGEHCS-561	1850.15	35.29	95.55%	77.9
93 of 226	17	551-KSLVGIGEHCSGLAVKS-567	1684.99	41.18	87.52%	76.3
94 of 226	17	557-GEHCSGLAVKSDYCGGN-573	1696.84	35.29	86.51%	81.2
95 of 226	17	563-LAVKSDYCGGNSCTCRP-579	1774.03	41.18	81.91%	81.8
96 of 226	17	569-YCGGNSCTCRPQAFGLW-585	1863.13	47.06	94.35%	87.6
97 of 226	17	575-CTCRPQAFGLWSADSL-591	1858.16	52.94	82.66%	87.6
98 of 226	17	581-AFLGWSADSLQGDKN-597	1815.02	47.06	87.15%	87.4
99 of 226	17	587-ADSLQGDKNIFANFI-603	1859.12	52.94	90.37%	87.6
100 of 226	17	593-GDKNIFANFILHDVNS-609	1907.15	47.06	93.73%	82.9
101 of 226	17	599-FANFILHDVNSGLTCS-615	1839.07	47.06	81.62%	87.6
102 of 226	17	605-HDVNSGLTCSLDLQKAN-621	1802.95	29.41	80.77%	82.1
103 of 226	17	611-LTCSLDLQKANTDIILG-627	1806.08	41.18	92.90%	87.3
104 of 226	17	617-LQKANTDIILGVCVNYD-633	1879.17	52.94	92.31%	87.8
105 of 226	17	623-DIILGVCVNYDLYGILG-639	1840.17	64.71	92.91%	93.4
106 of 226	17	629-CVNYDLYGILGQGFVE-645	1903.18	58.82	93.87%	93.5
107 of 226	17	635-YGILGQGFVEVNATYY-651	1907.14	58.82	80.15%	93.5
108 of 226	17	641-GIFVEVNATYYNSWQNL-657	2018.21	52.94	96.81%	93.9
109 of 226	17	647-NATYYNSWQNLLYDSNG-663	2023.09	41.18	96.42%	93.9
110 of 226	17	653-SWQNLLYDSNGNLYGFR-669	2047.21	41.18	94.81%	88.7
111 of 226	17	659-YDSNGNLYGFRDYITNR-675	2068.18	35.29	89.35%	84.0
112 of 226	17	665-LYGFRDYITNRTFMIRS-681	2153.49	47.06	80.42%	80.5
113 of 226	17	671-YITNRTFMIRSCYSGRV-687	2067.42	47.06	83.25%	79.8
114 of 226	17	677-FMIRSCYSGRVSAAFHA-693	1903.22	58.82	93.87%	78.4
115 of 226	17	683-YSGRVSAAFHANSSEPA-699	1750.85	41.18	95.39%	81.7
116 of 226	17	689-AAFHANSSEPAALLFRNI-705	1858.10	52.94	90.89%	82.5

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
117 of 226	17	695-SSEPALLFRNIKCNYVF-711	2001.34	52.94	81.22%	83.6
118 of 226	17	701-LFRNIKCNYVFNNLSLTR-717	2102.45	47.06	85.58%	80.1
119 of 226	17	707-CNYVFNNLSLTRQLQPIN-723	2024.29	41.18	90.90%	88.6
120 of 226	17	713-NSLTRQLQPINYFDSYL-729	2072.30	41.18	88.42%	88.8
121 of 226	17	719-LQPINYFDSYLGCVVNA-735	1916.18	58.82	93.14%	93.6
122 of 226	17	725-FDSYLGCVVNAYNSTAI-741	1837.04	58.82	92.66%	93.4
123 of 226	17	731-CVVNAYNSTAISVQTCD-747	1787.99	52.94	91.59%	93.2
124 of 226	17	737-NSTAISVQTCDLTVGSG-753	1652.81	35.29	95.06%	92.7
125 of 226	17	743-VQTCDLTVGSGYCVDYS-759	1809.99	47.06	87.05%	93.3
126 of 226	17	749-TVGSGYCVDYSKNRRSR-765	1948.14	29.41	82.76%	74.9
127 of 226	17	755-CVDYSKNRRSRGAIITG-771	1884.11	29.41	89.46%	74.2
128 of 226	17	761-NRRSRGAIITGYRFTNF-777	2017.24	29.41	80.21%	75.5
129 of 226	17	767-AITTYRFTNFEPFTVN-783	1978.19	41.18	88.43%	88.3
130 of 226	17	773-RFTNFEPFTVNSVNDL-789	1987.17	35.29	94.68%	88.3
131 of 226	17	779-PFTVNSVNDLSEPVGGL-795	1744.93	35.29	86.53%	93.0
132 of 226	17	785-VNDLSEPVGGLYEIQIP-801	1843.07	41.18	91.70%	93.4
133 of 226	17	791-PVGGLYEIQIPSEFTIG-807	1820.08	41.18	83.29%	93.3
134 of 226	17	797-EIQIPSEFTIGNMEEFI-813	1997.26	41.18	81.25%	93.8
135 of 226	17	803-EFTIGNMEEFIQTSSPK-819	1958.18	29.41	95.49%	88.2
136 of 226	17	809-MEEFIQTSSPKVTIDCA-825	1899.18	41.18	84.51%	87.9
137 of 226	17	815-TSSPKVTIDCAAFVCGD-831	1713.96	47.06	96.44%	86.7
138 of 226	17	821-TIDCAAFVCGDYAACKS-837	1738.00	64.71	97.21%	86.9
139 of 226	17	827-FVCGDYAACKSQLVEYG-843	1853.10	58.82	80.23%	87.6
140 of 226	17	833-AACKSQLVEYGSFCDNI-849	1848.09	52.94	93.28%	87.6
141 of 226	17	839-LVEYGSFCDNINAILTE-855	1901.13	52.94	97.49%	93.5
142 of 226	17	845-FCDNINAILTEVNELL-861	1936.18	52.94	92.62%	93.6
143 of 226	17	851-AILTEVNELLDTTQLQV-867	1900.17	47.06	82.99%	93.5
144 of 226	17	857-NELLDTTQLQVANSLMN-873	1904.14	41.18	96.64%	93.5
145 of 226	17	863-TQLQVANSLMNGVTLST-879	1777.04	41.18	91.88%	93.1
146 of 226	17	869-NSLMNGVTLSTKLKDG-885	1777.08	35.29	87.10%	81.9
147 of 226	17	875-VTLSTKLKDG VNFVDD-891	1865.08	35.29	90.08%	82.6
148 of 226	17	881-LKDG VNFVDDINFSPV-897	1893.09	41.18	91.80%	87.9
149 of 226	17	887-FNVDDINFSPVLGCLGS-903	1797.03	47.06	80.13%	93.2
150 of 226	17	893-NFSPVLGCLGSECSKAS-909	1698.94	41.18	89.16%	86.7
151 of 226	17	899-GCLGSECSKASSRSAIE-915	1684.87	35.29	87.92%	81.1
152 of 226	17	905-CSKASSRSAIEDLLFDK-921	1870.12	41.18	92.96%	78.1
153 of 226	17	911-RSAIEDLLFDKVKLS-927	1948.26	47.06	89.48%	78.8
154 of 226	17	917-LLFDKVKLS-933	1943.27	58.82	95.99%	83.2
155 of 226	17	923-KLSDVGFVEAYNNCTGG-939	1773.94	41.18	82.37%	87.1
156 of 226	17	929-FVEAYNNCTGGAEIRD-945	1872.05	47.06	94.01%	87.7
157 of 226	17	935-NCTGGAEIRDLICVQSY-951	1842.09	47.06	97.16%	87.6
158 of 226	17	941-EIRDLICVQSYGKIKVL-957	1977.40	52.94	82.75%	79.1
159 of 226	17	947-CVQSYGKIKVLPPLSE-963	1874.28	47.06	86.01%	82.6
160 of 226	17	953-GIKVLPPLSENQISGY-969	1828.14	41.18	93.84%	87.5
161 of 226	17	959-PLLENQISGYTLAATS-975	1764.95	41.18	92.65%	93.1

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
162 of 226	17	964-NQISGYTLAATSASLFP-980	1740.93	47.06	96.35%	93.0
163 of 226	17	970-TLAATSASLFLWTAATAA-986	1691.95	64.71	91.52%	92.9
164 of 226	17	976-ASLFLWTAAGVVPFYL-992	1824.16	70.59	90.59%	93.3
165 of 226	17	982-WTAAAGVVPFYLVNQYRI-998	1969.27	64.71	90.41%	88.3
166 of 226	17	988-VPFYLVNQYRINGLGVT-1004	1953.27	52.94	93.38%	88.2
167 of 226	17	994-VQYRINGLGVTMDVLSQ-1010	1893.20	47.06	93.76%	87.9
168 of 226	17	1000-GLGVTMDVLSQNQKLI-1016	1787.12	47.06	90.17%	87.2
169 of 226	17	1006-DVLSQNQKLIANAFNNA-1022	1860.07	47.06	94.48%	87.6
170 of 226	17	1011-NQKLIANAFNNALYAIQ-1027	1906.18	58.82	96.08%	88.0
171 of 226	17	1017-NAFNNALYAIQEGFDAT-1033	1858.99	52.94	90.72%	93.5
172 of 226	17	1023-LYAIQEGFDATNSALVK-1039	1840.07	52.94	82.11%	87.6
173 of 226	17	1029-GFDATNSALVKIQAVVN-1045	1746.99	52.94	96.14%	87.0
174 of 226	17	1035-SALVKIQAVVNAEAL-1051	1711.00	64.71	96.79%	86.7
175 of 226	17	1040-IQAVVNAEALNLLQ-1056	1795.04	58.82	83.18%	93.2
176 of 226	17	1046-AEALNLLQQLSNRF-1062	1916.13	47.06	88.18%	88.0
177 of 226	17	1052-NLLQQLSNRFGAISAS-1068	1833.04	41.18	92.71%	87.5
178 of 226	17	1058-LSNRFGAISASLQEILS-1074	1806.06	47.06	91.60%	87.3
179 of 226	17	1064-AISASLQEILSRLDALE-1080	1829.09	52.94	89.15%	87.5
180 of 226	17	1069-LQEILSRLDALEAEAQI-1085	1912.18	52.94	92.59%	88.0
181 of 226	17	1075-RLDALEAEAQIDRLING-1091	1897.13	47.06	83.20%	82.9
182 of 226	17	1081-AEAQIDRLINGRLTALN-1097	1868.13	47.06	80.69%	82.6
183 of 226	17	1087-RLINGRLTALNAYVSQQ-1103	1917.20	47.06	98.69%	83.0
184 of 226	17	1093-LTALNAYVSQQLSDSTL-1109	1824.02	47.06	84.40%	93.3
185 of 226	17	1099-YVSQQLSDSTLVKFSAA-1115	1844.05	47.06	93.59%	87.6
186 of 226	17	1105-SDSTLVKFSAAQAMEKV-1121	1812.08	47.06	81.00%	82.2
187 of 226	17	1111-KFSAAQAMEKVNCEVKS-1127	1870.19	47.06	96.64%	78.1
188 of 226	17	1117-AMEKVNCEVKSQSSRIN-1133	1923.21	35.29	84.64%	78.6
189 of 226	17	1123-ECVKSQSSRINFCGNGN-1139	1843.04	29.41	80.99%	82.4
190 of 226	17	1129-SSRINFCGNGNHIISLV-1145	1831.09	41.18	81.46%	82.3
191 of 226	17	1135-CGNGNHIISLVQNAPYG-1151	1756.96	41.18	84.98%	87.0
192 of 226	17	1141-IISLVQNAPYGLYFIHF-1157	1995.35	64.71	80.52%	88.4
193 of 226	17	1147-NAPYGLYFIHFSYVPTK-1163	2017.31	52.94	81.89%	83.7
194 of 226	17	1153-YFIHFSYVPTKYVTARV-1169	2091.43	58.82	84.97%	79.9
195 of 226	17	1159-YVPTKYVTARVSPGLCI-1175	1867.24	52.94	85.07%	82.6
196 of 226	17	1165-VTARVSPGLCIAGDRGI-1181	1684.99	47.06	80.34%	81.1
197 of 226	17	1171-PGLCIAGDRGIAPKSGY-1187	1674.94	41.18	80.60%	81.0
198 of 226	17	1177-GDRGIAPKSGYFVNVNN-1193	1807.99	35.29	84.24%	82.2
199 of 226	17	1183-PKSGYFVNVNNTWMYTG-1199	1978.21	41.18	93.81%	88.3
200 of 226	17	1189-VNVNNTWMYTGSGYYYP-1205	2029.20	47.06	83.07%	93.9
201 of 226	17	1195-WMYTGSGYYYPEPITEN-1211	2071.23	41.18	95.76%	94.1
202 of 226	17	1201-GYYYPEPITENNVVMS-1217	1975.20	47.06	81.68%	93.8
203 of 226	17	1207-PITENNVVMSTCAVNY-1223	1854.14	52.94	97.83%	93.4
204 of 226	17	1213-VVMSTCAVNYTKAPYV-1229	1845.21	64.71	95.44%	87.6
205 of 226	17	1219-CAVNYTKAPYVMLNTSI-1235	1888.23	58.82	89.60%	87.8
206 of 226	17	1225-KAPYVMLNTSIPNLPDF-1241	1920.26	47.06	80.56%	88.0

Table 1: Peptide Analysis (continued)

Peptide	Length	Sequence	Molecular Weight (amu)	Hydrophobicity	Purity by HPLC ¹	Peptide Content ²
207 of 226	17	1231-LNTSIPNLPDFKEELDQ-1247	1973.18	29.41	90.62%	88.3
208 of 226	17	1237-NLPDFKEELDQWFKNQ-1253	2152.36	29.41	93.52%	84.5
209 of 226	17	1243-EELDQWFKNQTSVAPDL-1259	2020.19	35.29	94.63%	88.5
210 of 226	17	1249-FKNQTSVAPDLSLDYIN-1265	1925.13	41.18	80.26%	88.0
211 of 226	17	1255-VAPDLSLDYINVTFLDL-1271	1908.18	58.82	87.41%	93.5
212 of 226	17	1261-LDYINVTFLDLQVEMNR-1277	2083.40	52.94	87.41%	88.8
213 of 226	17	1267-TFLDLQVEMNRLQEAIK-1283	2048.40	47.06	90.52%	83.9
214 of 226	17	1273-VEMNRLQEAIKVLNQS-1289	2035.36	47.06	86.26%	83.8
215 of 226	17	1278-LQEAIKVLNQSINLKD-1294	1989.30	47.06	85.14%	83.5
216 of 226	17	1284-VLNQSYINLKDIGTYEY-1300	2033.26	47.06	89.44%	88.6
217 of 226	17	1290-INLKDIGTYEYVWKP-1306	2188.50	52.94	89.28%	84.7
218 of 226	17	1296-GTYEYVWKPWYVWLLI-1312	2279.65	70.59	80.22%	89.7
219 of 226	17	1302-VKWPWYVWLLICLAGVA-1318	2017.51	82.35	82.55%	88.5
220 of 226	17	1308-VWLLICLAGVAMLVLLF-1324	1874.48	94.12	81.85%	93.5
221 of 226	17	1314-LAGVAMLVLLFFICCCT-1330	1817.39	88.24	92.08%	93.3
222 of 226	17	1320-LVLLFFICCCTGCGTSC-1336	1783.26	70.59	80.13%	93.2
223 of 226	17	1326-ICCCTGCGTSCFKKCGG-1342	1671.07	47.06	94.52%	81.0
224 of 226	17	1332-CGTSCFKKCGGCCDDYT-1348	1791.06	41.18	81.52%	82.0
225 of 226	17	1338-KKCGGCCDDYTYQELV-1354	1882.12	41.18	91.39%	82.7
226 of 226	18	1344-CDDYTYQELVIKTS-1361	2102.22	33.33	89.81%	84.2

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	2.0					1.0		3.0	4.0		1.0	2.0	1.0	1.0	1.0			1.0
	Actual	2.1					1.0		2.2	4.0		1.0	1.9	1.0	0.9	1.1			0.9
2 of 226	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
	Actual	2.0		1.1	0.0		1.0		1.7	2.1	1.0		1.0	1.0	1.9	1.9			0.8
3 of 226	Expected	1.0		3.0	1.0		1.0		2.0	1.0	1.0		1.0		2.0	2.0		1.0	1.0
	Actual	0.9		3.1	0.0		1.0		1.8	1.1	1.1		0.9		1.9	2.0		1.1	0.6
4 of 226	Expected			4.0	1.0		1.0		1.0	1.0	2.0			1.0	2.0	3.0		1.0	
	Actual			3.9	0.0		0.9		1.0	1.1	2.0			1.2	1.9	2.9		1.0	
5 of 226	Expected			4.0			1.0		2.0		1.0			3.0	2.0	3.0		1.0	
	Actual			4.2			1.1		2.0		1.1			3.1	2.0	2.8		0.9	
6 of 226	Expected			4.0			1.0		1.0		1.0			3.0	1.0	4.0			2.0
	Actual			4.2			1.0		1.1		1.0			2.9	0.9	3.9			2.1
7 of 226	Expected			3.0			2.0		1.0	1.0				1.0	1.0	4.0		2.0	2.0
	Actual			3.1			2.0		1.0	1.0				1.0	0.9	3.9		2.0	2.1
8 of 226	Expected		1.0	3.0			2.0			2.0						2.0		3.0	4.0
	Actual		1.1	2.9			2.0			2.1						1.9		3.0	4.0
9 of 226	Expected		1.0	2.0			1.0			4.0			1.0			3.0		3.0	2.0
	Actual		1.0	2.1			1.0			4.0			1.0			3.0		2.8	2.1
10 of 226	Expected		1.0	3.0			1.0			4.0			1.0	1.0		2.0		3.0	1.0
	Actual		0.9	3.1			1.1			3.9	3.1		1.0	1.1		1.8		2.9	1.1
11 of 226	Expected			2.0			2.0			2.0			1.0	1.0	2.0	4.0		3.0	
	Actual			2.0			2.0			2.0			1.0	1.1	1.9	3.9		3.0	
12 of 226	Expected	1.0	1.0	2.0			2.0			1.0	1.0	1.0		1.0	2.0	2.0		3.0	
	Actual	1.1	1.0	2.0			1.9			1.1	1.2	0.9		1.0	1.8	1.8		2.9	
13 of 226	Expected	1.0	1.0	1.0			2.0			3.0	1.0	1.0			4.0	1.0		1.0	1.0
	Actual	1.0	1.0	1.0			2.0			3.0	1.1	0.9			3.8	1.0		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)
14 of 226	Expected	1.0	1.0	1.0			1.0			4.0	2.0	1.0	1.0	1.0	2.0		1.0		1.0
	Actual	0.9	1.0	1.0			1.0			3.9	2.0	0.9	1.0	1.2	1.9		0.0		1.1
15 of 226	Expected		1.0	1.0						4.0	1.0		3.0	2.0	3.0		1.0		1.0
	Actual		1.0	1.0						3.9	1.0		3.1	2.0	2.8		0.0		1.1
16 of 226	Expected	1.0		2.0			1.0		2.0	2.0	1.0		4.0	2.0	1.0		1.0		
	Actual	1.0		2.1			1.0		2.0	2.0	1.1		3.9	2.0	0.8		0.0		
17 of 226	Expected	1.0		3.0			1.0		2.0	1.0	3.0		3.0		1.0	1.0			1.0
	Actual	1.1		3.1			1.0		1.8	0.9	3.1		2.9		0.9	1.0			1.1
18 of 226	Expected	1.0	1.0	3.0			1.0		2.0		4.0		1.0			1.0			3.0
	Actual	1.0	1.0	2.9			1.1		2.0		4.0		1.1			1.0			3.2
19 of 226	Expected		1.0	2.0		1.0			1.0		3.0	1.0	1.0	1.0	1.0	1.0		1.0	3.0
	Actual		1.0	2.1		1.0			0.7		3.2	0.9	1.1	1.1	0.8	0.9		1.0	2.8
20 of 226	Expected	1.0	1.0	1.0		1.0	1.0		3.0		1.0	1.0	1.0	1.0	2.0	1.0		1.0	1.0
	Actual	1.0	1.0	1.2		1.0	0.9		2.9		1.2	1.0	0.9	0.9	2.0	0.8		0.9	1.2
21 of 226	Expected	1.0		1.0		1.0	1.0		2.0				2.0	1.0	3.0	3.0		1.0	1.0
	Actual	1.0		1.2		0.8	1.1		2.1				1.9	0.9	3.0	2.9		0.9	1.2
22 of 226	Expected			1.0		1.0	1.0		2.0				1.0		3.0	3.0		1.0	4.0
	Actual			0.9		1.0	1.0		2.1				0.9		2.9	3.1		1.1	3.7
23 of 226	Expected		1.0	2.0		1.0			1.0				1.0	1.0	3.0	2.0		1.0	4.0
	Actual		1.1	2.1		0.9			1.1				1.0	1.0	2.8	1.9		1.0	3.5
24 of 226	Expected		1.0	3.0		2.0	1.0		1.0					1.0	2.0	2.0		1.0	3.0
	Actual		1.0	3.1		2.0	1.1		1.0					1.0	1.8	1.9		1.1	2.5
25 of 226	Expected		1.0	3.0		2.0	2.0		1.0	3.0	1.0				1.0	2.0		1.0	
	Actual		0.9	3.1		2.1	2.0		1.0	3.2	1.2				1.0	1.9		0.9	
26 of 226	Expected			2.0	1.0	3.0	2.0			3.0	1.0				1.0	1.0		1.0	2.0
	Actual			2.0	0.0	3.0	2.1			3.1	0.9				1.0	0.9		1.0	2.2
27 of 226	Expected			1.0	2.0	4.0	1.0			3.0	1.0	1.0			1.0			1.0	2.0
	Actual			1.2	0.0	4.2	1.0			2.9	0.8	1.1			0.8			1.1	2.1
28 of 226	Expected			1.0	3.0	4.0			1.0			1.0		1.0	1.0	1.0		2.0	2.0
	Actual			1.1	0.0	3.9			1.0			1.0		1.1	0.9	0.9		2.1	2.1
29 of 226	Expected			3.0	2.0	2.0	1.0	1.0	1.0	1.0			1.0	2.0		1.0		2.0	
	Actual			3.0	0.0	2.0	1.1	1.0	1.1	1.1		0.9		2.1		1.0		1.8	
30 of 226	Expected		1.0	2.0	1.0	2.0	1.0	2.0	1.0	2.0	1.0			2.0		1.0	1.0		
	Actual		1.0	2.1	0.0	2.0	1.0	2.0	1.1	2.1	1.0			2.0		0.9	0.0		
31 of 226	Expected		1.0	3.0		1.0	2.0	2.0		3.0	1.0			1.0		1.0	1.0		1.0
	Actual		0.9	3.0		1.0	1.9	2.0		2.9	1.1			0.9		0.9	0.0		1.2
32 of 226	Expected		1.0	1.0	1.0	1.0	1.0	1.0		3.0	2.0				1.0	1.0	1.0	1.0	2.0
	Actual		1.0	1.0	0.0	1.0	1.1	1.0		3.0	2.0				0.9	0.9	0.0	1.1	2.0
33 of 226	Expected		1.0	3.0	1.0		1.0			2.0	1.0		1.0		1.0	2.0		2.0	2.0
	Actual		1.1	3.1	0.0		1.0			1.8	1.1		1.1		0.9	1.8		2.2	1.5
34 of 226	Expected	1.0	1.0	4.0	1.0					2.0	1.0		1.0		1.0	1.0		3.0	1.0
	Actual	1.0	1.0	4.0	0.0					2.1	1.1		1.0		0.8	1.0		2.9	1.1
35 of 226	Expected	1.0		4.0		1.0		1.0		1.0			3.0			1.0		4.0	1.0
	Actual	1.0		4.2		1.1		1.0		1.0			2.9			0.9		3.8	1.0
36 of 226	Expected	1.0		2.0		2.0	2.0	1.0		1.0			3.0			1.0		4.0	
	Actual	1.0		1.9		2.2	2.1	1.0		1.0			2.9			1.0		3.9	
37 of 226	Expected	1.0		1.0		2.0	2.0	1.0					4.0			3.0		3.0	
	Actual	1.1		1.2		1.9	2.0	0.9					3.9			3.0		3.0	
38 of 226	Expected	1.0		1.0			3.0				1.0		3.0			4.0		2.0	2.0
	Actual	1.0		1.1			2.8				1.1		2.8			4.1		1.8	1.4
39 of 226	Expected			2.0			1.0			2.0	1.0		3.0			3.0		2.0	3.0
	Actual			2.2			1.0			2.0	1.1		2.9			2.9		1.9	2.4
40 of 226	Expected	1.0		1.0			1.0	1.0		3.0	1.0	1.0	2.0		1.0	1.0		1.0	3.0
	Actual	1.1		1.1			1.0	1.1		3.1	1.1	0.9	1.9		0.9	0.9		0.9	2.2
41 of 226	Expected	1.0		1.0			1.0	1.0		3.0		2.0	1.0	1.0	1.0			3.0	2.0
	Actual	1.0		1.0			1.0	1.0		3.1		2.0	1.0	1.1	0.9			2.8	2.1
42 of 226	Expected	1.0		1.0	1.0			1.0		2.0	1.0	2.0		1.0	2.0	1.0		2.0	2.0
	Actual	1.0		1.2	0.0			1.0		2.0	1.2	1.9		1.0	1.8	0.8		1.9	2.2
43 of 226	Expected			2.0	1.0		1.0			2.0	2.0	1.0	1.0	1.0	1.0	2.0		1.0	2.0
	Actual			2.1	0.0		1.1			2.1	2.2	0.9	1.1	1.0	0.9	1.8		0.9	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)
44 of 226	Expected			2.0	1.0	1.0	1.0			1.0	2.0		1.0	1.0	1.0	2.0	1.0	1.0	2.0
	Actual			1.9	0.0	1.0	1.0			1.0	2.0		1.0	1.2	0.8	1.9	0.0	1.0	2.2
45 of 226	Expected		1.0	1.0		2.0	1.0			2.0			1.0	1.0	1.0	3.0	1.0	2.0	1.0
	Actual		1.0	1.0		2.0	1.0			2.1			1.0	1.0	0.8	2.8	0.0	2.0	1.2
46 of 226	Expected	1.0	1.0	1.0		2.0				3.0			1.0	1.0	1.0	2.0	1.0	2.0	1.0
	Actual	1.0	1.0	1.1		2.0				2.9			1.1	1.0	0.9	1.8	0.0	2.0	1.2
47 of 226	Expected	1.0	1.0	3.0		2.0	1.0		2.0	2.0			2.0		1.0	1.0		1.0	
	Actual	1.0	1.0	3.3		2.1	1.1		1.2	2.0			2.1		0.8	0.9		1.0	
48 of 226	Expected	2.0		4.0	1.0	1.0	1.0		2.0	1.0		1.0	2.0		1.0				1.0
	Actual	1.9		4.2	0.0	1.0	1.1		1.4	1.0		1.0	2.1		0.8				1.1
49 of 226	Expected	1.0		3.0	1.0	1.0	1.0		3.0			2.0	2.0		2.0				1.0
	Actual	1.0		3.0	0.0	1.0	1.0		2.5			2.1	2.2		1.8				1.0
50 of 226	Expected			2.0	2.0	2.0			1.0		2.0	2.0	1.0		3.0	1.0			1.0
	Actual			2.0	0.0	1.9			1.2		2.1	2.0	1.2		2.9	1.0			0.8
51 of 226	Expected	1.0			1.0	2.0	1.0		2.0		2.0	1.0	1.0	2.0	2.0	2.0			
	Actual	1.1			0.0	2.0	1.1		2.1		2.0	0.9	1.0	2.1	2.0	1.9			
52 of 226	Expected	1.0		1.0	1.0	2.0	2.0		1.0	1.0	1.0			2.0	1.0	2.0		1.0	1.0
	Actual	1.0		1.1	0.0	1.9	2.0		1.0	1.1	1.0			2.0	0.9	1.8		1.0	1.1
53 of 226	Expected	1.0		1.0		2.0	2.0		1.0	1.0				3.0		2.0		2.0	2.0
	Actual	0.9		1.1		2.1	2.0		1.1	1.0				2.9		1.8		1.9	2.1
54 of 226	Expected	1.0	2.0	2.0		2.0	1.0		1.0	1.0				1.0		1.0		3.0	2.0
	Actual	1.0	2.1	2.0		2.0	1.0		1.0	1.0				1.0		0.9		2.9	2.1
55 of 226	Expected	1.0	2.0	3.0		1.0			1.0	2.0	1.0			2.0		1.0		1.0	2.0
	Actual	1.0	2.0	3.0		1.0			1.1	2.1	1.1			2.1		0.9		1.0	2.0
56 of 226	Expected	1.0	2.0	4.0	1.0	1.0			1.0	2.0	1.0			1.0			1.0	1.0	1.0
	Actual	1.0	2.0	3.9	0.0	1.0			1.0	2.0	1.0			1.0			0.0	1.0	1.1
57 of 226	Expected	1.0		5.0	1.0	1.0			1.0	3.0	1.0			1.0	1.0		1.0		1.0
	Actual	1.0		5.2	0.0	1.1			1.0	3.1	1.0			1.0	1.0		0.0		1.0
58 of 226	Expected	1.0		4.0		1.0			1.0	2.0	1.0			2.0	2.0		2.0		1.0
	Actual	1.0		3.9		1.0			1.0	2.0	1.0			2.0	1.9		0.0		1.1
59 of 226	Expected		1.0	3.0		1.0				1.0	2.0		1.0	2.0	3.0	1.0	1.0	1.0	1.0
	Actual		1.1	3.2		1.0				0.9	1.8		1.1	2.1	3.1	1.0	0.0		0.9
60 of 226	Expected		1.0	4.0	1.0	1.0				1.0	1.0	1.0	2.0	1.0	2.0	1.0	1.0		
	Actual		1.0	4.0	0.0	1.0				1.0	1.0	1.0	2.0	1.0	1.9	1.0	0.0		
61 of 226	Expected		1.0	3.0	1.0					1.0	1.0	2.0	3.0		4.0	1.0			
	Actual		1.0	3.1	0.0					1.1	1.0	2.0	2.9		3.9	1.0			
62 of 226	Expected	1.0		3.0	1.0	1.0			1.0	1.0		2.0	3.0		4.0				
	Actual	1.0		3.0	0.0	1.0			1.0	1.1		2.0	3.1		3.8				
63 of 226	Expected	1.0		4.0	1.0	1.0			2.0	1.0		1.0	2.0		3.0	1.0			
	Actual	1.0		4.1	0.0	1.0			2.1	1.0		1.0	2.2		3.0	1.0			
64 of 226	Expected	3.0		4.0	1.0	1.0			3.0		1.0		1.0		1.0	1.0		1.0	
	Actual	3.0		4.1	0.0	1.0			3.0		1.1		1.1		0.9	1.0		1.0	
65 of 226	Expected	2.0		3.0	2.0		1.0		2.0	2.0	1.0	1.0	1.0		2.0	1.0		1.0	1.0
	Actual	1.9		3.1	0.0		1.0		2.1	1.1	1.0	1.1	1.1		1.9	0.8		1.1	
66 of 226	Expected	2.0		1.0	1.0		1.0		3.0		2.0	1.0	2.0		2.0	1.0		1.0	
	Actual	1.9		1.1	0.0		1.0		3.1		2.0	0.9	2.2		2.0	1.0		1.0	
67 of 226	Expected	1.0	1.0	2.0	1.0		1.0		3.0		1.0	1.0	2.0	1.0	2.0	1.0			
	Actual	0.9	0.9	2.0	0.0		0.9		3.1		1.1	1.2	2.2	0.9	2.0	1.1			
68 of 226	Expected	1.0	1.0	3.0		1.0	1.0		2.0	2.0	2.0		1.0	1.0		1.0			1.0
	Actual	1.0	1.0	2.9		1.0	1.0		2.0	2.1	2.0		1.0	1.0		0.9			1.1
69 of 226	Expected		1.0	3.0		1.0	3.0		1.0	4.0	1.0			1.0				1.0	1.0
	Actual		0.9	3.0		1.0	2.9		1.2	3.8	1.1			0.9				1.0	1.0
70 of 226	Expected		1.0	3.0		2.0	2.0			4.0			1.0		1.0			2.0	1.0
	Actual		1.1	3.0		2.0	2.0			3.8			1.1		0.8			2.1	1.0
71 of 226	Expected	1.0	1.0	3.0		1.0	1.0		1.0	2.0			1.0		1.0	3.0		2.0	
	Actual	1.1	1.0	3.1		1.0	1.0		1.1	2.0			1.1		0.8	3.0		2.0	
72 of 226	Expected	1.0	1.0	2.0	1.0	1.0			1.0	1.0			1.0		2.0	3.0		3.0	
	Actual	1.1	0.8	1.9	0.0	1.1			0.8	1.3			1.0		1.9	3.1		3.0	
73 of 226	Expected	3.0		3.0	1.0	1.0				2.0				1.0	1.0	3.0		2.0	
	Actual	3.1		3.2	0.0	1.0				2.0				1.1	0.9	2.8		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)
74 of 226	Expected	2.0	1.0	2.0	1.0	1.0				2.0			1.0	1.0	2.0			2.0	2.0
	Actual	1.9	1.1	2.0	0.0	0.9				1.9			1.1	1.0	1.8			1.9	2.2
75 of 226	Expected	2.0	1.0	3.0						1.0			1.0	2.0	3.0	1.0	1.0		2.0
	Actual	1.9	1.0	3.2						1.0			1.0	2.0	2.8	1.1	0.0		2.1
76 of 226	Expected		2.0	2.0			1.0		1.0		1.0		3.0	1.0	3.0	1.0	1.0		1.0
	Actual		1.9	2.0			1.0		1.0		1.1		2.9	1.0	2.9	0.9	0.0		1.1
77 of 226	Expected		1.0	2.0		1.0	1.0		1.0		2.0		3.0	1.0	2.0	1.0	1.0		1.0
	Actual		1.0	2.1		1.1	1.0		1.0		2.0		3.0	1.0	1.8	0.9	0.0		1.0
78 of 226	Expected	1.0	2.0	1.0		1.0	2.0		1.0		1.0		3.0	2.0	1.0				2.0
	Actual	1.0	1.8	1.1		1.0	1.9		1.0		1.1		2.8	2.0	0.9				2.2
79 of 226	Expected	1.0	1.0	3.0			1.0	1.0		1.0	1.0		1.0	2.0	1.0	1.0			3.0
	Actual	1.0	1.0	3.1			1.0	1.0		1.0	1.0		1.0	2.0	0.8	1.0			3.2
80 of 226	Expected	2.0	1.0	2.0	1.0	1.0	1.0	2.0		1.0				1.0		1.0		1.0	3.0
	Actual	2.0	0.9	2.1	0.0	1.1	1.0	2.1		1.0				1.0		1.0		1.0	2.6
81 of 226	Expected	2.0		3.0	1.0	1.0		2.0			2.0		1.0	1.0		1.0		1.0	2.0
	Actual	1.9		3.0	0.0	1.0		1.9			2.1		1.1	1.1		0.9		1.0	1.4
82 of 226	Expected	2.0		1.0	3.0	1.0		1.0		1.0	3.0		2.0	2.0				1.0	
	Actual	1.8		1.0	0.0	0.9		1.0		1.2	3.1		2.0	2.1				0.9	
83 of 226	Expected	1.0		2.0	3.0		2.0			1.0	3.0		1.0	2.0	1.0				1.0
	Actual	0.9		2.0	0.0		2.2			1.1	3.0		0.9	1.9	0.9				1.2
84 of 226	Expected			2.0	3.0		4.0			1.0	2.0			2.0	2.0				1.0
	Actual			2.2	0.0		3.8			1.0	2.2			1.9	1.8				1.1
85 of 226	Expected			2.0	2.0		6.0	1.0			1.0			1.0	2.0	1.0			1.0
	Actual			2.1	0.0		5.8	1.1		1.1	1.1			1.0	2.1	0.8			1.0
86 of 226	Expected	1.0		3.0	1.0		5.0	1.0		1.0				2.0		2.0		1.0	
	Actual	1.0		2.9	0.0		5.1	1.0		1.0				2.0		1.9		1.1	
87 of 226	Expected	1.0		3.0	2.0		3.0	1.0	2.0					1.0		3.0		1.0	
	Actual	1.0		3.1	0.0		2.8	1.0	2.1					1.0		2.8		1.0	
88 of 226	Expected	1.0		4.0	2.0		1.0	1.0	2.0					2.0		3.0		1.0	
	Actual	0.9		4.2	0.0		0.9	1.1	2.0					2.2		2.9		0.9	
89 of 226	Expected	1.0		3.0	2.0		1.0	1.0	1.0	1.0			1.0	2.0		4.0			
	Actual	1.0		2.8	0.0		1.0	1.0	0.9	1.2			1.0	1.9		3.9			
90 of 226	Expected	1.0		1.0	1.0	1.0	1.0	1.0			2.0		1.0	3.0		4.0		1.0	
	Actual	1.0		0.8	0.0	1.1	1.0	1.0			2.1		1.0	2.8		3.8		1.1	
91 of 226	Expected	1.0			1.0	1.0	2.0			1.0	3.0		1.0	1.0	1.0	3.0		1.0	1.0
	Actual	0.9			0.0	1.0	2.0			1.1	3.0		1.0	1.1	0.8	2.9		1.0	1.2
92 of 226	Expected			2.0	2.0	2.0	1.0	1.0	1.0	2.0				1.0	2.0	1.0		1.0	1.0
	Actual			0.0	1.8	2.1	1.1	1.2	1.0	1.8				0.9	1.8	1.0		1.0	1.1
93 of 226	Expected	1.0			1.0	1.0	3.0	1.0	1.0	2.0	2.0				3.0				2.0
	Actual	1.0			0.0	0.9	2.9	0.9	1.1	2.0	2.1				2.8				2.1
94 of 226	Expected	1.0		2.0	2.0	1.0	4.0	1.0		1.0	1.0				2.0			1.0	1.0
	Actual	0.9		2.2	0.0	1.0	4.0	1.0		0.9	1.2				1.8			1.0	1.0
95 of 226	Expected	1.0	1.0	2.0	3.0		2.0			1.0	1.0			1.0	2.0	1.0		1.0	1.0
	Actual	1.1	1.1	2.0	0.0		1.9			0.9	1.1			1.1	2.0	1.0		0.9	1.0
96 of 226	Expected	1.0	1.0	1.0	3.0	1.0	3.0			1.0			1.0	1.0	1.0	1.0	1.0	1.0	
	Actual	1.0	1.0	1.1	0.0	1.0	3.1			0.9			0.9	1.1	0.9	1.0	0.0	1.2	
97 of 226	Expected	2.0	1.0	1.0	3.0	1.0	1.0			2.0			1.0	1.0	2.0	1.0	1.0		
	Actual	2.0	1.0	1.1	0.0	0.9	1.0			2.1			1.1	1.0	2.0	1.0	0.0		
98 of 226	Expected	2.0		3.0	2.0	1.0	2.0			2.0	1.0		1.0		2.0			1.0	
	Actual	1.8		3.3	0.0	1.0	1.9			1.9	1.1		0.9		2.1		0.0		
99 of 226	Expected	2.0		4.0	2.0	1.0	1.0		2.0	1.0	1.0		2.0		1.0				
	Actual	1.9		4.0	0.0	1.0	1.0		2.2	1.0	1.1		2.2		0.8				
100 of 226	Expected	1.0		5.0	1.0		1.0	1.0	2.0	1.0	1.0		2.0		1.0				1.0
	Actual	1.0		5.1	0.0		1.1	0.9	2.1	1.0	1.0		2.1		0.9				1.0
101 of 226	Expected	1.0		3.0	1.0		1.0	1.0	1.0	2.0			2.0		2.0	2.0			1.0
	Actual	0.9		2.9	0.0		1.1	1.0	1.0	2.1			2.0		2.0	1.8			1.1
102 of 226	Expected	1.0		4.0	1.0	1.0	1.0	1.0		2.0	1.0				2.0	2.0			1.0
	Actual	1.1		4.2	0.0	1.0	1.0	0.9		2.0	1.2				1.8	1.8			1.0
103 of 226	Expected	1.0		3.0	1.0	1.0	1.0		2.0	3.0	1.0				1.0	3.0			
	Actual	1.0		3.1	0.0	1.0	1.1		1.4	2.9	1.1				1.0	2.9			

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	1.0		2.0	2.0	1.0					1.0		1.0	2.0
	Actual	1.0		4.2	0.0	1.0	1.0		1.2	2.0	0.9					0.9		1.2	2.1
105 of 226	Expected			3.0	1.0		3.0		3.0	3.0								2.0	2.0
	Actual			3.2	0.0		2.9		1.8	2.9								1.9	2.1
106 of 226	Expected			2.0	1.0	2.0	3.0		2.0	2.0			1.0					2.0	2.0
	Actual			2.0	0.0	2.1	3.0		2.0	2.0			1.0					1.9	2.0
107 of 226	Expected	1.0		1.0		2.0	3.0		2.0	1.0			1.0			1.0		3.0	2.0
	Actual	1.1		1.1		1.9	2.8		1.9	0.9			1.0			1.0		2.9	2.2
108 of 226	Expected	1.0		3.0		2.0	1.0		1.0	1.0			1.0		1.0	1.0	1.0	2.0	2.0
	Actual	1.0		3.1		2.1	1.0		1.0	1.1			0.9		0.9	1.0	0.0	2.0	2.1
109 of 226	Expected	1.0		5.0		1.0	1.0			2.0					2.0	1.0	1.0	3.0	
	Actual	0.9		5.2		1.0	1.1			2.1					1.9	1.0	0.0	2.9	
110 of 226	Expected		1.0	4.0		1.0	2.0			3.0			1.0		2.0		1.0	2.0	
	Actual		1.1	4.1		0.9	2.0			3.0			1.1		1.9		0.0	2.0	
111 of 226	Expected		2.0	5.0			2.0		1.0	1.0			1.0		1.0	1.0		3.0	
	Actual		2.2	5.0			2.0		1.0	1.0			1.0		1.1	0.9		2.9	
112 of 226	Expected		3.0	2.0			1.0		2.0	1.0		1.0	2.0		1.0	2.0		2.0	
	Actual		2.9	2.2			1.0		2.1	0.9		0.9	2.2		1.0	1.9		1.9	
113 of 226	Expected		3.0	1.0	1.0		1.0		2.0			1.0	1.0		2.0	2.0		2.0	1.0
	Actual		2.9	0.9	0.0		1.2		1.8			0.9	1.0		1.9	2.0		1.9	1.2
114 of 226	Expected	3.0	2.0		1.0		1.0	1.0	1.0			1.0	2.0		3.0			1.0	1.0
	Actual	2.8	1.8		0.0		1.1	1.1	1.0			1.1	1.9		2.8			1.1	0.9
115 of 226	Expected	4.0	1.0	1.0		1.0	1.0	1.0					1.0	1.0	4.0			1.0	1.0
	Actual	4.0	0.9	1.0		1.0	1.0	1.0					1.0	1.0	3.9			1.0	1.1
116 of 226	Expected	4.0	1.0	2.0		1.0		1.0	1.0	2.0			2.0	1.0	2.0				
	Actual	4.0	1.1	2.1		0.9		0.9	1.1	2.1			2.0	1.0	1.8				
117 of 226	Expected	1.0	1.0	2.0	1.0	1.0			1.0	2.0	1.0		2.0	1.0	2.0			1.0	1.0
	Actual	1.0	1.0	2.1	0.0	0.9			1.0	1.9	1.1		2.0	0.9	1.8			1.0	1.1
118 of 226	Expected		2.0	4.0	1.0				1.0	2.0	1.0		2.0		1.0	1.0		1.0	1.0
	Actual		2.1	4.1	0.0				1.0	2.0	1.0		2.0		0.9	1.0		1.0	1.1
119 of 226	Expected		1.0	4.0	1.0	2.0			1.0	2.0			1.0	1.0	1.0	1.0		1.0	1.0
	Actual		1.0	4.1	0.0	2.1			1.2	2.1			0.9	1.1	1.0	1.0		0.9	0.9
120 of 226	Expected		1.0	3.0		2.0			1.0	3.0			1.0	1.0	2.0	1.0		2.0	
	Actual		0.9	3.2		2.0			1.0	3.0			1.0	1.0	2.1	0.9		2.0	
121 of 226	Expected	1.0		3.0	1.0	1.0	1.0		1.0	2.0			1.0	1.0	1.0			2.0	2.0
	Actual	1.1		3.1	0.0	1.0	1.0		1.0	2.0			1.1	1.0	0.9			1.9	1.6
122 of 226	Expected	2.0		3.0	1.0		1.0		1.0	1.0			1.0		2.0	1.0		2.0	2.0
	Actual	2.1		3.2	0.0		0.9		1.2	0.9			0.9		2.0	1.1		1.9	1.7
123 of 226	Expected	2.0		3.0	2.0	1.0			1.0						2.0	2.0		1.0	3.0
	Actual	2.0		3.2	0.0	1.0			1.1						1.9	1.9		1.0	2.6
124 of 226	Expected	1.0		2.0	1.0	1.0	2.0		1.0	1.0					3.0	3.0			2.0
	Actual	1.0		1.9	0.0	0.9	2.0		1.0	1.1					2.9	2.9			2.2
125 of 226	Expected			2.0	2.0	1.0	2.0			1.0					2.0	2.0		2.0	3.0
	Actual			2.0	0.0	0.9	1.9			1.0					2.1	2.2		1.9	3.0
126 of 226	Expected		3.0	2.0	1.0		2.0				1.0				3.0	1.0		2.0	2.0
	Actual		2.9	2.1	0.0		1.9				1.0				3.1	0.9		1.9	2.1
127 of 226	Expected	1.0	3.0	2.0	1.0		2.0		1.0		1.0				2.0	2.0		1.0	1.0
	Actual	1.0	2.9	1.9	0.0		2.1		1.1		0.9				2.2	1.9		1.0	1.0
128 of 226	Expected	1.0	4.0	2.0			2.0		1.0				2.0		1.0	3.0		1.0	
	Actual	1.1	4.0	2.0			2.1		1.1				2.1		0.8	2.9		1.1	
129 of 226	Expected	1.0	1.0	2.0		1.0	1.0		1.0				3.0	1.0		4.0		1.0	1.0
	Actual	0.9	1.0	2.2		1.1	1.0		1.0				2.9	1.0		4.0		0.9	1.1
130 of 226	Expected		1.0	4.0		1.0				1.0			3.0	1.0	2.0	2.0			2.0
	Actual		1.0	4.2		1.0				1.1			2.9	1.0	2.0	1.8			2.2
131 of 226	Expected			3.0		1.0	2.0			2.0			1.0	2.0	2.0	1.0			3.0
	Actual			3.1		1.0	2.0			2.0			1.0	2.0	1.9	0.9			3.2
132 of 226	Expected			2.0		3.0	2.0		2.0	2.0				2.0	1.0			1.0	2.0
	Actual			2.0		3.0	2.0		2.1	2.0				2.2	0.8			1.0	2.1
133 of 226	Expected					3.0	3.0		3.0	1.0			1.0	2.0	1.0	1.0		1.0	1.0
	Actual					3.0	3.1		3.0	1.0			1.0	2.0	0.9	1.0		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		5.0	1.0		4.0			1.0	2.0	1.0	1.0	1.0			
	Actual			1.2		4.9	1.1		4.0			1.1	2.1	1.0	0.8	0.9			
135 of 226	Expected			1.0		4.0	1.0		2.0		1.0	1.0	2.0	1.0	2.0	2.0			
	Actual			1.0		4.1	1.0		2.0		1.1	1.0	2.0	1.1	1.9	1.8			
136 of 226	Expected	1.0		1.0	1.0	3.0			2.0		1.0	1.0	1.0	1.0	2.0	2.0			1.0
	Actual	1.0		1.1	0.0	3.0			1.9		1.1	1.0	0.9	1.0	2.1	1.8			1.1
137 of 226	Expected	2.0		2.0	2.0		1.0		1.0		1.0		1.0	1.0	2.0	2.0			2.0
	Actual	2.2		2.0	0.0		1.1		1.0		1.0		1.1	0.9	1.9	1.8			1.9
138 of 226	Expected	4.0		2.0	3.0		1.0		1.0		1.0		1.0		1.0	1.0		1.0	1.0
	Actual	4.0		2.1	0.0		1.0		1.0		1.2		1.0		0.8	0.9		1.0	1.1
139 of 226	Expected	2.0		1.0	2.0	2.0	2.0			1.0	1.0		1.0		1.0			2.0	2.0
	Actual	2.0		1.0	0.0	2.1	2.0			1.1	1.1		0.9		0.8			2.0	2.1
140 of 226	Expected	2.0		2.0	2.0	2.0	1.0		1.0	1.0	1.0		1.0		2.0			1.0	1.0
	Actual	2.0		2.2	0.0	1.8	1.0		1.1	1.0	0.9		1.0		2.1			0.9	1.1
141 of 226	Expected	1.0		3.0	1.0	2.0	1.0		2.0	2.0			1.0		1.0	1.0		1.0	1.0
	Actual	1.0		3.1	0.0	1.9	1.0		2.1	2.0			1.0		0.9	1.0		1.0	1.1
142 of 226	Expected	1.0		5.0	1.0	2.0			2.0	3.0			1.0			1.0			1.0
	Actual	1.0		5.1	0.0	2.0			2.0	3.0			0.9			0.9			1.2
143 of 226	Expected	1.0		2.0		4.0			1.0	4.0						3.0			2.0
	Actual	0.9		2.1		4.0			1.0	4.0						3.0			2.1
144 of 226	Expected	1.0		4.0		3.0				4.0		1.0			1.0	2.0			1.0
	Actual	1.1		4.3		3.0				4.0		1.0			0.9	1.8			1.1
145 of 226	Expected	1.0		2.0		2.0	1.0			3.0		1.0			2.0	3.0			2.0
	Actual	1.0		2.2		1.8	1.1			3.0		1.0			1.8	2.9			2.2
146 of 226	Expected			3.0			2.0			3.0	2.0	1.0			2.0	2.0			2.0
	Actual			2.9			2.0			3.0	2.1	0.9			1.9	1.9			2.3
147 of 226	Expected			5.0			1.0			2.0	2.0		1.0		1.0	2.0			3.0
	Actual			4.9			1.0			1.9	2.1		1.0		0.9	2.1			3.2
148 of 226	Expected			6.0			1.0		1.0	1.0	1.0		2.0	1.0	1.0				3.0
	Actual			6.1			1.0		1.0	1.0	1.0		2.0	1.1	0.9				3.2
149 of 226	Expected			4.0	1.0		2.0	Expected	1.0	2.0			2.0	1.0	2.0				2.0
	Actual			4.2	0.0		2.0		1.1	1.9			2.0	1.0	1.9				1.9
150 of 226	Expected	1.0		1.0	2.0	1.0	2.0			2.0	1.0		1.0	1.0	4.0				1.0
	Actual	0.9		1.1	0.0	0.9	1.9			2.0	1.0		1.0	1.0	4.1				1.2
151 of 226	Expected	2.0	1.0		2.0	2.0	2.0		1.0	1.0	1.0				5.0				
	Actual	2.0	1.0		0.0	2.0	1.8		1.1	1.0	1.1				4.8				
152 of 226	Expected	2.0	1.0	2.0	1.0	1.0			1.0	2.0	2.0		1.0		4.0				
	Actual	2.0	0.9	2.0	0.0	1.0			1.1	1.9	2.1		1.0		3.8				
153 of 226	Expected	1.0	1.0	3.0		1.0			1.0	3.0	2.0		1.0		2.0				2.0
	Actual	1.0	0.9	3.1		0.9			1.0	3.0	2.1		1.1		2.0				2.3
154 of 226	Expected	1.0		2.0		1.0	1.0			3.0	2.0		2.0		1.0			1.0	3.0
	Actual	1.0		2.0		1.1	1.0			2.9	2.1		2.0		0.9			1.0	3.1
155 of 226	Expected	1.0		3.0	1.0	1.0	3.0			1.0	1.0		1.0		1.0	1.0		1.0	2.0
	Actual	1.0		3.1	0.0	1.0	3.1			1.0	1.1		1.0		0.8	1.0		1.0	2.1
156 of 226	Expected	2.0	1.0	3.0	1.0	2.0	2.0		1.0	1.0			1.0			1.0		1.0	1.0
	Actual	2.0	1.0	3.2	0.0	2.0	2.0		1.0	1.1			0.9			1.0		0.9	1.1
157 of 226	Expected	1.0	1.0	2.0	2.0	2.0	2.0		2.0	1.0					1.0	1.0		1.0	1.0
	Actual	1.0	1.0	2.0	0.0	1.9	1.9		2.0	1.1					1.0	0.9		1.1	1.2
158 of 226	Expected			1.0	1.0	2.0	1.0		3.0	2.0	2.0				1.0			1.0	2.0
	Actual			0.9	1.0	0.0	1.9	1.1	3.1	2.0	2.2				0.9			1.0	2.2
159 of 226	Expected				1.0	2.0	1.0		1.0	3.0	2.0			2.0	2.0			1.0	2.0
	Actual				0.0	1.9	1.0		1.0	3.0	2.0			2.0	2.0			1.0	2.1
160 of 226	Expected			1.0		2.0	2.0		2.0	3.0	1.0			2.0	2.0			1.0	1.0
	Actual			1.0		1.9	2.0		1.9	3.2	1.0			2.1	1.8			0.9	1.1
161 of 226	Expected	2.0		1.0		2.0	1.0		1.0	3.0				1.0	3.0	2.0			1.0
	Actual	2.0		1.0		1.8	1.0		1.1	3.0				1.0	3.0	2.1			1.0
162 of 226	Expected	3.0		1.0		1.0	1.0		1.0	2.0			1.0	1.0	3.0	2.0			1.0
	Actual	3.0		0.9		0.9	1.1		1.1	2.0			1.1	1.1	2.8	2.1			1.0
163 of 226	Expected	6.0								3.0			1.0	1.0	2.0	3.0	1.0		
	Actual	5.9								3.0			1.1	1.1	1.8	2.8	0.0		

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					1.0			3.0			2.0	2.0	1.0	1.0	1.0	1.0	1.0
	Actual	3.9					1.0			3.0			2.0	2.0	0.8	1.0	0.0	1.0	1.2
165 of 226	Expected	3.0	1.0	1.0		1.0	1.0		1.0	1.0			1.0	1.0		1.0	1.0	2.0	2.0
	Actual	2.9	1.0	1.0		1.0	1.0		1.1	1.0			1.0	1.0		0.8	0.0	2.0	2.2
166 of 226	Expected		1.0	2.0		1.0	2.0		1.0	2.0			1.0	1.0		1.0		2.0	3.0
	Actual		1.0	2.1		1.0	2.1		1.0	2.1			1.0	1.0		1.0		1.9	3.1
167 of 226	Expected		1.0	2.0		2.0	2.0		1.0	2.0		1.0			1.0	1.0		1.0	3.0
	Actual		1.0	2.2		1.9	2.1		1.0	2.1		1.0			0.9	1.0		1.0	3.1
168 of 226	Expected	1.0		2.0		2.0	2.0		1.0	3.0	1.0	1.0			1.0	1.0			2.0
	Actual	1.1		2.0		1.9	1.9		1.1	3.0	1.1	1.0			0.8	0.9			2.1
169 of 226	Expected	3.0		5.0		2.0			1.0	2.0	1.0		1.0		1.0				1.0
	Actual	3.0		5.0		1.9			1.0	2.0	1.1		1.0		0.9				1.0
170 of 226	Expected	4.0		4.0		2.0			2.0	2.0	1.0		1.0					1.0	
	Actual	4.0		3.8		1.9			2.1	2.0	0.9		1.1					1.1	
171 of 226	Expected	4.0		4.0		2.0	1.0		1.0	1.0			2.0			1.0		1.0	
	Actual	4.0		4.0		2.0	1.0		1.0	1.0			1.9			0.9		1.0	
172 of 226	Expected	3.0		2.0		2.0	1.0		1.0	2.0	1.0		1.0		1.0	1.0		1.0	1.0
	Actual	3.0		2.1		2.0	1.0		1.0	2.0	1.1		1.0		0.8	0.9		1.0	1.2
173 of 226	Expected	3.0		3.0		1.0	1.0		1.0	1.0	1.0		1.0		1.0	1.0			3.0
	Actual	2.9		3.1		1.1	1.0		1.0	1.0	1.1		0.9		1.0	0.8			2.6
174 of 226	Expected	5.0		2.0		2.0			1.0	2.0	1.0				1.0				3.0
	Actual	5.1		2.1		1.9			1.0	2.1	1.0				1.0				2.4
175 of 226	Expected	4.0		4.0		3.0			1.0	3.0									2.0
	Actual	3.9		4.0		2.8			1.1	3.1									1.4
176 of 226	Expected	3.0	1.0	4.0		3.0				4.0			1.0		1.0				
	Actual	2.9	1.1	3.9		2.8				4.1			1.1		0.9				
177 of 226	Expected	2.0	1.0	3.0		2.0	1.0		1.0	3.0			1.0		3.0				
	Actual	2.1	1.0	2.9		1.9	1.0		1.1	3.1			1.0		3.0				
178 of 226	Expected	2.0	1.0	1.0		2.0	1.0		2.0	3.0			1.0		4.0				
	Actual	2.0	1.0	1.1		1.9	1.0		2.0	3.1			1.0		3.8				
179 of 226	Expected	3.0	1.0	1.0		3.0			2.0	4.0					3.0				
	Actual	3.0	1.0	1.1		2.9			2.0	4.1					2.8				
180 of 226	Expected	3.0	1.0	1.0		5.0			2.0	4.0					1.0				
	Actual	3.1	1.0	1.1		5.0			2.1	4.0					0.9				
181 of 226	Expected	3.0	2.0	3.0		3.0	1.0		2.0	3.0									
	Actual	2.9	1.9	3.1		2.9	1.1		2.1	2.9									
182 of 226	Expected	3.0	2.0	3.0		2.0	1.0		2.0	3.0						1.0			
	Actual	2.9	2.0	3.0		1.8	1.1		2.1	3.1						1.0			
183 of 226	Expected	2.0	2.0	2.0		2.0	1.0		1.0	3.0					1.0	1.0		1.0	1.0
	Actual	2.1	1.8	1.9		2.3	0.9		1.0	2.9					0.9	1.0		1.1	1.0
184 of 226	Expected	2.0		2.0		2.0				4.0					3.0	2.0		1.0	1.0
	Actual	2.0		1.9		1.9				3.8					2.9	2.1		1.0	1.1
185 of 226	Expected	2.0		1.0		2.0				2.0	1.0		1.0		4.0	1.0		1.0	2.0
	Actual	2.1		1.0		2.2				2.1	1.0		0.9		3.9	0.9		1.0	1.9
186 of 226	Expected	3.0		1.0		2.0				1.0	2.0	1.0	1.0		3.0	1.0			2.0
	Actual	2.8		1.1		2.0				1.0	1.9	0.9	1.0		3.0	1.0			2.1
187 of 226	Expected	3.0		1.0	1.0	3.0					3.0	1.0	1.0		2.0				2.0
	Actual	3.1		1.0	0.0	2.8					3.0	1.0	1.0		2.1				2.2
188 of 226	Expected	1.0	1.0	2.0	1.0	3.0			1.0		2.0	1.0			3.0				2.0
	Actual	1.1	1.0	2.0	0.0	2.8			1.0		1.9	1.1			3.0				2.0
189 of 226	Expected		1.0	3.0	2.0	2.0	2.0		1.0		1.0		1.0		3.0				1.0
	Actual		1.0	3.1	0.0	1.8	2.0		1.1		1.0		1.0		2.9				1.0
190 of 226	Expected		1.0	3.0	1.0		2.0	1.0	3.0	1.0			1.0		3.0				1.0
	Actual		0.9	2.9	0.0		2.0	1.0	1.9	1.1			0.9		2.9				1.2
191 of 226	Expected	1.0		3.0	1.0	1.0	3.0	1.0	2.0	1.0				1.0	1.0			1.0	1.0
	Actual	1.1		2.9	0.0	1.0	2.9	0.9	1.2	1.0				1.1	0.9			1.1	1.1
192 of 226	Expected	1.0		1.0		1.0	1.0	1.0	3.0	2.0			2.0	1.0	1.0			2.0	1.0
	Actual	1.1		1.0		1.0	1.0	0.9	1.8	2.0			2.0	1.1	0.8			2.1	1.1
193 of 226	Expected	1.0		1.0			1.0	1.0	1.0	1.0	1.0		2.0	2.0	1.0	1.0		3.0	1.0
	Actual	1.1		1.1			1.0	0.9	0.8	1.1	1.1		2.0	2.1	0.9	1.0		3.1	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)
194 of 226	Expected	1.0	1.0					1.0	1.0		1.0		2.0	1.0	1.0	2.0		3.0	3.0
	Actual	1.1	1.0					0.8	0.9		1.1		2.0	1.0	1.0	2.0		2.9	3.1
195 of 226	Expected	1.0	1.0		1.0		1.0		1.0	1.0	1.0			2.0	1.0	2.0		2.0	3.0
	Actual	1.1	1.0		0.0		1.1		1.0	1.1	1.1			2.0	0.9	1.9		1.8	2.9
196 of 226	Expected	2.0	2.0	1.0	1.0		3.0		2.0	1.0				1.0	1.0	1.0			2.0
	Actual	2.0	2.0	1.1	0.0		3.1		2.2	1.0				1.0	1.0	0.8			2.0
197 of 226	Expected	2.0	1.0	1.0	1.0		4.0		2.0	1.0	1.0			2.0	1.0			1.0	
	Actual	2.1	1.0	1.1	0.0		3.9		2.0	1.1	1.1			2.0	0.8			1.0	
198 of 226	Expected	1.0	1.0	4.0			3.0		1.0		1.0		1.0	1.0	1.0			1.0	2.0
	Actual	1.0	1.0	4.0			2.9		1.0		1.0		1.0	1.0	0.9			1.0	2.2
199 of 226	Expected			3.0			2.0				1.0	1.0	1.0	1.0	1.0	2.0	1.0	2.0	2.0
	Actual			2.9			2.1				0.9	1.0	1.0	1.0	0.9	2.0	0.0	2.1	2.2
200 of 226	Expected			3.0			2.0					1.0		1.0	1.0	2.0	1.0	4.0	2.0
	Actual			2.9			2.1					1.0		1.1	0.9	1.9	0.0	4.2	2.1
201 of 226	Expected			1.0		2.0	2.0		1.0			1.0		2.0	1.0	2.0	1.0	4.0	
	Actual			1.2		1.8	2.0		1.0			1.0		2.0	1.0	1.8	0.0	4.1	
202 of 226	Expected			2.0		2.0	1.0		1.0			1.0		2.0	1.0	1.0		3.0	3.0
	Actual			2.1		1.9	1.0		1.1			1.0		2.1	0.9	1.0		2.9	2.8
203 of 226	Expected	1.0		3.0	1.0	1.0			1.0			1.0		1.0	1.0	2.0		1.0	4.0
	Actual	1.0		2.9	0.0	1.0			1.0			1.1		0.9	1.1	1.9		1.0	4.6
204 of 226	Expected	2.0		1.0	1.0						1.0	1.0		1.0	1.0	2.0		2.0	5.0
	Actual	2.1		1.1	0.0						1.1	0.9		1.1	0.8	1.9		2.1	4.3
205 of 226	Expected	2.0		2.0	1.0				1.0	1.0	1.0	1.0		1.0	1.0	2.0		2.0	2.0
	Actual	1.9		1.9	0.0				1.1	1.1	1.0	1.0		1.0	0.9	1.9		2.0	2.1
206 of 226	Expected	1.0		3.0					1.0	2.0	1.0	1.0	1.0	3.0	1.0	1.0		1.0	1.0
	Actual	1.0		3.1					1.0	2.0	1.0	1.0	1.1	3.1	0.8	0.9		1.0	1.1
207 of 226	Expected			4.0		3.0			1.0	3.0	1.0		1.0	2.0	1.0	1.0			
	Actual			4.1		3.1			1.1	3.0	1.1		1.1	2.1	0.8	0.9			
208 of 226	Expected			4.0		4.0				2.0	2.0		2.0	1.0		1.0	1.0		
	Actual			4.0		3.9				2.0	2.1		2.1	1.0		1.0	0.0		
209 of 226	Expected	1.0		3.0		4.0				2.0	1.0		1.0	1.0	1.0	1.0	1.0		1.0
	Actual	1.0		3.1		4.1				2.0	1.0		0.9	1.0	1.0	0.9	0.0		1.1
210 of 226	Expected	1.0		4.0		1.0			1.0	2.0	1.0		1.0	1.0	2.0	1.0		1.0	1.0
	Actual	0.9		4.0		1.1			1.0	1.8	0.9		0.9	0.9	1.9	1.2		1.0	1.2
211 of 226	Expected	1.0		4.0					1.0	4.0			1.0	1.0	1.0	1.0		1.0	2.0
	Actual	1.0		4.1					1.1	4.0			1.0	1.0	0.9	0.9		1.0	2.2
212 of 226	Expected		1.0	4.0		2.0			1.0	3.0		1.0	1.0			1.0		1.0	2.0
	Actual		1.1	4.1		2.0			0.9	3.1		1.1	1.0			0.9		0.9	2.1
213 of 226	Expected	1.0	1.0	2.0		4.0			1.0	3.0	1.0	1.0	1.0			1.0			1.0
	Actual	1.0	1.0	2.0		3.9			1.0	3.0	1.1	1.0	1.0			0.9			1.1
214 of 226	Expected	1.0	1.0	2.0		4.0			1.0	2.0	1.0	1.0			1.0			1.0	2.0
	Actual	1.1	0.9	2.0		4.0			1.1	2.1	1.1	0.9			0.8			1.0	2.2
215 of 226	Expected	1.0		3.0		3.0			2.0	3.0	2.0				1.0			1.0	1.0
	Actual	0.9		3.2		3.1			1.9	2.9	2.0				1.0			1.0	1.0
216 of 226	Expected			3.0		2.0	1.0		2.0	2.0	1.0				1.0	1.0		3.0	1.0
	Actual			3.0		1.9	1.1		2.0	2.0	1.2				0.9	1.0		3.1	1.0
217 of 226	Expected			2.0		1.0	1.0		2.0	1.0	2.0			1.0		1.0	2.0	3.0	1.0
	Actual			2.1		1.0	1.0		2.2	0.9	1.9			1.1		1.0	0.0	3.1	1.0
218 of 226	Expected					1.0	1.0		1.0	2.0	1.0			1.0		1.0	3.0	4.0	2.0
	Actual					0.9	1.0		1.1	2.1	1.0			1.0		0.9	0.0	4.0	2.1
219 of 226	Expected	2.0			1.0		1.0		1.0	3.0	1.0			1.0			3.0	1.0	3.0
	Actual	2.0			0.0		1.0		1.0	2.9	1.0			1.0			0.0	1.0	2.9
220 of 226	Expected	2.0			1.0		1.0		1.0	6.0		1.0	1.0				1.0		3.0
	Actual	2.1			0.0		1.0		1.0	6.0		1.0	1.0				0.0		2.9
221 of 226	Expected	2.0			3.0		1.0		1.0	4.0		1.0	2.0			1.0			2.0
	Actual	2.1			0.0		1.0		1.0	4.0		1.0	2.0			1.0			2.0
222 of 226	Expected				5.0		2.0		1.0	3.0			2.0		1.0	2.0			1.0
	Actual				0.0		2.1		1.0	3.0			2.1		1.0	1.9			1.1
223 of 226	Expected				6.0		4.0		1.0		2.0		1.0		1.0	2.0			
	Actual				0.0		4.0		1.0		2.2		1.0		0.8	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)
224 of 226	Expected			2.0	5.0		3.0				2.0		1.0		1.0	2.0		1.0	
	Actual			2.2	0.0		2.8				2.0		1.0		1.0	1.8		1.1	
225 of 226	Expected			2.0	3.0	2.0	3.0			1.0	2.0					1.0		2.0	1.0
	Actual			2.0	0.0	2.0	2.8			1.1	2.0					0.9		2.1	1.1
226 of 226	Expected			4.0	1.0	2.0	1.0	1.0	1.0	1.0	1.0				1.0	2.0		2.0	1.0
	Actual			3.9	0.0	2.1	1.1	1.0	0.5	1.0	1.0				1.0	1.9		1.8	0.6

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.

/Heather Couch/

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