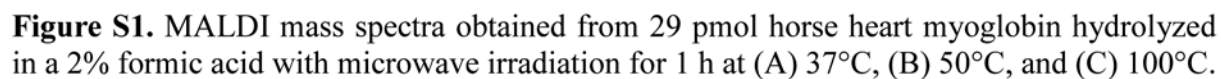


Supporting Information

Weak Acid Hydrolysis of Proteins

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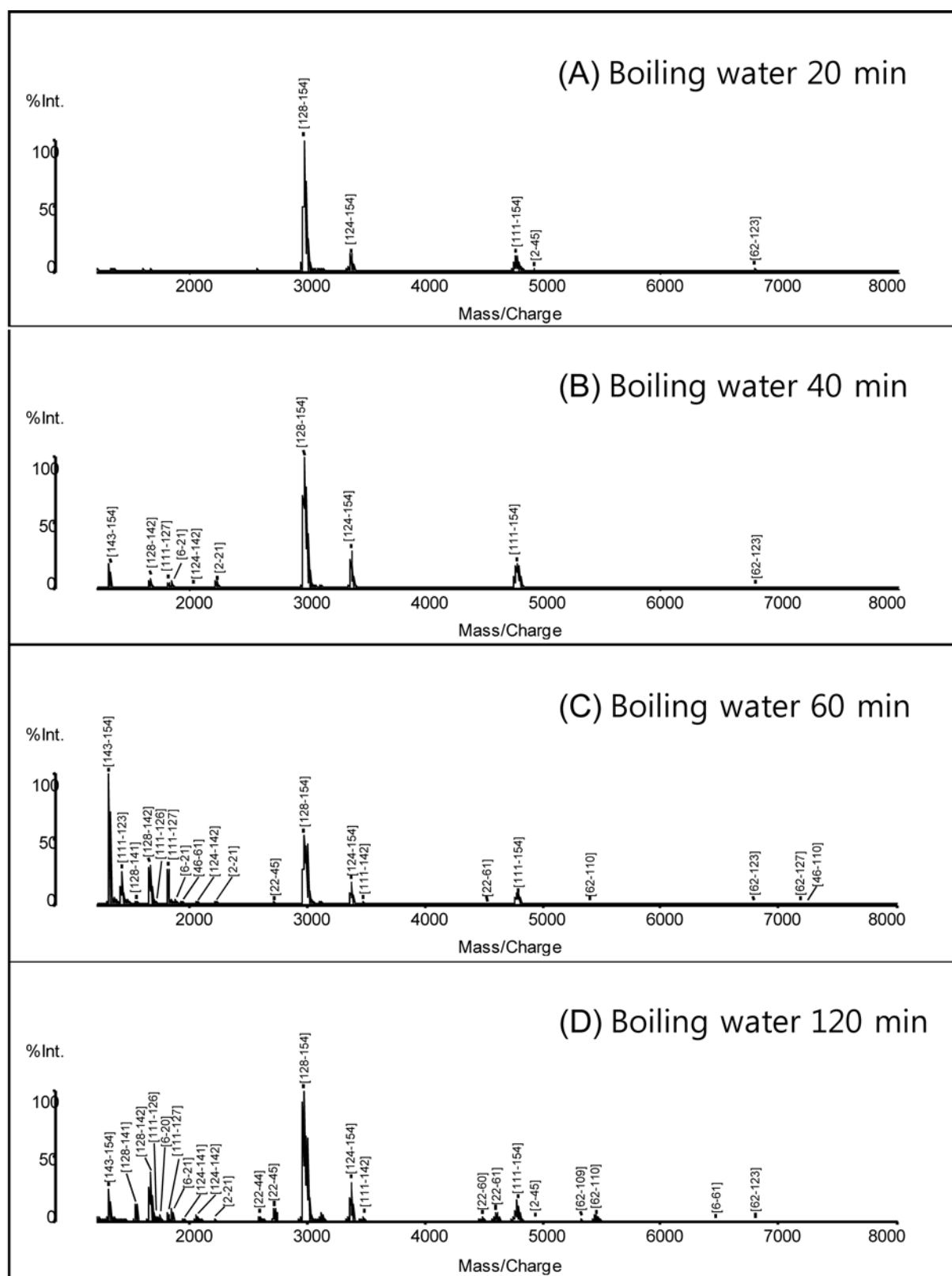


Figure S2. MALDI mass spectra from 29 pmol horse heart myoglobin hydrolyzed in a 2% formic acid in boiling water without microwave irradiation for (A) 20 min, (B) 40 min, (C) 60 min, and (D) 120 min.

Supplementary Table S1. Summary of identified peptides obtained from myoglobin following weak acid hydrolysis with microwave irradiation or in boiling water under various conditions.

Experimental <i>m/z</i> values	Theoretical average <i>m/z</i> values for [M+H] ⁺	Δ <i>Mass</i> (Daltons)	Peptide sequence	Position	Number of missed cleavages	Conditions of acidic cleavage						
						Microwave, 1 h			Boiling water			
						37 °C	50 °C	100 °C	20 min	40 min	60 min	120 min
1325.6	1325.5	-0.1	D.IAAKYKELGFQG.-	143-154	0	- ^{a)}	O	O ^{b)}	-	O	O	O
1422.4	1424.6	2.2	D.AIHVLHSHKHPGD.F	111-123	0	-	-	O	-	-	O	-
1550.5	1550.8	0.3	D.AQGAMTKALELFRN.D ^{c)}	128-141	0	-	-	O	-	-	O	O
1664.7	1665.9	1.2	D.AQGAMTKALELFRND.I	128-142	0	-	-	O	-	O	O	O
1701.0	1699.9	-1.1	D.AIHVLHSHKHPGDFGA.D ^{c)}	111-126	1	-	-	O	-	-	O	O
1743.8	1743.9	0.1	D.GEWQQVLNVWGKVEAD. ^{c)}	6-20	0	-	-	O	-	-	-	O
1816.2	1815.0	-1.2	D.AIHVLHSHKHPGDFGAD.A	111-127	1	-	-	O	-	O	O	O
1859.9	1859.0	-0.9	D.GEWQQVLNVWGKVEAD.I	6-21	0	-	-	O	-	O	O	O
1893.7	1893.2	-0.5	D.KFKHLKTEAEKASED.L	46-61	0	-	-	-	-	-	O	-
1941.3	1941.2	-0.1	D.FGADAQGAMTKALELFRN.D ^{c)}	124-141	1	-	-	O	-	-	-	O
2055.4	2056.3	0.9	D.FGADAQGAMTKALELFRND.I	124-142	1	-	-	O	-	O	O	O
2232.7	2231.4	-1.3	-GLSDGEWQQVLNVWGKVEAD.I	2-21	1	-	-	O	-	O	O	O
2591.9	2594.0	2.1	D.IAGHGQEVLRILFTGHPETL.EKED ^{c)}	22-44	0	-	-	O	-	-	-	O
2712.4	2709.1	-3.3	D.IAGHGQEVLRILFTGHPETL.EKFD.K	22-45	0	-	-	O	-	-	O	O
2971.9	2972.4	0.5	D.AQGAMTKALELFRNDIAAKY.KELGFQG.-	128-154	1	-	O	O	O	O	O	O
3364.4	3362.8	-1.6	D.FGADAQGAMTKALELFRNDIAAKYKELGFQG.-	124-154	2	-	O	O	O	O	O	O
3461.2	3461.9	0.7	D.AIHVLHSHKHPGDFGADAQG.AMTKALELFRND.I	111-142	2	-	-	O	-	-	O	O
4469.9	4468.1	-1.8	D.IAGHGQEVLRILFTGHPETL.EKFDKFKHLKTEAEKASE.D ^{c)}	22-60	1	-	-	O	-	-	-	O
4581.2	4583.2	2	D.IAGHGQEVLRILFTGHPETL.EKFDKFKHLKTEAEKASED.L	22-61	1	-	-	O	-	-	O	O
4768.9	4768.4	-0.5	D.AIHVLHSHKHPGDFGADAQG.AMTKALELFRNDIAAKYKEL.GFQG.-	111-154	3	-	O	O	O	O	O	O
4921.7	4921.5	-0.2	-GLSDGEWQQVLNVWGKVEAD.IAGHGQEVLRILFTGHPETL.EKFD.K	2-45	2	-	-	O	O	-	-	O
5313.1	5311.4	-1.7	D.LKKHGTVVLTALGGILKKKG.HHEAELKPLAQSHATKHKIP.IKYLEFIS.D ^{c)}	62-109	0	-	-	O	-	-	-	O
5426.0	5426.5	0.5	D.LKKHGTVVLTALGGILKKKG.HHEAELKPLAQSHATKHKIP.IKYLEFISD.A	62-110	0	-	-	O	-	-	O	O
6420.2	6423.2	3	D.GEWQQVLNVWGKVEADIAGH.GQEVLRILFTGHPETLEKFD.KFKHLKTEAEKASED.L	6-61	2	-	-	-	-	-	-	O
6835.5	6832.1	-3.4	D.LKKHGTVVLTALGGILKKKG.HHEAELKPLAQSHATKHKIP.IKYLEFISDAIHVLHSHKHP.GD.F	62-123	1	-	-	-	O	O	O	O
7221.9	7222.5	0.6	D.LKKHGTVVLTALGGILKKKG.HHEAELKPLAQSHATKHKIP.IKYLEFISDAIHVLHSHKHP.GDFGAD.A	62-127	2	-	-	-	-	-	O	-
7303.3	7300.6	-2.7	D.KFKHLKTEAEKASEDLKKH.GTVVLTALGGILKKKGHHEA.ELKPLAQSHATKHKIPIKYLEFISD.A	46-110	1	-	-	-	-	-	O	-
Total number of identified peptides												
Number of identified peptides with missed cleavages												
Ratio of missed cleavages												
Number of identified peptides with cleavages at the N-terminal aspartic acid												
Ratio of cleavage at N-terminus of aspartic acid to cleavage at C-terminus of aspartic acid												
Sequence coverage												
						0%	28.8%	100%	89.6%	100%	100%	100%
						0	0	31.8%	0	0	10%	30.4%
						0	0	7	0	0	2	7
						0	75.0%	54.5%	100%	70.0%	60.0%	60.9%
						0	0	0	0	0	2	7
						0	0	0	0	0	0	0
						0	3	12	5	7	12	14
						0	4	22	5	10	20	23