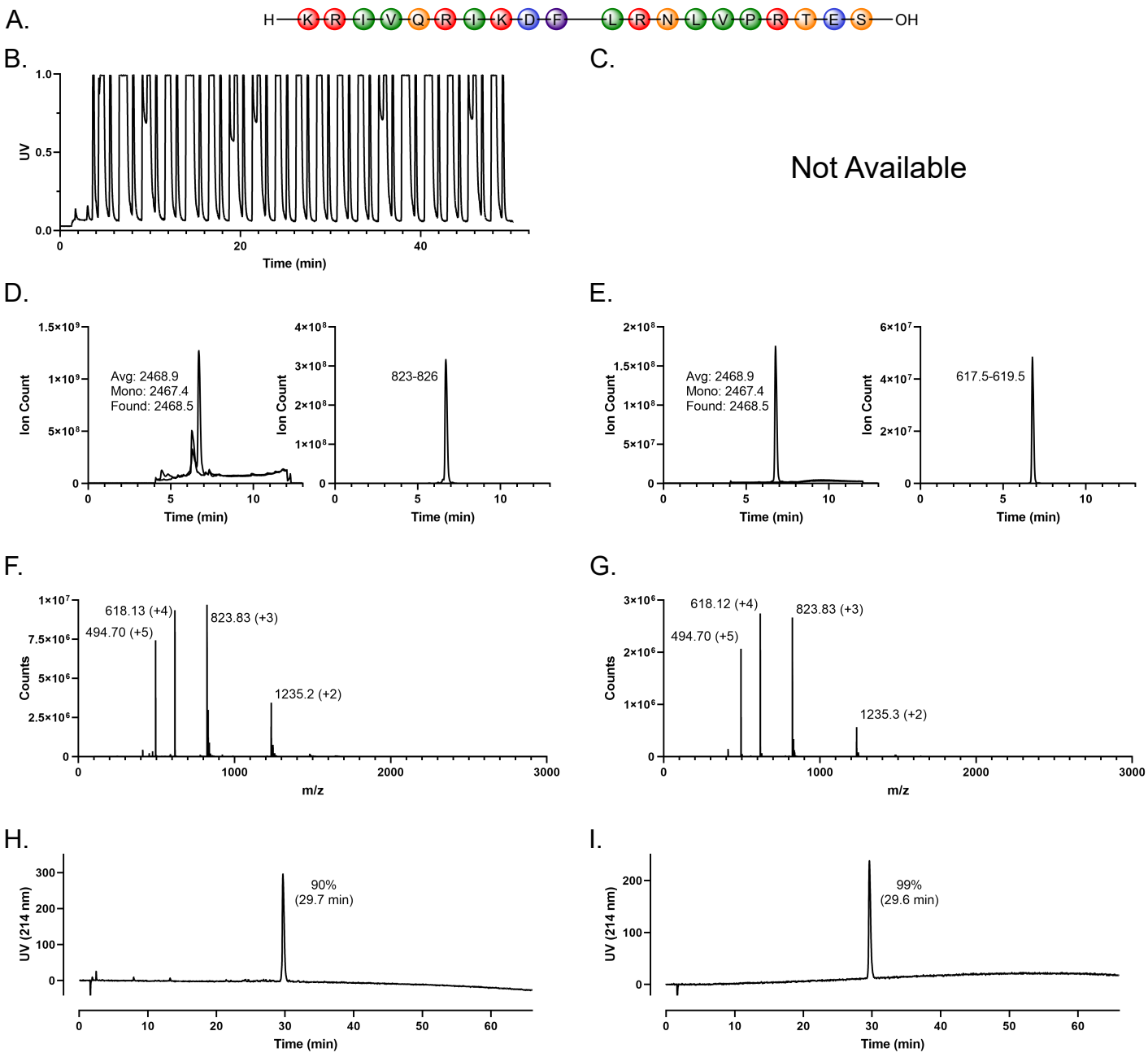
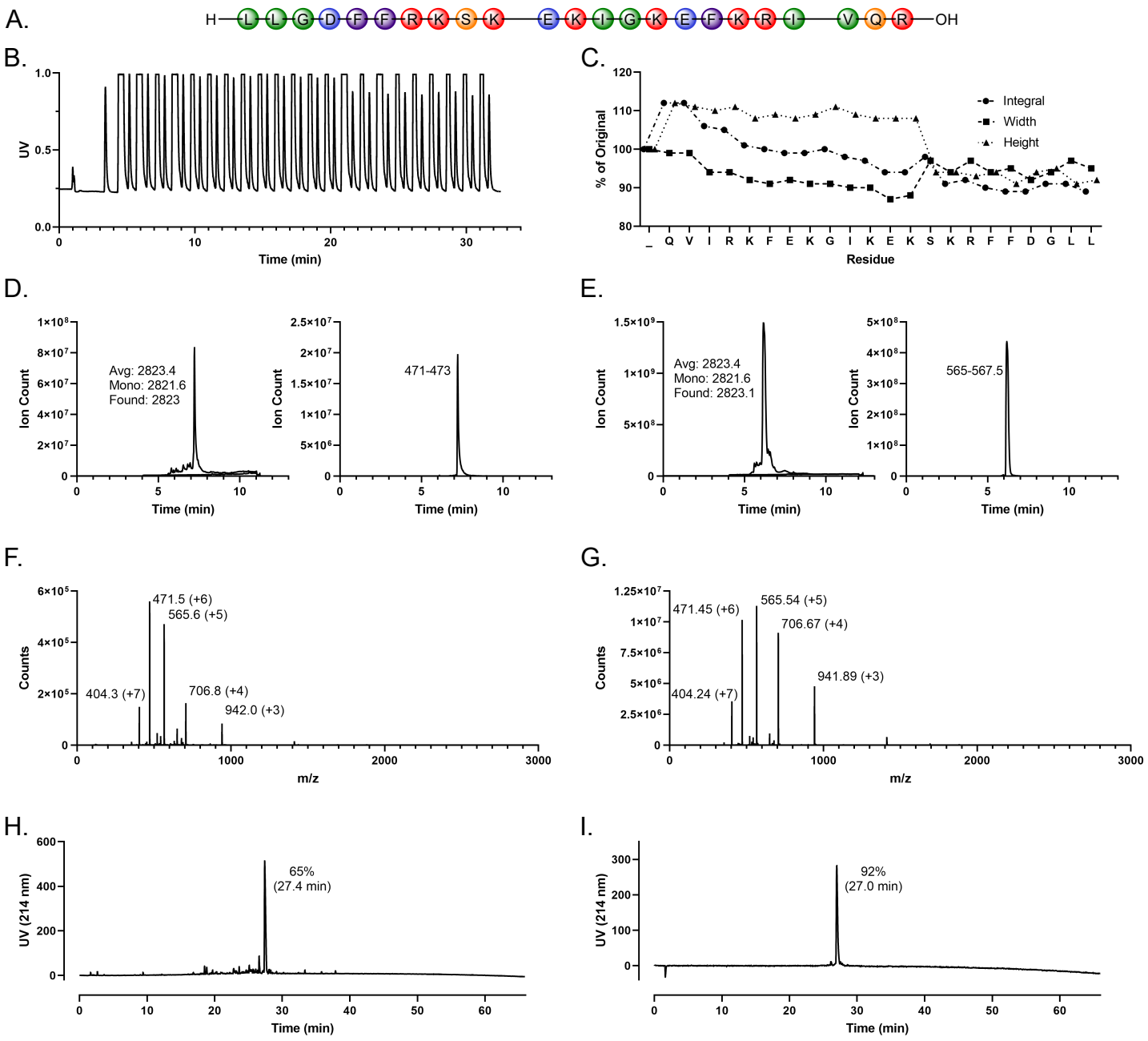
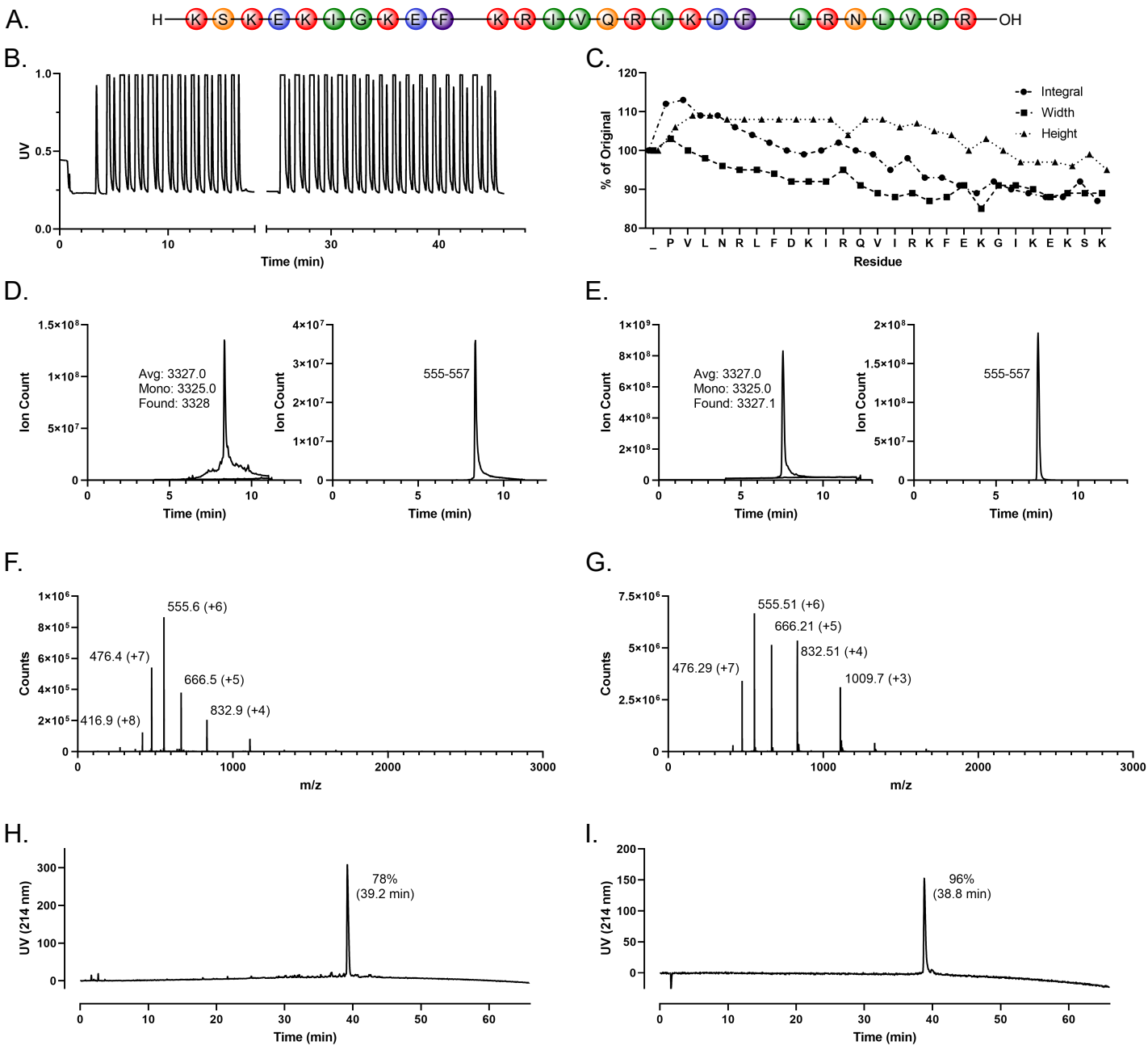


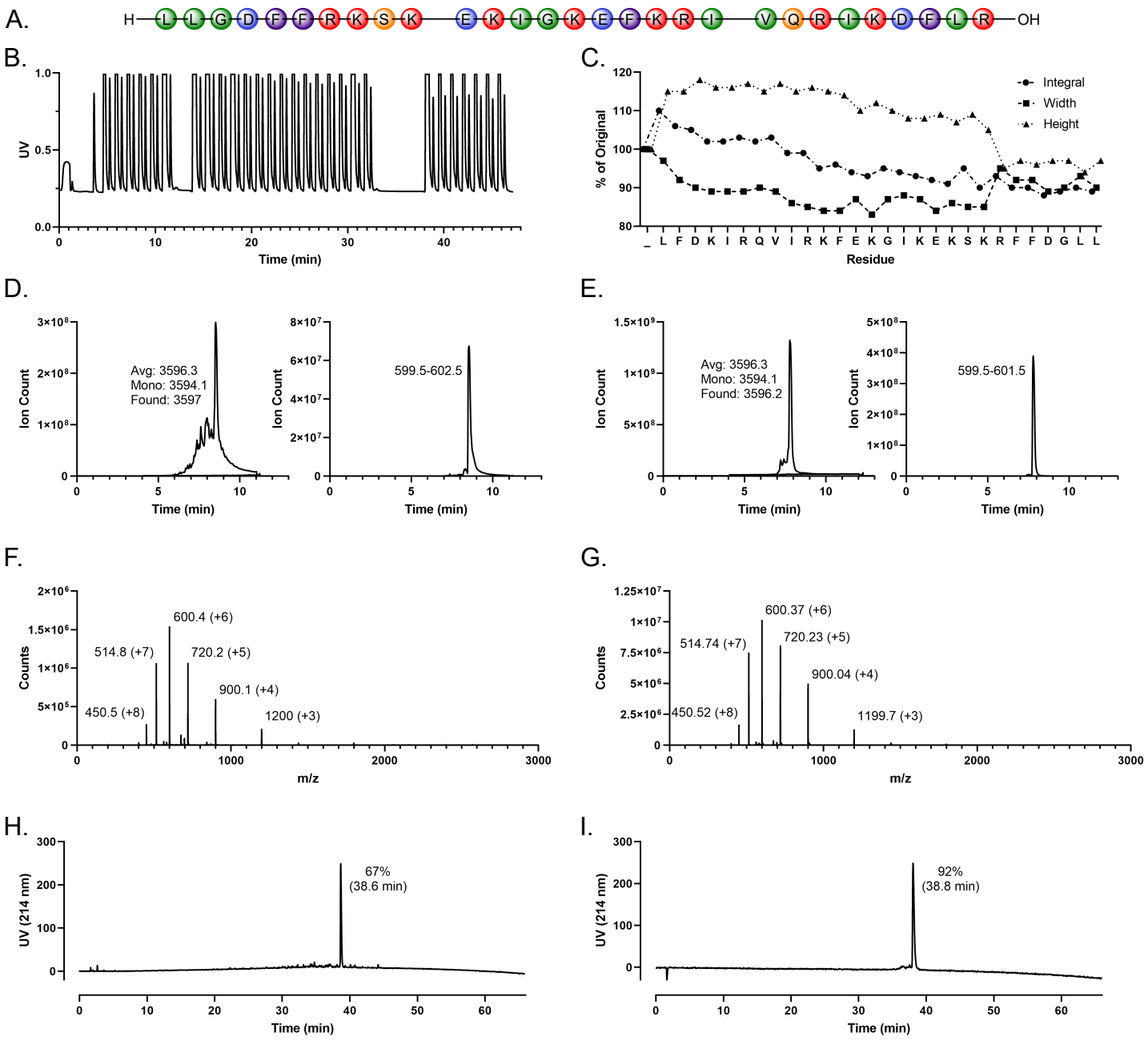
Supplementary Figure 1: A. KR-20 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 4th Generation – Length. **C.** Integrals unavailable for this sequence. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 3. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the indicated integral percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



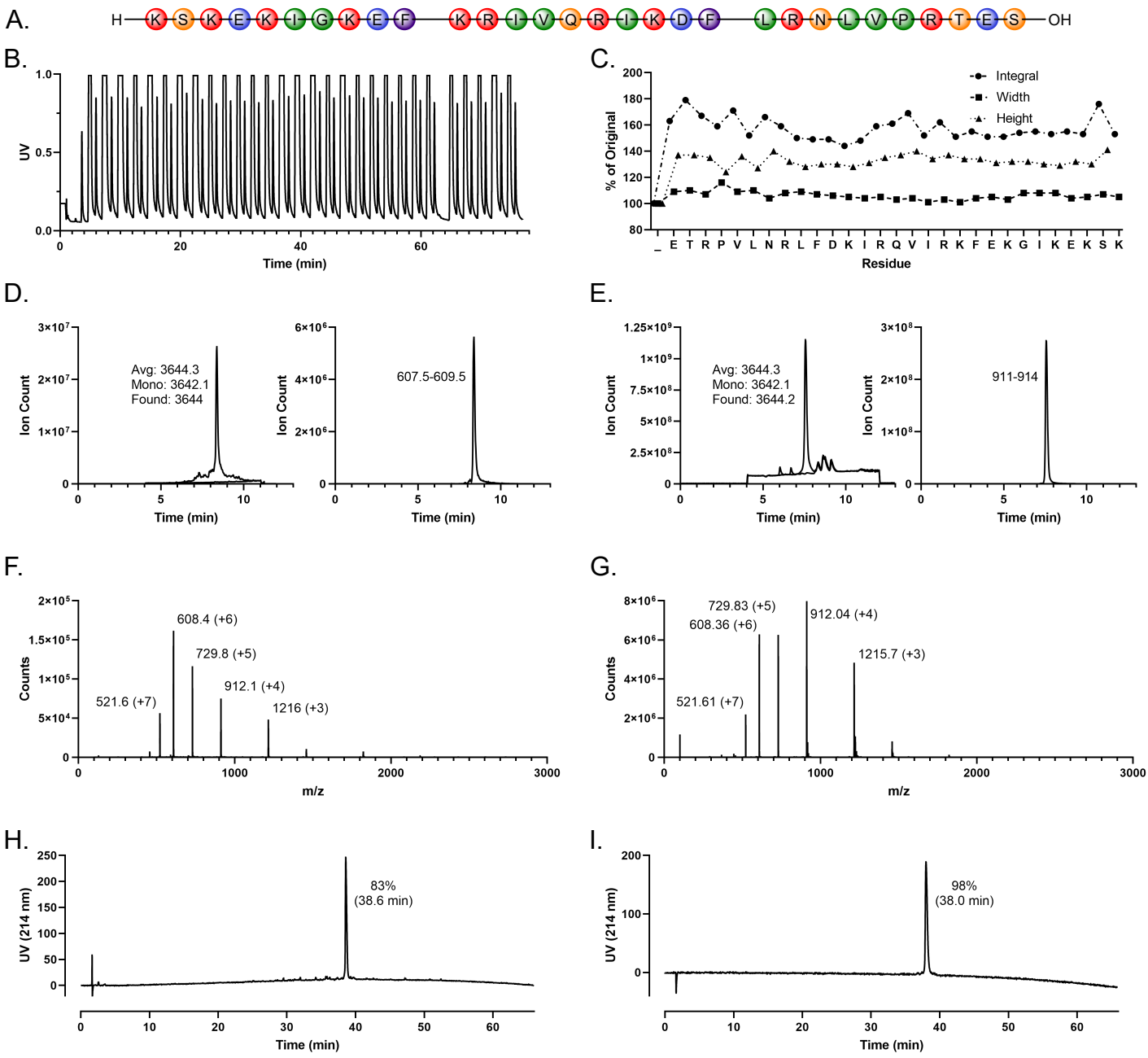
Supplementary Figure 2: A. LL-23 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the indicated integral percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



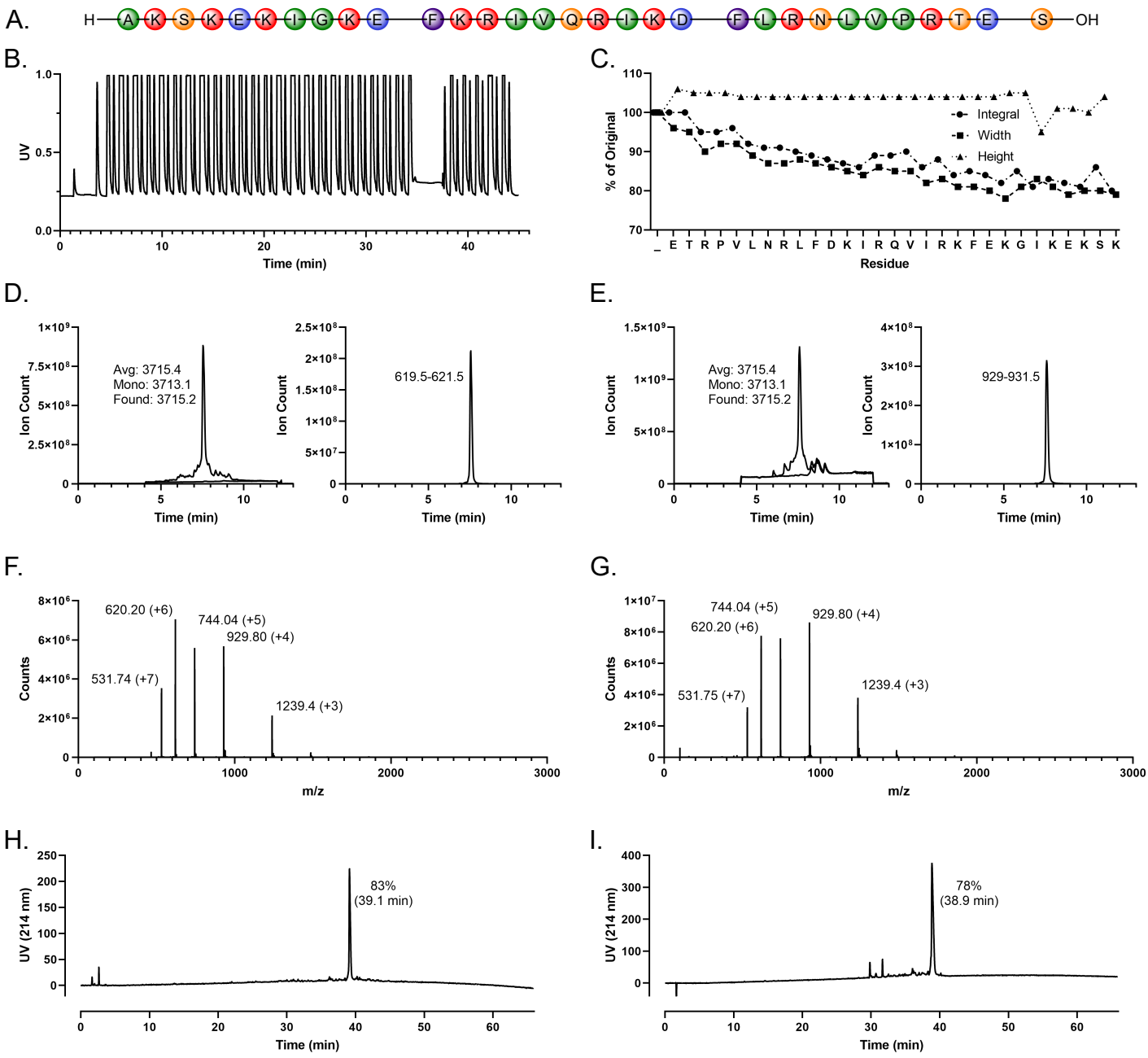
Supplementary Figure 3: A. KS-27 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. The x-axis is cut at a user-initiated pause; total time graphed includes the pause time. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



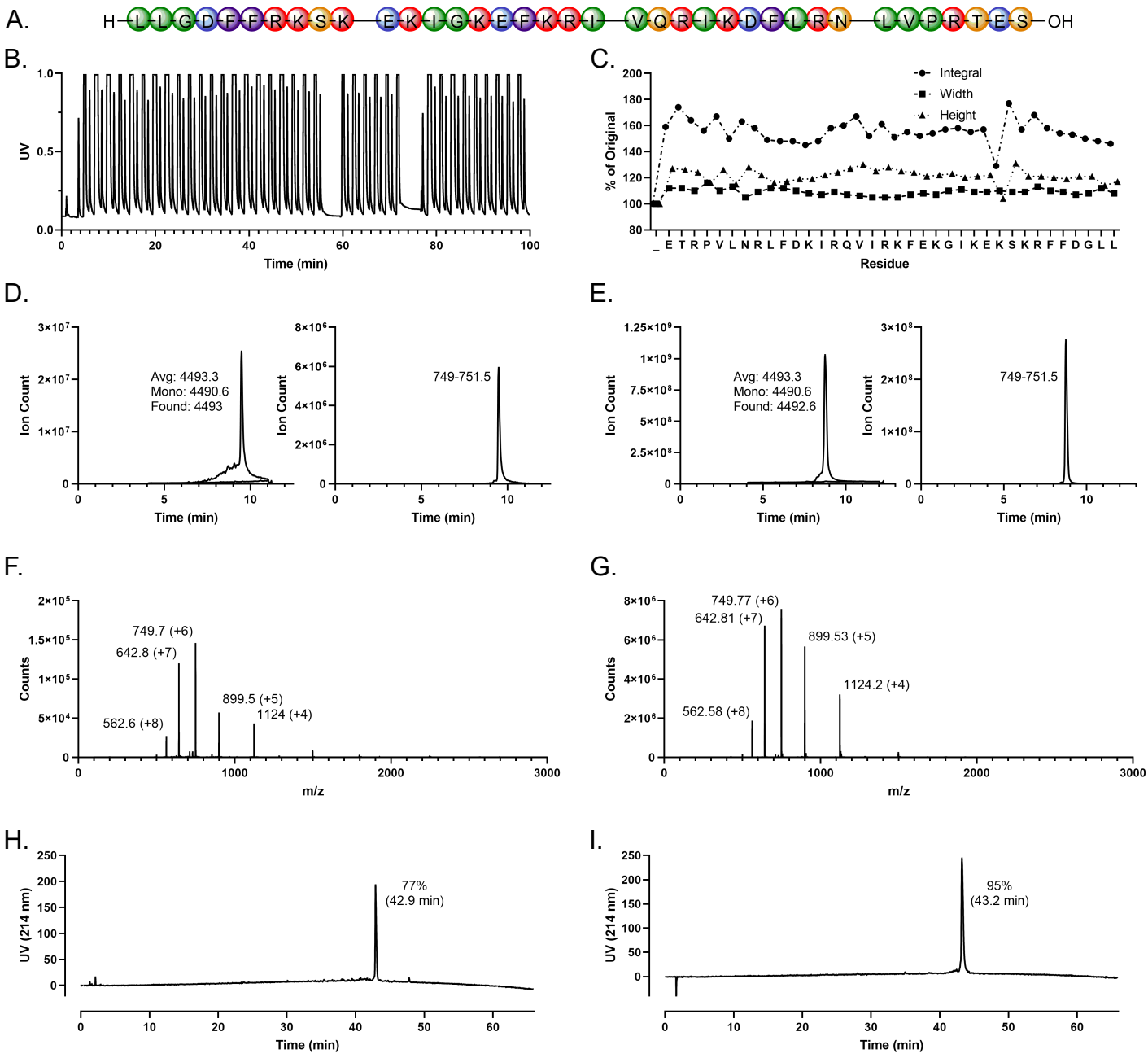
Supplementary Figure 4: A. LL-29 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. Spaces in the x-axis represent user-initiated pauses. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



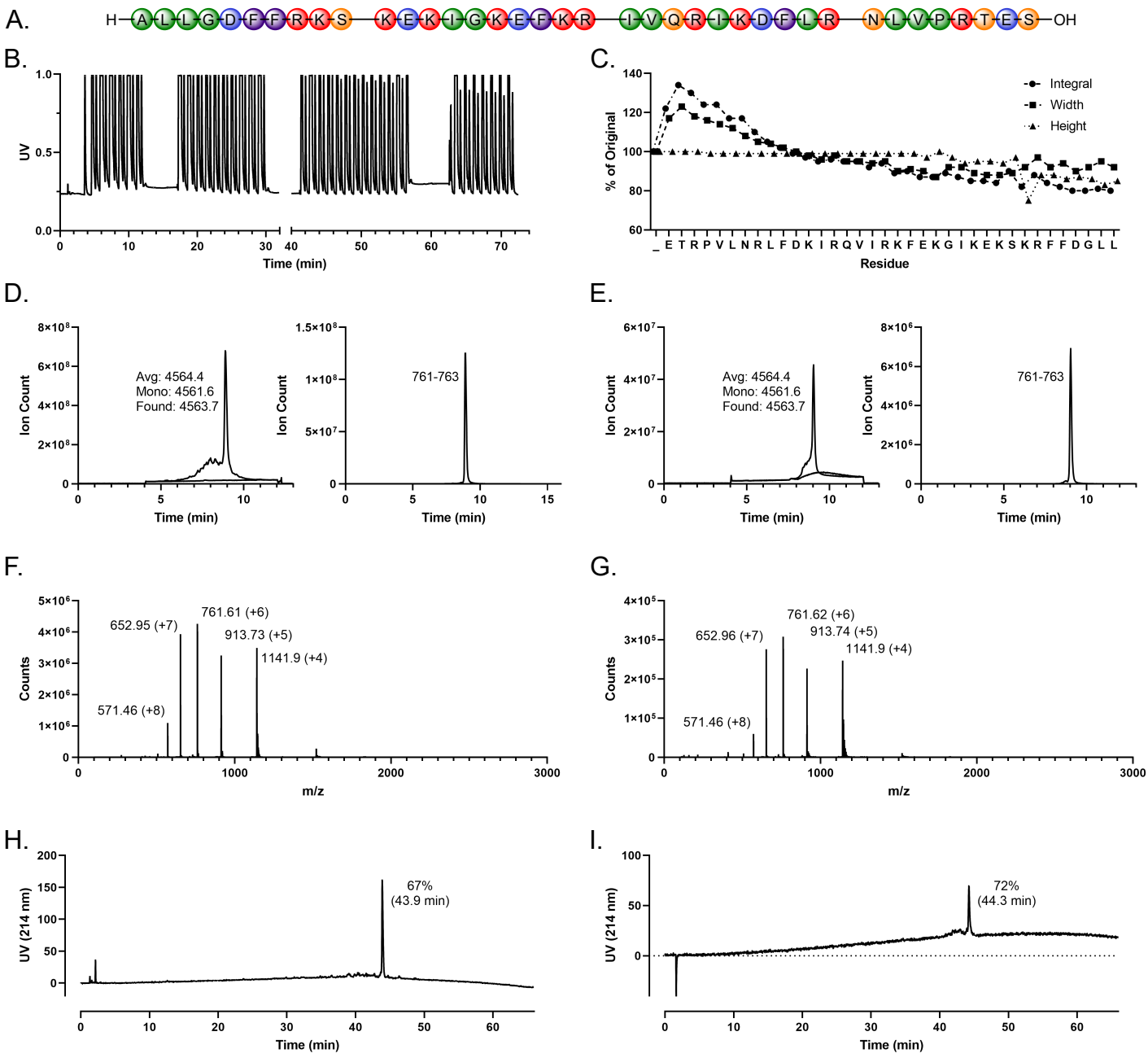
Supplementary Figure 5: A. KS-30 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Length. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



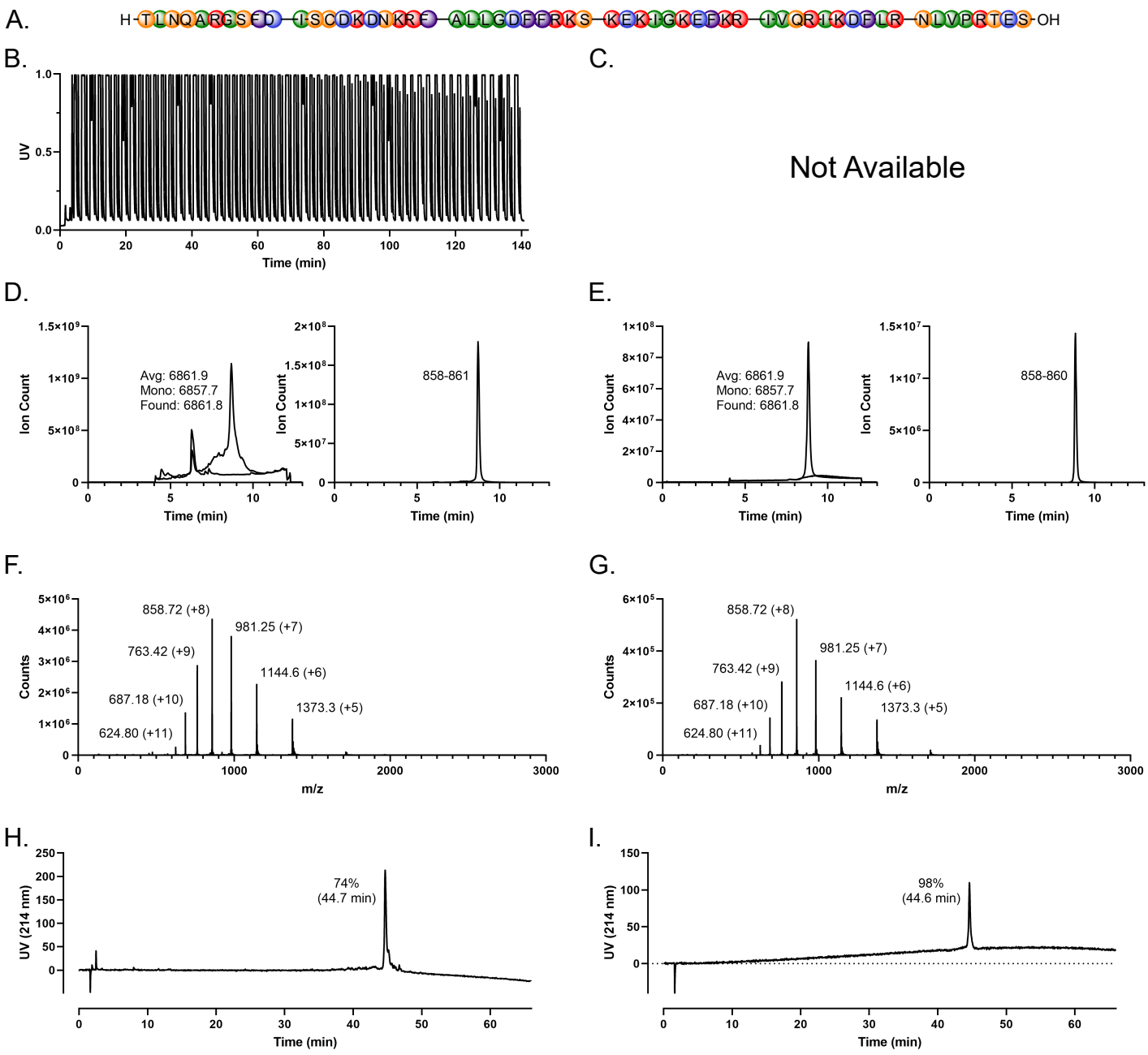
Supplementary Figure 6: A. RK-31 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed with batch addition of the N-terminal amino acid to a prior flow synthesis of KS-30 (not the one shown in **Supplementary Figure 5**). Spaces in the x-axis represent user-initiated pauses. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 3. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



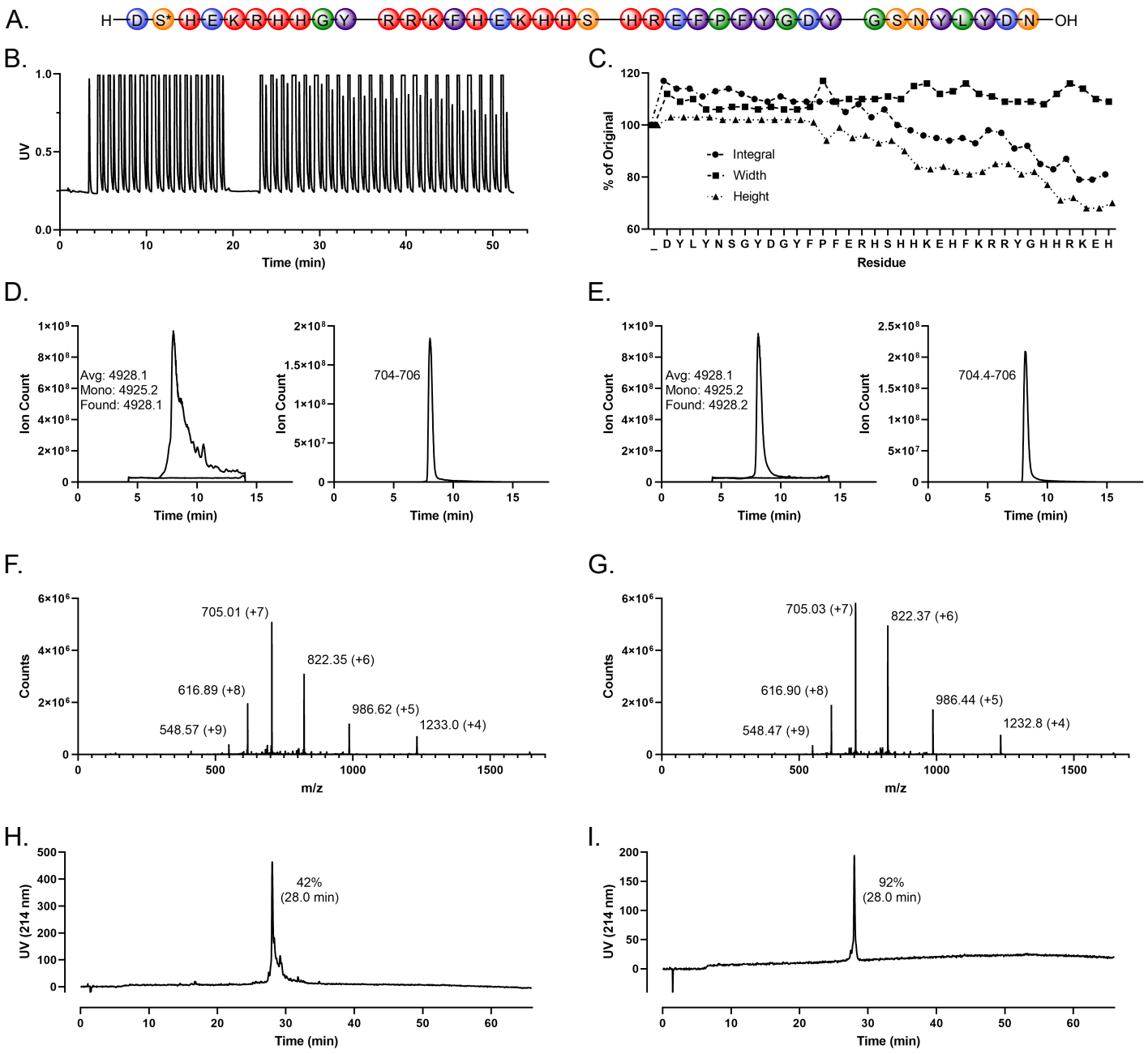
Supplementary Figure 7: A. LL-37 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Length. Spaces in the x-axis represent user-initiated pauses. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



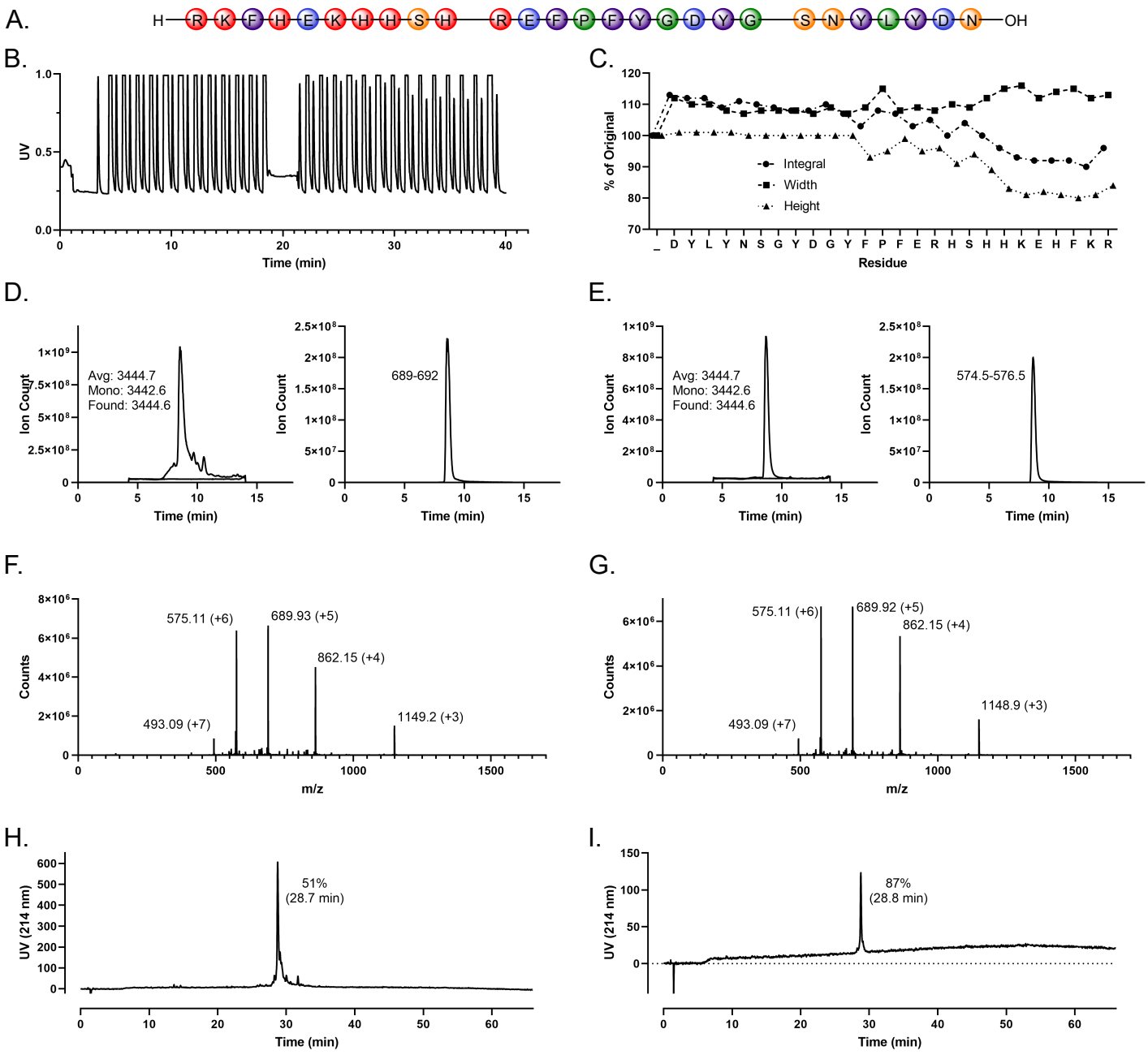
Supplementary Figure 8: A. ALL-38 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed with batch addition of the N-terminal amino acid to a prior flow synthesis of LL-37 (not the one shown in **Supplementary Figure 7**). Spaces in the x-axis represent user-initiated pauses. The x-axis is cut at a longer user-initiated pause; total time graphed includes the pause time. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 3. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



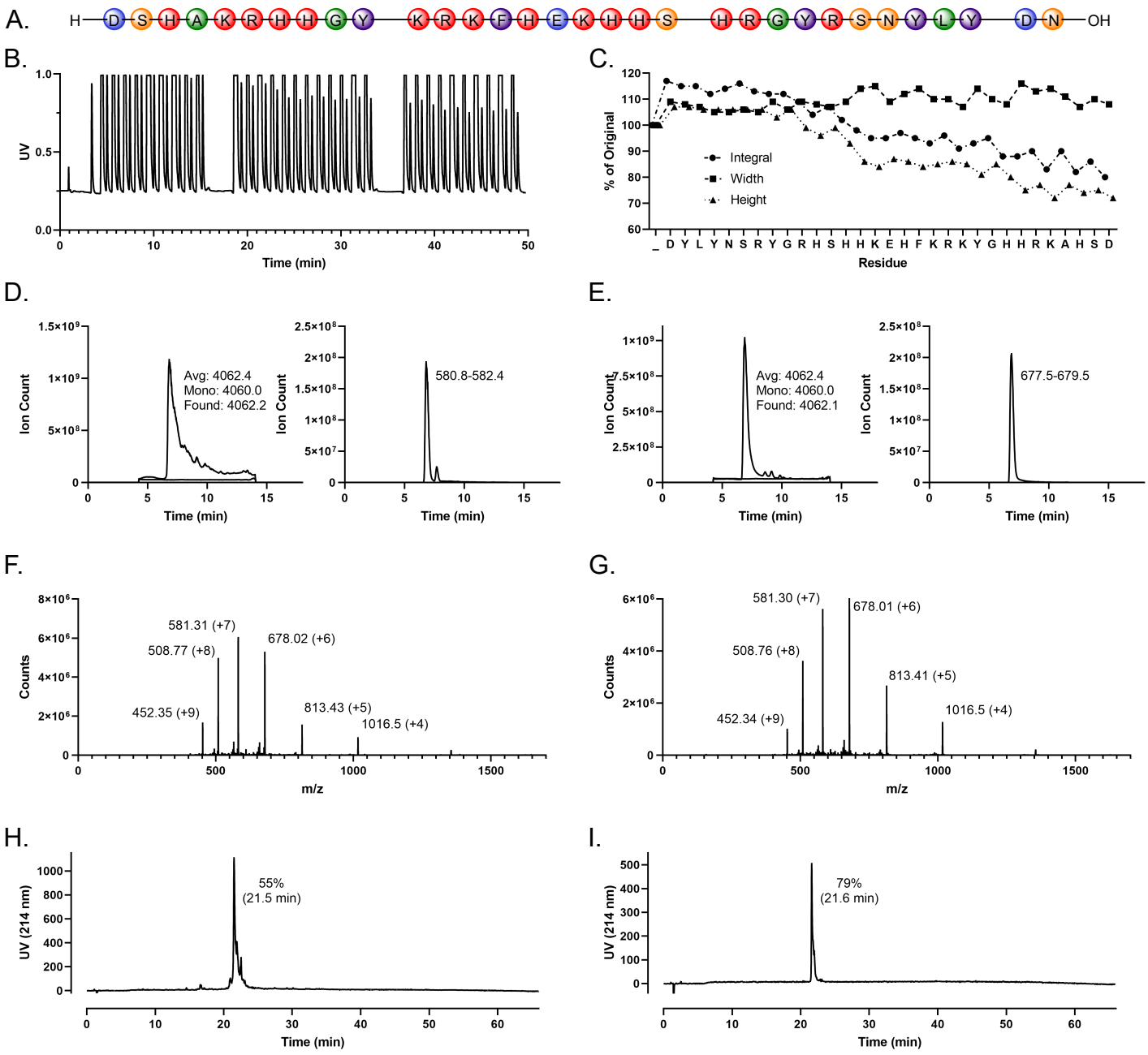
Supplementary Figure 9: A. TLN-58 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 4th Generation – Length. **C.** Integrals unavailable for this sequence. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 3. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



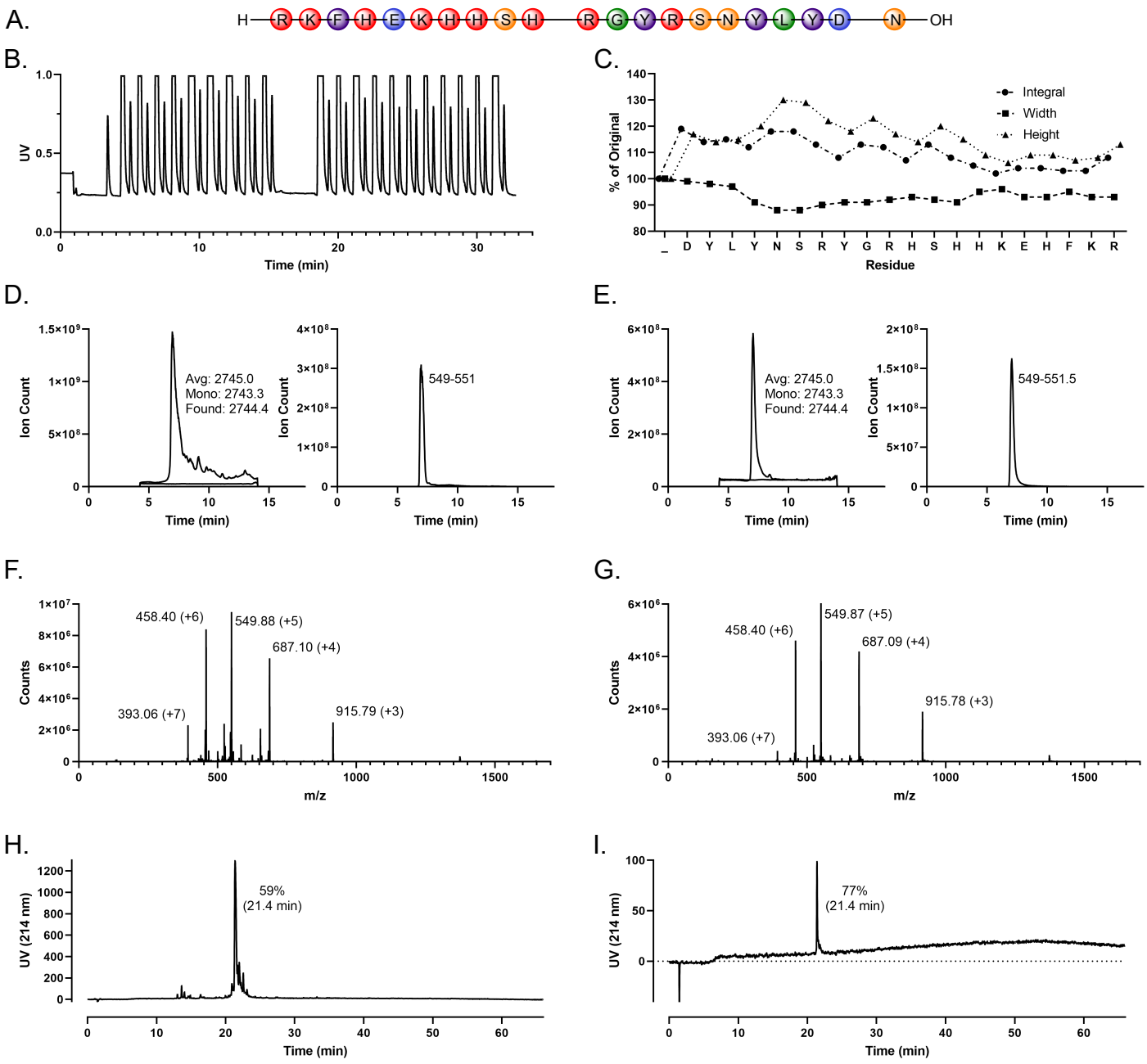
Supplementary Figure 10: A. Histatin 1 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. **B.** Synthesizer UV trace. 3rd Generation – Speed with batch addition of phospho-Ser2 and N-terminal Glu. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 2. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 2.



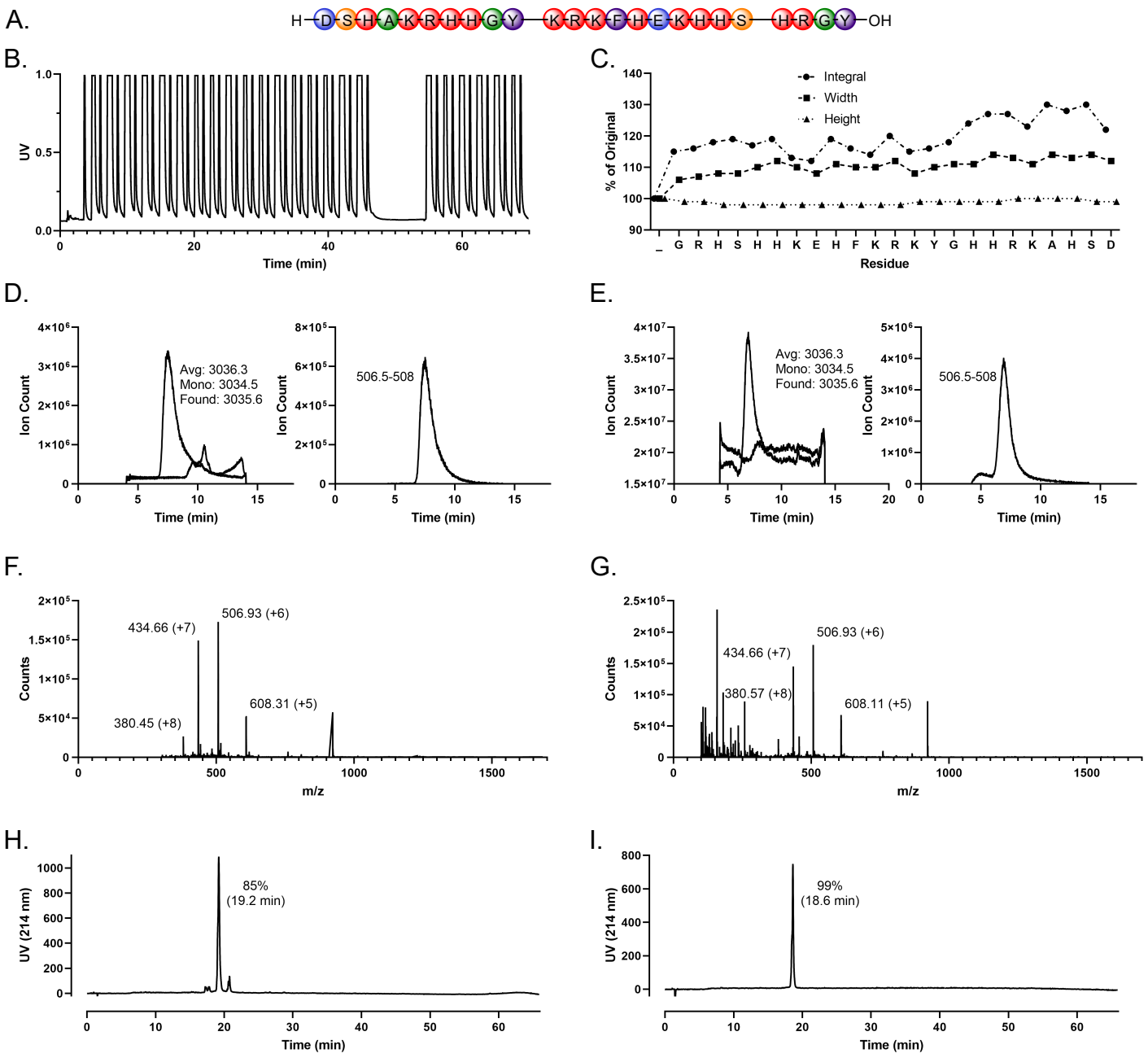
Supplementary Figure 11: A. Histatin 2 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 2. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 2.



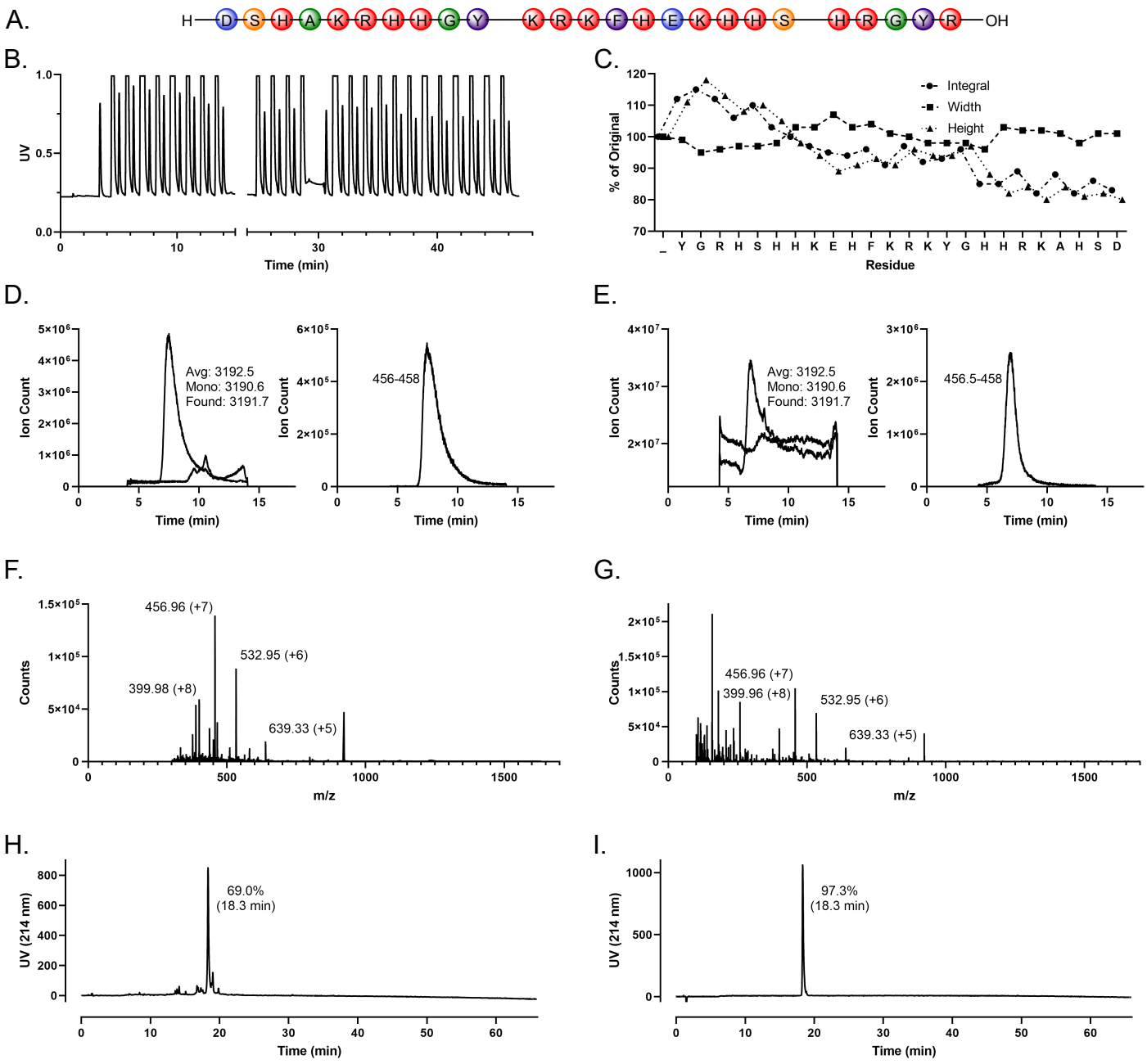
Supplementary Figure 12: A. Histatin 3 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 2. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 2.



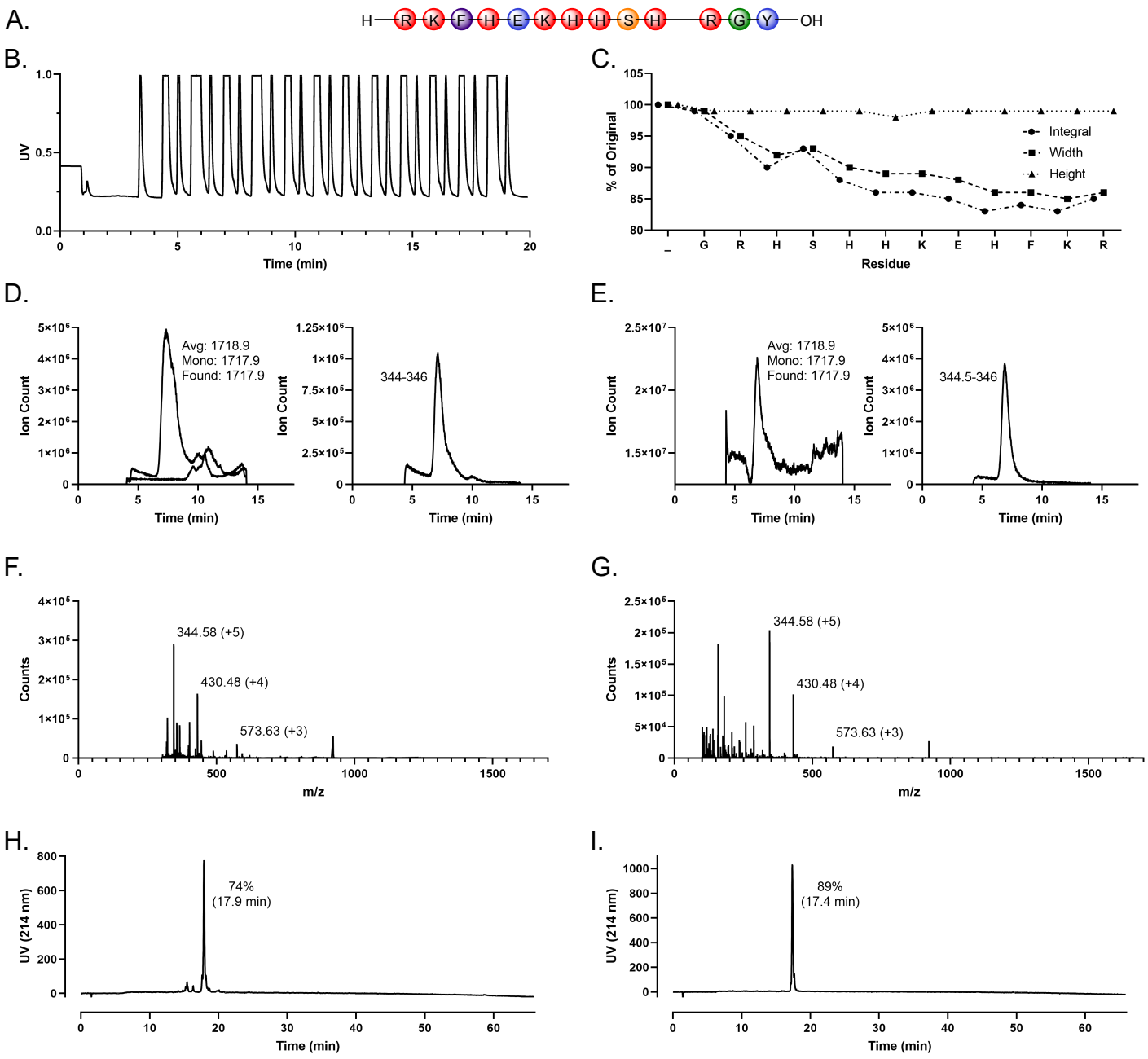
Supplementary Figure 13: A. Histatin 4 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 2. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 2.



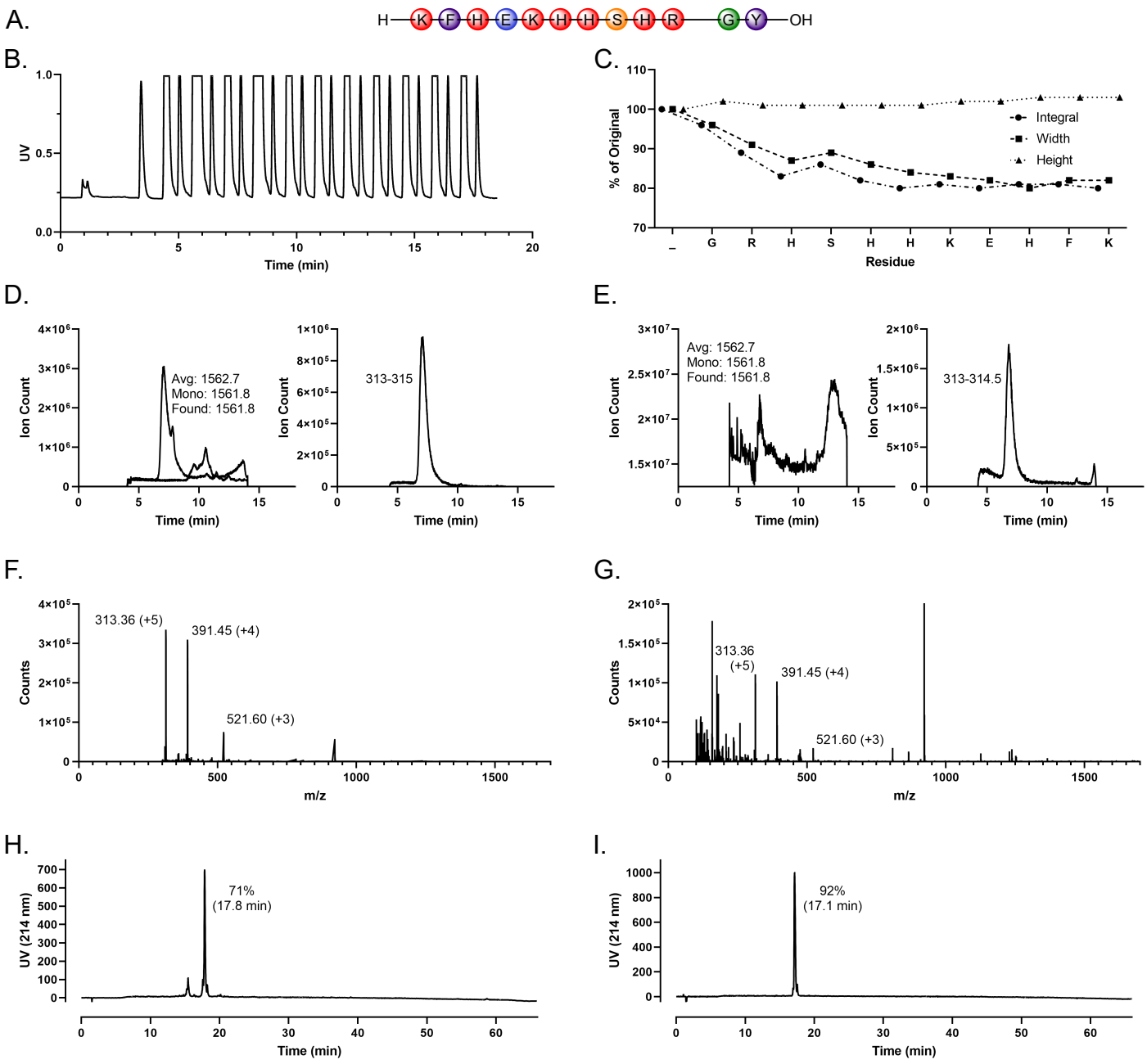
Supplementary Figure 14: A. Histatin 5 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. **B.** Synthesizer UV trace. 3rd Generation – Length. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 2. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 2.



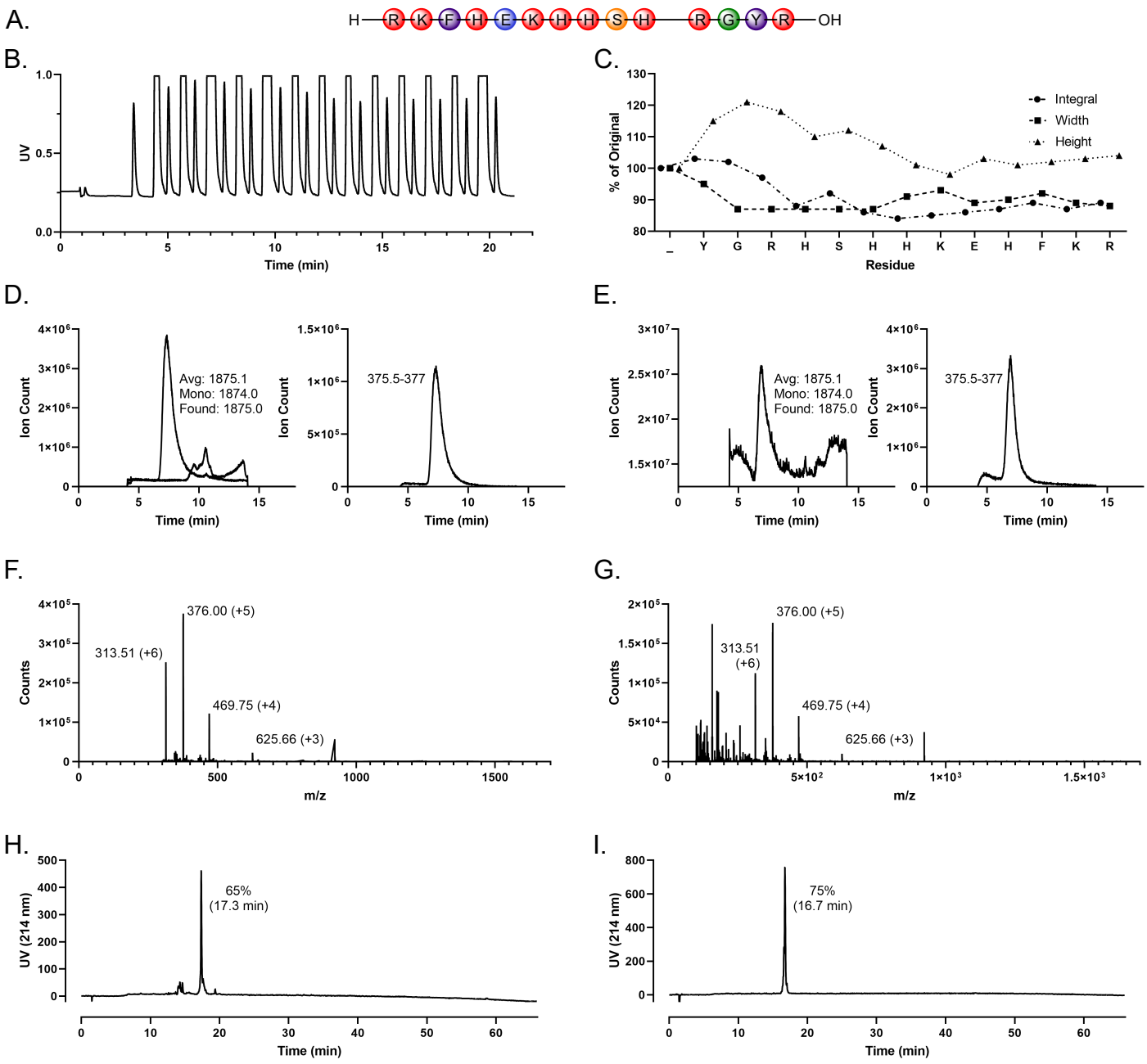
Supplementary Figure 15: A. Histatin 6 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. The x-axis is cut at a longer user-initiated pause; total time graphed includes the pause time. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 2. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 2.



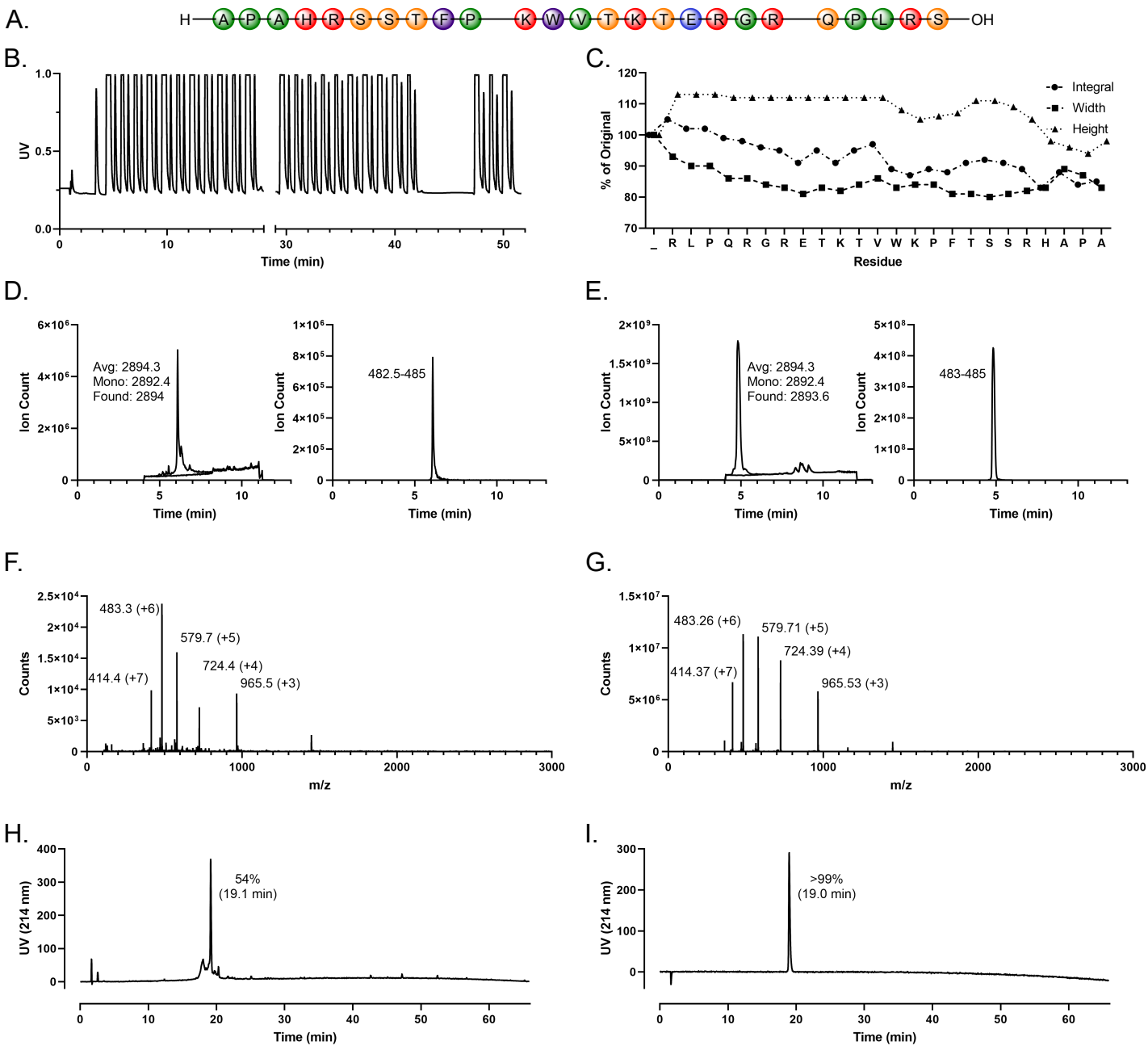
Supplementary Figure 16: A. Histatin 7 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 2. Blanks omitted from **D** and **E** due to poor baseline; see also main text. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 2.



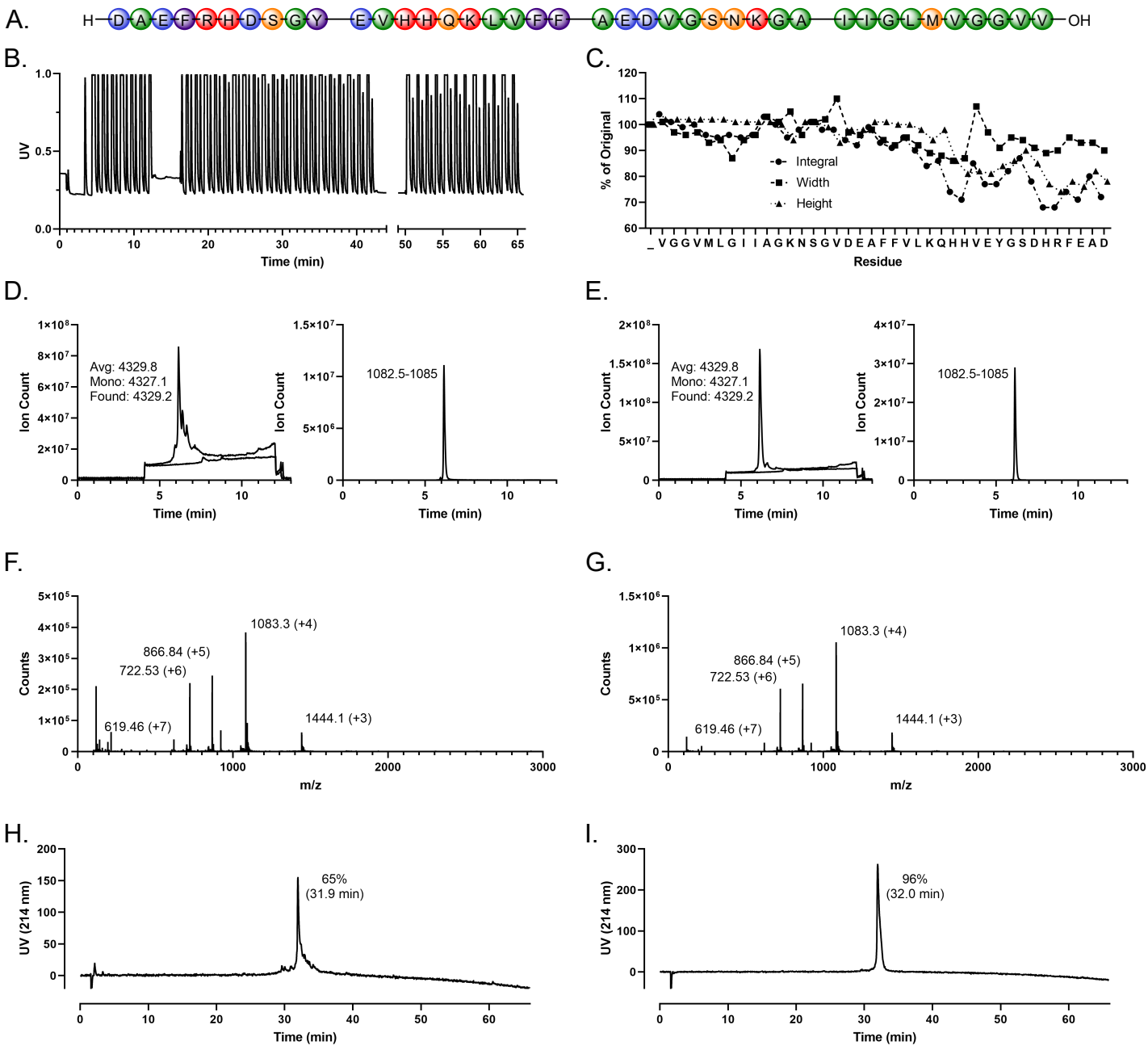
Supplementary Figure 17: A. Histatin 8 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 2. Blanks omitted from **D** and **E** due to poor baseline; see also main text. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 2.



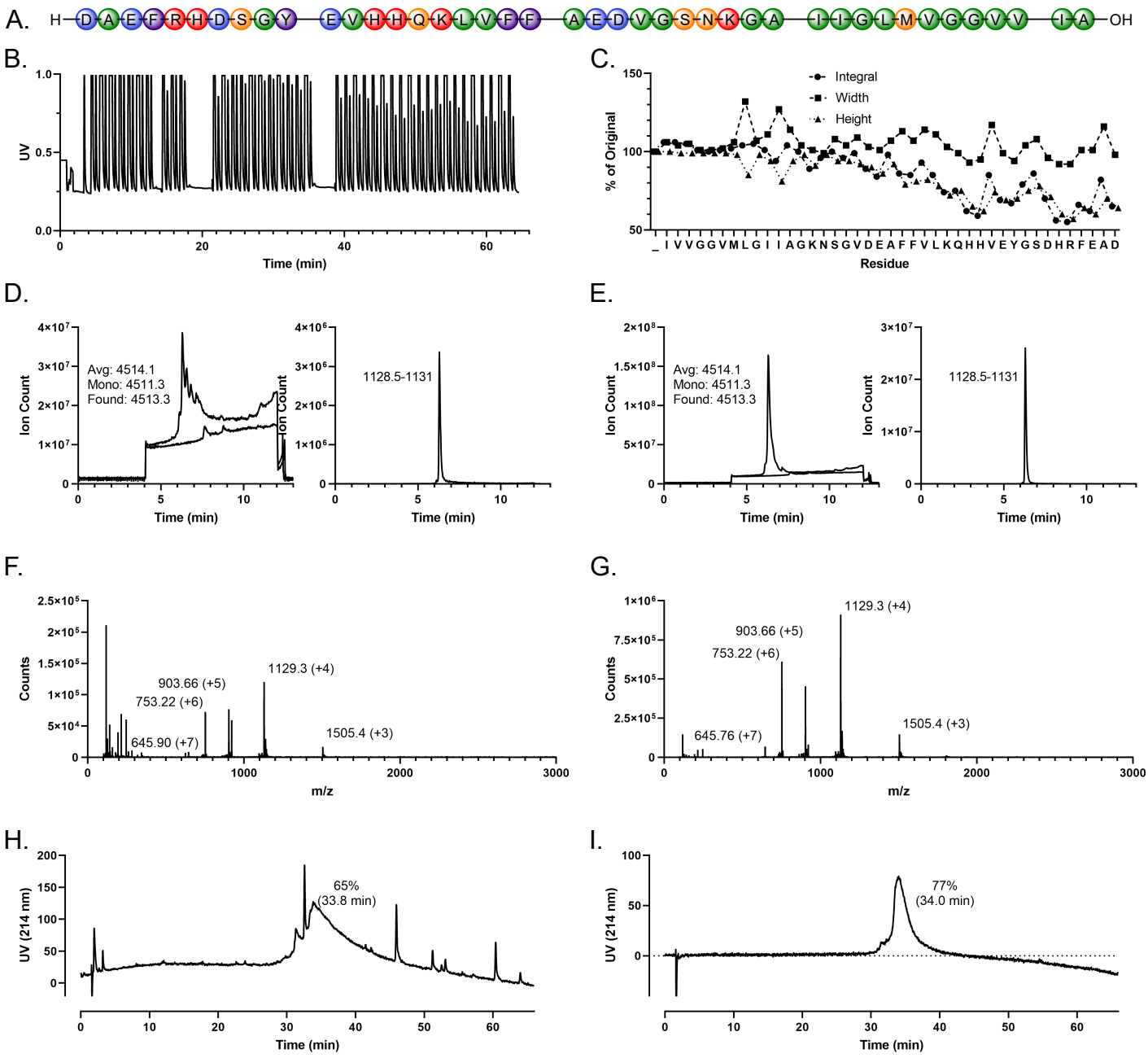
Supplementary Figure 18: A. Histatin 9 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 2. Blanks omitted from **D** and **E** due to poor baseline; see also main text. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. The charge states of the labeled ions are indicated in parentheses. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 2.



Supplementary Figure 19: A. Alarin sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. Spaces in the x-axis represent user-initiated pauses. The x-axis is cut at a longer pause; total time graphed includes the pause time. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



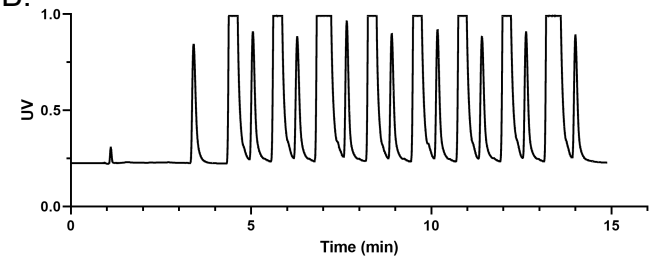
Supplementary Figure 20: A. Amyloid β 1-40 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. Spaces in the x-axis represent user-initiated pauses. The x-axis is cut at a longer pause; total time graphed includes the pause time. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 3. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



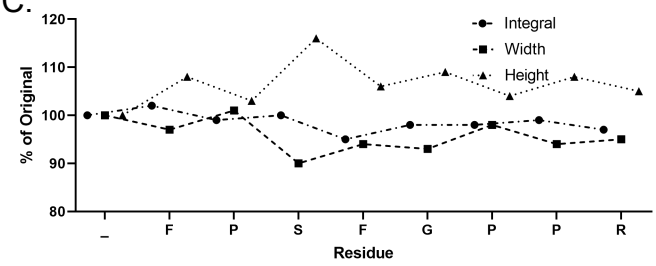
Supplementary Figure 21: A. Amyloid β 1-42 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 3. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.

A.

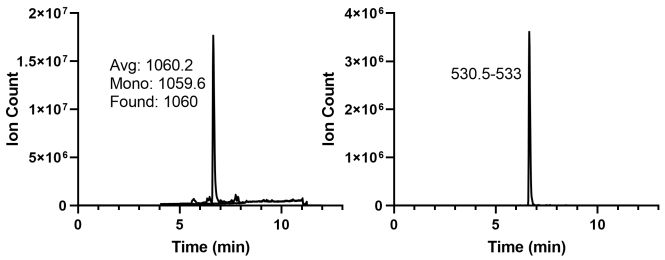
B.



C.



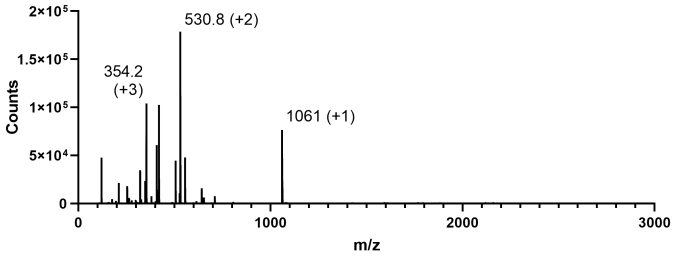
D.



E.

Not Available

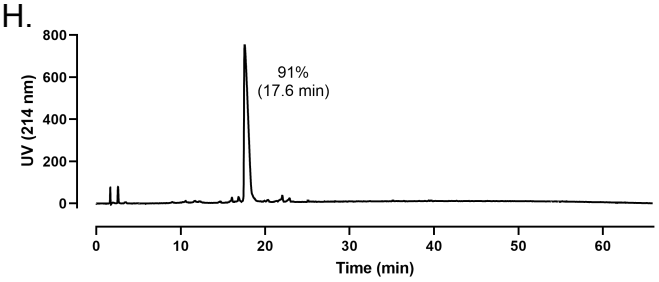
F.



G.

Not Available

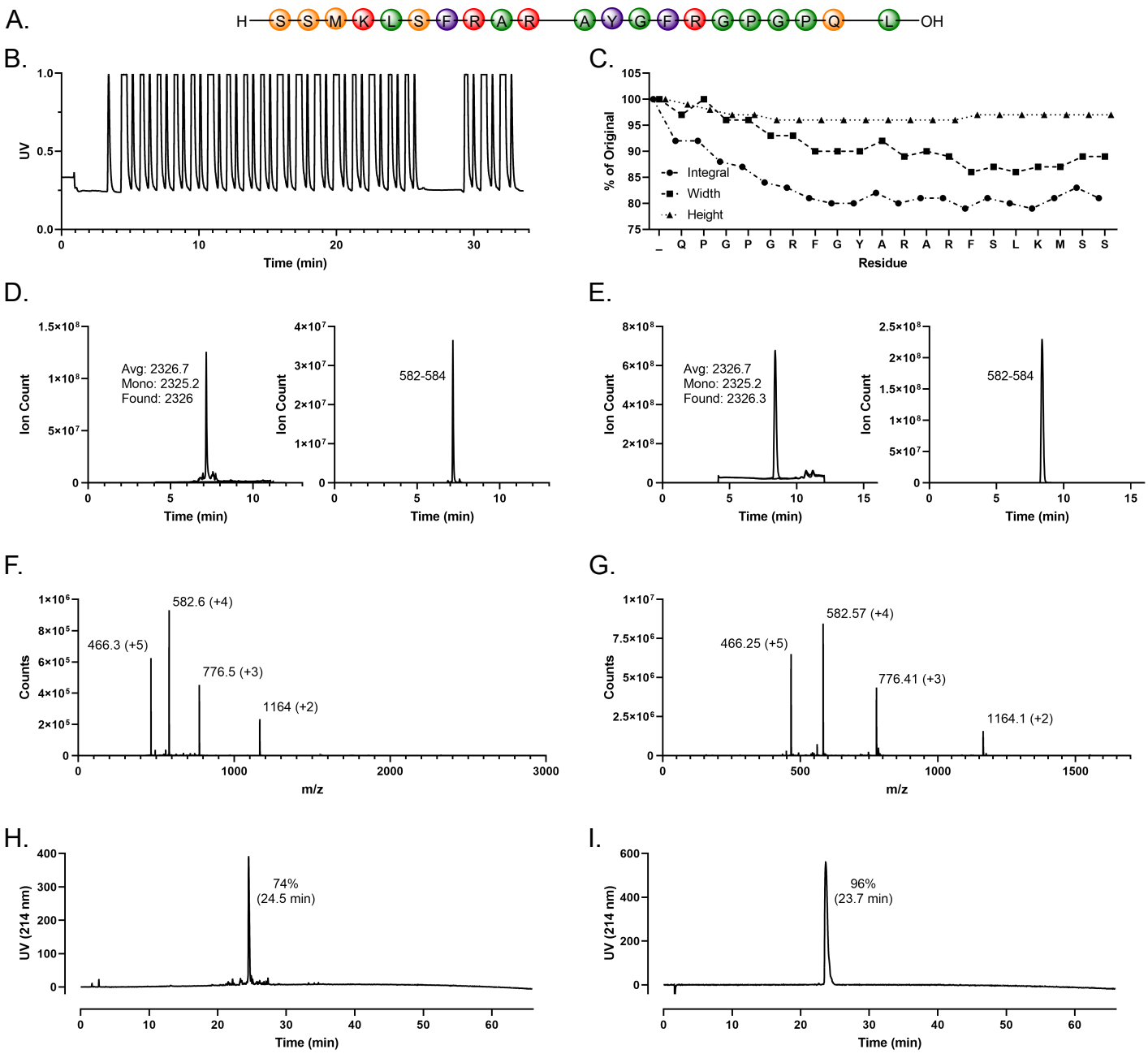
H.



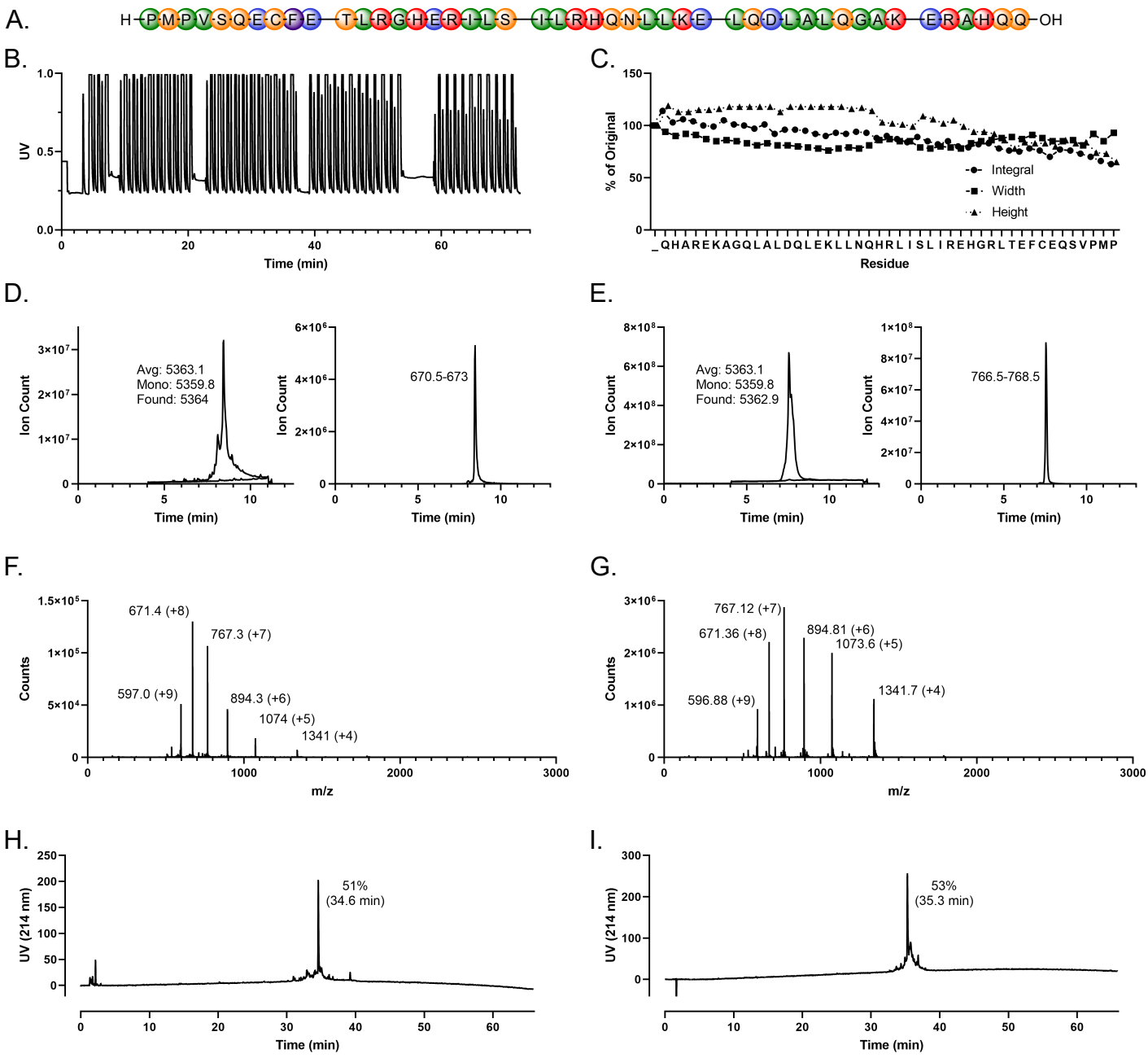
I.

Not Available

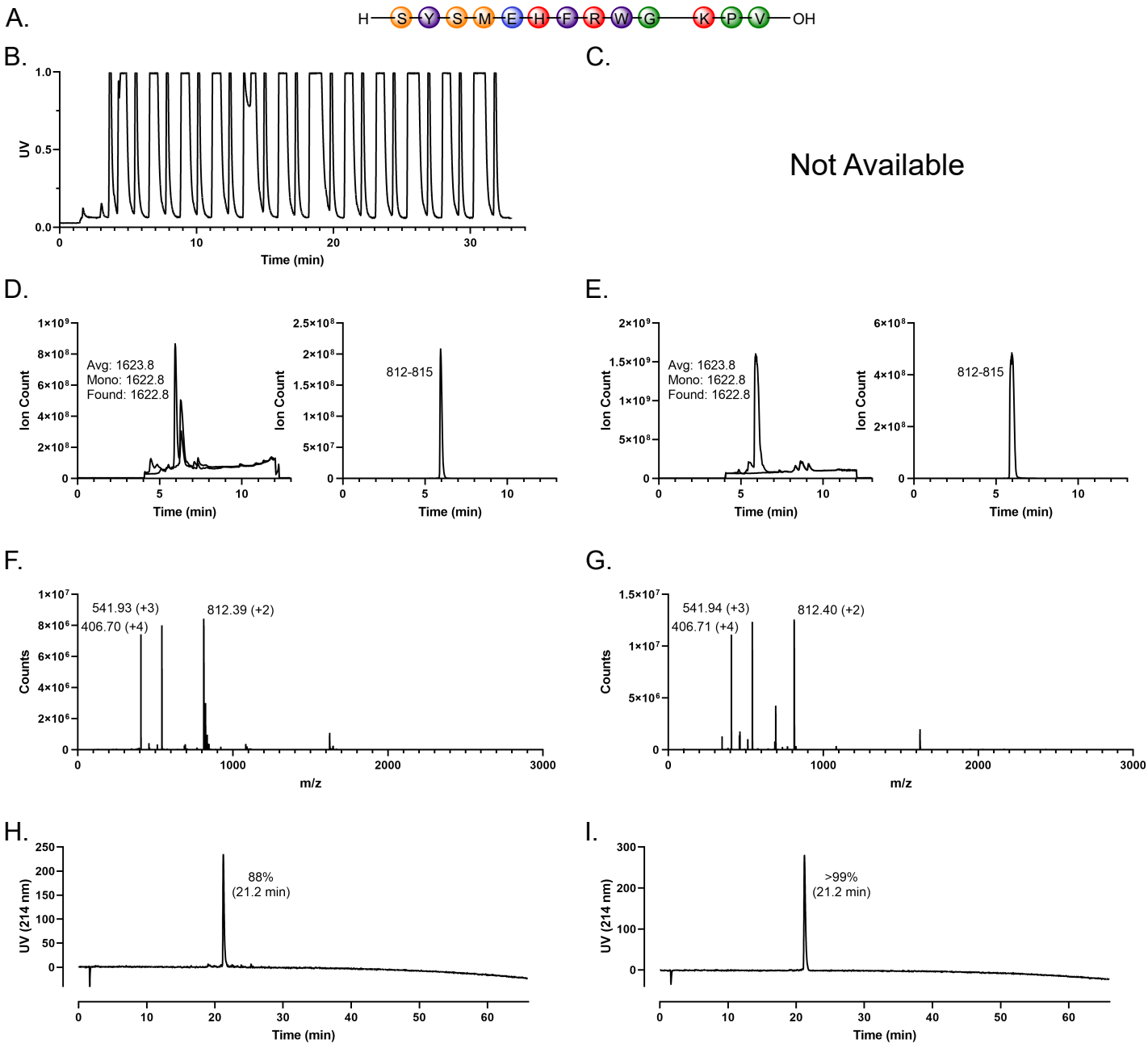
Supplementary Figure 22: A. Bradykinin sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** Not purified. **F.** Mass spectrum associated with the dominant peak of **D. G.** Not purified. **H.** Analytical HPLC trace of crude peptide with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1. **I.** Not purified.



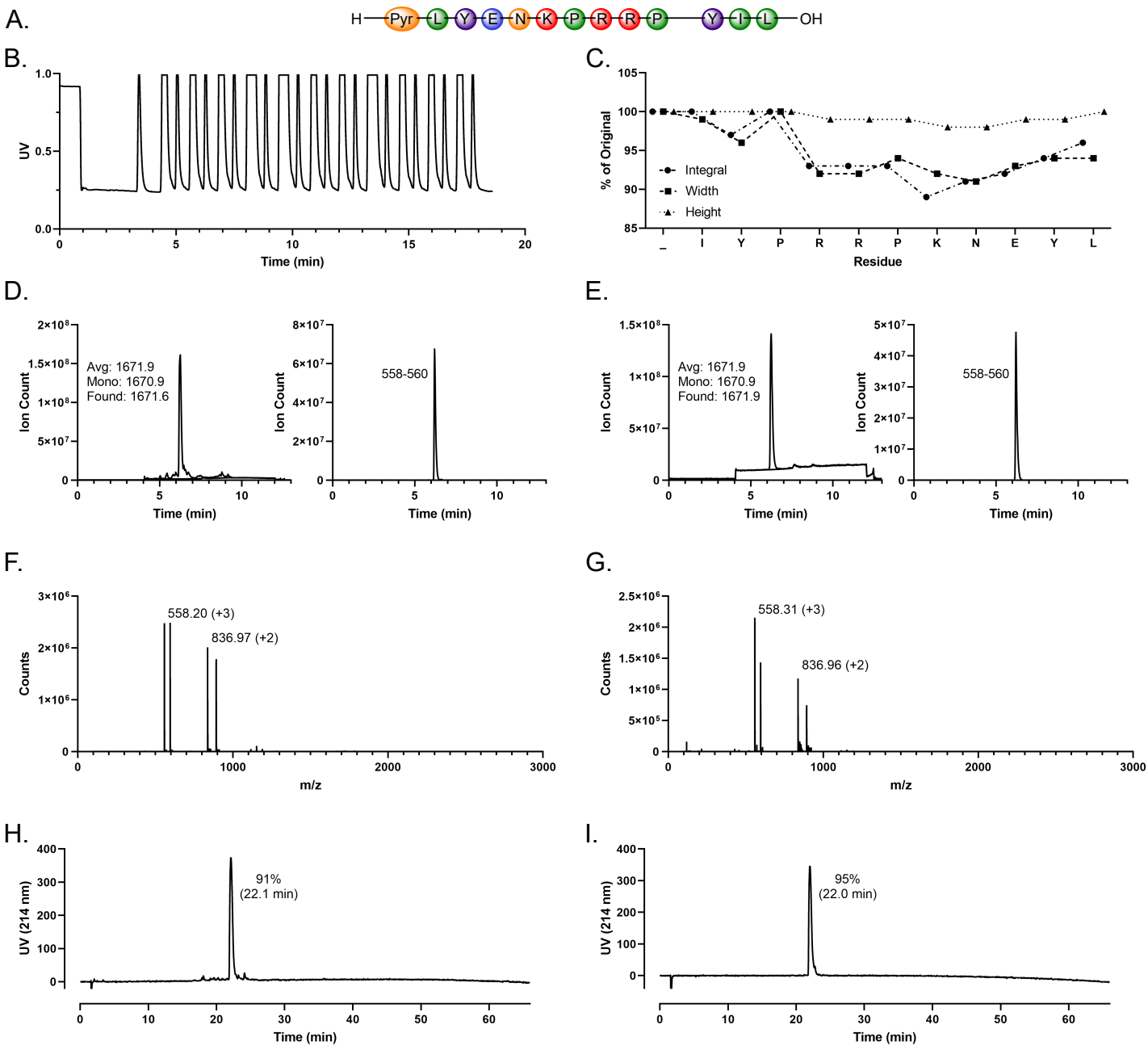
Supplementary Figure 23: A. Catestatin sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. Spaces in the x-axis represent user-initiated pauses. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 1. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



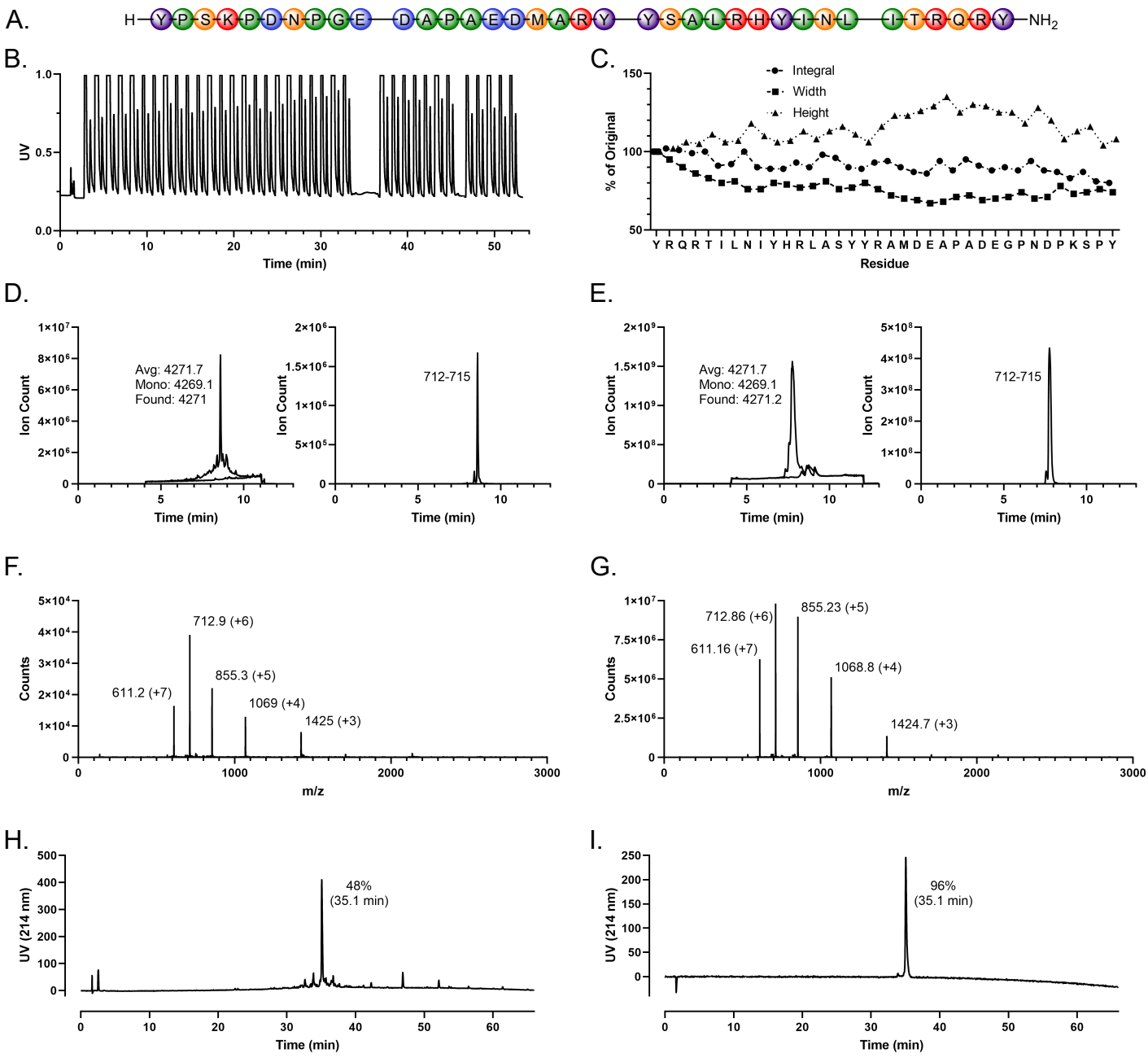
Supplementary Figure 24: A. CGA-N46 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



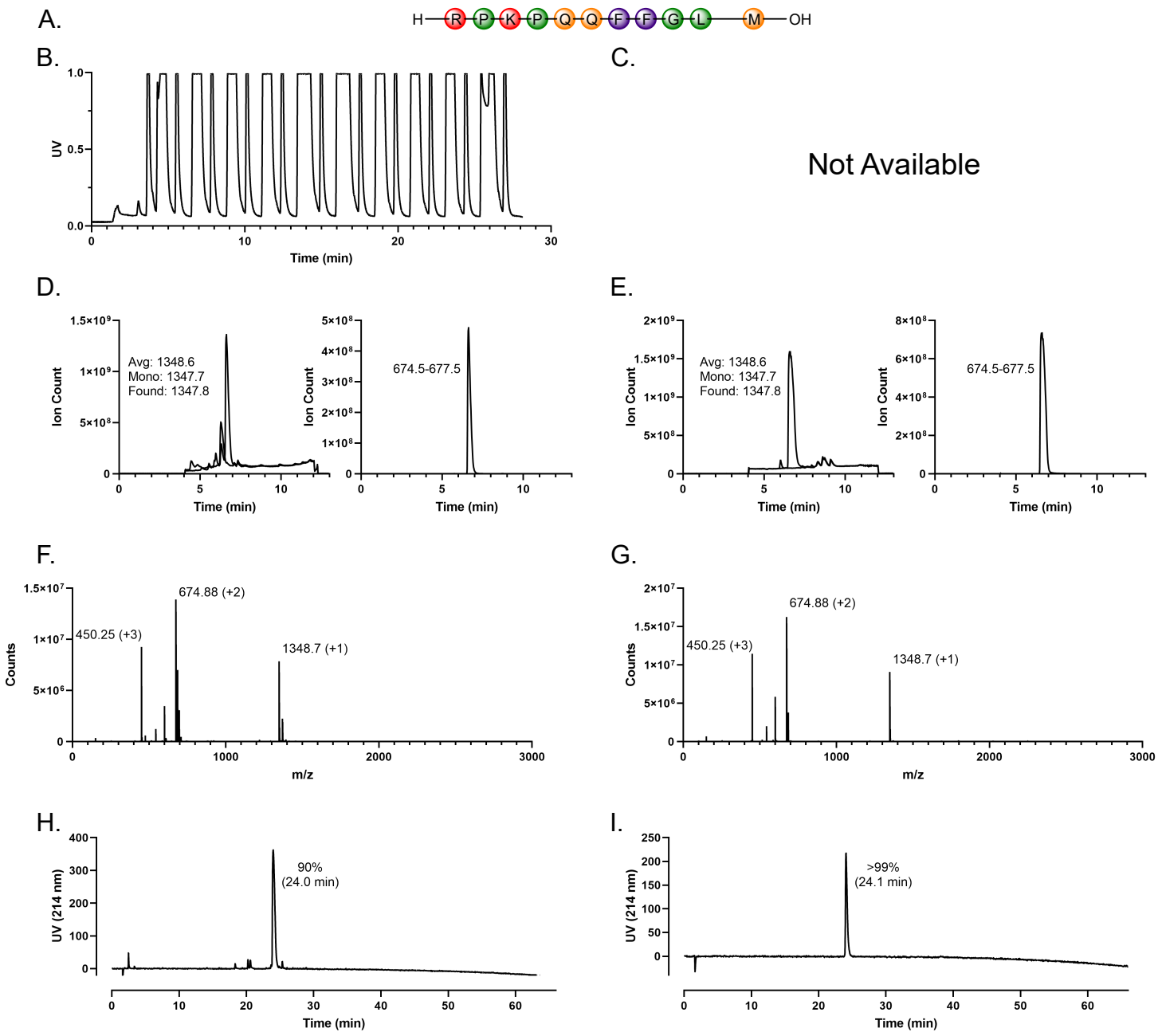
Supplementary Figure 25: A. α MSH sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 4th Generation – Length. **C.** Integrals unavailable for this sequence. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 3. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



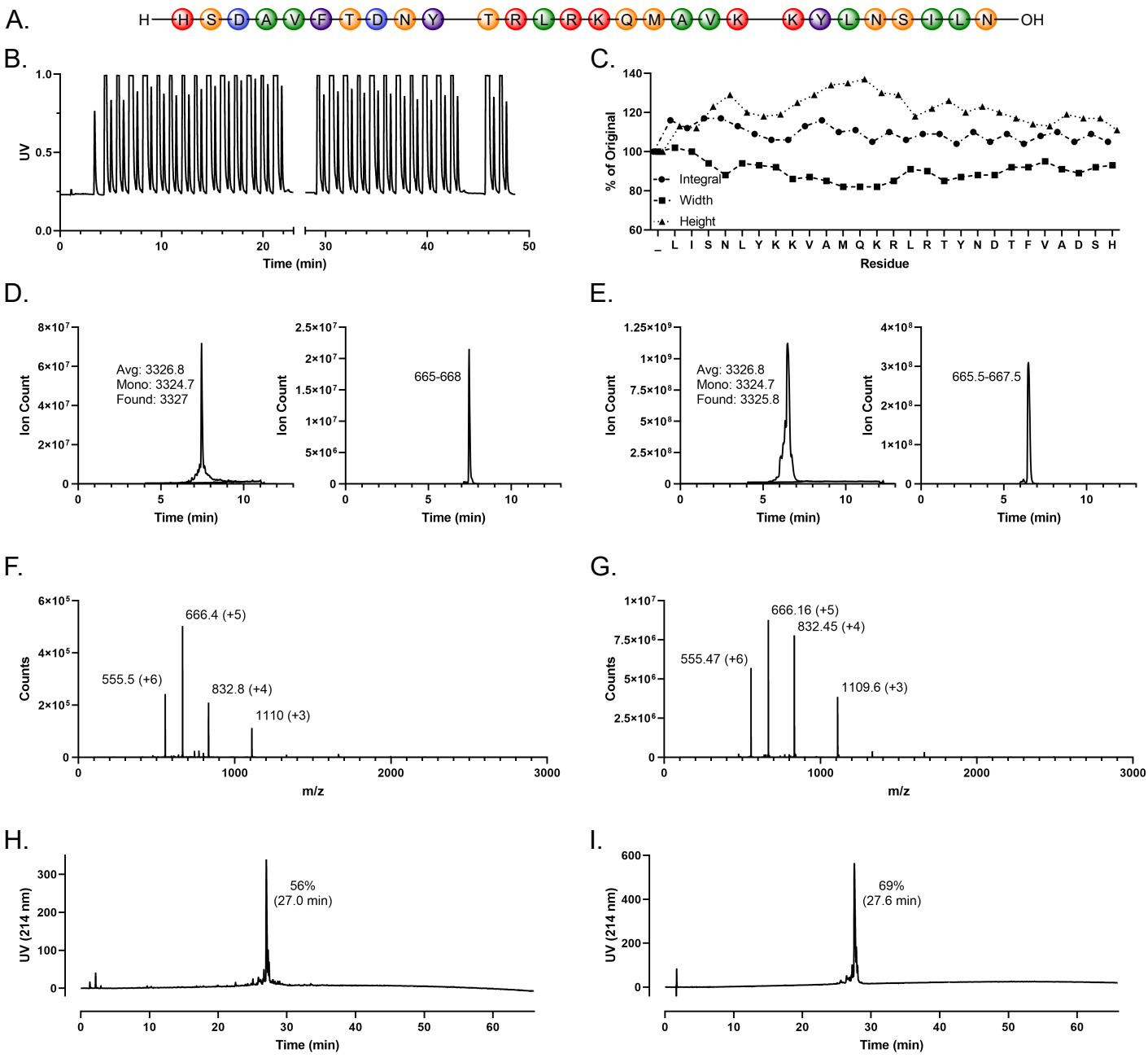
Supplementary Figure 26: A. Neurotensin sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic); see main text for discussion pertaining to this synthesis. **B.** Synthesizer UV trace. 3rd Generation – Speed with batch addition of N-terminal pyroglutamate. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 3. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



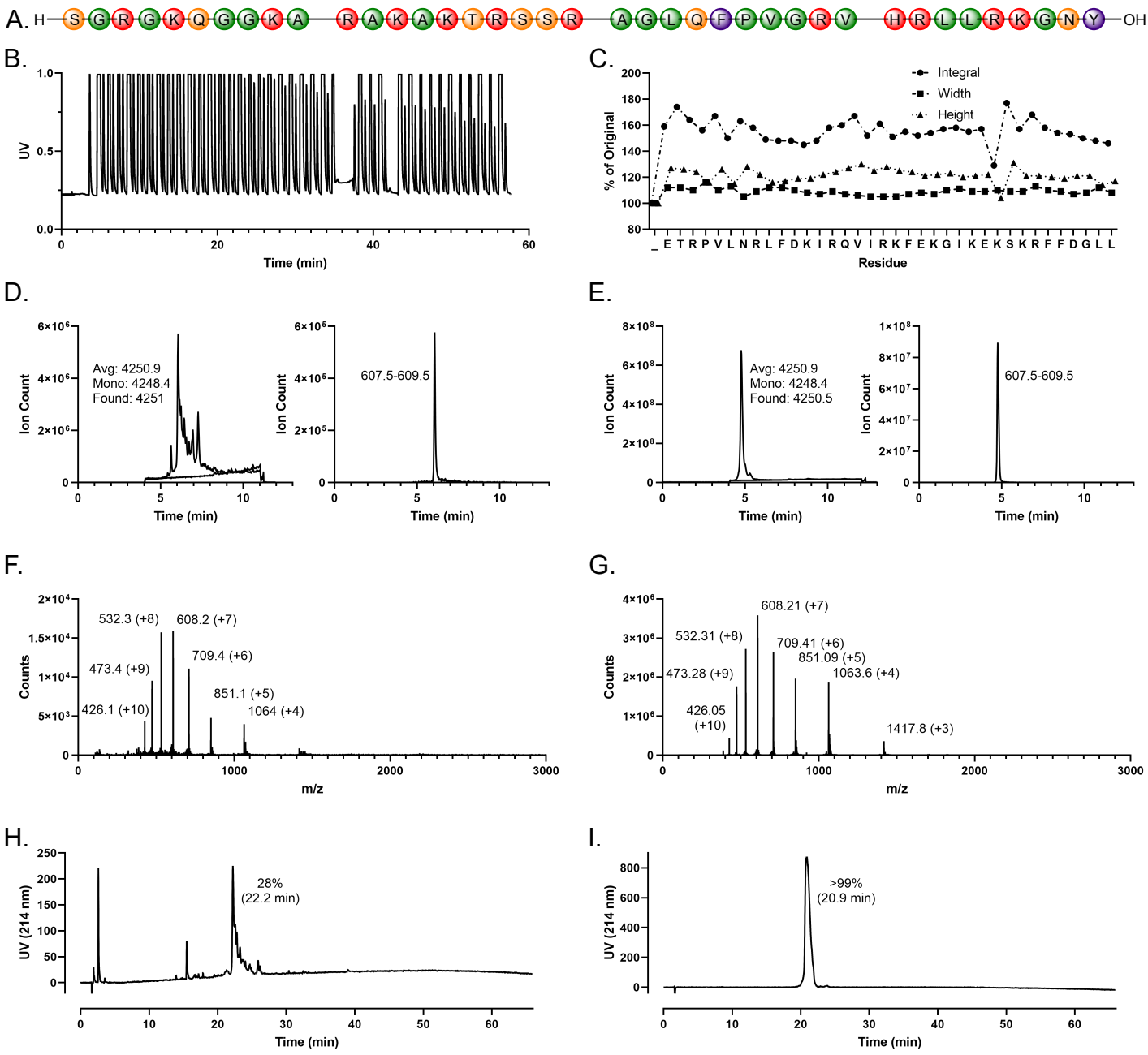
Supplementary Figure 27: A. Neuropeptide Y (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed on Rink Amide to yield C-terminal amide on acid cleavage. Spaces in the x-axis represent user-initiated pauses. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



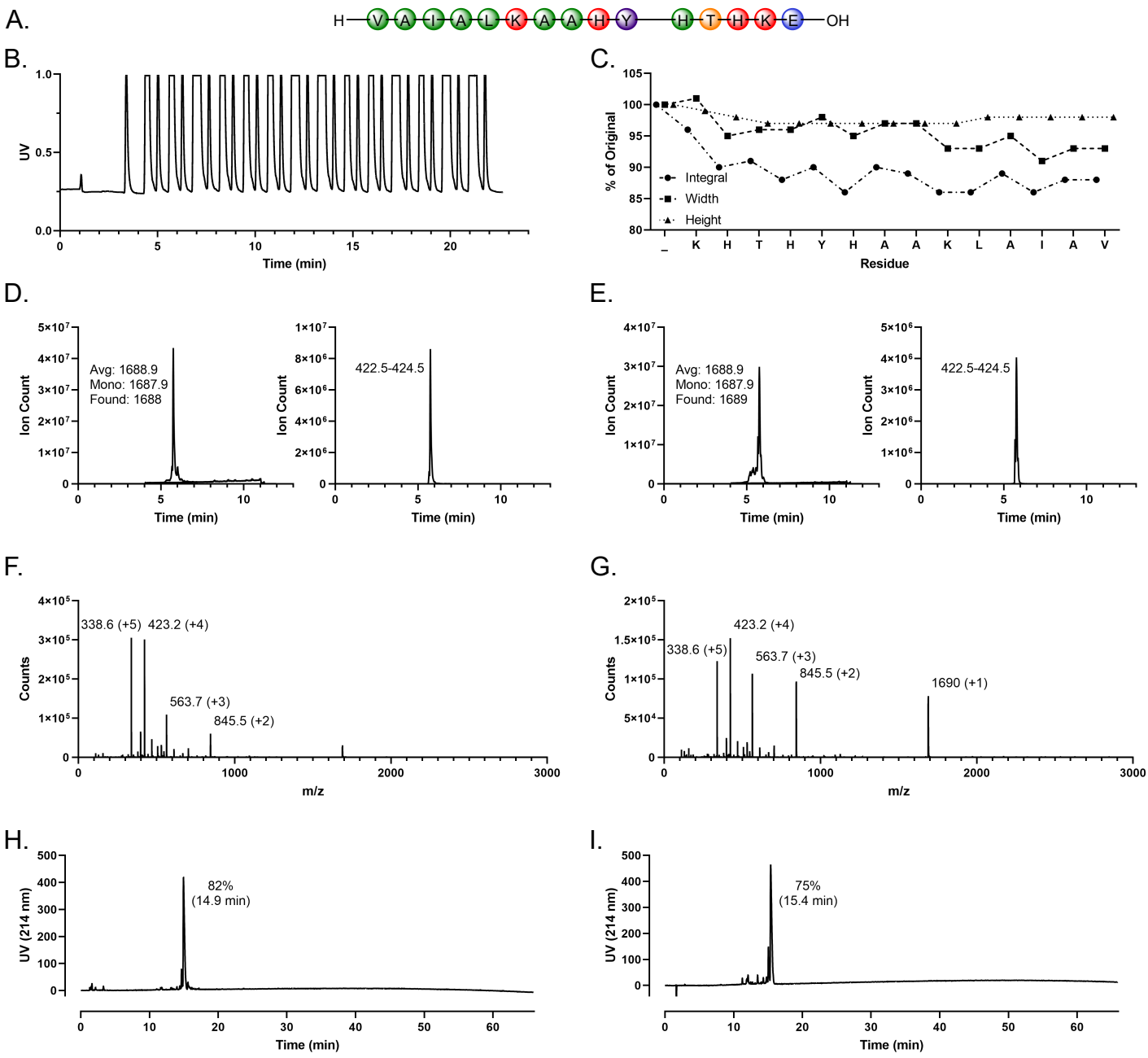
Supplementary Figure 28: A. Substance P sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 4th Generation – Length. **C.** Integrals unavailable for this sequence. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 3. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



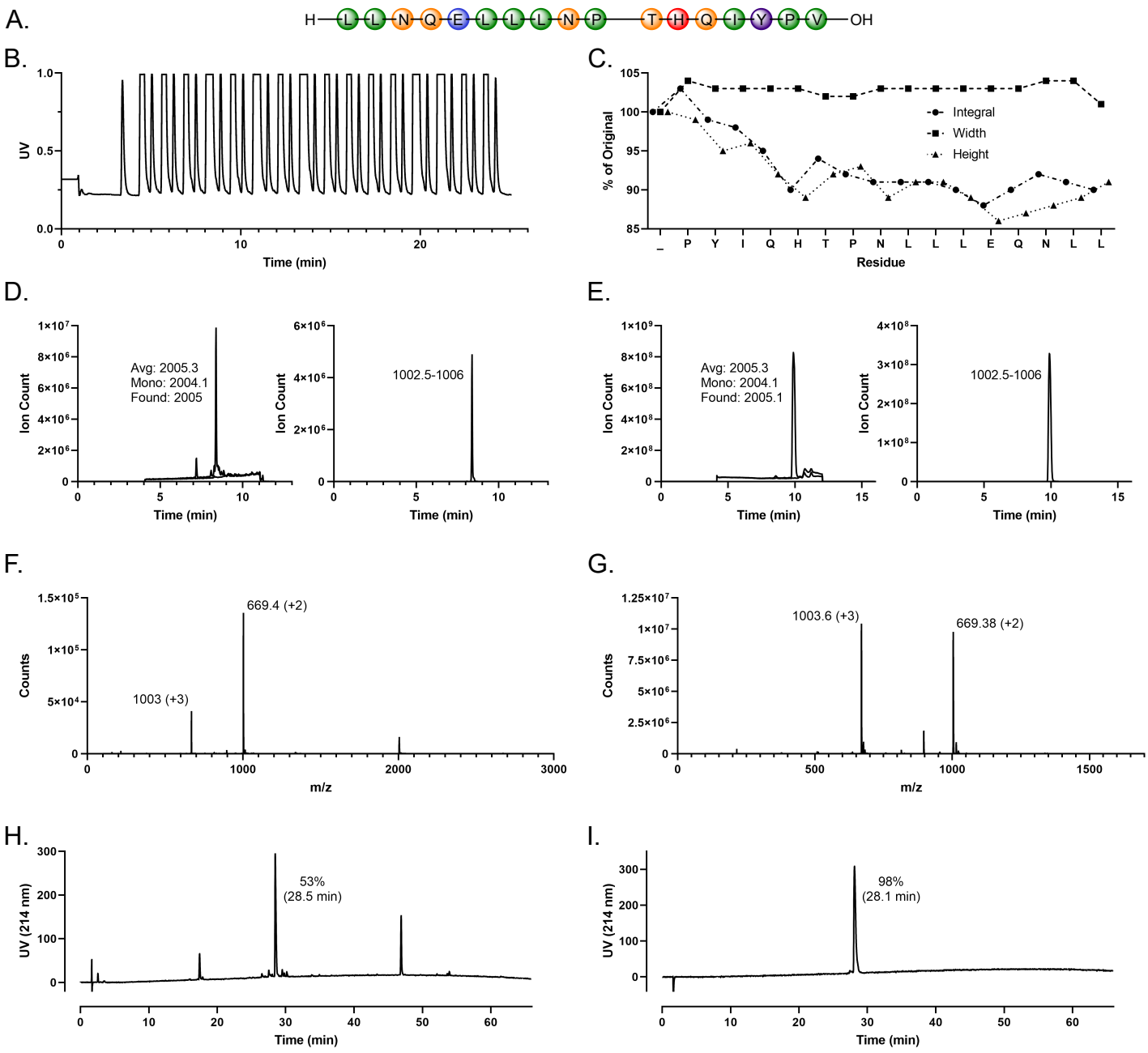
Supplementary Figure 29: A. Vasoactive Intestinal Peptide sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. Spaces in the x-axis represent user-initiated pauses. The x-axis is cut at a longer pause; total time graphed includes the pause time. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



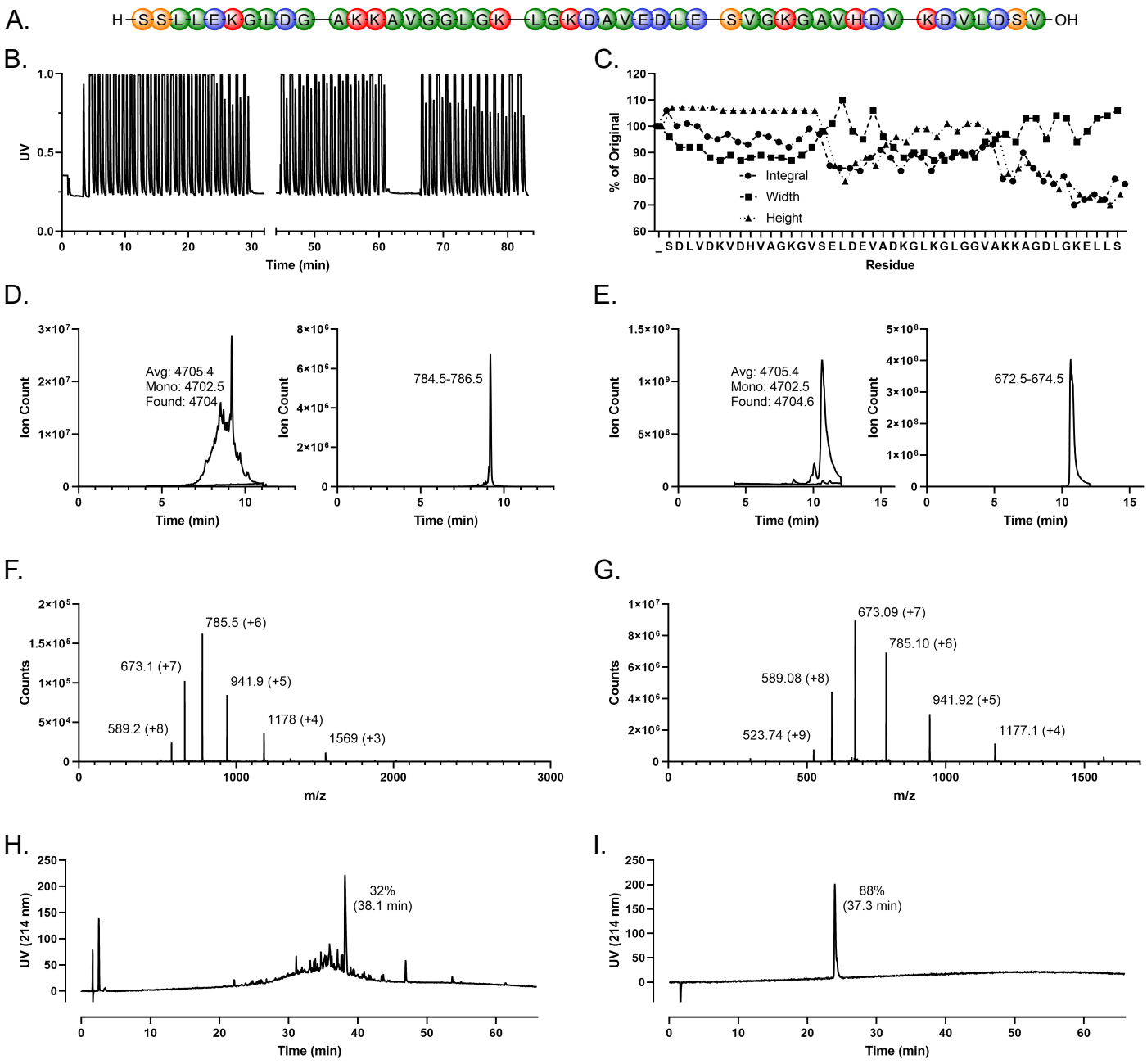
Supplementary Figure 30: A. Buforin I sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



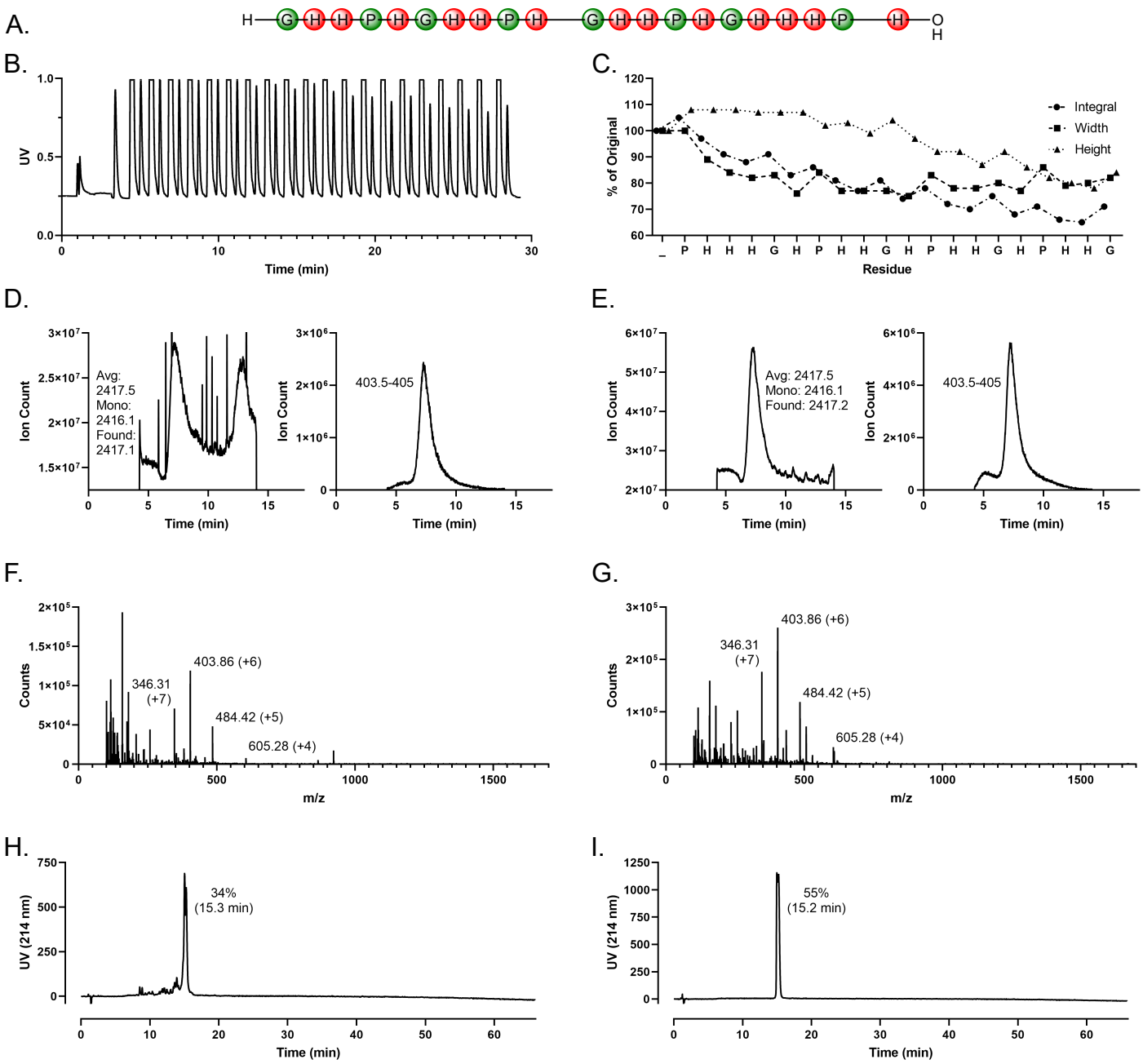
Supplementary Figure 31: A. Calcitermin sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 5. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



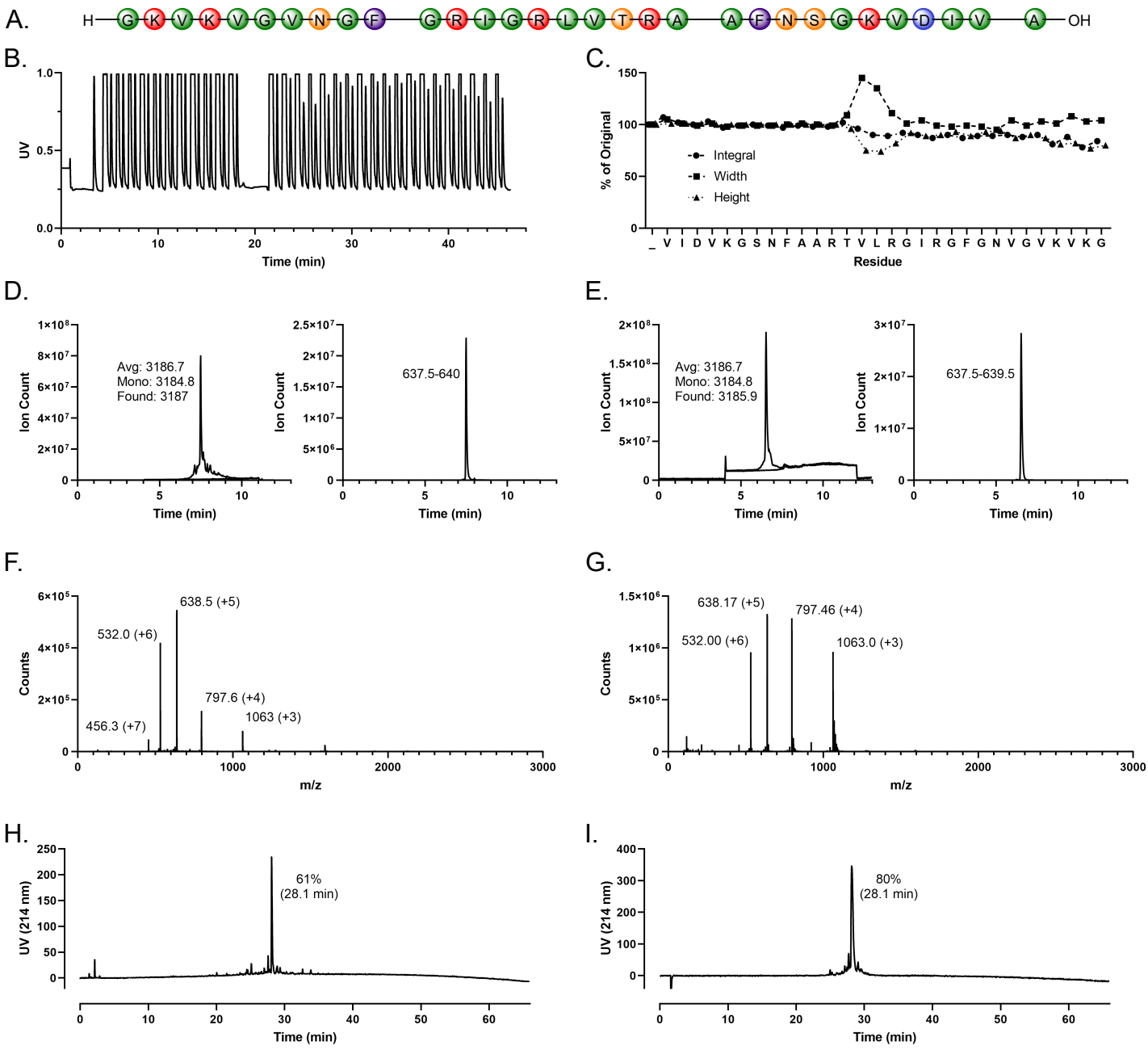
Supplementary Figure 32: A. β-casein 197 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 1. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



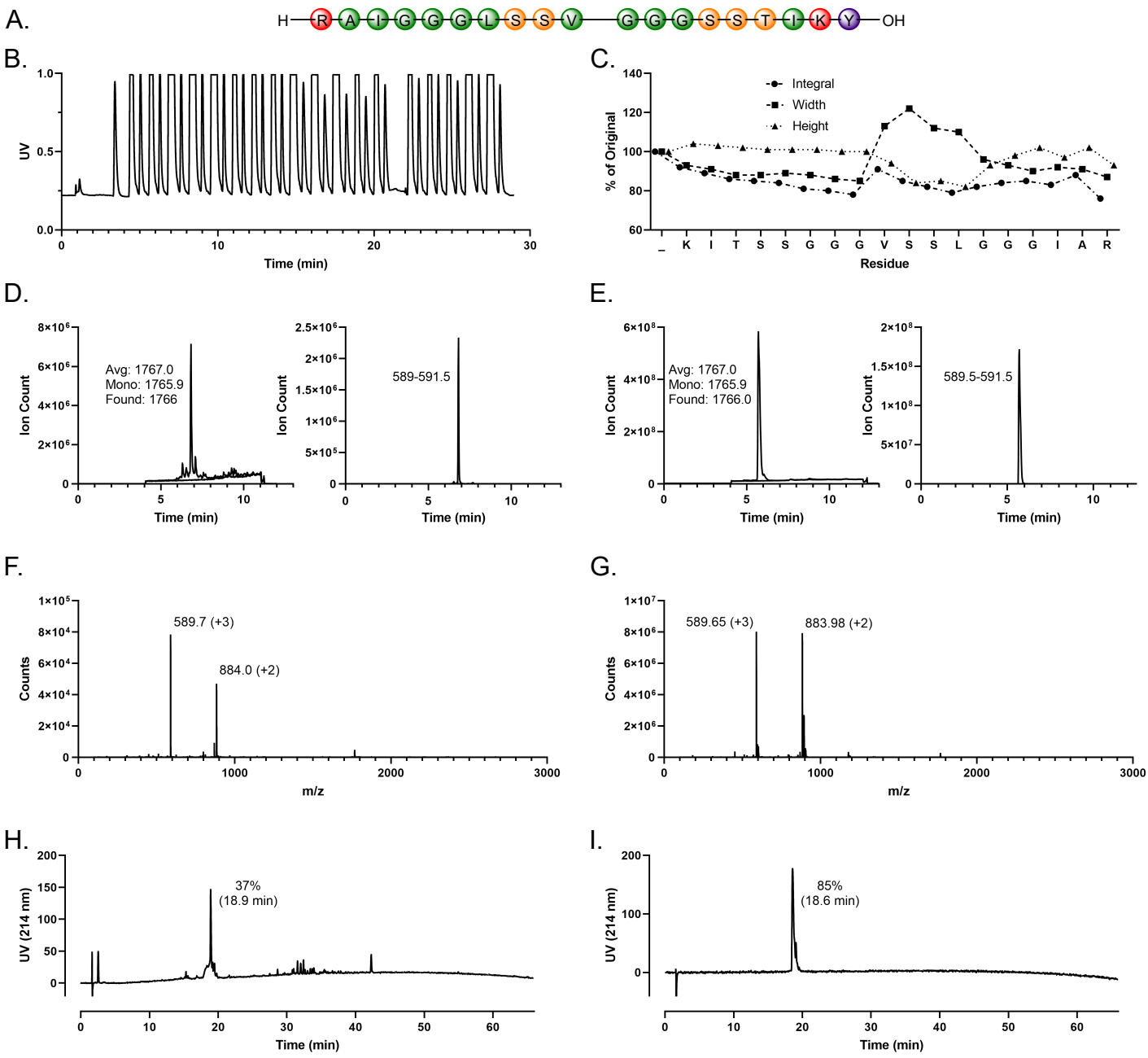
Supplementary Figure 33: A. Dermcidin sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. The x-axis is cut at a longer pause; total time graphed includes the pause time. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCM S Method 1. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



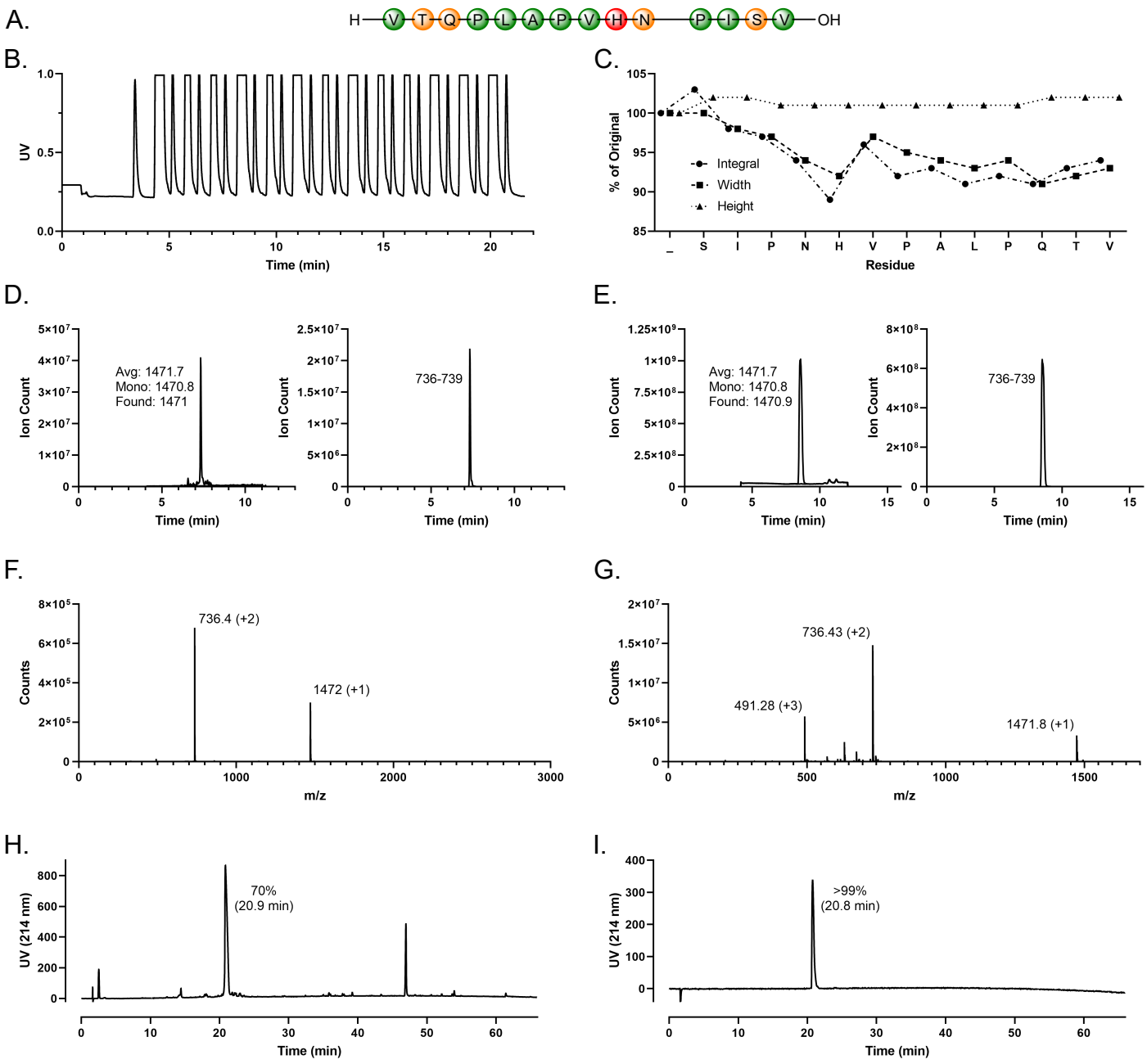
Supplementary Figure 34: A. GHH20 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 2. Blanks are omitted from panels **D** and **E** due to separate issues with each (MS spiking similar to the sample shown in **D** and substantial debris from prior runs in **E**). **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 2.



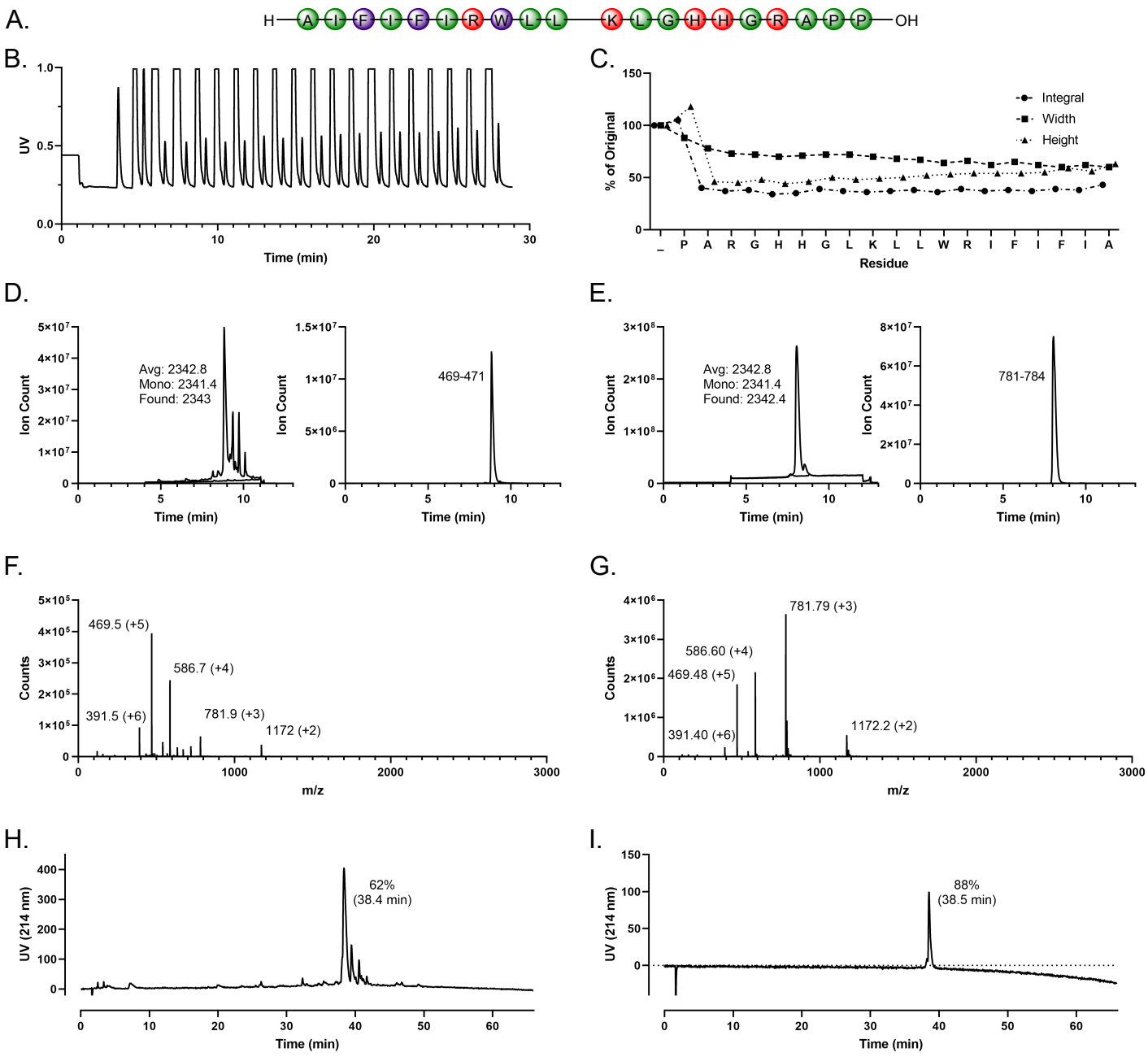
Supplementary Figure 35: A. hGAPDH sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



Supplementary Figure 36: A. KDAMP 19-mer sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



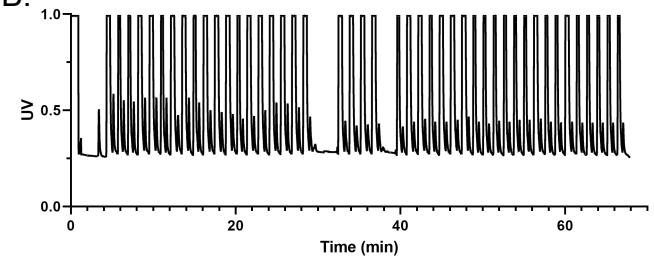
Supplementary Figure 37: A. PDC213 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 1. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.



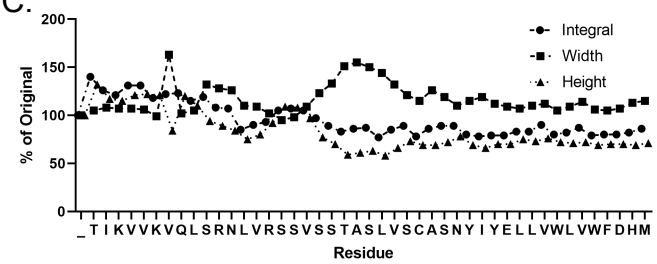
Supplementary Figure 38: A. Salusin β sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 3. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.

A.

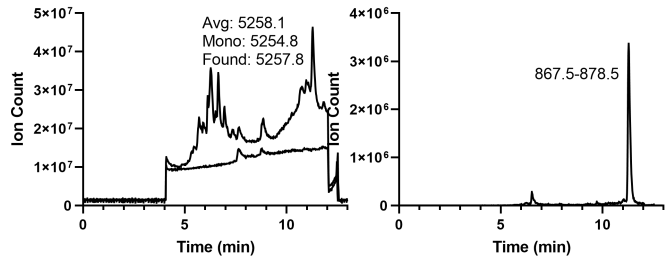
B.



C.



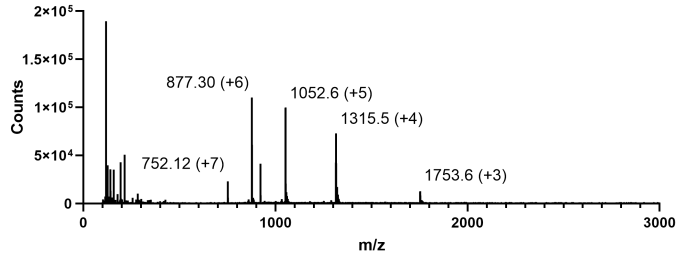
D.



E.

Not Available

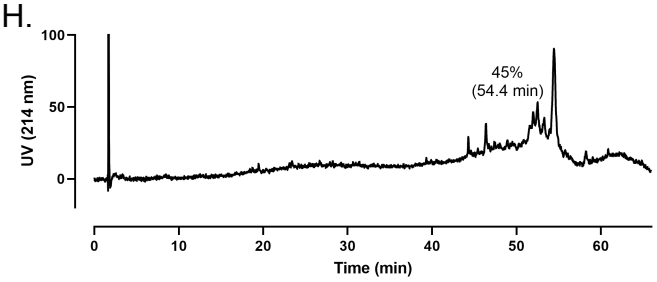
F.



G.

Not Available

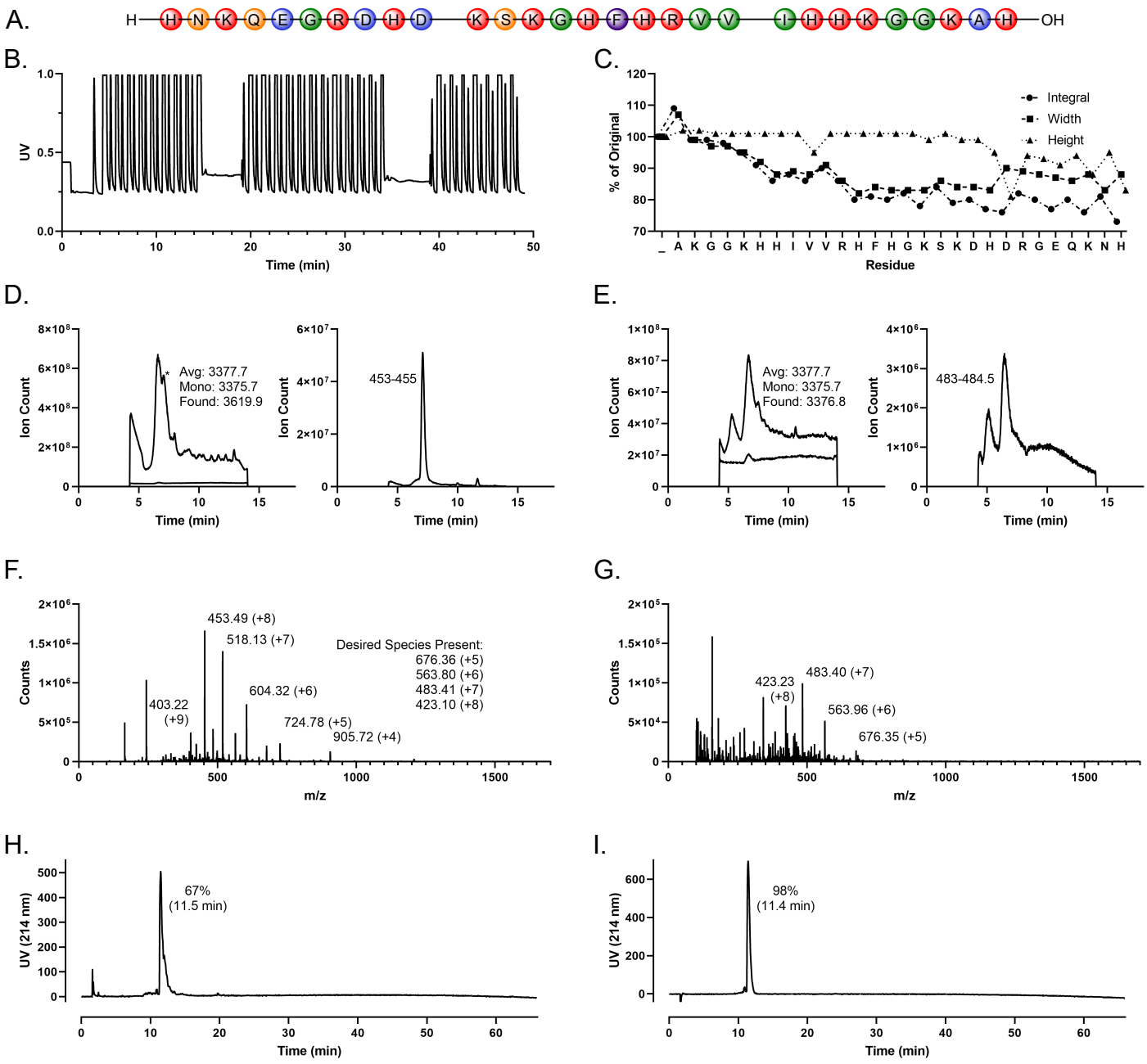
H.



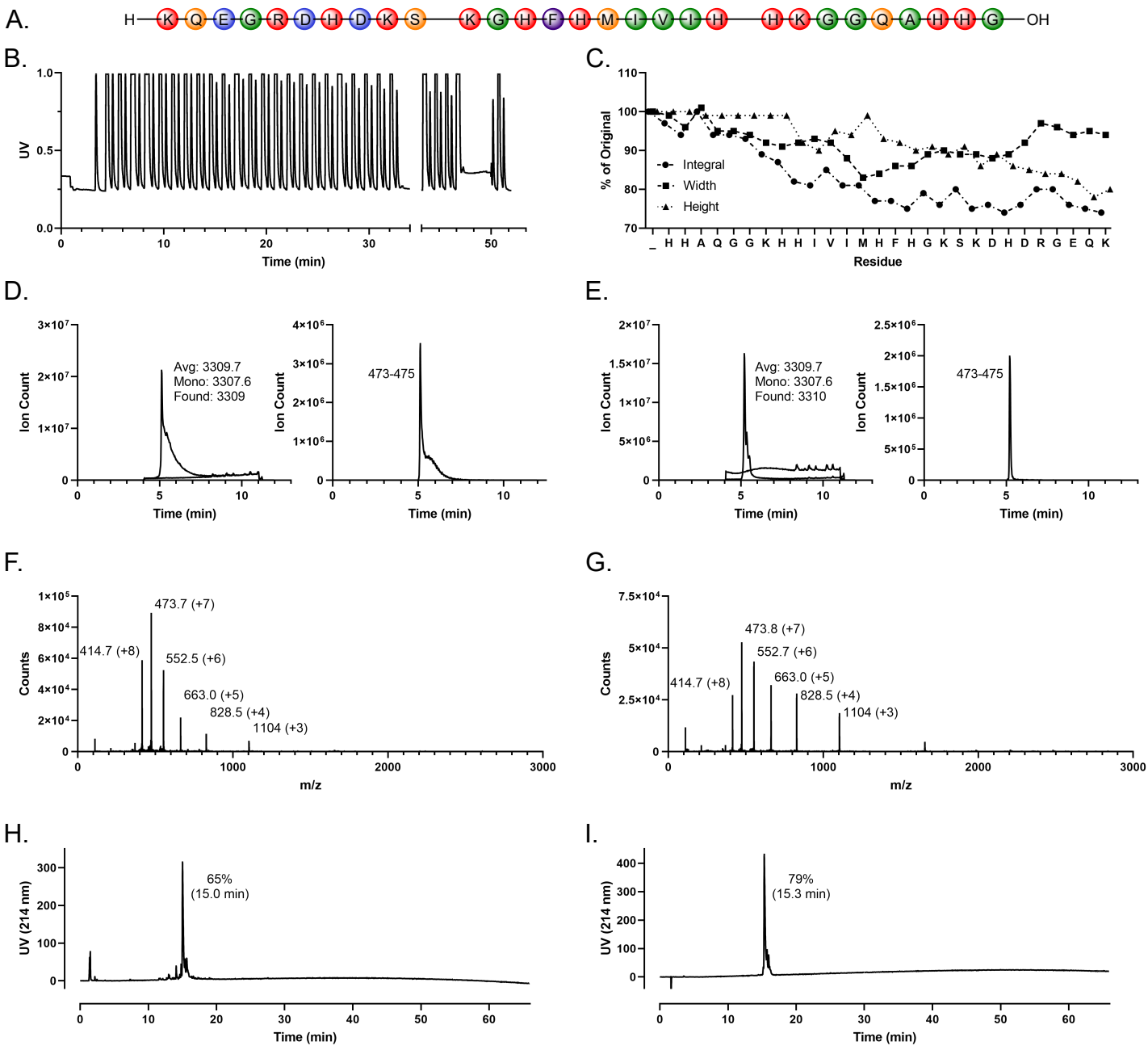
I.

Not Available

Supplementary Figure 39: A. Salvic sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace unavailable. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 3. Right panel EIC of crude AMP for the specified *m/z* range. **E.** Not completed. **F-G.** Mass spectra associated with the dominant peak of **D**. **E.** Not completed. **H.** Analytical HPLC trace of crude peptide with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1. **I.** Not completed.

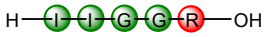


Supplementary Figure 40: A. SgI-29 sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion of the right shoulder of the dominant peak (starred), LCMS Method 2. Right panel EIC in the specified *m/z* range, centered on the most abundant ion in the spectrum shown in **F**. **E.** Left panel TIC of purified AMP overlaid on Blank run, LCMS Method 2. Right panel EIC in the specified *m/z* range, centered on the most abundant ion in the spectrum shown in **G**. **F-G.** Mass spectra associated with the aforementioned peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.

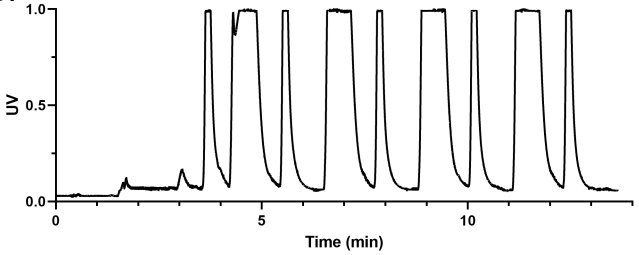


Supplementary Figure 41: A. SgII Peptide A sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. The x-axis is cut at a longer pause; total time graphed includes the pause time. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 5. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 5. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1.

A.



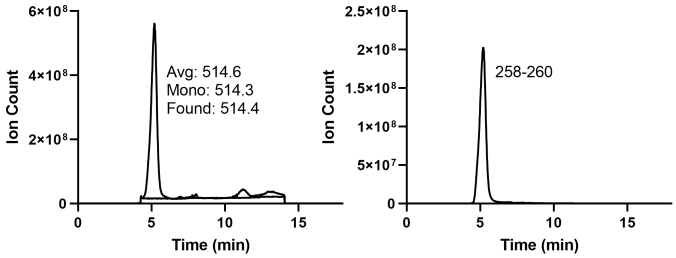
B.



C.

Not Available

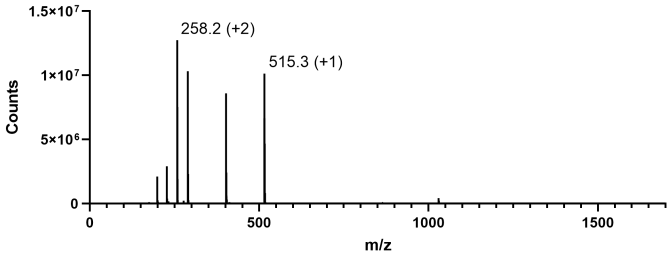
D.



E.

Not Available

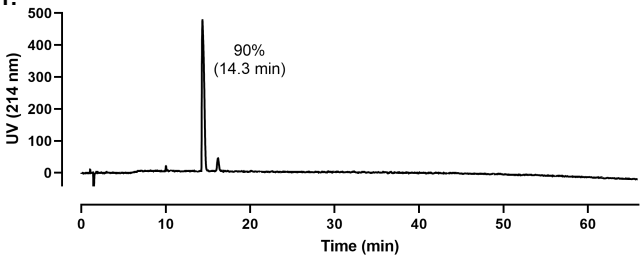
F.



G.

Not Available

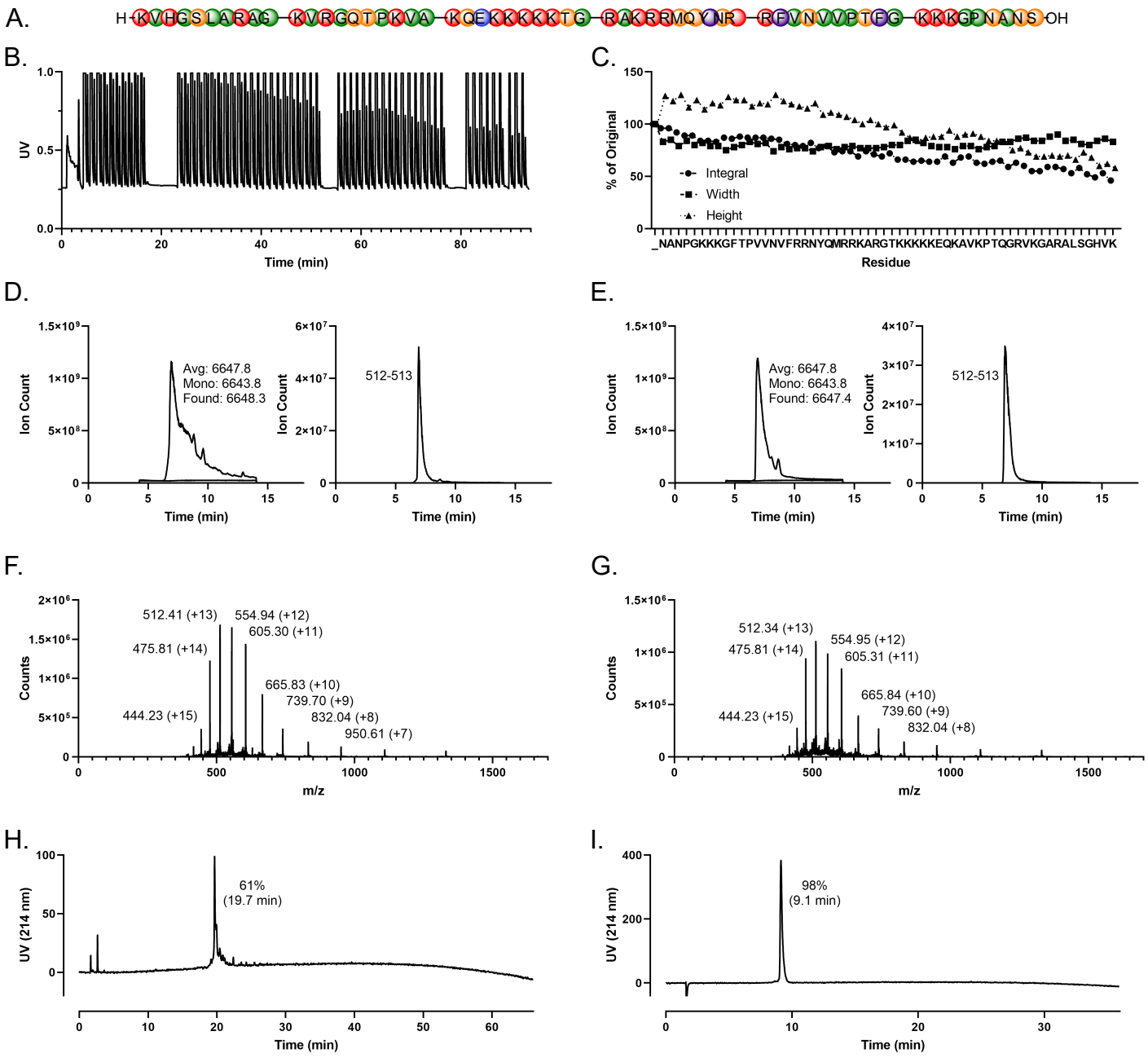
H.



I.

Not Available

Supplementary Figure 42: A. Cathepsin G sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). **B.** Synthesizer UV trace. 4th Generation – Length. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** Not completed. **F.** Mass spectrum associated with the dominant peak of **D**. **E.** Not completed. **H.** Analytical HPLC trace of crude peptide with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 2. **I.** Not completed.



Supplementary Figure 43: A. Ubiquicidin sequence (red = cationic, blue = anionic, orange = polar, green = nonpolar, purple = aromatic). Spaces in the x-axis represent user-initiated pauses. **B.** Synthesizer UV trace. 3rd Generation – Speed. **C.** Integrals and peak width and height expressed as percentages relative to the first cycle. **D.** Left panel TIC of crude AMP overlaid on Blank run with the predicted average and monoisotopic masses as well as the observed mass as calculated from the most abundant ion, LCMS Method 2. Right panel EIC of crude AMP for the specified *m/z* range. **E.** TIC and EIC of purified AMP, LCMS Method 2. **F-G.** Mass spectra associated with the dominant peaks of **D** and **E**, respectively. **H-I.** Analytical HPLC traces of crude and purified peptide, respectively, with the integrated percentage of the dominant peak (retention time in parentheses), HPLC Method 1a.

A.

```
KR-20       ------------------------------------KRIVQRIKDFLRNLVPRTES  20
KS-30       ----------------------------KSKEKIGKEFKRIVQRIKDFLRNLVPRTES  30
RK-31       ----------------------------RKSKEKIGKEFKRIVQRIKDFLRNLVPRTES  31
LL-37       --------------------LLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES  37
ALL-38      ------------------ALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES  38
TLN-58      TLNQARGSFDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES  58
LL-23       --------------------LLGDFFRKSKEKIGKEFKRIVQR--------------  23
LL-29       --------------------LLGDFFRKSKEKIGKEFKRIVQRIKDFLR--------  29
KS-27       ----------------------------KSKEKIGKEFKRIVQRIKDFLRNLVPR---  27
                                                  ******
```

B.

```
Histatin-1      DSHEKRHHGYRRKFHEKHHSHREFPFYGDYGSNYLYDN      38
Histatin-2      -----------RKFHEKHHSHREFPFYGDYGSNYLYDN      27
Histatin-3      DSHAKRHHGYKRKFHEKHHSHRGYR------SNYLYDN      32
Histatin-4      -----------RKFHEKHHSHRGYR------SNYLYDN      21
Histatin-5      DSHAKRHHGYKRKFHEKHHSHRGY--------------      24
Histatin-6      DSHAKRHHGYKRKFHEKHHSHRGYR-------------      25
Histatin-7      -----------RKFHEKHHSHRGY--------------      13
Histatin-8      ------------KFHEKHHSHRGY--------------      12
Histatin-9      -----------RKFHEKHHSHRGYR-------------      14
                           **********
```

C.

```
β Amyloid 1-42      DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA    42
β Amyloid 1-40      DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--    40
                    ****************************************
```

D.

```
SgI-29      HNKQEGRDHDKSKGHFHRVVIHHKGGKAH--     29
SgII        --KQEGRDHDKSKGHFHMIVIHHKGGQAHHG     29
              *************** :*******:**
```

Supplementary Figure 44: A. Cathelicidin alignment. **B.** Histatin alignment. **C.** β amyloid alignment. **D.** Semenogelin-derived peptide alignment.