

**Supporting Information**

# Proton-driven Amide Bond Cleavage Pathways of Gas-Phase Peptide Ions Lacking Mobile Protons

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Figure S1. The structure of the lowest energy CS → SB transition structure of  $[\text{GGR}+\text{H}]^+$  determined at the B3LYP/6-31+G(d,p) level of theory.

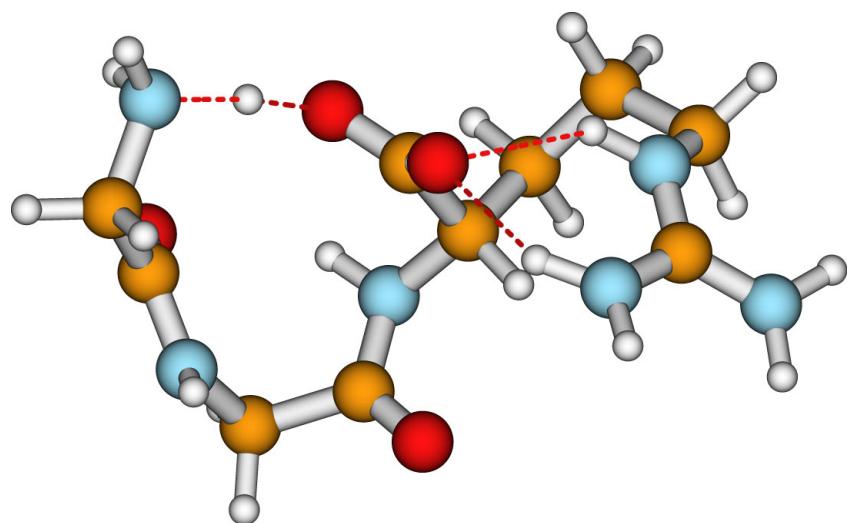


Figure S2. Structures and relative energy of the lowest energy  $b_n$ - $y_m$  TSs for  $[\text{GGGR}+\text{H}]^+$  determined at the B3LYP/6-31+G(d,p) level of theory with the relative energies corrected for zero-point vibration energy (ZPE) using B3LYP/6-31G(d) level of theory. (a) The Salt-bridge  $b_2$ - $y_2$  Transition Structure; (b) The Anhydride  $b_3$ - $y_1$  Transition Structure.

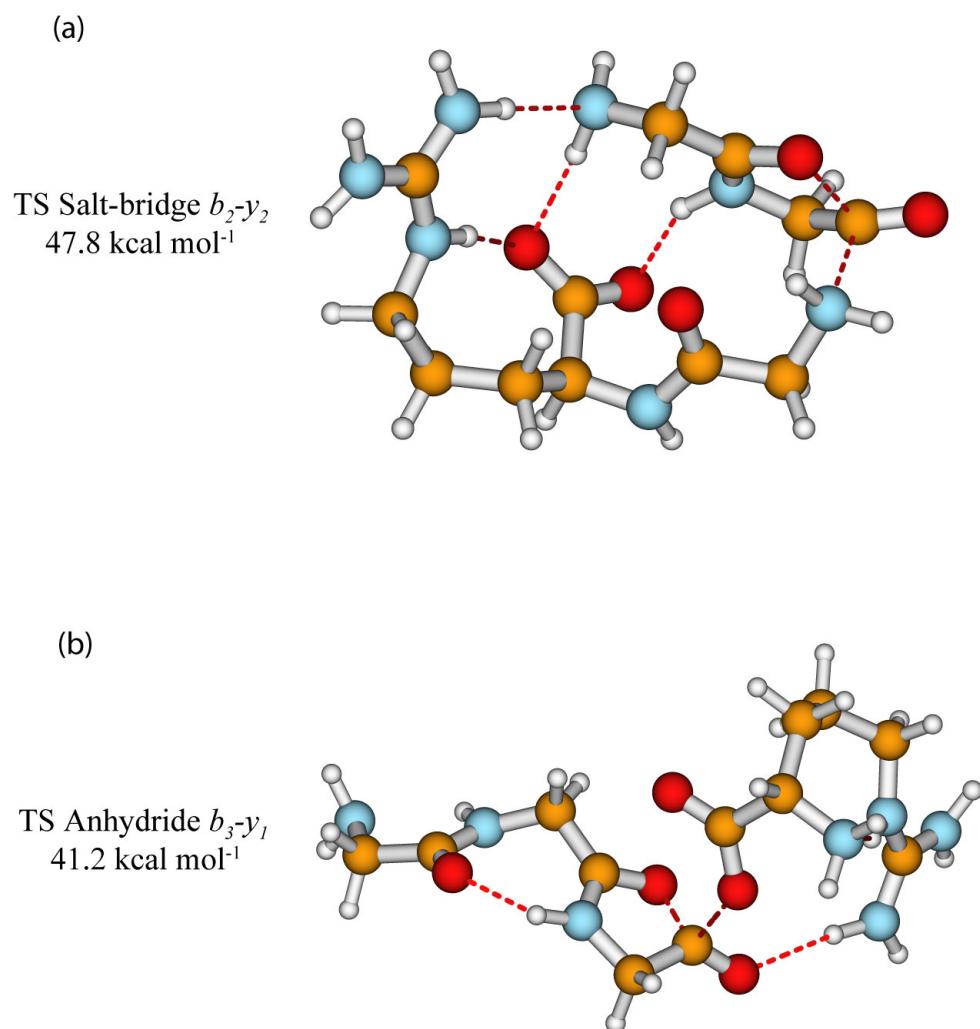


Figure S3. Structures and relative energy of the lowest energy  $b_n-y_m$  TSs for  $[\text{GGGGR}+\text{H}]^+$  determined at the B3LYP/6-31+G(d,p) level of theory with the relative energies corrected for zero-point vibration energy (ZPE) using B3LYP/6-31G(d) level of theory. (a) The Anhydride  $b_2-y_3$  Transition Structure; (b) The Salt-bridge  $b_3-y_2$  Transition Structure; (c) The Anhydride  $b_4-y_1$  Transition Structure.

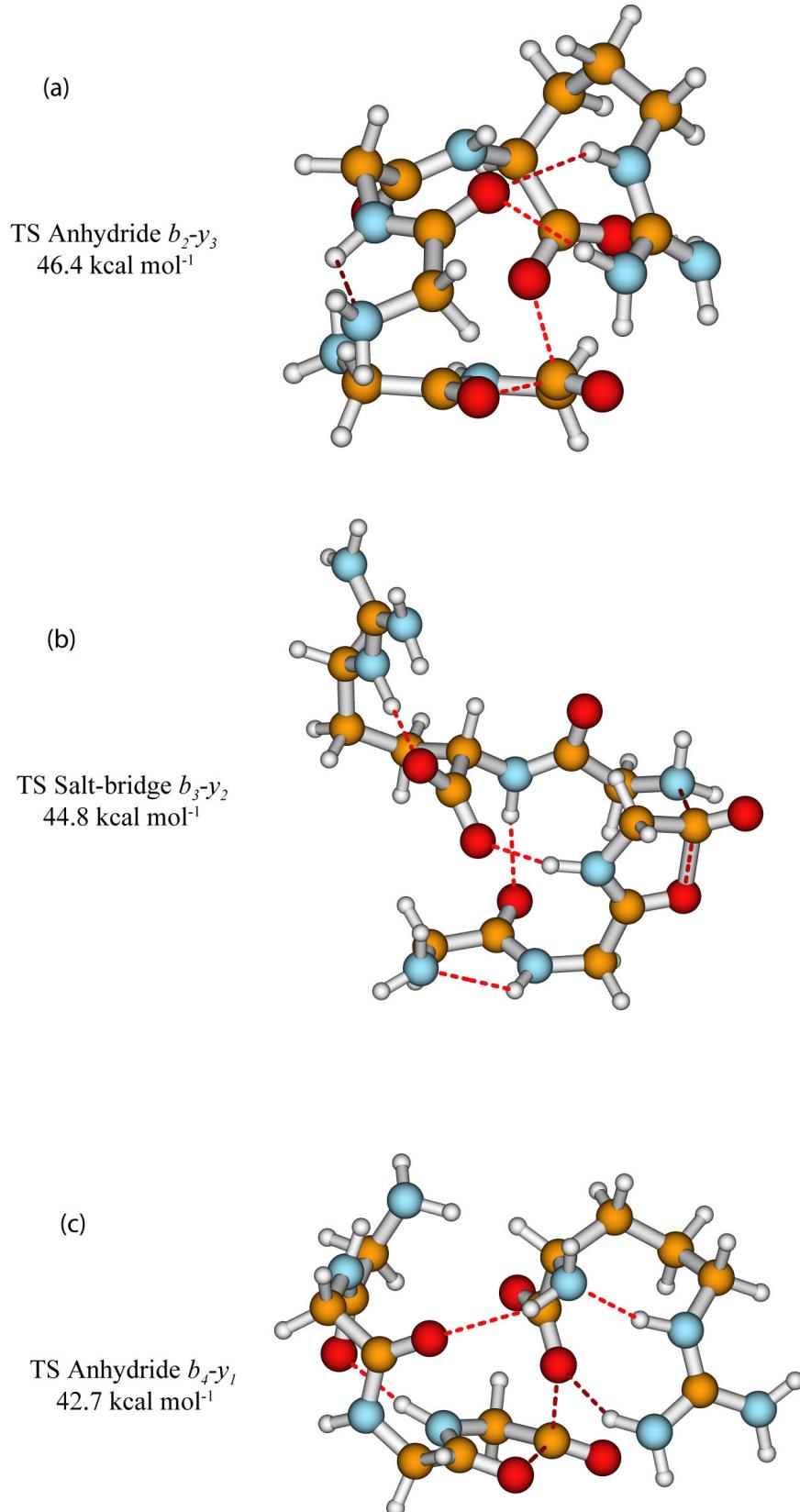


Table S1. Total and relative energies of the various of  $[GGR+H]^+$  determined at the B3LYP/6-31+G(d,p) level of theory with the relative energies corrected for zero-point vibration energy (ZPE) using B3LYP/6-31G(d) level of theory.

Structure	$E_{\text{Total}} + \text{ZPE}$ /H	$E_{\text{rel}}$ / kcal mol $^{-1}$	$\Delta G_{298}/$ kcal mol $^{-1}$	$\Delta S_{298}/$ cal K $^{-1}$ mol $^{-1}$
CS Global Minimum	-1022.732645	0.0	0.0	0.0
CS N-term. Prot.	-1022.691145	26.1	27.9	-8.5
CS G(1)-G(2) amide N Prot.	-1022.669234	39.8	40.5	-4.2
CS G(1)-R amide N Prot.	-1022.68833	40.1	40.0	-2.3
CS G(1)-G(2) amide O Prot.	-1022.67566	22.0	22.6	-3.9
CS G(1)-R amide O Prot.	-1022.705649	16.9	17.1	-1.9
SB N-term. Prot.	-1022.714126	11.6	13.5	-9.5
SB G(1)-G(2) amide N Prot.	-1022.670681	38.9	39.1	-1.7
SB G(1)-R amide N Prot.	-1022.684293	30.3	30.2	-0.1
SB G(1)-G(2) amide O Prot.	-1022.696598	22.6	23.4	-4.4
SB G(1)-R amide O Prot.	-1022.702927	18.7	19.2	-3.4
Imine enol G(1)-G(2)	-1022.714666	11.3	10.3	3.5
Imine enol G(2)-R	-1022.713844	11.8	12.0	-1.3

Table S2. MALDI-TOF/TOF peak intensities of sequence ions and neutral losses from the MS/MS of  $[G_nR+H]^+$  peptides.

Protonated System	Assignment	Relative Intensity
<b>GGR</b>	$[GGR+H-NH_3]^+$	57
	$b_2$	32
	$a_2 / R$ (87)	7
	$y_1^*$	100
	$y_1^*$	82
	$y_2$	21
<b>GGGR</b>	$[G_3R+H -NH_3]^+$	82
	$[G_3R+H-2NH_3]^+$	21
	$b_2$	31
	$a_2 / R$ (87)	1
	$y_3^*$	5
	$y_3$	56
	$y_2^*$	21
	$y_2$	100
	$b_3$	77
	$y_1^*$	92
	$y_1$	82
<b>GGGGR</b>	$[G_4R+H -NH_3]^+$	100
	$b_2$	13
	$a_2 / R$	4
	$y_3^*$	21
	$y_3$	68
	$b_3$	30
	$y_2^*$	13
	$y_2$	70
	$b_4$	38
	$b_4^\circ$	28
	$a_4$	15
	$y_1$	64
	$y_1^*$	56
	$y_4^*$	9
	$y_4$	26

Table S3. Ion trap (LCQ, Thermo San Diego, (ACN:H<sub>2</sub>O 1:1 0.1% Formic Acid)) peak intensities for MS/MS of [G<sub>n</sub>R+H]<sup>+</sup> peptides.

Protonated System	Assignment	Relative Intensity
<b>GGR</b>	[GGR+H-H <sub>2</sub> O-NH <sub>3</sub> ] <sup>+</sup>	100
	[GGR+H-NH <sub>3</sub> ] <sup>+</sup>	59
	y <sub>1</sub> *	89
	y <sub>1</sub>	28
	b <sub>2</sub>	6
<b>GGGR</b>	[G <sub>3</sub> R+H-H <sub>2</sub> O-NH <sub>3</sub> ] <sup>+</sup>	40
	[G <sub>3</sub> R+H-NH <sub>3</sub> ] <sup>+</sup>	100
	y <sub>3</sub> *	6
	b <sub>3</sub>	11
	y <sub>1</sub> *	15
	y <sub>1</sub>	10
	b <sub>2</sub>	3.5
	y <sub>2</sub> *	2.5
	y <sub>2</sub>	16
<b>GGGGR</b>	[G <sub>3</sub> R+H-2NH <sub>3</sub> ] <sup>+</sup>	28
	[G <sub>3</sub> R+H-H <sub>2</sub> O-NH <sub>3</sub> ] <sup>+</sup>	31
	[G <sub>3</sub> R+H-NH <sub>3</sub> ] <sup>+</sup>	100
	y <sub>4</sub> *	1
	y <sub>4</sub>	3
	b <sub>4</sub>	16.5
	a <sub>4</sub> *	4
	a <sub>4</sub>	3
	y <sub>1</sub> *	8
	y <sub>1</sub>	6
	b <sub>3</sub>	6
	y <sub>2</sub> *	2
	y <sub>2</sub>	6
	b <sub>2</sub>	1
	y <sub>3</sub> *	2.5
	y <sub>3</sub>	13

Table S4. FT-ICR (Bruker 9.4 T FT-ICR, (ACN:H<sub>2</sub>O 1:1 0.1% Formic Acid)) QCID peak intensities of sequence ions and neutral losses from the MS/MS of [G<sub>n</sub>R+H]<sup>+</sup> peptides.

Protonated System	Assignment	Relative Intensity
<b>GGR</b>	[GGR+H-H <sub>2</sub> O-NH <sub>3</sub> ] <sup>+</sup>	100
	[GGR+H-NH <sub>3</sub> ] <sup>+</sup>	32
	y <sub>2</sub> *	14
	y <sub>1</sub> *	97
	y <sub>1</sub>	47
<b>GGGR</b>	[G <sub>3</sub> R+H-H <sub>2</sub> O-NH <sub>3</sub> ] <sup>+</sup>	100
	[G <sub>3</sub> R+H-2NH <sub>3</sub> ] <sup>+</sup>	42
	[G <sub>3</sub> R+H-NH <sub>3</sub> ] <sup>+</sup>	83
	[G <sub>3</sub> R+H-H <sub>2</sub> O-2NH <sub>3</sub> ] <sup>+</sup>	48
	y <sub>3</sub>	56
	y <sub>1</sub> *	89
	y <sub>1</sub> *	86
	y <sub>2</sub>	85
<b>GGGGR</b>	[G <sub>3</sub> R+H-2NH <sub>3</sub> ] <sup>+</sup>	67
	[G <sub>3</sub> R+H-H <sub>2</sub> O-NH <sub>3</sub> ] <sup>+</sup>	78
	[G <sub>3</sub> R+H-NH <sub>3</sub> ] <sup>+</sup>	100
	[G <sub>3</sub> R+H-H <sub>2</sub> O-2NH <sub>3</sub> ] <sup>+</sup>	43
	y <sub>4</sub> *	5
	y <sub>4</sub> **	27
	y <sub>4</sub> **	12
	y <sub>4</sub> **	11
	b <sub>4</sub>	45
	a <sub>4</sub> *	18
	a <sub>4</sub>	11
	y <sub>1</sub> *	46
	y <sub>1</sub>	40
	b <sub>3</sub>	6
	y <sub>2</sub> *	6
	y <sub>2</sub>	43
	b <sub>2</sub>	1
	y <sub>3</sub> *	9
	y <sub>3</sub> **	80
	y <sub>3</sub>	15

Table S5. Total and relative energies of the various minima and transition structures of  $[GGG+H]^+$  determined at the B3LYP/6-31+G(d,p) level of theory with the relative energies corrected for zero-point vibration energy (ZPE) using B3LYP/6-31G(d) level of theory.

Structure	$E_{\text{Total}} + \text{ZPE}$ Corr./ H	$E_{\text{rel}}$ / kcal mol <sup>-1</sup>
CS Global Minimum	-700.683445	0.0
<b>TS classical<sup>7</sup> <math>b_2-y_I</math></b>	<b>-700.636209</b>	<b>29.6</b>
TS Imine enol $b_2-y_I$	-700.614794	43.1

This demonstrates that the imine enol mechanism is much less favorable for systems which do not contain arginine, where the normally invoked  $b_n-y_m$  mechanism still prevails. The salt-bridge structures collapsed to form charge-solvated structures during the TS optimizations, indicating there non-applicability of this mechanism is these systems too.

Full citation for Reference 19:

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