Electronic Supplementary Information

Excited-state proton transfer in protonated adrenaline revealed by cryogenic UV photodissociation spectroscopy

Jordan Dezalay,^a Michel Broquier,^a Satchin Soorkia,^a Keisuke Hirata,^{b,c} Shun-ichi Ishiuchi,^{b,c} Masaaki Fujii^{*b,c,d} and Gilles Grégoire^{*a,d}

^a Université Paris-Saclay, CNRS, Institut des Sciences Moléculaires d'Orsay, F-91405 Orsay, France. E-mail : gilles.gregoire@universite-paris-saclay.fr

^b Laboratory for Chemistry and Life Science, Institute of Innovative Research, Tokyo Institute of Technology, 4259, Nagatsuta-cho, Midori-ku, Yokohama, 226-8503, Japan. Email: mfujii@res.titech.ac.jp

^c School of Life Science and Technology, Tokyo Institute of Technology. 4259 Nagatsutacho, Midori-ku, Yokohama, Kanagawa, 226-8503, Japan.

^d Tokyo Tech World Research Hub Initiative (WRHI), Institute of Innovation Research, Tokyo Institute of Technology, 4259, Nagatsuta-cho, Midori-ku, Yokohama, 226-8503, Japan

*Corresponding authors: <u>mfujii@res.titech.ac.jp</u>; <u>gilles.gregoire@universite-paris-saclay.fr</u>



a) UV PID

b) UV + probe

Fig. S1 Difference mass spectra of the UV photodissociation of AdH⁺ (m/z 184) recorded for a short fragmentation time of 1 μ s with (a) UV only (laser on – laser off) and (b) in the pump-probe scheme (pump and probe laser – pump only). The C_{α}-C_{β} bond cleavage fragments are m/z 139, m/z 46 and m/z 44, the water loss (m/z 166) and its secondary fragment at m/z 135. On the pump-probe scheme, the probe photon (550 nm) opens the H loss channel at m/z 183 along with its secondary fragment at m/z 44 and depletes all the fragmentation channels initially observed by the pump only.



Fig. S2 Comparison of the simulated vibronic spectra of the G1-STR3 and G1-STR4 structure with the spectroscopy of conformer C. G1-STR3 provides a better agreement in the low frequency region below 200 cm⁻¹.



Fig. S3 Franck-Condon active modes in the vibronic spectrum of the AdH⁺ G1-STR1 conformer. The frequency modes below 100 cm⁻¹ involve motion of the methyl-amino moiety above the catechol ring. The v_{18} mode is the first in-plane breathing mode of the catechol ring.





Fig. S4 Franck-Condon active modes in the vibronic spectrum of the AdH^+ T1-STR1 conformer.





Fig. S5 Franck-Condon active modes in the vibronic spectrum of the AdH^+ G1-STR3 conformer.

G1-STR4



Fig. S6 Franck-Condon active modes in the vibronic spectrum of the AdH^+ G1-STR4 conformer.



Fig. S7 UV photodissociation spectroscopy of AdH⁺ recorded with the ns dye laser (0.2 cm⁻¹ resolution) and the ps OPA laser (10 cm⁻¹ resolution) recorded on the C_{α} - C_{β} bond break fragment.



Fig. S8 Optimized structure of the ${}^{1}\pi\pi^{*}$ state and ESPT form of AdH⁺ G1-STR1 conformer along with the most relevant bond distances and dihedral angles. In the S₁ structure, the lengthening of the N-H bond along with the slight ring puckering favor the ESPT reaction.