

CORRECTION

Correction: The Translocation Domain of Botulinum Neurotoxin A Moderates the Propensity of the Catalytic Domain to Interact with Membranes at Acidic pH

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A reference was incorrectly omitted in Table 1. The authors have provided the reference and a corrected table here.

Table 1. Comparison of the secondary structure of the three proteins based on the far-UV CD spectra at pH 7 (BeStSel [46]) with the secondary structure observed in the crystal structure of BoNT/A (3BTA) (STRIDE PDB).

	BeStSel				STRIDE PDB			
	LC	H _N	LC-H _N	LC + H _N isolated	LC	H _N	LC-H _N	LC + H _N isolated
alpha	28.3	51.8	39.6	40.05	30.2	50.2	40.7	40.2
beta	17.3	7	14.2	12.15	14	1.4	9.7	7.7
Others ¹	54.4	41.2	46.2	47.8	55.8	48.4	49.6	52.1

¹Others: turns and random coils

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46. Micsonai A, Wien F, Kernya L, Lee YH, Goto Y, Réfrégiers M, Kardos J. Accurate secondary structure prediction and fold recognition for circular dichroism spectroscopy. Proc Natl Acad Sci U S A. 2015; 112: E3095–E3103. doi [10.1073/pnas.1500851112](https://doi.org/10.1073/pnas.1500851112). PMID:26038575.

Reference

- Araye A, Goudet A, Barbier J, Pichard S, Baron B, England P, et al. (2016) Correction: The Translocation Domain of Botulinum Neurotoxin A Moderates the Propensity of the Catalytic Domain to Interact with Membranes at Acidic pH. PLoS ONE 11(4): e0153401. doi: [10.1371/journal.pone.0153401](https://doi.org/10.1371/journal.pone.0153401) PMID: [27070312](#)

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