PLOS ONE

CORRECTION

Correction: Software-aided approach to investigate peptide structure and metabolic susceptibility of amide bonds in peptide drugs based on high resolution mass spectrometry

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In Fig 6 the images for buserelin metabolites M2 and M3 are incorrectly switched. Please see the corrected Fig 6 here.

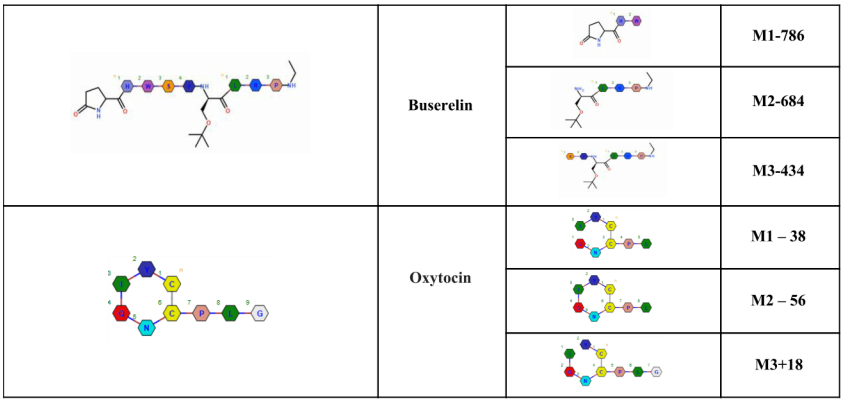

Fig 6. Proposed metabolites of buserelin and oxytocin found in 120 min incubations with chymotrypsin.

https://doi.org/10.1371/journal.pone.0200772.g001

Reference

1. Radchenko T, Brink A, Siegrist Y, Kochansky C, Bateman A, Fontaine F, et al. (2017) Software-aided approach to investigate peptide structure and metabolic susceptibility of amide bonds in peptide drugs based on high resolution mass spectrometry. PLoS ONE 12(11): e0186461. https://doi.org/10.1371/journal.pone.0186461 PMID: 29091918

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