

CORRECTION

Correction: The a1,6-Fucosyltransferase Gene (fut8) from the Sf9 Lepidopteran Insect Cell Line: Insights into fut8 Evolution

The PLOS ONE Staff

There is an error in the legend for <u>Fig. 3</u>, "Conserved aa and motifs found in all the α 1,6-fucosyltransferases sequences". Please view <u>Fig. 3</u> and its complete, correct legend here:





Citation: The *PLOS ONE* Staff (2015) Correction: The α1,6-Fucosyltransferase Gene (*fut8*) from the *Sf9* Lepidopteran Insect Cell Line: Insights into *fut8* Evolution. PLoS ONE 10(4): e0122944. doi:10.1371/ journal.pone.0122944

Published: April 7, 2015

Copyright: © 2015 The PLOS ONE Staff. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

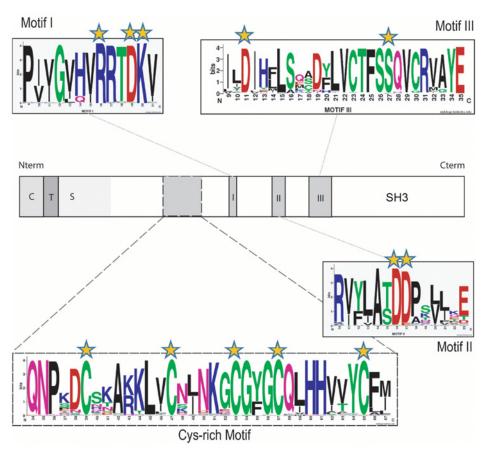


Fig 3. Conserved aa and motifs found in all the α 1,6-fucosyltransferases sequences. Schematic representations of the FUT8 protein showing the cytoplasmic (C), transmembrane (T) and stem region (S) characteristic of α 1,6-fucosyltransferases. The catalytic domain is in white and motifs I, II and III in grey. In addition, a region found only in α 1,6-fucosyltransferase with conserved cysteine residues is indicated by dashed lines and was named "Cys-rich" domain. Conserved aa and those implicated in the enzymatic activity are highlighted with orange stars. The conserved peptide sequences used to generate the motif I, motif II and motif III sequence logos were extracted from multiple alignments of 96 α 1,6-fucosyltransferase sequences identified in the databases (Table S2) and visualized at the Weblogos site at Berkeley, as described previously [63]. In the logos, aa are colored according to their chemical properties: polar aa (G, C, S, T, Y) are green, basic (K, R, H) are blue, acidic (D, E) are red, hydrophobic (A, V, L, I, P, W, F, M) are black and neutral polar aa (N, Q) are pink. The overall height of the stacks indicates the sequence conservation at a given position, while the height of the symbol within the stack indicates the relative frequency of each aa at that position. [70, 71]

doi:10.1371/journal.pone.0122944.g001

Reference

 Juliant S, Harduin-Lepers A, Monjaret F, Catieau B Violet M-L Cérutti P, et al. (2014) The α1,6-Fucosyltransferase Gene (fut8) from the Sf9 Lepidopteran Insect Cell Line: Insights into fut8 Evolution. PLoS ONE 9(10): e110422. doi: 10.1371/journal.pone.0110422