

## Erratum

# The types and prevalence of alternative splice forms [*Current Opinion in Structural Biology* 2006, 16:362–367]<sup>☆</sup>

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*Current Opinion in Structural Biology* 2006, 16:557

Available online 11th July 2006

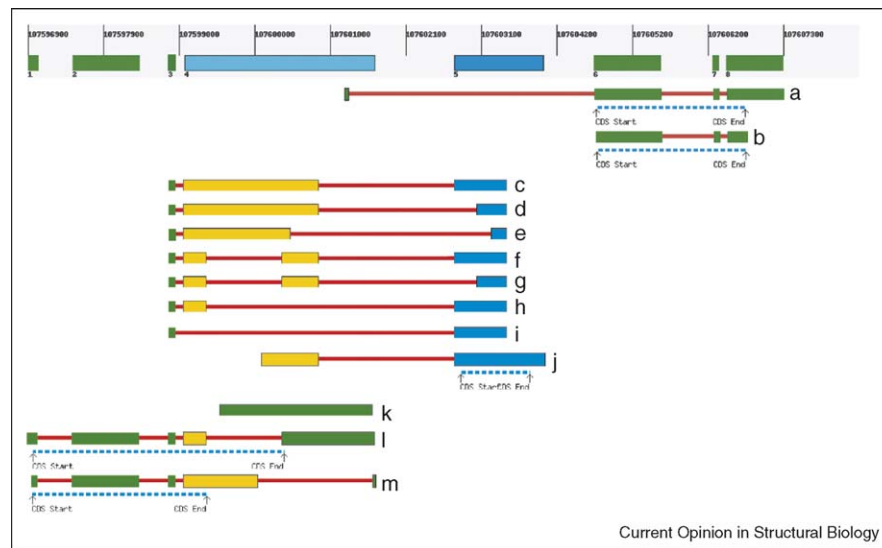
0959-440X/\$ – see front matter

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DOI 10.1016/j.sbi.2006.06.010

Unfortunately, a mistake was introduced into Figure 1 of this review during the editing process. The correct version of the figure is reproduced below. We apologise to the authors and readers for any confusion this may have caused.

Figure 1



A transcription unit (TU) of mouse full-length cDNAs, as displayed in the browser of the SPAED database (<http://www.spaed.unibas.ch>) [16]. Thin red bars correspond to introns and thicker bars correspond to exons. Green indicates an invariant exon, yellow an exon with evidence of donor site variation, blue an exon with acceptor site variation and light blue an exon with evidence of intron retention. Cassette exons are indicated by a black outline surrounding the exon. The bars at the top show the genomic exons in this TU and their splice annotation. This TU corresponds to a polycistron [32] encoding the known genes hyaluronidase 1 (Hyal1, transcripts l and m) and hyaluronidase 3 (Hyal3, transcripts a and b), and *N*-acetyltransferase 6 (Fus2, transcript j).

<sup>☆</sup> DOI of original article: 10.1016/j.sbi.2006.05.002.