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ERRATUM

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Complement C2 receptor inhibitor trispanning: from man to schistosome

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The text above Fig. 3 referring to part **a** should read: "As shown in Fig. 3a there is a 50% identity and 73% similarity across the region".

Figures 1 and 3 should have appeared in colour.
In the legend to Fig. 3, the text referring to parts **b** and **c** should be transposed.
The colour figures and their legends are published here.

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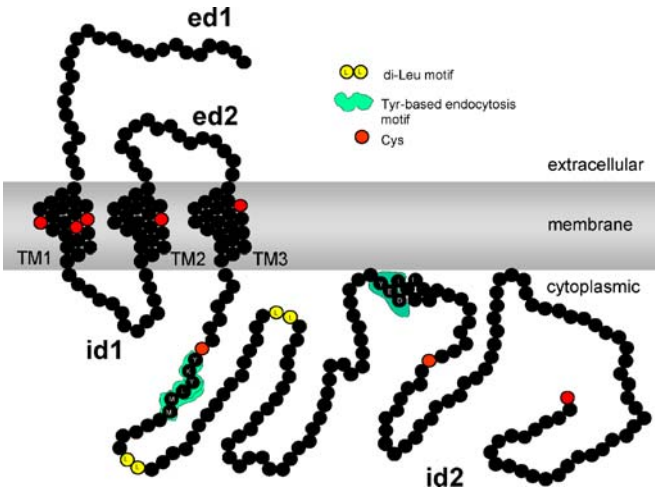

Fig. 1 Schematic topology predicition of CRIT showing N-terminal extracellular domains (ed1 and ed2), three N-terminal transmembrane domains (TM1, TM2 and TM3), two intracytoplasmic domains (id1) and the cytoplasmic tail (id2). Also indicated are tyrosine-based endocytosis motifs in id2, as well as cysteine residues shown in *red*

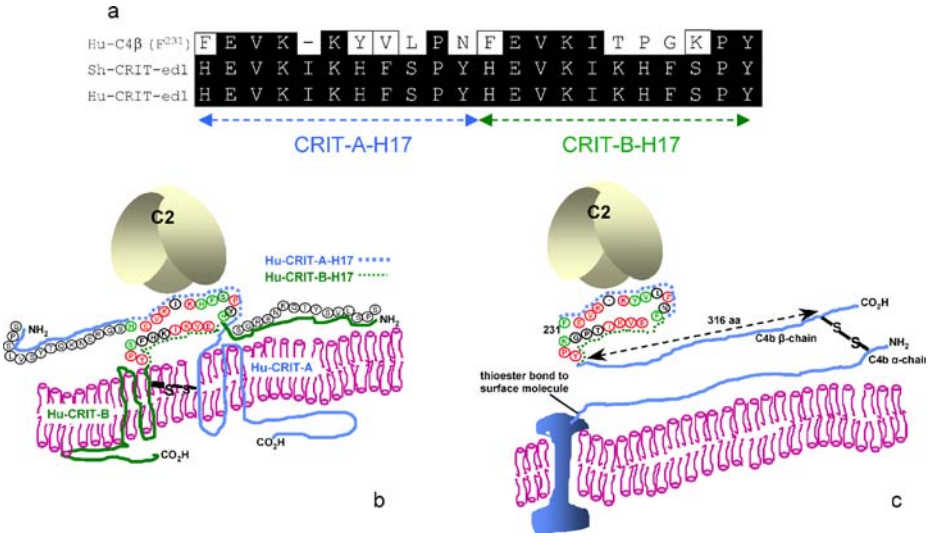

Fig. 3 Alignment of amino acid sequence of the CRIT-ed1 domain of the human c4 β-chain F^{231}–Y^{251} with *S. haematobium* and human CRIT-ed1. **a** The C-terminal 11 -amino-acid CRIT-ed1, the so called CRIT-H17 motif, is shown. In this schematic, two such motifs have been placed contiguosly to represent how two such regions may come into close proximity in a CRIT homodimer made up of CRIT-A and CRIT-B. **b** A schematic of two CRIT molecules constituting a homodimer in which two CRIT-H17 motifs might be brought together in such a way as to represent the equivalent of the CRIT-ed1 domain in the C4 β-chain. **c** A schematic of the β-chain of C4, with emphasis on the predicted C2-binding ed1 domain