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## Characterization of the Mouse *Cblc/Cbl3* Gene

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**The mouse *Cblc/Cbl3* gene was cloned and characterized. It comprises 12 exons and encodes a putative protein of 496 amino acid residues which shares an overall 67% identity with its human ortholog; it also shares 70% of amino acid identity with mouse CBL over their conserved SH2 and Ring finger domains. Mouse *Cblc* mRNA is expressed in embryo and adult tissues and has a rather ubiquitous distribution.** © 2001

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Transmembrane receptors (RTKs) and cytoplasmic molecules (PTKs) endowed with tyrosine kinase activity are major components of cell communication processes. Their recycling and degradation is tightly regulated by a number of factors. The cytoplasmic CBL adaptor proteins play a role in the negative regulation and degradation of RTKs and PTKs. In mammals, there are three CBL related proteins known to date: CBL, CBLb, and CBLc/CBL3, best characterized in humans. They are encoded by paralogous genes (1). CBLs function as ubiquitin E3 ligase proteins (2); when bound to an RTK and phosphorylated, they recruit ubiquitin-activating and conjugating enzymes that target RTKs and other proteins to the proteasome degradation machinery (3–8). The primarily suppressive function of CBL proteins is exemplified by the defects observed in null mutant mice obtained by gene targeting (9–13) or in non vertebrate animal models (14–16). CBL proteins are constituted of a N-terminus domain, a RING finger domain and a C-terminus extension of variable length containing proline-rich sequences. The N-terminus region is sometimes called the PTB domain; actually, upon characterization of its three-dimensional structure (17), it has been subdivided into three subregions that include a four helix bundle (4F), a calcium-binding EF-hand domain and an unusual SH2 domain.

The human *CBLc/CBL3* gene was recently characterized (1, 18, 19). To gather more information on the third member of the CBL family, as well as a to take necessary first step towards the use animal models for

studying this molecule, we cloned the mouse *Cblc* gene and studied its structure and its expression in the adult and during development.

### MATERIALS AND METHODS

*cDNA and cosmid cloning and analysis.* Mouse *Cblc* cDNA was obtained by PCR amplification of reverse transcribed RNA from several tissues [kidney, prostate, 17.5 days postconception (d.p.c.) embryos]. Specific primers designed from the mouse coding sequence were used: (5'-CGGCGGCAGCCCCGCAAGGGTG-3' and 5'-ACAGCTTGGCCGGAAGATATA-3'). A 794-bp PCR product, named "troncus," was cloned. The "troncus" fragment was used to performed 3' RACE-PCR (Marathon cDNA amplification Kit, Clontech) to isolate the full length cDNA.

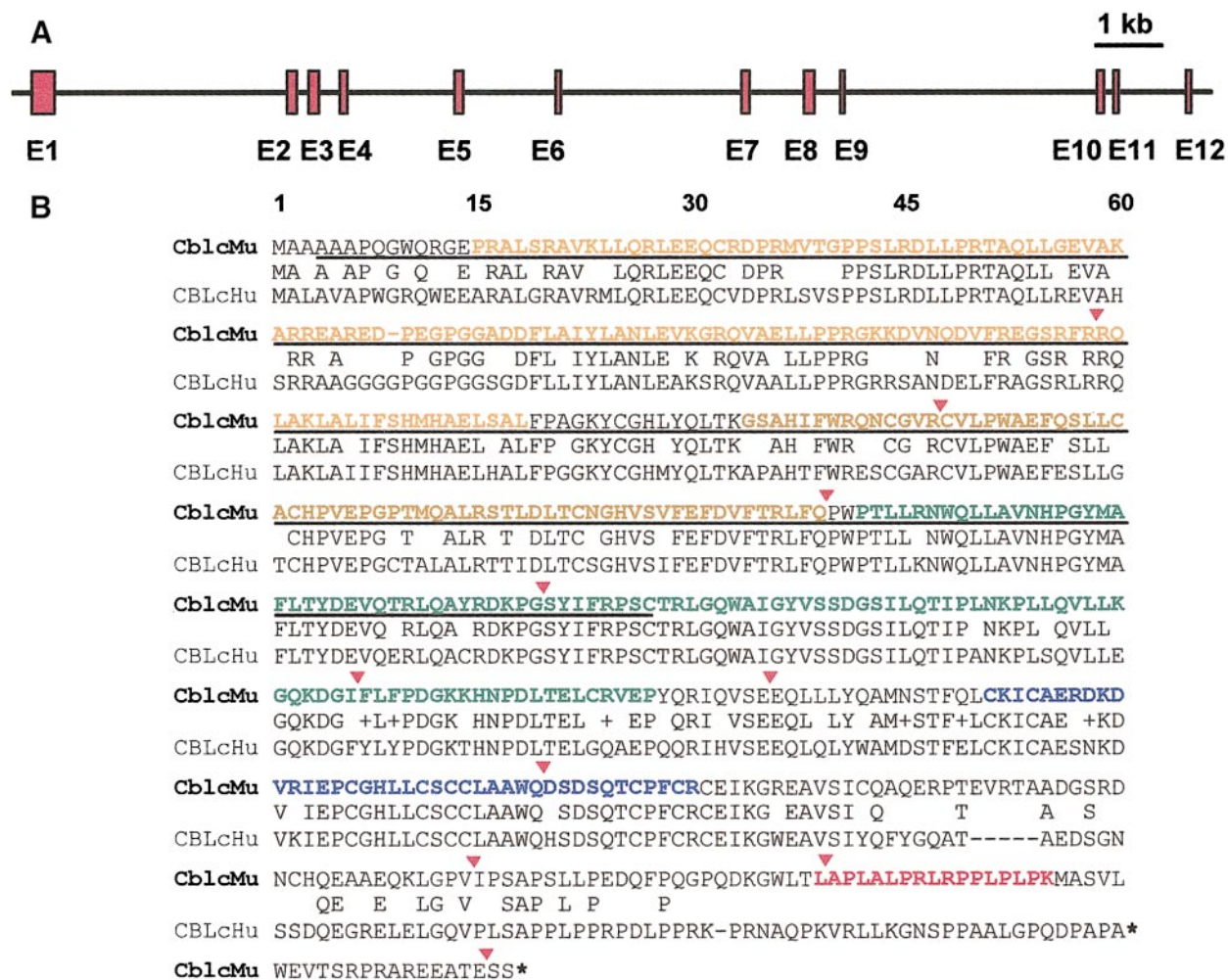
Mouse cosmid clones were isolated from a RZPD library (129/ola library No. 121) using a human cDNA probe (1). Eight clones were obtained and characterized by restriction enzyme patterns and DNA sequence (Genome Express, Grenoble, France) analyses. These clones were used to identified the coding regions. In addition, we scanned the emerging mouse genome sequence (<http://www.ncbi.nlm.nih.gov/blast/blast.cgi>) with the full length *Cblc* cDNA. The mouse *Cblc* gene sequence is present in clone RP23-33H23 (AC073760). A draft genomic sequence was obtained which confirmed our data.

Alignment was done using NCBI software (<http://www.ncbi.nlm.nih.gov/gorf/bl2.html>).

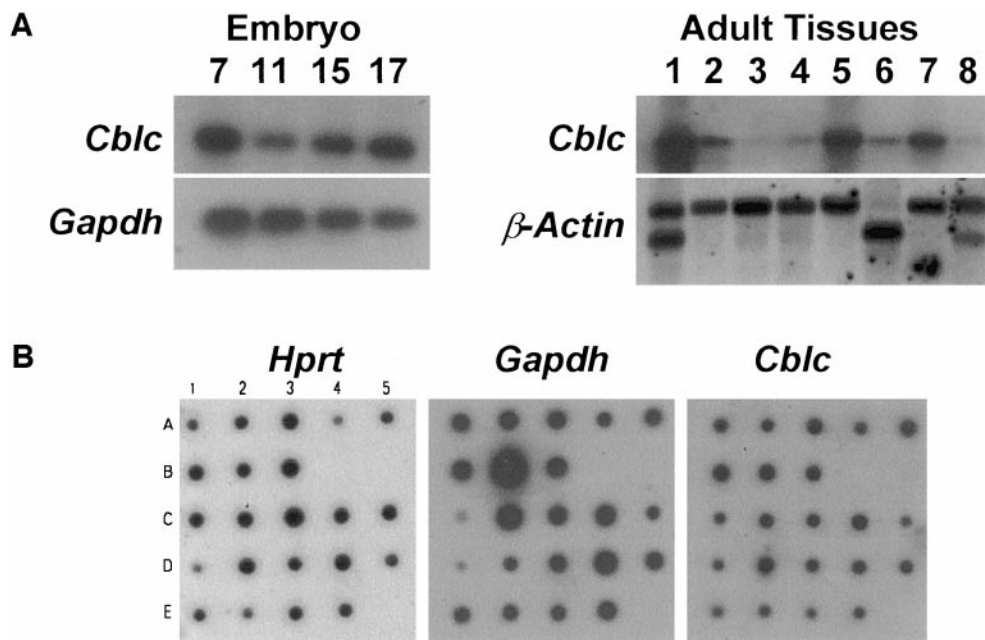
*Northern and dot blot hybridization analyses.* The mouse *Cblc* cDNA probe "troncus" was used to hybridize the Clontech Northern (Mouse tissues Cat 7762-1 and Mouse Embryo Cat 7763-1) and Dot blot (Cat 7771-1) membranes. Northern blot membranes contain 2 µg of total RNA in each lane. They were first hybridized with the *Cblc* probe and second with a murine *Gapdh* or  $\beta$ -actin probes. The control dot blot images (using an *Hprt* probe) and adult Northern blot (using a  $\beta$ -Actin probe) were provided by the furnisher.

*Nonradioactive in situ hybridization analysis.* Dioxigenin-labeled sense or antisense riboprobes were synthesized in the presence of digoxigenin-dUTP (Boehringer Mannheim) by T3 sense or T7 antisense RNA polymerase from the "troncus" fragment of 5' coding sequences of mouse *Cblc* cDNA, cloned into pBS-KS+ plasmid and digested by *Xba*I (sense) or *Xho*I (antisense) restriction enzymes.

The study was done on 14–16 µm fresh-frozen tissue sections of embryos of 12.5, 13.5, and 14.5 d.p.c. and on adult mouse tissues. The protocol described by Philippe *et al.* (20) was used. Detection was carried out by anti-digoxigenin antibody conjugated with alkaline-phosphatase (1:5000, Boehringer Mannheim). Colorimetric reaction with nitro-blue tetrazodium and 5-bromo-4-chloro-3-indolyl-1-phosphate (NBT/BCIP) was carried out at room temperature: 2 h for control samples and only 15 min for positive sections.



**FIG. 1.** Mouse *Cblc* gene structure. (A) Structure of the mouse *Cblc* gene showing exon-intron organization. (B) Alignment of amino-acid sequences of mouse CBLc and human CBLc. Identical amino acid residues are shown in between the two sequences. According to "SMART" software (<http://smart.embl-heidelberg.de/>), the amino acid stretch shown in green is a potential SH2 domain, the ring finger (as defined in 25) is shown in blue and the proline-rich region is shown in red. Two other domains (as defined in 17) are indicated: the four helix bundle (in yellow) and the EF-hand fold (in brown). The exon-intron boundaries are schematized by red arrowheads. The "troncus" probe region is



**FIG. 2.** Mouse *Cblc* mRNA expression. (A) Northern blot analysis of *Cblc* expression in adult mouse tissues and mouse embryos. Northern blot membranes containing polyA<sup>+</sup> RNAs (2  $\mu$ g per lane) from adult mouse tissues or embryos at different stages of gestation were hybridized with a 794-bp <sup>32</sup>P 5' mouse *Cblc* fragment and *Gapdh* or  $\beta$ -*Actin* control probes. Mouse Embryo Northern blot: day 7; day 11; day 15; day 17 of gestation. Mouse multiple tissues Northern blot: heart (lane 1); brain (lane 2); spleen (lane 3); lung (lane 4); liver (lane 5); skeletal muscle (lane 6); kidney (lane 7); testis (lane 8). (B) Dot blot analysis of *Cblc* expression in adult mouse tissues and mouse embryos. Mouse RNA Master Blot containing polyA<sup>+</sup> RNAs (100–500 ng per dot) was hybridized with the hypoxanthine guanine phosphoribosyl transferase (*Hprt*) <sup>32</sup>P-labeled probe and 5' *Cblc* mouse probe. Brain (A1); eye (A2); liver (A3); lung (A4); kidney (A5); heart (B1); skeletal muscle (B2); smooth muscle (B3); pancreas (C1); thyroid (C2); thymus (C3); submaxillary gland (C4); spleen (C5); testis (D1); ovary (D2); prostate (D3); epididymis (D4); uterus (D5); embryo day 7 (E1); embryo day 11 (E2); embryo day 15 (E3); embryo day 17 (E4).

## RESULTS AND DISCUSSION

### Mouse *Cblc* Gene Cloning

Mouse *Cblc* cDNA was obtained by PCR amplification of reverse transcribed RNA from several tissues. To characterize the 3' end of *Cblc* cDNA, RACE-PCR was carried out on liver mRNA. The human *CBLc* cDNA probe col7, derived from EST zm28c07 (Accession No. AA112513) (1) was used to screen a mouse cosmid library from RZPD (<http://www.tel.de/s/R/RZPD.htm>). Eight positive cosmid clones were isolated. Cosmids B and F (Clone ID MPMGc121M0228Q4 and MPMGc121H07398Q3, respectively) were selected for further analysis. Mapping and sequencing of fragments reacting positively with the human *CBLc* probe identified exons 1 to 5 of the mouse *Cblc* gene. The structure of the mouse *Cblc* gene is shown in Fig. 1A. The gene comprises 12 exons which are distributed over 17 kb of genome.

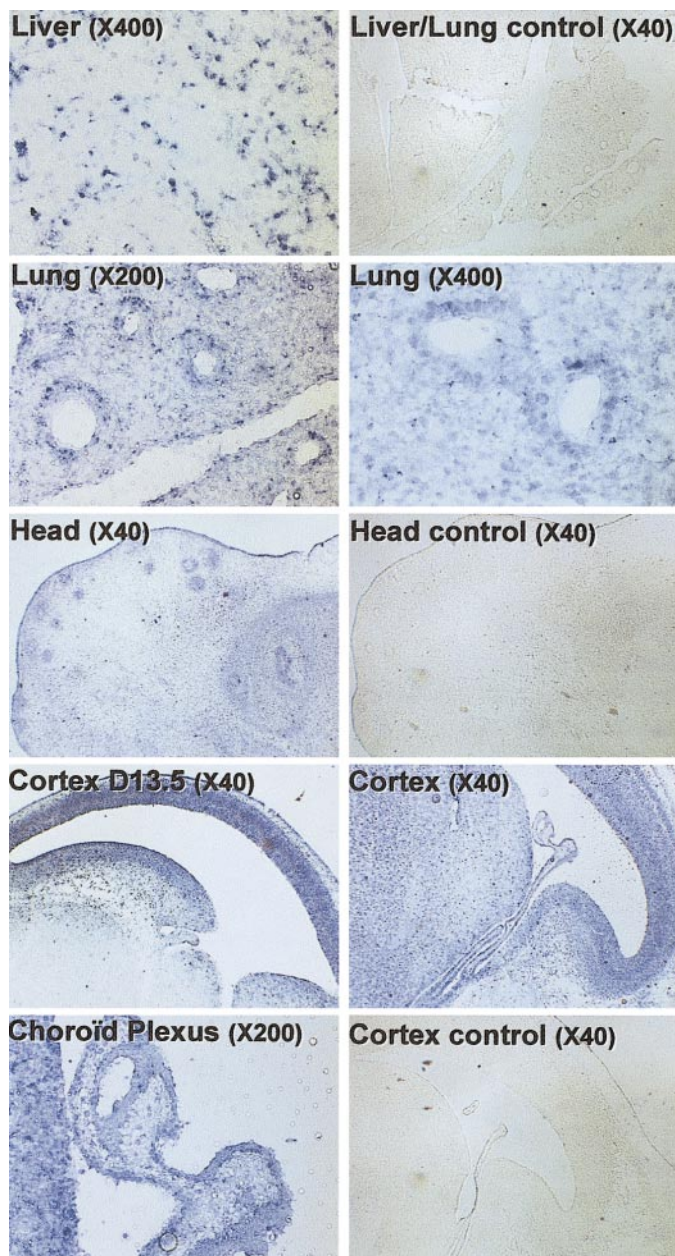
Cloning and sequencing of the reconstituted cDNA yielded a deduced amino-acid sequence for the putative mouse CBLc/CBL3 protein. The mouse CBLc protein is 496 amino acids long and has a typical ring finger motif and a SH2 domain, two features shared by all CBL proteins. The alignment of mouse CBLc and human CBLc protein sequences is shown in Fig. 1B. Overall, mouse and human CBLc proteins share 67% amino-acid identity. As compared to the other CBL products, CBLc is shorter and lacks a C-terminus tail present in both CBL and CBLb. Mouse CBL and CBLc proteins share 70% amino acid identity over their conserved N-terminal portion (Fig. 1C). Whereas for CBL as well as CBLb, the C-terminus is well conserved between human and mouse, the C-terminal tail of murine CBLc differs greatly from that of human CBLc; however, the last proline-rich motif is preserved. This difference explains why the commercial antibodies, which are di-

underlined. The corresponding nucleotide sequence has the GenBank Accession No. AF319956. (C) Comparison of amino-acid sequence identities between different CBL proteins: the percentage of identity of amino acid residues between the various regions (including the so-called PTB region with 4H, four helix bundle; EF, EF-hand fold; and SH2, SH2 domain) of CBL proteins (Mm, *Mus musculus*; Hs, *Homo sapiens*; Dm, *Drosophila melanogaster*; Ce, *Caenorhabditis elegans*) is indicated below a schematic representation of the putative CBLc protein (the color code is the same as in B).

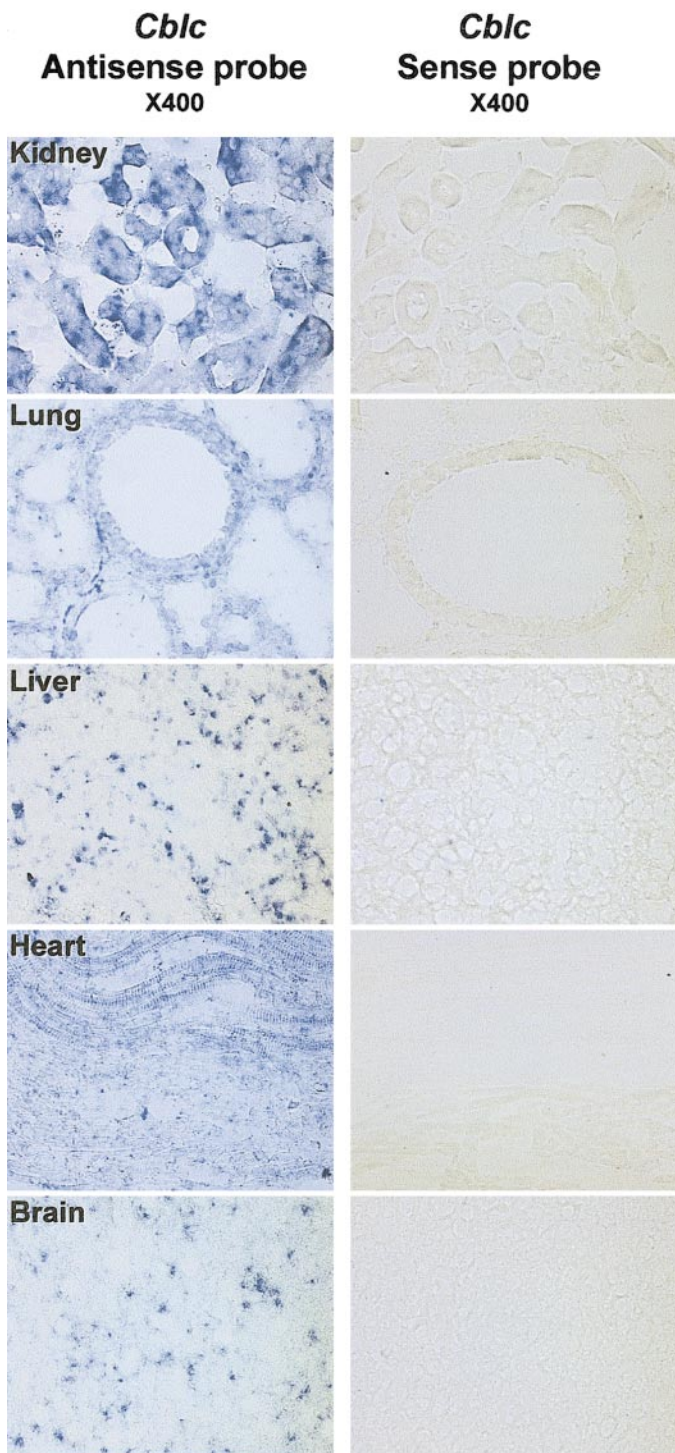
rected against the last amino acids of the human CBLc protein, are unable to recognize the mouse protein.

### *Cblc* Expression

We first performed Northern blot analyses of *Cblc* expression in mouse tissues and embryos. Forward and reverse oligonucleotide primers were designed in exons 1 and 5, respectively, and used to amplify reverse-transcribed RNA from 17.5 d.p.c. embryo. This PCR



**FIG. 3.** *In situ* hybridization analysis of *Cblc* mRNA expression in mouse embryonic tissues. All organs express *Cblc* with various degrees and distribution. Details of liver, lung, head, and brain are shown. Control sense probe does not show any signal.



**FIG. 4.** *In situ* hybridization analysis of *Cblc* mRNA expression in adult mouse tissues. Several sections of adult tissues were analyzed by *in situ* hybridization. All tissues tested express *Cblc* mRNA. Details of kidney, lung, liver, heart, and brain are shown. Control sense probe does not show any signal.

product was used as probe in Northern blot analyses. *Cblc* was expressed in all tissues tested as a 1.7-kb transcript (Fig. 2A). Mouse embryos of 7, 11, 15, and

17 d.p.c. express *Cblc*. No cross reacting signal with *Cbl* and *Cblb* mRNA was seen. To extend these data, we performed a dot blot expression study on mouse tissues. *Cblc* mRNA was found expressed in all tissues tested. However, expression was weaker in lymphohematopoietic organs such as thymus and spleen (Fig. 2B). As for mouse *Cblc*, analysis of the human *CBLC*/*CBL3* mRNA showed ubiquitous expression, with strong signals in endodermally-derived organs (18, 19). In contrast to human *CBLC*, mouse *Cblc* mRNA is also found in brain and in heart.

We next performed *in situ* hybridization on embryonic and adult tissues. *In situ* data correlated well with Northern blot results. *Cblc* is expressed in embryonic tissues. Figure 3 shows examples of *in situ* hybridization signals in the 14.5 d.p.c. fetal liver, with a punctuate perilobular labeling, lung where epithelial structures are prominently stained, head where the primordia of follicles of vibrissae and eyes are strongly labeled, in the 13.5 and 14.5 d.p.c. fetal brain with a strong staining of cortex neurons and choroid plexus. *Cblc* mRNA was found in all adult tissues tested. Figure 4 shows examples of *in situ* hybridization signals: *Cblc* mRNA is present in the epithelial cells of the kidney nephron, the airway structures of the lung, the liver where the punctuate labeling is seen, as well as in myocardium and brain neurons.

The human *CBL* and *CBLB* genes are ubiquitously expressed but the mRNA levels of expression are variable according to tissues (21–23). Major transcripts of 11 and 4.4 kb are detected for *CBL* and *CBLB*, respectively. *CBL* and *CBLB* are specifically highly expressed, and play a role in lymphohematopoietic organs (8, 21–24). Accordingly, *Cbl*  $-/-$  (9) and *Cblb*  $-/-$  (12, 13) mice show immunological defects. In contrast, *Cblc* although also ubiquitously expressed, shows high expression in epithelial structures but its expression is lower in lymphohematopoietic tissues. It is possible that, depending on specific territories, differences in mRNA and/or protein levels are maintained between the three CBLs allowing differential regulation of signaling cascades. The CBL proteins play a major role in protein degradation via the ubiquitin pathway, but their respective spectrum and specificity of interaction with target proteins is not precisely known. Occupation of overlapping but slightly distinctive expression territories may be one way to exert their role in the degradation of different proteins.

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