Functional characterization of alternatively spliced human SECISBP2 transcript variants

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ABSTRACT

Synthesis of selenoproteins depends on decoding of the UGA stop codon as the amino acid selenocysteine (Sec). This process requires the presence of a Sec insertion sequence element (SECIS) in the 3′-untranslated region of selenoprotein mRNAs and its interaction with the SECIS binding protein 2 (SBP2). In humans, mutations in the SBP2-encoding gene Sec insertion sequence binding protein 2 (SECISBP2) that alter the amino acid sequence or cause splicing defects lead to abnormal thyroid hormone metabolism. Herein, we present the first in silico and in vivo functional characterization of alternative splicing of SECISBP2. We report a complex splicing pattern in the 5′-region of human SECISBP2, wherein at least eight splice variants encode five isoforms with varying N-terminal sequence. One of the isoforms, mtSBP2, contains a mitochondrial targeting sequence and localizes to mitochondria. Using a minigene-based in vivo splicing assay we characterized the splicing efficiency of several alternative transcripts, and show that the splicing event that creates mtSBP2 can be modulated by antisense oligonucleotides. Moreover, we show that full-length SBP2 and some alternatively spliced variants are subject to a coordinated transcriptional and translational regulation in response to ultraviolet type A irradiation-induced stress. Overall, our data broadens the functional scope of a housekeeping protein essential to selenium metabolism.

INTRODUCTION

Selenocysteine (Sec), the 21st amino acid in the genetic code, is incorporated into a subset of proteins termed selenoproteins in response to an in-frame UGA codon (1). Since the UGA codon most commonly signals translation termination, its decoding as Sec relies on the presence of several unique, evolutionary conserved structures and protein factors. The major cis-acting determinant for Sec incorporation is the Sec insertion sequence (SECIS) element, a stem–loop RNA structure located within the 3′-untranslated region (UTR) of all eukaryotic selenoprotein mRNAs (2,3). This element acts by recruiting the specialized protein complexes required for the read-through of UGA and translation of selenoproteins. An additional RNA structure able to support UGA codon read-through, named the Sec redefinition element (SRE), has been recently identified within the coding region of selenoprotein N, a few nucleotides downstream of the UGA codon (4). While the SECIS element is absolutely required for Sec incorporation, the SRE appears to play only a fine-tuning role in determining the UGA decoding efficiency for some selenoproteins (5). Synthesis, delivery and incorporation of Sec into polypeptide chains is supported by selenocysteyl-tRNA[Ser]Sec(1) and by a set of specialized proteins [reviewed in (6)], including SECIS binding protein 2 (SBP2) (7,8), Sec-specific elongation factor eEFSec (9,10), ribosomal protein L30 (11),

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the 43 kDa RNA binding protein (SECp43) and Sec synthase (12). Although much progress has been made in delineating individual components required for selenoprotein synthesis, the overall mechanism that directs this process is not fully understood.

SBP2 is one of the most studied selenoprotein synthesis factors, initially shown to be required for this process in reticulocyte lysates and in vitro assays (8,13). Consistent with this, we have shown that SBP2 depletion in human cells leads to decreased selenoprotein synthesis (14). Hereafter, we refer to SBP2 as protein, whereas Sec insertion sequence binding protein 2 (SECISBP2) in italicized letters refers to gene or transcript. The first in vivo evidence showing that SBP2 is epistatic to selenoprotein synthesis was recently provided in a study that identified mutations in SECISBP2 in families presenting with clinical evidence of abnormal thyroid hormone metabolism (15). This was manifested through lack of functional selenoenzyme deiodinase 2 (DIO2) and dramatically reduced levels of selenoprotein P in affected individuals (15). Detailed biochemical and functional characterization of SBP2 has been carried out; however, its regulation at the gene and transcript level requires further studies.

Alternative splicing represents a functionally important and a major regulatory pathway of gene expression and ultimately protein function. Recent genomic studies have indicated that at least 60% of mammalian genes are subjected to alternative splicing (16), providing a significant contribution to protein diversity beyond that encoded in the genome sequence. Most alternative splicing events affect the coding sequence and it is believed that half of these alter the reading frame (17), and a third lead to nonsense mediated decay (NMD) of the RNA product (18). Defects in alternative splicing and generation of aberrant ratios of mRNA transcripts from a single gene are now also recognized as major contributors to human disease and it is estimated that at least 15% of the mutations that cause hereditary disease affect pre-mRNA splicing (19). Splicing defects have also been associated with cancers and a genome wide analysis of human expressed sequence tags (ESTs) found strong evidence for cancer specific splice variants in 316 human genes (20–24). To date, this level of regulation has not been explored for any of the factors involved in Sec incorporation, including SBP2.

SBP2 is the only protein of the Sec incorporation machinery so far linked to a clinical condition (15). Interestingly, one of the mutations identified in patients alters the splicing of SECISBP2 by creating an alternative donor splice site, which produces a transcript with a 26 bp intron retention. This event alters the reading frame upstream of the SBP2 RNA-binding domain, giving rise to a truncated, non-functional protein. The regulation of SBP2 expression by alternative splicing thus appears to have significant implications for its function. Prompted by these findings, we herein carried out in silico, as well as functional analysis of alternative splicing of SECISBP2. We now provide evidence for a complex alternative splicing pattern in the 5′-region of human SECISBP2 that give rise to eight spliced variants generated through different exon combinations. All alternative splicing events are confined within the region of SBP2 that is dispensable for Sec incorporation in vitro, but may be involved in regulation of selenoprotein synthesis in vivo. Interestingly, one of the alternatively spliced isoforms contains a mitochondrial targeting sequence (MTS). We designated this transcript as mitochondrial Sec insertion sequence binding protein 2 (mtSECISBP2). First, using a minigene-based in vitro splicing assay we delineated the splicing events within the 5′-region of SECISBP2 and showed that splicing of mtSECISBP2 can be modulated by antisense oligonucleotides (ASOs). We furthermore demonstrated that the protein encoded by mtSECISBP2 does indeed localize to mitochondria and that transcription and translation of SBP2 is regulated in a coordinated manner in response to stress.

MATERIALS AND METHODS

In silico identification of alternatively spliced forms of SBP2

The previously characterized human full-length SECISBP2 gene (GeneBank ID: NM_024077) was used to search against both the EST and the non-redundant (NR) nucleotide databases to identify alternative forms of human SECISBP2 gene. Sequence analyses were performed using BLAST programs (available at http://www.ncbi.nlm.nih.gov/BLAST/) with default parameters. Tissue- and cell-type information of various ESTs was also retrieved from EST database. Identified sequences that were homologous to SECISBP2 were then mapped to human genomic sequences to analyze genomic structures of detected alternative forms. Cellular localizations of proteins were predicted by PSORT II (http://psort.ims.u-tokyo.ac.jp/form2.html).

Cell culture and treatments

The cell lines human embryonic kidney 293T, human cervical carcinoma C33A, human cervical carcinoma HeLa and normal foreskin fibroblast (NFF) cells, were maintained in RPMI 1640 medium supplemented with 10% fetal calf serum (Gibco-BRL, Gaithersburg, MD, USA) and 1% penicillin/streptomycin, in a humidified atmosphere containing 5% CO₂. For Ultraviolet A (UVA) treatments, media was removed and kept at 37°C, and phosphate buffered saline (PBS) was added. Cells were subjected to a dose of 50 kJ/m² of UVA irradiation. Control cells were maintained in PBS at room temperature, in the dark, for the duration of treatment. Following irradiation, the PBS was replaced with the media and cells were allowed to recover for the time indicated.

Generation of minigenes

SECISBP2 minigene splicing cassette was generated by amplifying genomic sequences starting from exon 1 through exon 4 of the SECISBP2 gene with high-fidelity Pfx polymerase (Invitrogen, Carlsbad, CA, USA) and genomic DNA (Clontech Laboratories, Inc. Palo Alto, CA, USA). Appropriate primers were used to reduce the size of intron 2 from ~5.6 kb to 356 nt that include 184 residues of the 5′-end of intron 2 and 172 residues of the
3’-end of intron 2. An ~2.3 kb amplified fragment from genomic SECISBP2 containing entire exon 1, entire intron 1, entire exon 2, partial intron 2 (only 356 nt), entire exon 3, entire intron 3 and entire exon 4 was cloned into pCI vector (Promega) between Xho I and Not I site. Subsequently, genomic sequences from the pCI vector were subcloned into a SBP2-GFP plasmid described previously (14). Here, appropriate primers were used to replace exon 1 through exon 4 of SBP2 cDNA sequence with ~2.3 kb genomic sequence described above (Figure 2A). The complete SBP2 minigene sequence is provided as supplementary data. Mutations were introduced using the Quick-Change site directed mutagenesis kit (Stratagene) as per manufacturer’s instructions.

**Antisense oligonucleotides**

ASOs were synthesized by Dharmacon, Inc. The sequences of the oligonucleotides used are as follows: mG(3’)-mA(mC)(mG)(mA)(mU)(mC)(mG)(mA)(mU)(mC)(mG)(mC)(mG)(mG)(mA)(mU)-mC(mG)(mC)(mG)(mA)-mA(mC)-mG(mU)-mG(mC)-mA(mA)-mA(mG)-mA(mC)-mA(mA)-mA(mG)-mU(mG)+mU(mA)-mA(mA)-mA(mG)-mU(mG)+mU(mA)-mA(mA)-mA(mC) for the control ASO (GATC) and mC(mU)+mG(mC)-mU(mA)-mA(mG)-mA(mU)-mA(mU)-mA(mA)+mG(mU)-mA(mA)-mA(mG)-mU(mG)+mU(mA)-mA(mA)-mA(mC) for the SBP2 specific ASO spanning the intron 2-exon 3a boundary (In2E3a). In these sequences, the letter m represents an O-methyl modification at the second position of a sugar residue and an asterisk represents a phosphorothioate modification of the backbone.

**Transfections and in vivo splicing assays**

All reagents were used according to the manufacturer’s recommendations. Transient transfections of cells with plasmid DNA or antisense oligonucleotides were performed with Lipofectamine 2000 (Invitrogen). Cells were plated into 6-well plates 24 h prior to transfection so that their density on the day of transfection was 70%, 2.0 µg of plasmid DNA was used per well. For co-transfection experiments, cells were transfected with 1.0 µg of plasmid DNA and 100 nM of ASO per well. Total RNA was isolated 24 h after transfection with Trizol reagent (Invitrogen). To generate cDNA, reverse transcription was carried out with a SuperScript II reaction kit (Invitrogen) using oligo(dT) primer. Generally, 1.0 µg of total RNA was used per 20 µl of reaction mixture. Minigene-specific spliced products were subsequently amplified with forward primer annealing in the vector sequence (P1GF) 5’-GCTAGCGCATCCGGACCTCA GT-3’, and the reverse SBP2-specific primer annealing in exon3b 5’-CTTAAACAGAGCTTTCATTTCTTG TTTACCTAG-3’ for full-length SECISBP2 and 5’-CAGTGCAGAAATGT TTATCGTAG-3’ for mtsSECISBP2, and the same reverse primer 5’-CTTCTGTGTCGCTGTTATGG-3’. Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) was used as an internal standard (Fwd 5’-CTGACACACACAC TGCTTAG-3’; Rev 5’-GTCTTCGGGTTGGCATGTG AT-3’). Real-time RT-PCR was performed using Platinum SYBR Green qPCR SuperMix-UDG (Invitrogen) in a Rotor-Gene 6000 (Corbett Life Science) according to the instructions provided with the kit. Cycling conditions were used as suggested in the SYBR Green kit instructions. Results were analyzed using relative quantification software (Corbett Life Science).

**Cell lysis and western blotting**

Cells were lysed in universal immunoprecipitation buffer (UIP) as described previously (14). Proteins were separated on 4-12% gradient gels (Invitrogen) unless otherwise stated. Western blotting was performed using the following antibodies: anti-SBP2 and anti-HSP70 antibodies raised in house as described previously (14), anti-actin (Sigma), anti-GFP (Molecular Probes, Invitrogen) and anti-SBP2 antibodies (EC1) (Everest Biotech, Oxfordshire, UK). Except for Figure 4B, images were acquired using an LAS-3000 luminescent image analyzer (Fujifilm Life Science, Stanford, CA, USA). The western blot in Figure 4B was developed using traditional X-ray film.

**Fluorescence microscopy**

Cells, untransfected or transfected with GFP-tagged proteins, were washed in PBS twice and fixed with 4% paraformaldehyde in PBS for 30 min at room temperature. 4’,6-Diamidino-2-phenylindole (DAPI) was used to stain the nuclei and MitoTracker CMXRos (Molecular Probes, Invitrogen) (50 nM) was used to stain mitochondria. For immunofluorescence, coverslips were blocked in 3% horse serum in PBS, incubated with anti-SBP2 antibody (EC1) at 1:250 dilution, followed by incubation with an Alexa fluor 488 dye-conjugated secondary antibody (Molecular Probes, Invitrogen). Colocalization of SBP2 with mitochondria was detected using a double immunofluorescent procedure. Coverslips were mounted with ProLong Gold (Molecular Probes, Invitrogen). Images were acquired in 20 z-sections by using a state-of-the art DeltaVision PD system microscope (Applied Precision, Washington, USA) with a 60× or 100× objective. Images were subsequently deconvolved with 10 cycles of the DeltaVision PD software.

**RESULTS**

**Human SBP2 is alternatively spliced**

In humans, the SECISBP2 gene spans a 43 kb region on chromosome 9q22.1 and consists of 17 exons.
Following reverse transcription PCR (RT-PCR) of the 5'-end of SECISBP2 using mRNA isolated from 293T cells, we observed a second PCR product, shorter than the full-length transcript (data not shown). Sequence analysis of this band identified two alternatively spliced SECISBP2 variants: one lacking exon 2, and the second lacking part of exon 3, further designated exon 3a. To further examine whether additional SECISBP2 splice variants were present in humans, we searched EST and NR databases using known full-length SECISBP2 sequences and mapped and quantified the identified cDNAs onto the genomic sequence. This search confirmed that full-length SECISBP2 is indeed the most abundant transcript, currently represented by ~120 ESTs and 5 complete mRNAs, and led to the identification of seven alternatively spliced SECISBP2 variants arising through different exon combinations. These variants are as listed in Table 1 along with their proposed nomenclature. A schematic representation of the genomic organization of human SECISBP2 is shown in Figure 1A, and the spliced variants for which sufficient sequence was available to determine their complete 5'-exon combination are presented in Figure 1B. The three functional domains of SBP2: the RNA binding domain, the Sec insertion domain and the ribosome interacting domain, are located within the C-terminal part of the protein (8,25), which corresponds to exons 12–16. Interestingly, all alternative splicing events occur upstream of exon 11, within the region dispensable for Sec insertion in vitro.

Sequence analysis of exon/intron boundaries showed that nearly all splice sites within the 5'-region of SECISBP2 conform to consensus sequences (AAG|GU or CAG|GU at the 5'-exon/intron boundary and CAG|G at the 3'-end) (26) with only a few deviations (Table 2). The majority of exons have one donor and one acceptor splice site; however, exons 3 and 7 have multiple acceptor sites, denoted as a, b, c or d. A very complex splicing pattern was noted between exons 6 and 7, with four possible splicing combinations. The most common acceptor site was the 7a site. The 6–7b splice variant appeared to be rare, however, an encoding mRNA derived from brain tissue (Table 1) was present in the EST database. The variants 6–7c and 6–7d were covered by several ESTs.

All SECISBP2 transcripts for which sufficient 5'-sequence information was available appear to begin with exon 1. This suggests the usage of a common promoter, located upstream of exon 1. As mentioned above, the overwhelming majority of SECISBP2 transcripts include all exons. However, the alternatively spliced SECISBP2 variants seem to be expressed in normal as well as in cancer-derived tissues (Table 1). The best represented alternatively spliced transcript lacked exon 3a as evidenced by 24 ESTs from normal and cancer-derived tissues and cell lines, and was also covered by three complete mRNAs (Table 1). Despite the presence of a large number of ESTs covering the 5'-region of SECISBP2 sequence, no alternative splicing events were detected downstream of exon 10.

**Alternative splicing of SECISBP2 creates several open reading frames**

We next examined the nucleotide sequences of the various transcripts for their potential to encode complete open reading frames (ORFs), and found that five SBP2 isoforms initiating from five different ATG start sites can be encoded (Figure 1C). As previously shown, the full-length SBP2 is translated using the first ATG codon in exon 1. This main ORF is however abrogated for some of the variants as premature termination codons (PTCs) are generated, suggesting a possibility of the use of alternative ATG start sites. As indicated in Figure 1B, these potential alternative translation initiation sites (referred by amino acid numbering in full-length SBP2) are methionine (Met) 69 within exon 3a for SBP2_Δ2, and Met 233 within exon 5 for SBP2_Δ3 and they are in the same frame as full-length SBP2. However, for the mtSECISBP2 and SECISBP2E6 transcripts, the first ATG codon downstream of the PTC is created in a different frame in exon 2 (Met 33) and in exon 6 (Met 283) respectively (Figure 1B). These reading frames create a short N-terminal amino acid composition different to full-length SBP2 (i.e., 27 aa for mtSBP2 MVRVLRSCLMP QLCSHILVSCGTTSDR, and 11 aa for SBP2E6 MP LPILVHQ), however, these reconnect with the full-length SBP2 reading frame at the next splice site. Interestingly, motif analysis using the PSORTII program predicted the existence of a classical MTS within the exon 3a-deleted variant (Figure 1C), and this form is further designated as mitochondrial SBP2, mtSBP2. The alternate reading frame for SBP2E6 did not seem to encode any targeting signals or motifs different to full-length SBP2. The complex splicing pattern between exon 6 and 7 was interesting as all splicing variations lead to changes in the amino acid composition of the encoded proteins. The splicing from exon 6–7c and 6–7d lead to deletion of a stretch of 38 or 39 amino acids (aa 294–331) from exon 7 (294ELSWTPMGYVRQTLSTELSAAPKNVT517). Interestingly, motif analysis using the PSORTII program predicted the existence of a classical MTS within the exon 3a-deleted variant (Figure 1C), and this form is further designated as mitochondrial SBP2, mtSBP2. The alternate reading frame for SBP2E6 did not seem to encode any targeting signals or motifs different to full-length SBP2. The complex splicing pattern between exon 6 and 7 was interesting as all splicing variations lead to changes in the amino acid composition of the encoded proteins. The splicing from exon 6–7c and 6–7d lead to deletion of a stretch of 38 or 39 amino acids (aa 294–331) from exon 7 (294ELSWTPMGYVRQTLSTELSAAPKNVT517), however, the reading frame starting in exon 1 is maintained throughout both isoforms. The ESTs covering the SECISBP2_Δ9 transcript did not have sufficient sequence upstream of the splicing event in order to determine its translation initiation sites; however, ORF prediction indicated that the reading frame in exon 1 can be maintained despite exon 9 skipping.

**Evolutionary aspects of splicing events within SBP2**

We next investigated the extent of alternative splicing events in SBP2 in other species. We thus analyzed the distribution of SECISBP2 homologs, the conservation of splicing events and evolution of the SECISBP2 gene in genomic and EST databases. As recently established, selenoprotein genes are widely distributed among eukaryotes including all vertebrates and most arthropods, nematodes, protozoa and lower plants (27–29). Selenoproteins were lost in fungi, land plants, some insects and most eukaryotic parasites. We found that SECISBP2 homologs are present in all selenoprotein-containing genomes, and absent in EST and genomic databases of organisms lacking Sec utilization, suggesting that SECISBP2 co-evolved...
Table 1. Alternatively spliced human SECISBP2 transcripts

<table>
<thead>
<tr>
<th>Transcript name</th>
<th>Exon combination</th>
<th>No. of ESTs</th>
<th>Normal tissue or cell line</th>
<th>Primary tumors</th>
<th>Cancer derived or transformed cell lines</th>
<th>Complete mRNAs</th>
</tr>
</thead>
<tbody>
<tr>
<td>SECISBP2</td>
<td>1–17</td>
<td>~120</td>
<td>Present in most tissues</td>
<td>Present in several tumors</td>
<td>Present in several cell lines</td>
<td>NM024077, AK090608, AK174632, BC036109, AF380995</td>
</tr>
<tr>
<td><em>mtSECISBP2</em></td>
<td>1.2–3b,4,5,6 ...</td>
<td>24</td>
<td>Pooled glandular (CB956376) Pancreas (BM315064) ES cell lines (CN256608, CN256604, CX870404) T-lymphocytes (CR994587) Liver Cho-CK cell line (CB126125) Thymus (DB160135) Small intestine (DA926236) Fetal brain (DA803510) Thalamus (DA407353) Corpus callosum (DA283160) Testis (DB459197, DC399547) Pooled mixed tissue (CV092893)</td>
<td>Retinoblastoma (BE252177) Choriocarcinoma (BG481218) Terratocarcinoma (DA754929, DA758978) Tongue tumor (DA450129)</td>
<td>Lymphoma (BQ049808) Osteosarcoma (BG113716) Neuroepithelioma (DA903910) Lymphoma (CR747151)</td>
<td>AL138681, AK290182, AM392812</td>
</tr>
<tr>
<td>SECISBP2_A2</td>
<td>1–3a,4,5 ...</td>
<td>2</td>
<td>ES cell line (CV811081)</td>
<td>Genitourinary tract high-grade tumor (AW630547)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SECISBP2_A3</td>
<td>1.2–4,5 ...</td>
<td>3</td>
<td>Testis (DB459197)</td>
<td>293T cell line (this study)</td>
<td>293T cell line (this study)</td>
<td></td>
</tr>
<tr>
<td>SECISBP2_A7a</td>
<td>1–5,6b–7b ...</td>
<td>3</td>
<td>Uterus (AI129567, AI128470)</td>
<td>Genitourinary tract high-grade tumor (AW630547)</td>
<td>Mammary gland tumor (BP313796)</td>
<td>AB208940</td>
</tr>
<tr>
<td>SECISBP2_c</td>
<td>3,4,5, 6a–7c ...(aa TRAD)</td>
<td>5</td>
<td>ES cell line (CN256603, CX787609)</td>
<td>Squamous cell carcinoma (BP352801)</td>
<td>Large cell carcinoma (BQ430224)</td>
<td></td>
</tr>
<tr>
<td>SBP2_7d</td>
<td>3.4, 6a–7d ...(aa TRD)</td>
<td>5</td>
<td>Pancreas (BE669723)</td>
<td>Retinoblastoma (BC01189, BE79955)</td>
<td>Prostate cancer (EC508545)</td>
<td></td>
</tr>
<tr>
<td>SECISBP2_9</td>
<td>8–10 ...</td>
<td>2</td>
<td>Retinal pigment epithelium (CA389610)</td>
<td>Leiomysarcoma (BU902304)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

SECISBP2 transcripts that were identified experimentally or by EST database searches are listed according to the nomenclature proposed in the text. Information on exon combination, number of ESTs present, tissue of origin and corresponding GenBank accession numbers are given. ES = embryonic stem.
**Figure 1.** Schematic representation of human SECISBP2 transcript variants. (A) Genomic organisation of SECISBP2 showing the 17 exons and their sizes in base pairs (bp). Locations of the functional domains are indicated. (B) Alternatively spliced SECISBP2 transcript variants generated through different exon combinations are shown schematically. Arrowheads indicate translation start sites. Designation for the encoded protein isofoms, the corresponding Met start codon number [based on numbering in the full-length human SBP2 sequence (NP_076982)] and predicted molecular weights (MW) of isoforms are indicated to the right of each transcript. (C) An alternative reading frame used for translation of the mitochondrial SBP2 isoform (mtSBP2) initiates in exon 2 (indicated by arrow). The encoded mitochondrial targeting sequence is underlined.

**Table 2.** Splice site boundaries of SECISBP2 transcript variants

<table>
<thead>
<tr>
<th>Donor exon (nt)</th>
<th>Acceptor exon (nt)</th>
<th>Intro size(kb)</th>
<th>EXON/intron/EXON (splice site consensus: ...AGguagu...)(y)hgnyagG...</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (116)</td>
<td>2 (146)</td>
<td>1.04</td>
<td>AGCCAG guaagg_uaauuuuuuucuccag</td>
</tr>
<tr>
<td>1 (116)</td>
<td>*3a (121)</td>
<td>6.81</td>
<td>AGCCAG guaagg_uaauuuuuuuuauucag</td>
</tr>
<tr>
<td>2 (146)</td>
<td>*3a (121)</td>
<td>5.63</td>
<td>GACAGA guaugu_uuaacuuuuuacucag</td>
</tr>
<tr>
<td>2 (146)</td>
<td>*3b (129)</td>
<td>5.63</td>
<td>GACAGA guaugu_uaccccucacccacccag</td>
</tr>
<tr>
<td>2 (146)</td>
<td>4 (142)</td>
<td>5.63</td>
<td>GACAGA guaugu_uuuuuuaacucucucucucag</td>
</tr>
<tr>
<td>2 (146)</td>
<td>4 (142)</td>
<td>0.20</td>
<td>UUUAAG guagug_uuuuuuuuuucucucucucag</td>
</tr>
<tr>
<td>2 (146)</td>
<td>5 (227)</td>
<td>2.67</td>
<td>AAUAAG guuaaa_uuuuuuuuuuuuuuucacag</td>
</tr>
<tr>
<td>3 (250)</td>
<td>4 (142)</td>
<td>0.20</td>
<td>UUUAAG guagug_uuuuuuuuuuuuuuucucucucucag</td>
</tr>
<tr>
<td>3 (250)</td>
<td>5 (227)</td>
<td>2.67</td>
<td>AAUAAG guuaaa_uuuuuuuuuuuuuuucacag</td>
</tr>
<tr>
<td>4 (142)</td>
<td>6 (78)</td>
<td>4.02</td>
<td>UCAAGA guagugga_uuaguguuuuuuucucucucucucag</td>
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<tr>
<td>4 (142)</td>
<td>7a (209)</td>
<td>1.53</td>
<td>(CAAGA...</td>
</tr>
<tr>
<td>5 (227)</td>
<td>6 (78)</td>
<td>4.02</td>
<td>UCAAGA guagugga_uuaguguuuuuuucucucucucucucag</td>
</tr>
<tr>
<td>6 (79)</td>
<td>*7a (209)</td>
<td>1.53</td>
<td>(CAAGA...</td>
</tr>
<tr>
<td>6 (79)</td>
<td>*7b (171)</td>
<td>1.53</td>
<td>(CAAGA...</td>
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<tr>
<td>6 (79)</td>
<td>*7c (95)</td>
<td>1.53</td>
<td>(CAAGA...</td>
</tr>
<tr>
<td>7 (79)</td>
<td>*7d (92)</td>
<td>1.53</td>
<td>(CAAGA...</td>
</tr>
<tr>
<td>8 (123)</td>
<td>10 (132)</td>
<td>2.76</td>
<td>(CAAGA...</td>
</tr>
</tbody>
</table>

The donor and acceptor exons are listed with their sizes in nucleotides (nt) in brackets. Intron sizes are given in kilobases (kb). Boundaries of splice sites was identified from the genomic DNA sequence (http://genome.ucsc.edu) and compared to the consensus of splice site motifs (16). Consensus nucleotides at the 5' and 3' splice sites are indicated in bold letters and splice sites are indicated with a vertical line. The polypyrimidine stretch is shown in italics.

**Exons with alternative donor or acceptor sites.**
Characterization of SBP2 splicing in vivo and modulation with antisense oligonucleotides

The identification of alternative splicing within the 5’-region of human SECISBP2 prompted us to further characterize and quantify the occurrence of these events in vivo. We were particularly interested in the mtSECISBP2 variant since it appeared to be the best represented transcript after the full-length transcript. To gain a better insight into the expression pattern of the two transcripts, we first quantified their relative expression levels in a cDNA panel from various human tissues by real-time RT-PCR using isoform-specific primers spanning the exon 2–3a boundary for SECISBP2, and the exon 2–3b boundary for mtSECISBP2. As shown in Figure 2A, SECISBP2 and mtSECISBP2 were expressed in all tissues tested, with the highest expression levels for both transcripts in testis. The ratio between the SECISBP2 and mtSECISBP2 was on average ~4.4:1 in most tissues, which is consistent with the bioinformatics data presented in Table 1. However, colon, thymus and leukocytes had a ~2:1 ratio, indicating that mtSECISBP2 is most abundantly expressed relative to SECISBP2 in these tissues. We also confirmed the expression of mtSECISBP2 variant in a number of normal and cancer-derived cell lines including ones used in this study (data not shown).

As a second approach to characterize and potentially modulate SECISBP2 splicing in vivo, we generated a SECISBP2 minigene construct (WT minigene), schematically presented in Figure 2B. We also generated two mutant minigene constructs: one harbouring a point mutation at the exon 3a 3’ splice site 5′AG>AA (named Ex3AG>AAΔT) which should abrogate the splicing at this site and hence deplete the production of mtSECISBP2; and a second construct harbouring a point mutation 5′AG>AAΔT which should abrogate the splicing at this site and hence deplete the production of mtSECISBP2; and a second construct harbouring a point mutation (5′AG>AAΔT) which should abrogate the splicing at this site and hence deplete the production of mtSECISBP2. These were transiently transfected into several cell lines including 293T, C33A and HeLa, and the expressed proteins were analyzed by western blotting. Blots were probed with anti-GFP antibodies (which is tagged at the C-terminus of SBP2), and with anti-SBP2 antibodies raised against a central region of SBP2 (exon 6–8) to

Several SBP2 isoforms are expressed from the minigene

We next investigated the translation pattern of the alternatively spliced SBP2 isoforms using the minigene constructs. These were transiently transfected in several cell lines including 293T, C33A and HeLa, and the expressed proteins were analyzed by western blotting. Blots were probed with anti-GFP antibodies (which is tagged at the C-terminus of SBP2), and with anti-SBP2 antibodies raised against a central region of SBP2 (exon 6–8) to
ensure that the proteins detected are products that initiate at different ATG codons within the N-terminal region of SBP2 rather than degradation products. A representative example of the minigenes' expression pattern in 293T cells is shown Figure 3A. Consistent with the data obtained from the splicing assay, full-length SBP2 initiating from the ATG in exon 1, was by far the highest expressed protein from the WT and Ex2ATG>CTG minigenes.
weight prediction, this band could represent a protein initiating from ATG codons in exon 3a or exon 3b. We speculate that the increased expression of this band in the Ex2ATG>CTG mutant could be the consequence of lack of translation initiation in exon 2 due to abrogation of the ATG codon with a consequent promotion of translation from downstream ATG codons. Although we could not detect the mtSBP2 isoform expressed from the minigenie by western blotting, its expression levels could be below the detection limit, but still responsible for regulating the expression of other downstream ATG-initiating isoforms (Figure 3A lane 1 compared to lane 2). However, this possibility remains to be investigated. We also noted that translation of the SBP2E3b isoform from the Ex3AG>AAΔT minigenie did not increase significantly when a point mutation that abrogates the full-length SBP2 reading frame is introduced (Figure 3A lane 4). This suggests that the ATG codon context in exon 3b is rather weak, or that expression of this isoform is strictly regulated. The overall SBP2 splicing pattern was similar in other cell lines tested despite variations in transfection efficiency (data not shown).

We showed above (Figure 2B) that the In2E3a ASO is extremely efficient at increasing the levels of the mtSECISBP2 transcript both off the minigenie and endogenously. We therefore tested if co-transfecting the WT minigenie with the In2E3a ASO could induce the expression of the mtSBP2 protein. As shown Figure 3B, a band that corresponds to the predicted size of mtSBP2-GFP was indeed apparent in In2E3a ASO co-transfected cells, but not in control ASO transfected cells, demonstrating that this isoform can be translated in vivo, albeit very inefficiently. Although the In2E3a ASO proved efficient at inducing splicing of endogenous mtSECISBP2 transcript, we were unable to detect the endogenous mtSBP2 protein following In2E3a ASO transfection, despite extensive efforts in several cell lines. Overall, these results showed that full-length SECISBP2 is the most abundant and preferentially translated SBP2-encoding transcript. However, the alternatively spliced transcripts generated are also translated into protein, albeit far less efficiently.

**The mtSBP2 isoform localizes to mitochondria**

One of the main aims of the minigenie splicing assay was to analyze the expression and localization of the protein encoded by the most common alternate SECISBP2 transcript-mtSBP2. Although the assay convincingly showed expression of the mtSECISBP2 transcript, it proved less amenable at analyzing the protein expression. Thus, in order to determine if the predicted mtSBP2 does indeed localize to mitochondria, we expressed the mtSBP2-encoding cDNA (commencing at the ATG codon in exon 2) fused N-terminal to GFP (mtSBP2-GFP) in C33A cells, and analyzed its subcellular localization by co-staining with the mitochondrial marker MitoTracker Red CMX-Ros. The full-length FLSBP2-GFP construct and a construct lacking the putative MTS encoded by the alternate reading frame in exon 2 (SBP2_Δ2-GFP) were used for comparison. Localization of the proteins was visualized using a Z-scanning

**Figure 3.** Minigenie-based expression of SBP2 isoforms. (A) The minigenies (described in the legend to Figure 2) were transfected into 293T cells and the proteins expressed were separated on 4-12% gradient gels and analyzed by western blotting with anti-GFP and anti-SBP2 antibodies. Western blots with the two antibodies show similar staining pattern and thus confirm the expression of several SBP2 isoforms initiating from alternative ATG codons. E3aSBP2-GFP, E3bSBP2-GFP and E5SBP2-GFP refer to isoforms initiating at ATG codons in exons 3a, 3b and 5 respectively. (B) Western blots of cells co-transfected with wild-type (WT) minigenie and the In2E3a antisense oligonucleotides that promotes splicing of the mtSECISBP2 transcript show translation of the mtSBP2GFP isoform. Actin was used as a control for protein loading.

(Figure 3A lanes 1 and 2), however, the presence of multiple bands detected by both antibodies suggested that proteins initiating from other ATG start codons are expressed. Due to the small differences in their size (85.9 kDa, 86 kDa, 80 kDa) some of them could not be resolved and identified easily. However, the nucleotide deletion (T^367) in exon 3b of the Ex3AG>AAΔT minigenie which abrogates the ORFs starting at ATG codons in exons 1, 2 or 3a by creating PTCs, enabled us to identify two of the additional bands as the SBP2 isoforms initiating in exon 3b from Met 139 and in exon 5 from Met 233 (Figure 3A lane 4). Thus, using the minigenie-based in vivo splicing assay we have been able to convincingly show that alternative splicing of SECISBP2 may have a functional relevance as multiple SBP2 isoforms initiating from different ATG start codons and containing different N-termini amino acid composition are being expressed.

Intriguingly, we could not detect a decrease in a band representing the mtSBP2 protein expressed from the Ex2ATG>CTG mutant construct (Figure 3A lane 2). On the contrary, a small increase in expression of the band below the full-length SBP2 was consistently seen (Figure 3A lane 2). According to molecular
microscope followed by image deconvolution. Interestingly, mtSBP2-GFP expressing cells exhibited distinct cytoplasmic fluorescence, which overlapped significantly with the MitoTracker staining as indicated by the intense yellow staining in Figure 4A (Pearson coefficient 0.879). FLSBP2-GFP protein displayed a strong peri-nuclear punctate staining, however, this fluorescence did not overlap significantly with the MitoTracker staining (Figure 4A bottom panels, Pearson coefficient 0.264). Most likely, this pattern represents a ribosomal/endoplasmic reticulum (ER) staining which is the believed functional localization of SBP2 (14,32). Similar to FLSBP2-GFP, SBP2_Δ2-GFP localized throughout the cytoplasm and showed marginal co-localization with MitoTracker (data not shown). This data established that the MTS encoded by the alternative reading frame in exon 2 is functional, and required for targeting the mtSBP2-GFP protein to the mitochondria. It should be noted that only ~10% of cells transfected with the mtSBP2-GFP plasmid displayed strong mitochondrial localization as shown in Figure 4A, and some of the transfected cells also displayed a diffuse cytoplasmic fluorescence that did not co-localize with the MitoTracker staining (data not shown). Indeed, western blot of mtSBP2-GFP transfected cells showed the presence of additional proteins initiating in exon 3b and exon 5 (Figure 4B, lane 4), which explained the cytoplasmic localization of these proteins.
fluorescence observed. Notably, mtSBP2-GFP was poorly expressed in comparison to other isoforms and we consistently observed this in several cell lines tested. It is also interesting to note that cells transfected with a construct that lacks exon 2 (SBP2Δ2-GFP) expressed high levels of proteins initiating in exons 3a, 3b and 5 (Figure 4B, lane 4), while lack of exon 3a (SBP2Δ3a-GFP) did not seem to have a similar effect on proteins initiating in exons 3b and 5 (Figure 4B, lane 3). These results suggest that exon 2 might play a role in regulating the expression of some of the SBP2 isoforms by suppressing translation initiation at ATG start sites in exons 3a, 3b and 5. These results are also in agreement with the results from the minigene assay where mutation to the exon 2 ATG start site led to increased translation from exon 3b.

We also sought to determine whether the mtSBP2 isoform, or additional spliced variants could be detected endogenously in cells using our previously described anti-SBP2 antibody raised against an epitope in exons 6–8 (aa 279–378 in SBP2) (14) which should detect most isoforms, if expressed. However, we were unable to detect any SBP2 isoforms other than the full-length SBP2 by western blotting. Similarly, analysis of mitochondrial fractions of cells failed to reveal the existence of mtSBP2 by western blotting. Notably, a new anti-peptide antibody raised against the C-terminus of SBP2 (referred to as anti-SBP2 EC1) was shown to be very specific for SBP2 (data not shown). We used this antibody in immunofluorescence-based detection of mtSBP2 due to similar level of staining in SBP2-depleted and normal cells. Notably, a new anti-peptide antibody raised against the C-terminus of SBP2 (referred to as anti-SBP2 EC1) was shown to be very specific for SBP2 (data not shown). We used this antibody in immunofluorescence of C33A cells and found that the majority of cells showed a distinct punctuated cytoplasmic staining (Figure 4C, middle panel). Interestingly, while most cells also showed some punctuated staining along the mitochondria, ~5–10% of cells displayed a clear mitochondrial staining. We also sought to determine whether the mtSBP2 isoform, or additional spliced variants could be detected endogenously in cells using our previously described anti-SBP2 antibody raised against an epitope in exons 6–8 (aa 279–378 in SBP2) (14) which should detect most isoforms, if expressed. However, we were unable to detect any SBP2 isoforms other than the full-length SBP2 by western blotting. Similarly, analysis of mitochondrial fractions of cells failed to reveal the existence of mtSBP2 by western blotting. Notably, a new anti-peptide antibody raised against the C-terminus of SBP2 (referred to as anti-SBP2 EC1) was shown to be very specific for SBP2 (data not shown). We used this antibody in immunofluorescence-based detection of mtSBP2 due to similar level of staining in SBP2-depleted and normal cells. Notably, a new anti-peptide antibody raised against the C-terminus of SBP2 (referred to as anti-SBP2 EC1) was shown to be very specific for SBP2 (data not shown). We used this antibody in immunofluorescence of C33A cells and found that the majority of cells showed a distinct punctuated cytoplasmic staining (Figure 4C, middle panel). Interestingly, while most cells also showed some punctuated staining along the mitochondria, ~5–10% of cells displayed a clear mitochondrial staining. We also investigated the UVA stress response pattern of the SBP2 isoforms expressed by the minigene constructs. We conducted a similar time course experiment in response to UVA treatment in HeLa cells expressing wild-type SBP2 protein (WT-SBP2GFP), the exon 2 ATG>CTG mutated SBP2 (ATGm-SBP2GFP) and the SBP2 mutated protein that initiates translation from exon 3b (E3b-SBP2GFP). As shown in Figure 5C, all minigene products showed a similar down-regulation pattern in response to stress, as seen for endogenous SBP2. Similar results were obtained in NFF cells (data not shown). From these experiments we thus conclude that mutation of the ATG codon in exon 2 and thus the lack of mtSBP2 expression does not affect the response of the full-length SBP2 to UVA-induced oxidative stress, and that the spliced variants E3b-SBP2GFP and E5-SBP2GFP (data not shown) have a similar pattern of regulation as full-length SBP2 in response to stress. Importantly, these experiments established a coordinated transcriptional and translational mechanism of SBP2 regulation in response to oxidative stress, and revealed that the alternatively spliced transcripts and the corresponding proteins have a similar pattern of regulation as the full-length SBP2.

**DISCUSSION**

SBP2 is a critical factor for selenoprotein synthesis, with roles in SECIS element binding, ribosome binding and Sec incorporation. Much of recent work has elaborated on...
Figure 5. Coordinated transcriptional and translational regulation of SBP2 following UVA treatment. (A) Real-time RT-PCR using transcript specific primers shows a similar transcriptional induction of both transcripts in HeLa cells over 24 h. (B) Western blot using anti-SBP2 antibodies shows the translational response of endogenous SBP2 and HSP70 a different time points after UVA irradiation. Quantitation of FLSBP2 transcript and protein levels is presented in the graph below. Error bars represent the standard error of the mean (SEM). Transcript levels were normalized against GAPDH and protein levels were normalized against actin. (C) Western blots show the translational response of WT, Ex2ATG->CTG and Ex3AG->AA minigene-derived proteins to UVA treatment. HSP70 was used as a marker for UVA-induced stress and actin shows protein loading.

Understanding its role in the translation of 25 mammalian selenoproteins, by detailed molecular and biochemical characterization. Mutations in the SECISBP2 gene that either alter the reading frame through splicing defects or alter the interaction of SBP2 with a subset of SECIS elements due to amino acid substitutions, result in abnormal thyroid hormone function in humans (15,25). In this study, we presented the first detailed \textit{in vivo} and \textit{in silico} characterization of human SECISBP2 alternative splicing and highlighted a new mode of transcriptional and translational regulation. Interestingly and intriguingly, the most abundant SBP2 variant after the full-length SBP2 contains a MTS, which we showed is functional and required for targeting of the mtSBP2 protein to mitochondria. A small proportion of the endogenous SBP2 pool is also localized to the mitochondria, however, only a small fraction of cells appeared to have strong mitochondrial SBP2 localization. This suggests that the mitochondrial localization of SBP2 may be tightly regulated and may occur predominantly during certain, yet unidentified conditions.

The identification of a potential mitochondrial human-specific SBP2 isoform was an intriguing and somewhat puzzling finding when viewed against the known SBP2 function in decoding UGA as Sec during selenoprotein translation. This process is unlikely to occur within the inner mitochondria for the following reasons: (i) analysis of the mitochondrial genome using the SECISearch program (34) suggests that the human mitochondrial genome does not contain any genes with SECIS elements and hence does not encode selenoproteins; (ii) UGA codes for tryptophan in the human mitochondrial genome; and (iii) mitochondrial matrix translation uses a mechanism similar to that of prokaryotes. These facts would argue against the requirement of a mitochondrial SBP2 isoform with canonical function in Sec incorporation. However, emerging evidence suggests that translationally active cytoplasmic ribosomes, or polysomes, are present on the outer membrane of the mitochondria and that about 50% of mRNAs coding for mitochondria-localized products are primarily associated with mitochondria-bound polysomes (35–37). Targeting mRNAs to the mitochondria is mediated by conserved secondary structures in their 3’ UTR (36). Although this process is poorly understood, it is possible that the conservation of localized translation might assist in the co-translational import of hydrophobic proteins into mitochondria to prevent their aggregation in the cytoplasm, or to simply provide a more efficient way of translation, as one mRNA molecule can serve in several rounds of translation. The mitochondrial SBP2 isoform could thus function in the translation of selenoproteins targeted to mitochondria such as thioredoxin reductase 2 (TxnRd2/TR3) (1,38), mitochondrial form of phospholipid glutathione peroxidase (PHGpX/GPx4) (39) and glutathione peroxidase 1 (GPx1) (40) on mitochondria-bound cytoplasmic ribosomes. Alternatively, mtSBP2 could be involved in binding to mRNA structures, possibly also in non-selenoprotein encoding mRNAs that target the message to the outer mitochondrial ribosomes. The high-resolution images we obtained of both over-expressed mtSBP2-GFP and endogenous mtSBP2 pointed
to a localization of the mtSBP2 isoform on the outer mitochondrial surface, in specific punctate clusters. This localization would indeed be in agreement with the functional localization of SBP2 at polysomes. The fact that we could not detect mtSBP2 in mitochondrial subfractions of cells by western blotting argues for a possible loose interaction between mtSBP2 and the organelle, which may be easily disrupted during the fractionation procedure. But if mtSBP2 is localized on the outer surface of the mitochondria, why would it require a classical type of MTS that generally targets proteins to the inner mitochondrial matrix? Although this question remains to be answered, our findings are relevant to a recent report showing that DAKAP1, a multifunctional protein with roles in cAMP dependent protein kinase (PKA) regulation and mRNA binding, can be targeted to the cytosolic side of the outer membrane of the mitochondria by use of a classical MTS. DAKAP1 contains a bi-functional targeting motif that switches to encode either an MTS, such as the one present in mtSBP2, or an ER targeting signal (41). Although the precise mechanism of how this protein attaches to the mitochondria outer membrane remains unknown at present, it is possible to reconcile the idea that proteins that localize on the cytosolic side of the mitochondrial membrane can be targeted there by classical MTSs. The MTS in mtSBP2 may thus facilitate the localization of the protein to the cytosolic side of the mitochondria via active mitochondrial import. More detailed studies will be required to investigate this aspect of mtSBP2 localization as well as the precise role of this isoform in the cell. The low expression of mtSBP2 isoform in the cell lines tested indicates that its synthesis could be dependent on tissue-specific translation factors and may be maximized in tissues or organs with high demand for mitochondrial selenoproteins. A prime candidate would be testis, where PHGPx is the most abundant selenoprotein. Indeed, the expression of this isoform in the cell lines tested indicates that its synthesis is expected to involve specific factors that may dictate the differential binding of SBP2 to different selenoprotein mRNAs (25,43). The high sequence variability in the N-terminal region of SBP2 could thus serve as a protein–protein interaction domain and function in the recruitment of such factors prior to interaction with the SECIS element.

In a previous study we showed that acute oxidative stress caused by H<sub>2</sub>O<sub>2</sub> and sodium selenite had an inhibitory effect on selenoprotein synthesis, and that this was mediated by oxidation of SBP2 redox-sensitive cysteine residues and its depletion from the ribosomes (14). In the current study, using UVA-irradiation as a cause of oxidative stress we found that SBP2 responded by coordinated transcripitional and translational changes following stress. Importantly, SECISBP2 and mtSECISBP2 transcripts were simultaneously and immediately induced during treatment, and stabilized during the recovery phase. At the protein level, SBP2 was degraded and levels remained approximately half of the initial levels for ~16 h post-irradiation. The SBP2 isoforms that we could monitor using the minigene showed similar down-regulation as full-length SBP2, suggesting that their intracellular function is most likely related to the function of full-length SBP2 in SECIS binding and Sec incorporation. However, our data does not exclude the possibility that mtSBP2 or any other SBP2 isoforms may perform additional functions unrelated to selenium metabolism.

This is the first report validating the occurrence and significance of alternative splicing associated with SECISBP2, an essential gene linked to selenium metabolism. Although, we have focussed mainly on one spliced variant, mtSECISBP2, there remain other variants of significant interest. Having shown that an ASO-based approach could be used to generate specific spliced variants, future studies could be tailored to examine their functions. Recent years have seen a dramatic evolution in our understanding of translational regulation by microRNAs, a class of small RNA that could be synthesized by a stem-loop containing transcript generated from RNA Polymerase II (45). To a broader significance, it remains to be seen if some of the poorly translatable SECISBP2 spliced variants including mtSBP2 are meant between the nucleus and cytoplasm (14), however, its requirement for selenoprotein synthesis in vivo has not been determined. Interestingly, the NLS is located within exon 8, which is common to all alternatively spliced SBP2 isoforms suggesting that this motif may indeed play an important role in the function of SBP2 in the nucleus in vivo. Consistent with this, recent studies have suggested a new role of SBP2 in protection of selenoprotein encoding mRNAs from nonsense mediated decay by binding to these mRNAs in the nucleus (42,43). The human selenoproteome consists of 25 selenoproteins (44) but the SECIS core element and the binding site for SBP2 are well conserved. As a result, Sec incorporation with regard to SECIS element binding would not require variability within the SBP2 RNA binding region which could explain the lack of alternate splicing in the C-terminal region of SBP2. In contrast, the hierarchy of selenoprotein synthesis is expected to involve specific factors that may dictate the differential binding of SBP2 to different selenoprotein mRNAs (25,43). The high sequence variability in the N-terminal region of SBP2 could thus serve as a protein–protein interaction domain and function in the recruitment of such factors prior to interaction with the SECIS element.
to generate microRNAs and/or serve as potential targets of microRNAs.

SUPPLEMENTARY DATA
Supplementary Data are available at NAR Online.

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