Frame 1: Predicate MUTATE

<table>
<thead>
<tr>
<th>Argument Structure for Biology</th>
<th>PropBank Argument Structure</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Arg1:</strong> physical location where mutation happen</td>
<td>Sense = to undergo and cause</td>
</tr>
<tr>
<td>// exon, intron //</td>
<td>to undergo mutation</td>
</tr>
<tr>
<td><strong>Arg2:</strong> mutated entity</td>
<td><strong>Arg0:</strong> agent</td>
</tr>
<tr>
<td>// gene //</td>
<td><strong>Arg1:</strong> entity undergoing</td>
</tr>
<tr>
<td><strong>Arg3:</strong> changes at molecular level</td>
<td><strong>mutation</strong></td>
</tr>
<tr>
<td><strong>ArgR:</strong> changes at phenotype level</td>
<td></td>
</tr>
</tbody>
</table>

Match to MUTATE senses in WordNet: sense 1 – undergo mutation

**Sentence 1.1** The exon 5 mutated allele with the premature translation termination resulted in severe deficiency of Hex A.

**Pred:** mutate

**Arg1:** exon 5
**Arg2:** allele
**Arg3:** [with] the premature translation termination
**ArgR:** resulted in severe deficiency of Hex A

**Sentence 1.2** The gene mutated in variant late-infantile neuronal ceroid lipofuscinosis (CLN6) and in nclf mutant mice encodes a novel predicted transmembrane protein.

**Pred:** mutate

**Arg1:** -
**Arg2:** gene
**Arg3:** [in] variant late-infantile neuronal ceroid lipofuscinosis (CLN6) and in nclf mutant mice
**ArgR:** encodes a novel predicted transmembrane protein

**Sentence 1.3** Transient expression of the exon 8 mutated alpha-chain cDNA in COS-1 cells resulted in deficiency of enzymatic activity.

**Pred:** mutate

**Arg1:** exon 8
**Arg2:** alpha-chain cDNA in COS-1 cells
**Arg3:** -
**ArgR:** resulted in deficiency of enzymatic activity

Frame 2: Predicate INITIATE

<table>
<thead>
<tr>
<th>Argument Structure for Biology</th>
<th>PropBank Argument Structure</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Arg0:</strong> agent</td>
<td>Sense = begin</td>
</tr>
<tr>
<td>//gene//</td>
<td><strong>Arg0:</strong> agent</td>
</tr>
<tr>
<td><strong>Arg1:</strong> entity created</td>
<td><strong>Arg2:</strong> theme (-creation)</td>
</tr>
<tr>
<td>//transcription or translation//</td>
<td><strong>Arg3:</strong> instrument</td>
</tr>
<tr>
<td><strong>Arg2:</strong> specific location on gene</td>
<td><strong>Arg4:</strong> method</td>
</tr>
<tr>
<td>//exon or intron//</td>
<td></td>
</tr>
<tr>
<td><strong>Arg3:</strong> location as tissue or cell</td>
<td></td>
</tr>
<tr>
<td><strong>Arg4:</strong> method</td>
<td></td>
</tr>
</tbody>
</table>

Match to INITIATE senses in WordNet: sense 1 – bring into being

**Sentence 2.1** Apparently HeLa cells either initiate transcription at multiple sites within RPS14 exon 1, or capped 5' oligonucleotides are removed from most S14 mRNAs posttranscription.

**Pred:** initiate

**Arg0:** -
**Arg1:** transcription
**Arg2:** [at] multiple sites within RPS14 exon 1
**Arg3:** HeLa cells
**Arg4:** -

**Sentence 2.2** I kappa B-epsilon translation initiates from an internal ATG codon to give rise to a protein of 45 kDa, which exists as multiple phosphorylated isoforms in resting cells.

**Pred:** initiate

**Arg0:** -
**Arg1:** I kappa B-epsilon translation
**Arg2:** [from] an internal ATG codon
**Arg3:** -
**Arg4:** -

**Sentence 2.3** Since RTKs initiate signaling by recruiting downstream components to the activated receptor, proteins that are immediately downstream of an activated RTK can be identified by first identifying sequences in the RTK that are necessary to activate downstream signaling (Schlessinger and Ullrich, 1992; Pawson, 1995).

**Pred:** initiate

**Arg0:** RTKs
**Arg1:** signaling
**Arg2:** -
**Arg3:** -
**Arg4:** [by] recruiting downstream components to the activated receptor