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Avoid regions of secondary structure; namely intra-primer homology (more than 3 bases that complement within the primer) or inter-primer homology (forward and reverse primers having complementary sequences). These circumstances can lead to self-dimers/hairpins or primer-dimers instead of annealing to the desired DNA sequences. Thus have a ...

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**Primer | Definition of Primer by Merriam-Webster**

Structures Primer, A. Description. For Introduction to Structures, a required course for students of architecture, engineering technology, construction technology, and construction management.

**Kaufman, Structures Primer, A | Pearson**

A primer on structured settlements. Structured settlements are still a minefield for personal injury lawyers not familiar with them. Fortunately, two of Canada's leading brokers, McKellar Group of Guelph, Ont., and Henderson Struct-ured Settlements Inc., based in Ancaster, Ont., have provided some easy-to-read guidelines.

**A primer on structured settlements | Law Times**

$T_a = 0.3 \times T_m(\text{primer}) + 0.7 T_m(\text{product}) - 14.9$ . where,  $T_m(\text{primer})$  = Melting Temperature of the primers.  $T_m(\text{product})$  = Melting temperature of the product. 4. GC Content: The GC content (the number of G's and C's in the primer as a percentage of the total bases) of primer should be 40-60%. 5.

**Primer Design Guide for PCR :: Learn Designing Primers for PCR**

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This controls whether the primer should span an exon junction on your mRNA template. The option "Primer must span an exon-exon junction" will direct the program to return at least one primer (within a given primer pair) that spans an exon-exon junction. This is useful for limiting the amplification only to mRNA.

**Primer designing tool**

Don't forget to match the GC content and the  $T_m$  within a primer pair. Also try to avoid having a GC clamp (more than 3-4 G's or C's consecutively) within your primer sequences. 4. Ends matter: 3' and 5' end of the primer. The 3' end of a primer is extremely critical for a successful PCR; especially the last 5-6 nucleotides.