

# Generic legend

base pair annotations  
 - covarying mutations  
 - compatible mutations  
 - no mutations observed

— connector (zero length)

— variable-length region

C variable-length loop

|| variable-length stem

⊖ variable-length stem-loop

□ modular sub-structure

⊖ modular hairpin

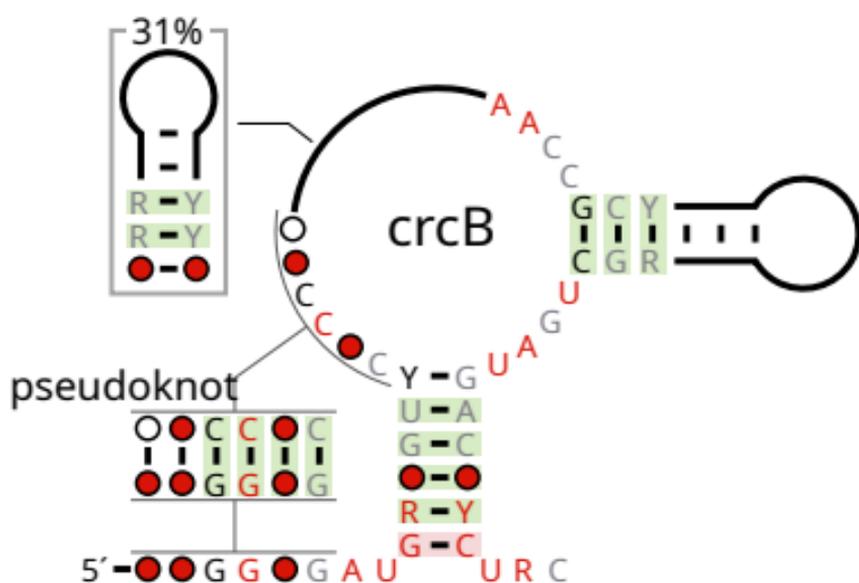
nucleotide present      nucleotide identity

● 97%	● 75%	N	97%
● 90%	○ 50%	N	90%
		N	75%

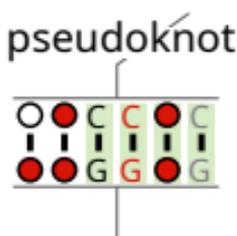
—?— possible stem

R = A or G. Y = C or U. "nt" = nucleotides. "P1" = pairing element 1. "SD" = Shine-Dalgarno (predicted ribosome-binding site). "start" = start codon.

## Example with pseudoknot and modular structure



## Putting "pseudoknot" over the connector



## Example with labels for stem, SD & start

