

# Generic legend

base pair annotations

- covarying mutations
- compatible mutations
- no mutations observed

— connector (zero length)

— variable-length region

C variable-length loop

II variable-length stem

variable-length stem-loop

modular sub-structure

modular hairpin

nucleotide present

- 97%
- 90%
- 75%
- 50%

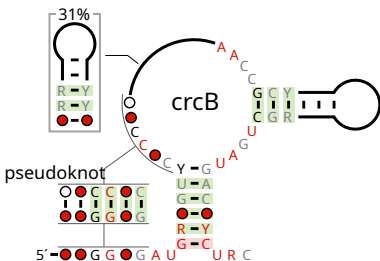
nucleotide identity

- N 97%
- N 90%
- N 75%

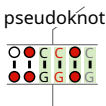
—?— possible stem

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

