Generic legend

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

nucleotide present
● 97% ● 75%
● 90% 50%

nucleotide identity
N 97%
N 90%
N 75%

—?— possible stem

— connector (zero length)
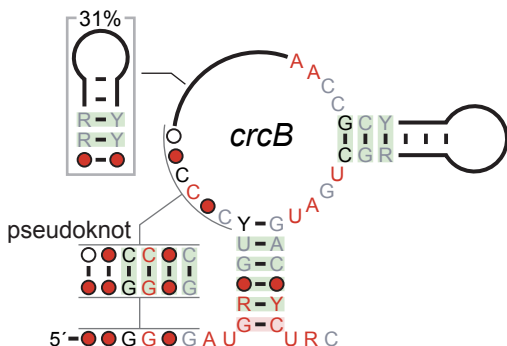— variable-length region
C variable-length loop
⊟ variable-length stem
⊙⊞ variable-length stem-loop
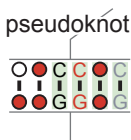▢ modular sub-structure
⊡ modular hairpin

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