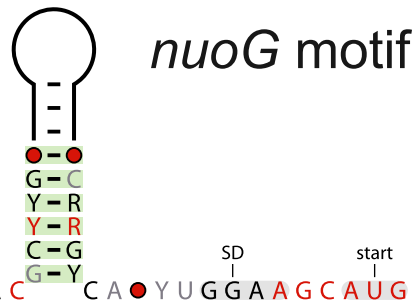
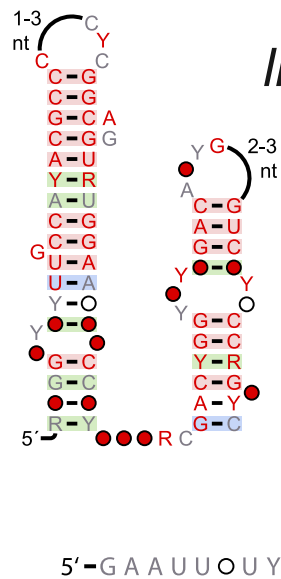
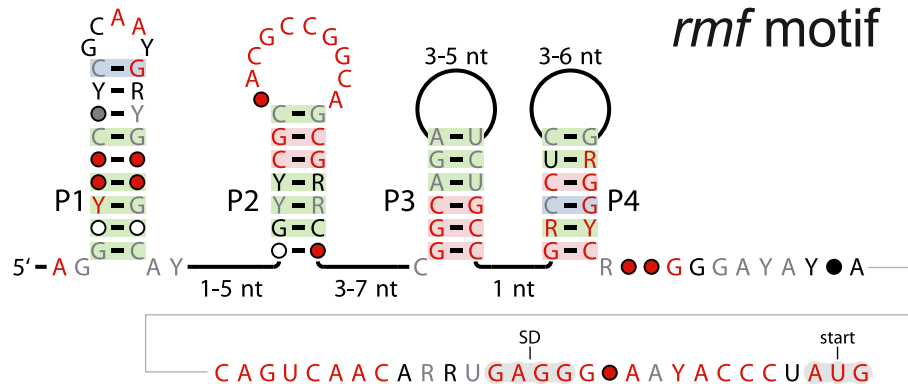
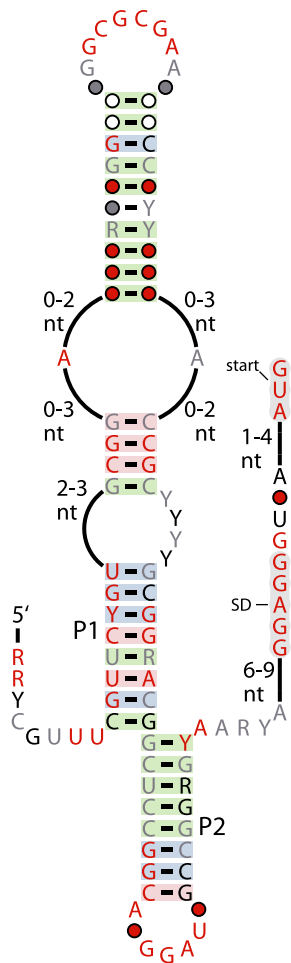


Termite-flg motif



base pair annotations

- covarying mutations
- compatible mutations
- no mutations observed

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

- connector (zero length)
- variable-length region
- variable-length loop
- variable-length stem-loop

R = A or G. Y = C or U.

"nt" = nucleotides.

"P1" = pairing element 1.

"SD" = Shine-Dalgarno (predicted ribosome-binding site).

"start" = start codon.