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Family: **CRISPR-DR57 (RF01370)**
Description: **CRISPR RNA direct repeat element**

442 sequences14 species0 structures

SummarySequencesAlignmentSecondary structureSpeciesTreesStructuresMotif matchesDatabase referencesCuration

Secondary structure

This section shows a variety of different secondary structure representations for this family. [More...](#)
You can view the secondary structure of the family using the [VARNA](#) applet. You can see more information about VARNA itself [here](#).

R-scapeseqconsbpconscoventmaxcmnormrchie

Current Rfam structure

0 out of 7 basepairs are significant at E-value=0.05

Colours

☐ Statistically significant basepair with covariation

☐ 97% conserved nucleotide

☐ 90% conserved nucleotide

☐ 75% conserved nucleotide

☐ 50% conserved nucleotide

Nucleotides

R: A or G

Y: C or U

Tip: The diagrams are interactive: you can pan and zoom to see more details or hover over nucleotides and basepairs.


R-scape optimised structure

0 out of 7 basepairs are significant at E-value=0.05

R-scape is a method for testing whether **covariation analysis** supports the presence of a conserved RNA secondary structure. This page shows R-scape analysis of the secondary structure from the Rfam seed alignment and a new structure with covariation support that is **compatible** with the same alignment.
To find out more about the method, see the R-scape paper by [Rivas et al., 2016](#). The structures are visualised using [R2R](#).

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