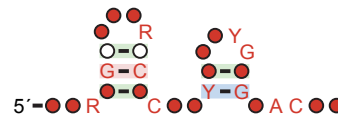


**A**

```
# STOCKHOLM 1.0
human      ACACGCGAAA.GCGCAA.CAAACGUGCACGG
chimp      GAAUGUGAAAAACACCA.CUCUUGAGGACCU
bigfoot    UUGAG.UUCG..CUCGUUUUCUCGAGUACAC
#=GC SS_cons ...<<<.....>>>....<<.....>>....
//
```

**B**

demo1

**C**

A "hit id", which identifies this sequence by the name "chimp".

This identifies the line as being the secondary structure consensus.

All stockhom files begin with "# STOCKHOLM 1.0"

A gap within this sequence.

An unpaired column

This column is not represented in the drawing in part B, because it is mostly gaps.

All stockhom files end with "//".

```
# STOCKHOLM 1.0
human      ACACGCGAAA.GCGCAA.CAAACGUGCACGG
chimp      GAAUGUGAAAAACACCA.CUCUUGAGGACCU
bigfoot    UUGAG.UUCG..CUCGUUUUCUCGAGUACAC
#=GC SS_cons ...<<<.....>>>....<<.....>>....
//
```

**D**

The consensus line inferred by R2R. 'n' corresponds to a gap. '-' is a gap. The numbers below define the degree of conservation (colors in the diagrams).

```
# STOCKHOLM 1.0
human      ACACGCGAAA.GCGCAA.CAAACGUGCACGG
chimp      GAAUGUGAAAAACACCA.CUCUUGAGGACCU
bigfoot    UUGAG.UUCG..CUCGUUUUCUCGAGUACAC
#=GC SS_cons
#=GC cons  nnRnGnnnnR-nCnCnnYnnnYGnGnACnn
#=GC cons  111114111104111110111111111111
#=GC cov_SS_cons ...202.....202.....12.....21.....
//
```

This column is classified as a gap by R2R.

Covariation

No mutation observed

Compatible mutation

**E**

intermediate/demo1.cons.sto