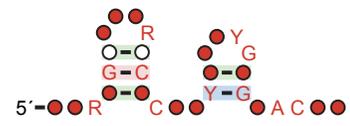


**A**

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

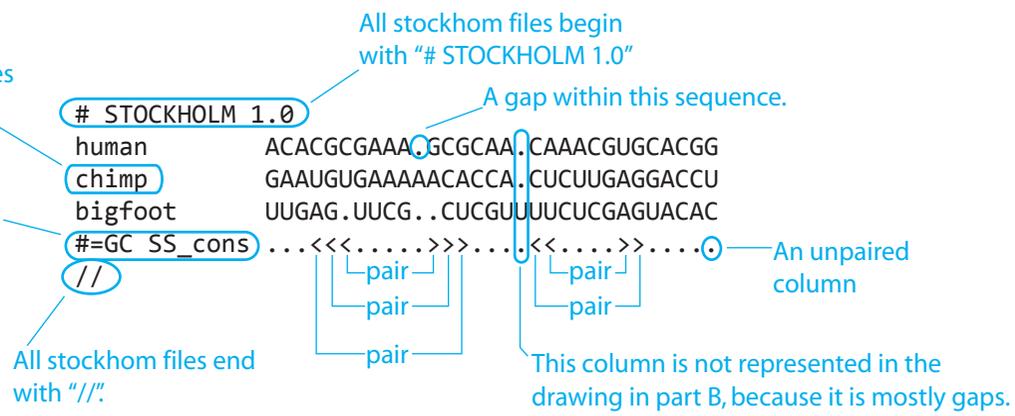
**B**

demo1

**C**

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

This identifies the line as being the secondary structure consensus.

**D**

The consensus line inferred by R2R. 'n' corresponds to a circle in the diagrams. '.' 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  11111411111041111101111111111111
#=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