

Package ‘asciiruler’

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Type Package

Title Render an ASCII Ruler

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Description An ASCII ruler is for measuring text and is especially useful for sequence analysis. Included in this package are methods to create ASCII rulers and associated GenBank sequence blocks, multi-column text displays that make it easy for viewers to locate nucleotides by position.

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Depends R (>= 2.14)

Imports stringr

Collate 'asciiruler.R'

RoxygenNote 6.0.1

Suggests testthat

NeedsCompilation no

Repository CRAN

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References

Inspired by <http://codegolf.stackexchange.com/questions/4910/ascii-ruler-generation>

Examples

```
asciiruler(low=-30,high=30,borders=TRUE)
```

```
genbank_seqblock      Generate a GenBank sequence block
```

Description

```
,
'
'      1      6      11     16     21     26     31     36     41     46     51     56
'      |      |      |      |      |      |      |      |      |      |      |
'      |||||      |||||      |||||      |||||      |||||      |||||      |||||
'      1 GATCACAGGT CTATCACCT ATTAACCACT CACGGGAGCT CTCCATGCAT TTGGTATTTT
'      61 CGTCTGGGGG GTGTGCACGC GATAGCATTG CGAGACGCTG GAGCCGGAGC ACCCTATGTC
'      121 GCAGTATCTG TCTTTGATTC CTGCCCCATC CTATTATTTA TCGCACCTAC GTTCAATATT
'      181 ACAGGCGAAC ATACTTACTA AAGTGTGTTA ATTAATTAAT GCTTGTAGGA CATAATAATA
'      241 ACAATTGAAT GTCTGCACAG CCGCTTTCCA CACAGACATC ATAACAAAAA ATTTCCACCA
'      301 AACCCCCCTC CCCCCGCTTC TGGCCACAGC ACTTAAACAC ATCTCTGC
'
```

Usage

```
genbank_seqblock(string, start = 1L, end = 0L, blocksize = 10L,
  width = 60L, sep = " ", line_break = "\n", ruler = TRUE, ...)
```

Arguments

string	the sequence string to display
start	the substring start, should be 1 or greater
end	substring end, should be >start, negative to trim
blocksize	number of characters in each block
width	width of the sequence block
sep	space character between blocks
line_break	the line break character(s)
ruler	display an ascii ruler
...	additional arguments passed to asciiruler

Value

delimited GenBank block string ready to cat

Examples

```
my_sequence<- 'GATCACAGGTCTATCACCTATTAACCACTCACGGGAGCTCTCCATGCATTTGGTATTTTCGTCTGGGGG
GTATGCACGCGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCCTATGTCGCAGTATCTGTCTTTGATTC
CTGCCTCATCCTATTATTTATCGCACCTACGTTCAATATTACAGGCGAACATACTTACTAAAGTGTGTTA
ATTAATTAATGCTTGTAGGACATAATAATAACAATTGAATGTCTGCACAGCCACTTCCACACAGACATC'
my_seqblock<-genbank_seqblock(my_sequence)
cat(my_seqblock)
```

```
print.asciiruler      Print an asciiruler
```

Description

Print an asciiruler

Usage

```
## S3 method for class 'asciiruler'
print(x, ...)
```

Arguments

x	the asciiruler
...	additional arguments

```
width      Get the total width of an ascii ruler
```

Description

Get the total width of an ascii ruler

Usage

```
width(x, ...)
```

Arguments

x	the asciiruler
...	additional arguments

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