Package ‘MINTplates’

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Title Encode ``License-Plates'' from Sequences and Decode Them Back

Version 1.0.1

Description It can be used to create/encode molecular ``license-plates'' from sequences and to also decode the ``license-plates'' back to sequences. While initially created for transfer RNA-derived small fragments (tRFs), this tool can be used for any genomic sequences including but not limited to: tRFs, microRNAs, etc. The detailed information can reference to Pliatiska V, Loher P, Telonis AG, Rigoutsos I (2016) <doi:10.1093/bioinformatics/btw194>. It can also be used to annotate tRFs. The detailed information can reference to Loher P, Telonis AG, Rigoutsos I (2017) <doi:10.1038/srep41184>.

Depends R (>= 3.2.3)

License GPL (>= 2)

RoxygenNote 7.1.1

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NeedsCompilation no

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**annotate_tRF**  
*Annotate a tRF sequence*

**Description**
Obtain tRF ID, type, whether exclusive to tRNA space, and tRNA sources of the tRF with its sequence.

**Usage**
```
annotate_tRF(sequence)
```

**Arguments**
- `sequence`: tRF sequence.

**Value**
- tRF ID, type, whether exclusive to tRNA space, and tRNA sources of the tRF.

**References**

**Examples**
```
sequence='TCCCTGGTGTTCTAGTTAGGTCCGGC'
annotate_tRF(sequence)
```

---

**deseqs**  
*Decode license-plates*

**Description**
Decode the license-plates using the lookup table.

**Usage**
```
deseqs(plates)
```

**Arguments**
- `plates`: The license plates being decoded.

**Value**
- The sequences they decode to.
enseqs

References

Examples

plates=c("tRF-18-BS6PDFD2","tRF-20-51K36026")
deseqs(plates)

enseqs Encode sequences

Description
Encode the sequences into their corresponding license plates with given prefix (if given one).

Usage
enseqs(sequences, prefix = "")

Arguments
sequences The sequences being encoded.
prefix The prefix to use for the license plate.

Value
The license plates they encode to.

References

Examples
seqs=c("AACCGGGCAGAAGCACCA","GAGCCCCAGTGGAACCACCA")
enseqs(seqs,"tRF")
source_tRNA

---

### exclusive

**Determine whether the tRFs are exclusive to tRNA space**

**Description**

Determine whether the tRFs are exclusive to tRNA space with the tRF sequences.

**Usage**

```r
exclusive(sequences)
```

**Arguments**

- `sequences` tRF sequences.

**Value**

Whether the tRFs are exclusive to tRNA space.

**References**


**Examples**

```r
sequences=c("TCCCTGGTGTTAGTTAGGATTCGGC", "TCCCTGGTGTTAGTTAGGATTCGGCG")
exclusive(sequences)
```

---

### source_tRNA

**Obtain the tRNA source of a tRF**

**Description**

Obtain the tRNA source of a tRF with the tRF sequence.

**Usage**

```r
source_tRNA(sequence)
```

**Arguments**

- `sequence` tRF sequence.

**Value**

Sources of the tRF.
source_tRNA2

References


Examples

```r
sequence = 'TCCCTGGTGCTCTAGTGGTTAGGATTCGGC'
source_tRNA(sequence)
```

---

**source_tRNA2**  
*Obtain the tRNA sources of tRFs*

**Description**

Obtain the tRNA sources of tRFs with the tRF sequences.

**Usage**

```r
source_tRNA2(sequences)
```

**Arguments**

- `sequences`: tRF sequences.

**Value**

Sources of the tRFs.

**References**


**Examples**

```r
sequences = c('TCCCTGGTGCTCTAGTGGTTAGGATTCGGC', 'TCCCTGGTGCTCTAGTGGCT', 'TCCCTGGTGCTCTAGTGGCTAATGGTTA')
source_tRNA2(sequences)
```
Description

Obtain the type of tRFs with the tRF sequences.

Usage

tRFtype(sequences)

Arguments

sequences  tRF sequences.

Value

The type of tRFs.

References


Examples

sequences=c("TCCCTGGTGCTCTGGGTTAGGATTCGGC","AAAAATTTTGGTCACTCCAAATAAAA")
tRFtype(sequences)
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