

Structural Bioinformatics and Molecular Modeling

CRBM-CNRS Montpellier



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T-REKS

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T-REKS is an algorithm for *de novo* detection and alignment of repeats in sequences based on K-means algorithm. Minimal length of repeat arrays is 9 for true homorepeats and 14 for other repeats with potential biological meaning.

Citing T-REKS: T-reks: identification of tandem repeats in sequences with a k-means based algorithm. Jorda J, Kajava AV(2009). Bioinformatics 25 (20), 2632-2638

Search in a file :

or Paste sequences:

Sequence type : Protein DNA

Percentage of similarity - Psim:

Filter the overlapping repeats:

Disable the sequence splitting:

01:00:06

Research of repeats is requested:

```
repeat not found in sequence
0 sequences have been detected as tandem repeats containing.
Memory usage: 286,376 bytes.
```