Mass Calculator

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1. Overview

This application computes mass for molecules and peptides.

2. Usage

```
usage: MassCalc <fasta> [-a] [-h] [-p <arg>] [-v]
 -a,--average-enabled       enable average mass type
                            by default: disabled (monoisotopic mode).
 -h,--help                  print this message.
 -p,--precision <arg>       define the decimal precision for output mass,
                            by default: 6.
 -v,--version               print the version info.
```

3. Fasta sequence format

The fasta sequences are by default amino-acids. As fasta sequences can be of molecular or other monomer types, we define the following specific format:

```
> sequence header
MONOMER-TYPE:SEQUENCE

// examples
> molecule
ATOM:CH3

> peptide with explicit monomer type
AA:ANKIOLERFG

> peptide by default
ANKIOLERFG
```

4. Releases

The latest version is v1.2 - [Download app](#).