Composition module

# Create composition library

## Input:

Dictionary of peptideObjects

{‘PEPTIDECK’: <peptideObject>, ….}

### (Relevant) Attributes:

**sequence**

The full peptide sequence

**charge**

The charge of the precursor

**includedPeaks**

The MS1 peaks that are isolated

**fragments**

A dictionary of the m/z of all peaks. Keys have the format ‘y3 h1++’.

## Output:

Dictionary of compensationObjects

{‘PEPTIDECK’: <compensationObject>, ….}

### Attributes:

**sequence**

The full peptide sequence

**charge**

The charge of the precursor

**includedPeaks**

The MS1 peaks that are isolated

**fragments**

A list of peaks in the format ‘y3 h1++’.