

# Java Proteomic Library

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## 1. Overview

The *Proteome Informatics Group* (PIG) at the *Swiss Institute of Bioinformatics* (SIB) is involved in the development of proteomics applications and services mainly available at [ExPASy](#) server.

In order to share code and ease maintenance, we developed a proteomic library in Java (Java Proteomic Library for JPL) of objects and routines commonly used in proteomics. The JPL is an on-going open-source project providing classes for the analysis of mass spectrometry proteomic data and enabling rapid bioinformatics application development in the Java programming language.

It is composed of several modules. The library contains APIs for manipulating basic biological objects such as peptide or protein sequences, post- translational modifications and mass spectra. It provides objects for protein digestion and peptide fragmentation taking into account various ion types and modifications.

It also supplies readers and writers and support different standard data file formats (fasta, mgf, mz(X)ML, dta, sptxt or msp).

JPL is a unit testing driven project and requires Java JDK 5 or higher.

## 2. News

### 2.1. 2012/01/24

New version of tool [Liberator](#).

### 2.2. 2012/01/17

New release 1.0.

**Warning:**

The migration to this new release lead to drastic changes such as massive class refactoring (renaming and few package movement) - by mostly removing the JPL- and JPLI- prefixes in every classes. If you have some old-style JPL code to update, please, follow this [link](#).

### 2.3. 2011/11/09

New [ProteinDigester](#) tool.

## 2.4. 2011/09/06

New [QuickModViewer](#) tool.

## 3. License

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