



Application Programming Interface (API)

FlowRepository implements an Application Programming Interface (API) that allows third party software tools to browse public datasets and download data and annotations associated with these datasets. The current API is a beta version that will likely be extended in the future, namely to support authentication, data submission and querying.

If you are a developer interested to communicate with FlowRepository computationally, please contact us at flowrepository-admin@isac-net.org and ask for a client ID. At this point, a client ID needs to be generated for you in order to be able to use FlowRepository API. Below, we describe the communication protocol that can be used to communicate with FlowRepository.

Communication protocol

The text YourClientID in all URLs shall be replaced with your client ID, a unique identifier assigned to you/your software tool based on your request. Client identifiers allow us to keep track of who is using FlowRepository API as well as customize the API for certain clients (if needed in the future).

Step 1): Start with an HTTP GET request of <http://flowrepository.org/list?client=YourClientID>
FlowRepository will return an XML that lists all the public experiments including basic metadata, in this format:

```
<FlowRepository>
  <api-version>0.1</api-version>
  <response-with-details type="boolean">>false</response-with-details>
  <public-experiments type="array">
    <experiment>
      <id>FR-FCM-ZZZ3</id>
      <public-url>http://flowrepository.org/id/FR-FCM-ZZZ3</public-url>

      <xml-details-url>http://flowrepository.org/list/FR-FCM-ZZZ3?client=YourClientID</xml-details-url>
      <name>Identification of B cells through negative gating</name>
      <created type="datetime">2011-04-18T21:36:25Z</created>
      <primary-researcher>...</primary-researcher>
      <purpose>...</purpose>
      <conclusion>...</conclusion>
      <miflowcyt-score type="float" unit="%">89.8275</miflowcyt-score>
      <keywords type="array">...</keywords>
      <related-publications type="array">...</related-publications>
      <organizations type="array">...</organizations>
      <fcs-files-count type="integer">284</fcs-files-count>
      <attachments-count type="integer">10</attachments-count>
    </experiment>
    ...
  </public-experiments>
</FlowRepository>
```

Step 2): Parse the XML and find out, which experiment (dataset) is of your interest. Then, make a second HTTP GET request to get the xml-details-url, such as <http://flowrepository.org/list/FR-FCM-ZZZ3?client=YourClientID> FlowRepository will return a similar XML response, which will be for one experiment only, but with more details including details about all the FCS files and other files attached to the experiment, e.g.:

```
<FlowRepository>
  <api-version>0.1</api-version>
  <response-with-details type="boolean">>true</response-with-details>
  <public-experiments type="array">
    <experiment>
      <id>FR-FCM-ZZZ3</id>
      <public-url>http://flowrepository.org/id/FR-FCM-ZZZ3</public-url>
      <xml-details-url>...</xml-details-url>
      <name>Identification of B cells through negative gating</name>
      <created type="datetime">2011-04-18T21:36:25Z</created>
      <primary-researcher>...</primary-researcher>
      <primary-investigator>...</primary-investigator>
      <uploader>...</uploader>
      <experiment-dates>...</experiment-dates>
      <purpose>...</purpose>
      <conclusion>...</conclusion>
      <comments>...</comments>
      <quality-control-measures>...</quality-control-measures>
      <miflowcyt-score type="float" unit="%">89.8275</miflowcyt-score>
      <keywords type="array">...</keywords>
      <related-publications type="array">...</related-publications>
      <organizations type="array">...</organizations>
      <fcs-files-count type="integer">284</fcs-files-count>
      <fcs-files type="array">
        <fcs-file>
          <file-name>a2006_01T2pb05i_A1_A01.fcs</file-name>
          <fcs-version>FCS3.0</fcs-version>
          <file-size unit="byte" type="integer">9599761</file-size>
          <md5sum>f503d32bd899e98fd7dde6cccee46a11</md5sum>
          <url>http://flowrepository.org/experiments/3/fcs\_files/21/download</url>
          ...
        </fcs-file>
      </fcs-files>
      <attachments-count type="integer">10</attachments-count>
      <attachments type="array">
        <attachment>
          <file-name>a2006analysis.jo</file-name>
          <file-size unit="byte" type="integer">15114009</file-size>
          <md5sum>d8a8ab50dd39f4b6b8f480bf2115d303</md5sum>
          <description>a2006 FlowJo analysis file</description>
          <url>http://flowrepository.org/experiments/3/attachments/1/download</url>
          ...
        </attachment>
      </attachments>
    </experiment>
  </public-experiments>
</FlowRepository>
```

Step 3): Parse this "detailed" XML and extract the information of the FCS files and other attachments that you may be interested in. Each of these files may be downloaded via an HTTP GET request of the URL specified with each of these files. You may also use the additional information (e.g., the MD5 sums) to make sure you retrieved the file correctly.

Feedback

Please feel free to contact us if you have any questions or if you find any issues or if you have any suggestions in terms of how this interface could be improved to serve your needs. Also, please note that this API is still under development in the sense that we will likely be improving and extending it in the future. For example, the basic "initial" list is getting a bit long (and slow) with the increased number of publicly available datasets. Therefore, we are exploring options of API based searching capabilities as well as "paging" options for the initial list. Finally, this API is for reading public data only. As one of our longer term goals, we would like to provide read/write API-based access, however, this will require additional work to address authentication, authorization and data integrity issues.