

Here is a sample of an ExpressionView XML file (ALL test data).  
To improve readability, we only show the first entry of the lists.  
Comments are written in red.

```
<?xml version="1.0" encoding="UTF-8"?>
<ged>
  # summary of data
  <summary>
    <description>ExpressionView data file</description>
    <version>1.0</version>
    <nmodules>8</nmodules>
    <ngenes>3522</ngenes>
    <nsamples>128</nsamples>
  </summary>

  # description of experiment
  <experimentdata>
    <title>Gene expression profile of adult T-cell acute lymphocytic leukemia identifies distinct subsets of patients with
different response to therapy and survival.</title>
    <name>Chiaretti et al.</name>
    <lab>Department of Medical Oncology, Dana-Farber Cancer Institute, Department of Medicine, Brigham and
Women's Hospital, Harvard Medical School, Boston, MA 02115, USA.</lab>
    <abstract>Gene expression profiles were examined in 33 adult patients with T-cell acute lymphocytic leukemia (T-
ALL). Nonspecific filtering criteria identified 313 genes differentially expressed in the leukemic cells. Hierarchical clustering
of samples identified 2 groups that reflected the degree of T-cell differentiation but was not associated with clinical
outcome. Comparison between refractory patients and those who responded to induction chemotherapy identified a single
gene, interleukin 8 (IL-8), that was highly expressed in refractory T-ALL cells and a set of 30 genes that was highly
expressed in leukemic cells from patients who achieved complete remission. We next identified 19 genes that were
differentially expressed in T-ALL cells from patients who either had a relapse or remained in continuous complete
remission. A model based on the expression of 3 of these genes was predictive of duration of remission. The 3-gene model
was validated on a further set of T-ALL samples from 18 additional patients treated on the same clinical protocol. This study
demonstrates that gene expression profiling can identify a limited number of genes that are predictive of response to
induction therapy and remission duration in adult patients with T-ALL.</abstract>
    <url></url>
    <annotation>hgu95av2</annotation>
    <organism>Homo sapiens</organism>
  </experimentdata>

  # list of genes
  <genes>
    # column names and titles for genes (shown in the datagrid)
    <genetags>
      <id>#</id>
      <score>Score</score>
      <name>Name</name>
      <symbol>Symbol</symbol>
      <entrezid>EntrezID</entrezid>
    </genetags>

    # individual gene
    <gene>
      <id>1</id>
      <score/>
      <name>33500_i_at</name>
      <symbol>LOC100126583</symbol>
      <entrezid>100126583</entrezid>
    </gene>

    ...

  </genes>

  # list of samples
  <samples>
    # column names and titles for samples (shown in the datagrid)
    <sampletags>
      <id>#</id>
      <score>Score</score>
      <name>Name</name>
      <diagnosis> Date of diagnosis</diagnosis>

```

```
<sex> Gender of the patient</sex>
<age> Age of the patient at entry</age>
</sampltags>
```

**# individual sample**

```
<sample>
  <id>128</id>
  <score/>
  <name>LAL4</name>
  <diagnosis>NA</diagnosis>
  <sex>NA</sex>
  <age>NA</age>
</sample>
```

...

```
</samples>
```

**# list of modules**

```
<modules>
```

**# column names and titles for modules (shown in the datagrid)**

```
<moduletags>
  <id>#</id>
  <name>Name</name>
  <iterations>iterations</iterations>
  <oscillation>oscillation</oscillation>
  <thr_row>thr.row</thr_row>
  <thr_col>thr.col</thr_col>
  <freq>freq</freq>
  <rob>rob</rob>
  <rob_limit>rob.limit</rob_limit>
</moduletags>
```

**# column names and titles for go categories (shown in the datagrid)**

```
<gotags>
  <id>#</id>
  <go>GO</go>
  <term>Term</term>
  <ontology>Ontology</ontology>
  <pvalue>PValue</pvalue>
  <oddsratio>OddsRatio</oddsratio>
  <expcount>ExpCount</expcount>
  <count>Count</count>
  <size>Size</size>
</gotags>
```

**# column names and titles for kegg pathways (shown in the datagrid)**

```
<keggtags>
  <id>#</id>
  <kegg>KEGG</kegg>
  <pathname>Path Name</pathname>
  <pvalue>PValue</pvalue>
  <oddsratio>OddsRatio</oddsratio>
  <expcount>ExpCount</expcount>
  <count>Count</count>
  <size>Size</size>
</keggtags>
```

**# individual module**

```
<module>
  <id>1</id>
  <name>module 1</name>
  <iterations>22</iterations>
  <oscillation>0</oscillation>
  <thr_row>2.7</thr_row>
  <thr_col>1.4</thr_col>
  <freq>1</freq>
  <rob>21.98</rob>
  <rob_limit>21.98</rob_limit>
```

```

# list of genes contained in module
<containedgenes>214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231,
232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251</containedgenes>
# gene scores
<genescores>-0.94, -0.88, 0.74, -0.76, -1.00, -0.84, -0.74, -0.76, -0.85, -0.88, 0.78, -0.80, -0.95, 0.78, 0.79,
0.79, 0.83, 0.92, 0.83, -1.00, 0.79, 0.89, -0.84, -0.91, -0.82, -0.83, -0.80, 0.73, -0.86, -0.78, -0.74, -0.80, -0.73, 0.87, -0.82,
-0.92, 0.77, 0.95</genescores>
# list of samples contained in module
<containedsamples>63, 64, 65, 54, 66, 67, 55, 56, 53, 57, 29, 58, 62, 30, 59, 68, 69, 60, 70, 61, 71</
containedsamples>
# sample scores
<samplescores>-0.62, -1.00, -0.77, -0.40, -0.28, -0.70, -0.48, -0.14, -0.36, -0.63, -0.26, -0.48, -0.22, -0.27,
-0.46, -0.34, -0.07, -0.76, -0.25, -0.08, -0.36</samplescores>
# list of intersecting modules
<intersectingmodules>7</intersectingmodules>

# list of go categories
<gos>
# individual go category
<go>
  <id>1</id>
  <go>GO:0006955</go>
  <term>immune response</term>
  <ontology>BP</ontology>
  <pvalue>6.78e-07</pvalue>
  <oddsratio>10.13</oddsratio>
  <expcount>2.72</expcount>
  <count>16</count>
  <size>213</size>
</go>
...
</gos>

# list of kegg pathways
<keggs>
# individual kegg pathway
<kegg>
  <id>1</id>
  <kegg>05310</kegg>
  <pathname>Asthma</pathname>
  <pvalue>9.67e-05</pvalue>
  <oddsratio>36.43</oddsratio>
  <expcount>0.26</expcount>
  <count>5</count>
  <size>14</size>
</kegg>
...
</keggs>
</module>
...
</modules>

# gene expression data
# rounded to two digits, encoded in Base64
# loop over genes, loop over samples
<data>
9/oH7P8U9hPu/xj47e7p9iHp8PL++/ft6v8YN+3p8AEMBvb07fX2C/gG4wgg7/f9AxBQJf7fHm
6ej94AX48Pbu6+AA7OH29fPu7enu5uv89R3+8Qgm8vcH6vn89/H16u7zAgAEA+716fjk5+zq6AXu
...
</data>
</ged>

```