

Description of APATML–XML output of APAT System

APATML v1.3

<results>

The main tag that wraps various kinds of annotations produced by different servers.

Contains

<input> tag and <result> tag.

Input Data

<input>

Contains details of the input sequence

Contains:

<seqid> and <seq> tags.

Example:

```
<input>
  <seqid>sp| P96118|TROC_TREPA Zinc transport system membrane protein troC -
  Treponema pallidum</seqid>
  <seq>M</seq>
  <seq>H</seq>
  <seq>A</seq>
  <seq>L</seq>
  <seq>M</seq>
  <emailaddress>s.v.v.deevi@rdg.ac.uk</emailaddress>
  <parameter server='targetp' param='origin' value='non-plant' />
  <parameter server='psort' param='origin' value='yeast' />
</input>
```

<seqid>

Contains the protein sequence identification details.

<seq>

Contains the amino acids of the input protein (one residue per tag).

<emailaddress>

Contains the emailaddress entered by the users.

<parameter>

This is an empty tag containing the information in its attributes.

Attributes:

- server : says about name of the server for which this parameter applies
- param : says about type or name of the parameter
- value : says about value stored in it for the parameter

<result>

Includes the output from one particular server.

Attributes:

- program : says about name of the annotation server
- version : (optional) says about version of the annotation server

Contains:

<function>, <info>, <run> and <predictions> tags.

Example:

```
<result program="NetPhos" version="2.0">
  <function>...</function>
  <info href='...'>...</info>
  <run>...</run>
  <predictions>...</predictions>
</result>
```

<function>

Describes the function of the annotation server.

Example:

```
<function>Protein Phosphorylation sites prediction</function>
```

<info>

Describes the tool being used and is hyperlinked to the actual server if it is a webbased tool or just says it is a local server if it is one.

Attributes:

href: (optional) provides the URL for the webserver. This attribute is absent in case of local server.

<run>

Contains <params> tag that describes run parameters and date.

Example:

```
<run>
  <params>
    <param name = 'Serine' value = 'Checked' />
    <param name = 'Threonine' value = 'Checked' />
    <param name = 'Tyrosine' value = 'Checked' />
    <param name = 'Generate Graphics' value = 'unChecked' />
    <param name = 'Threshold' value = '0.500' />
  </params>
  <date>Fri Nov 19 15:30:38 GMT 2004</date>
</run>
```

<params>

Contains tags that represent the run parameters.

Contains:

<param> tags

<param>

Contains name and value associated with the parameter as attributes. (One or more tags)

Attributes:

name: name of the parameter.

value: value assigned for the parameter.

<date>

Contains details about day, date, time of run.

<predictions>

Contains the predictions from the server.

Contains:

<link><perres-number>, <perres-character>, <threshold>, <perdom> and <perseq> tags (all optional).

<link>

Contains link for prediction from the actual webserver being used in it's unparsed form. It is available for a limited time. This tag is not applicable for local servers and servers whose output pages are handled by cgi scripts where a separate URL for the output page can't be provided.

Attributes:

href : Contains the URL for the output page from the webserver which is stored in \$link(before getting results into a variable) if possible to do so (not possible for cgi scripts).

Per-residue output data**<perres-number>**

Describes numeric annotation at the per-residue level. The actual values appear in <value-perres> tags.

Attributes:

name : name of the type of numeric data stored in the array (like 'p-score').

clrmin : minimum value for colouring range.

clrmax : maximum value for colouring range.

graph : (optional) whether a graph is required or not (1 for yes and 0 for no).

graphtype : (optional, required if graph = 1) type of graph to be used 'bars' or 'lines'.

Contains:

<value-perres>

Example:

```
<perres-number name = 'P-score' clrmin = '0.0' clrmax = '1.0' graph='1'  
  graphtype='bars'>  
  <value-perres residue='1'>0.000000</value-perres>  
  <value-perres residue='2'>0.000000</value-perres>  
  <value-perres residue='3'>0.000000</value-perres>  
  <value-perres residue='4'>0.000000</value-perres>  
  <value-perres residue='5'>0.000000</value-perres>  
</perres-number>
```

<value-perres>

These tags specify a value to be assigned to each residue.

Attributes:

residue : sequential number of the residue in the protein sequence.

<perres-character>

Describes text annotation at the per-residue level. The actual values appear in <value-perres> tags.

Attributes:

name : name of the type of numeric data stored in the array (like 'p-score').

Contains:

<value-perres> (see description above)

Example:

```
<perres-character name='sspred'>  
  <value-perres residue='1'>C</value-perres>  
  <value-perres residue='2'>C</value-perres>  
  <value-perres residue='3'>H</value-perres>  
  <value-perres residue='4'>H</value-perres>  
  <value-perres residue='5'>H</value-perres>  
</perres-character>
```

<threshold>

Used to indicate residues that pass some prediction threshold – i.e. Those that are considered 'positive' predictions and should therefore be highlighted. The actual residues are indicated with <thr-res> tags and a <description> tag explains the meaning of the threshold prediction.

Contains:

<description> and <thr-res> tags

Example:

```
<threshold>
  <description>P-scores greater than 0.5 are considered as
  positive predictions</description>
  <thr-res>1</thr-res>
  <thr-res>4</thr-res>
</threshold>
```

<description>

Description of what the threshold represents.

<thr-res>

Stores the residue numbers (one per tag) of those residues that pass the threshold value.

Per-domain output data

<perdom>

Describes annotations (either numeric or character) that apply to a continuous range of residues.

Attributes:

class : (optional) contains the name of the server; used for servers that produce multiple types of annotation.

name : (optional) annotation name applied to the domain.

highlight : whether to highlight the value or not (1 for yes and 0 for no).

rangemin : minimum sequence number of the range of the annotated region.

rangemax : maximum sequence number of the range of the annotated region.

Contains:

<value-perdom> and <perdom-description> tags

Example:

```
<perdom class="PRINTS" name="SH2_DOMAIN" highlight="1" rangemin="6"
rangemax="102">
  <value-perdom label="match">
VYHGKISRETGEKLLLATGLDGSYLLRDESVPGVYCLCVLYHGYIYTYRVSQTETGSWS
AETApgvhkRYFRKIKNLISAFQKPDQGIVIPLYPV
  </value-perdom>
  <value-perdom label="score">16.381</value-perdom>
</perdom>
```

<value-perdom>

Includes either numeric or character data of annotation. Typically used for indicating confidence or match region.

Attributes:

label : A description of what the value refers to (e.g. 'Confidence, e-value, match pattern')

<perdom-description>

Provides an extended general description of the kind of domain predicted.

Attributes:

class : (optional) contains the name of the server and is used for servers that produce multiple types of annotation.

name : annotation name applied to the domain.

Example:

```
<perdom-description class="PRINTS" name="SH2_DOMAIN">
The SH2 domain is the Src Homology domain which is characteristic of
intracellular signal-transducing proteins
</perdom-description>
```

Per-sequence output data

<perseq>

Sequence level annotation that contains either number or character output from the server. Actual values are stored in <value-perseq> tags containing either numeric or character data along with a <description> tag that briefly describes the kind of prediction/output.

Attributes:

name : name of the prediction/type of output.

Example 1:

```
<perseq name="mTP-pred">  
  <description>Mitochondrial targeting peptide (mTP) prediction  
  score</description>  
  <value-perseq highlight="0">0.031</value-perseq>  
</perseq>
```

Example 2:

```
<perseq name="Loc-pred">  
  <description>SUBCELLULAR LOCATION PREDICTION</description>  
  <value-perseq highlight="1">SECRETORY PATHWAY, i.e. THE SEQUENCE CONTAINS  
  A SIGNAL PEPTIDE,SP.</value-perseq>  
</perseq>
```

<value-perseq>

Contains the actual value (output) of prediction.

Attributes:

highlight : whether to highlight the value or not (1 for yes and 0 for no).

<description>

More detailed description of the prediction/output.