Description of APATML–XML output of APAT System

`<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>
</input>
```

`<seqid>`

Contains the protein sequence identification details.

`<seq>`

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

Output Data

`<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>`, `<run>` and `<predictions>` tags.

Example:

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

`<function>`

Describes the function of the annotation server.

Example:

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

`<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:

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

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 (1for 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 (1for 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">
VYHGKISRETGEKLLLATGLDGSYLLRDSESVPGVYCLCVLYHGYIYTYRVSQTETGSWS
AETApgvhkRYFRKIKNLISAFQKPDQGIVIPLQYPV
    </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.