PhyloXML

A gene family tree can be downloaded in PhyloXML format. The following information is included:

For a leaf node (a gene):

- branch length
- name (gene_id)
- taxonomy scientific_name
- sequence accession (UniProt ID)

For a non-leaf node:

- branch length
- events (duplication or speciation)

Example:

```xml
<phyloxml>
    <phylogeny rooted="true">
        <name>3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE</name>
        <description>PTHR10556</description>
        <clade>
            <branch_length>0.83</branch_length>
            <events>
                <duplications>1</duplications>
            </events>
            <clade>
                <branch_length>1.2449999999999999</branch_length>
                <events>
                    <speciations>1</speciations>
                </events>
                <clade>
                    <branch_length>0.187</branch_length>
                    <events>
                        <speciations>1</speciations>
                    </events>
                    <clade>
                        <branch_length>0.162</branch_length>
                        <events>
                            <duplications>1</duplications>
                        </events>
                        <clade>
                            <name>AMTR_s00004p00149160</name>
                            <branch_length>2</branch_length>
                            <taxonomy>
                                <scientific_name>Amborella trichopoda</scientific_name>
                            </taxonomy>
                            <sequence>
                                <accession source="UniProtKB">W1NET2</accession>
                            </sequence>
                        </clade>
```

PANTHER family name

PANTHER family id

gene_id

a leaf node

UniProt_id