

Generic Gene Page XML

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Background, or Why?

- To provide a simple and consistent interchange format for commonly needed gene information.
- <http://biology.plosjournals.org/perlserv/?request=get-document&doi=10.1371/journal.pbio.0060175&ct=1>
- I.e., making automated mining of gene info across species easier, if one wanted to, say, submit them to Wikipedia.



```
<gene>
  <data_provider>FlyBase</data_provider>
  <accession>FBgn0000490</accession>
  <name type="primary">dpp</name>
  <name type="synonym">Dpp</name>
  <dbReference type="INTERPRO" key="69" id="IPR001111"/>
  <dbReference type="orthologs" key="93" id="HOMSA:ENP44"/>
  <organism>
    <name type="common">fruit fly</name>
    <name type="scientific">Drosophila melanogaster</name>
    <dbReference type="NCBI Taxonomy" key="107" id="7227"/>
  </organism>
  <mapLocations>
    <mapLocation map="genome" chromosome="2L"
      position="2428454..2459609" units="bp"/>
  </mapLocations>
  <ontology>
    <dbReference type="GO" key="108" id="GO:0007455">
      <property type="term" value="antennal disc morph"/>
      <property type="evidence_code" value="inferred"/>
    </dbReference>
  </ontology>
  <literature>
    <dbReference type="pubmed" key="3368" id="17034783"/>
  </literature>
</gene>
```



How to implement

- Subclass `Bio::GMOD::GenericGenePage`
 - `Bio::GMOD::GenericGenePage::Chado`
- Implement some abstract classes, like
 - name
 - accessions
 - synonyms
 - ontology_terms
 - 7 others
- Override `new()`



To use

```
my $page = Bio::GMOD::GenericGenePage->new($id);  
my $xml = $page->render_xml();
```



Current providers

- SGN
- FlyBase
- Sample yeast set at gmod.org:
 - http://gmod.org/cgi-bin/gbrowse/chado_yeast/



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