

Feature and Annotation HOWTO

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This is a HOWTO written in DocBook format that explains how to use the SeqFeature and Annotation objects of Bioperl.

then tell this object to make a version of itself as a fl

FEATURES	Location/Qualifiers
source	1..1846

```
print ref($seq_object);  
# results in "Bio::Seq::RichSeq"
```

The SeqFeature::Generic object uses tag/value pairs to store information, and the values are always returned as arrays. A simple way to access all the data in the features of a Seq object would look something like this:

```
for my $feat_object ($seq_object->get_SeqFeatures) {  
    print "primary tag: ", $feat_object->primary_tag, "\n";  
    for my $tag ($feat_object->get_all_tags) {  
        print "    tag: ", $tag, "\n";  
        for my $value ($feat_object->get_tag_values($tag)) {  
            print "        value: ", $value, "\n";  
        }  
    }  
}
```

This bit would print out something lik

```
        if ($feat_object->has_tag("db_xref"));  
    }
```

Important

/gene="Phe-tRNA"


```
for my $feature ($seqobj->top_SeqFeatures){
  if ( $feature->location->isa('Bio::Location::SplitLocationI')
      && $feature->primary_tag eq 'CDS' ) {
    for my $location ( $feature->location->sub_Location ) {
```



```
my $anno_collection = $seq_obj->annotation;
```

Now we can access each

And from this array of Annotations let's extract a hash containing the `as_text` strings as keys and the concatenated tagnames and object types as values:

```
my %tagname_type = map {$_->as_text,($_->tagname . " " . ref($_)) }  
    @annotations;
```

The contents of the `%tagname_type` hash will look like the table below.
