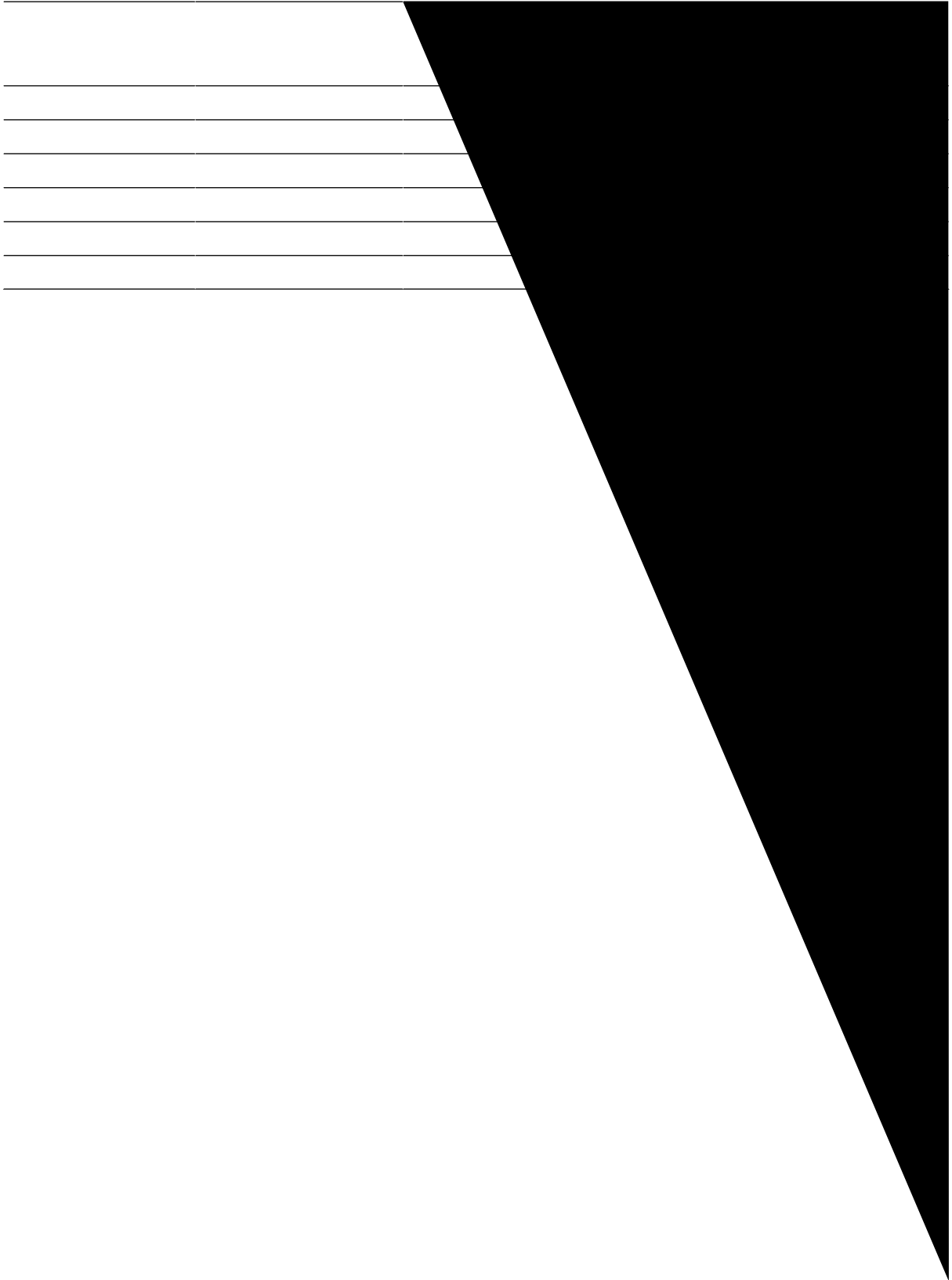


1. Introduction

Importing sequences with annotations is a basic part of most bioinformatics tasks. Bioperl supports importing (Importion) TFASTA files. C

4. Modifying th.

Database-name sections can be repeated, in which case the client should try each service in turn from top to bottom.



To use the registry from a Perl script, use the following idiom:

```
1 use Bio::DB::Registry;
2 $registry = Bio::DB::Registry->new;
3 $db = 1; $registry->get_database('embl');
```