Ruby RESTful client

```ruby
require 'rubygems'
require 'activeresource'

@url = 'http://current.mirmaid.org'
class Precursor < ActiveResource::Base; self.site = @url; end
class Mature < ActiveResource::Base; self.site = @url; end

# 1) Get the 'comment' attribute for the cel-let-7 precursor
puts Precursor.find('cel-let-7').comment

# 2) Get the mature sequences for the hsa-mir-21 precursor
Mature.find(:all, :from => '/precursors/hsa-mir-21/matures').each do |m|
  puts m.sequence
end
```

Perl RESTful client

```perl
use strict;
use REST::Client; # These modules can be installed easily with 'cpan'
use XML::Simple;
use Data::Dumper;

my $client = REST::Client->new();
my $xs = XML::Simple->new(NoAttr=>1,KeyAttr=>[]);
$client->setHost("http://current.mirmaid.org");

# 1) Get the 'comment' attribute for the cel-let-7 precursor
$client->GET('/precursors/cel-let-7.xml');
my $precursor = $xs->XMLin($client->responseContent());
print $precursor->{'comment'}."\n";

# 2) Get the mature sequences for the hsa-mir-21 precursor
$client->GET('/precursors/hsa-mir-21/matures.xml');
my $matures = $xs->XMLin($client->responseContent())->{'mature'};
foreach my $m (@$matures) {
  print $m->{'sequence'}."\n" }
```

Command-line RESTful client

(Retrieves the 157 C. elegans mature miRNA sequences in fasta format)

```shell
> curl current.mirmaid.org/species/cel/matures.fa
```

R RESTful client

(Retrieves the 157 C. elegans mature miRNA sequences in fasta format)

```r
> Library(Biostrings)
> read.RNAStringSet(url(http://current.mirmaid.org/species/cel/matures.fa), format="fasta")
```