

Working with biological sequence data

We will use the Biopython package

<http://biopython.org>



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Biopython

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Introduction





Biopython is a set of freely available tools for biological computation written in [Python](#) by an international team of developers.

It is a distributed collaborative effort to develop Python libraries and applications which address the needs of current and future work in bioinformatics. The source code is made available under the [Biopython License](#), which is extremely liberal and compatible with almost every license in the world.

We are a member project of the [Open Bioinformatics Foundation \(OBF\)](#), who take care of our domain name and hosting for our mailing list etc. The OBF used to host our development repository, issue tracker and website but these are now on [GitHub](#).

This wiki will help you download and install Biopython, and start using the libraries and tools.

Get Started	Get help	Contribute
Download Biopython	Tutorial (PDF)	What's being worked on
Installation help (PDF)	Documentation on this wiki	Developing on Github
	Cookbook (working examples)	Google Summer of Code

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Applications on

root



Channels

Refresh



notebook

 4.3.1

Web-based, interactive computing notebook environment. Edit and run human-readable docs while describing the data analysis.

Launch



qtconsole

4.2.1

PyQt GUI that supports inline figures, proper multiline editing with syntax highlighting, graphical calltips, and more.

Launch



snvdr



anaconda-fusion

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Description

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_license



1.1



alabaster

Configurable, python 2+3
compatible sphinx theme

0.7.9



anaconda



4.3.0



anaconda-client

Anaconda.org command line client
library

1.6.0



appnope



0.1.0



appscript



1.0.1



astroid

Abstract syntax tree for python
with inference support

1.4.9



astropy

Community-developed python
library for astronomy

1.3



babel



2.3.4



backports



1.0



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All



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1.1



_nb_ext_conf



0.3.0



accelerate



2.3.1



accelerate_cudalib



2.0



affine



2.0.0



alabaster

Configurable, python 2+3
compatible sphinx theme[0.7.9](#)

alpaca_static



1.5.22



anaconda

[4.3.0](#)

anaconda-build



1.15.0



anaconda-clean



1.1.0

839 packages available (root)

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biopython



Freely available tools for biological computation

1.68



scikit-bio



Python package for bioinformatics

0.5.1



Create



Clone






Import



Remove

2 packages available matching "bio" (root)

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Create



Clone



Import






Remove

2 packages available matching "bio" (root)

Apply

Clear

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All



Channels

[Update index...](#)

bio



root

Proceed with the following actions?



The following actions will be applied:

Install:

- biopython

Cancel

Ok



T

Description

Version



Freely available tools for biological computation

1.68



Python package for bioinformatics

0.5.1



Create



Clone



Import



Remove

2 packages available matching "bio" (root)

[Apply](#)[Clear](#)

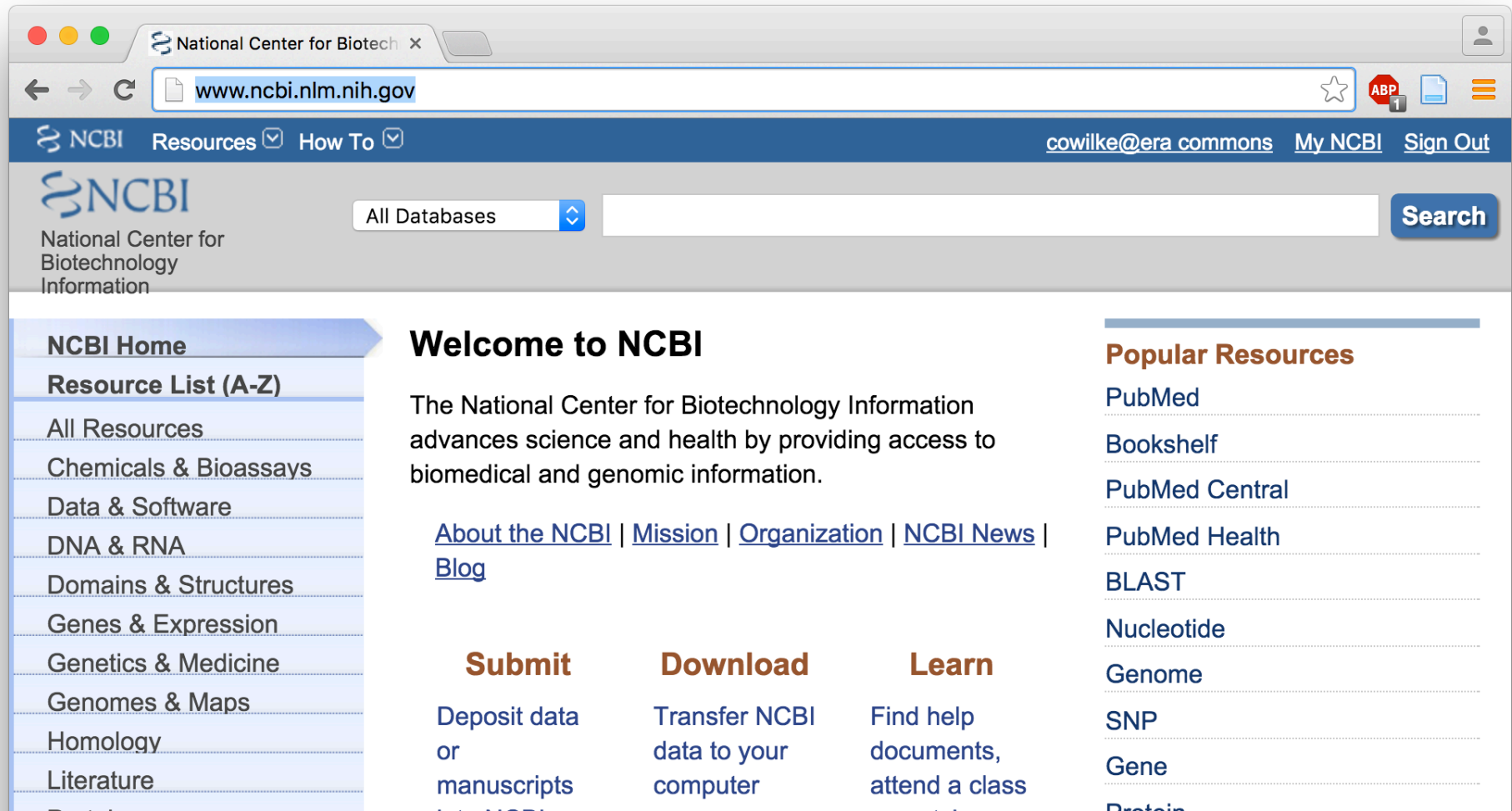
Testing whether Biopython is properly installed

```
In [1]: import Bio
```

```
Out[1]:
```

Getting biological data: The NCBI databases

<http://www.ncbi.nlm.nih.gov/>



The screenshot shows the NCBI website homepage. At the top, there's a browser window with the address bar showing 'www.ncbi.nlm.nih.gov'. Below the browser window, the NCBI logo is on the left, and a navigation bar contains 'Resources' and 'How To' dropdown menus. On the right of the navigation bar, there's a user profile icon, a star, a red 'ABP' badge, a document icon, and a hamburger menu. Below the navigation bar, there's a search bar with a dropdown menu set to 'All Databases' and a 'Search' button. On the left side, there's a 'NCBI Home' section with a 'Resource List (A-Z)' and a list of resources: All Resources, Chemicals & Bioassays, Data & Software, DNA & RNA, Domains & Structures, Genes & Expression, Genetics & Medicine, Genomes & Maps, Homology, and Literature. In the center, there's a 'Welcome to NCBI' section with a paragraph about the center's mission and a list of links: About the NCBI, Mission, Organization, NCBI News, and Blog. Below this, there are three columns: 'Submit' (Deposit data or manuscripts), 'Download' (Transfer NCBI data to your computer), and 'Learn' (Find help documents, attend a class). On the right side, there's a 'Popular Resources' section with a list of resources: PubMed, Bookshelf, PubMed Central, PubMed Health, BLAST, Nucleotide, Genome, SNP, Gene, and Protein.

NCBI National Center for Biotechnology Information

Resources How To

cowilke@era commons My NCBI Sign Out

All Databases Search

NCBI Home

Resource List (A-Z)

- All Resources
- Chemicals & Bioassays
- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

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Submit

Deposit data or manuscripts

Download

Transfer NCBI data to your computer

Learn

Find help documents, attend a class

Popular Resources

- PubMed
- Bookshelf
- PubMed Central
- PubMed Health
- BLAST
- Nucleotide
- Genome
- SNP
- Gene
- Protein

Try search for "KT220438"

The screenshot shows a web browser window with the address bar displaying `www.ncbi.nlm.nih.gov/gquery/?term=KT220438`. The page title is "KT220438 - GQuery: Glob: x". The NCBI logo and navigation links (Resources, How To) are visible in the header. The search bar contains "KT220438" and a "Search" button. The results section shows "Results found in 2 databases for 'KT220438'". A highlighted box contains the following information:

[Influenza A virus \(A/NewJersey/NHRC_93219/2015\(H3N2\)\) segment 4 hemagglutinin \(HA\) gene, complete cds](#)
1,701 bp cRNA.
Lab_host: MDCK. Country: USA: New Jersey. Segment: 4. Isolation_source: nasopharyngeal swab. Collection_date: 17-Jan-2015.
Accession: **KT220438.1** GI: 887493048
[GenBank](#) [FASTA](#) [Graphics](#)

Below the highlighted box, there are two sections: "Literature" and "Genes".

Literature		Genes	
Books	0	EST	0
	books and reports		expressed sequence tag sequences
MeSH	0		collected information about
	ontology used for PubMed indexing		

Direct link to search results

<http://www.ncbi.nlm.nih.gov/gquery/?term=KT220438>

A genbank record is just a simple text file

LOCUS KT220438 1701 bp cRNA linear VRL 20-JUL-2015
 DEFINITION Influenza A virus (A/NewJersey/NHRC_93219/2015(H3N2)) segment 4
 hemagglutinin (HA) gene, complete cds.
 ACCESSION KT220438
 VERSION KT220438.1 GI:887493048
 KEYWORDS .
 SOURCE Influenza A virus (A/New Jersey/NHRC_93219/2015(H3N2))
 ORGANISM Influenza A virus (A/New Jersey/NHRC_93219/2015(H3N2))
 Viruses; ssRNA viruses; ssRNA negative-strand viruses;
 Orthomyxoviridae; Influenzavirus A.
 REFERENCE 1 (bases 1 to 1701)
 AUTHORS Sitz,C.R., Thammavong,H.L., Balansay-Ames,M.S., Hawksworth,A.W.,
 Myers,C.A. and Brice,G.T.
 TITLE GEISS Influenza Surveillance Response Program
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1701)
 AUTHORS Sitz,C.R., Thammavong,H.L., Balansay-Ames,M.S., Hawksworth,A.W.,
 Myers,C.A. and Brice,G.T.
 TITLE Direct Submission
 JOURNAL Submitted (29-JUN-2015) Operational Infectious Diseases, Naval
 Health Research Center, 140 Sylvester Rd., San Diego, CA 92106, USA
 COMMENT ##Assembly-Data-START##
 Sequencing Technology :: Sanger dideoxy sequencing
 ##Assembly-Data-END##
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 Jersey/NHRC_93219/2015(H3N2))"
 /mol_type="viral cRNA"
 /strain="A/NewJersey/NHRC_93219/2015"
 /serotype="H3N2"

FEATURES

source

Location/Qualifiers

1..1701

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Jersey/NHRC_93219/2015(H3N2))"

/mol_type="viral cRNA"

/strain="A/NewJersey/NHRC_93219/2015"

/serotype="H3N2"

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/segment="4"

/lab_host="MDCK"

/country="USA: New Jersey"

/collection_date="17-Jan-2015"

gene

1..1701

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CDS

1..1701

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/product="hemagglutinin"

/protein_id="AKQ43545.1"

/db_xref="GI:887493049"

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SSFFSRLNWLTHLNYTYPALNVTMPNNEQFDKLYIWGVHHPGTDKDQIFLYAQSSGRI
TVSTKRSQQAVIPNIGSRPRIRDIPSRSISYWTIVKPGDILLINSTGNLIAPRGYFKI
RSGKSSIMRSDAPIGKCKSECITPNGSIPNDKPFQNVNRITYGACPRYVKHSTLKLAT
GMRNVPEKQTRGIFGAIAGFIENGWEGMVDGWYGFRHQNSEGRGQAADLKSTQAAIDQ
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ORIGIN

```

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181 aattcctcaa taggtgaaat atgcgacagt cctcatcaga tccttgatgg agaaaactgc
241 acactaatag atgctctatt gggagaccct cagtgtgatg gctttcaaaa taagaaatgg
301 gacctttttg ttgaacgaag caaagcctac agcaactgct acccttatga tgtgccggat
361 tatgcctccc ttaggtcact agttgcctca tccggcacac tggagtttaa caatgaaagc
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481 agtagtttct ttagtagatt aaattggttg acccacttaa actacacata cccagcattg
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