

NCBI 简介

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- NCBI是啥？有啥？What
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BLAST使用

BioPython使用

NCBI是啥？

Introduction to NCBI----What?



国家生物技术信息中心（ National Center for Biotechnology Information，简称NCBI）是美国国家医学图书馆（ NLM）的一部分（该图书馆是美国国家卫生研究所的一部分）。

The National Center for Biotechnology Information



***Created in 1988 as a part of the
National Library of Medicine at NIH***

- Establish public databases
- Research in computational biology
- Develop software tools for sequence analysis
- Disseminate biomedical information

NCBI Databases and Services

- GenBank **primary sequence database**
- Free public access to biomedical literature
 - PubMed **free Medline (3 million searches per day)**
 - PubMed Central **full text online access**
- Entrez **integrated molecular and literature databases**
- BLAST **highest volume sequence search service**
(100 – 200 K searches per day)
- VAST **structure similarity searches**
- Software and Databases

NCBI数据库和工具

- ▶ **生物数据库**
 - 文献数据库
 - 核酸数据库
 - 基因组资源库
 - ENTREZ数据库
- ▶ **生物信息工具**
 - 数据挖掘的工具
 - 序列分析工具
 - 三维结构显示和相似查询的工具
- ▶ **图谱 (MAPS)**
- ▶ **癌症协作研究项目**
- ▶ **FTP数据下载**

NCBI怎么用？

Introduction to NCBI----How?

Entrez全数据库搜索 Example:血红蛋白 β 链HBB

查看基因信息

下载FASTA格式数据

Run BLAST

BLAST

BLAST (Basic Local Alignment Search Tool) allows rapid sequence comparison of a query sequence against a database.

The BLAST algorithm is fast, accurate, and web-accessible.

BLAST--步骤

- 选择一个BLAST程序
- 选择你所感兴趣的序列，输入到BLAST中
- 选择一个用于搜索的数据库
- 为搜索和输出格式选择可选参数

BLAST--Step1 选择一个BLAST程序

Basic BLAST

Choose a BLAST program to run.

<u>nucleotide blast</u>	Search a nucleotide database using a nucleotide query <i>Algorithms: blastn, megablast, discontinuous megablast</i>
<u>protein blast</u>	Search protein database using a protein query <i>Algorithms: blastp, psi-blast, phi-blast, delta-blast</i>
<u>blastx</u>	Search protein database using a translated nucleotide query
<u>tblastn</u>	Search translated nucleotide database using a protein query
<u>tblastx</u>	Search translated nucleotide database using a translated nucleotide query

BLAST—Step2 输入

可以输入Accession number/gi/FASTA序列
或上传一个文件

NCBI/BLAST/blastn suite **Standard Nucleotide BLAST**

[blastn](#) [blastp](#) [blastx](#) [tblastn](#) [tblastx](#)

BLASTN programs search nucleotide databases using a nucleotide query. [more...](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#) **Query subrange** [?](#)

From

To

Or, upload file 未选择任何文件 [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

☐ **Align two or more sequences** [?](#)

FASTA格式介绍

- 第一行是由大于号 “>” 起始的任意文字说明
- 从第二行开始为序列本身，只允许使用既定的核苷酸或氨基酸编码符号

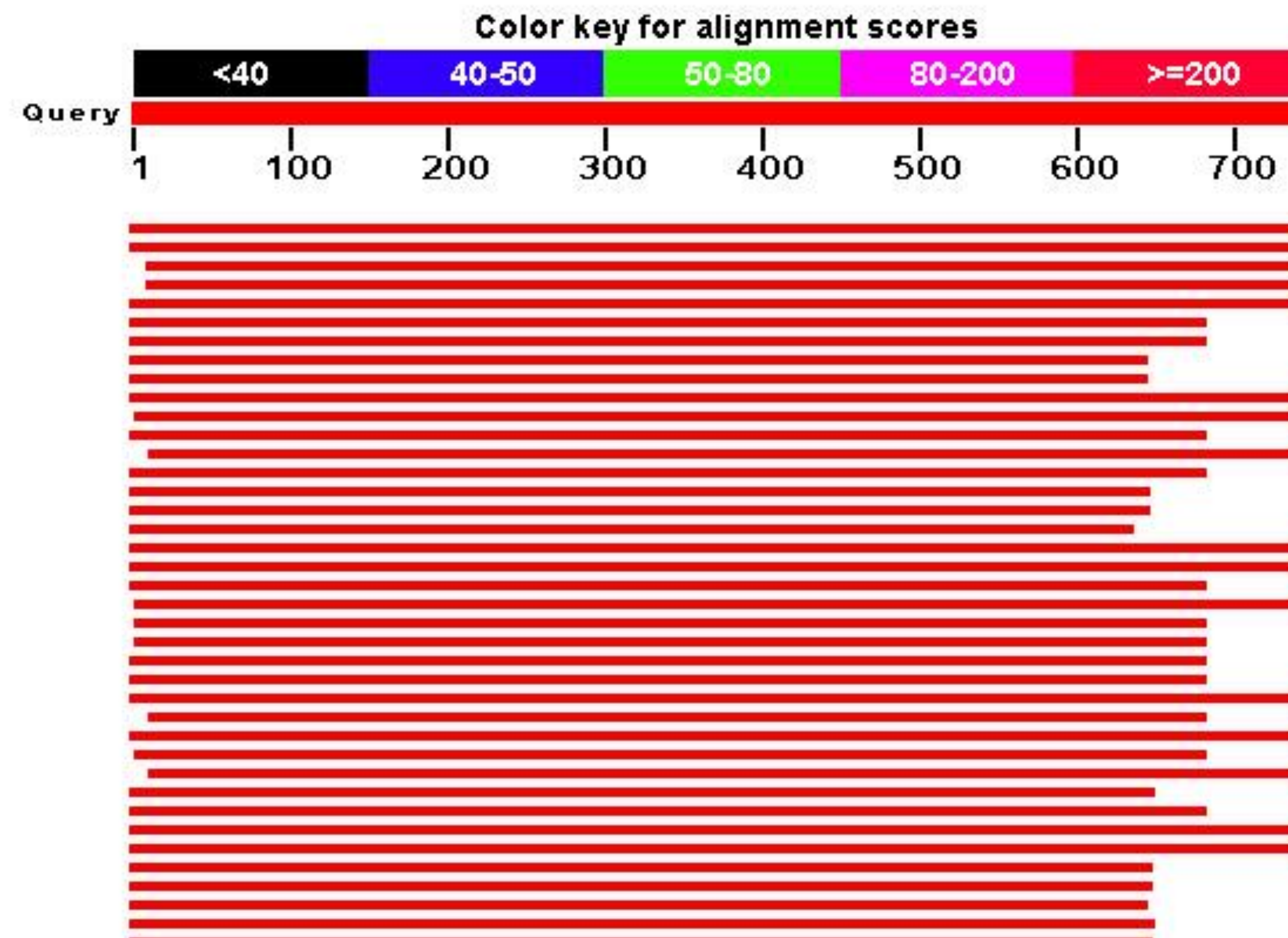
```
>gi|1679627|gb|U41284.1|HSU41284 Homo sapiens cytochrome c oxidase (COX5B) gene, partial cds
GAGCTCAGGAGTTTGAGAGCAGCCTGGGCAACATAGAGAGACCCATCTCTAGAAAAACAATAATTAGC
CAGACCCACACTGTAGTGCCTGTAGTCCAGCCACTCTGGAGGCTGAGGTGAGAGGATGGCTTGGGCAC
AGGAGGGCAAGACTTCAGTGAGCCTTGATTGTATCAGTGCAC TTCAGACTAGGC AACAGAGTGAGACCT
GTCTCAAAAAAATTAAOCTTGTTGAAC TG TATG TGATGOCOCCTTTCTG TG TTAGAAATACATCTTTTAT
TTGTTTACTTTT TACTTTTATCATCATCACTTG TAAAATAC TTAG AAGTTTAAGACATCCTTTTATCCT
TGAACCATTTGAGGGTAAGTTT TGATCTTAAACATAATGTATGGAC TCCTGTGACTTTGTGAAGCTGTAT
```

BLAST—Step3 Result

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments



- Download: <http://biopython.org/wiki/Download>
- Example:
- 用BioPython转录翻译
- 用BioPython进行BLAST