

# Introduction à la Bioinformatique 2025



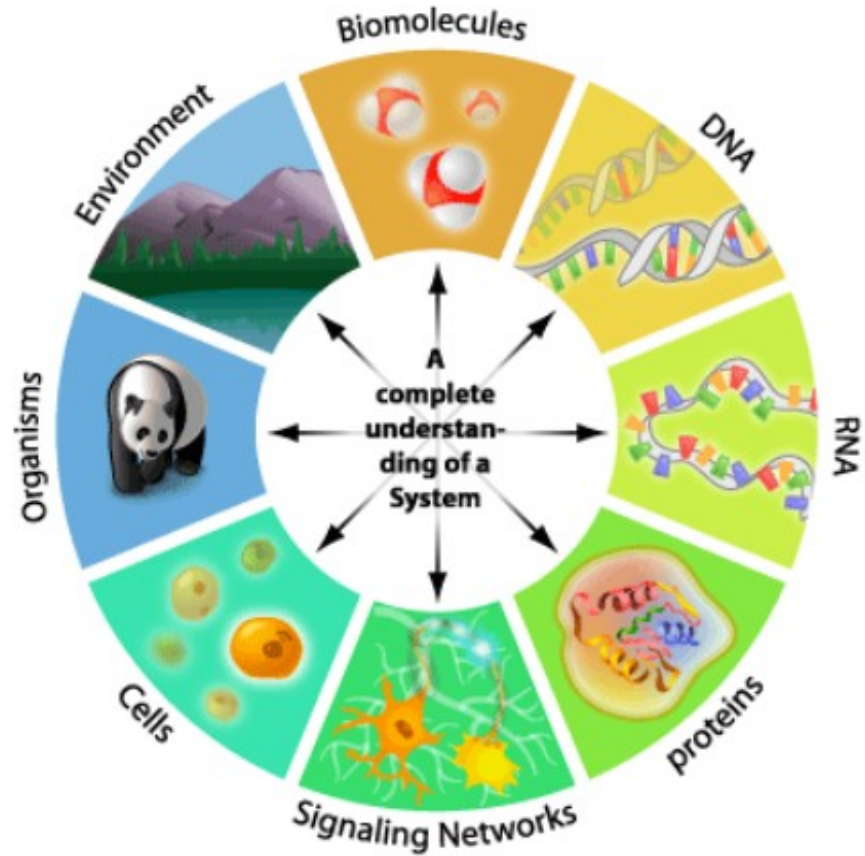
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Biologie moléculaire –  
Bioinformatique

# Introduction aux bases de données et aux ressources

Recherche de séquences

## Objectifs du cours

- Comprendre la structure et la disposition des ressources de données du NCBI et de l'EBI
- Comprendre la différence entre les bases de données, les outils et les repositories.
- Recherche de données dans des bases de données spécifiques à l'aide de numéros d'accès, de noms de gènes, etc.
- Utiliser les ressources NCBI et EBI

[illegible]

# Introduction

- Plusieurs bases de données et ressources en ligne
- Besoin de savoir laquelle :
  - ✓ Quelles sont les bases de données et les ressources existantes
  - ✓ Quels sont les outils disponibles pour exploiter ces ressources ?
  - ✓ Quels sont les outils disponibles pour rechercher dans les ressources?



# Bases de données biologiques



# Bases de données biologiques

- Bases de données biologiques sont :
  - ✓ Publique ou privée
  - ✓ Protéine, nucléotide, structure, littérature, annotation...
  - ✓ Généralisée ou spécialisée
  - ✓ Centré sur la séquence (aa ou nt) ou le génome

# Bases de données biologiques

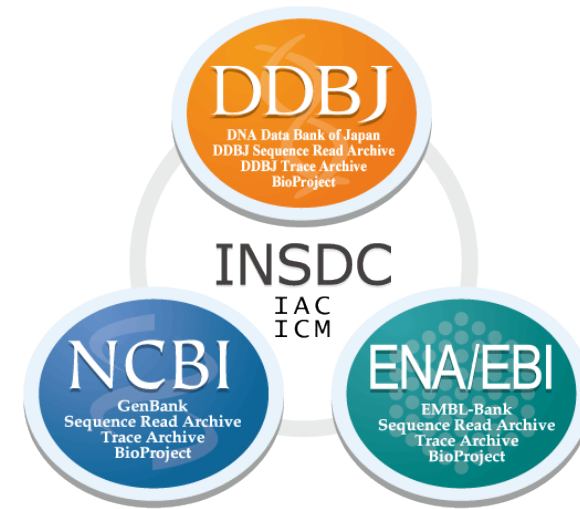
Quelques noms de banques de données:

- ❖ **Séquences en acides nucléiques** (DNA et mRNA); [EMBL](#), [GenBank](#), [DDBJ](#)
- ❖ **Séquences en acides aminés** (protéines); [Swiss-Prot](#), [wwPDB](#)
- ❖ **Références bibliographiques**; [PubMed](#)
- ❖ **Informations générales sur les gènes et/ou les maladies**; [EntrezGene](#), [OMIM](#), [HMGD](#)
- ❖ **informations sur la structure tridimensionnelle des protéines ou de l'ADN**; [PDB](#)
- ❖ Il existe aussi des banques spécialisées, comme Newt, qui donne des informations sur la classification des espèces



# Bases de données primaires

- International Nucleotide Sequence Database Collaboration (INSDC)
- Données de séquences génomiques stockées dans 3 bases de données publiques
- Chacun a son propre numéro d'accès et ses propres outils



# Bases de données secondaires

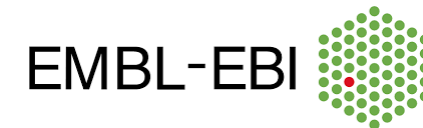
- Des bases de données spécialisées construites à partir de données de séquences primaires
- Fournissent plusieurs ressources et annotations différentes

# Ressources bioinformatiques les plus populaires

- National Centre for Biotechnology Information (NCBI)



- European Bioinformatics Institute (EMBL-EBI)



# Recherche dans les bases de données: NCBI



ncbi



[Tous](#)

[Vidéos](#)

[Images](#)

[Livres](#)

[Maps](#)

[Plus](#)

Outils

Environ 87 900 000 résultats (0,49 secondes)

<https://www.ncbi.nlm.nih.gov> [Traduire cette page](#)

## National Center for Biotechnology Information

The **National Center for Biotechnology Information** advances science and health by providing access to biomedical and genomic information. About the **NCBI** | ...

### PubMed

PubMed® comprises more than 32 million citations for biomedical ...

### BLAST

Nucleotide - Standard Protein  
BLAST - Nucleotide BLAST - ...

### Nucleotide

Nucleotide. The Nucleotide database is a collection of ...

[Autres résultats sur nih.gov »](#)

### Gene

Advanced search - RefSeqGene -  
OMIM - Genome Workbench

### Proteins

Protein - Protein Clusters -  
Identical Protein Groups - ...

### All Resources

A database of human genes and genetic disorders. NCBI ...

## National Center for Biotechnology Information



Entreprise

Le National Center for Biotechnology Information, en français « Centre américain pour les informations biotechnologiques », est un institut national américain pour l'information biologique moléculaire. [Wikipédia](#)

**Fondateur** : [Claude Denson Pepper](#)

**Création** : 4 novembre 1988

**Organisation mère** : [United States National Library of Medicine](#)

# Recherche dans les bases de données: NCBI

The image shows the NCBI homepage. At the top, there is a navigation bar with 'NCBI Resources' and 'How To' menus. A callout box with a red arrow points to the 'All Databases' dropdown menu. Below the navigation bar is a 'COVID-19 Information' banner with links to public health, research, SARS-CoV-2 data, prevention, and treatment information. A 'UNITE' banner follows, promoting a new NIH initiative to end structural racism. The main content area is divided into three columns. The left column contains a 'Resource List (A-Z)' sidebar. The middle column features a 'Welcome to NCBI' message and six interactive tiles: 'Submit', 'Download', 'Learn', 'Develop', 'Analyze', and 'Research'. The right column lists 'Popular Resources' and 'NCBI News & Blog' updates.

NCBI Resources How To Sign in to NCBI

NCBI National Center for Biotechnology Information

All Databases

Menu déroulant des différentes BD de NCBI

COVID-19 Information

Public health information (CDC) | Research information (NIH) | SARS-CoV-2 data (NCBI) | Prevention and treatment information (HHS) | Español

UNITE

A new NIH initiative to end structural racism and achieve racial equity in the biomedical research enterprise.

LEARN MORE

Ending Structural Racism

NCBI Home

Resource List (A-Z)

All Resources

Chemicals & Bioassays

Data & Software

DNA & RNA

Domains & Structures

Genes & Expression

Genetics & Medicine

Genomes & Maps

Homology

Literature

Proteins

Sequence Analysis

Taxonomy

Training & Tutorials

Variation

Welcome to NCBI

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

About the NCBI | Mission | Organization | NCBI News & Blog

Submit

Deposit data or manuscripts into NCBI databases

Download

Transfer NCBI data to your computer

Learn

Find help documents, attend a class or watch a tutorial

Develop

Use NCBI APIs and code libraries to build applications

Analyze

Identify an NCBI tool for your data analysis task

Research

Explore NCBI research and collaborative projects

Popular Resources

PubMed

Bookshelf

PubMed Central

BLAST

Nucleotide

Genome

SNP

Gene

Protein

PubChem

NCBI News & Blog

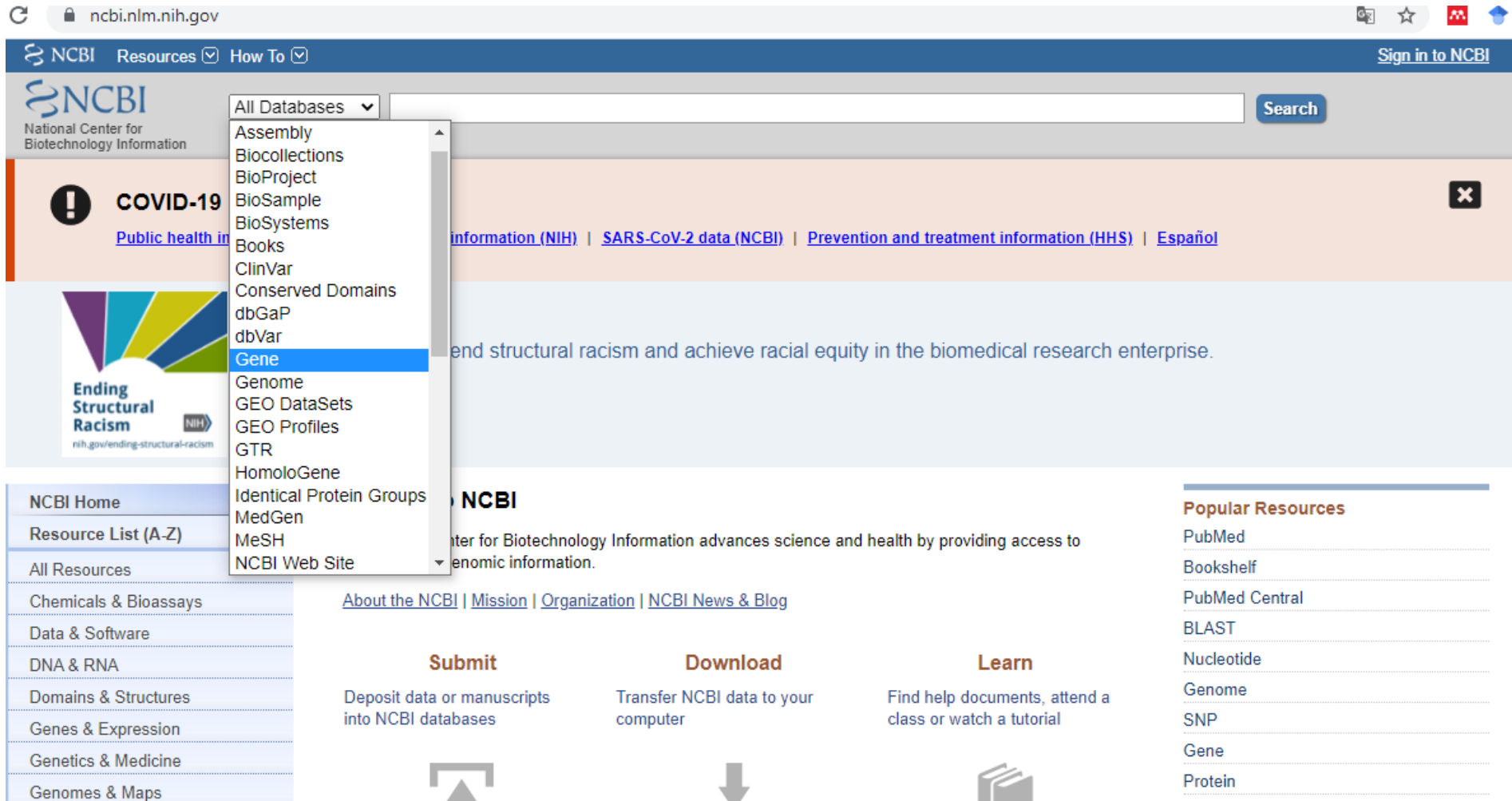
BLAST+ 2.12.0 now available with more efficient multithreaded searches

09 Jul 2021

BLAST+ 2.12.0 programs feature better multithreaded searches and support a

Codeathon from the Couch — NCBI

# Recherche dans les bases de données: NCBI



The screenshot shows the NCBI website interface. The browser address bar displays `ncbi.nlm.nih.gov`. The NCBI logo and navigation links (Resources, How To) are at the top. A search bar is present with a 'Search' button. A dropdown menu titled 'All Databases' is open, listing various databases including Assembly, Biocollections, BioProject, BioSample, BioSystems, Books, ClinVar, Conserved Domains, dbGaP, dbVar, Gene (highlighted), Genome, GEO DataSets, GEO Profiles, GTR, HomoloGene, Identical Protein Groups, MedGen, MeSH, and NCBI Web Site. The main content area features a COVID-19 public health information banner and a banner about ending structural racism. The footer includes links to About the NCBI, Mission, Organization, and NCBI News & Blog, as well as sections for Submit, Download, and Learn. A 'Popular Resources' sidebar on the right lists PubMed, Bookshelf, PubMed Central, BLAST, Nucleotide, Genome, SNP, Gene, and Protein.

ncbi.nlm.nih.gov

NCBI Resources How To Sign in to NCBI

NCBI National Center for Biotechnology Information

COVID-19 Public health information

Ending Structural Racism

All Databases

- Assembly
- Biocollections
- BioProject
- BioSample
- BioSystems
- Books
- ClinVar
- Conserved Domains
- dbGaP
- dbVar
- Gene
- Genome
- GEO DataSets
- GEO Profiles
- GTR
- HomoloGene
- Identical Protein Groups
- MedGen
- MeSH
- NCBI Web Site

NCBI

NCBI Home

Resource List (A-Z)

All Resources

Chemicals & Bioassays

Data & Software

DNA & RNA

Domains & Structures

Genes & Expression

Genetics & Medicine

Genomes & Maps

Submit

Deposit data or manuscripts into NCBI databases

Download

Transfer NCBI data to your computer

Learn

Find help documents, attend a class or watch a tutorial

Popular Resources

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



# Bases de données de NCBI

- NCBI comprend plus de 30 bases de données
- la littérature : [PubMed Central](#) (PMC), [Bookshelf](#) et [PubReader](#)
- La santé: [ClinVar](#), [dbGaP](#), [dbMHC](#), the [Genetic Testing Registry](#), [HIV-1/Human Protein Interaction Database](#) et [MedGen](#)
- Les génomes: [BioProject](#), [Assembly](#), [Genome](#), [BioSample](#), [dbSNP](#), [dbVar](#), [Nucleotide](#), [Probe](#) et [RefSeq](#).
- Les gènes: [Gene](#), [Gene Expression Omnibus](#) (GEO), [HomoloGene](#), [PopSet](#), [Refseq](#) et [UniGene](#).
- Les protéines: [Protein](#), the [Conserved Domain Database](#) (CDD), [COBALT](#), [Conserved Domain Architecture Retrieval Tool](#) (CDART), the [Molecular Modeling Database](#) (MMDB), [Refseqp](#) et [Protein Clusters](#).
- Les produits chimiques: [Biosystems](#) et [PubChem](#)

# EMBL - EBI

- Maintenir la gamme la plus complète au monde de bases de données moléculaires librement accessibles et actualisées
- Proposer des formations en ligne et en direct pour l'utilisation de leurs ressources.
- <https://www.ebi.ac.uk/training>

# EMBL - EBI

The EMBL-EBI website has been redesigned. Please [send us feedback](#) about this page.

EMBL's European Bioinformatics Institute

## EMBL-EBI

Unleashing the potential of big data in biology



Search

Example searches: [blast keratin bfl1](#) | [About EBI Search](#)

Find data resources →

Submit data →

Explore our research →

Train with us →

### Latest news →



Organisations should embrace open science faster – interview with Prof. Dame Janet Thornton

17 May 2022



Europe PMC: Harnessing the power of text mining to accelerate life sciences research

12 May 2022



2.4 billion sequences now available in the latest MGnify protein database release

11 May 2022



[Predicted complexes from ModelArchive now on PDBe-KB pages](#)

6 May 2022

# EMBL - EBI

## Services

[Overview](#)[A to Z](#)[Data submission](#)[Research infrastructure development programme](#)[Support](#)

The European Bioinformatics Institute (EMBL-EBI) maintains the world's most comprehensive range of freely available and up-to-date molecular data resources.

Developed in collaboration with our colleagues worldwide, our services let you share data, perform complex queries and analyse the results in different ways. You can work locally by downloading our data and software, or use our [web services](#) to access our resources programmatically.

— You can read more about our services in the journal [Nucleic Acids Research](#)

## Tools & Data Resources



### Tools

#### Clustal Omega



Multiple sequence alignment of DNA or protein sequences. Clustal Omega replaces the older ClustalW alignment tools.

[Web API](#)[Multiple sequence alignment](#)

#### InterProScan



InterProScan searches sequences against InterPro's predictive protein signatures.

[Web API](#)[Protein feature detection](#)[Sequence motif recognition](#)

#### BLAST [protein]



Fast local similarity search tool for protein sequence databases.

[Web API](#)[Sequence similarity search](#)

#### BLAST [nucleotide]



Fast local similarity search tool for nucleotide sequence databases.

### Data resources

#### Ensembl



Genome browser, API and database, providing access to reference genome annotation

[Web API](#)[EMBL-EBI Terms of use](#)

#### UniProt



A comprehensive resource for protein sequence and functional annotation.

[Web API](#)[CC-BY](#)

#### PDBe



The European resource for the collection, organisation and dissemination of 3D structural data (from PDB and EMDB) on biological macromolecules and their complexes.

[Web API](#)[CC0](#)

#### Europe PMC



A database to search the worldwide life sciences literature

[Web API](#)[EMBL-EBI Terms of use](#)

### Browse by type

[DNA & RNA](#)[Gene Expression](#)[Proteins](#)[Structures](#)[Systems](#)[Chemical biology](#)[Ontologies](#)[Literature](#)[Cross domain](#)

## Programmatic access

EMBL-EBI web services allow you to query our large biological data resources programmatically, so that you can develop data analysis pipelines or integrate public data with your own applications. The Web Services technology we use are built on open standards to ensure client and server software from various sources will work well together.

[Browse EMBL-EBI web services](#)

## Principles of service provision

### Open

Our data and tools are freely available, without restriction. The only exception is potentially identifiable human genetic information, for which access depends

# Bases de données spécialisées

- Il existe un grand nombre de bases de données spécialisées

- ❖ La plupart des séquences sont également dans la banque GenBank/EMBL
- ❖ Peut contenir des génomes entiers
- ❖ Peut contenir des ressources spécialisées
- ❖ Contient des outils spécifiques pour l'exploitation des données

# Bases de données spécialisées

- Plasmodium <https://plasmodb.org/plasmo/app>
- Les collections spécialisées de Sanger  
<https://www.sanger.ac.uk>
- Base de données sur les hépatites  
[https://hcv.lanl.gov/content/sequence/HCV/news/old\\_news.html](https://hcv.lanl.gov/content/sequence/HCV/news/old_news.html)
- Base de données de recherche sur la grippe  
influenza  
<https://www.fludb.org/brc/home.spg?decorator=influenza>



# Design d'amorce utilisant Primer Blast

 An official website of the United States government [Here's how you know](#)



**National Library of Medicine**  
National Center for Biotechnology Information

 tibionez@gmail.com

## Primer-BLAST

A tool for finding specific primers

Finding primers specific to your PCR template (using Primer3 and BLAST).

Primers for target on one template

Primers common for a group of sequences

[Retrieve recent results](#) [Publication](#) [Tips for finding specific primers](#)

[Save search parameters](#) [Reset page](#)

### PCR Template

Enter accession, gi, or FASTA sequence (A refseq record is preferred) ?

[Clear](#)

Range ?

[Clear](#)

	From	To
Forward primer	<input type="text"/>	<input type="text"/>
Reverse primer	<input type="text"/>	<input type="text"/>

Or, upload FASTA file

Choisir le fichier aucun fichier sélectionné

### Primer Parameters

Use my own forward primer  
(5'→3' on plus strand)

[Clear](#)

Use my own reverse primer  
(5'→3' on minus strand)

[Clear](#)

PCR product size

Min	Max
<input type="text" value="70"/>	<input type="text" value="1000"/>

# of primers to return

Primer melting temperatures  
(T<sub>m</sub>)

Min	Opt	Max	Max T <sub>m</sub> difference
<input type="text" value="57.0"/>	<input type="text" value="60.0"/>	<input type="text" value="63.0"/>	<input type="text" value="3"/> ?

### Exon/intron selection

A refseq mRNA sequence as PCR template input is required for options in the section ?

Exon junction span

?

Exon junction match

Min 5' match	Min 3' match	Max 3' match
<input type="text" value="7"/>	<input type="text" value="4"/>	<input type="text" value="8"/>

Minimal and maximal number of bases that must anneal to exons at the 5' or 3' side of the junction ?

Intron inclusion

☐ Primer pair must be separated by at least one intron on the corresponding genomic DNA ?

Intron length range

Min	Max
<input type="text" value="1000"/>	<input type="text" value="10000"/> ?

### Primer Pair Specificity Checking Parameters

Specificity check

☒ Enable search for primer pairs specific to the intended PCR template ?

<input type="text" value="1UUU"/>	<input type="text" value="1UUU"/> ?
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### Primer Pair Specificity Checking Parameters

Specificity check

☒ Enable search for primer pairs specific to the intended PCR template ?

# Take home

- Une grande quantité de données existent
- Les bases de données primaires stockent les données brutes des séquences
- Les bases de données secondaires fournissent des informations sur l'annotation des données de séquence.
- Il est important de savoir comment et où les données sont stockées
- NCBI et EBI sont les deux ressources les plus populaires pour obtenir des données biologiques.