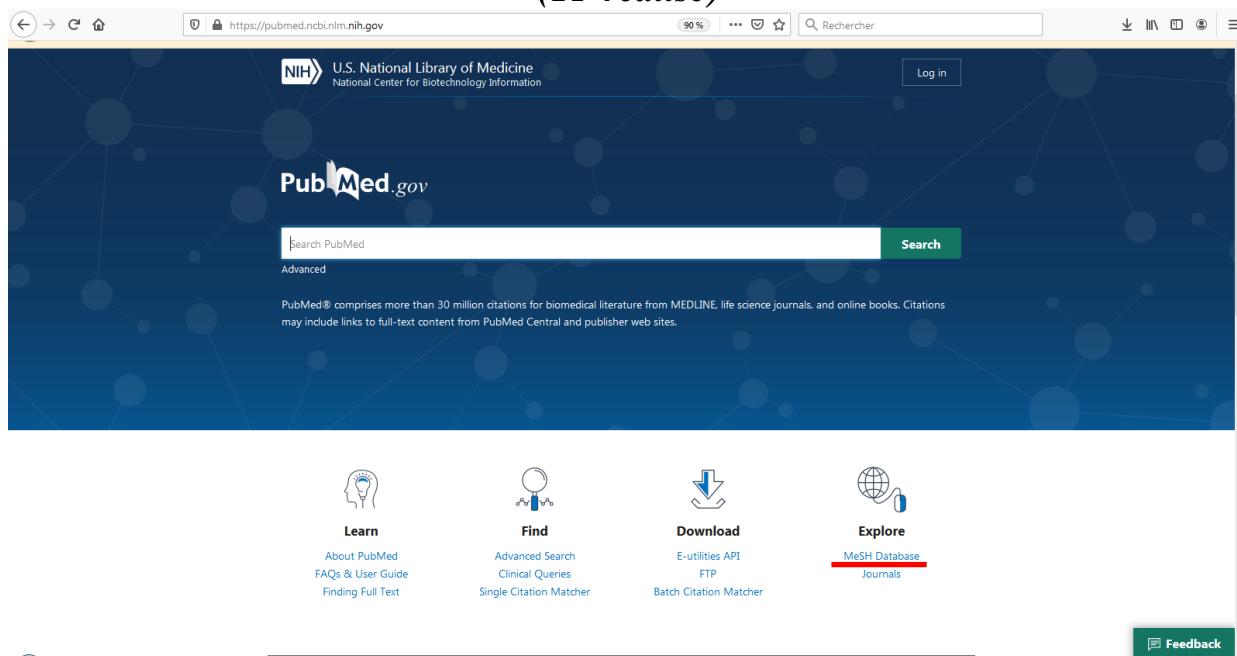


TP2 : Recherche des séquences dans les bases de données (Genbank) **(TP réalisé)**

Application :

- Trouver dans la base Genbank la séquence dont le numéro d'accesion est le suivant : MT020781
Il s'agit de la séquence du génome du coronavirus (Severe acute respiratory syndrome coronavirus 2 isolate).
- Résumer les informations accompagnant la séquence.

TP3 : Bases de données bibliographiques (Pubmed) **(TP réalisé)**



Applications

- Trouver des articles sur le coronavirus dans Pubmed
- Trouver des informations sur coronavirus covid-19 dans le service MeSH database.
- Pour plus d'informations sur le coronavirus, consulter les articles suivants :
 - [Case-Fatality Rate and Characteristics of Patients Dying in Relation to COVID-19 in Italy.](#)
Onder G, et al. JAMA. 2020. PMID: 32203977.
 - [Rapid Progression to Acute Respiratory Distress Syndrome: Review of Current Understanding of Critical Illness from COVID-19 Infection.](#)
Goh KJ, et al. Ann Acad Med Singapore. 2020. PMID: 32200400
 - [Treatment for severe acute respiratory distress syndrome from COVID-19.](#)
Matthay MA, et al. Lancet Respir Med. 2020. PMID: 32203709.
 - [Should COVID-19 Concern Nephrologists? Why and to What Extent? The Emerging Impasse of Angiotensin Blockade.](#)
Perico L, et al. Nephron. 2020. PMID: 32203970 Review.
 - [Rational use of face masks in the COVID-19 pandemic.](#)
Feng S, et al. Lancet Respir Med. 2020. PMID: 32203710.

TP4 : Comparaison des séquences (Alignment)

1- Comparaison d'une séquence nucléique avec une base de données nucléique

- Le programme utilisé est Blast de Genbank sur le site du NCBI

- Il existe 5 types de BLAST (blastn, blastp, blastx, tblastn, tblastx)

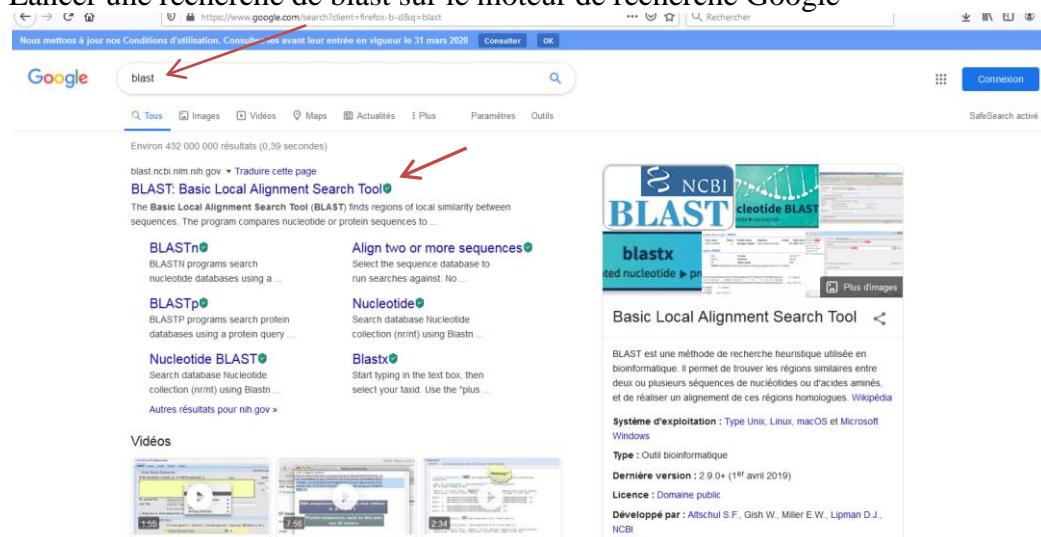
Pour comparer la séquence nucléotidique avec les séquences nucléotidiques de la base de données genbank on utilise le Blastn (Nucleotide BLAST).

Lancer une recherche BLAST pour la séquence suivante :

```
gggggggggtt tccggattta ttgggcgtaa gcgagcgcag gcgggttttt aagtctgatg tgaaaaggccct  
cggttaacc gaggaagcgc atcggaaact gggaaacttg agtgcagaag aggacagtgg aactccatgt  
gtagcgtga aatgcgtaga tatatggaag aacaccatgg cgcgaaggcg ctgtctggtc tgtaactgac  
gctgaggctc gaaagcatgg gtagcgaaca ggattagata ccctggtagt ccatgcccgt aacgatgaaat  
gcttaggttt ggggggttcc cgcccttcag tgccgcagct aacgcattaa gcattccgccc tggggagtag  
gaccgcaagg ttgaaactca aaggaattga cgggggccccg cacaaggcggt ggagcatgtg gtttaattcg  
aagcaacgcg aagaacctta ccaggtcttg acatctttg atcacctgag agatcagggtt tccccttcgg  
ggccaaaatg acagggtgtg catgggtgtc gtcagctcgt gtcgtgagat gtgggttaaa gtcccccaac  
gagcgcaacc cttatgacta gttgccagca ttttagttggg cactctagta agactgcccgg tgacaaaccg  
gaggaaggtg gggatgacgt caaatcatca tgcccttat gacctggctt acacacgtgc tacaatggat  
ggtacaacga gttgcgagac cgcgaggtca agctaatttc ttaaaggccat ttcagttcg gactgttaggc  
tgcaactcgc ctacacgaag tcggaatcgc tagtaatcgc ggatcagcac atacgttccc
```

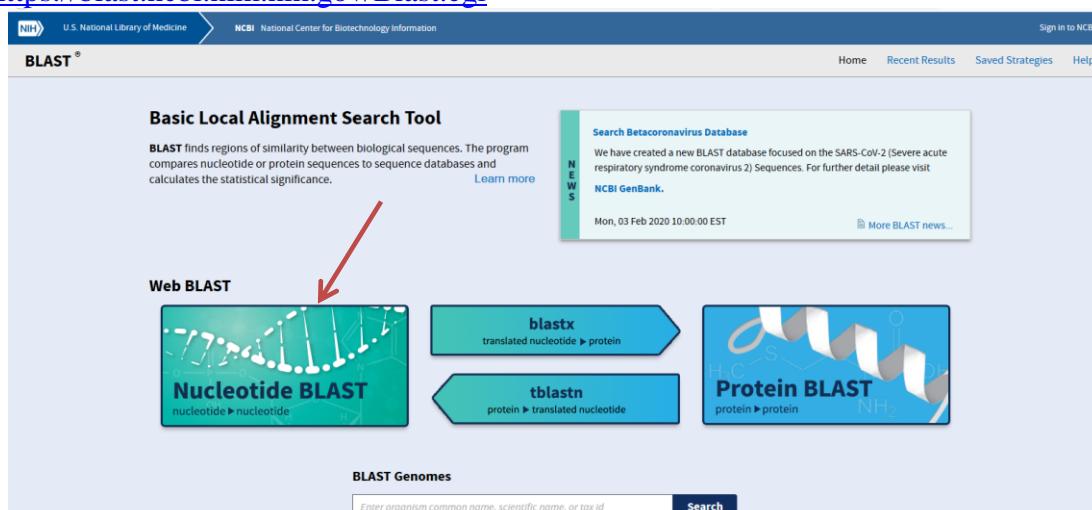
Les étapes :

Lancer une recherche de blast sur le moteur de recherche Google

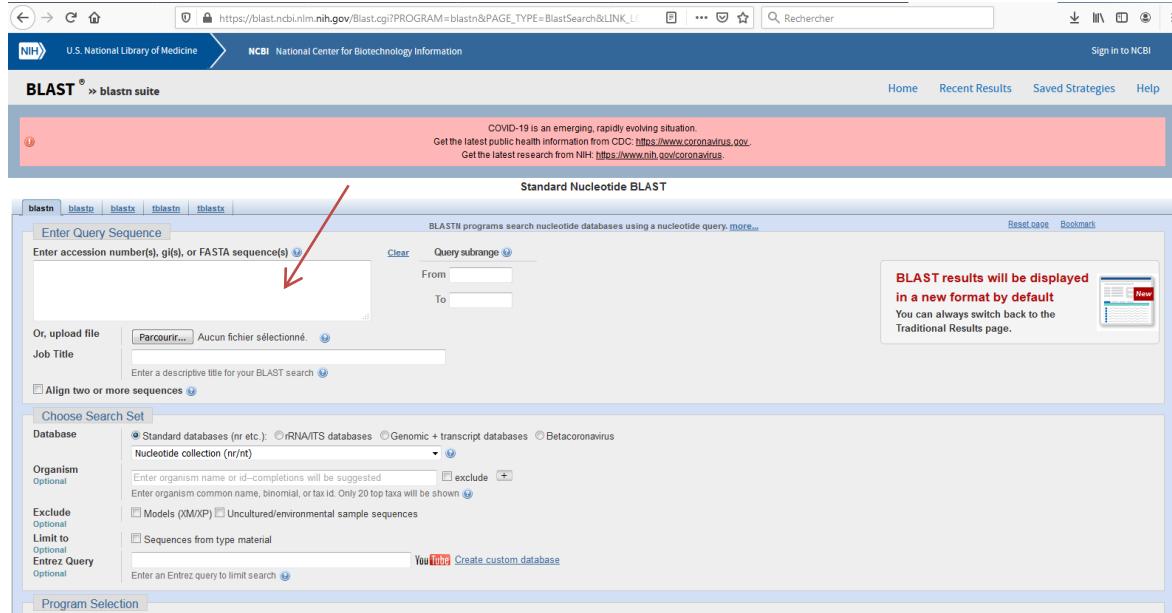


Cliquer sur le premier résultat : Blast : Basic local alignment Search Tool

<https://blast.ncbi.nlm.nih.gov/Blast.cgi>

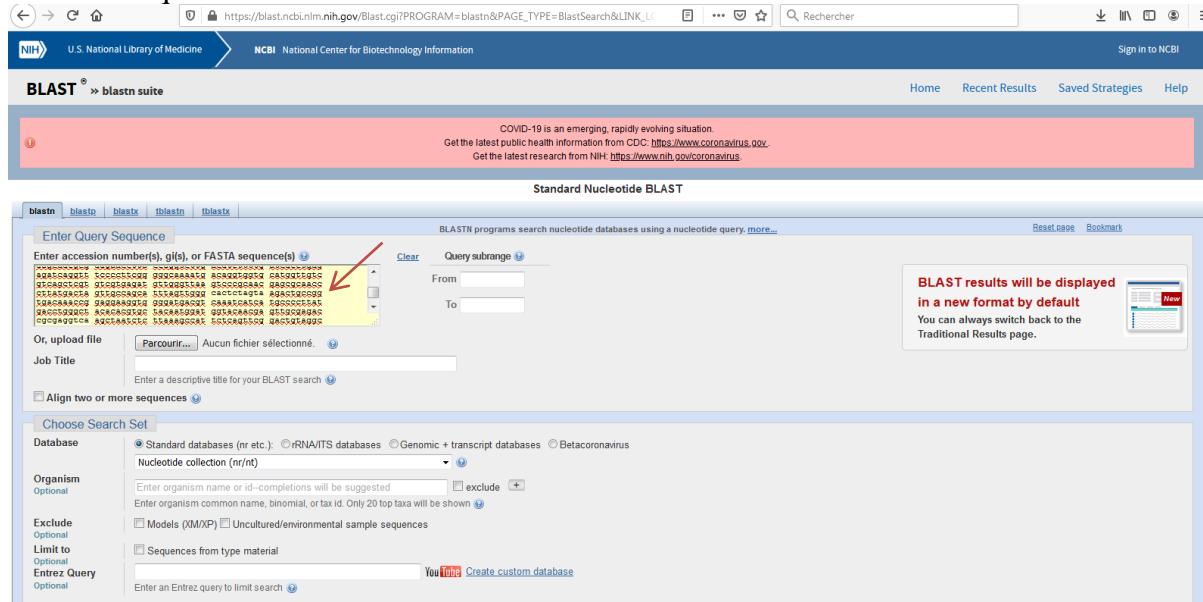


Choisir le nucleotide BLAST



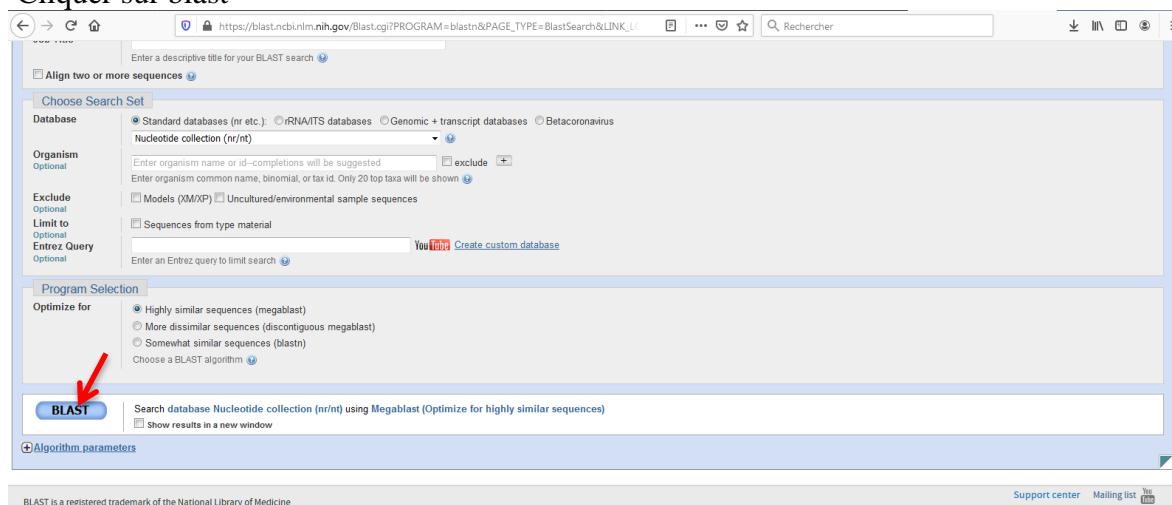
The screenshot shows the 'Standard Nucleotide BLAST' search page. At the top, there's a red banner with COVID-19 information. Below it, the 'Enter Query Sequence' field is highlighted with a red arrow. The page includes fields for accession numbers, upload files, job titles, and search parameters like databases and organism names.

Entrer la séquence dans la fenêtre



This screenshot shows the same BLAST interface as above, but with a sequence (ATGCGTACG...) pasted into the 'Enter Query Sequence' field. The sequence is highlighted with a red arrow. The rest of the interface remains consistent with the first screenshot.

Cliquer sur blast



The final screenshot shows the completed search parameters. A red arrow points to the large blue 'BLAST' button at the bottom left of the form. The page also includes a 'Program Selection' section with optimization options and a summary of the search parameters at the bottom.

Le programme blast va comparer la séquence (la séquence requête ou query) avec les séquences de la base.

Les résultats de BLAST

La page résultat est divisée en 3 parties :

- La liste des séquences avec leur score et leur E-value

The screenshot shows the NCBI BLAST results page for job ID TPWP4M50016. The search parameters are set to Nucleotide Sequence, Program BLASTN, and Database nt. The query sequence is lcl|Query_62969. The results table lists 100 significant alignments, each with a checkbox, a link to the sequence details, and columns for Max Score, Total Score, Query Cover, E value, Per. Ident., and Accession number. A red arrow points to the E value column header. The table includes a header row and 100 data rows. The page also features a navigation bar at the top and various filtering options on the left and right sides.

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident.	Accession
<input checked="" type="checkbox"/>	Lactobacillus casei strain B1 16S ribosomal RNA gene _partial sequence	1570	1570	99%	0.0	99.77%	KY764324.1
<input checked="" type="checkbox"/>	Lactobacillus casei strain BM10 16S ribosomal RNA gene _partial sequence	1561	1561	99%	0.0	99.53%	KY764329.1
<input checked="" type="checkbox"/>	Lactobacillus casei strain 2SA3 16S ribosomal RNA gene _partial sequence	1557	1557	98%	0.0	99.88%	KC967210.1
<input checked="" type="checkbox"/>	Lactobacillus fermentum strain MBO003 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MT071603.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain ES81 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MT044251.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain NS16 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MT044244.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain NS12 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MT044245.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain ABK 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN994625.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain CACC 566 chromosome _complete genome	1554	7759	98%	0.0	99.76%	CP048003.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain TD 062 chromosome _complete genome	1554	7759	98%	0.0	99.76%	CP044361.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain 1490 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN750022.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain MG5191 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN749945.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain MG5190 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN749944.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain MG5189 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN749943.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain MG5179 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN749939.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain f3 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN744424.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain f2 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN744423.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain MG5310 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN720512.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain MG5245 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN704668.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain LMT13-95 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN689621.1
<input checked="" type="checkbox"/>	uncultured bacterium partial 16S rRNA gene	1554	1554	98%	0.0	99.76%	LR650498.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain SHTR-1 16S ribosomal RNA gene _partial sequence	1554	1554	98%	0.0	99.76%	MN599715.1

Plus le score est grand, plus la qualité est bonne et plus le pourcentage d'identité est élevé

- Une vue graphique générale (Graphic summary) des séquences résultats avec différentes couleurs



- Résultat détaillé, fournissant pour chaque séquence résultat (subject), l'alignement avec la séquence requête (query).

