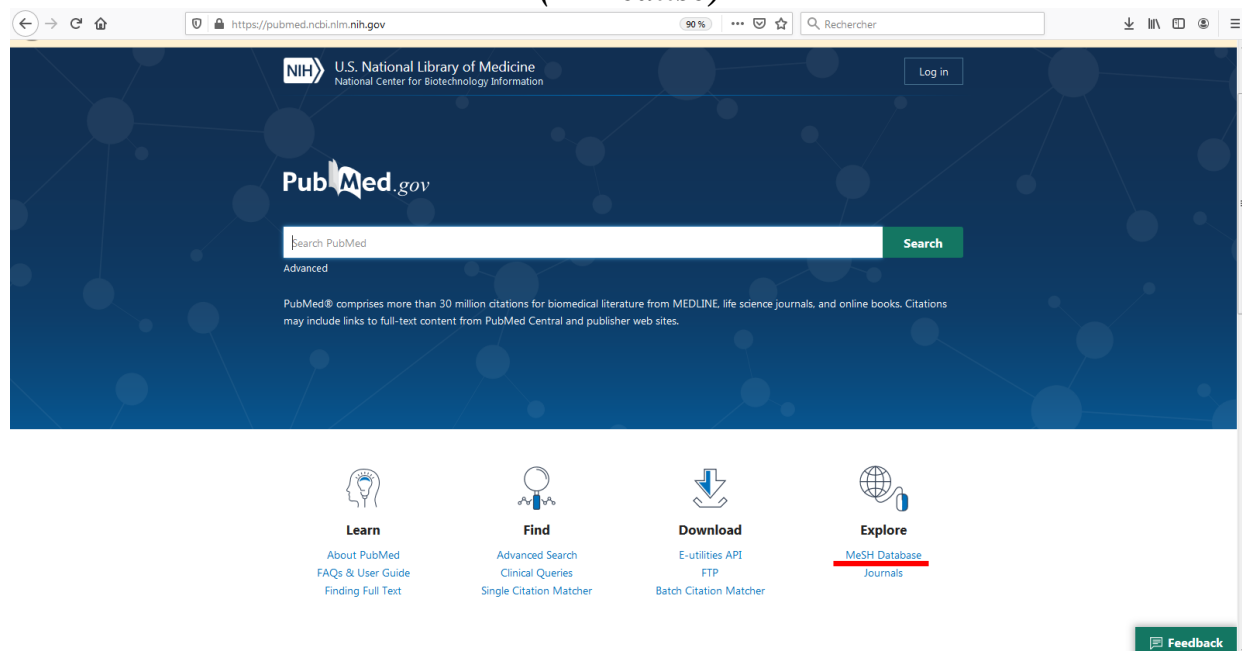


TP2 : Recherche des séquences dans les bases de données (Genbank) **(TP réalisé)**

Application :

- Trouver dans la base Genbank la séquence dont le numéro d'accèsion 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 (Alignement)

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)

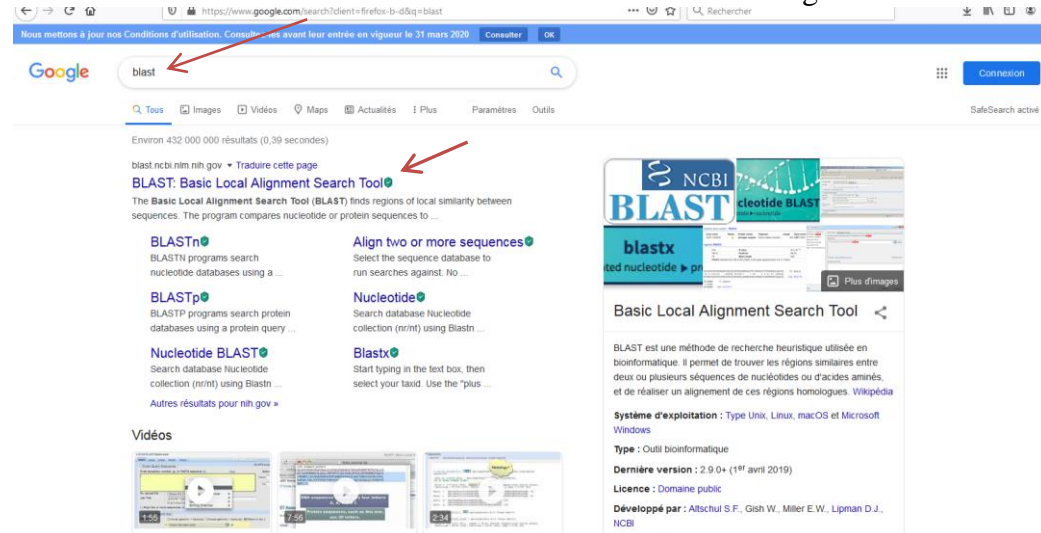
Pour comparer la séquence nucléotidique avec les séquences nucléotidiques de la base de données genbank on utilise le Blastn (Nucleotide BLAST).

Lancer une recherche BLAST pour la séquence suivante :

```
ggggggggtt   tccggattta   ttgggcgtaa   gcgagcgcag   gcggtttttt   aagtctgatg   tgaaagccct
cggcttaacc   gaggaagcgc   atcggaaact   gggaaacttg   agtgcagaag   aggacagtgg   aactccatgt
gtacggtga    aatgcgtaga   tatatggaag   aacaccagtg   gcgaaggcgg   ctgtctggtc   tgtaactgac
gctgaggtc    gaaagcatgg   gtacgaaca    ggattagata   ccctggtagt   ccattgccgt   aacgatgaat
gctaggtgtt   ggagggtttc   cgcccttcag   tgccgcagct   aacgcattaa   gcattccgcc   tggggagtac
gaccgcaagg   ttgaaactca   aaggaaattga  cggggggccc   cacaagcggg   ggagcatgtg   gtttaattcg
aagcaacgcg   aagaacctta   ccaggtcttg   acatcttttg   atcacctgag   agatcaggtt   tccccctcgg
gggcaaaatg   acaggtgggtg  catggtgtgc   gtcgtgagat   gttgggttaa   gttccgcaac   gtcccgaac
gagcgaacc    cttatgacta   gttgccagca   tttagttggg   cactctagta   agactgccgg   tgacaaaccg
gaggaaggtg   gggatgacgt   caaatcatca   tgccccttat   gacctgggct   acacacgtgc   tacaatggat
ggtacaacga   gttgcgagac   cgcgaggtca   agctaattct   ttaaagccat   tctcagttcg   gactgtaggc
tgcaactcgc   ctacacgaag   tcggaatcgc   tagtaatcgc   ggatcagcac   gcgcggtga   atacgttccc
gggccttgta   caccssca
```

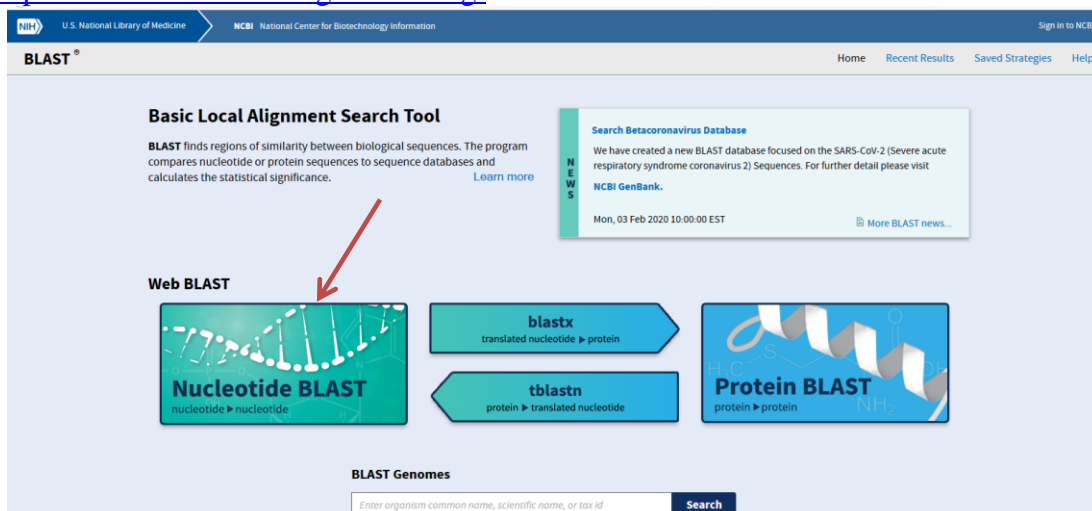
Les étapes :

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

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LC

NIH U.S. National Library of Medicine NCBI National Center for Biotechnology Information Sign in to NCBI

BLAST® » blastn suite Home Recent Results Saved Strategies Help

COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: <https://www.coronavirus.gov>.
Get the latest research from NIH: <https://www.nih.gov/coronavirus>.

Standard Nucleotide BLAST

blastn blasto blastx tblastn tblastx

BLASTn programs search nucleotide databases using a nucleotide query. [more...](#) [Reset cases](#) [Bookmark](#)

Enter Query Sequence

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

From

To

Or, upload file [Parcourir...](#) Aucun fichier sélectionné. [?](#)

Job Title

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

☐ Align two or more sequences [?](#)

Choose Search Set

Database ☒ Standard databases (nr etc.) ☐ rRNA/ITS databases ☐ Genomic + transcript databases ☐ Betacoronavirus

Nucleotide collection (nr/nt) [?](#)

Organism [Optional](#)

Enter organism name or id-completions will be suggested [?](#) ☐ exclude [?](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

☐ Sequences from type material

Entrez Query [Optional](#)

[You find](#) [Create custom database](#)

Enter an Entrez query to limit search [?](#)

Program Selection

Entrer la séquence dans la fenêtre

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LC

NIH U.S. National Library of Medicine NCBI National Center for Biotechnology Information Sign in to NCBI

BLAST® » blastn suite Home Recent Results Saved Strategies Help

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Get the latest research from NIH: <https://www.nih.gov/coronavirus>.

Standard Nucleotide BLAST

blastn blasto blastx tblastn tblastx

BLASTn programs search nucleotide databases using a nucleotide query. [more...](#) [Reset cases](#) [Bookmark](#)

Enter Query Sequence

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

From

To

Or, upload file [Parcourir...](#) Aucun fichier sélectionné. [?](#)

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Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

☐ Sequences from type material

Entrez Query [Optional](#)

[You find](#) [Create custom database](#)

Enter an Entrez query to limit search [?](#)

Program Selection

Optimize for ☒ Highly similar sequences (megablast) ☐ More dissimilar sequences (discontiguous megablast) ☐ Somewhat similar sequences (blastn) [Choose a BLAST algorithm](#)

BLAST Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences) ☐ Show results in a new window

[Algorithm parameters](#)

Cliquer sur blast

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LC

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Get the latest research from NIH: <https://www.nih.gov/coronavirus>.

Standard Nucleotide BLAST

blastn blasto blastx tblastn tblastx

BLASTn programs search nucleotide databases using a nucleotide query. [more...](#) [Reset cases](#) [Bookmark](#)

Enter Query Sequence

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

From

To

Or, upload file [Parcourir...](#) Aucun fichier sélectionné. [?](#)

Job Title

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

☐ Align two or more sequences [?](#)

Choose Search Set

Database ☒ Standard databases (nr etc.) ☐ rRNA/ITS databases ☐ Genomic + transcript databases ☐ Betacoronavirus

Nucleotide collection (nr/nt) [?](#)

Organism [Optional](#)

Enter organism name or id-completions will be suggested [?](#) ☐ exclude [?](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

☐ Sequences from type material

Entrez Query [Optional](#)

[You find](#) [Create custom database](#)

Enter an Entrez query to limit search [?](#)

Program Selection

Optimize for ☒ Highly similar sequences (megablast) ☐ More dissimilar sequences (discontiguous megablast) ☐ Somewhat similar sequences (blastn) [Choose a BLAST algorithm](#)

BLAST Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences) ☐ Show results in a new window

[Algorithm parameters](#)

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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

← → ↻ 🏠 <https://blast.ncbi.nlm.nih.gov/Blast.cgi> ... 📧 ⭐ 🔍 Rechercher

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Get the latest research from NIH: <https://www.nih.gov/coronavirus>.

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[◀ Edit Search](#) [Save Search](#) [Search Summary ▼](#)

Job Title Nucleotide Sequence
RID 7PWP4M50016 [Search expires on 03-26 23:03 pm](#) [Download All ▼](#)
Program BLASTN [Citation ▼](#)
Database nt [See details ▼](#)
Query ID lcl|Query_62969
Description None
Molecule type dna
Query Length 859
Other reports [Distance tree of results](#) [MSA viewer](#) ⓘ

Filter Results
Organism only top 20 will appear ☐ exclude
Type common name, binomial, taxid or group name
[+ Add organism](#)
Percent Identity to **E value** to **Query Coverage** to
[Filter](#) [Reset](#)

Descriptions [Graphic Summary](#) [Alignments](#) [Taxonomy](#)

Sequences producing significant alignments [Download ▼](#) [Manage Columns ▼](#) Show 100 ⓘ

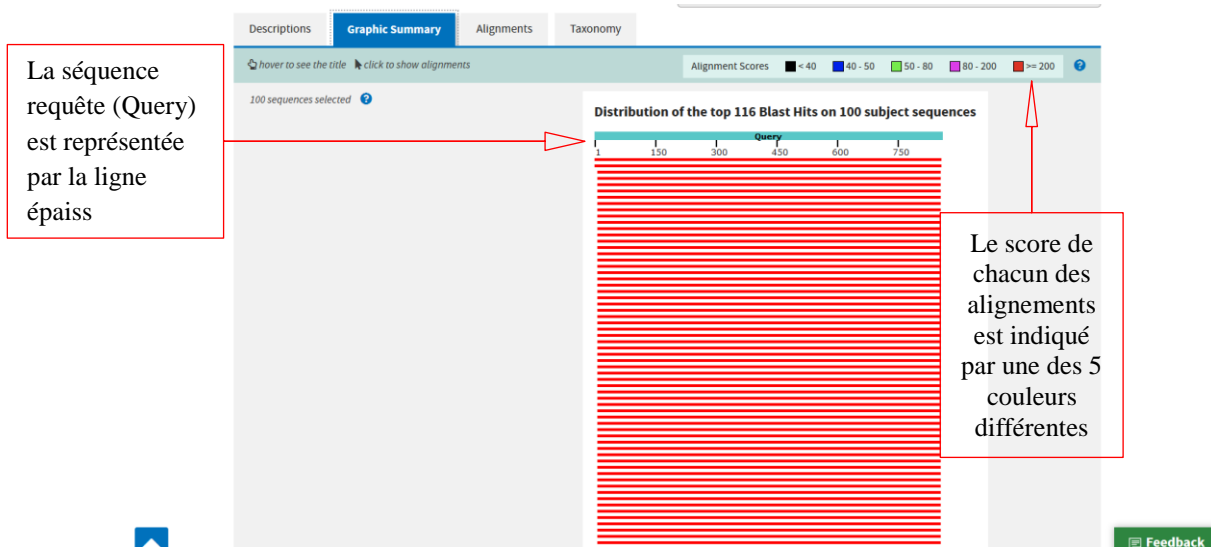
☒ select all 100 sequences selected [GenBank](#) [Graphics](#) [Distance tree of results](#)

	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 ZSA3 16S ribosomal RNA gene, partial sequence	1567	1567	98%	0.0	99.88%	KC867210.1
<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%	MT044253.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain NS16 16S ribosomal RNA gene, partial sequence	1554	1554	98%	0.0	99.76%	MT044251.1
<input checked="" type="checkbox"/>	Lactobacillus paracasei strain NS12 16S ribosomal RNA gene, partial sequence	1554	1554	98%	0.0	99.76%	MT044244.1
<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	7769	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

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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).

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

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise CDS feature Download

100 sequences selected

Download GenBank Graphics

Lactobacillus casei strain B1 16S ribosomal RNA gene, partial sequence
Sequence ID: [KY764324.1](#) Length: 860 Number of Matches: 1

Range 1: 1 to 856 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
1570 bits(850)	0.0	854/856(99%)	1/856(0%)	Plus/Plus
Query 1	g g g g g g g g g g T T T C C G G A T T T A T T G G G C G T A A G C G A G C G C A G G C G G T T T T T A A G T C T G A T G	60		
Sbjct 1	G G G G G G G G T T C C G G A T T T A T T G G G C G T A A G C G A G C G C A G G C G G T T T T A A G T C T G A T G	60		
Query 61	T G A A A G C C C T C G G C T T A A C G A G G A G C G C A T C G G A A A C T G G G A A A C T T G A G T C C A G A A G	120		
Sbjct 61	T G A A A G C C C T C G G C T T A A C G A G G A G C C A T C G G A A A C T T G A G T C C A G A A G	120		
Query 121	A G G A C A G T G G A A C T C C A T G T G T A G C G G T G A A A T G C T A G A T A T A T G G A A G A A C A C C A G T G	180		
Sbjct 121	A G G A C A G T G G A A C T C C A T G T G T A G C G G T G A A A T G C T A G A T A T A T G G A A G A A C A C C A G T G	180		
Query 181	G C G A A G G C G C T G T C T G T C T G T A A C T G A C G C T G A G G C T C G A A A G C A T G G G T A G C G A A C A	240		
Sbjct 181	G C G A A G G C G C T G T C T G T C T G T A A C T G A C G C T G A G G C T C G A A A G C A T G G G T A G C G A A C A	240		
Query 241	G G A T T A G A T A C C C T G G T A G T C C A T G C C G T A A A C G A T G A A T G C T A G T G T G G A G G G T T T C	300		
Sbjct 241	G G A T T A G A T A C C C T G G T A G T C C A T G C C G T A A A C G A T G A A T G C T A G T G T G G A G G G T T T C	300		
Query 301	C G C C C T T C A G T G C C G A G C T A A C G C A T T A A G C A T T C C G C C T G G G G A G T A C G A C C G A A G G	360		
Sbjct 301	C G C C C T T C A G T G C C G A G C T A A C G C A T T A A G C A T T C C G C C T G G G G A G T A C G A C C G A A G G	360		
Query 361	T T G A A A C T C A A A G A A T T G A C G G G G C C C G C A A G C G G T G G A G C A T G T G G T T A A T T C G	420		
Sbjct 361	T T G A A A C T C A A A G A A T T G A C G G G G C C C G C A A G C G G T G G A G C A T G T G G T T A A T T C G	420		

Feedback