Fiche technique du logiciel d'identification de l'ADN

Utiliser BLAST logiciel d'identification de séquences par comparaison avec des séquences déjà rencontrées

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

Démarche d'analyse de séquences

- Sélectionner Nucléotide BLAST

NIH	U.S. National Library of Medicine NCBI National Center for Biotechnology Information	
BL	ST [®] Home Recent F	esults
0	COVID-19 is an emerging, rapidly evolving situation. Get the latest public health information from COC <u>https://www.icounsavinus.gov</u> Get. the latest research from Vith <u>https://www.itsps.counsavinus.</u> Find NCB1SABS-Col-2 literature, sequence, and clinical content: <u>https://www.itsps.coursav</u> .	
	BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. Learn more the statistical significance. BLAST expression of the sequence databases and calculates the statistical significance. Learn more the sequence databases and calculates the statistical significance. Learn more the sequence databases and calculates the statistical significance. Learn more the sequence database and calculates the statistical significance. Learn more the sequence database and calculates the statistical significance. Learn more the sequence database and calculates the statistical significance. Learn more the sequence database and calculates the statistical significance. Learn more the sequence database and calculates the statistical significance. Learn more the sequence database and calculates the statistical significance. Learn more the sequence database and calculates the statistical significance database and calculates	
	Web BLAST Image: Distribution of the state of the st	

Coller la séquence inconnue dans la case prévue à cet effet.

Appuyer sur **« somewhat simalar sequences »** puis sur **« blast »** pour lancer la recherche / parfois un peu long

← ⇒ C fi	D blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome	으 ☆ 🛞 📒
BLAST [®] Home Recent	Easile Local Alignment Search Tool Results Swed Brainges Fielp	My NCBI W [Sign in] [Register]
NCBI/ BLAST/ blastn	suite Standard Nucleotide BLAST	
blastn blastp blas	sts folasts	
Enter Query Se	IQUENCE BLASTN programs search nuceoble databases using a nucleoble database.	age poornars
Enter accession n	umber(s), gi(s), or FASTA sequence(s) 🕖 Carry subarge 🖗 From To	
Or, upload file	Choose File No file chosen	
Job Title		
	Enter a descriptive title for your BLAST search 😡	
Align two or mo	re sequences 😡	
Choose Searc	h Set	
Database	© Human genomic + transcript ◎ Mouse genomic + transcript ® Others (nr etc.):	
Organism Optional	Nucleide collection (mm) Enter organism name or Id-completions will be sup Enter organism common name, binomial, or tax id. On/y 20 bax will be aboun that organism common name, binomial, or tax id. On/y 20 bax will be aboun	
Exclude	Models (XMXP) Unoulturedienvironmental sample sequences	
Entrez Query		
Optional	Enter an Entrez query to limit search 😡	
Program Selec	ction	
Optimize for	Highly similar sequences (megablast)	
	More dissimilar sequences (discontiguous megablast)	
_	Somewhat similar sequences (blastn)	
1	unose a source agencier 👷	
BLAST	Search database Hucleotide collection (nrint) using Blastn (Optimize for somewhat similar sequences)	
Algorithm parame	ters	

Obtention de résultats

1- Les résultats sont les noms des séquences trouvées dans la base de données qui ressemblent à notre séquence inconnue : ils sont classés du plus grand au plus petit pourcentage de similitudes.

Si 100% d'identité, on peut confirmer l'identité de l'espèce inconnue. En dessous de 85%, on ne peut rien conclure.

ne Recent Results Save	Basic Local Alignment Search Tool d Strategies Holp						M1 [22
AST/ blastn suite/ Formatting	g Results - BY8ZSKRC015		M. (11)				
and Resubmit Save Searc	ch Strategies Formatting options Download		103	How to read	this pa	ge Blast	report de
otide Sequence (1798 le	etters)						
RID BV8ZSKRCD)15 (Expires on 12-28 22:59 pm)						
Query ID Icl 24071	Database Name	nr					
Description None alecule type nucleic acid	Description	Nucleotide collection (nt) BLASTN 2.2.29t Is Citation					
uery Length 1798	r tog un	DENOTITIZIZZO P SITERIO					
	transition of the last						
her reports: Moearch Sum	mary Taxonomy reports [Distance tree of results]						
phic Summary							
criptions							
17							
1 Alignments Downloa	nd -< SearBank Couchlics Distance tree of results Description		Max	Total Query	E	Ident A	coession
Alignments Downlos Crostratus 185 rRNA get	ed + <u>GenRant</u> <u>Grantics</u> <u>Distance tree of results</u> Description		Max score 3232	Total Query score cover 3232 100%	E velue 0.0	Ident A	coession 3391.1
Alignments Downlos Crostratus 185 (RNA per Chaetoceros sp. p442 18	ed × GentRant Graphics Distance tree of results Description the State St		Max score 3232 2994	Total Query score cover 3232 100% 2994 100%	E velue 0.0	Ident Ad 100% X80 97% AJS	coession 1391.1 535187.1
Alignments Downlos Crostratus 185 (RNA per Chaetoceros sp. p442 18 Chaetoceros penuvianus (Max soore 3232 2994 2892	Total Query score cover 3232 100% 2994 100% 2892 81%	E value 0.0 0.0 0.0	Ident Ar 100% X80 97% AJ5 99% HO	coession 3391.1 535187.1 912850.1
Alignments Downlos Crostratus 185 (RNA pe Chaetoeros pp. p4/2 19) Chaetoeros peruvianus i Unoutured eukaryote per	No 2 Gentiliant Conchics Distance tree of results Description SIS RNA gens, slone p442 strain ECTSSUT-Chaptersens ISS small subunit ribosomal RNA gens, partial sequence prior SSU RNA, partial sequence, come. DS3M34		Max score 3232 2994 2892 2715	Total Query score cover 3232 100% 2994 100% 2892 91% 2715 93%	E velue 0.0 0.0 0.0 0.0	Ident A	coession 3391.1 535187.1 912850.1 275034.1
Alignments Downlos Constratus 185 (RNA pe Chaetoceros pp. p4/2 19 Chaetoceros peruviorus r Unostured extanute extanute extanute extanute extanute extanute extanute extanute extanute extan			Max score 3232 2994 2892 2715 2553	Total Query scora cover 3232 100% 2994 100% 2892 91% 2715 93% 2553 91%	E velue 0.0 0.0 0.0 0.0 0.0	Ident Ad 100% X87 97% AJE 99% HO 98% AB 94% HQ	Coession 1391.1 535187.1 1912850.1 275034.1 1912824.1
Alignments Downloa Crostatus 185 (RNA pe Chaetoceros pp. p4/2 18 Chaetoceros pp. p4/2 18 Chaetoceros penvironic i Upoytured extende per Hemisulus strain Biockmantialia brootman		5 mosomal RNA gate, partal seguence	Max score 3232 2994 2892 2715 2553 2645	Total Query scora sovar 3232 100% 2994 100% 2892 91% 2715 93% 2553 91% 2645 99%	E 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Ident Ad 100% X82 97% AJ5 99% HO 96% AB2 94% HO 92% HO	coession 3391_1 535187.1 912850.1 275034.1 912824.1 912824.3
Alignments Domitio Crostratus 155 (RNA as Chastoceros per virau: Unostrate statistica est Inostrate estancia est Inostrate estancia est Chastoceros mente istati Bockmaniala brockman Chastoceros muellei ate		S roosonal RNA gara, partal asguanga	Max score 3232 2994 2892 2715 2553 2645 2545	Total Query scora covar 3232 100% 2994 100% 2892 91% 2715 93% 2553 51% 2545 99%	E volue 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Ident Ad 100% X80 97% AJ5 99% HO 98% AB5 94% HO 92% HO 92% AP0	coession 1391.1 1355187.1 1912850.7 1912824.1 1912855.1 1912565.1 19125656.1
Alignments Donation Constants 155 (RNA are Creations as p4/2) Chastoners pervirans : Undiffued extravite set Herisalus cherois stain Kodomannials intoximm Chastocers ambelia stat Chastocers activitians :		5 mosomal RNA gate, partial seguence	Max soore 3232 2994 2892 2715 2553 2645 2645 2645 2645	Total Query scora oover 3232 100% 2994 100% 2892 91% 2715 93% 2553 91% 2645 99% 2538 60%	E volue 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Ident Ar 100% X82 97% AJ 99% HO 98% AB 94% HO 92% HO 92% DO	Coession 1391.1 135167.1 1912650.1 1912624.1 1912624.1 1912655.1 1912565.1 1912565.1
Alignments Domnlo Crostratus 155 (RNA ap Chastocers an P42 18 Chastocers an P42 18 Chastocers and reaction Recimanial process Chastocers and the control		S ribosomal FINA gene, partai seguence gene, partai seguence	Max soore 2232 2994 2892 2715 2555 2645 2645 2648 2638	Total Query score cover 3232 100% 2994 100% 2892 91% 2715 93% 2553 91% 2555 91% 2545 99% 2545 99%	E value 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Ident Ar 100% XIC 97% Ar 99% HO 98% AR 94% HO 92% HO	 coession 3391.1 535187.1 912850.1 912824.1 912824.3 912825.1 925856.1 825856.1 825856.1 82758.5 8758.95.1
Alignments Download Grosstatus 155 (RNA av Chaesocars pr. pr42 19 Chaesocars privanse. Unoutured existivate cer Herinkus precisi prani Stackores anneliei stat Chaesocars antelinist	Gentilant, Crachics Distance tree of results Description de Gentilant, Crachics Distance tree of results Description de Gentilant, Crachics Distance tree of results Description de Gentilant, Crachics Distance tree Description de Gentilant, Crachics Distance description	S ribosomal HNA gene, partal sequence gene, partal sequence	Mex score 3232 2994 2892 2715 2553 2645 2535 2545 2538 2638 2638 2638	Total Query scora bover 3232 100% 2994 100% 2892 81% 2715 53% 2645 9% 2645 9% 2648 9% 2648 8% 2638 8% 2638 8%	E volue 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	Ident Ar 100% XXX 97% ArX 97% HO 98% HO 92% HO	ccession 3391_1 535187.1 912850.1 912850.1 912855.1 912565.1 925696.1 925696.1 925696.1 925695.1 925695.1 925695.1 91223.1
Alignments Donnto Constants 155 (RNA an Chastocero ap. pr42 15 Chastocero ap. pr42 1 Chastoceros pervurans. Unottuned extancte cer Herisikus atensis statin Beckimanista brockman Chastoceros caloitans at Chastoceros presiti stati Biddubis tideas looke: Attava begoenis statin		S ribosomal RNA gara, partai seguance gara, partai seguance	Mex score 3232 2994 2715 2553 2645 2638 2638 2638 2638 2639 2639 2632	Total Query scora sover 3232 100% 2994 100% 2892 81% 2715 53% 2645 99% 2645 99% 2645 99% 2645 98% 2628 89% 2629 88% 2629 98% 2620 98% 2622 99%	E velue 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	Ident Ar 100% XZ 97% Ar 99% HO 98% HO 92% HO 92% HO 92% HO 92% Ar 92% Ar 92% JXH 91% Ar	 coession 3391_1 535187.1 912850.1 912824.1 912824.1 912824.1 912824.1 912824.1 912824.1 912824.1 912825.3 625896.1 827758.5 82758.5 101228.1 485450.1
Alignments Download Crossistis 185 (RNA ar Crossistis 195 (RNA ar Crossis 195 (RNA ar Crossis 195 (RNA ar Crossistis 195 (RNA ar		5 ribosomal RNA gara, partal saguance gana, partal sequance	Max 2007a 2094 2892 27115 2553 2646 2645 2645 2645 2645 2645 2645 2645	Total Query scors sover 3232 100% 2094 100% 2892 81% 2553 51% 2645 99% 2638 90% 2639 83% 2638 99% 2632 99% 2632 99% 2612 99% 2618 99%	E 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Ident Ar 100% XZ 97% Ar 99% HO 98% HO 92% HO 92% HO 92% HO 92% Ar 92% Ar 92% JXH 91% Ar 91% JXH	 coession 3391.1 535187.1 912850.1 912854.1 912824.1 912824.1 912825.9 925896.1 82758.1 82758.1 82758.1 91228.1 485450.1 91220.1 91230.1
Alignments IS/RA4 as Constatus IS/RA4 as Chastocera pay-ratus Chastocera pay-ratus Unoutland existynte eer Heriukus sinesi brostvan Chastocera calkinas zi Chastocera calkinas zi Chastocera partielli sita Atheya bogcontis stran Mindusellis paskanotis stran		S ribosomal FNA gere, partal sequence	Max soars 3232 2994 2892 2715 2553 2645 2533 2645 2538 2638 2638 2638 2638 2638 2638 2638 26	Total Query scors sover 3232 100% 2934 100% 2892 81% 2553 51% 2545 99% 2545 99% 2638 69% 2639 69% 2632 88% 2618 89% 2618 89%	E 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Ident All 100% XZ 97% All 98% HQ 98% HQ 94% HQ 92% HQ 92% HQ 92% HQ 92% HQ 92% HQ 91% AY 91% AY 92% HQ	 coession 3391.1 535187.1 912850.1 912854.1 912824.1 912825.1 925896.1 925896.1
Alignments Donnto Alignments Donnto Constances 155 (RNA) as Chaetocores pervurance. Unsutured extanyote set Heriniulus shores around Bodynaminal branchara s Chaetocores celevitare s Chaetocores medieni s Chaetocores medieni s	Sectional Control is Control in the control in	S ribosomal FNA gana, partal aeguance gana, partal sequence ng, partal sequence	Max 2007 3232 2994 2992 2715 2695 2645 2645 2645 2645 2658 2658 2658 2658 2658 2658 2658 265	Total Query zoora govar 3232 100% 2894 100% 2894 100% 2892 81% 2715 93% 2655 51% 2645 9% 2638 9% 2638 9% 2632 9% 2638 9% 2638 9% 2639 9% 2638 9% 2638 9% 2638 9% 2638 9% 2638 9% 2638 9% 2638 9% 2638 9% 2638 9% 2638 9% 2618 8% 2618 8% 2618 2618	E value 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	Ident Ar 100% XE 97% Ar 98% Ar 98% Ar 92% Ar 92% Ar 92% Ar 92% Ar 91% Ar 91% Ar 91% Ar 91% Ar 92% Ar	 coession 3391.1 3391.2 3391.2 50.34.1 912824.1 912824.2 827563.2 8287756.2 8287756.2 8287756.2 82876756.2 82876756.2 82876756.2 8287756.2 8287756.2 82876756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 8287756.2 <
Alignments Donnto Alignments Donnto Constitutes 155://RNA are Chastoceros per urans; Unolfused extension per urans; Chastoceros per		S mosomal FNA gee, partal seguence pre, partal seguence	Misx score 3232 2094 2892 2715 2553 2645 2555 2656 2656 2656 2656 2656 2622 2638 2622 2638 2622 2638 2653 2655 2655 2655 2655 2655 2656 2656	Total Query zoora oover 3232 100% 2994 100% 2892 81% 2715 93% 2645 99% 2645 59% 2645 59% 2628 80% 2628 96% 2629 88% 2628 99% 2618 59% 2618 66% 2611 67%	E value value 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	Ident Ar 100% X2 97% Ar 99% HO 98% HO 92% HO 92% HO 92% AY 92% AY 92% AY 92% AY 91% AY 91% AY 92% LX 92% LX 92% LX 92% LX	00000000000000000000000000000000000000

2- Cliquer sur **Accession** au bout de la ligne correspondant à l'espèce trouvée Vous trouverez ainsi son nom et sa classification

3- Aller sur le site suivant et regarder la vidéo descriptive de certains spécimens http://planktonchronicles.org/fr/episodes/

ou

Chercher sur un moteur de recherche le milieu de vie / taxonomie de l'espèce trouvée