

## Résultat pour Séquence inconnue 1

### Notre résultat

RESULTS	
Seed used	: 1111111111
Pattern match	: AGCGGGGTAGAGGAATTGGTTTACTCATCAGGCTCATGACCTGAAGACTGCAGGTTCTGAATCCTGTCCCCGCC
Sequence match	: AGCGGGGTAGAGGAATTGGTCGACTCATCAGGCTCATGACCTGAAGACTGCAGGTTCTGAATCCTGTCCCCGCC
ID	: >M cat Carica_papaya
Fusion score	: 347
Bit score	: 503
E value	: 8.87221492294373e-146
Q2.2 AA	(deduced) : GGDRIRTCQLQVMSLSRPIPLR...
Q2.2 Anticodon	(deduced) : GGC GGG GAC AGG AUUC GAAC CUG AGU CUU CAG GUC AUG AGU C GAC CAU UCC UCU ACC CCG CU

### BLAST (nucléotides) :

Descriptions		Graphic Summary		Alignments		Taxonomy				
Sequences producing significant alignments						Download	Select columns	Show	100	?
<input checked="" type="checkbox"/> select all 100 sequences selected						GenBank	Graphics	Distance tree of results	MSA Viewer	
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	
<input checked="" type="checkbox"/>	<a href="#">Malus asiatica isolate hh mitochondrion, complete genome</a>	<a href="#">Malus asia...</a>	137	137	100%	1e-28	100.00%	374023	<a href="#">PP493238.1</a>	
<input checked="" type="checkbox"/>	<a href="#">Pyrus betulifolia mitochondrion, complete genome</a>	<a href="#">Pyrus betu...</a>	137	137	100%	1e-28	100.00%	432493	<a href="#">ON478165.1</a>	
<input checked="" type="checkbox"/>	<a href="#">Sorbus aucuparia mitochondrion, complete genome</a>	<a href="#">Sorbus au...</a>	137	275	100%	1e-28	100.00%	384977	<a href="#">NC_052880.1</a>	
<input checked="" type="checkbox"/>	<a href="#">Malus halliana isolate cs1 mitochondrion, complete genome</a>	<a href="#">Malus halli...</a>	137	137	100%	1e-28	100.00%	181618	<a href="#">PP498824.1</a>	
<input checked="" type="checkbox"/>	<a href="#">Malus niedzwetzkyana mitochondrion, complete genome</a>	<a href="#">Malus nie...</a>	137	275	100%	1e-28	100.00%	385872	<a href="#">PQ165102.1</a>	
<input checked="" type="checkbox"/>	<a href="#">Malus x robusta isolate bl mitochondrion, complete genome</a>	<a href="#">Malus x ro...</a>	137	137	100%	1e-28	100.00%	374023	<a href="#">PP493236.1</a>	
<input checked="" type="checkbox"/>	<a href="#">Malus domestica genome assembly, organelle: mitochondrion</a>	<a href="#">Malus do...</a>	137	413	100%	1e-28	100.00%	400843	<a href="#">OX352770.1</a>	

En filtrant par organisme, on n'obtient pas de match significatif pour Carica papaya. On retrouve cependant le genre Malus qui correspond à notre séquence inconnue.

## Séquence inconnue 2 :

Avec les critères de filtre par défaut, on n'obtient pas de match dans notre database. Si on utilise un seed plus flexible, on peut possiblement obtenir quelque chose:

RESULTS	
Seed used	: 11100000111
Pattern match	: ACATCCTTAGCTCAGTAGGATAGAGCAACAGCCTTCTAAGCTGGTGGTCACAGGTTCAAATCCTGTAGGATGT
Sequence match	: ACATTCTTAGCTCAGTTGGATAGAGCAACGGCCTTCTAAGCTGTAGGTCACAGGTTCAAATCCTGTAGAATGT
ID	: >R tct Mesostigma_viride
Fusion score	: 311
Bit score	: 451
E value	: 3.995690382092034e-130
Q2.2 AA (deduced)	: TFYRI*TCDLQLRRPLLYPTELRM...
Q2.2 Codon (deduced)	: ACAUUCUACAGGAUUUGAACCUUGACCUACAGCUUAGAAGGCCGUUGCUCUAUCCAACUGAGCUAAGAAGU

BLAST (nucléotides) :

Sequences producing significant alignments										Download	Select columns	Show	100	?
<input checked="" type="checkbox"/> select all	30 sequences selected									GenBank	Graphics	Distance tree of results	MSA Viewer	
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession					
<input checked="" type="checkbox"/>	<a href="#">Nephroselmis olivacea mitochondrion, complete genome</a>	<a href="#">Nephrosel...</a>	135	135	100%	4e-28	100.00%	45223	<a href="#">NC_008239.1</a>					
<input checked="" type="checkbox"/>	<a href="#">Candidatus Stammera capleta isolate BHILEGBA chromosome</a>	<a href="#">Candidatu...</a>	106	106	86%	3e-19	96.83%	274464	<a href="#">CP144850.1</a>					
<input checked="" type="checkbox"/>	<a href="#">Candidatus Stammera capleta isolate ECOKPGPJ chromosome</a>	<a href="#">Candidatu...</a>	106	106	86%	3e-19	96.83%	250393	<a href="#">CP144810.1</a>					
<input checked="" type="checkbox"/>	<a href="#">Candidatus Stammera capleta isolate 1 chromosome, complete genome</a>	<a href="#">Candidatu...</a>	106	106	86%	3e-19	96.83%	260485	<a href="#">CP043975.1</a>					
<input checked="" type="checkbox"/>	<a href="#">Candidatus Stammera capleta isolate KMIDBMKN chromosome</a>	<a href="#">Candidatu...</a>	100	100	86%	1e-17	95.24%	274655	<a href="#">CP144822.1</a>					
<input checked="" type="checkbox"/>	<a href="#">Candidatus Stammera capleta isolate EPMLGANN chromosome</a>	<a href="#">Candidatu...</a>	100	100	86%	1e-17	95.24%	274554	<a href="#">CP144819.1</a>					
<input checked="" type="checkbox"/>	<a href="#">Marchantia polymorpha subsp. ruderalis Tak-1 mitochondrial DNA, co...</a>	<a href="#">Marchanti...</a>	99.0	99.0	97%	5e-17	91.55%	186197	<a href="#">AP025456.1</a>					
<input checked="" type="checkbox"/>	<a href="#">Riccia fluitans isolate RF2 mitochondrion, complete genome</a>	<a href="#">Riccia fluit...</a>	99.0	99.0	97%	5e-17	91.55%	185615	<a href="#">OR220799.1</a>					

Cependant, pas de résultat correspondant avec notre recherche. La recherche avec filtre Mesostigma viride ne donne pas de résultat pertinent. On retrouve cependant Nephroselmis Olivacea en premier résultat de BLAST, ce qui correspond à notre séquence inconnue.

Séquence inconnue 3:

Aussi une séquence qui ne retourne pas de match avec les critères par défaut.

En allégeant le minimum e value, on obtient :

```
RESULTS
Seed used      : 1110000111
Pattern match  : CGCGGAGTAGAGCAGTTTG
Sequence match : CGCAAAAAGAATTGTTT
ID             : >G|gcc|Chlorokybus_atmophyticus
Fusion score   : 23
Bit score      : 36
E value        : 3.380959969945252e-05
Q2.2 AA       (deduced) : KTILFC...
Q2.2 Codon     (deduced) : AAAACAAUUCUUUUUGCG
```

Match de mauvaise qualité avec un mauvais score.

BLAST (nucléotides) :

Descriptions	Graphic Summary	Alignments	Taxonomy						
Sequences producing significant alignments									
Download									
Select columns									
Show 100									
?									
<input checked="" type="checkbox"/> select all 100 sequences selected									
<a href="#">GenBank</a> <a href="#">Graphics</a> <a href="#">Distance tree of results</a> <a href="#">MSA View</a>									
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	<a href="#">Phoenix dactylifera cultivar Khanezi isolate K2 mitochondrion, complet...</a>	<a href="#">Phoenix d...</a>	137	190	100%	1e-28	100.00%	715120	<a href="#">MH176159.1</a>
<input checked="" type="checkbox"/>	<a href="#">Phoenix dactylifera mitochondrion, complete genome</a>	<a href="#">Phoenix d...</a>	137	137	100%	1e-28	100.00%	715001	<a href="#">NC_016740.1</a>
<input checked="" type="checkbox"/>	<a href="#">Phoenix dactylifera cultivar Naghal mitochondrion, complete genome</a>	<a href="#">Phoenix d...</a>	137	190	100%	1e-28	100.00%	715094	<a href="#">MH176158.1</a>
<input checked="" type="checkbox"/>	<a href="#">Coelogyne viscosa chloroplast, complete genome</a>	<a href="#">Coelogyne...</a>	124	177	100%	9e-25	98.59%	160081	<a href="#">OR687507.1</a>
<input checked="" type="checkbox"/>	<a href="#">Curcuma longa chloroplast, complete genome</a>	<a href="#">Curcuma l...</a>	124	177	100%	9e-25	98.59%	162180	<a href="#">MK109020.1</a>
<input checked="" type="checkbox"/>	<a href="#">Dendrobium capillipes chloroplast, complete genome</a>	<a href="#">Dendrobiu...</a>	124	177	100%	9e-25	98.59%	159400	<a href="#">NC_072707.1</a>
<input checked="" type="checkbox"/>	<a href="#">Ochagavia elegans isolate S79 plastid, complete genome</a>	<a href="#">Ochagavia...</a>	124	177	100%	9e-25	98.59%	158163	<a href="#">NC_045385.1</a>
<input checked="" type="checkbox"/>	<a href="#">Calla palustris chloroplast, complete genome</a>	<a href="#">Calla palus...</a>	124	177	100%	9e-25	98.59%	162794	<a href="#">MN046887.1</a>
<input checked="" type="checkbox"/>	<a href="#">Yucca brevifolia x Yucca jaegeriana chloroplast, complete genome</a>	<a href="#">Yucca brev...</a>	124	177	100%	9e-25	98.59%	157953	<a href="#">MW281814.1</a>
<input checked="" type="checkbox"/>	<a href="#">Hechtia confusa isolate IR2189 voucher CICY:Ramirez 2189 chloropla...</a>	<a href="#">Hechtia co...</a>	124	177	100%	9e-25	98.59%	157118	<a href="#">NC_080292.1</a>
<input checked="" type="checkbox"/>	<a href="#">Calamus henryanus voucher N_XT068 (IBSC) chloroplast, complete g...</a>	<a href="#">Calamus h...</a>	124	124	95%	9e-25	98.59%	157536	<a href="#">NC_079715.1</a>
<input checked="" type="checkbox"/>	<a href="#">Gymnadenia crassinervis chloroplast, complete genome</a>	<a href="#">Gymnaden...</a>	124	177	100%	9e-25	98.59%	154124	<a href="#">MW322684.1</a>
<input checked="" type="checkbox"/>	<a href="#">Chiloschista yunnanensis voucher KUN1513873 chloroplast, complete...</a>	<a href="#">Chiloschist...</a>	124	124	95%	9e-25	98.59%	143431	<a href="#">MZ681474.1</a>
<input checked="" type="checkbox"/>	<a href="#">Hosta jonesii isolate NamHae chloroplast, complete genome</a>	<a href="#">Hosta jonesii</a>	124	177	100%	9e-25	98.59%	156724	<a href="#">MZ919311.1</a>
<input checked="" type="checkbox"/>	<a href="#">Allium rude strain CMS-S chloroplast, complete genome</a>	<a href="#">Allium rude</a>	124	177	100%	9e-25	98.59%	153697	<a href="#">NC_042158.1</a>
<input checked="" type="checkbox"/>	<a href="#">Musa mannii chloroplast, complete genome</a>	<a href="#">Musa mannii</a>	124	177	100%	9e-25	98.59%	170636	<a href="#">OK012348.1</a>

Correspond aux informations de la séquence inconnue (Phoenix dactylifera), mais pas à notre recherche.

Résultat pour Séquence inconnue 4:

Notre résultat :

RESULTS	
Seed used	: 11111111111
Pattern match	: GCATTCTTAGCTCAGCTGGATAGAGCAACAACCTTCTAAGTTGAAGGTCACAGGTTCAAATCCTGTAGGATGC
Sequence match	: GCATTCTTAGCTCAGTTGGATAGAGCAACAACCTTCTAAGTTGAAGGTCACAGGTTCAAATCCTGTAGATGC
ID	: >R tct Marchantia_polymorpha
Fusion score	: 347
Bit score	: 503
E value	: 8.87221492294373e-146
Q2.2 AA	(deduced) : AFYRI*TCDLQLRRLLLYPTELRM...
Q2.2 Anticodon	(deduced) : GCAUUCUACAGGAUUUGAACCUUGACCUUACAACUUGAAGGUUGUCUCUAUCCAACUGAGCUAAGAAUGC

BLAST (nucléotides) :

Descriptions	Graphic Summary	Alignments	Taxonomy					
Sequences producing significant alignments								
Download								
Select columns								
Show 100								
select all 100 sequences selected								
GenBank								
Graphics								
Distance tree of results								
MSA Viewer								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> <a href="#">Nitella hyalina mitochondrion, complete genome</a>	<a href="#">Nitella hyal...</a>	137	137	100%	1e-28	100.00%	80193	<a href="#">NC_017598.1</a>
<input checked="" type="checkbox"/> <a href="#">Nitellopsis obtusa isolate KGK5729 mitochondrion, complete genome</a>	<a href="#">Nitellopsis ...</a>	137	137	100%	1e-28	100.00%	60236	<a href="#">MW556320.1</a>
<input checked="" type="checkbox"/> <a href="#">Chara braunii S276 mitochondrial DNA, complete sequence</a>	<a href="#">Chara bra...</a>	137	137	100%	1e-28	100.00%	67059	<a href="#">AP018556.1</a>
<input checked="" type="checkbox"/> <a href="#">Chara vulgaris mitochondrion, complete genome</a>	<a href="#">Chara vulg...</a>	137	137	100%	1e-28	100.00%	67738	<a href="#">ON406421.1</a>
<input checked="" type="checkbox"/> <a href="#">Chara vulgaris mitochondrion, complete genome</a>	<a href="#">Chara vulg...</a>	137	137	100%	1e-28	100.00%	67737	<a href="#">NC_005255.1</a>
<input checked="" type="checkbox"/> <a href="#">Racomitrium ericoides mitochondrion, complete genome</a>	<a href="#">Niphotrich...</a>	132	132	100%	5e-27	98.65%	106727	<a href="#">NC_026540.1</a>

Pour la séquence inconnue 4, si on filtre par espèce:

Descriptions	Graphic Summary	Alignments	Taxonomy					
Sequences producing significant alignments								
Download		Select columns	Show 100					
<input checked="" type="checkbox"/> select all 3 sequences selected								
<a href="#">GenBank</a> <a href="#">Graphics</a> <a href="#">Distance tree of results</a> <a href="#">MSA Viewer</a>								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> <a href="#">Marchantia polymorpha subsp. ruderalis Tak-1 mitochondrial DNA, com...</a>	<a href="#">Marchantia...</a>	124	244	98%	5e-30	97.26%	186197	<a href="#">AP025456.1</a>
<input checked="" type="checkbox"/> <a href="#">Marchantia polymorpha subsp. ruderalis strain KBDI00084 mitochondrio...</a>	<a href="#">Marchantia...</a>	124	244	98%	5e-30	97.26%	186196	<a href="#">MK202951.1</a>
<input checked="" type="checkbox"/> <a href="#">Marchantia polymorpha subsp. ruderalis mitochondrial DNA, complete g...</a>	<a href="#">Marchantia...</a>	124	244	98%	5e-30	97.26%	186196	<a href="#">NC_037508.1</a>

Ce qui semble donner un match raisonnable avec notre recherche. Ne correspond cependant pas aux informations de la séquence inconnue (Chara Vulgaris)