Du bateau au laboratoire :
Le plancton, source de biodiversité

Qu'est ce que le plancton ?
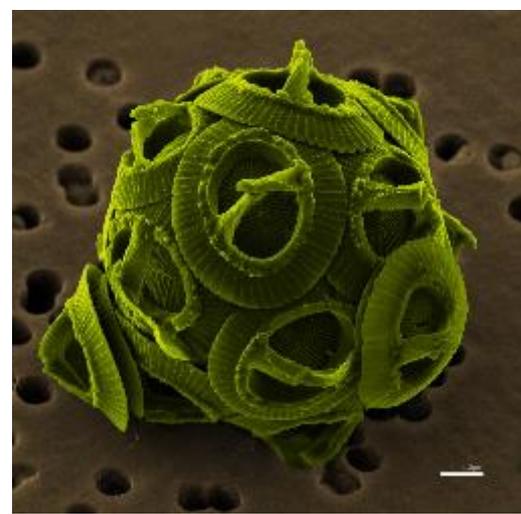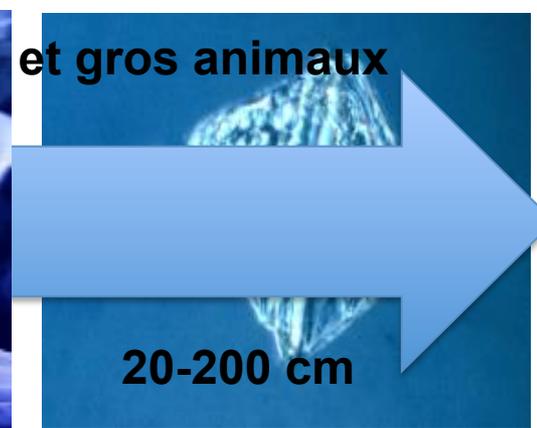
Coccolithophores
(5 à 35µ)

Méduses
(jusqu'à 200cm)

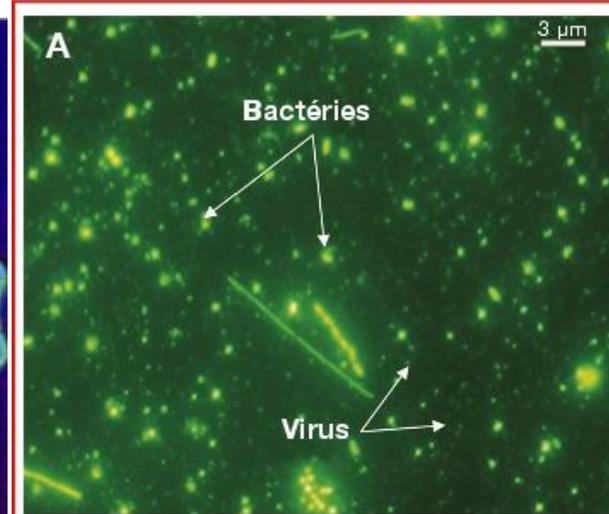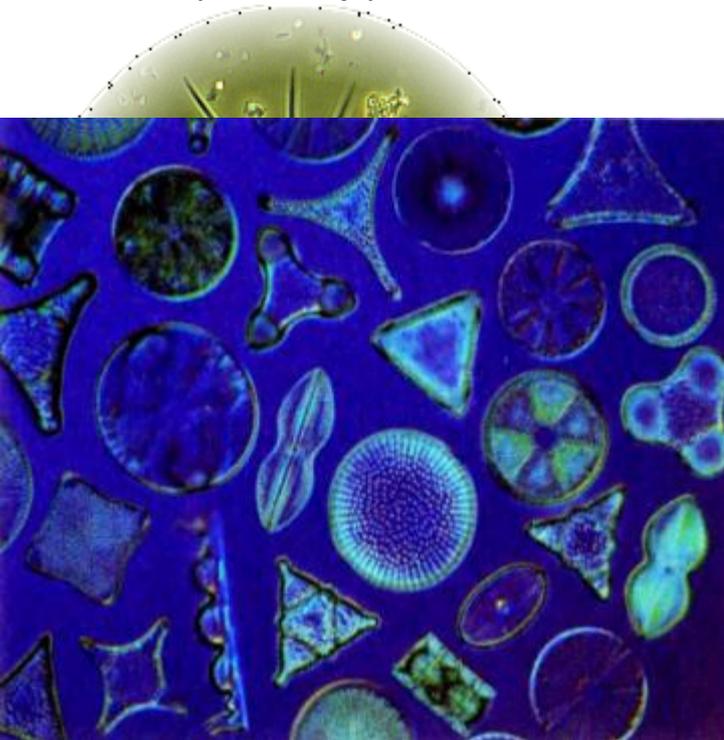et gros animaux

20-200 cm

Larve de mollusque
(60µ)

30% du plancton actuel ...onnu.
...es analyses ...permettent-
...valuer la ...ersité ?

Virus (≤0,2µ)
Bactéries (0,2 à 2µ)

Radiolaires
(50 à 300 µ)

Bactéries

Virus

Plancton et biodiversité

Recueil du plancton
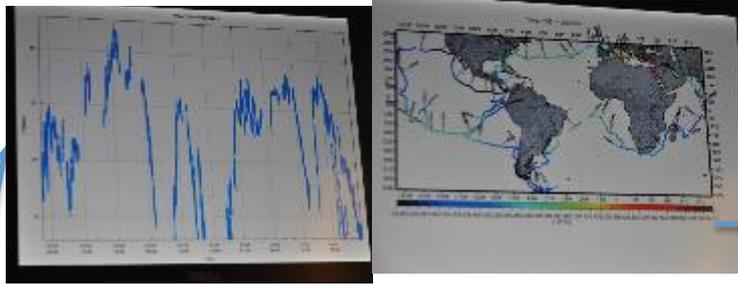
Enregistrement de diverses conditions

Analyse aux laboratoires de :
-**Roscoff**
- **Villefranche**
- **Paris VI**

Chaque échantillon de 50 ml génère environ 10 000 images, soit autant d'organismes à identifier.

FLOW CAM

Filtres différents

conservation

Analyses génétiques
- **Roscoff**
- **GENOSCOPE**
- **Barcelone**
- **Arizona,**
- **….**

1ʳᵉ étape : réalisation d'une électrophorèse en TP
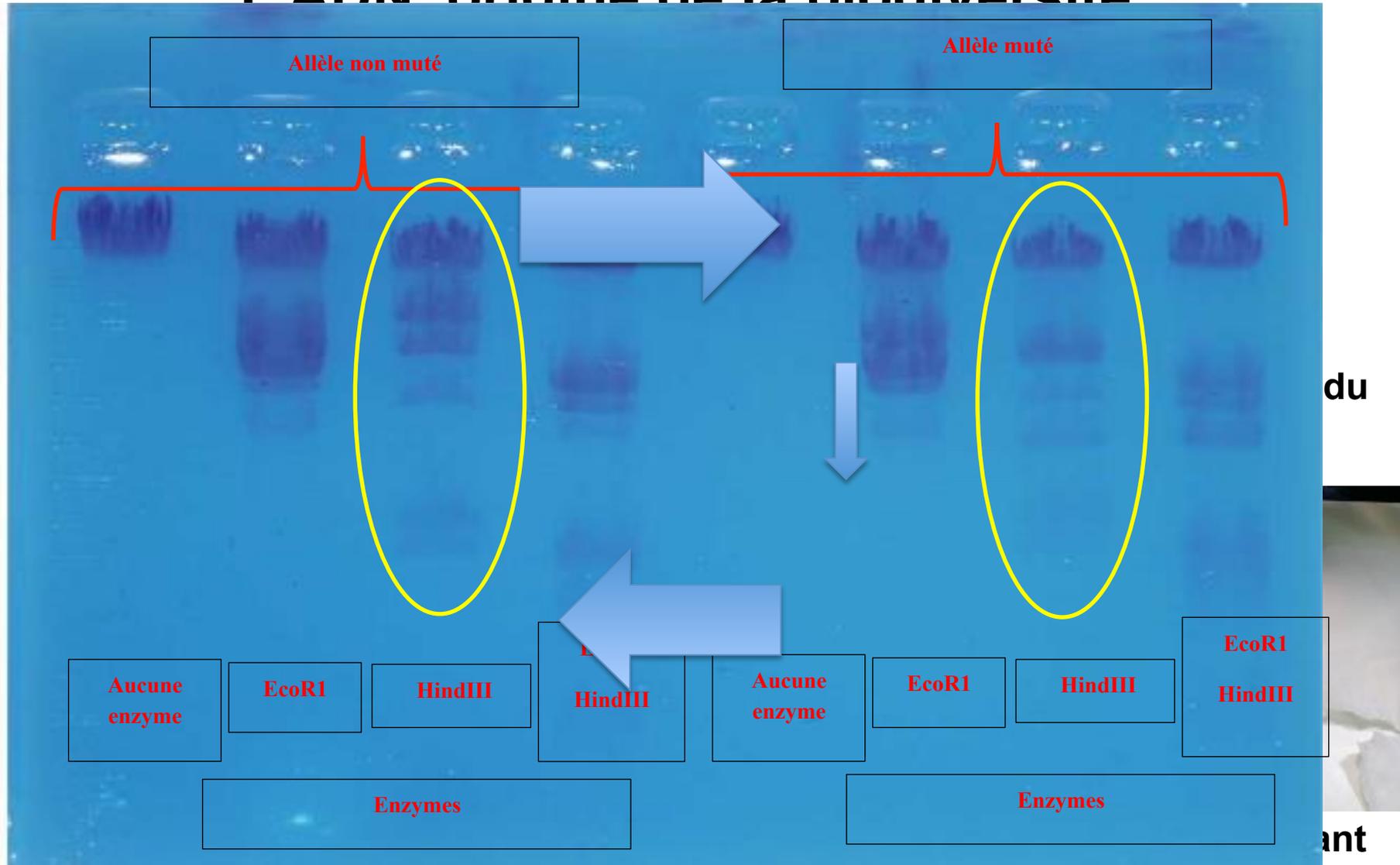
Nos résultats

Deux enzymes de restriction.

GCCGGTGAGAATTCGGCCTTTC...
CGGCCACTCTTAAGCCGGAAAG...

TTAAAAAAGTCGTTTCTGCAAGCTTGGCTGTATAGTCAACTAACTCTTCTGTCGA...
AATTTTTTCAGCAAAGACGTTCGAACCGACATATCAGTTGATTGAGAAGACAGCT...

...CTGCAAGCTTGGCTGT...
...GACGTTCGAACCGACA...

1220   1230
3055 3060 3050 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200 3210
3130   31

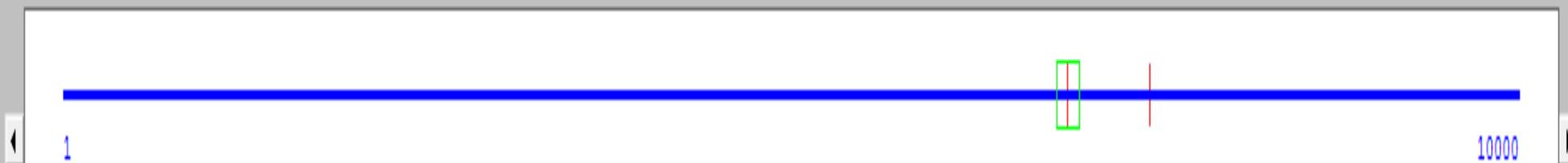**Site EcoRI**   **Site HIND III**

Sens migration

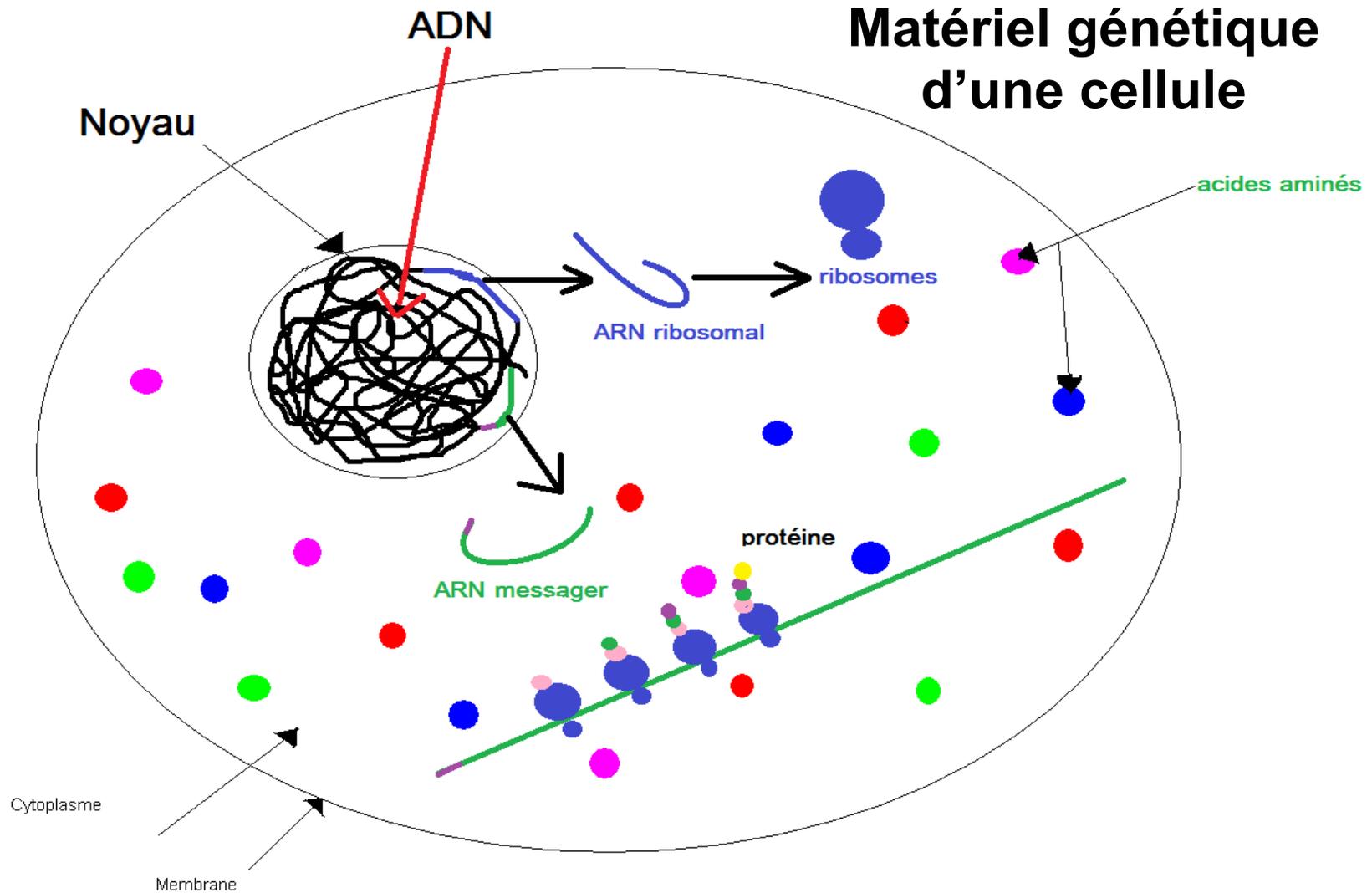1   10000

GCCTTCAACAAACAAAAAGATGGGAATCCCAATGATTCGTCATCTGCGAGGCTGTTCTTAATATCTTCAACTGAAAGCTTTAGAGCGATTTATCTTCTGAACCAGACTCTTGTCATTTGTTTTGGTAAAGAGAAAGTTTTTCCATCGATTTTATGAAT
CGGAAGTTGTTTGTTTTTTCTACCCTTAGGGTTACTAAGCAGTAGACGCTCCGACAAGAATTATAGAAGTTGACTTCGAAATCTCGCTAAATAGAAGACTTGGTCTGAGAACAGTAAACAAAACCATTTCTCTTTTCAAAAAGGTAGCTAAAATACTTA

2ᵉ étape : visite du GENOSCOPE
Séquençage de l'ADN

Matériel génétique d'une cellule

ADN

Noyau

acides aminés

ribosomes

ARN ribosomal

ARN messager

protéine

Cytoplasme

Membrane

Broyage et extraction ADN, ARN

Stockage et conservation des échantillons

Dénaturation de l'ADN par l'azote liquide et centrifugation
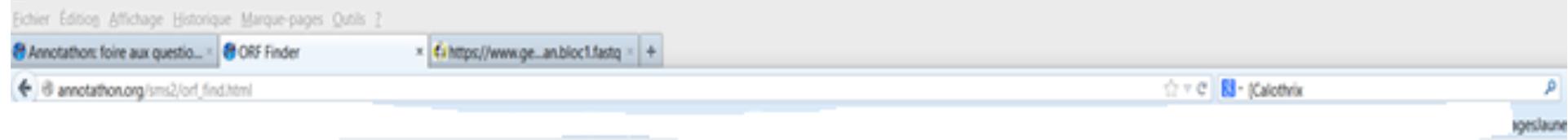
```
@G3:64TC8AAXX:4:1:8922:1322/1
TTGGCGGGCTTCCGTTGAATCCTGAATTTGAAAAATCCATCCATGTTTTTGTCAACAACTGCCTTCTGGCA
AAGCAAACGTGACGATGGTGAATCGCAAGAATTTGCTCCTTGGAGCATCACTCCATTTGATATGTAGTGGT
GTAGCTAG
+
IIIIIIIIIIIIIIIIIIIIIIIGIIFHIIIHIIIIIIIIIIIHGIIIIIIIIIGIIIIIIIIIIIIIIIGI
IHDGIEHIDBGFEDCEEECIFEEIIDGDHGGGD:HDBHEB@D@@BB@BBBDBEBB>@CE5=;=?@>B?D@>
A;>>>8=?
@G3:64TC8AAXX:4:1:13959:1323/1
ACCAGCGGGCATCTTCTGCAATTTCATATATGTCAGGGATCATTGCAGTAGGGTATTTTTTCTTTTTTAGA
ACCGATCTGCGAGAGAAACTCTTTGACATGCATTCTCTTCTATCCCTCCAGGAGGTGCACAGATTGCAACA
CAGGATTG
+
HIIIIIIIIIIIIIIIHIHIIHIIIIIIFIHIDHGHIIIHIIGIIGIFIEHGGG=BGGGDDIIIIIIHI=HE
HGHIDGGHIIHBHBFBBEEBEDBDGEEDDGDEDEEBCEEEEEEEDDEEAADBBB?0A?=?==34:?;6=@@
@>B=2=.?|
@G3:64TC8AAXX:4:1:6314:1324/1
CGAAAAAGCATTATCATCCTTAACAAAAGCCATTAGTATTCAACGAGAAACGATGACAAGGTCAATCTTG
GTCTTACCTATAATATAAGAGGTGTTATTCATAGTAACTTAAAACAATATGAACCTGCACTAGAGTATTTT
AATAACGCC
```

échantillon

ATT ……

AA ….

…ajoutées par le séquenceur

Index of /sadc/projet_AMC/MetaGenome

Site GENOSCOPE – séquences échantillons ...ption

📁 Parent Directory   -

❓ AMC_DTEMOSW_4_64TC8AAXX.IND12_shuffled_clean.bloc1.fastq   27-Feb-2013 16:07 4.4M

❓ AMC_DTEMOSW_4_64TC8AAXX.IND12_shuffled_clean.bloc2.fastq   27-Feb-2013 16:07 4.4M

AMC_DTEMOSW_4_64TC8AAXX.IND12_shuffled_clean.bloc3.fastq   27-Feb-2013 16:07 4.4M

AMC_DTEMOSW_4_64TC8AAXX.IND12_shuffled_clean.bloc4.fastq   27-Feb-2013 16:07 4.4M

AMC_DTEMOSW_4_64TC8AAXX.IND12_shuffled_clean.bloc5.fastq   27-Feb-2013 16:07 4.6M

AMC_DTEMOSW_4_64TC8AAXX.IND12_shuffled_clean.bloc6.fastq   27-Feb-2013 16:07 4.9M

AMC_DTEMOSW_4_64TC8AAXX.IND12_shuffled_clean.bloc7.fastq   27-Feb-2013 16:07 5.1M

❓ AMC_DTEMOSW_4_64TC8AAXX.IND12_shuffled_clean.bloc8.fastq   27-Feb-2013 16:07 5.2M

AMC_DTEMOSW_4_64TC8AAXX.IND12_shuffled_clean.bloc9.fastq   27-Feb-2013 16:07 5.2M

multi-sensor hybrid histidine kinase [Flavobacteriales bacterium ALC-1] >gb|EDP71559.1| multi-sensor hybrid histidine kinase [Flavobacteriales bacterium ALC-1]   54.3 54.3 90% 3e-07 60% ZP_02192061.1

Histidine kinase [Formosa sp. AK20] >gb|EMC94483.1| Histidine kinase [Formosa sp. AK20]   42.4 42.4 100% 0.004 42% ZP_23739615.1

serine/threonine protein kinases [uncultured Cytophagia bacterium]   41.2 149 100% 0.009 42% CCF99360.1

hypothetical protein APPUASWS_10687, partial [Arthrospira platensis str. Paraca] >gb|EKX79040.1| hypothetical protein APPUASWS_10687, partial [Arthrospira platensis str. Paraca]   41.2 41.2 100% 0.009 43% ZP_11274755.1

hypothetical protein LYNGBM3L_15000 [Moorea producens 3L] >gb|EGJ34556.1| hypothetical protein LYNGBM3L_15000 [Moorea producens 3L]   41.6 41.6 98% 0.009 43% ZP_08426220.1

Tetratricopeptide repeat family [Coleofasciculus chthonoplastes PCC 7420] >gb|EDX73040.1| Tetratricopeptide repeat family [Coleofasciculus chthonoplastes PCC 7420]   40.8 146 100% 0.012 43% ZP_05028994.1

hypothetical protein [Monosiga brevicollis MX1] >gb|EDQ84735.1| predicted protein [Monosiga brevicollis MX1]   40.4 40.4 100% 0.015 40% XP_001750385.1

hypothetical protein [Arthrospira platensis NIES-39] >dbj|BAI88364.1| hypothetical protein [Arthrospira platensis NIES-39]   40.4 40.4 100% 0.019 43% YP_005066802.1

hypothetical protein Mic7113_3433 [Microcoleus sp. PCC 7113] >gb|AFZ19152.1| tetratricopeptide repeat protein [Microcoleus sp. PCC 7113]   39.7 39.7 98% 0.023 43% YP_007122568.1

hypothetical protein BACCOP_00471 [Bacteroides coprocola DSM 17136] >gb|EDV02436.1| putative flagellar protein FliS [Bacteroides coprocola DSM 17136]   39.3 39.3 98% 0.043 37% ZP_03008626.1


Sequences producing significant alignments:

Select: All None Selected 0

Alignments   Download ▾ GenPept Graphics Distance tree of results Multiple alignment

Description	Max score	Total score	Query cover	E value	Max ident	Accession
hypothetical protein PSYMP_26948 [Pseudomonas syringae pv. morsprunorum str. M302280] >ref|ZP_16714292.1| hypothetical protein PSYAC_07957 [Pseudomonas syringae pv. actinidiae str. M302091] >gb|EGH14187.1| hypothetical protein PSYMP_2694	31.6	31.6	76%	2.5	32%	ZP_16666773.1
hypothetical protein TcasGA2_TC010915 [Tribolium castaneum]	32.0	32.0	75%	5.3	36%	EFA03059.1

espèce	fréquence
arthrospira platensis	20
Oscillatoria acuminata	3
Nematostella vectensis	60
Microscilla marina	14
Crocosphaera watsonii	75
monosiga brevicollis	8
Zobellia galactanivorans	41

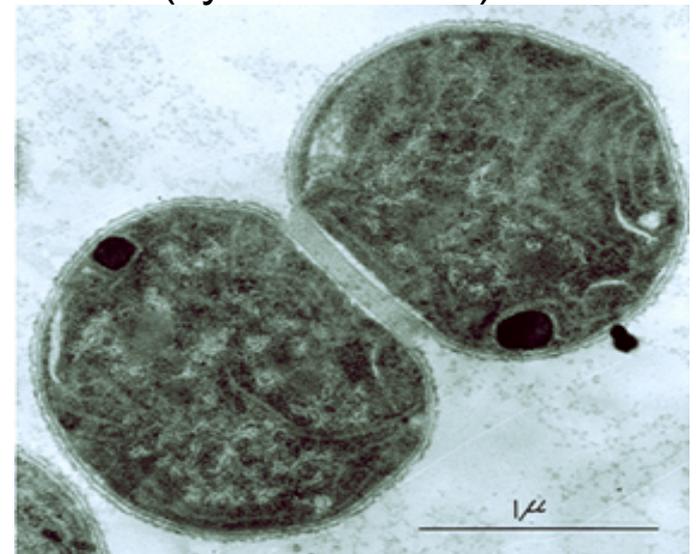fréquence de détection d'une espèce sur 100 séquences comparées
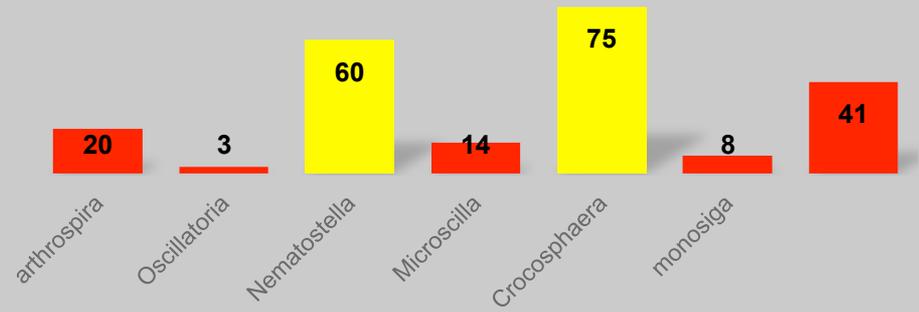
Nematostella vectensis
(anémone de mer)

Espèce
indéterminée
(site TARA)

Crocosphaera watsonii
(cyanobactérie)

Tous les élèves remercient
pour leur collaboration
et leur disponibilité…

- **Xavier BOUGEARD** – Chargé de mission éducation Tara-expéditions

- **Julie POULAIN** – Chef d'équipe séquençage GENOSCOPE

- **Nathalie AIACH –** Technicienne séquençage GENOSCOPE

- **Sabine LAVOREL et Vincent CHARBONNIER** – IFE