

Γονιδιωματική
Συγκριτική γονιδιωματική[3]

Τμήμα Γεωπονίας, Ιχθυολογίας
και Υδάτινου Περιβάλλοντος

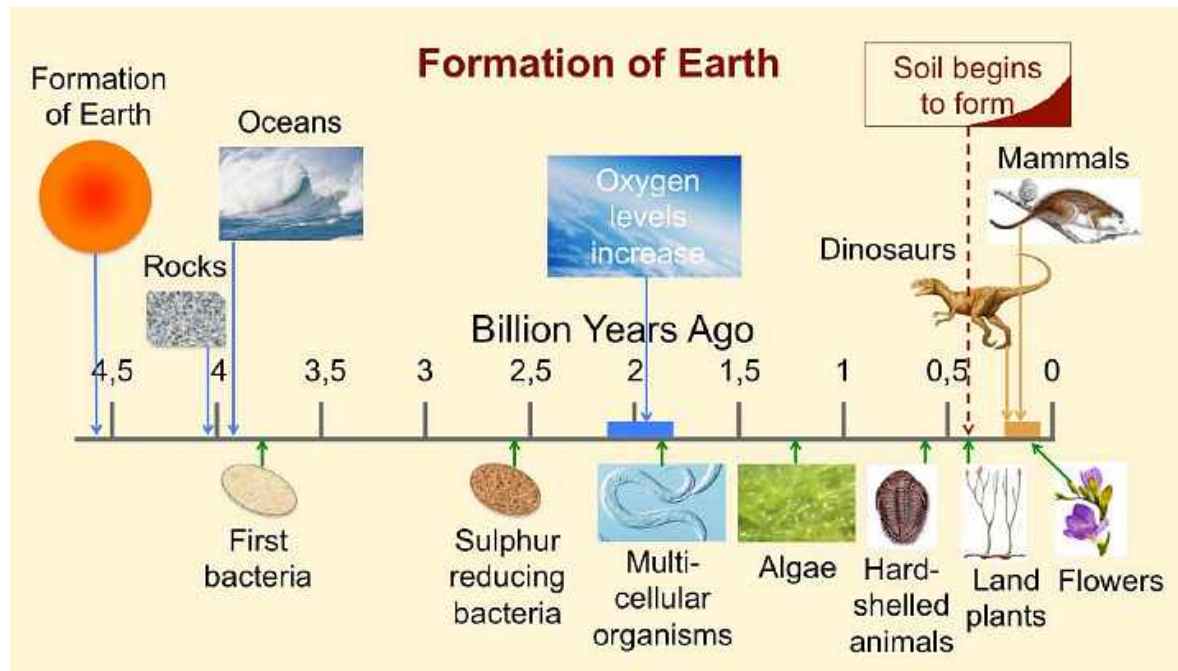
Μεζίτη Αλεξάνδρα

Η εξέλιξη της ζωής

3.5 bya: εμφάνιση των πρώτων μορφών ζωής → Προκαρυωτικές μορφές

2 bya: εμφάνιση Ευκαρυωτών

<https://prezi.com/eu7ymodemtyw/timeline-the-evolution-of-life-on-earth/>



***** Αρκετές ομοιότητες μεταξύ των οργανισμών σήμερα αποδεικνύουν την ύπαρξη κοινού προγόνου- η ποικιλότητα αποτελεί αποτέλεσμα αποκλίσεων. *****

Η ανάλυση αλληλουχιών αποτελεί την πιο σαφή απόδειξη για τις σχέσεις μεταξύ των ειδών

Τάξινομική

Ταξινόμηση Ευκαρυωτικών οργανισμών (Linnaeus)

Αλληλούχηση, Παλαιοντολογία, Συγκριτική ανατομία, Εμβρυολογία

Ταξινόμηση Προκαρυωτικών οργανισμών

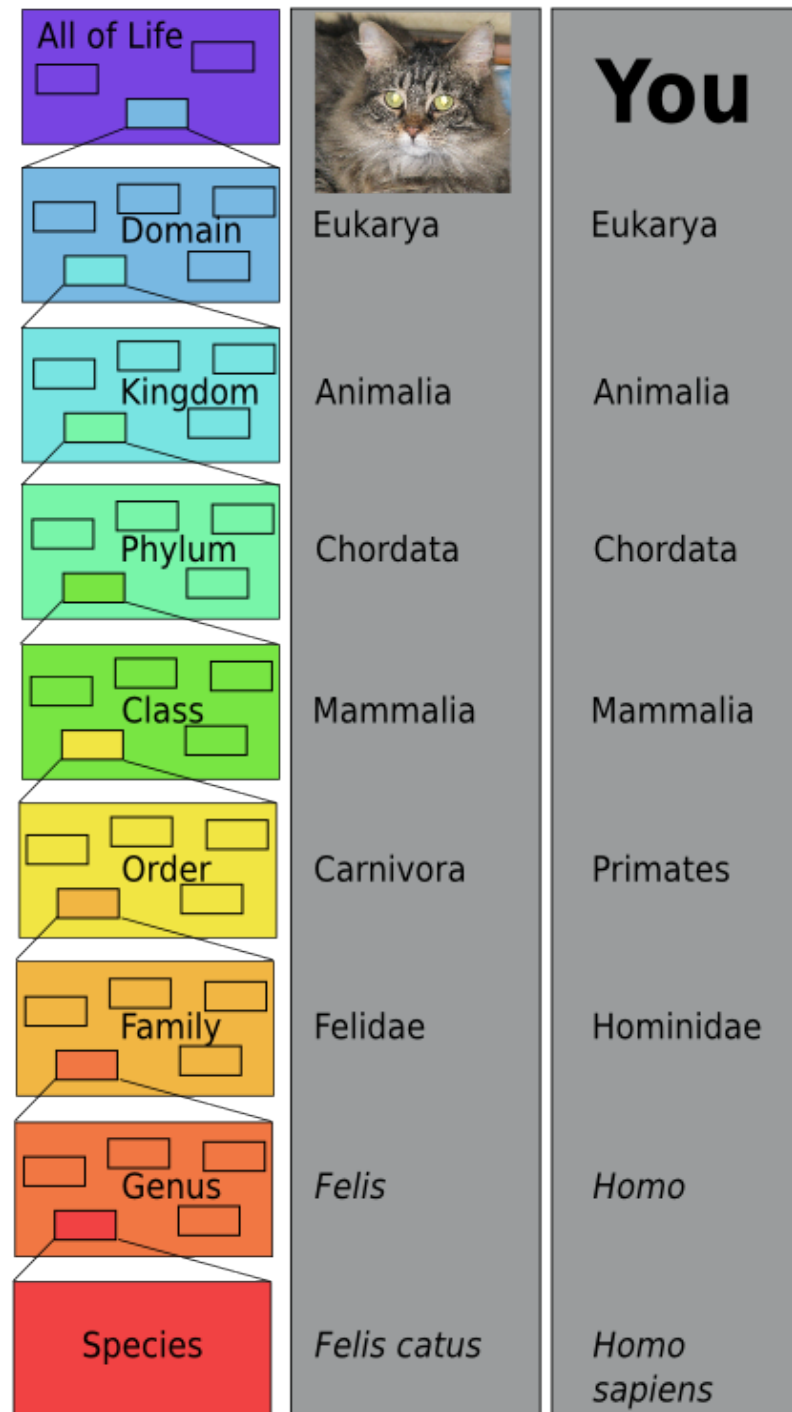
Μορφολογία, Φυσιολογία, Βιοχημεία,

Αλληλούχηση

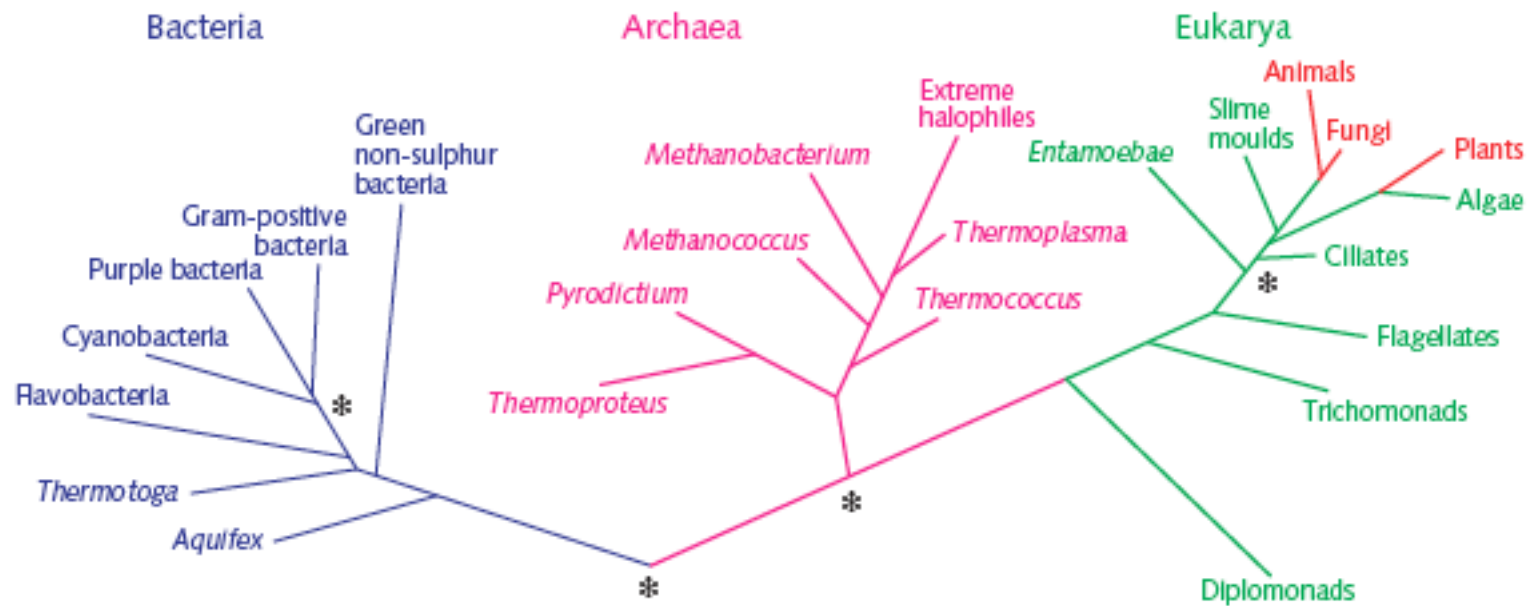
→ Υβριδοποίηση DNA

→ γονίδια (16S rRNA)

C. Woese: Τα Προκαρυωτικά είδη καθορίζονται από τις ομοιότητες των 16S rRNA αλληλουχιών. Διαφορές > 2.5-3% θεωρούνται ότι ανήκουν σε διαφορετικά είδη.



Το ριβόσωμα και οι τρεις Επικράτειες



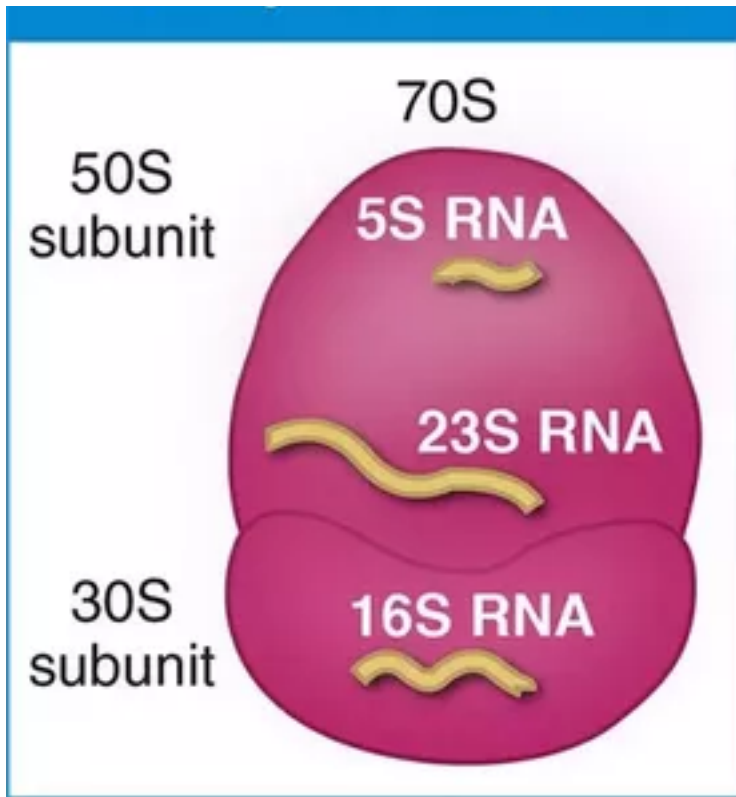
Woese, PNAS 2000, 97: 8392-8396

- Αρκετές ομοιότητες ανάμεσα στους οργανισμούς ώστε να αποδειχθεί ότι υπάρχει ένας κοινός πρόγονος → καθολικότητα χημικών δομών (DNA, RNA, πρωτεΐνες) και των βιολογικών τους ρόλων.
- Με βάση τα γονίδια του ριβοσωμικού RNA όλοι οι οργανισμοί χωρίστηκαν σε τρεις Επικράτειες (Βακτήρια, Αρχαία, Ευκαρυώτες) από τον C.Woese.
- Χρονολόγηση σημαντικών γεγονότων βάσει των διαφορών στις αλληλουχίες.
- Σημασία της οριζόντιας μεταφοράς γονιδίων.

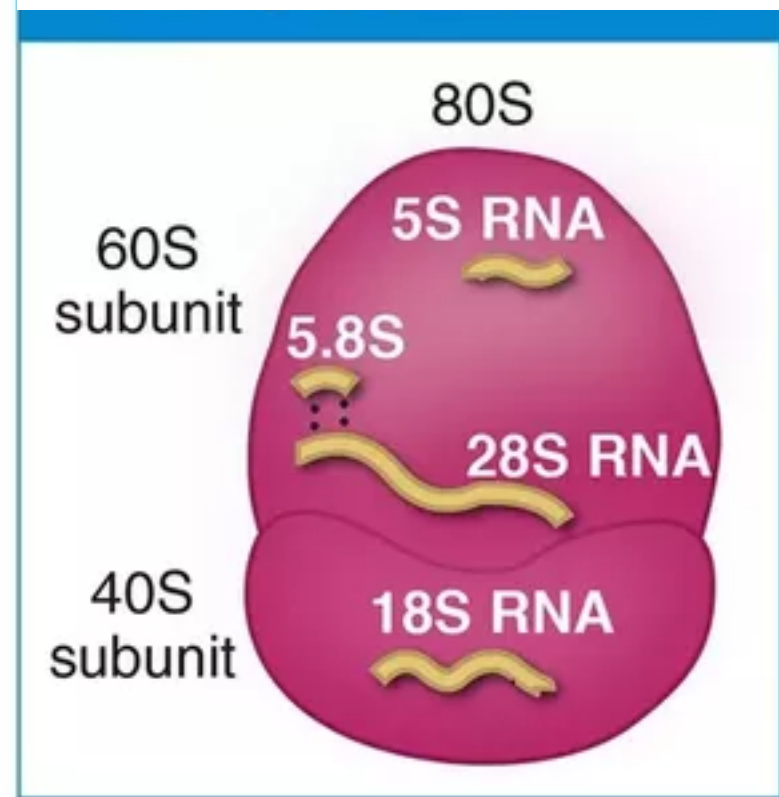
Το ριβόσωμα

Τα εργοστάσια παραγωγής πρωτεϊνών των κυττάρων

Προκαρυωτικό ριβόσωμα

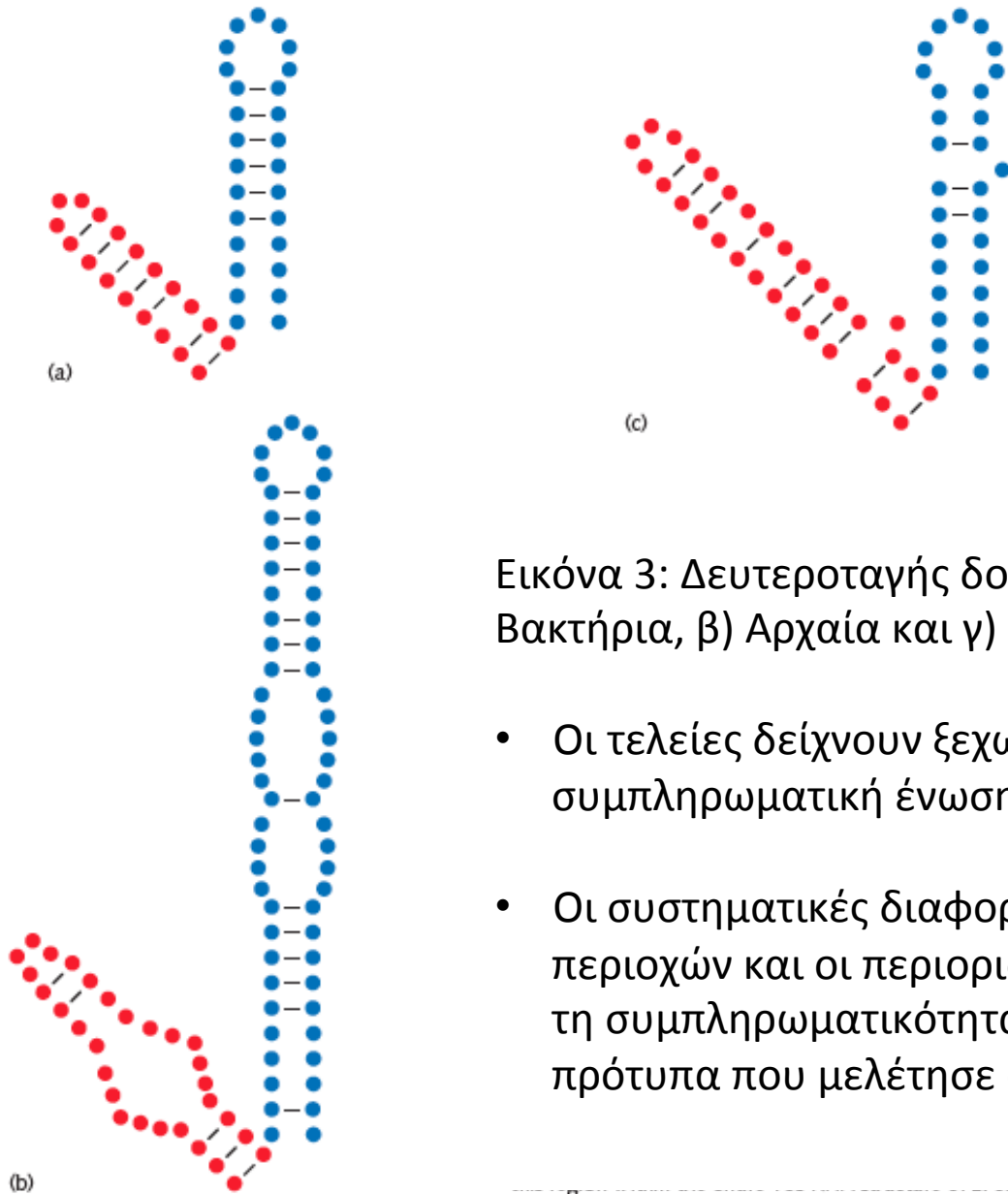


Ευκαρυωτικό ριβόσωμα



Εικόνα 1: Διαφορές των Προκαρυωτικών Και Ευκαρυωτικών ριβοσωμάτων

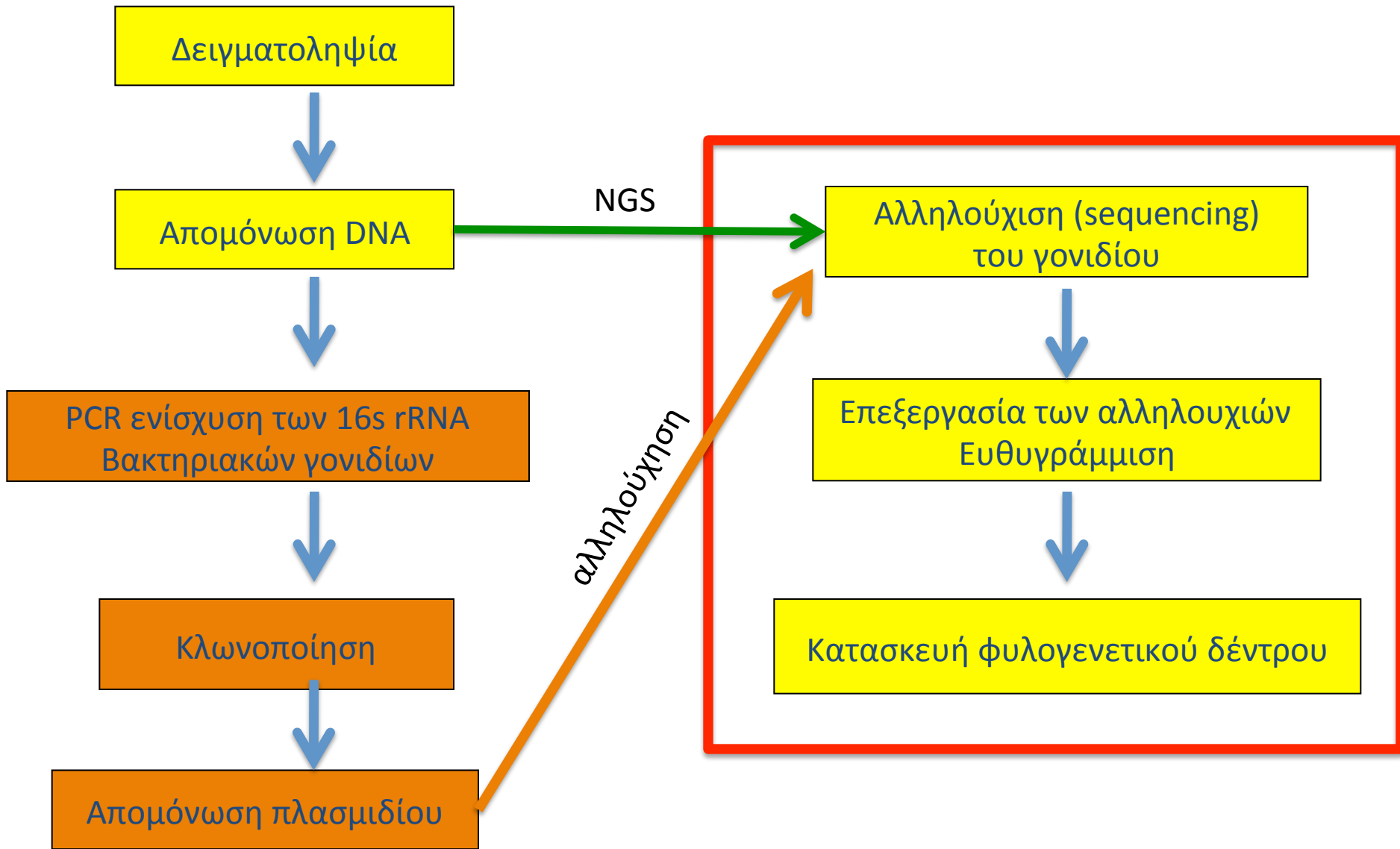
Δευτεροταγής δομή



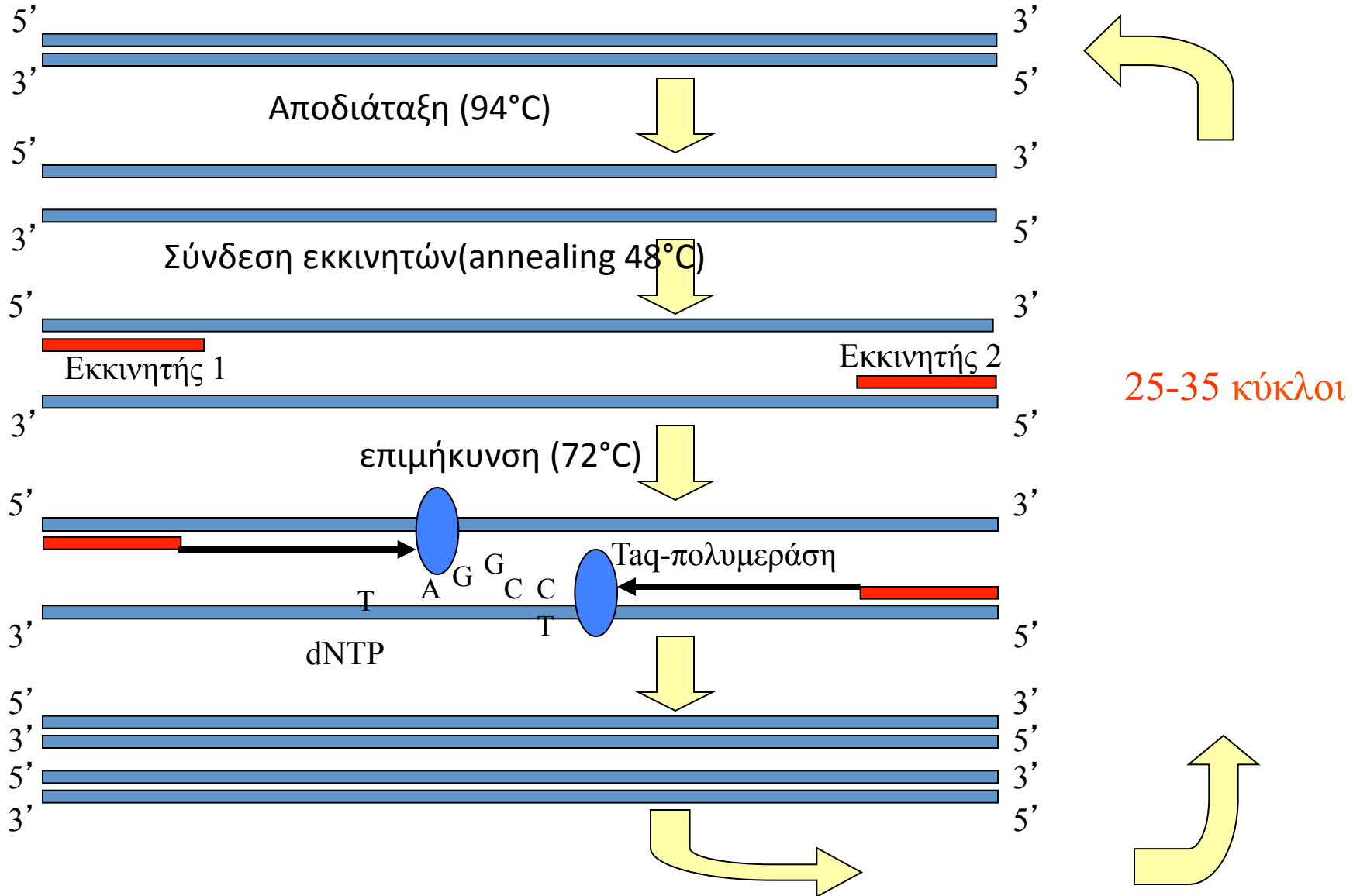
Εικόνα 3: Δευτεροταγής δομή 16S και 18S rRNA σε α) Βακτήρια, β) Αρχαία και γ) Ευκαρυώτες.

- Οι τελείες δείχνουν ξεχωριστές βάσεις και οι γραμμές συμπληρωματική ένωση βάσεων.
- Οι συστηματικές διαφορές στο μήκος των ελικοειδών περιοχών και οι περιορισμοί που υποδεικνύονται από τη συμπληρωματικότητα των βάσεων συνέβαλαν στα πρότυπα που μελέτησε ο Woese.

Μεθοδολογία

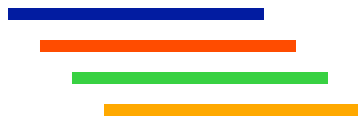


Αλυσιδωτή αντίδραση πολυμεράσης Polymerase chain reaction (PCR)

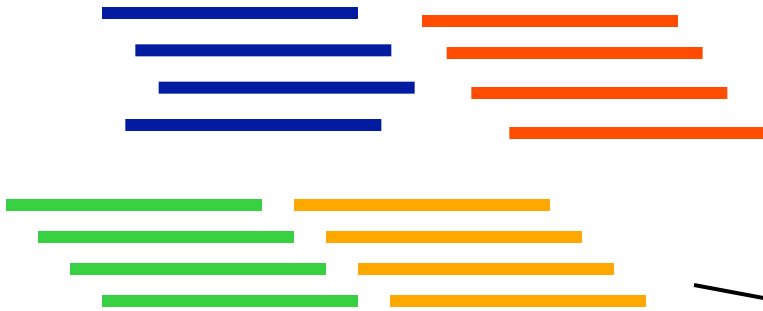


Κλωνοποίηση

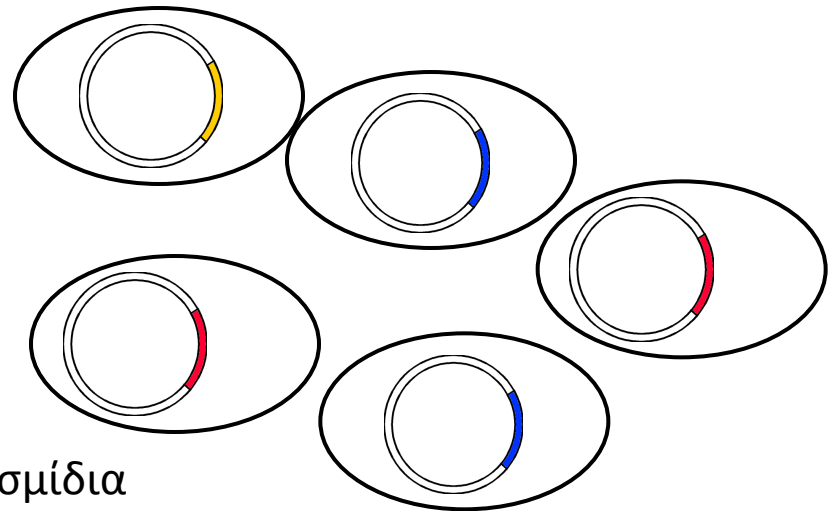
Περιβαλλοντικό δείγμα



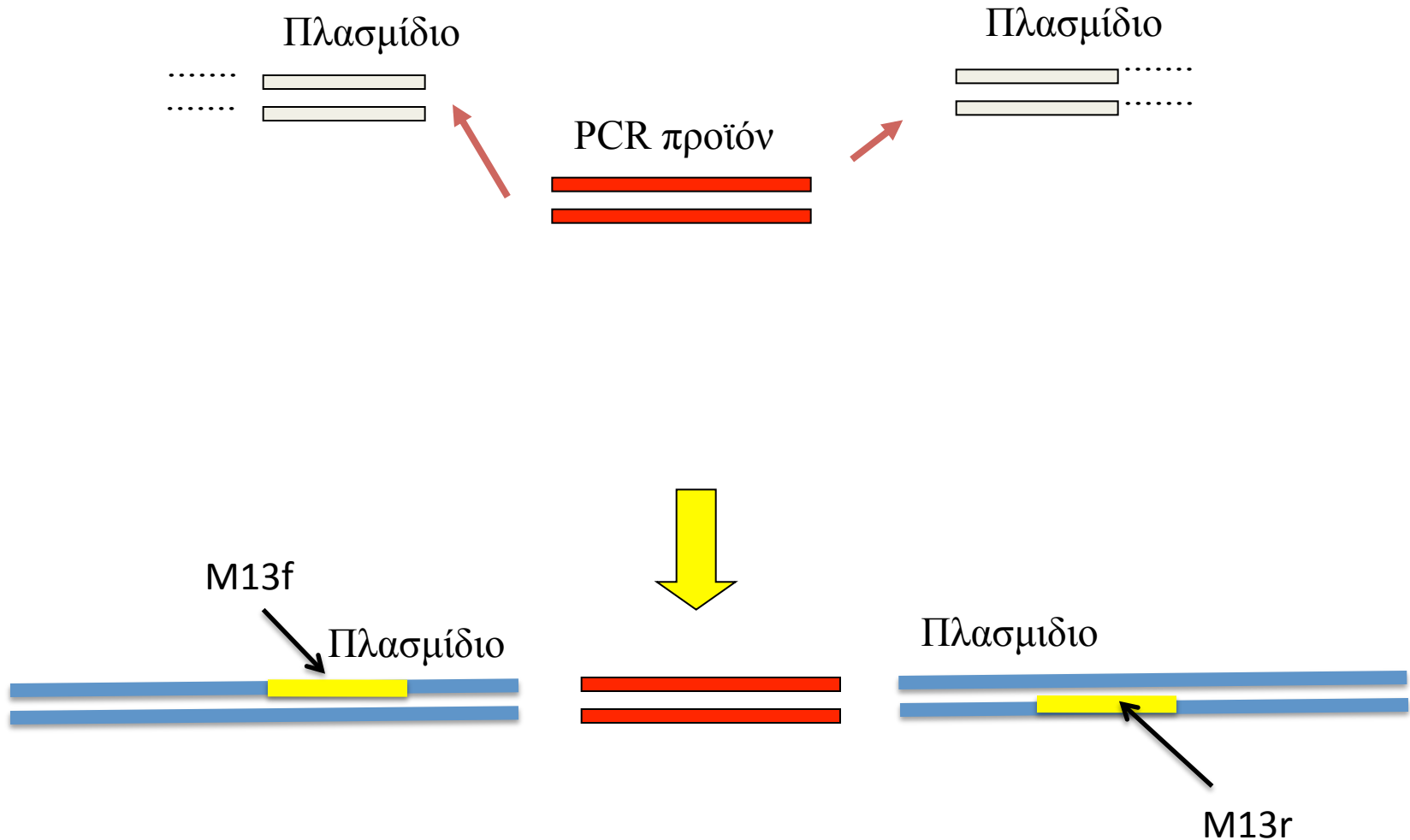
„γενική“ PCR



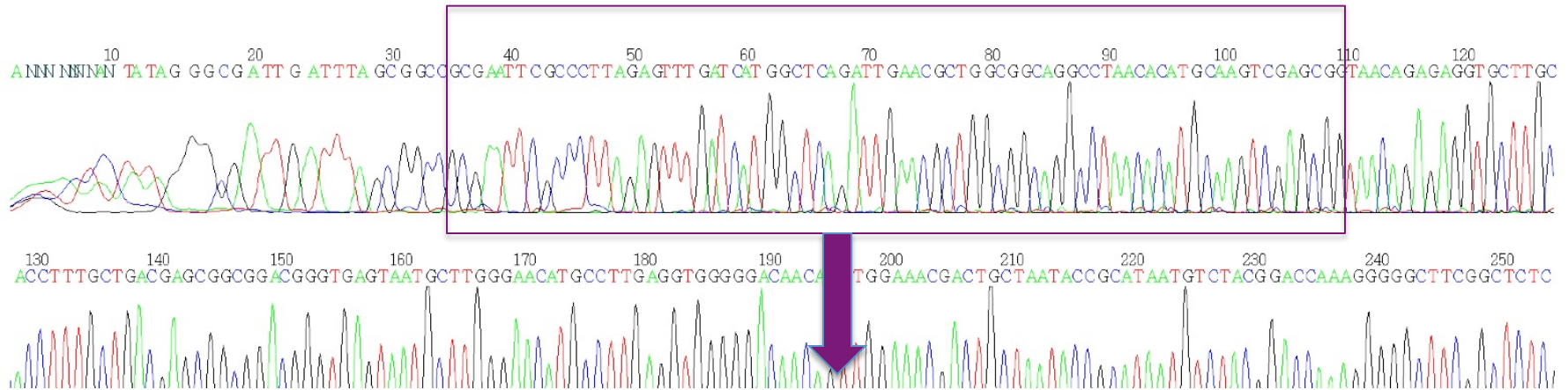
Σύνδεση με πλασμίδια
Της *Escherichia coli*



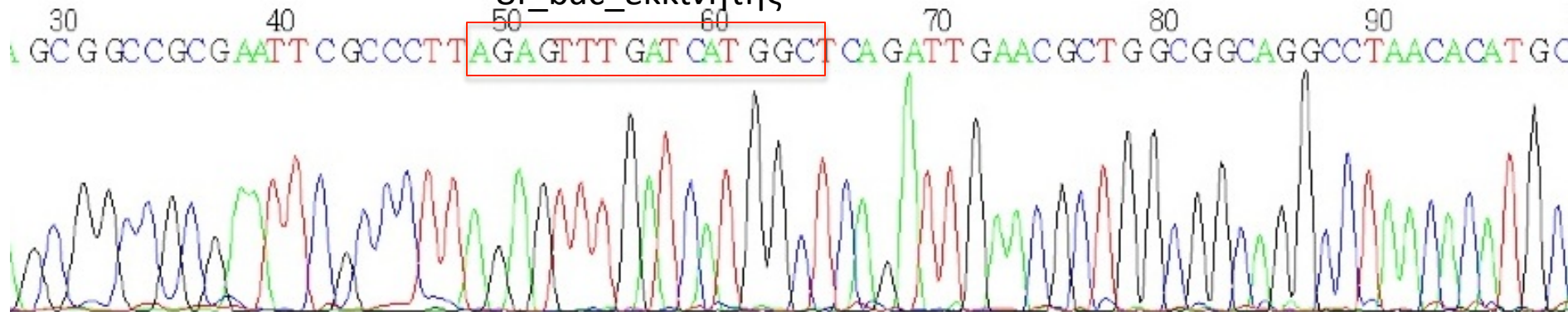
T-A cloning of PCR fragments



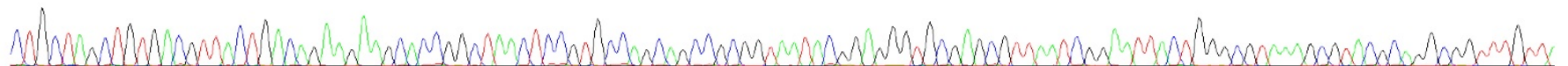
File: NF1-M13F.ab1 Run Ended: 2009/2/4 11:53:51 Signal G:1266 A:893 C:794 T:830
 Sample: NF1_M13F Lane: 62 Base spacing: 17.132507 909 bases in 10688 scans Page 1 of 2



8f_bac_εκκλινητής



510 520 530 540 550 560 570 580 590 600 610 620 630
 CTGCTAGCTGTGACGTTACTGACAGAAGAACACCGGCTAACTCCGTGCCAGCAGCCCGGTAATAACGGAGGGTGCAGCGCTAATCGGAATTACTGGCGTAAAGCGTACGCAGGCGGTTTGTTA



>NF13-M13F_forward

AGAGTTTGGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAACAGAGAGGTGCT
TGCACCTTTGCTGACGAGCGGCGGACGGGTGAGTAATGCTTGGGAACATGCCTTGAGGTGGGGGACAACAGTTGGA
AACGACTGCTAATACCGCATAATGTCTACGGACCAAAGGGGGCTTCGGCTCTCGCCTTTAGATTGGCCCAAGTGGGAT
TAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATCCCTAGCTGGTTTGAGAGGATGATCAGCCACACTGGGA
CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCA
TGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTCTCAGTCAGGAGGAAAGGTTAGTAGTTAATACCTGCT
AGCTGTGACGTTACTGACAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAGCG
TTAATCGGAATTACTGGGCGTAAAGCGTACGCAGGCGGTTTGTAAAGCGAGATGTGAAAGCCCCGGGCTAACCTGG
GAACTGCATTTGAACTGGCAAAGTACTAGAGTGTGATAGAGGGTGGTAGAATTTAGGTGTAGCGGTGAAATGCGT**AGA
GATCTGAAGGAATACCGATGGCGAAGGCAGCCACCTGGGTCAACACTGACGCTCATGTACGAAAGCGTGGGGAGCA
AACGGGATTAGATACCCCGGTAGTCCACGCCGTAAACGGTGTCTACTAGAAGCTCGGAGCCTCGGTTCTGTTTTCAA
AGCTAACGCATTAAGT**

>NF13-M13R (αντίστροφα συμπληρωματικο...Γιατι???)

**AGAGATCTGAAGGAATACCGATGGCGAAGGCAGCCACCTGGGTCAACACTGACGCTCATGTACGAAAGCGTGGGGAG
CAAACGGGATTAGATACCCCGGTAGTCCACGCCGTAAACGATGTCTACTAGAAGCTCGGAGCCTCGGTTCTGTTTTCA
AAGCTAACGCATTAAGT**AGACCGCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACACTTGACATACAGAGAACTTACCAG
AGATGGTTTGGTGCCTTCGGGAACTCTGATACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAGATGTTGGGTTA
AGTCCCGCAACGAGCGCAACCCTATCCTTAGTTGCTAGCAGGTAATGCTGAGAACTCTAAGGAGACTGCCGGTGATA
AACCGGAGGAAGGTGGGGACGACGTCAAGTCATCATGGCCCTTACGTGTAGGGCTACACACGTGCTACAATGGCGCA
TACAGAGTGCTGCGAACCTGCGAAGGTAAGCGAATCACTTAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGA
CTCCATGAAGTCGGAATCGCTAGTAATCGCGTATCAGAATGACGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCC
CGTCACACCATGGGAGTGGGTTGCTCCAGAAGTAGATAGTCTAACCTCGGGAGGACGTTTACCACGGAGTGATTCAT
GACTGGGGTGAAGTCGTAACAAGGTA

>NF13_16S rRNA gene

AGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAACAGAGA
GGTGCTTGCACCTTTGCTGACGAGCGGCGGACGGGTGAGTAATGCTTGGGAACATGCCTTGAGGTGGGGGA
CAACAGTTGGAAACGACTGCTAATACCGCATAATGTCTACGGACCAAAGGGGGCTTCGGCTCTCGCCTTTAG
ATTGGCCCAAGTGGGATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATCCCTAGCTGGTTTGAG
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ACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTCTCA
GTCAGGAGGAAAGGTTAGTAGTTAATACCTGCTAGCTGTGACGTTACTGACAGAAGAAGCACCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGTACGCAG
GCGGTTTGTAAAGCGAGATGTGAAAGCCCCGGGCTCAACCTGGGAAGTGCATTCGAACTGGCAAAGTAGAG
TGTGATAGAGGGTGGTAGAATTTAGGTGTAGCGGTGAAATGCGT**AGAGATCTGAAGGAATACCGATGGCG**
AAGGCAGCCACCTGGGTCAACACTGACGCTCATGTACGAAAGCGTGGGGAGCAAACGGGATTAGATACCC
GGTAGTCCACGCCGTAAACGGTGTCTACTAGAAGCTCGGAGCCTCGGTTCTGTTTTTCAAAGCTAACGCATTA
AGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGT
GGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACACTTGACATACAGAGAACTTACCAGAG
ATGGTTTGGTGCCTTCGGGAAGTCTGATACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAGATGTTG
GGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTAGTTGCTAGCAGGTAATGCTGAGAACTCTAAGGAGAC
TGCCGGTGATAAACCGGAGGAAGGTGGGGACGACGTCAAGTCATCATGGCCCTTACGTGTAGGGCTACACA
CGTGCTACAATGGCGCATAACAGAGTGCTGCGAACCTGCGAAGGTAAGCGAATCACTTAAAGTGCGTCTAGT
CCGATTGGAGTCTGCAACTCG
ACTCCATGAAGTCGGAATCGCTAGTAATCGCGTATCAGAATGACGCGGTGAATACGTTCCCGGGCCTTGTAC
ACACCGCCCGTCACACCATGGGAGTGGGTTGCTCCAGAAGTAGATAGTCTAACCTCGGGAGGACGTTTACC
ACGGAGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTA

http://blast.ncbi.nlm.nih.gov/

The screenshot shows the BLAST Basic Local Alignment Search Tool website. The browser window title is "BLAST: Basic Local Alignment Search Tool". The address bar shows "http://blast.ncbi.nlm.nih.gov/". The page has a blue header with the BLAST logo and navigation tabs: Home, Recent Results, Saved Strategies, and Help. Below the header, there is a section for "NCBI/ BLAST Home" with a search box and a link to "more...". A "New" banner promotes "Primer-BLAST" for PCR primers. The "BLAST Assembled Genomes" section lists various species genomes for search, including Human, Mouse, Rat, Arabidopsis thaliana, Oryza sativa, Bos taurus, Danio rerio, Drosophila melanogaster, Gallus gallus, Pan troglodytes, Microbes, and Apis mellifera. The "Basic BLAST" section lists different BLAST programs: nucleotide blast, protein blast, blastx, tblastn, and tblastx, each with a brief description and algorithms. The "Specialized BLAST" section is partially visible at the bottom. On the right side, there are sections for "News" (Align two sequences form) and "Tip of the Day" (Using Tree View to Examine Relationships Between Sequences).

http://blast.ncbi.nlm.nih.gov/

BLAST Basic Local Alignment Search Tool

- Home
- Recent Results
- Saved Strategies
- Help

NCBI/ BLAST Home

BLAST finds regions of similarity between biological sequences. [more...](#)

New Designing or Testing PCR Primers? Try your search in **Primer-BLAST**.

BLAST Assembled Genomes

Choose a species genome to search, or [list all genomic BLAST databases](#).

- [Human](#)
- [Mouse](#)
- [Rat](#)
- [Arabidopsis thaliana](#)
- [Oryza sativa](#)
- [Bos taurus](#)
- [Danio rerio](#)
- [Drosophila melanogaster](#)
- [Gallus gallus](#)
- [Pan troglodytes](#)
- [Microbes](#)
- [Apis mellifera](#)

Basic BLAST

Choose a BLAST program to run.

- [nucleotide blast](#) Search a **nucleotide** database using a **nucleotide** query
Algorithms: blastn, megablast, discontinuous megablast
- [protein blast](#) Search **protein** database using a **protein** query
Algorithms: blastp, psi-blast, phi-blast
- [blastx](#) Search **protein** database using a **translated nucleotide** query
- [tblastn](#) Search **translated nucleotide** database using a **protein** query
- [tblastx](#) Search **translated nucleotide** database using a **translated nucleotide** query

Specialized BLAST

News

[Align two sequences form.](#)

The Align two sequences link on the BLAST home page now uses the standard BLAST submission form.
Tue, 03 Feb 2009 16:00:00 EST

[More BLAST news...](#)

Tip of the Day

[Using Tree View to Examine Relationships Between Sequences.](#)

The new Tree View option on the NCBI Web BLAST service presents a dendrogram or tree display that clusters sequences according to their distances from the query sequence.

[More tips...](#)

Επιλογή: nucleotide blast
Database: others (nr etc.)

Firefox File Edit View History Bookmarks Tools Window Help

Nucleotide BLAST: Search nucleotide databases using a nucleotide query

http://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Nucleotides&PROGRAM=blastn&MEGABLAST=on&BLAST_PROGR...

Getting Started Most Visited Latest Headlines Welcome to Facebook... Apple Yahoo! Google Maps YouTube Wikipedia News Popular Cool OSX Apps Statistics Workshops

BLAST Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

My NCBI [Sign In] [Register]

NCBI/ BLAST/ blastn suite

blastn blastp

blastx tblastn tblastx

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

Enter Query Sequence

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

From

To

Or, upload file [Browse...](#)

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database Human genomic + transcript Mouse genomic + transcript Others (nr etc.):

Nucleotide collection (nr/nt)

Organism

Optional Enter organism name or id--completions will be suggested

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Entrez Query

Optional Enter an Entrez query to limit search

Program Selection

Optimize for Highly similar sequences (megablast)

More dissimilar sequences (discontiguous megablast)

Somewhat similar sequences (blastn)

Αντιγραφή της αλληλουχίας

Done

NCBI/ BLAST/ blastn suite/ Formatting Results - SR7RZJJB01N

Edit and Resubmit Save Search Strategies Formatting options Download

ApH1_test

Query ID |c|46691
Description ApH1_test
Molecule type nucleic acid
Query Length 689

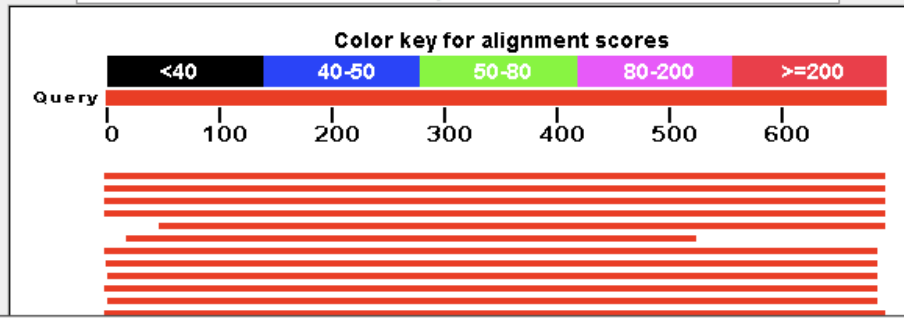
Database Name nr
Description All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
Program BLASTN 2.2.22+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments





▼ Descriptions

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

Sequences producing significant alignments:
(Click headers to sort columns)

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
DQ860037.1	Uncultured bacterium clone F2B 16S ribosomal RNA gene, partial sequer	1146	1146	100%	0.0	96%	
DQ856531.1	Uncultured bacterium clone C2E 16S ribosomal RNA gene, partial sequer	1146	1146	100%	0.0	96%	
DQ856501.1	Uncultured bacterium clone C1B 16S ribosomal RNA gene, partial sequer	1146	1146	100%	0.0	96%	
DQ856551.1	Uncultured bacterium clone C3M 16S ribosomal RNA gene, partial sequer	1140	1140	100%	0.0	96%	
FJ930399.1	Uncultured bacterium clone C3C9-2 16S small subunit ribosomal RNA ge	909	909	93%	0.0	92%	
DQ153194.1	Uncultured bacterium clone C1B 16S ribosomal RNA gene, partial sequer	832	832	73%	0.0	96%	
EU799602.1	Uncultured bacterium clone 1C227220 16S ribosomal RNA gene, partial	824	824	98%	0.0	88%	
FJ752850.1	Uncultured alpha proteobacterium clone NdGal99 16S ribosomal RNA ge	815	815	98%	0.0	88%	
EF572142.1	Uncultured bacterium clone S23_241 16S ribosomal RNA gene, partial s	813	813	98%	0.0	88%	
EU805031.1	Uncultured bacterium clone 6C233013 16S ribosomal RNA gene, partial	808	808	98%	0.0	88%	
EU802254.1	Uncultured bacterium clone 4C229555 16S ribosomal RNA gene, partial	802	802	98%	0.0	88%	
FJ656486.1	Uncultured bacterium clone AR68 16S ribosomal RNA gene, partial sequ	795	795	100%	0.0	87%	
EU361356.1	Uncultured Kordiimonas sp. clone HF130_16I04 small subunit ribosomal	785	785	95%	0.0	88%	
FJ656487.1	Uncultured bacterium clone SJ49 16S ribosomal RNA gene, partial sequer	784	784	100%	0.0	87%	
AM749667.1	Kiloniella laminariae partial 16S rRNA gene, type strain LD81T	784	784	99%	0.0	87%	
FM165264.1	Uncultured bacterium partial 16S rRNA gene, clone v1t42	780	780	99%	0.0	87%	
GU289640.1	Kordiimonas sp. MEBIC06554 16S ribosomal RNA gene, partial sequence	778	778	97%	0.0	87%	
DQ351777.1	Uncultured alpha proteobacterium clone Belgica2005/10-140-4 16S ribo	776	776	100%	0.0	87%	
EU287361.1	Uncultured bacterium clone S26-61 16S ribosomal RNA gene, partial sec	774	774	100%	0.0	87%	
FM165263.1	Uncultured bacterium partial 16S rRNA gene, clone v1t35	773	773	99%	0.0	87%	
AM162574.1	Uncultured alpha proteobacterium 16S rRNA gene, clone 3iSOMBO30	773	773	99%	0.0	87%	
F3504707.1	Uncultured marine bacterium clone Atrif4_10 16S ribosomal RNA gene	771	771	98%	0.0	87%	



GenBank: DQ856531.1

Uncultured bacterium clone C2E 16S ribosomal RNA gene, partial sequence

[Features](#) [Sequence](#)

LOCUS DQ856531 1465 bp DNA linear ENV 17-AUG-2007

DEFINITION Uncultured bacterium clone C2E 16S ribosomal RNA gene, partial sequence.

ACCESSION DQ856531

VERSION DQ856531.1 GI:114159775

KEYWORDS ENV.

SOURCE uncultured bacterium

ORGANISM [uncultured bacterium](#)
Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 1465)
AUTHORS Li,K., Guan,W., Wei,G., Liu,B., Xu,J., Zhao,L. and Zhang,Y.
TITLE Phylogenetic analysis of intestinal bacteria in the Chinese mitten crab (*Eriocheir sinensis*)
JOURNAL J. Appl. Microbiol. 103 (3), 675-682 (2007)
PUBMED [17714401](#)

REFERENCE 2 (bases 1 to 1465)
AUTHORS Li,K., Guan,W., Xu,J., Zhang,Y. and Zhao,L.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2006) Lab of Molecular Ecology and Ecogenomics, College of Life Science and Technology, Shanghai Jiaotong University, Shanghai, P.R. China

FEATURES
source Location/Qualifiers
1..1465
/organism="uncultured bacterium"
/mol_type="16S ribosomal RNA"

Change Region Shown ▾

Customize View ▾

Analyze This Sequence

- ▶ Run BLAST
- ▶ Pick Primers

Recent activity

[Turn Off](#) [Clear](#)

- Uncultured bacterium clone C2E 16S ribosomal RNA gene, partial sequence
- Uncultured bacterium clone F2B 16S ribosomal RNA gene, partial sequence
- Uncultured delta proteobacterium clone KorMud-V1C168 16S ribosomal RNA gene,

» See more...

All links from this record

PubMed home

http://www.ncbi.nlm.nih.gov/pubmed/

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Facebook Twitter KA Torrents Mininova Vuze Blog [2]

PubMed home

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PubMed.gov
U.S. National Library of Medicine
National Institutes of Health

Search: Nucleotide [Limits](#) [Advanced search](#) [Help](#)

DQ856531.1

Welcome to PubMed

PubMed comprises more than 19 million citations for biomedical articles from MEDLINE and life science journals. Citations may include links to full-text articles from PubMed Central or publisher web sites.

Using PubMed

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- [Topic-Specific Queries](#)

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- [Journals Database](#)
- [Clinical Trials](#)
- [E-Utilities](#)
- [LinkOut](#)

Done

http://www.ncbi.nlm.nih.gov/pubmed/

Ευθυγράμμιση ομόλογων νουκλεοτιδίων

The screenshot displays the ARB_EDIT4 software interface. The title bar reads "ARB_EDIT4 *1* [ali_16s]". The menu bar includes "File", "Create", "Edit", "View", "Block", and "Properties". The toolbar contains various editing and alignment tools such as "QUIT", "HELP", "Position", "E.coli", "Base", "IUPAC", "Helix No.", "JUMP", "GET", "Align", "Insert", "5'...3'", "UNDO", "REDO", "Protect", and "0". A search bar on the right contains the text "This is ARB Edit4 [Build 03_08_22]".

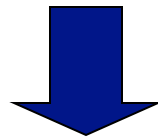
The main window shows a sequence alignment of 16S rRNA. The top section displays the alignment for "SAI: HELIX_NR", "SAI: HELIX", and "SAI: Ecoli (usually)". The bottom section shows a list of species with their corresponding sequences:

Species	data type	Sequence
Escherichia coli	0data	A-A-A--CGG-UAG-CU-A-A-UΔ-C-C-#-C-A-U-A-A-----C-----G-U-C-----G-CA-A
Pseudoalteromonas macleodii	5data	A-A-A--CGA-CUG-CU-A-A-UΔ-C-C-#-C-A-U-A-A-----U-----G-U-C-----U-UC-G
Shewanella benthica	5data	A-A-A--CAA-CUG-CU-A-A-UΔ-C-C-#-C-A-U-A-C-----G.....*.*.G-----U-AC-G
Roseobacter denitrificans	0data	A-A-A--CGA-AGG-GU-A-A-UΔ-C-C-#-U-A-U-A-C-----G-----C-C-G-----U-UC-G
Flavobacterium johnsoniae	5data	A-A-A--UUU-GGG-UU-A-A-UΔ-C-C-U-#-A-U-A-G-----U-A-U-U-A-U-A-G-A-G-Y-G-----G-CA-U
Anabaena circinalis	5data	A-A-A--CGG-UGG-CU-A-A-UΔ-C-C-#-G-A-U-G-U-----G-C-G-----G-AG-A
Rhodococcus rhodnii	5data	A-A-A--CUG-GGU-CU-A-A-UΔ-C-U-G-G-A-U-A-----U-G-A-G-C-A-G-U-G-G-U-U-----G-CA-U
Pirellula sp.	5data	A-A-A--CUG-GCA-GU-A-A-UΔ-C-C-G-G-A-U-A-A-----U-----A-U-C-----U-AC-G
Mycoplasma bovis	5data	A-A-A--CAU-CGG-AU-A-A-UΔ-C-C-G-A--AU-A-C-----#-U-A-U-U-A-U-U-U-U-U-----G-CA-U
Aquifex aeolicus	0data	A-A-A--CGG-GGG-CU-A-A-UΔ-C-C-C-C-A-U-A-A-----U-G-C-G-A-G-C-G-G-----ACUA-A

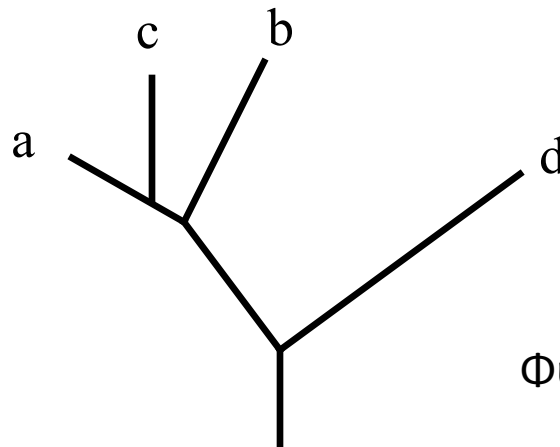
- ομόλογες θέσεις στην ίδια κολόνα

Κατασκευή φυλογενετικών δέντρων

είδος a	acgucucucuucaagcuaacgucggaacacacucgscgcauuu
είδος bCC.....
είδος cC.....
είδος dAAA.....



Συγκριτική ανάλυση αλληλουχιών



Φυλογενετικό δέντρο

Group I

1) FJ712590, 2) GQ866111, 3) AY770727, 4) GQ240858, 5) FJ157340,
6) AY292947 7) FJ649512, 8) DQ103597

Group II

1) FJ712614, 2) GQ866105, 3) AY770726, 4) GQ240857, 5) FJ157339
6) AY292917, 7) FJ649511, 8) DQ103596

- 3 κοντινότεροι συγγενείς
- Χαρακτηρισμένος κοντινότερος συγγενής (αν έχουν πάνω από 93% ομοιότητα).
- Που έχει εντοπιστεί ο συγκεκριμένος φυλότυπος
- Δημοσίευση (αν υπάρχει)
- Ταξινομική