



Departamento de Genética
USP Ribeirão Preto-FMRP



GENOMAS PROCARIOTOS

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Ribeirão Preto – Março/ 2020

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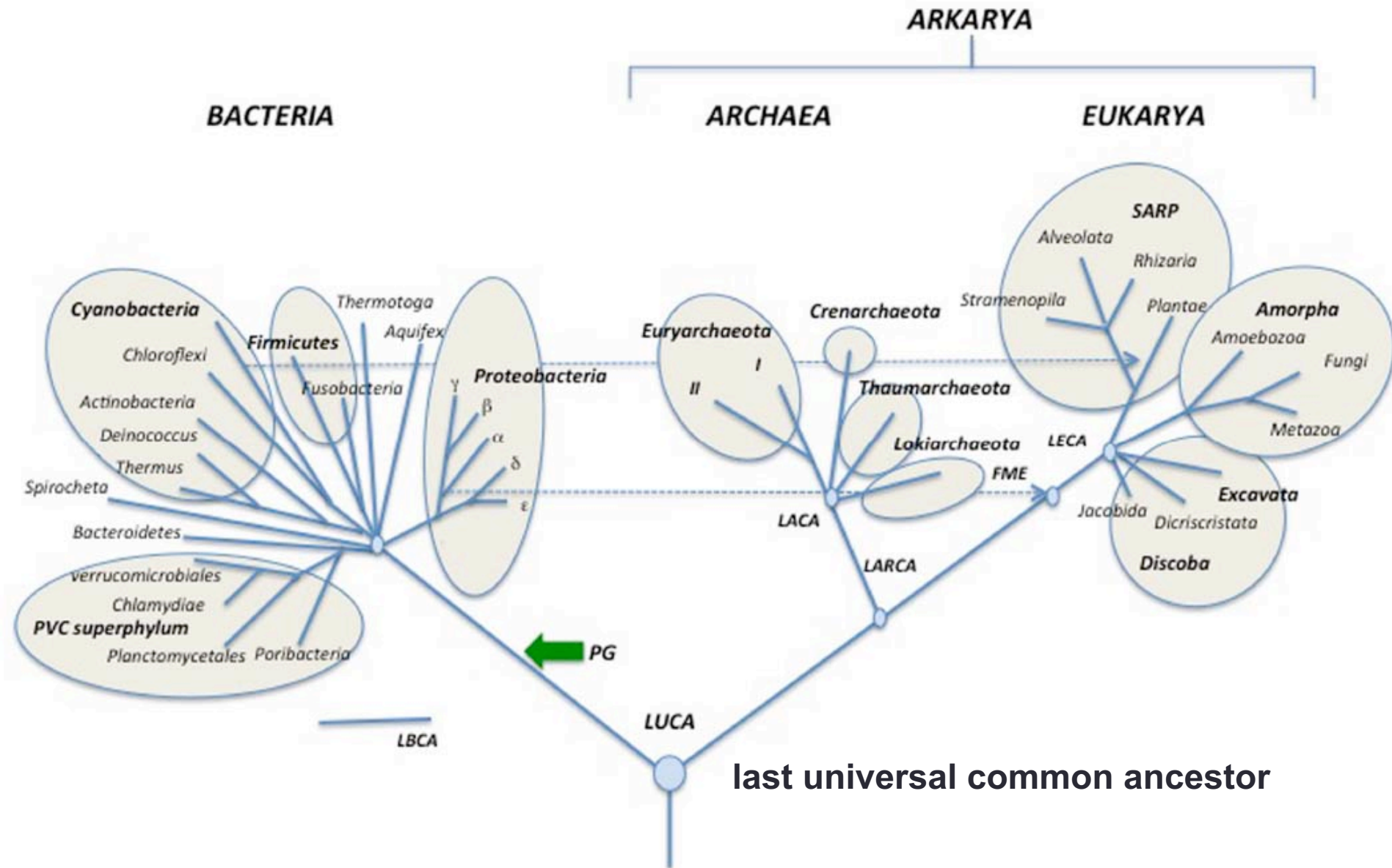
Conteúdos Principais:

- Distribuição dos Procariotos
- Filogenia principais grupos
- Variação da infecção hospitalar ao longo de 3 anos
- Projeto Microbioma Humano
- Microbioma do Trato Gastro Intestinal
- Bactérias mais comuns do ambiente hospitalar
 - *Staphylococcus aureus*
 - *Neisseria meningitidis*
- Exercícios

Distribuição dos procariotos

Habitat	Número de procariotos ($\times 10^{28}$)	Carbono total em procariotos ($\times 10^{15}$ g)
Sub-superfície Oceano	355	303
Sub-superfície Terrestre	25-250	22-215
Solo	26	26
Oceanos, lagos e rios	12	2,2
Corpo Humano	0,00004	

Filogenia: principais grupos

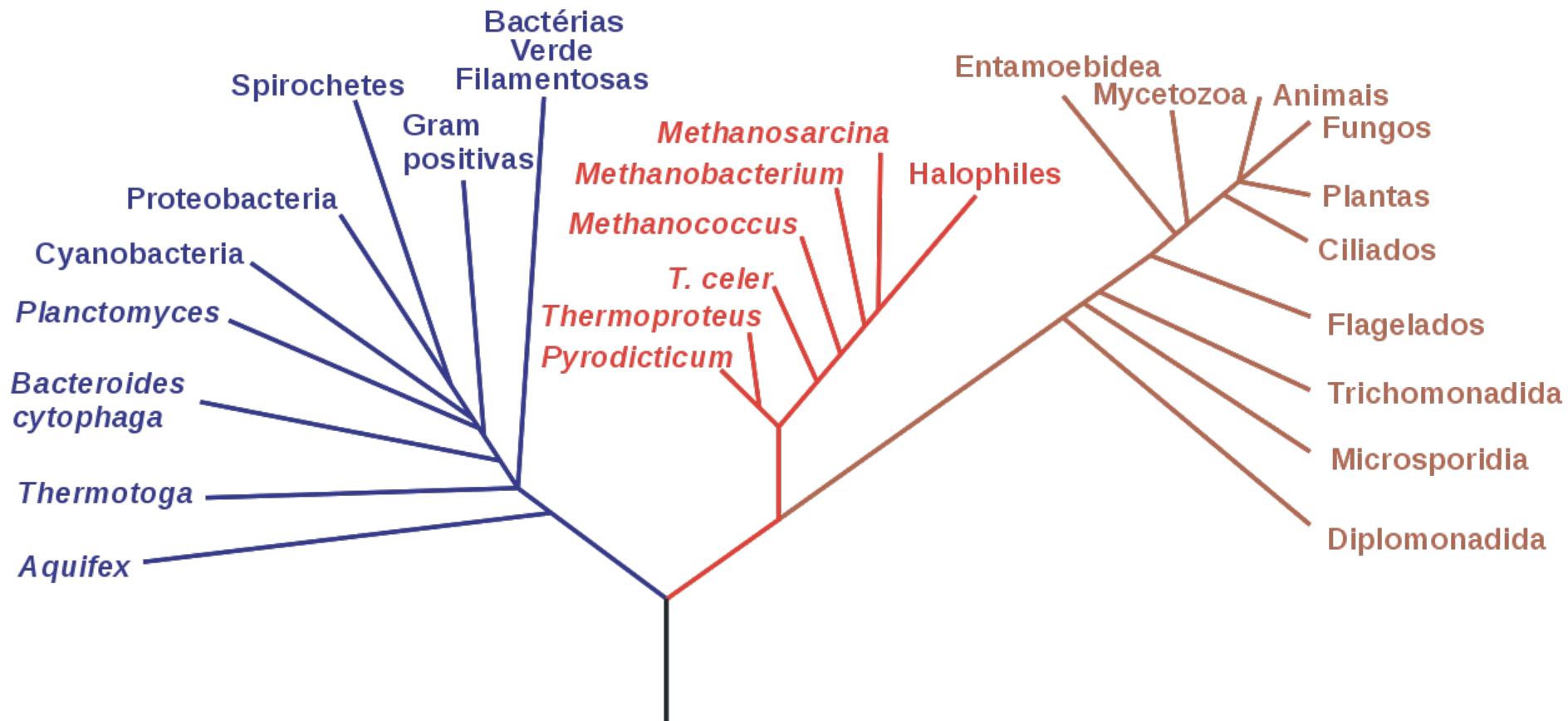


Filogenia: principais grupos

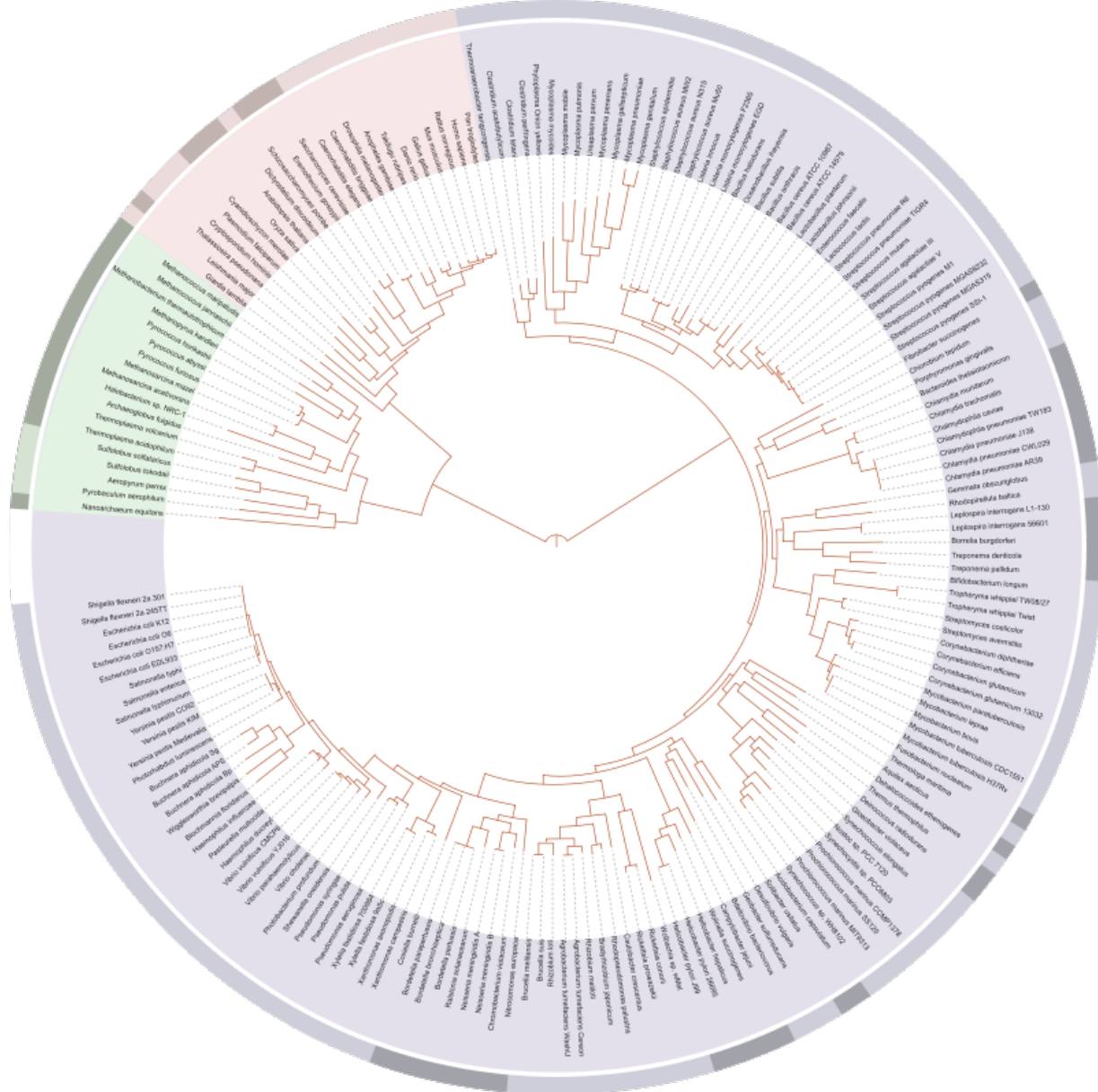
Bacteria

Archaea

Eukaria



Filogenia: principais grupos



Taxonomia

Filo

Classe

Ordem

Família

Gênero

International Nucleotide Sequence Database Collaboration

The **International Nucleotide Sequence Database Collaboration (INSDC)** consists of a joint effort to collect and disseminate **databases** containing **DNA** and **RNA** sequences.^[1] It involves the following computerized **databases**: **DNA Data Bank of Japan** (Japan), **GenBank** (USA) and the **European Nucleotide Archive** (UK). New and updated data on **nucleotide** sequences contributed by research teams to each of the three databases are synchronized on a daily basis through continuous interaction between the staff at each the collaborating organizations.

<http://www.insdc.org/>

International Nucleotide Sequence Database Collaboration



ABOUT INSDC

POLICY

ADVISORS

DOCUMENTS

International Nucleotide Sequence Database Collaboration

- The International Nucleotide Sequence Database Collaboration (INSDC) is a long-standing foundational initiative that operates between [DDBJ](#), [EMBL-EBI](#) and [NCBI](#). INSDC covers the spectrum of data raw reads, through alignments and assemblies to functional annotation, enriched with contextual information relating to samples and experimental configurations.

Data type	DDBJ	EMBL-EBI	NCBI
Next generation reads	Sequence Read Archive	European Nucleotide Archive (ENA)	Sequence Read Archive
Capillary reads	Trace Archive		Trace Archive
Annotated sequences	DDBJ		GenBank
Samples	BioSample		BioSample
Studies	BioProject		BioProject

ENA
European Nucleotide Archive

NCBI

DDBJ

Lista dos genomas bacterianos sequenciados

Contents [\[hide\]](#)

- 1 Abditibacteriota
- 2 Actinobacteria
- 3 Aquificae
- 4 Armatimonadetes
- 5 Bacteroidetes/Chlorobi group
- 6 Caldisei
- 7 Chlamydiae/Verrucomicrobia group
- 8 Chloroflexi
- 9 Chrysiogenetes
- 10 Cyanobacteria
- 11 Deferribacteres
- 12 *Deinococcus-Thermus*
- 13 Dictyoglomi
- 14 Elusimicrobia
- 15 Fibrobacteres/Acidobacteria group

- 16 Firmicutes
- 17 Fusobacteria
- 18 Gemmatimonadetes
- 19 Nitrospirae
- 20 Planctomycetes
- 21 Proteobacteria
 - 21.1 Alphaproteobacteria
 - 21.2 Betaproteobacteria
 - 21.3 Gammaproteobacteria
 - 21.4 Delta/epsilon subdivisions
 - 21.5 Zetaproteobacteria
- 22 Spirochaetes
- 23 Synergistetes
- 24 Tenericutes
- 25 Thermodesulfobacteria
- 26 Thermotogae

ETIOLOGICAL STRUCTURE OF HEALTHCARE- ASSOCIATED INFECTIONS IN ST. MARINA UNIVERSITY HOSPITAL OF VARNA FOR THE PERIOD 2011-2015

¹*Monov D.,*

²*Paunov Tz.,*

³*Mileva S.,*

³*Deneva D.,*

⁴*Zeleva E.*

Bulgaria, Varna;

¹*Educational Scientific sector "Health inspector" Medical College - Varna Medical University Varna,*

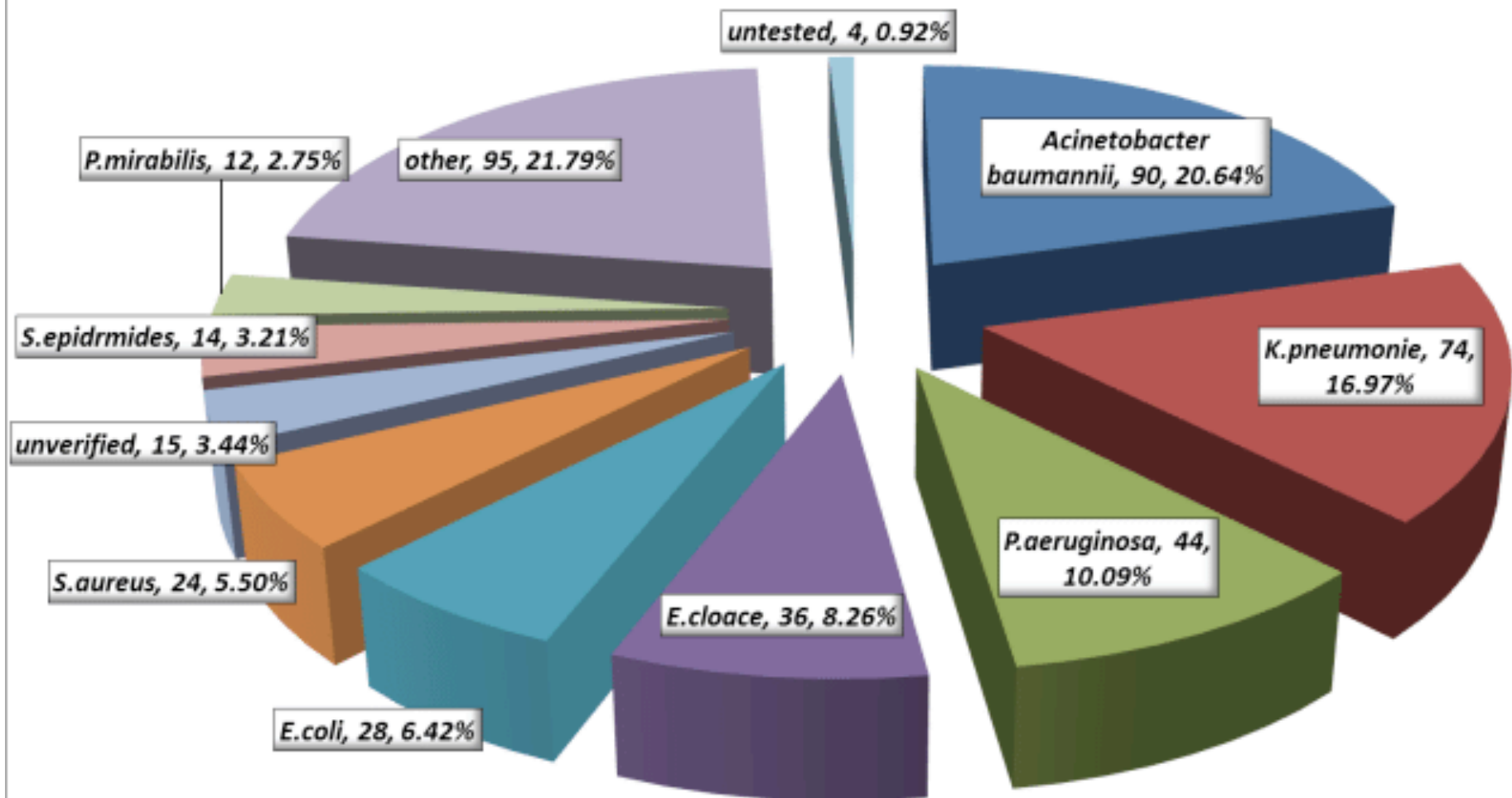
²*Medical University of Varna, Department of "Hygiene and epidemiology",*

³*"St. Marina" University Hospital of Varna,*

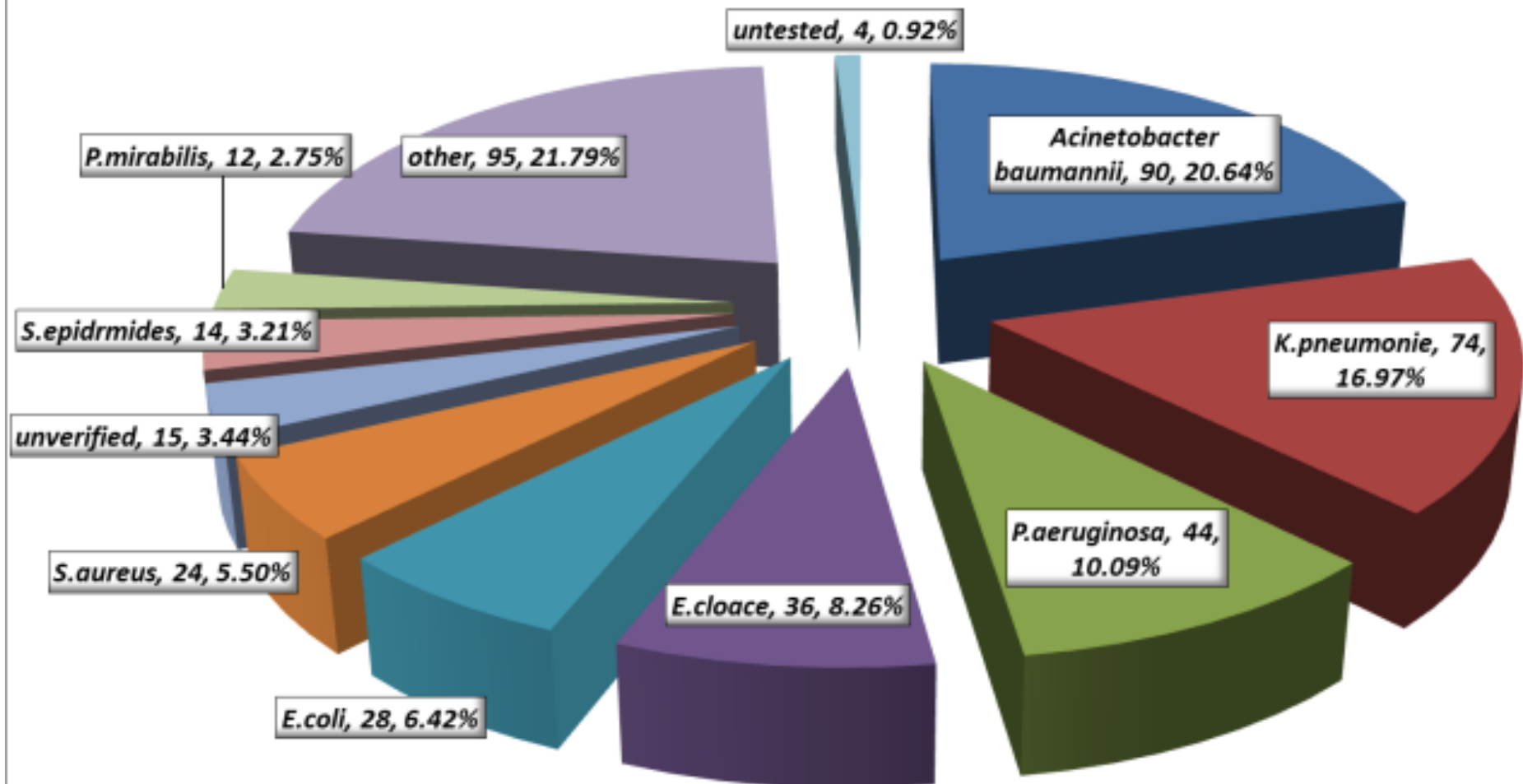
⁴*Medical University of Varna, Sliven branch, Department of "Nursing care"*



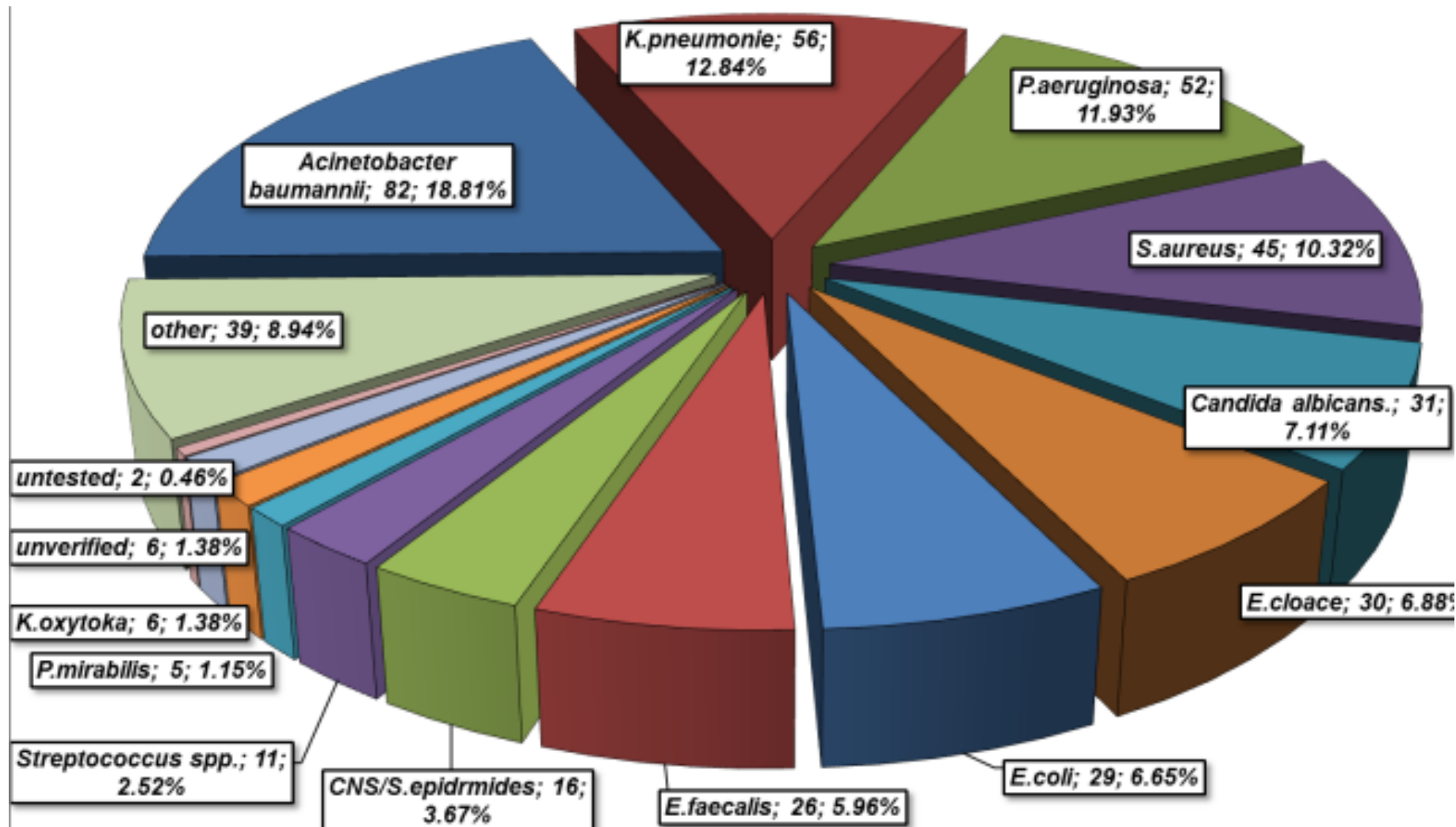
Filos grupo Bacteria detectadas Hospital St Marina Varna – 2013 - Bulgária



Filos grupo Bacteria detectadas Hospital St Marina Varna – 2014 - Bulgária



Filos grupo Bacteria detectadas Hospital St Marina Varna – 2015 - Bulgária



Conclusões

Depois de 2012, a principal causa etiológica de infecções não comensais é *Actinetobacter baumannii* que é responsável por 13% das infecções em 2012; 24% em 2013; 20% em 2014 e 18% em 2015.

O principal patógeno não comensais foi *Pseudomonas aeruginosa* que é responsável por 9% das infecções em 2012; 10% em 2013; 12% em 2014 e 10% em 2015.

Conclusões

***Staphylococcus aureus* foi o patógeno com o aumento mais significativa, como porcentagem das infecções não comensais: de 5.5% em 2014 para 10% em 2015.**



HMP1



NIH Human Microbiome Project



Overview

Membership

Publications

Resources

Data

Outreach

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Tools and Technology

Tools

Protocols



Walkthroughs



Tools

Software and online resources used by, or developed as part of the HMP are provided here.

Please be aware that HMP1 funding ended in 2012, and therefore some of these resources may have changed, moved or been discontinued. This list is no longer regularly maintained.

Microbial Reference Genomes

Sampling, Sequencing, & Analyses of 16S RNA

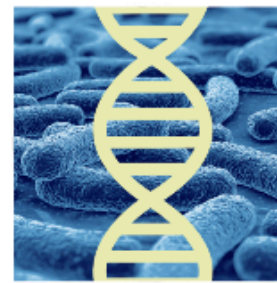
Sampling, Sequencing & Analysis of Whole Metagenomic Sequence

NIH Human Microbiome Project



Characterization of the microbiomes of healthy human subjects at five major body sites, using 16S and metagenomic shotgun sequencing.

[Enter HMP1](#)



Characterization of microbiome and human host from three cohorts of microbiome-associated conditions, using multiple 'omics technologies.

[Enter iHMP](#)

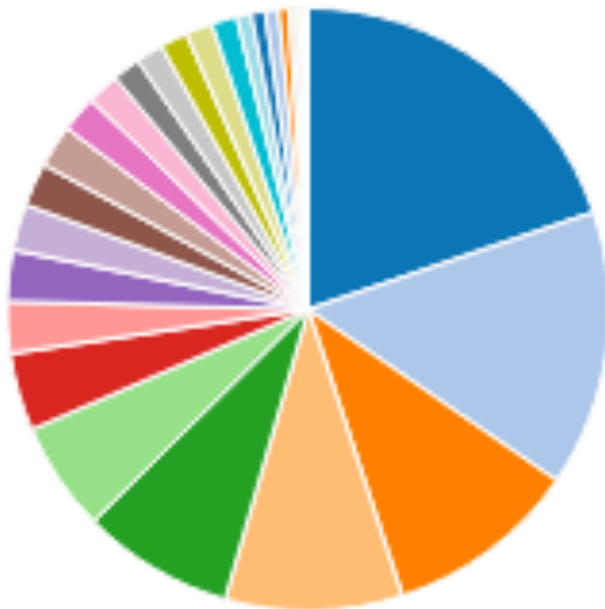
[Enter HMP Integrated Portal](#) 



Projeto Microbioma Humano

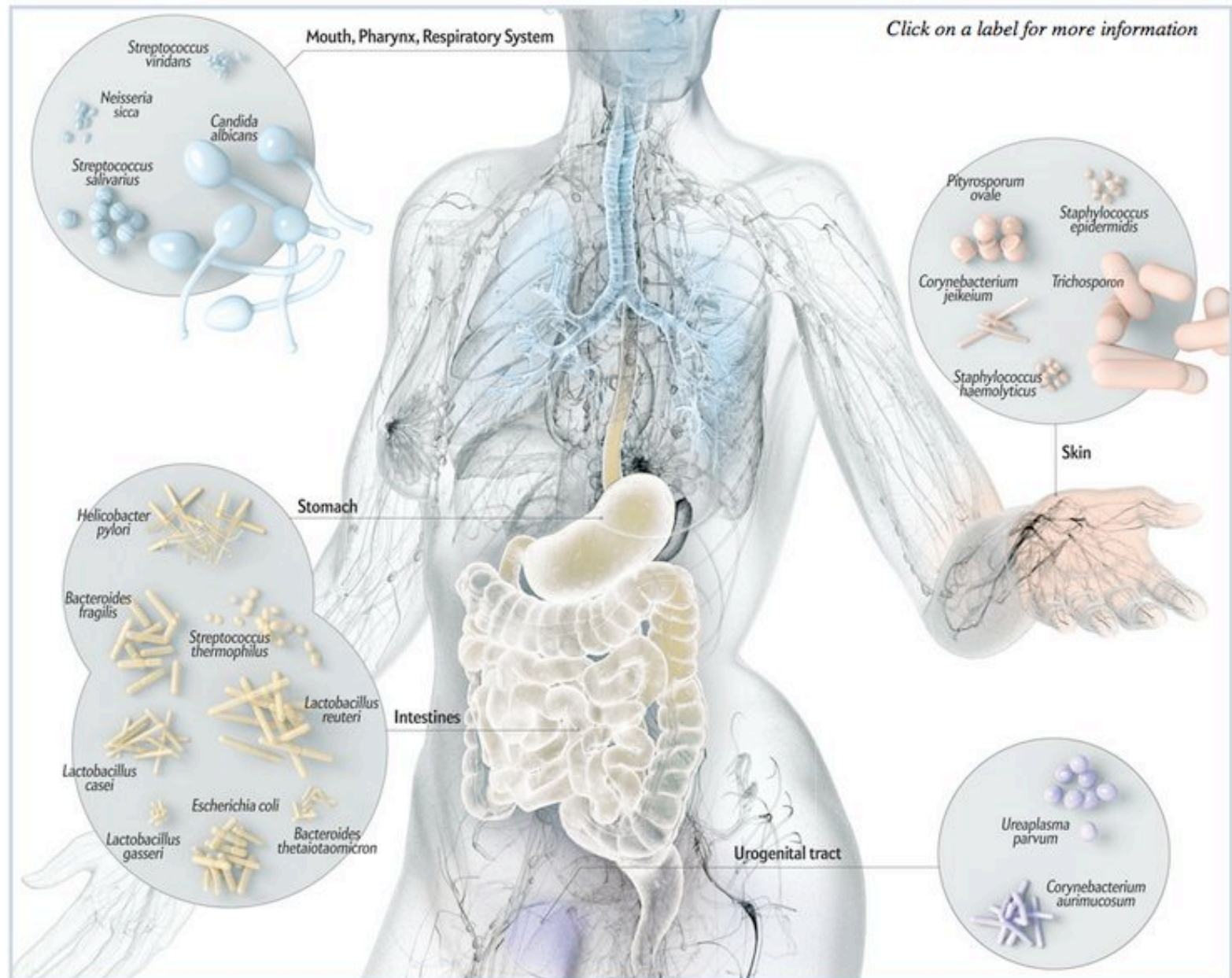
O Que é o Projeto Microbioma Humano?

- ❑ Um consórcio que envolve 45 Instituições de pesquisa e iniciado em 2008. Teve como objetivo caracterizar as comunidades microbianas encontradas em várias partes do corpo humano e analisar o papel desses micróbios na saúde humana e nas patologias.

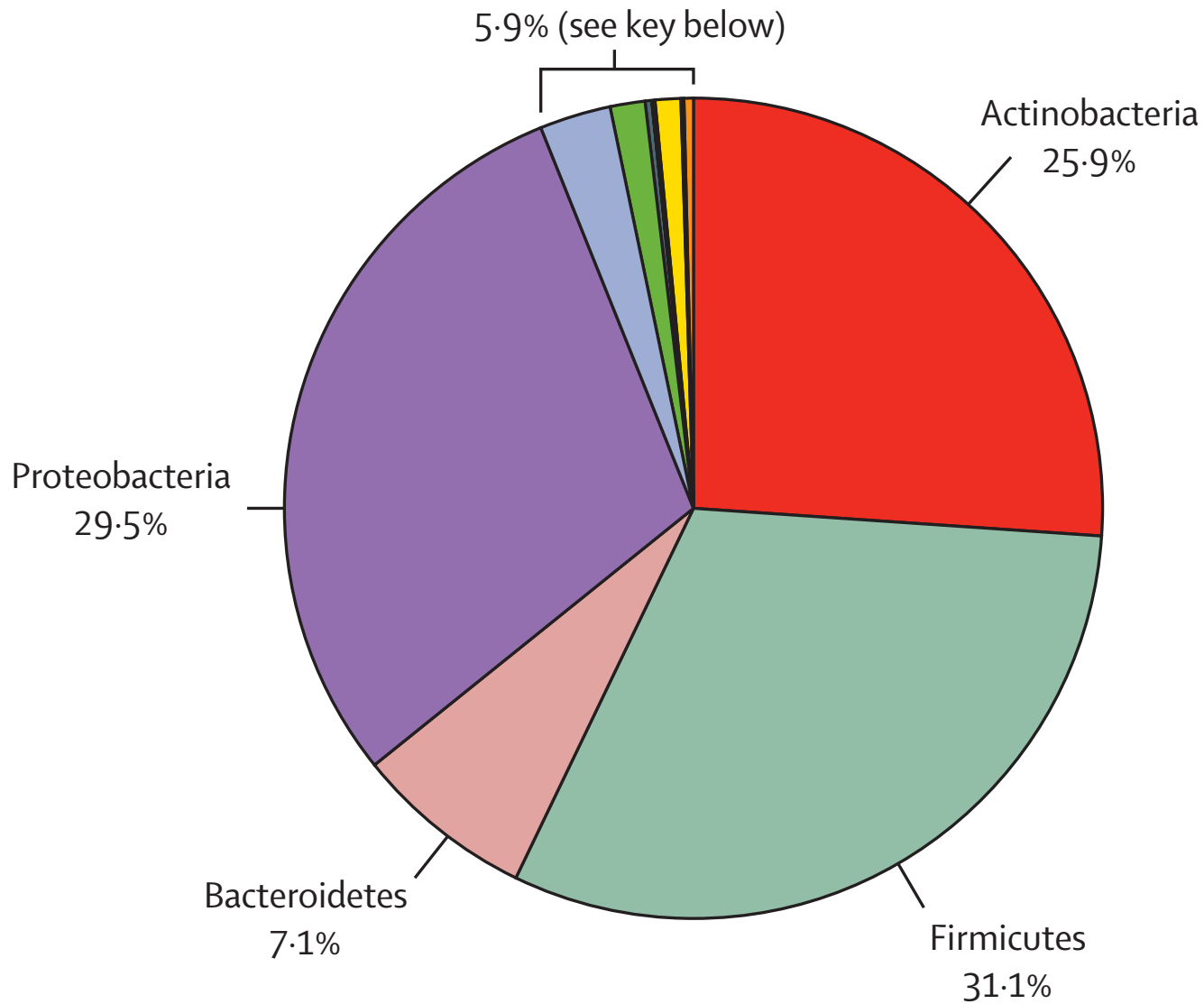


- ◆ Foram analisadas 30,000 amostras de 48 locais do corpo humano .

Microbioma Humano

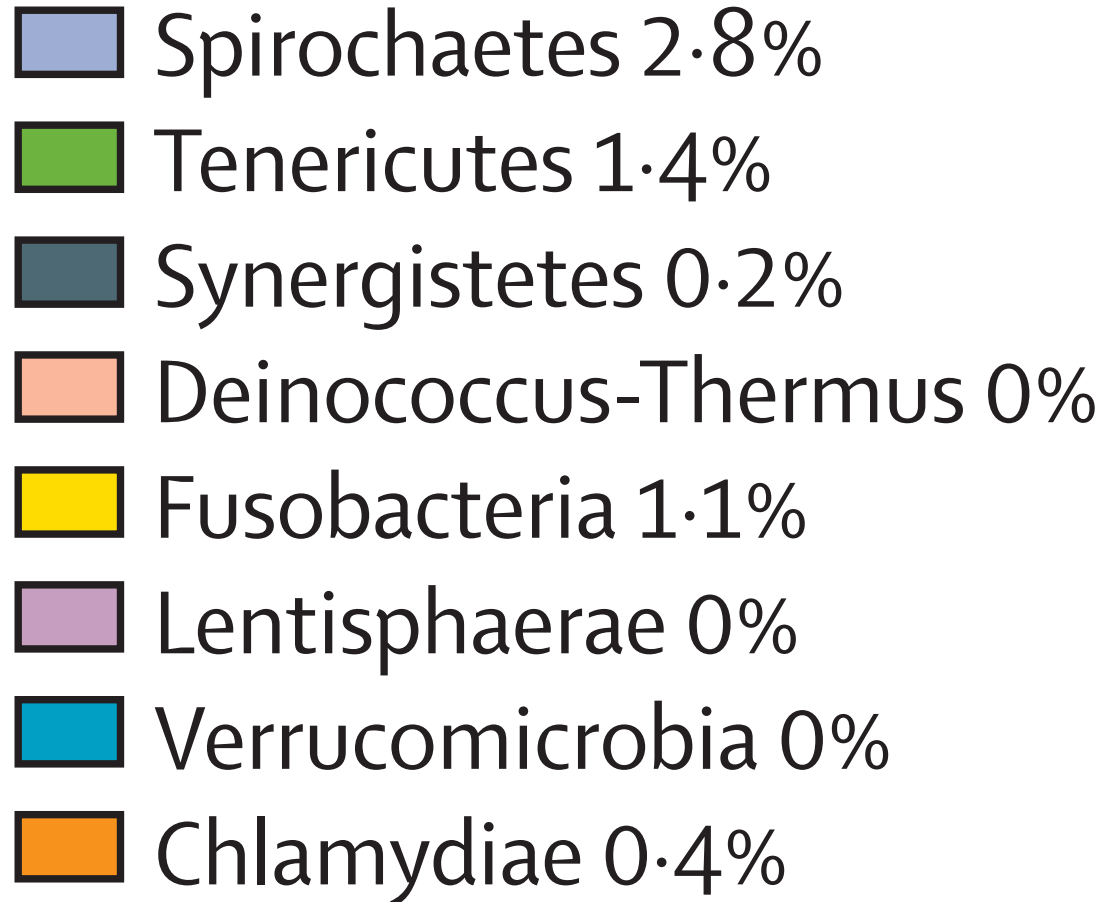


Filos do grupo Bacteria detectadas em humanos

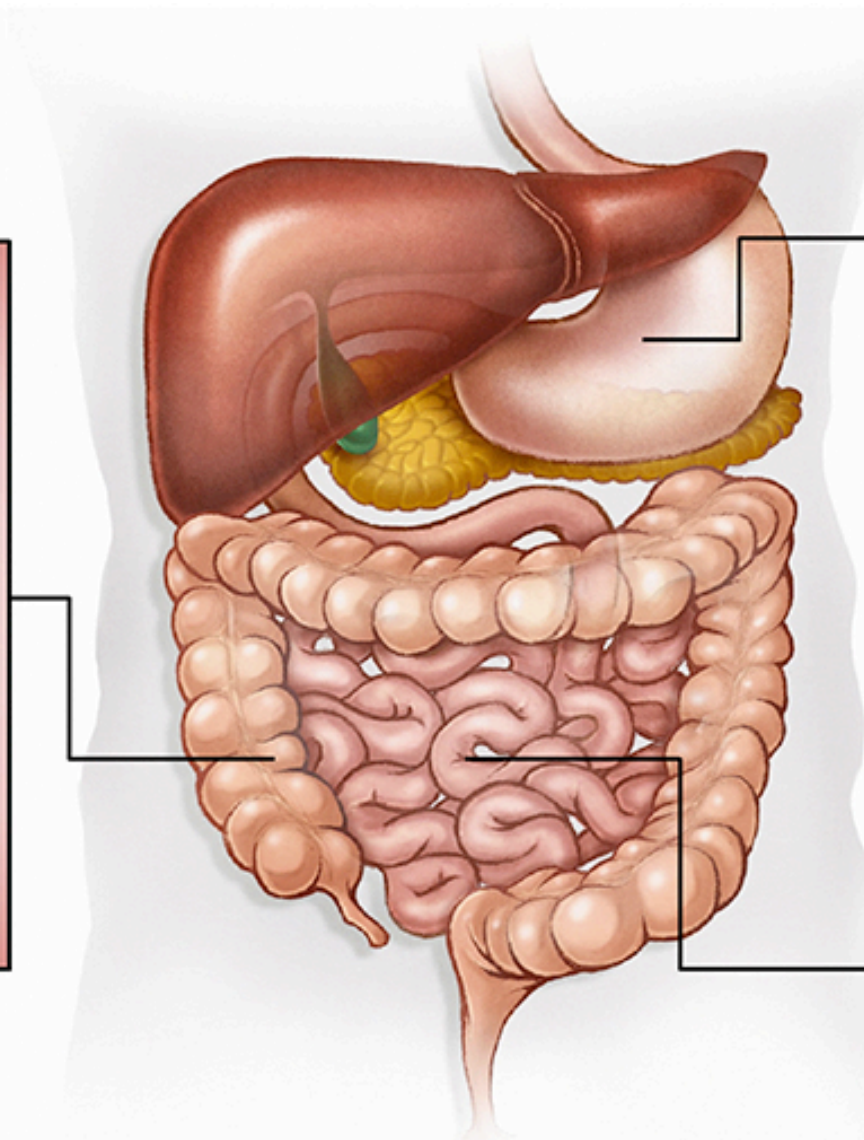


Hugon et al 2015 Lancet S1473-3099(15)00293-5

Filos grupo Bacteria detectadas em humanos



Microbioma trato gastrointestinal



Colon

$> 10^{11}$ bacteria mL^{-1}

Alistipes spp.
Anaerostipes spp.
Bacteroides spp.
Bifidobacterium spp.
Clostridium cluster spp.
Dorea spp.
Eubacterium spp.
Faecalibacterium spp.
Parabacteroides spp.
Roseburia spp.
Ruminococcus spp.

Stomach

$10^2 - 10^4$ bacteria mL^{-1}

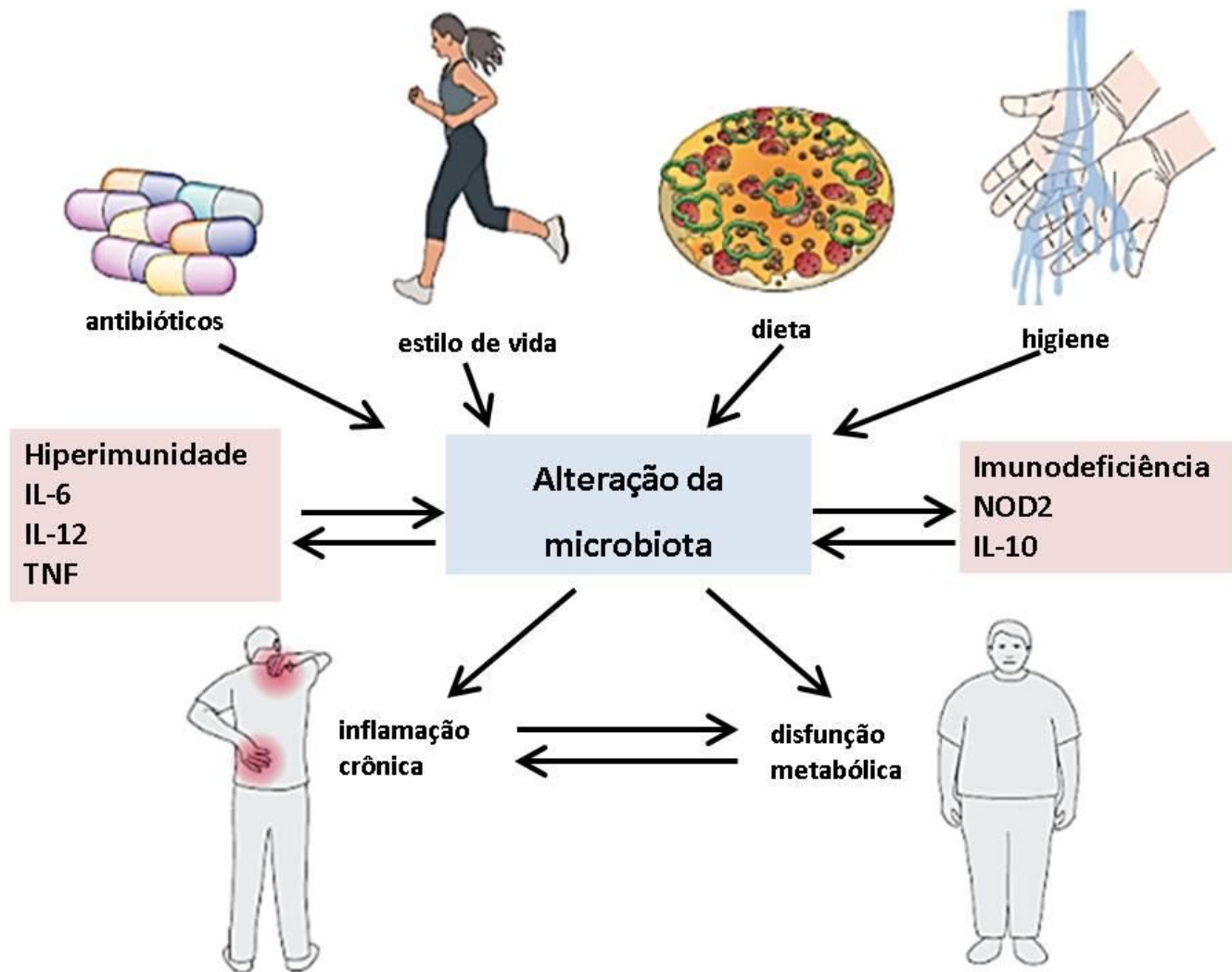
Lactobacillus spp.
Propionibacterium spp.
Streptococcus spp.
Staphylococcus spp.

Small intestine

$10^7 - 10^8$ bacteria mL^{-1}

Escherichia spp.
Bacteroides spp.
Clostridium cluster XIVa spp.
Lactobacillus spp.
Streptococcus spp.
Veillonella spp.

Fatores ambientais que afetam a microbiota intestinal



Microbioma trato gastrointestinal

Qual é o período do desenvolvimento humano que ocorre a formação do microbiota do trato gastrointestinal?

- ☐ A colonização do microbioma humano inicia-se algumas horas após o parto.
- ☐ Do nascimento aos 3 anos de idade é o período em que ocorre a colonização do trato gastro-intestinal de forma contínua e progressiva, com aumento gradual da diversidade filogenética.
- ☐ A amamentação influencia o tipo de colonização intestinal.
- ☐ A introdução dos alimentos sólidos está associada com o aumento da abundância de Bacteroidetes e uma mudança que facilita a utilização do lactato, carboidrato, biosíntese de vitamina e degradação de xenobióticos.

Bactérias mais comuns ambiente hospitalar

- ☐ *Acinetobacter baumannii*
- ☐ *Candida albican*
- ☐ *Candida parapsilosis*
- ☐ *Enterococcus faecalis*
- ☐ *E. coli*
- ☐ *Klebsiella pneumoniae*
- ☐ ***Staphylococcus aureus***
- ☐ *Staphylococcus coagulase*
- ☐ *Stenotrophomonas maltophilia*

Staphylococcus aureus

European nucleotide archive

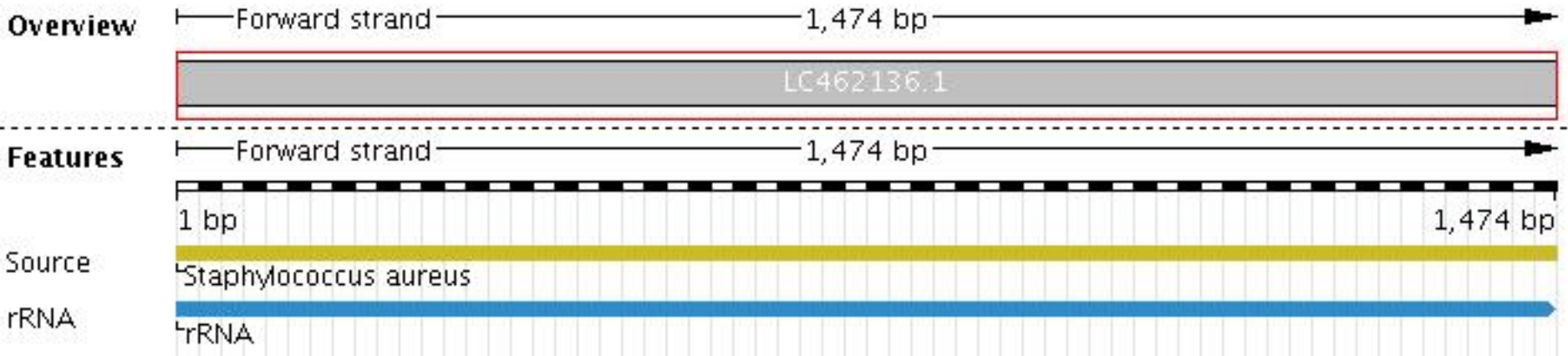
Firmicutes

Bacilli

Bacillales

Staphylococcaceae

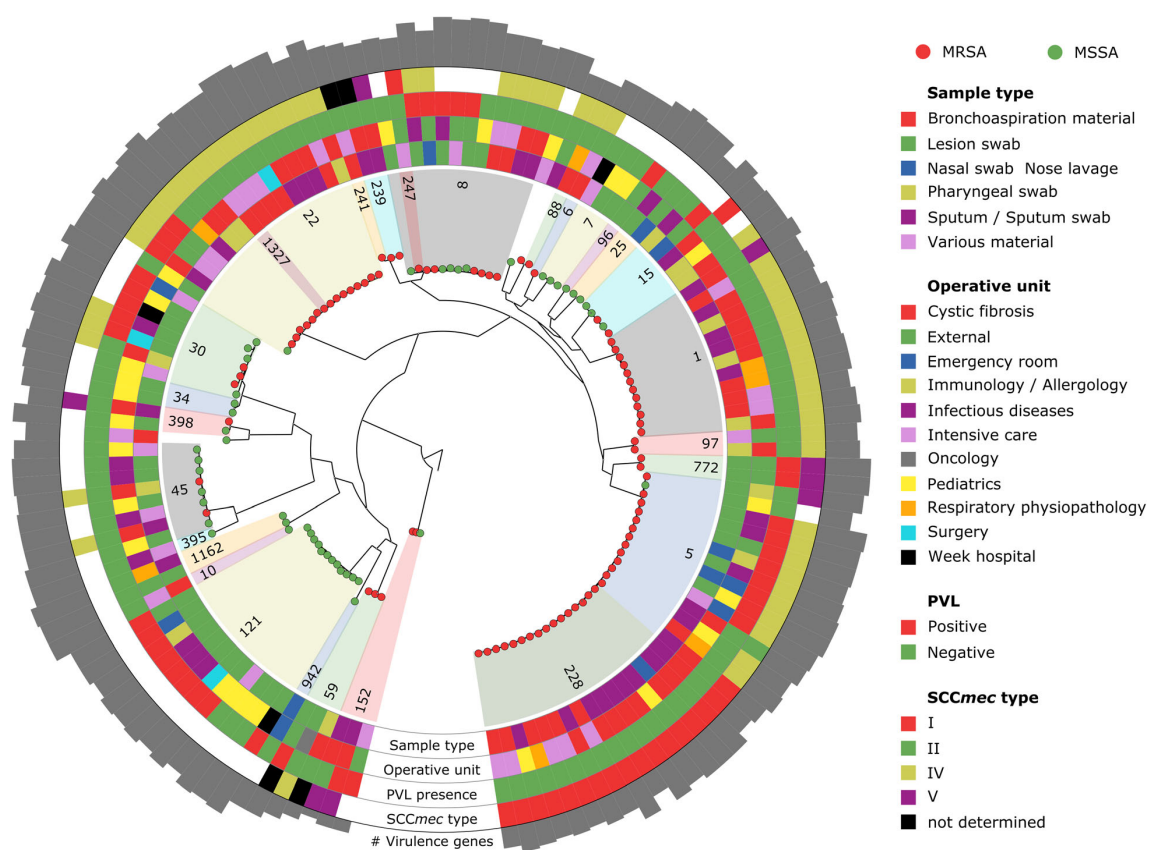
Staphylococcus



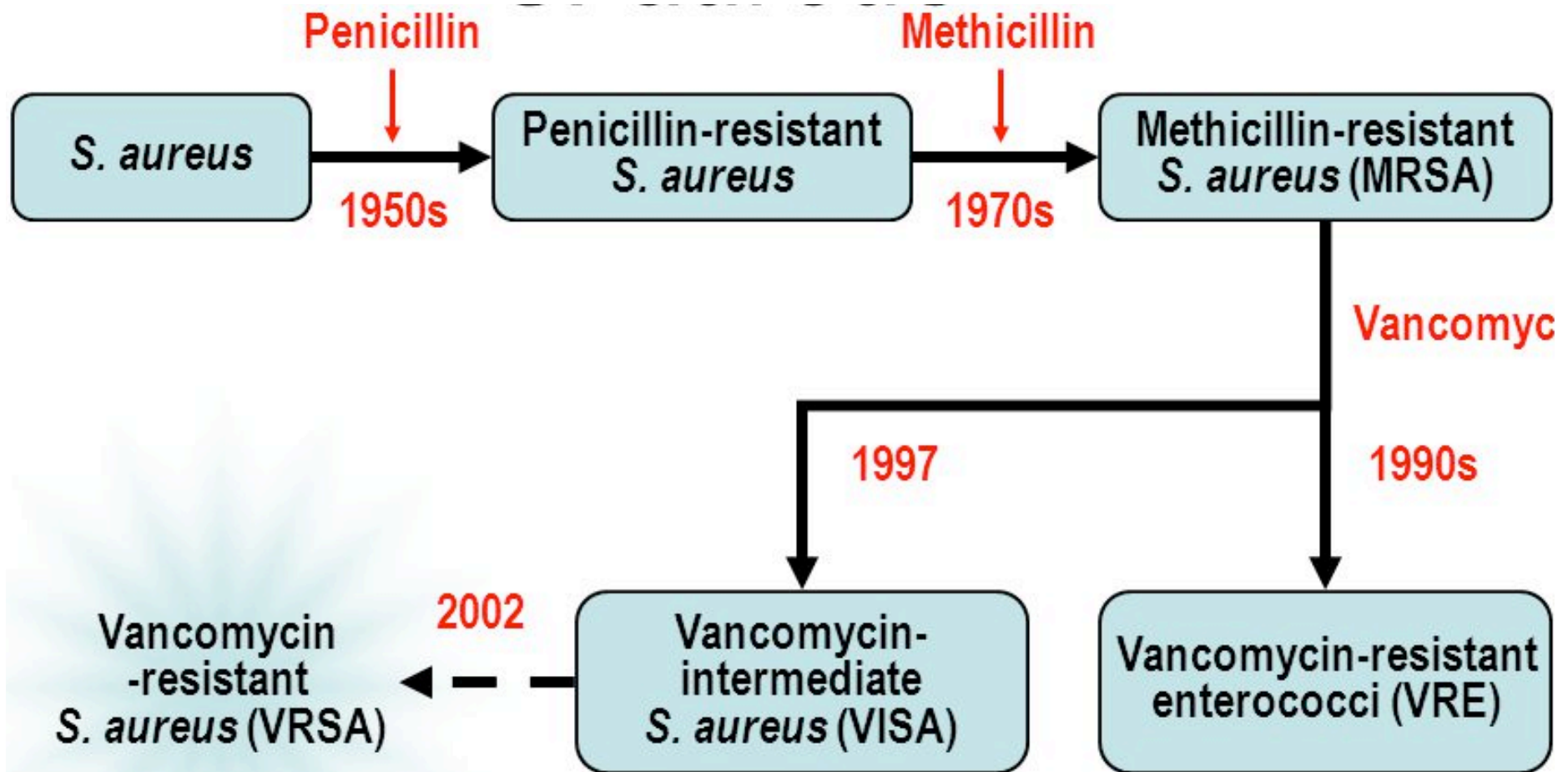
Staphylococcus aureus

❑ *Staphylococcus aureus*: problema clínico crescente devido o desenvolvimento agressivo de resistência a antibióticos.

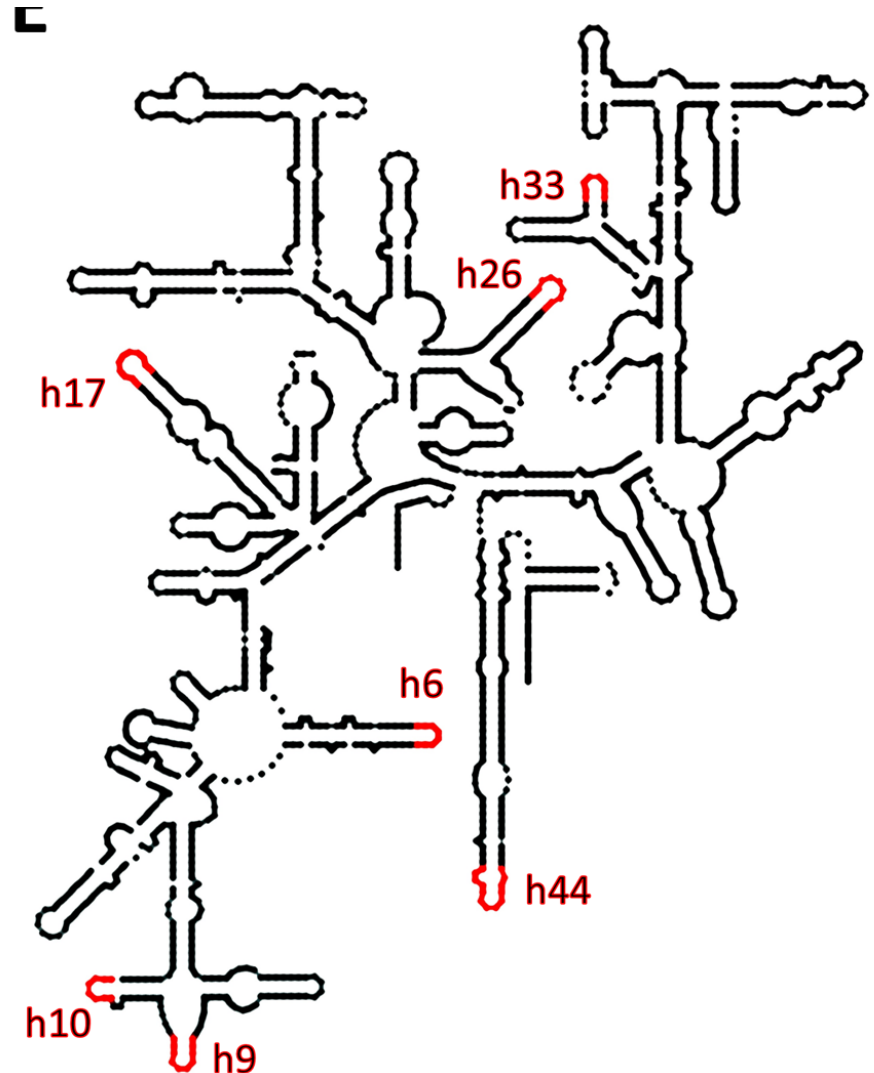
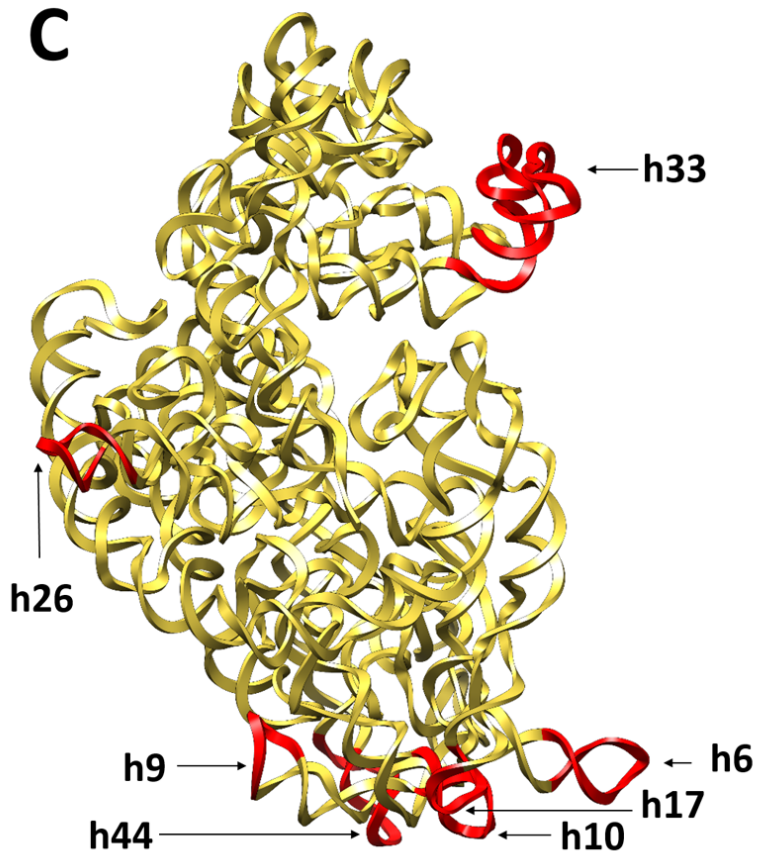
◆ Principal causa de infecção bacteriana nos países desenvolvidos.



Resistência a antibióticos em *S. aureus*

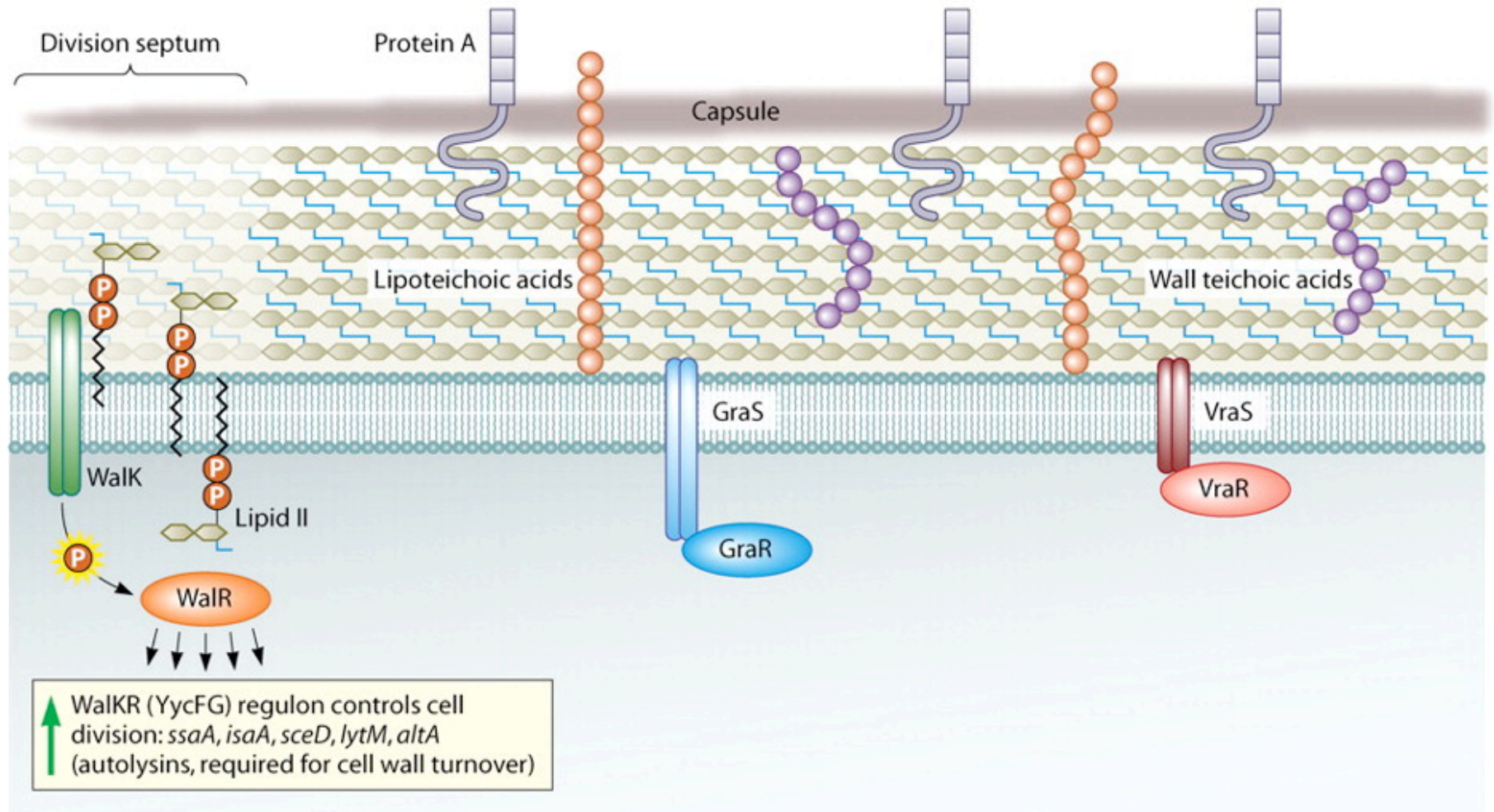


16S rRNA *S. aureus*

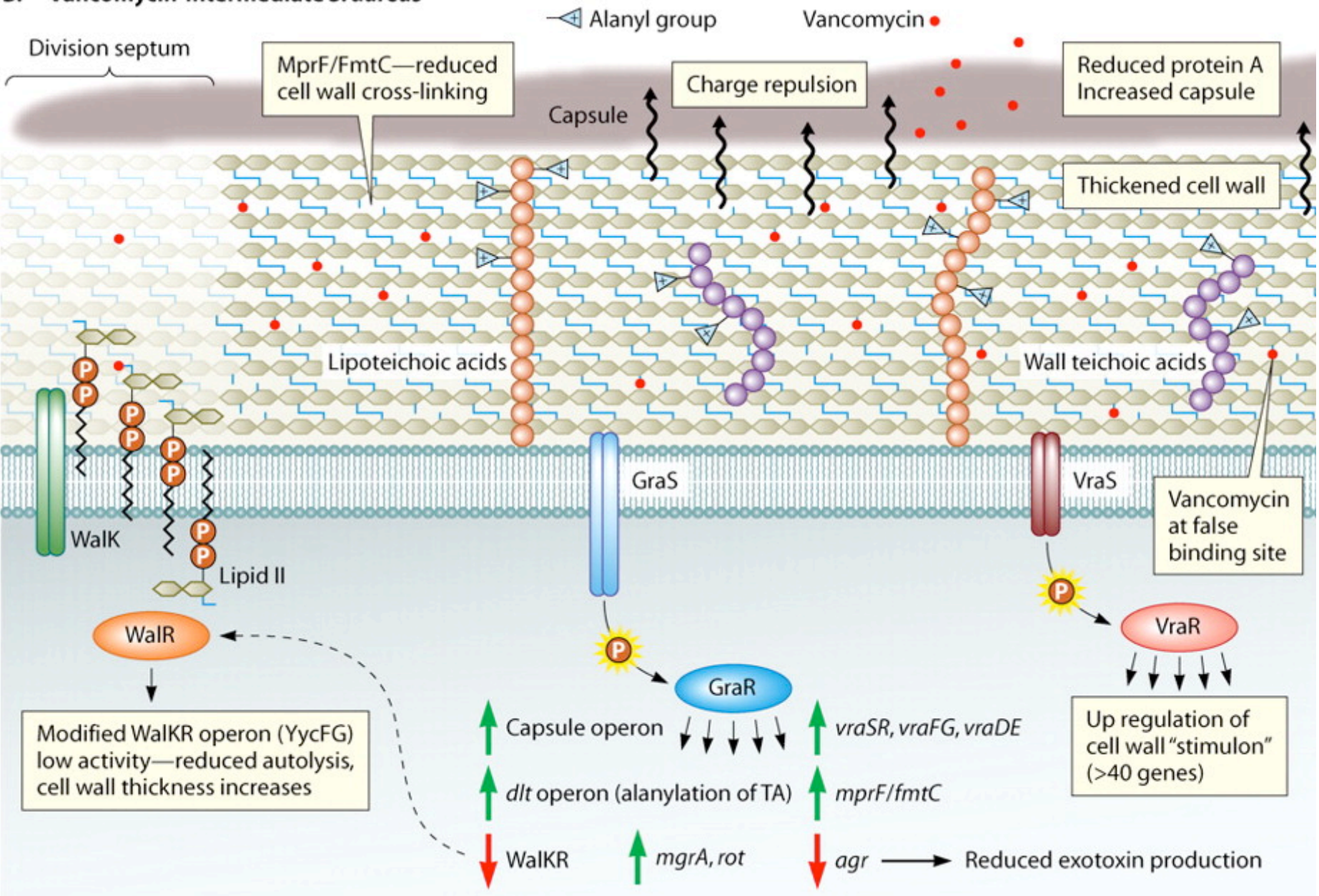


S. aureus sensível a vancomycin

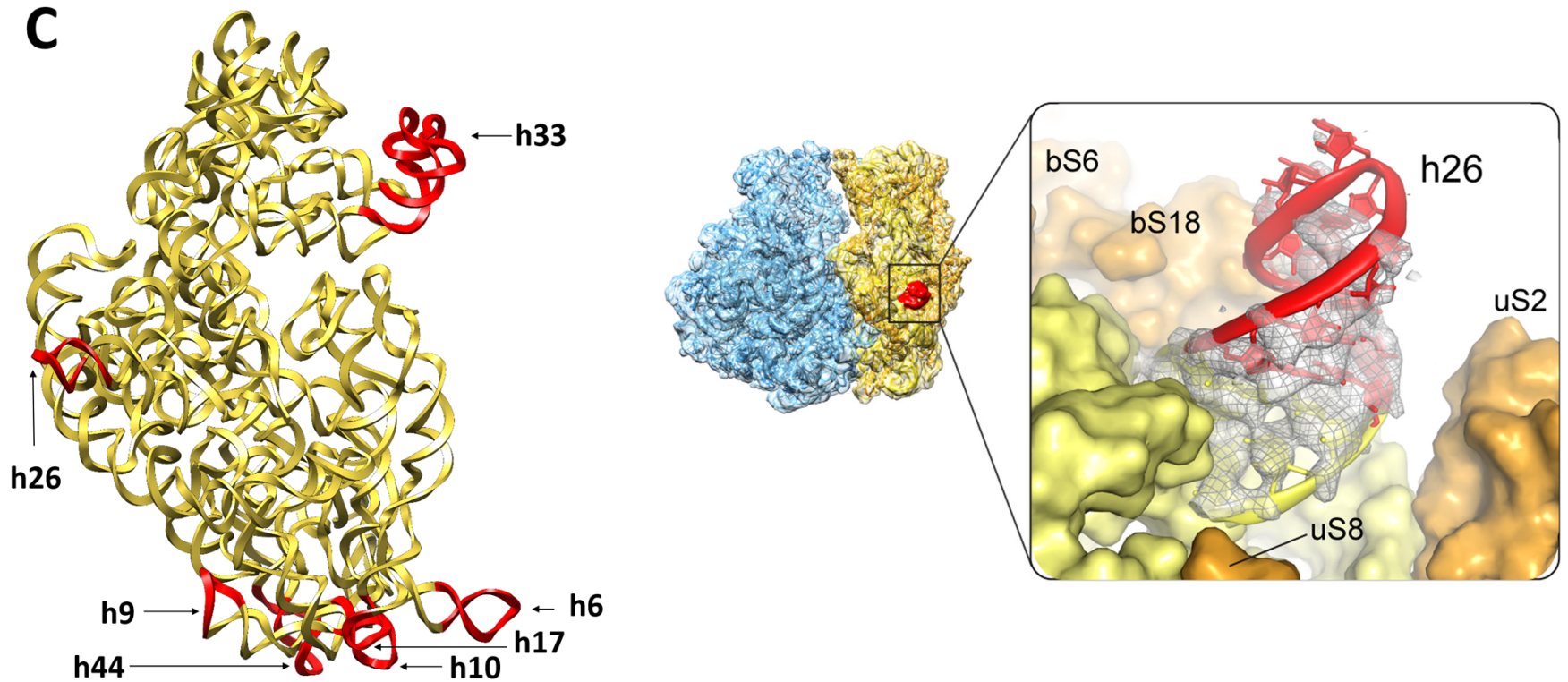
A. Vancomycin-susceptible *S. aureus*



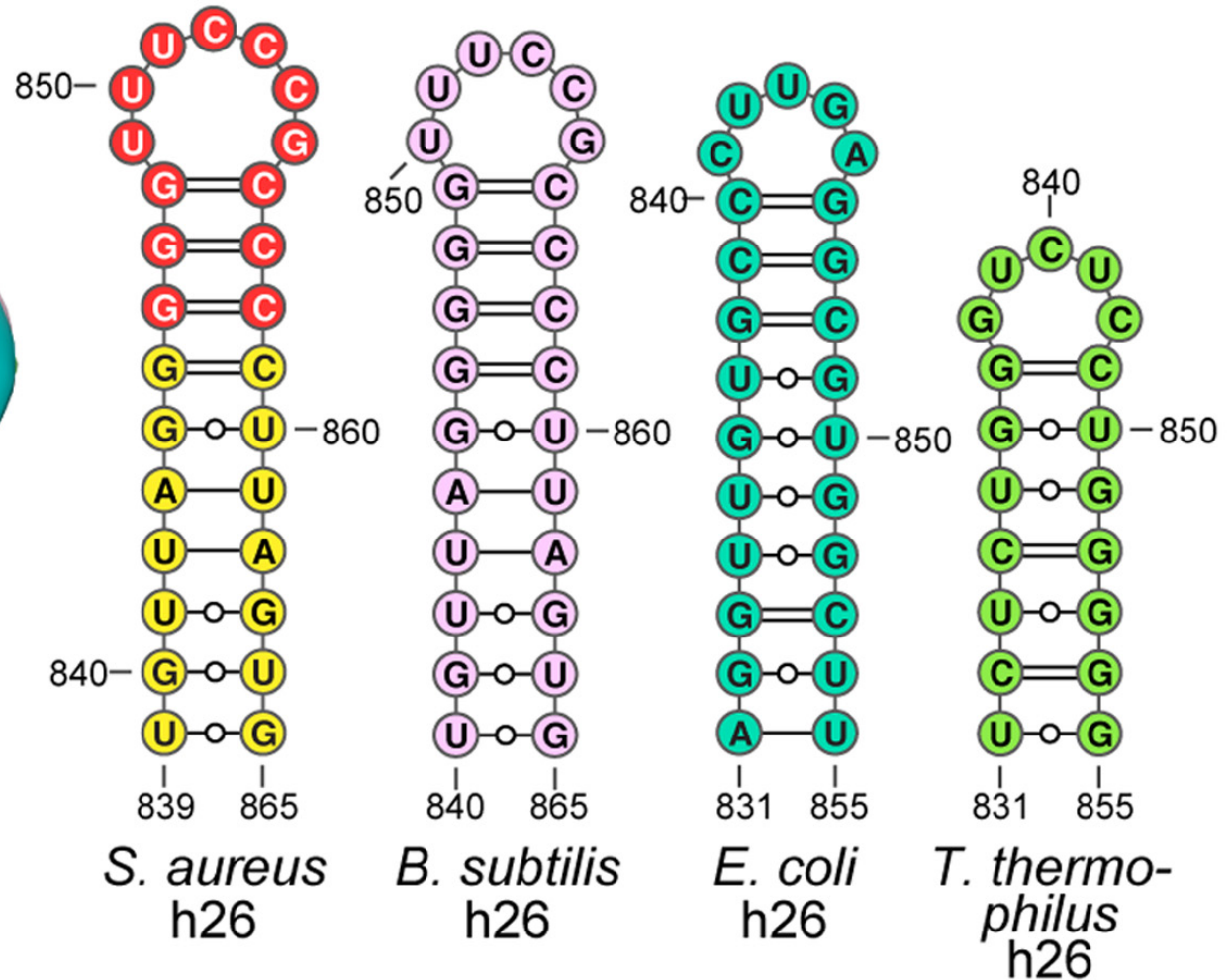
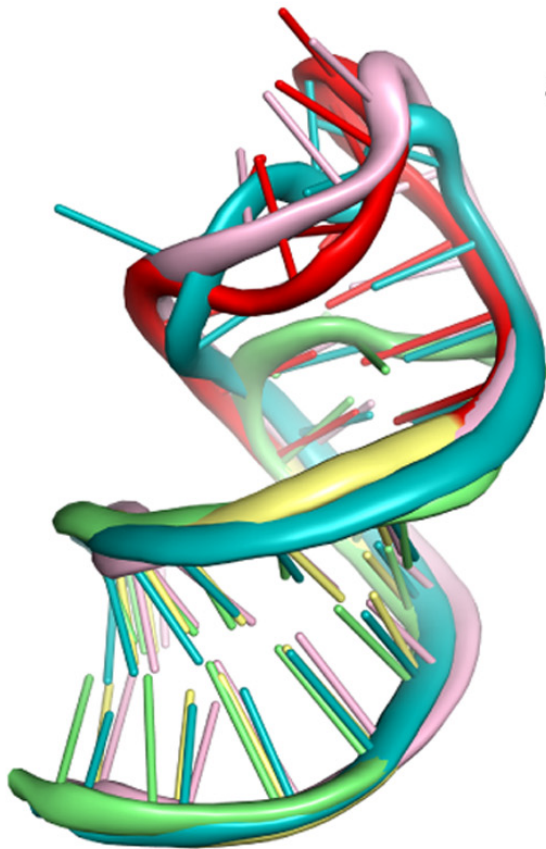
B. Vancomycin-intermediate *S. aureus*



16S rRNA *S. aureus*

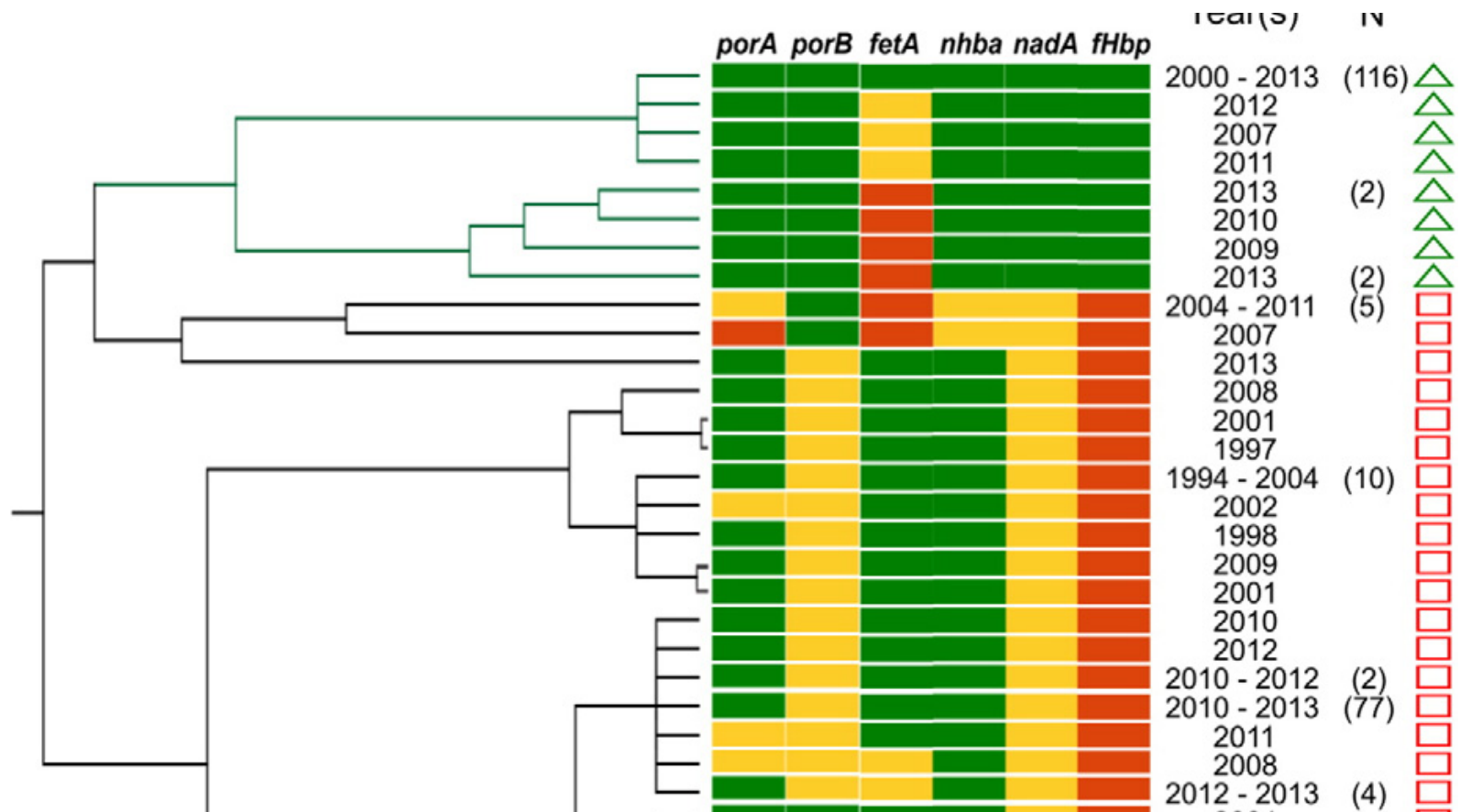


16S rRNA *S. aureus*



Neisseria meningitidis

- ❑ *Neisseria meningitidis*: serogrupo B – principal causa de meningite e septicemia em crianças e adolescentes.



Neisseria meningitidis

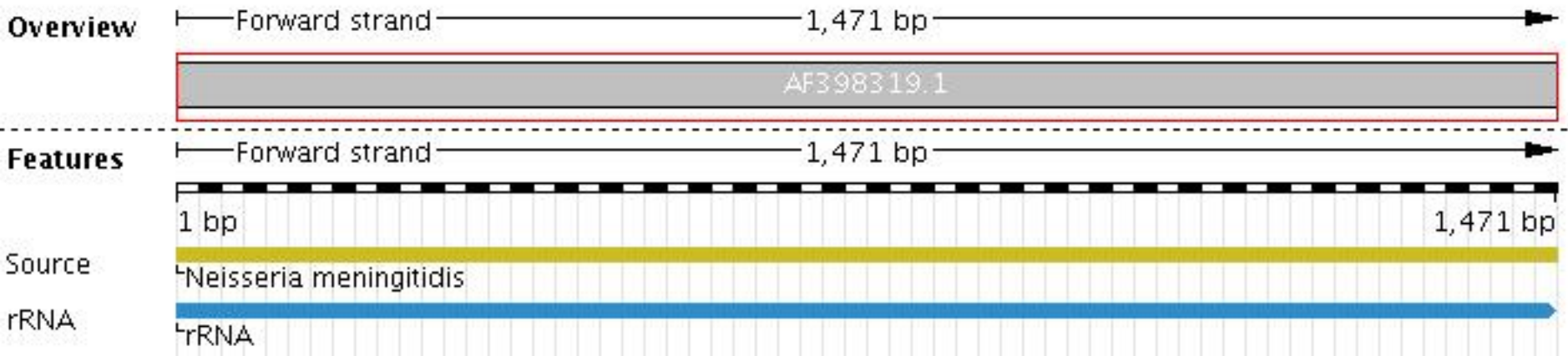
Proteobacteria

Betaproteobacteria

Neisseriales

Neisseriaceae

Neisseria



Exercícios

- ❑ Determine: Filo, Classe, Ordem e Família das principais bactérias de ambiente hospitalar
- ❑ Qual o Filo mais abundante?
- ❑ Qual o tamanho do 16S rRNA das principais bactérias de ambiente hospitalar?

Bibliografia

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Mustapha et al., 2015: Genomic Epidemiology of Hypervirulent Serogroup W, ST-11 *Neisseria meningitidis*. EBioMedicine 2:1447-1455

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Manara et al., 2018: Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of *Staphylococcus aureus* strains in a paediatric hospital. Genome Medicine 10:82.

Khusainov et al., 2016: Structure of the 70S ribosome from human pathogen *Staphylococcus aureus*. Nucl. Acid. Res. 44:10491.