

wgMLST  
SCHEMA

# BIONUMERICS®

MICROBIAL DATA ANALYSIS SOFTWARE

*Streptococcus pyogenes*

## WHAT IS wgMLST AND WHY DO YOU NEED A SCHEMA FOR IT?

Whole genome MLST (wgMLST) is an extension of the more traditional MLST, allowing a much higher typing resolution. It offers a fast and cost-effective way to analyze bacterial genomes. A schema is essential for the wgMLST technique to work as it defines the loci to which allele numbers are assigned. It represents the basis for a stable nomenclature that you can use to communicate about outbreaks, epidemics, evolution, etc...

## WHY DID WE DEVELOP A *STREPTOCOCCUS PYOGENES* wgMLST SCHEMA?

*Streptococcus pyogenes* is an infrequent, but usually pathogenic, part of the skin microbiota. Many important human diseases, which can range from mild skin infections to life-threatening systemic diseases, are caused by *S. pyogenes*. Some strains are toxigenic causing infections that may lead to the potentially life-threatening streptococcal toxic shock syndrome. These toxigenic strains can be quickly characterized using a well-defined wgMLST schema.

*Streptococcus pyogenes* subschemes

2,728 wgMLST loci + 7 MLST loci

## HOW WILL IT HELP YOU?



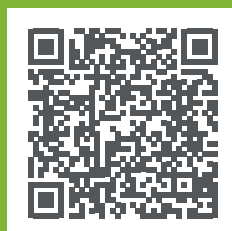
Turnaround  
time < 30 min



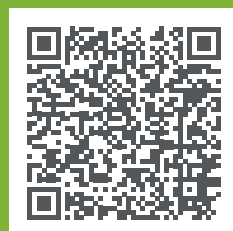
Simultaneous  
sample processing  
possible

- ✓ Defines a **robust set of loci**, validated and approved by our microbiologists
- ✓ Contains **minimal sample artifacts**, while keeping great discriminatory power
- ✓ Represents the known **diversity** of the species
- ✓ Allows **detection of markers** specific to a certain strain, enabling powerful classification and outbreak identification

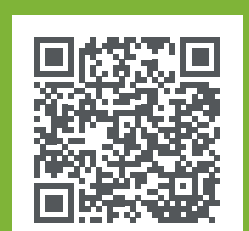
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