SI NO

□ □ Solo PAER?

Parecería interesante incluir otros organismos, valorar necesidad de definir tabla “RESISTOMAS” independientes por “organismo”.

□ □ Blank value (#ND)

Metadata (General)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| OK | FIELD | TYPE | DESCRIPTION | VALUES | NOTES |
| □ | ID | Alphanumerical | Unique identifier for a strain |  |  |
| □ | Project |  |  |  |  |
| □ | Data analysis project |  |  |  |  |
| □ | ORGANISM | Alphanumerical | Organism sequenced | * #ND * Pseudomonas aeruginosa |  |
| □ | ST |  | Sequence type (analysed by MLST definition) | * 0000 to 0000 * #ND |  |
| □ | Isolation date | Numerical | DD/MM/YY | * 0000 to 9999 * #ND |  |
| □ |  |  |  |  |  |

Metadata (Clinical)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| OK | FIELD | TYPE | DESCRIPTION | VALUES | NOTES |
| □ | Patient\_ID in the project | Alphanumerical | Unique identifier for the patient |  |  |
| □ | SAMPLE\_TYPE | Alphanumerical | Sample type for the strain | Definido para GEMARA, utilizarlo |  |
| □ | HOSPITAL\_NAME |  |  |  |  |
| □ | HOSPITAL\_WARD |  |  |  |  |
| □ | REGION |  |  |  |  |
| □ | COUNTRY |  |  |  |  |

Fenotypical and molecular information

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  | OK | FIELD | TYPE | DESCRIPTION | VALUES | NOTES |
|  |  |  |  |  |  | □ | Antibiotic Susceptibility Method | Alphanumerical | Method used for AST | Broth microdilution  Gradient test  Disk diffussion   * MIC * #ND |  |
|  |  |  |  |  |  |  | Antimicrobials | MIC value (numeric) |  |  |  |
|  |  |  |  |  |  | □ | Clinical interpretation (original) |  |  |  |  |
|  |  |  |  |  |  |  | ECDC-Resistance profile (original) |  |  |  |  |
|  |  |  |  |  |  |  | IDSA-Resistance profile (original) |  |  |  |  |
|  |  |  |  |  |  |  | Detección molecular de beta-lactamasas |  |  |  |  |
|  |  |  |  |  |  |  | Test CLOXA |  |  |  |  |
|  |  |  |  |  |  |  | Test MBL |  |  |  |  |
|  |  |  |  |  |  |  | Test BLEE |  |  |  |  |
|  |  |  |  |  |  |  | Test carbapenemasas clase A |  |  |  |  |
|  |  |  |  |  |  |  | Serotipo (O antigen) |  |  |  |  |
|  |  |  |  |  |  |  | CEVS (C. elegans virukence score) |  |  |  |  |
|  |  |  |  |  |  |  | LD50 (G. mellonella) |  |  |  |  |
|  |  |  |  |  |  |  | Hipermutador |  |  | SI, NO, DESCONOCIDO |  |

Sequence information

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| OK | FIELD | TYPE | DESCRIPTION | VALUES | NOTES |
| □ | TECHNIQUE | Alphanumerical | Sequencing technology | * Illumina * Oxford Nanopore * #ND |  |
| □ | PLATFORM | Alphanumerical | Platform used to sequence | * MiSeq, NovaSeq, HiSeq2000 * minION, gridION |  |
| □ | SOURCE | Alphanumerical |  | * Local * 3rd Part * #ND |  |
| □ | ST | Alphanumerical | Sequencetype (MLST) | * acsA, aroE, guaA, mutL, nuoD, ppsA, trpE * Analized MLST through allele combination |  |
|  | O-type |  | O-antigen type |  |  |
| □ | RESISTOME | Alphanumerical | Horizontally acquired resistance determinantsome analysis | * ges and InDels * Beta-lactamasas * AMES * Others |  |
| □ |  |  | Mutational | * List of chromosomic AR related genes |  |
|  | VIRULENCE MARKERS |  |  | exoS, exoU, exoT, exoY |  |
|  | MUTOME |  |  | * List of chromosomic genes |  |
| □ | ALIGNMENT | File | De Novo assembly |  |  |
| □ |  |  |  |  |  |
| □ | RAW DATA | File | Fastq | * Fastq |  |
|  |  |  |  |  |  |

# ID (alphanumerical): Unique identifier for a strain

# SEQUENCETYPE\_MLST (NUMERICAL): SEQUENCETYPE DEFIN