MLST Results

Sequence Type: *Unknown ST**

*Please note that one or more loci do not match perfectly to any previously registered MLST allele.
We recommend verifying the results by traditional methods for MLST.

SETTINGS:

Organism: *Pseudomonas aeruginosa*

MLST Profile: *paeruginosa*

Genes in MLST Profile: *7*

Locus	%Identity	HSP Length / Allele Length	Gaps	Allele
acs	99.74%	390/390	0	*acs_28*
aro	100%	349/498	0	*aro_122*
gua	100%	373/373	0	*gua_11*
mut	100%	442/442	0	*mut_11*
nuo	100%	366/366	0	*nuo_4*
pps	100%	370/370	0	*pps_12*
trp	100%	443/443	0	*trp_3*

extended output

CONTIGS INFO:

Technology: *Illumina Single End Reads*

N50: *2670*

acs*: WARNING, Identity: 99.74%, Length/HSP: 390/390, Gaps: 0, *acs_28* is the best match for *acs

```
MLST allele seq:  ggcccgttggccaacggcgccaccaccattctgttcgagggcgtgccgaactaccccgac
Hit in genome:    ggcccgttggccaacggcgccaccaccattctgttcgagggcgtgccgaactaccccgac

MLST allele seq:  gtgacccgcgtggcgaaaatcatcgacaagcacaaggtcaacatcctctacaccgcgccg
Hit in genome:    gtgacccgcgtggcgaaaatcatcgacaagcacaaggtcaacatcctctacaccgcgccg

MLST allele seq:  accgcgatccgcgcgatgatggccgaaggcaaggcggcggtggccggtgccgacggttcc
Hit in genome:    accgcgatccgcgcgatgatggccgaaggcaaggcggcggtggccggtgccgacggttcc

MLST allele seq:  agcctgcgtctgctcggttcggtgggcgagccgatcaacccggaagcctggcagtggtac
Hit in genome:    agcctgcgtctgctcggttctgtgggcgagccgatcaacccggaagcctggcagtggtac

MLST allele seq:  tacgagaccgtcggccagtcgcgctgcccgatcgtcgacacctggtggcagaccgagacc
Hit in genome:    tacgagaccgtcggccagtcgcgctgcccgatcgtcgacacctggtggcagaccgagacc

MLST allele seq:  ggcgcctgcctgatgacccgctgccgggcgcccacgcgatgaagccgggctctgcagcc
Hit in genome:    ggcgcctgcctgatgacccgctgccgggcgcccacgcgatgaagccgggctctgcagcc

MLST allele seq:  aagccgttcttcggcgtggtaccggcactg
Hit in genome:    aagccgttcttcggcgtggtaccggcactg
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***aro*: WARNING, Identity: 100%, Length/HSP: 498/349, Gaps: 0, *aro_122* is the best**

match for *aro*

```
MLST allele seq: atgtcaccgtgccgttcaaggaagaggcctatcgtctggtggacgaattgagcgagcggg
Hit in genome:

MLST allele seq: ccacccgggccggggcggtgaacaccctgatccgcctcgccgacggtcgcctgcgcggcg
Hit in genome:

MLST allele seq: acaacaccgacggcgcgggcttgctgcgggacctgacggcgaacgccggggtcgagctgc
Hit in genome:                              gacctgacggcgaacgccggggtcgagctgc

MLST allele seq: gcggcaagcgggttctcctgctcggcgccggcggtgcggtgcgtggggtgctcgaaccct
Hit in genome:   gcggcaagcgggttctcctgctcggcgccggcggtgcggtgcgtggggtgctcgaaccct

MLST allele seq: tcctcggcgagtgcccggcggagttgctgatcgccaaccgcacggcgcggaaggccgtgg
Hit in genome:   tcctcggcgagtgcccggcggagttgctgatcgccaaccgcacggcgcggaaggccgtgg

MLST allele seq: acctggccgagcggttcgccgacctcggcgcgggtgcacggctgcggtttcgccgaggtcg
Hit in genome:   acctggccgagcggttcgccgacctcggcgcgggtgcacggctgcggtttcgccgaggtcg

MLST allele seq: aagggcctttcgacctgatcgtcaacggcacctcggccagtcttgccggcgacgtgccgc
Hit in genome:   aagggcctttcgacctgatcgtcaacggcacctcggccagtcttgccggcgacgtgccgc

MLST allele seq: cgctggcgcagagcgtgatcgagcccggccgtaccgtctgctacgacatgatgtatgcca
Hit in genome:   cgctggcgcagagcgtgatcgagcccggccgtaccgtctgctacgacatgatgtatgcca

MLST allele seq: aggaaccgactgccttca
Hit in genome:   aggaaccgactgccttca
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gua*: PERFECT MATCH, Identity: 100%, Length/HSP: 373/373, Gaps: 0, *gua_11* is the best match for *gua

```
MLST allele seq: ctgctaggcctctccggcggcgtggactcctcggtggtcgccgcgctgctgcacaaggcc
Hit in genome:   ctgctaggcctctccggcggcgtggactcctcggtggtcgccgcgctgctgcacaaggcc

MLST allele seq: atcggcgaccaactgacctgcgtgttcgtcgacaacggcctgctgcgcctgcacgaaggc
Hit in genome:   atcggcgaccaactgacctgcgtgttcgtcgacaacggcctgctgcgcctgcacgaaggc

MLST allele seq: gaccaggtgatggccatgttcgccgagaacatgggcgtgaaggtgatccgcgccaacgcc
Hit in genome:   gaccaggtgatggccatgttcgccgagaacatgggcgtgaaggtgatccgcgccaacgcc

MLST allele seq: gaggacaagttcctcggccgcctggccggcgtcgccgacccggaagagaagcgcaagatc
Hit in genome:   gaggacaagttcctcggccgcctggccggcgtcgccgacccggaagagaagcgcaagatc

MLST allele seq: atcggccgcaccttcatcgaagttttcgacgaagaagccaccaagctgcaggacgtgaag
Hit in genome:   atcggccgcaccttcatcgaagttttcgacgaagaagccaccaagctgcaggacgtgaag

MLST allele seq: ttcctcgcccagggcaccatctaccccgacgtgatcgagtcggccggcgccaagaccggc
Hit in genome:   ttcctcgcccagggcaccatctaccccgacgtgatcgagtcggccggcgccaagaccggc

MLST allele seq: aaggcccacgtga
Hit in genome:   aaggcccacgtga
```

mut*: PERFECT MATCH, Identity: 100%, Length/HSP: 442/442, Gaps: 0, *mut_11* is the best match for *mut

```
MLST allele seq: ctgcaggaagtcatcaagcgcctggcgctggcccgtttcgacgtggctttccacctgcgc
Hit in genome:   ctgcaggaagtcatcaagcgcctggcgctggcccgtttcgacgtggctttccacctgcgc

MLST allele seq: cacaacggcaagaccatcttcgccctgcacgaggcgcgagacgagctggcccgcgcgcgc
Hit in genome:   cacaacggcaagaccatcttcgccctgcacgaggcgcgagacgagctggcccgcgcgcgc
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```
MLST allele seq:  cgggtcggcgcggtgtgcggccaggcattcctcgagcaggcgctgccgatcgaggtcgag
Hit in genome:    cgggtcggcgcggtgtgcggccaggcattcctcgagcaggcgctgccgatcgaggtcgag

MLST allele seq:  cgcaacggcctgcacctgtggggttgggtcggcttgccgaccttctcccgcagccagccg
Hit in genome:    cgcaacggcctgcacctgtggggttgggtcggcttgccgaccttctcccgcagccagccg

MLST allele seq:  gacctgcagtacttctatgtgaacgggcgcatggtgcgcgacaagctggtcgcccacgcg
Hit in genome:    gacctgcagtacttctatgtgaacgggcgcatggtgcgcgacaagctggtcgcccacgcg

MLST allele seq:  gtgcgccaggcttatcgcgacgtgctgtacaacggccggcatccgaccttcgtgctgttc
Hit in genome:    gtgcgccaggcttatcgcgacgtgctgtacaacggccggcatccgaccttcgtgctgttc

MLST allele seq:  ttcgaagtcgatccggcggtggtggacgtcaacgtgcacccgaccaagcacgaagttcgc
Hit in genome:    ttcgaagtcgatccggcggtggtggacgtcaacgtgcacccgaccaagcacgaagttcgc

MLST allele seq:  ttccgtgacagccggatggtcc
Hit in genome:    ttccgtgacagccggatggtcc
```

nuo*: PERFECT MATCH, Identity: 100%, Length/HSP: 366/366, Gaps: 0, *nuo_4* is the best match for *nuo

```
MLST allele seq:  atgttcctcaacctcggcccgaaccacccgtccgcccacggcgcgttccgcatcatcctg
Hit in genome:    atgttcctcaacctcggcccgaaccacccgtccgcccacggcgcgttccgcatcatcctg

MLST allele seq:  caactggacggcgaggagatcatcgactgcgtcccggagatcggctaccaccaccgcggc
Hit in genome:    caactggacggcgaggagatcatcgactgcgtcccggagatcggctaccaccaccgcggc

MLST allele seq:  gccgagaagatggccgagcgccagtcctggcacagtttcatcccctacaccgaccgcatc
Hit in genome:    gccgagaagatggccgagcgccagtcctggcacagtttcatcccctacaccgaccgcatc

MLST allele seq:  gactacctcggcgggggtgatgaacaacctgccctacgtactctcggtggagaagctcgcc
Hit in genome:    gactacctcggcgggggtgatgaacaacctgccctacgtactctcggtggagaagctcgcc

MLST allele seq:  gggatcaaggtgccccagcgggtcgacgtgatccggatcatgatggcggagttcttccgt
Hit in genome:    gggatcaaggtgccccagcgggtcgacgtgatccggatcatgatggcggagttcttccgt

MLST allele seq:  atcctgaaccacctgctgtacctgggcacctatatccaggacgtcggcgccatgacccccg
Hit in genome:    atcctgaaccacctgctgtacctgggcacctatatccaggacgtcggcgccatgacccccg

MLST allele seq:  gtgttc
Hit in genome:    gtgttc
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pps*: PERFECT MATCH, Identity: 100%, Length/HSP: 370/370, Gaps: 0, *pps_12* is the best match for *pps

```
MLST allele seq:  catcgtccaggcacgcccggaaaccgtgaagagccgcgccagcgccacggtcatggagcg
Hit in genome:    catcgtccaggcacgcccggaaaccgtgaagagccgcgccagcgccacggtcatggagcg

MLST allele seq:  ctacctgctgaaagagaaggggaccgtcctggtggaagggcgtgccatcggccagcgcat
Hit in genome:    ctacctgctgaaagagaaggggaccgtcctggtggaagggcgtgccatcggccagcgcat

MLST allele seq:  cggtgccggtccggtcaaggtgatcaacgacgtgtcggaaatggacaaggtccaaccggg
Hit in genome:    cggtgccggtccggtcaaggtgatcaacgacgtgtcggaaatggacaaggtccaaccggg

MLST allele seq:  tgacgtcctggtctccgacatgaccgacccggactgggagccggtgatgaagcgcgccag
Hit in genome:    tgacgtcctggtctccgacatgaccgacccggactgggagccggtgatgaagcgcgccag

MLST allele seq:  cgccatcgtcaccaaccgcggcgggcgtacctgccacgcggcgatcatcgctcgcgaact
Hit in genome:    cgccatcgtcaccaaccgcggcgggcgtacctgccacgcggcgatcatcgctcgcgaact

MLST allele seq:  aggcatcccggcggtggtcggttgcggcaacgccacccagatcctgcaggatggccaggg
Hit in genome:    aggcatcccggcggtggtcggttgcggcaacgccacccagatcctgcaggatggccaggg

MLST allele seq:  ggtgaccgtt
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Hit in genome:      ggtgaccgtt
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trp: PERFECT MATCH, Identity: 100%, Length/HSP: 443/443, Gaps: 0, trp_3 is the best match for trp

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MLST allele seq: tgtcgtgggcagctcgccggaggtgctggtacgggtcgaggatggcctggtgacggtgcg
Hit in genome:   tgtcgtgggcagctcgccggaggtgctggtacgggtcgaggatggcctggtgacggtgcg

MLST allele seq: cccgatcgccggtacccgtccgcgcgggatcaacgaagaggccgacctggcgctggagca
Hit in genome:   cccgatcgccggtacccgtccgcgcgggatcaacgaagaggccgacctggcgctggagca

MLST allele seq: ggatctgctgtcggacgccaaggagatcgccgagcacctgatgctgatcgacctggggcg
Hit in genome:   ggatctgctgtcggacgccaaggagatcgccgagcacctgatgctgatcgacctggggcg

MLST allele seq: caacgacgtggggcgggtgtccgacatcggcgcggtgaaggtcaccgaaaaaatggtgat
Hit in genome:   caacgacgtggggcgggtgtccgacatcggcgcggtgaaggtcaccgaaaaaatggtgat

MLST allele seq: cgaacgttactccaacgtcatgcacatcgtgtccaacgtcaccgggcaattgcgcgaggg
Hit in genome:   cgaacgttactccaacgtcatgcacatcgtgtccaacgtcaccgggcaattgcgcgaggg

MLST allele seq: gctcagcgcgatggacgcgctgcgggcgatcctgccggcgggtacgctgtccggcgcgcc
Hit in genome:   gctcagcgcgatggacgcgctgcgggcgatcctgccggcgggtacgctgtccggcgcgcc

MLST allele seq: gaagatccgcgccatggagatcatcgacgagctggagccggtcaagcgtggagtctacgg
Hit in genome:   gaagatccgcgccatggagatcatcgacgagctggagccggtcaagcgtggagtctacgg

MLST allele seq: cggcgcggtcggctacctggcat
Hit in genome:   cggcgcggtcggctacctggcat
```

trp: PERFECT MATCH, Identity: 100%, Length/HSP: 443/443, Gaps: 0, trp_3 is the best match for trp