
In Silico Molecular Analysis of Carbapenemase-Negative Carbapenem-Resistant *Pseudomonas aeruginosa* Strains in Greece

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Figure S1: Diagram of the transcriptional regulatory mechanisms controlling MexAB-OprM efflux pumps in *Pseudomonas aeruginosa*: transcriptional repression of the mexAB-oprM operon is mediated directly by MexR and NalD proteins and indirectly by NalC, which represses ArmR protein, an anti-repressor of MexR.

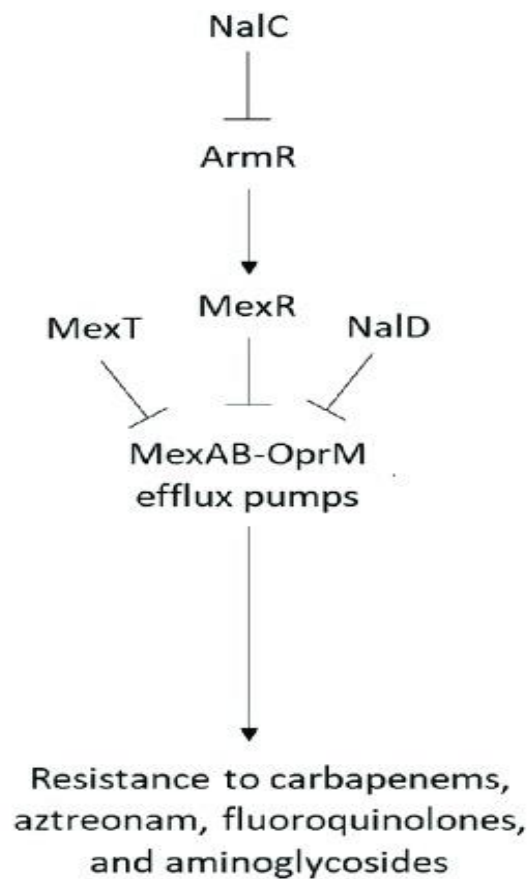


Table S1: Sequences of the *Pseudomonas aeruginosa* strains, aligned with ClustalW (using default parameters), where occurrences of frame shifts or stop codons have been detected. Premature stop codons are visually highlighted in red, while the first nucleotide or gap signifying a frame shift is highlighted in green. In *oprD* gene, premature stops codons were detected in strains 3, 6, 20 and 21, while in strain 8, a deletion of 20 amino acids was detected due to the presence of a premature stop codon. In the *nalC* gene, strain 18 exhibited a premature stop codon, whereas strain 19 displayed a frame shift was detected at position 18. In the *mexR* gene, a premature stop codon was detected in strain 1; in strain 18 exhibited a frame shift, due to a 7-nucleotide gap at position 266.

oprD

CLUSTAL 2.1 multiple sequence alignment

PAO1	ATGAAAGTGATGAAGTGGAGCGCCATTGCACTGGCGGTTTCCGCAGGTAGCACTCAGTTC
8	ATGAAAGTGATGAAGTGGAGCGCCATTGCACTGGCGGTTTCCGCAGGTAGCACTCAGTTC
20	ATGAAAGTGATGAAGTGGAGCGCCATTGCACTGGCGGTTTCCGCAGGTAGCACTCAGTTC
6	ATGAAAGTGATGAAGTGGAGCGCCATTGCACTGGCGGTTTCCGCAGGTAGCACTCAGTTC
3	ATGAAAGTGATGAAGTGGAGCGCCATTGCACTGGCGGTTTCCGCAGGTAGCACTCAGTTC
21	ATGAAAGTGATGAAGTGGAGCGCCATTGCACTGGCGGTTTCCGCAGGTAGCACTCAGTTC

PAO1	GCCGTGGCCGACGCATTCGTCAGCGATCAGGCCGAAGCGAAGGGGTTTCATCGAAGACAGC
8	GCCGTGGCCGACGCATTCGTCAGCGATCAGGCCGAAGCGAAGGGGTTTCATCGAAGACAGC
20	GCCGTGGCCGACGCATTCGTCAGCGATCAGGCCGAAGCGAAGGGGTTTCATCGAAGACAGC
6	GCCGTGGCCGACGCATTCGTCAGCGATCAGGCCGAAGCGAAGGGGTTTCATCGAAGACAGC
3	GCCGTGGCCGACGCATTCGTCAGCGATCAGGCCGAAGCGAAGGGGTTTCATCGAAGACAGC
21	GCCGTGGCCGACGCATTCGTCAGCGATCAGGCCGAAGCGAAGGGGTTTCATCGAAGACAGC

PAO1	AGCCTCGACCTGCTGCTCCGCAACTACTATTTCAACCGTGACGGCAAGAGCGGCAGCGGG
8	AGCCTCGACCTGCTGCTCCGCAACTACTATTTCAACCGTGACGGCAAGAGCGGCAGCGGG
20	AGCCTCGACCTGCTGCTCCGCAACTACTATTTCAACCGTGACGGCAAGAGCGGCAGCGGG
6	AGCCTCGACCTGCTGCTCCGCAACTACTATTTCAACCGTGACGGCAAGAGCGGCAGCGGG
3	AGCCTCGACCTGCTGCTCCGCAACTACTATTTCAACCGTGACGGCAAGAGCGGCAGCGGG
21	AGCCTCGACCTGCTGCTCCGCAACTACTATTTCAACCGTGACGGCAAGAGCGGCA-CGGG
	***** ****
PAO1	GACCGCGTCGACTGGACCCAAGGCTTCCTCACCACCTATGAATCCGGCTTCACCCAAGGC
8	GACCGCGTCGACTGGACCCAAGGCTTCCTCACCACCTATGAATCCGGCTTCACCTCAAGGC
20	GACCGCGTCGACTGGACC-AAGGCTTCCTCACCACCTATGAATCCGGCTTCACCCAAGGC
6	GACCGCGTCGACTGGACCCAAGGCTTCCTCACCACCTATGAATCCGGCTTCACCCAAGGC
3	GACCGCGTCGACTGGACCCAAGGCTTCCTCACCACCTATGAATCCGGCTTCACCCAAGGC
21	GACCGCGTCGACTGGACCCAAGGCTTCCTCACCACCTATGAATCCGGCTTCACCCAAGGC
	***** *****

PAO1 ACTGTGGGCTTCGGCGTCGATGCCTTCGGCTACCTGGGCCTGAAGCTCGACGGCACCTCC
8 ACCGTGGGCTTCGGCGTCGATGCCTTCGGCTACCTGGGCCTGAAGCTCGACGGCACCTCC
20 ACCGTGGGCTTCGGCGTCGATGCCTTCGGCTACCTCGGCC**TGA**AGCTCGACGGCACCTCG
6 ACTGTGGGCTTCGGCGTCGATGCCTTCGGCTACCTCGGCCTGAAGCTCGACGGTACCTCT
3 ACCGTGGGCTTCGGCGTCGATGCCTTCGGCTACCTCGGTCTGAAGCTCGACGGCACCTCG
21 ACCGTGGGCTTCGGCGTCGATGCCTTCGGCTACCTCGGT**TGA**AGCTCGACGGCACCTCG
** ***** ** ***** **

PAO1 GACAAGACCGGCACCGGCAACCTGCCGGTGATGAACGACGGCAAGCCGCGCGATGACTAC
8 GACAAGACCGGCACCGGCAACCTGCCGGTGATGAACGACGGCAAGCCGCGCGATGACTAC
20 GACAAGACCGGCACCGGCAACCTGCCGGTGATGAACGACGGCAAGCCGCGCGACGACTAC
6 GACAAGAGCGGCACCGGCAACCTGCCAGTAATGAACGACGGAACCCCCGTGACGACTAC
3 GACAAGAGCGGTACCGGCAACCTGCCGGTGATGAACGACGGCACGCCCCGTGACGACTAC
21 GACAAGAGCGGTACCGGCAACCTGCCGGTGATGAACGACGGCACGCCCCGTGACGACTAC
***** ** ***** ** ***** * *** ** * *****

PAO1 AGCCGCGCCGGCGGCGCCGTGAAGGTGCGCATCTCCAAGACCATGCTGAAGTGGGGCGAG
8 AGCCGCGCCGGCGGCGCCGTGAAGGTGCGCATCTCCAAGACCATGCTGAAGTGGGGCGAG
20 AGCCGCGCTGGCGGCGCCCTGAAGGTGCGCATTTCCAAGACCATGCTGAAGTGGGGCGAA
6 AGCCGCGCCGGTGGCGCCGTGAAGGTACGCATCTCCAAGACCATGCTGAAGTGGGGCGAG
3 AGCCGCGCCGGTGGCGCCGTGAAGGTACGCATCTCCAAGACCATGTTGAAGTGGGGCGAG
21 AGCCGCGCCGGTGGCGCCGTGAAGGTACGCATCTCCAAGACCATGTTGAAGTGGGGCGAG
***** ** ***** ***** ***** *****

PAO1 ATGCAACCGACCGCCCCGGTCTTCGCCGCTGGCGG-CAGCCGCCTGTTCCCGCAGACCGC
8 ATGCAACCGACCGCCCCGGTCTTCGCCGCTGGCGG-CAGCCGCCTGTTCCCGCAGACCGC
20 ATGCAACCTACCGCGCCGGTCTTCGCCGCCGGCGG-CAGCCGCCTGTTCCCGCAGACCGC
6 ATGCAGCCGACCGCTCCGGTCTTCGCCGCTGGGGGGCAGCCGCCTGTTCCCCCAGACCGC
3 ATG**TAG**CCGACCGCTCCGGTCTTCGCCGCCGGCGG-CAGCCGCCTGTTCCCGCAGACCGC
21 ATGCAGCCGACCGCTCCGGTCTTCGCCGCCGGCGG-CAGCCGCCTGTTCCCGCAGACCGC
*** * ** ***** ***** ** ** ***** *****

PAO1 GACCGGCTTCCAGCTGCAGAGCAGCGAATTCGAAGGGCTCGACCTCGAGGCAGGCCACTT
8 GACCGGCTTCCAGCTGCAGAGCAGCGAATTCGAAGGGCTCGACCTCGAGGCAGGCCACTT
20 GACCGGCTTCCAACTGCAGAGCAGTGAATTCGAAGGGCTCGATCTCGAAGCGGGCCACTT
6 GACCGGCTTCCAGCTGCAGAGCAGCGAATTCGAAGGGCTCGACCTCGAGGCAGGCCACTT
3 GACCGGCTTCCAACTGCAGAGCAGCGAATTCGAAGGGCTCGATCTCGAAGCGGGCCACTT
21 GACCGGCTTCCAACTGCAGAGCAGCGAATTCGAAGGGCTCGATCTCGAAGCGGGCCACTT
***** ***** *** ***** ***** ** *****

PAO1 CACCGAGGGCAAGGAGCCGACCACCGTCAAATCGCGTGGCGAACTCTATGCCACCTACGC
8 CACCGAGGGCAAGGAGCCGACCACCGTCAAATCGCGTGGCGAACTCTATGCCACCTACGC
20 CACCGAGGGCAAGGAGCCGACCACCGTCAAATCGCGTGGCGAACTCTATGCCACCTACGC
6 CACCGAGGGCAAGGAGCCGACCACCGTCAAATCGCGTGGCGAACTCTATGCCACCTACGC
3 CACCGAAGGCAAGCAGGGCACCACCACCAAGTCGCGCGGCGAACTCTACGCAACCTATGC
21 CACCGAAGGCAAGCAGGGCACCACCACCAAGTCGCGCGGCGAACTCTACGCAACCTATGC
***** **

PAO1 AGGCGAGACCGCCAAGAGCGCCGATTTCATTGGGGCCGCTACGCAATCACCGATAACCT
8 AGGCGAGACCGCCAAGAGCGCCGATTTCATTGGGGCCGCTACGCAATCACCGATAACCT
20 AGGCGAGACCGCCAAGAGCGCCGATTTCATTGGGGCCGCTACGCAATCACCGATAACCT
6 AGGCGAGACCGCCAAGAGCGCCGATTTCATTGGGGCCGCTACGCAATCACCGATAACCT
3 AGGCGAGACCGCCAAGAGCGCCGATTTCATTGGGGCCGCTACGCAATCACCGATAACCT
21 AGGCGAGACCGCCAAGAGCGCCGATTTCATTGGGGCCGCTACGCAATCACCGATAACCT

PAO1 CAGCGCCTCCCTGTACGGCGCCGAACCTCGAAGACATCTATCGCCAGTATTACCTGAACAG
8 CAGCGCCTCCCTGTACGGCGCCGAACCTCGAAGACATCTATCGCCAGTATTACCTGAACAG
20 CAGCGCCTCCCTGTACGGCGCCGAACCTCGAAGACATCTATCGCCAGTATTACCTGAACAG
6 CAGCGCCTCCCTGTACGGCGCCGAACCTCGAAGACATCTATCGCCAGTATTACCTGAACAG
3 CAGCGCCTCCCTGTACGGTGTGAACTCGAAGACATCTATCGTCAGTATTACCTGAACAG
21 CAGCGCCTCCCTGTACGGTGTGAACTCGAAGACATCTATCGTCAGTATTACCTGAACAG

PAO1 CAACTACACCATCCCCTGGCATCCGACCAATCGCTGGGCTTCGATTTCAACATCTACCG
8 CAACTACACCATCCCCTGGCATCCGACCAATCGCTGGGCTTCGATTTCAACATCTACCG
20 CAACTACACCATCCCCTGGCATCCGACCAATCGCTGGGCTTCGATTTCAACATCTACCG
6 CAACTACACCATCCCCTGGCATCCGACCAATCGCTGGGCTTCGATTTCAACATCTACCG
3 CAACTACACCATCCCCTGGCATCCGACCAATCGCTGGGCTTCGATTTCAACATCTACCG
21 CAACTACACCATCCCCTGGCATCCGACCAATCGCTGGGCTTCGATTTCAACATCTACCG

PAO1 CACAAACGATGAAGGCAAGGCCAAGGCCGGCGACATCAGCAACACCACTTGGTCCCTGGC
8 CACAAACGATGAAGGCAAGGCCAAGGCCGGCGACATCAGCAACACCACTTGGTCCCTGGC
20 CACAAACGATGAAGGCAAGGCCAAGGCCGGCGACATCAGCAACACCACTTGGTCCCTGGC
6 CACAAACGATGAAGGCAAGGCCAAGGCCGGCGACATCAGCAACACCACTTGGTCCCTGGC
3 CACAAACGATGAAGGCAAGGCCAAGGCCGGCGACATCAGCAACACCACTTGGTCCCTGGC
21 CACAAACGATGAAGGCAAGGCCAAGGCCGGCGACATCAGCAACACCACTTGGTCCCTGGC

PAO1 GGCAGCCTACACTCTGGATGCGCACACTTTTACCTTGGCCTACCAGAAGGTCCATGGCGA
8 GGCAGCCTACACTCTGGATGCGCACACTTTTACCTTGGCCTACCAGAAGGTCCATGGCGA
20 GGCAGCCTACACTCTGGATGCGCACACTTTTACCTTGGCCTACCAGAAGGTCCATGGCGA
6 GGCAGCCTACACTCTGGATGCGCACACTTTTACCTTGGCCTACCAGAAGGTCCATGGCGA
3 GGCAGCCTACACTCTGGATGCGCACACTTTTACCTTGGCCTACCAGAAGGTCCATGGCGA
21 GGCAGCCTACACTCTGGATGCGCACACTTTTACCTTGGCCTACCAGAAGGTCCATGGCGA

PAO1 TCAGCCGTTTGATTATATCGGCTTCGGCCGCAACGGCTCTGGCGCAGGTGGCGACTCGAT
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6 TCAGCCGTTTGATTATATCGGCTTCGGCCGCAACGGCTCTGGCGCAGGTGGCGACTCGAT
3 TCAGCCGTTTGATTATATCGGCTTCGGCGAGAACGGTTCCGGCGGCGGCGGTGACTCGAT
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***** ** ** ** **

PAO1 TTTCTCGCCAACTCTGTCCAGTACTCCGACTTCAACGGCCCTGGCGAGAAATCCTGGCA
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20 TTTCTCGCCAACTCTGTCCAGTACTCCGACTTCAACGGCCCTGGCGAGAAATCCTGGCA
6 TTTCTCGCCAACTCTGTCCAGTACTCCGACTTCAACGGCCCTGGCGAGAAATCCTGGCA
3 TTTCTCGCCAACTCCGTGCAGTACTCCGACTTCAACGGCCCCGGCGAGAAATCCTGGCA
21 TTTCTCGCCAACTCCGTGCAGTACTCCGACTTCAACGGCCCCGGCGAGAAATCCTGGCA
***** ** *****

PAO1 GGCTCGCTACGACCTGAACCTAGCCTCCTATGGCGTTCCCGGCCTGACTTTCATGGTCCG
8 GGCTCGCTACGACCTGAACCTAGCCTCCTATGGCGTTCCCGGCCTGACTTTCATGGTCCG
20 GGCTCGCTACGACCTGAACCTAGCCTCCTATGGCGTTCCCGGCCTGACTTTCATGGTCCG
6 GGCTCGCTACGACCTGAACCTAGCCTCCTATGGCGTTCCCGGCCTGACTTTCATGGTCCG
3 GGCCCGCTACGACCTGAACCTCGCCTCCTATGGCGTTCCCGGCCTGACTTTCATGGTCCG
21 GGCCCGCTACGACCTGAACCTCGCCTCCTATGGCGTTCCCGGCCTGACTTTCATGGTCCG
*** *****

PAO1 CTATATCAATGGCAAGGACATCGATGGCACCAAGATGTCTGACAACAACGTCGGCTATAA
8 CTATATCAATGGCAAGGACATCGATGGCACCAAGATGTCTGACAACAACGTCGGCTATAA
20 CTATATCAATGGCAAGGACATCGATGGCACCAAGATGTCTGACAACAACGTCGGCTATAA
6 CTATATCAATGGCAAGGACATCGATGGCACCAAGATGTCTGACAACAACGTCGGCTATAA
3 CTATATCAATGGCAAGGACATCGATGGCACCAAGATGTCTGACAACAACGTCGGCTATAA
21 CTATATCAATGGCAAGGACATCGATGGCACCAAGATGTCTGACAACAACGTCGGCTATAA

PAO1	GAACTACGGCTACGGCGAGGATGGCAAGCACCACGAAACCAACCTCGAAGCCAAGTACGT
8	GAACTACGGCTACGGCGAGGATGGCAAGCACCACGAAACCAACCTCGAAGCCAAGTACGT
20	GAACTACGGCTACGGCGAGGACGGCAAGCACCACGAGACCAACCTCGAAGCCAAGTACGT
6	GAACTACGGCTACGGCGAGGACGGCAAGCACCACGAGACCAACCTCGAAGCCAAGTACGT
3	GAACTACGGCTACGGCGAGGACGGCAAGCACCACGAGACCAACCTGGAAGCCAAGTACGT
21	GAACTACGGCTACGGCGAGGACGGCAAGCACCACGAGACCAACCTGGAAGCCAAGTACGT

PAO1	GGTCCAGTCCGGTCCGGCCAAGGACCTGTCGTTCCGCATCCGCCAGGCCTGGCACCGTGC
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6	GGTCCAGTCCGGTCCGGCCAAGGACCTGTCGTTCCGCATCCGCCAGGCCTGGCACCGTGC
3	GGTCCAGTCCGGTCCGGCCAAGGACCTGTCGTTCCGCATCCGCCAGGCCTGGCACCGCGC
21	GGTCCAGTCCGGTCCGGCCAAGGACCTGTCGTTCCGCATCCGCCAGGCCTGGCACCGCGC

PAO1	CAACGCCGACCAGGGCGAAGGCGACCAGAACGAGTTCCGCCTGATCGTCGACTATCCGCT
8	CAACGCCGAC TAG GGCGAAGGCGACCAGAACGAGTTCCGCCTGATCGTCGACTATCCGCT
20	CAACGCCGACCAGGGCGAAGGCGACCAGAACGAGTTCCGCCTGATCGTCGACTATCCGCT
6	CAACGCCGACCAGGGCGAAGGCGACCAGAACGAGTTCCGCCTGATCGTCGACTATCCGCT
3	CAACGCCGACCAGGCCGAAGGCGACCAGAACGAGTTCCGCCTGATCGTCGACTATCCGCT
21	CAACGCCGACCAGGCCGAAGGCGACCAGAACGAGTTCCGCCTGATCGTCGACTATCCGCT

PAO1	GTCGATCCTGTAA
8	GTCGATCCTGTAA
20	GTCGATCCTGTAA
6	GTCGATCCTGTAA
3	GTCGATCCTGTAA
21	GTCGATCCTGTAA

nalC

CLUSTAL 2.1 multiple sequence alignment

PAO1	ATGAACGATGC-TTCTCCCCGTCTGACCGAACGCGGCAGGCAACGCCGCCGCGCCATGCT
19	ATGAACGATGCGTCCCC C CGTCTGACCGAACGCGGCAGGCAACGCCGCCGCGCCATGCT
18	ATGAACGATGCGTCCCCCCCCGTCTGACCGAACGCGGCAGGCAACGCCGCCGCGCCATGCT

PAO1 CGACGCCGCTACCCAGGCCTTTCTCGAACACGGTTTCGAAGGCACCACCCTGGACATGGT
19 CGACGCCGCTACCCAGGCCTTTCTCGAACACGGTTTCGAAGGCACCACCCTGGACATGGT
18 CGACGCCGCCACCCAGGCCTTTCTCGAACACGGTTTCGAAGGCACCACCCTGGACATGGT

PAO1 GATAGAACGGGCCGGTGGTTCACGGGGGACCCTGTACAGCTCCTTCGGCGGCAAGGAGGG
19 GATAGAACGGGCCGGTGGTTCACGGGGGACCCTGTACAGCTCCTTCGGCGGCAAGGAGGG
18 GATTGAACGGGCCGGTGGTTCACGGGGAACCCTGTACAGCTCCTTCGGCGGCAAGGAAGG
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PAO1 CCTGTTCGCCGCGGTGATCGCCACATGATCGGGGAAATCTTCGACGACAGCGCCGATCA
19 CCTGTTCGCCGCGGTGATCGCCACATGATCGAGGAAATCTTCGACGACAGCGCCGATCA
18 CCTGTTTGCCGCGGTGATCGCCACATGATCGAGGAAATCTTCGACGACAGCGCCGATCA

PAO1 GCCGCGCCCCGCCGCCACGCTGAGCGCCACCCTCGAGCATTTTCGGCCGGCGCTTTCTCAC
19 GCCGCGCCCCGCCGCCACGCTGAGCGCCACCCTCGAGCATTTTCGGCCGGCGCTTTCTCAC
18 GCCGCGCCCCGCCGCCACGCTGAGCGCCACCCTCGAGCATTTTCGGCCGGCGCTTCCTCAC

PAO1 CAGCCTGCTCGATCCCCGCTGCCAGAGCCTCTATCGCCTGGTGGTGGCGGAATCCCCGCG
19 CAGCCTGCTCGATCCCCGCTGCCAGAGCCTCTATCGCCTGGTGGTGGCGGAATCCCCGCG
18 CAGCCTGCTCGATCCCCGCTGCCAGAGCCTCTATCGCCTGGTGGTGGCGGAATCTCCGCG

PAO1 GTTTCGGCGATCGGCAAGTCCTTCTACGAGCAGGGGCCGAGCAGAGCTATCTGCTGCT
19 GTTTCGGCGATCGGCAAGTCCTTCTACGAGCAGGGGCCGAGCAGAGCTATCTGCTGCT
18 GTTTCGGCGATCGGCAAGTCCTTCTACGAGCAGGGGCCGAGCAGAGCTACCTGCTGCT

PAO1 CAGCGAGCGACTGGCCGCGGTGCTCCTCACATGGACGAGGAAACGCTCTACGCGGTGGC
19 CAGCGAGCGACTGGCCGCGGTGCTCCTCACATGGACGAGGAAACGCTCTACGCGGTGGC
18 CAGCGAGCGACTGGTAGCGGTGCCCCCCCACATGGACGAGGAAACGCTCTACGCGGTGGC

PAO1 CTGCCAGTTTCTCGAGATGCTCAAGGCCGACCTGTTCTCAAGGCCCTCAGCGTGCCGA
19 CTGCCAGTTTCTCGAGATGCTCAAGGCCGACCTGTTCTCAAGGCCCTCAGCGTGCCGA
18 CTGCCAGTTTCTCGAGATGCTCAAGGCCGACCTGTTCTCAAGGCCCTCAGCGTGCCGA

PAO1 CTTCCAGCCGACCATGGCGTGCTGGAAACCCGCCTCAAGCTGTCGGTGGACATCATCGC
19 CTTCCAGCCGACCATGGCGTGCTGGAAACCCGCCTCAAGCTGTCGGTGGACATCATCGC
18 CTTCCAGCCGACCATGGCACTGCTGGAAACCCGCCTCAAGCTGTCGGTGGACATCATCGC

PA01 CTGCTACCTGGAACACCTGTCGCAGAGCCCCGCGCAGGGCTGA
19 CTGCTACCTGGAACACCTGTCGCAGCGCCCCGCGCAGGGCTGA
18 CTGCTACCTGGAACACCTGTCGCAGCGCCCCGCGCAGGGCTGA

mexR

CLUSTAL 2.1 multiple sequence alignment

PA01 ATGAACTACCCCGTGAATCCCACCTGATGCCC GCGCTGATGGCGGTCTTCCAGCATGTG
18 ATGAACTACCCCGTGAATCCCACCTGATGCCC GCGCTGATGGCGGTCTTCCAGCATGTA
1 ATGAACTACCCCGTGAATCCCACCTGATGCCC GCGCTGATGGCGGTCTTCCAGCATGTG

PA01 CGGACGCGCATCCAGAGCGAGCTCGATTGCCAGCGACTCGACCTGACCCCGCCCCGACGTC
18 CGGACGCGCATCCAGAGCGAGCTCGATTGCCAGCGACTCGACCTGACCCCGCCCCGACGTC
1 CGGACGCGC-----GCTCGATTGCCAGCGACTCGACCTGACCCCGCCCCGACGTC

PA01 CATGTATTGAAGCTTATCGACGAACAACGCGGGCTGAACCTGCAGGACCTGGGACGCCAG
18 CATGTATTGAAGCTTATCGACGAACAACGCGGGCTGAACCTGCAGGACCTGGGACGCCAG
1 CATGTATTGAAGCTTATCGACGAACAACGCGGGCTGAACCTGCAGGACCTGGGACGCCAG

PA01 ATGTGCCGCGACAAGGCACTGATCACCCGGAAGATCCGCGAGCTGGAGGGAAGAAACCTG
18 ATGTGCCGCGACAAGGCACTGATCACCCGGAAGATCCGCGAGCTGGAGGGAAGAAACCTG
1 ATGTGCCGCGACAAGGCACTGATCACCCGGAAGATCCGCGAGCTGGAGGGAAGAAACCTG

PA01 GTCCGCGCGAGCGCAACCCAGCGACCAGCGAGCTTCCAGCTCTTCCTCACCAGACGAG
18 GTCCGCGCGAGCGCAACCCAGCG-----CAGCTTCCAGCTCTTCCTCACCAGACGAG
1 GTCCGCGCGAGCGCAACCCAGTGAACAGCGAGCTTCCAGCTCTTCCTCACCAGACGAG

PA01 GGGCTGGCCATCCACCAGCATGCGGAAGCCATCATGTACGCGTGCATGACGAGTTGTTT
18 GGGCTGGCCATCCACCAGCATGCGGAAGCCATCATGTACGCGTGCATGACGAGTTGTTT
1 GGGCTGGCCATCCACCAGCATGCGGAAGCCATCATGTACGCGTGCATGACGAGTTGTTT

PA01 GCCCCGCTACCCCGGTGGAACAGGCCACCCTGGTGCATCTCCTCGACCAGTGCCTGGCC
18 GCCCCGCTACCCCGGAGGAACAAGCCACCCTGGTGCATCTCCTCGACCAATGCCTGGCC

1 GCCCCGCTCACCCGGAGGAACAAGCCACCCTGGTGCATCTCCTCGACCAATGCCTGGCC
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PAO1 GCGCAACCGCTTGAGGATATTTAA
18 GCGCAACCGCTTGAGGATATTTAA
1 GCGCAACCGCTTGAGGATATTTAA
