

> IS26 **Family: IS6**

Length=820

Score = 1620 bits (817), Expect = 0.0
Identities = 817/817 (100%), Gaps = 0/817 (0%)
Strand=Plus/Minus

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Query 1 ACTGTTGCAAAGTTAGCGATGAGGCAGCCTTTTGTCTTATTCAAAGGCCTTACATTTCAA 60
      |||
Sbjct 817 ACTGTTGCAAAGTTAGCGATGAGGCAGCCTTTTGTCTTATTCAAAGGCCTTACATTTCAA 758

Query 61 AAACCTCTGCTTACCAGGCGCATTTGCGCCAGGGGATCACCATAATAAAATGCTGAGGCCT 120
      |||
Sbjct 757 AAACCTCTGCTTACCAGGCGCATTTGCGCCAGGGGATCACCATAATAAAATGCTGAGGCCT 698

Query 121 GGCCTTTGCGTAGTGACGCATCACCTCAATACCTTTGATGGTGGCGTAAGCCGCTTCA 180
      |||
Sbjct 697 GGCCTTTGCGTAGTGACGCATCACCTCAATACCTTTGATGGTGGCGTAAGCCGCTTCA 638

Query 181 TGGATTTAAATCCCAGCGTGGCGCCGATTATCCGTTTCAGTTTGCCATGATCGCATTCAA 240
      |||
Sbjct 637 TGGATTTAAATCCCAGCGTGGCGCCGATTATCCGTTTCAGTTTGCCATGATCGCATTCAA 578

Query 241 TCACGTTGTTCCGGTACTTAATCTGTCTGGTGTCAACGTCAGACGGGCACCGGCCTTCGC 300
      |||
Sbjct 577 TCACGTTGTTCCGGTACTTAATCTGTCTGGTGTCAACGTCAGACGGGCACCGGCCTTCGC 518

Query 301 GTTTGAGCAGAGCAAGCGCGGACCATAGGCGGGCGCTTTATCCGTGTTGATGAATCGCG 360
      |||
Sbjct 517 GTTTGAGCAGAGCAAGCGCGGACCATAGGCGGGCGCTTTATCCGTGTTGATGAATCGCG 458

Query 361 GGATCTGCCACTTCTTCACGTTGTTGAGGATTTTACCCAGAAACCGGTATGCAGCTTTGC 420
      |||
Sbjct 457 GGATCTGCCACTTCTTCACGTTGTTGAGGATTTTACCCAGAAACCGGTATGCAGCTTTGC 398

Query 421 TGTTACGACGGGAGGAGAGATAAAAAATCGACAGTGCGGCCCCGGCTGTCGACGGCCCCGGT 480
      |||
Sbjct 397 TGTTACGACGGGAGGAGAGATAAAAAATCGACAGTGCGGCCCCGGCTGTCGACGGCCCCGGT 338

Query 481 ACAGATACGCCCAGCGGCCATTGACCTTCACGTAGGTTTCATCCATGTGCCACGGGCAAA 540
      |||
Sbjct 337 ACAGATACGCCCAGCGGCCATTGACCTTCACGTAGGTTTCATCCATGTGCCACGGGCAAA 278

Query 541 GATCGGAAGGGTTACGCCAGTACCAGCGCAGCCGTTTTTCCATTTCAGGCGCATAACGCT 600
      |||
Sbjct 277 GATCGGAAGGGTTACGCCAGTACCAGCGCAGCCGTTTTTCCATTTCAGGCGCATAACGCT 218

Query 601 GAACCCAGCGGTAAATCGTGGAGTGATCGACATTCACCTCCGCGTTACGCCAGCATCTCCT 660
      |||
Sbjct 217 GAACCCAGCGGTAAATCGTGGAGTGATCGACATTCACCTCCGCGTTACGCCAGCATCTCCT 158

Query 661 GCAGCTCACGGTAACGTATGCCGTATTTGCAGTACCAGCGTACGGCCACAGAATGATGT 720
      |||
Sbjct 157 GCAGCTCACGGTAACGTATGCCGTATTTGCAGTACCAGCGTACGGCCACAGAATGATGT 98

Query 721 CACGCTGAAAATGCCGGCCTTTGAATGGGTTTCATGTGCAGCTCCATCAGCAAAAGGGGAT 780
      |||
Sbjct 97 CACGCTGAAAATGCCGGCCTTTGAATGGGTTTCATGTGCAGCTCCATCAGCAAAAGGGGAT 38

Query 781 GATAAGTTTATCACCACCGACTATTTGCAACAGTGCC 817
      |||
Sbjct 37 GATAAGTTTATCACCACCGACTATTTGCAACAGTGCC 1
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Supplementary Figure S1. Presence of IS26 in *P. aeruginosa* strain B19083-1. While IS26 is not exclusive to *P. aeruginosa*, its detection in this strain highlights its widespread distribution across various bacterial species. S26 plays a crucial role in the dissemination of antibiotic resistance and genome rearrangement.

CLUSTAL O(1.2.4) multiple sequence alignment

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gb|AAG06466.1|+|cprS      MKRGLSLIPVGGGVTLILAGVLLVYTRMLGDYGETGALYLLSMMEEEEGLYFAQRYQED  60
PY0Hw3_10925              MKRGLSLIPVGGGVTLILAGVLLVYTRMLGDYGETGALYLLSMMEEEEGLYFAQRYQED  60
                           *****

gb|AAG06466.1|+|cprS      PATPADSYFFKGSVGTAGLPKLRMLDTPPYKSIGAMQLLGNWDDDEEEDDDAPSDD  120
PY0Hw3_10925              PATPADSYFFKGSVGTAGLPKLRMLDTPPYKSIGAMQLLGNWDDDEEEDDDAPSDD  120
                           *****

gb|AAG06466.1|+|cprS      AYVVVRQPLADGKTLTYLDNDAAGSIDTPLSDAIIDARVRQTWIVTLSVTLPSLAAGVLL  180
PY0Hw3_10925              AYVVVRQPLADGKTLTYLDNDAAGSIDTPLSDAIIDARIRQTWIVTLSVTLPSLAAGVLL  180
                           *****

gb|AAG06466.1|+|cprS      VWFIVAPLRKLTWWSMTLDDLAPDSQRPRFNYRELNVLADTLWNSVTRIKDFSQREERFL  240
PY0Hw3_10925              VWFIVAPLRKLTWWSMTLDDLAPDSQRPRFNYRELNVLADTLWNSVTRIKDFSQREERFL  240
                           *****

gb|AAG06466.1|+|cprS      RYASHELRTPLAVIGMNLLELDQPGRAPSPHALQRIIRSALGMQMTETLLWLSRESGEL  300
PY0Hw3_10925              RYASHELRTPLAVIGMNLLELDQPGRAPSPHALQRIIRSALGMQMTETLLWLSRESGEL  300
                           *****

gb|AAG06466.1|+|cprS      RDDGHIEVGRLLLEELLEEQQALSQRRGLTFHLDVEPHSLPQTRARIIGNLLRNALQYSD  360
PY0Hw3_10925              RDDGHIEVSRLLLEELLEEQQALSQRRGLTFHLDVEPHSLPQTRARIIGNLLRNALQYSD  360
                           *****.*****

gb|AAG06466.1|+|cprS      EGVVEIVVRDRSLLISNPIGAAQGTESMAFGYGLGLDLVQRLCQKSGWRLHYSSDEQRF  420
PY0Hw3_10925              EGVVEIVVRDRSLLISNPIGAAQGTESMAFGYGLGLDLVQRLCQKSGWRLHYSSDEQRF  420
                           *****

gb|AAG06466.1|+|cprS      RCELLFPATPD      431
PY0Hw3_10925      RCELLFPATPD      431
                           *****

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Supplementary Figure S2. Alignment of *Pseudomonas aeruginosa* HW3 Strain with the Reference Strain *cprS* (gb|AAG06466.1|) using Clustal Omega. The mutations D108N, V159I, and E386D are observed.