Sequence of the *Bacillus subtilis* spectinomycin resistance gene region

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The sequence (GenBank accession number M31102) of the *spc^r* gene region of *B. subtilis* strain 1A241 (Bacillus Genetic Stock Center) was determined from a DNA fragment that conferred *spc^r* to the wild type strain. Four complete and one incomplete open reading frames (ORF) were observed with ORF1 (nt 58–546), ORF2 (nt 563–739), ORF3 (773–1210), ORF4 (nt 1215–2507), and incomplete ORF5 (nt 2565–2912) coding for proteins homologous to *E. coli* ribosomal proteins S5, L30, L15, SecY, and Adk, respectively (1, 2).

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TGATCGCTCGTGAAGCTGGACCTAAATTTTAATAAAAGAGAGGACACATGATTATGCGTCTGATTGACCAAGCAAATTAGAGTTAGAAGACGCT    100
M R R I D P S K L E L E E R
TAGTTACGGTTAACCAGCGTAGCGAAAGTGGTCTGCTTTCGGCTTCGAGCTCTAGTCTGTTGCGGTGACAAAAACGGACACGTAGGATTGCGTACTGG    200
L V T V N R V A K G G R R F R F A A L V V V G D K N G H V G F G T G
TAAAGCACAAAGTACCAAGCGATTGCGAAAGCTGTTGAAGATGCGAAAAAGAAATTGATTGAAGTACCAATGGTTGGAACCTACAATCCACACGAA
K A Q E V P E A I R K A V E D A K K N L I E V P M V G T T I P H E
ATCATCGGACGTTTCGGTGCAGTAACATCTTGTAAACCTGCTCTGAAAGTACTGGAAGTTATCGCTGGAGGCCCTGACGTGCGGTACTTGAGCTAG    400
I I G R F G A G N I L L K P A S E G T G V I A G G P V R A V L E L
CTGGTGTAGCTGATATCCTTTCTAAGTCTTAGGTTCTAACACACCGATCAACATGATTGCTGCAACACTTCAAGGTTTAAAGTAACTAAACGCTGCTGA
A G V A D I L S K S L G S N T P I N M I R A T L Q G L S E L K R A E
AGACGTTGCGAAGCTTCGTGGAATACTGTAGAAAGCTGTTAGGATAAGGAGGGAACATTAATGGCTAAATTAGAAATTACCTCAAACGAAAGTGAAT    600
D V A K L R G K S V E E L L G M A K L E I T L K R S V I
CGGTGCGCGGAAGACCAACGCGTACTGTAAAGCACTTGGTTTAAAGAAAAACAAACCAACTGTTGTTTCATGAAGCAACGCTGCGGATCGGTGATG
G R P E D Q R V T V R T L G L K K T N Q T V V H E D N A A I R G M
ATTAATAAAGTATCTCATTTAGTTCTGTTAAAGAAACATAAAAAATTTGATCGGATAAGGAGGTGCTCTAATGAACCTCATGAATTAAGAACTTCAG    800
I N K V S H L V S V K E Q M K L H E L K P S
AAGGTTACGCAAAACCGCTAATCGCTAGGTCGCTGATTGCTTCTGGCAACGCTAAACAGCTGGTAAAGGTCACAAAGTCAAAACGCTGCTTCTGG
E G S R K T R N R V G R I G S G N G K T A G K G H K G Q N A R S R
CGGCGGTGTACGCCCTGGATTGAGGGGGGACAAATGCTTTTATCCAAAGCTGCTTCAACGTTGTTCACTAACATCAACCGCAAGGAAATACGCTGTA    1000
G G V R P G F E G G Q M P L F Q R L P K R G F T N I N R K E Y A V
GTCAACCTAGACAAATTGAACGGTTTTCGAGAAGGACGGAAGTCACTCTGAACTTCTTAGAGACTGGTGTATTAGCAAACTTAATGCGAGGATAA
V N L D K L N G F A E G T E V T P E L L L E T G V I S K L N A G V
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K I L G N G K L E K K L T V K A N K P S A S A K E A V E A A G G T A
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E V I L F K T I S N F M R V S D I R N K I I F T L L M L I V F R
CATAGTGCCTTTATCTGCTGCTTACGTTAAGCTGAAGCGTACAGGCACAGCTCAAAATGGGTGTTTGTATCTCCTTAATACATTTGGCGCGGT
I G A F I P V P Y V N A E A L Q A Q S O M G V F D L L N T F G G G
GGCCTTACCAATTTCCATTTTCGCAATGGGAATTACTCCTTATATCAAGGCTTCGATCATTCAGCTGCTCAGATGGATGGTACCGCAAGTTTA    1500
A L Y I P S I F A M G I T P Y I T A S I I I Q L L Q M D V V P K F
CCGAGTGCTTAAGCAAGGTGAAGTTGGCGCGCGTAAATTAGCTCAGTTTCAACAGGTACTTACGATTGCTGCTGTTTCAACGCTTAGGTATGTC
T E W S K Q G E V G R R K L A Q F T R Y F T I V L G F I Q A L G M S
ATATGGAATCAACAACTGCGCAACGGTATGCTGATCGAAAAATCCGGTGTATGACATATCTTATCATTGCTTTAGTGCTCACTGCGCGGAATGCGCTTT
Y G F N N L A N G M L I E K S G V S T Y L I I A L V L T G G T A F
TTAATGTCGCTTGGGAAACAAATTAATCTCATGAGTAGGCAACGGAATATCGATCATTATCTCGCGGGGATGTGTCTAGTATCCAAAAACAAATG
L M W L G E Q I T S H G V G N G I S I I I F A G I V S S I P K T I
GGCAATATATGAGACTCAATTTGTCGCGAGCAACGATCAGTTGTTTATCATATTGTGAAGTGGCACTTCTGTGATTGCGATTTCAGCAGTTATTG
G Q I Y E T Q F V G S N D Q L F I H I V K V A L L V I A I L A V I V
TGGAGTTATTTTCAATCAGCAAGCGGTACGGAATAATGCGATTCAATATGCTAAAGGCACAGGTGCTTCACTGCTGCGGAGGTCACTACACCTT
G V I F I Q Q A V R K I A I Q Y A K G T G R S P A G G G Q S T H L
CCATTGAAAGTGAATCCTGACGGGTTATTCGGTAATCTTTGCGGTTGCGTTTGTATAACGCGCGGACGATCGCGTCACTTTTGGAAACAAACGATG
P L K V N P A G V I P V I F A V A F L I T P R T I A S F F G T N D
TGACAAAGTGATTCAAAACAACTTTGATAATACGATCCGGTGGGTATGGCGATATATGTTGCGTTGATTATGCGCTTTACGTACTTTTATGCTTTTGT
V T K W I Q N N F D N T H P V G M A I Y V A L I I A F T Y F Y A F V
ACAGGTAACCCGTAACAAATGGCTGATAACCTTAAAAACAGGCTGCTATATCCCGGGGTCGTCACGGGAAATGACTCAAGATAGAATAACGAGC
Q V N P E Q M A D N L K K Q G G Y I P G V R P G K M T Q D R I T S
ATTTTGTATGACCTACGTTTGTGGTTCTATATCTTAGCGGTGATTTCATCTTCTCTATCTTTTCAATCAATTCGCTGGATTGCGCTCAAGGTGAC
I L Y R T F V G S I F L A V I S I L P I F F I Q F A G L P Q S A
AAATTTGGCGGAACATCTTTGTTAATGTTGTCGGGGTAGCCTTGGAGACAAATAGAAACAACTAGAAAGCAAGTGGTGAACGAACTACCGGTGATTAT
Q I G G T S L L I V V G V A L E T M K Q L E S Q L V K R N Y R G F M
GAAAACTAGAGAAATGGAATTTATCCATTCCTCTTAATAAGAGAGAGCGGGGAAATCCGAATGAACCTAGTCTTAATGGGGCTTCTGTTGGTGGCT
K N M N L V L M G L P G A G
AAAGGCACACAGGCGCAAGCAATTTGTTGAGGATTATGGGATTCCTCATATCTCAACAGGAGATATGTTCCGTGCTGCTATGAAAGAAAGAACCACTCG
K G T G Q E R I V E D Y G I P H I S T G D M F R A A M K E E T P L
GACTGCAAGCAAAATCTTATATGAGGAGAGCTGCTACCTGACGAGTCAATCGGAATTTGAAAGAGAGACTTGGCAAGATGATTGTGAAAG
G L E A K S Y I D K G E L V P D E V T I G I V K E R L G K D D C E R
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G F L L D G F P R T V A Q A E A L E E I L E E Y G K P I D Y V I N
ATTGAAGTCGAC
I E V D

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