

Fig. 36. LEU-regulation of gene *leuA* in  $\alpha$ -proteobacteria. The start and regulatory codons of the leader peptide are in bold, the stop codon is in bold italic, the left shoulder – in green, the right shoulder – in violet.

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Atu      UCGCCGUGCGGUGCACUCUCGCUUCUUAGCCCUCGACCUUACACGCGGUUGCCGGUCCAGUGAGGAGC***CCCGCGGGCGAAACCCGCUGGGCAACGCUCUCAUCUCGAAAUCUCAUUUUUAUCUGGAUUUAGGCUCUCA
SI859A1 *****CUCUCGCUUCUACGCCCUUCUCUUCUUAGCUGCGGCCGUCGGACCCGUUGACCUGAAGGGGCGUCCCGCGGUCGAGCCGGCACUGUGGUCCGACCCGGCCCGCGCGCUCAGCCCCUUCGCUUUACAAGACGGUU
BR, BME, BruAbl GAUGUUUGCGUUCUGGACUCGCUUCUUACCCUCGGCCUUAGCGGCGAUCGCCGGGUCGUUGAGAGGAGC**GUCCGCGGUCCAUCUUCGGUCUCGCCGGACCUGUGCUCUUUCAGAAAACCAUAUAAUCGAUCAGCAUUUGUC
FP2506 *****GGCCCUUCUUUCUCUCUUAGACCGGACCGUCUGGCCGUUAGCAAGGGGUCAGGCGGUCGUCUCAGGUCUGACAGAGGUCUCUCGCCACGAGACUUCCUCCUUCAAAUCUCAAGACCGAUG
ml      GUGCGCGCGCUUGUUCGACCCCUGCUUUCUCGGCCCUUAUCGGCGAUCGCCGGUUCGCUGAAGGAGCCG***CCCGCGGUCGAACCGCGCGAACGCCAUGCUCUUGGCCAGUCUCAAAAUUGGAGUCACAUCAAGCGAACGA
Meso    ACGGCUCGUGCGCUUUCCAGCCUCCUUUCUCGGCCCUUAUCGGCGAUCGCCGGCCGCUGAAGGAGCCG***CCCGCGGAUCGAUCCCGUGAUCGUGUCGCUCUUCCGUCAGAAACUGGAUUUGAAGCCUUGACAGGCGG
RHE, RL  *****CUGACCUCGCUUCUUUCUCGGCCCUUACGCGCGGUUGCCGGUCCUUUGAGGAGC***CCCGCGGGCGAAACCCGCCGGCCAUCGUCUCGCAGUCACUUUAAAAUUGACCCAAUGACCGAAGGUCC
Smed    CCGUCGCGCCUUUCGCCUCCUUCUUUCUCGGCCCUUAUUGCGGUUGCCGGUUCGCUGAGGAGC***CCCGCGGGCGAAACCCGCCGGCACAUGCUCUCCAAAUCAGACAAGCUGAACCAAUCGCGCGCCCGC
SMc     CCUGCGCGCCACCGCAUCCCUUCUUUCUCGGCCCUUAUCGGCGGUUGCCGGUUCGCUGAGGAGC***CCCGCGGGCGAAACCCGCCGGCACCUGCUCUCGAAAUCAGAAAAGCUGAACCAAUCGCGCGCCCGC
Dshi    GCUGGCCACAGCGCGCGGUGCUGCGGUCUCUCUCUUAGCCCCUCUCUGAGCGUGCC***UCCGGCGGACCGCUCAGAGGUAAUCCGGCCAAUUCGCGACAGACAGCUGAGAGCUUAC
Jann    GCAGCCCCCGCUGCACGCGACCUGCUUGGUCUCUCUCUUAGCCCCUCUCUGAGCGUGCC***UCCGCGGACCGCUCAGAGGUAAUCCGGCCAAUUCGCGACAGACAGCUGAGAGCUUAC
SKA53   AUGGCACAGACAUCCGGCACUGUCCCGCCCUCUACUUCUUAGCAGCGCCUGAGCGUGCCUGG***UCCGCGGACCGCUCAGAGGUAAUCCGGCCAAUUCGCGACAGACAGCUGAGAGCUUAC
OB2597  GCGCGCGCGUCACGCGCGCCCGCCCUCCGCCUACUCCUAAUCCCCUCUCUGAGCGUGCC***UCCGGCGGACGCUCAGAGGUAAUCCGGCCAAUUCGCGACAGACAGCUGAGAGCUUAC
OG2516  UCCGCCAUUCCCGCGCGCGUCCCUCGGCCUCUCUCUUACCCCCUCUCUGAGCGUGCC***CAUCCGCGGACCGCUCAGAGGUAAUCCGGCCAAUUCGCGACAGACAGCUGAGAGCUUAC
RB2654  AACCAGCCUUUGGCCGGUUUGCUGCGUAGUGCCCUCUUCUUAGUUGCCUCUCUGAGCGUGCC***UUGGGCGGACGCUCAGAGGUAAUCCGGCCAAUUCGCGACAGACAGCUGAGAGCUUAC
Rsph17025 ACGCCCCUCCAGGCUGUGGCUGCCCGUGCGCUUCUUUCUUAGCUGCCUCUCUGAGCGUGCC***CUUGGGCGGACCGCUCAGAGGUAAUCCGGCCAAUUCGCGACAGACAGCUGAGAGCUUAC
RD1     ACCGCACGCACCCUCCGCGCCACGGCUGCCCUACUCUCUCUAAUCCCCUCUCUGAGCGUGCC***UUCGGCGGACCGCUCAGAGGUAAUCCGGCCAAUUCGCGACAGACAGCUGAGAGCUUAC
ISM     *****CGUGCCCGCCCGCUUGCCCUACUCUGAUCCUAAGCCCCUCUCUGAGCGUGCC***CUUGGGCGGACCGCUCAGAGGUAAUCCGGCCAAUUCGCGACAGACAGCUGAGAGCUUAC
RTM1035 GCCCUCGGCGCGACCUUGCGCUUGGCCCUCCGUCUUCUCUAAUCCCCUCUCUGAGCGUGCC***CCGGCGGACCGCUCAGAGGUAAUCCGGCCAAUUCGCGACAGACAGCUGAGAGCUUAC
NAS141  CGCGCUCGCGCACUUUCCUCCGUGCCAACCUACUCUCUCUAAUCCCCUCUCUGAGCGUGCC***UCCGGCGGACCGCUCAGAGGUAAUCCGGCCAAUUCGCGACAGACAGCUGAGAGCUUAC
OM2255  ACGCAUAAUGCACUUUUAGCAUUAUCUGCACUCUUAUUACUGAGCUCCUCUCUGAGCGUGCC***UGGCGAAAGCUCAGGGGAUAGCAAUGGCCAAAUAUUAUAAAAGAAAAUAAA***
amb     GUUUCGCUCCGCUUUCGCCGGUCUCUCUCUCUCUCCGACUAACCGCGGUCGCGGGGUAAGGUCAUUCGCGGCGGCCCGCGGCGGAAAGACCGGGUCGCGCUCCCCAUUACAGCAGUCAGACCAUAAAGGAGGACCAGG
Magn    AUGUGUGUUCCGGCCUUCGGCGCCCUCGUCUCUCUCUCUAACCAGCGGUCGCGGGGUAAGGUCAUUCGCGGCGGCCCGCGGCGCCAAAGACCGGGUCGCGCUUUCUCAUCGCCAAAAAGAUCAAGGAGGACCAGGCC
Swit    *****AUGACGCGCGCCGUUCGCCCUUCUCUCUCUUCGACCUUACGCGCCUUAGCGCGCGAUUCGCUUGGGUCGAAACAGGCCCGCAAGCACGGCGUCUAAGGGUCCCGAGCGCGCAUUUCGUUGGGGUCGAAACA

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