# Conservative region of *ddl* promoter in *Staphylococci*

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                          (1) 1        10        20        30        40        50
    p-ddl-8325        (1) --------------CTCACTAATGTTTATATCA--ATTTTACATGACTTT
    p-ddl-Mu50        (1) --------------CTCACTAATGTTTATATCA--ATTTTACATGACTTT
    p-ddl-MW2         (1) --------------CTCACTAATGTTTATATCA--ATTTTACATGACTTT
    p-ddl-S.capitis   (1) ----------------ATAAATAG-TCTACATTGATTTTACATGACTTT
    p-ddl-S.caprae    (1) ----------------ATAAATAG-TCTACATTGATTTTACATGACTTT
    p-ddl-S.epidermidis (1) ---TTCATTCATATTTTCTAATCAAATATATATTAATTTTACATGACTTC
    p-ddl-S.pasteuri  (1) ATAATCTTTCATCTTTCATCCATAATTATATAACGATTTTACATGACTTT
    p-ddl-S.warneri   (1) -TAATCATTCATCTTTCATCCATAATTATATAACGATTTTACATGACTTT
    p-ddl-S.simiae    (1) -------------CCACACTTATAGTTATTTTA--ATTTTACATGACTTT
    p-ddl-N315        (1) --------------CTCACTAATGTTTATATCA--ATTTTACATGACTTT
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                         (51) 51        60        70        80        90        100
    p-ddl-8325       (35) TTAAAAATTAGCTAGAATATCACAGTGATATCAGCTATAGATTTCAATTT
    p-ddl-Mu50       (35) TTAAAAATTAGCTAGAATATCACAGTGATATCAGCTATAGATTTCAATTT
    p-ddl-MW2        (35) TTAAAAATTAGCTAGAATATCACAGTGATATCAGCTATAGATTTCAATTT
    p-ddl-S.capitis  (33) TTTTAAATTTGCTAGAATATCAAAG---TGGCAAGTCGACAAATTATATA
    p-ddl-S.caprae   (33) TTTTAAATTTGCTAGAATATCAAAG---TGGCAAGTCGACAAATTATATA
    p-ddl-S.epidermidis (48) TTTTAAATTTGCTAGAATATCACAG---AATGATAGCACCTTATTAACTT
    p-ddl-S.pasteuri (51) ATAGAAATTTGCTAGAATATCAAGTCTAAATGCAATAACCAATTTATTTC
    p-ddl-S.warneri  (50) ATAGAAATTTGCTAGAATATCAAGTTCAATTGCAATAACCATTTTATTTC
    p-ddl-S.simiae   (36) TACTAAATTAGCTAGAATATCCAGATGATAAAACAACTAGAATACATAAC
    p-ddl-N315       (35) TTAAAAATTAGCTAGAATATCACAGTGATATCAGCTATAGATTTCAATTT
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                        (101) 101       110       120       130       140       150
    p-ddl-8325       (85) GAATTAGGA---ATAAAATAGAAGGGAATA-TTGTTCTGATTATAAATGA
    p-ddl-Mu50       (85) GAATTAGGA---ATAAAATAGAAGGGAATA-TTGTTCTGATTATAAATGA
    p-ddl-MW2        (85) GAATTAGGA---ATAAAATAGAGGGGAATA-TTGTTCTGATTATAAATGA
    p-ddl-S.capitis  (80) GAAATAAGCT--TTCTTTTCCATTCAAAG--GTAGAGGAATTAAAACAG-
    p-ddl-S.caprae   (80) GAAATAAGCT--TTCTTTTCCATTCAAAG--GTAGAGGAATTAAAACAG-
    p-ddl-S.epidermidis (95) TTAATATGTA--ATAGTCATAATAAAAATATGTATATTAGCGCAAATTG-
    p-ddl-S.pasteuri (101) ATAGAAAGT---ATTAGATTAAATA-TAGG-TTTGGTTAAACAACTTTG-
    p-ddl-S.warneri  (100) TAAGGGAGT---ATTAGATTGAATAGTAGG-TTTGGTAAAAGAACTTTG-
    p-ddl-S.simiae   (86) GAAATAACATTGATAATCTTAAAGAGAACT-GTAACATAATTAGATAGGG
    p-ddl-N315       (85) GAATTAGGA---ATAAAATAGAAGGGAATA-TTGTTCTGATTATAAATGA
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                        (151) 151       160       170       180       190       200
    p-ddl-8325      (131) ATCAACATAGATACAGACACATAAGTCCTCGTTTTTAAAATGCAAAATAG
    p-ddl-Mu50      (131) ATCAACATAGATACAGACACATAAGTCCTCGTTTTTAAAATGCAAAATAG
    p-ddl-MW2       (131) ATCAACATAGATACAGACACATAACGCCTCGTTTTTAAAATGCAAAATAG
    p-ddl-S.capitis (125) --TCACTAAAAATTAGATTTATTG---ATGGATTAACAAATGCAATTGAT
    p-ddl-S.caprae  (125) --TCACTAAAAATTAGATTTATTG---ATGGATTATCAAATGCAATTGAT
    p-ddl-S.epidermidis (142) --TCATTAAAATTTAGTTCTATAT---TTAGATTATCAAATGCAATTGAA
    p-ddl-S.pasteuri (145) --CCATATATATTAATAGA-------------TTATAAAATGCAAAAGTC
    p-ddl-S.warneri (145) --CCCTTTATATTAATAGA-------------TTATAAAATGCAAAAGTC
    p-ddl-S.simiae  (135) A-CGGTAAATATTCACATT-ATAGCGCTT--ATTTTGAAATGCAAAATAA
    p-ddl-N315      (131) ATCAACATAGATACAGACACATAAGTCCTCGTTTTTAAAATGCAAAATAG
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             (201) 201        210        220        230        240        250
  p-ddl-8325 (181) CATTAAAATGTGATACTATTAAGATTCAAAGATGCG---AATAAATCAAT
  p-ddl-Mu50 (181) CATTAAAATGTGATACTATTAAGATTCAAAGATGCG---AATAAATCAAT
   p-ddl-MW2 (181) CATTAAAATGTGATACTATTAAGATTCAAAGATGCG---AATAAATCAAT
p-ddl-S.capitis (170) TTTAGAAATATGATAATATTAAGTTTCAGAGAC-CGTTATGTACAT-TGA
p-ddl-S.caprae (170) TTTAGAAATATGATAATATTAAGTTTCAGAGAC-CGTTATGTACAT-TGA
p-ddl-S.epidermidis (187) TTTAAAAATATGATAATATTAAGTTTCAGAAGC-CGTTATGTACTT-AAA
p-ddl-S.pasteuri (180) CTATCAAATATGATAATATTAAGTTTCAGAGAAGACTT-TGTATATTAAA
p-ddl-S.warneri (180) CTATCAAATATGATAATATTAAGTTTCAGAGAAGACTT-TGTATATTAAA
 p-ddl-S.simiae (181) CAATAAAATATGATACTATTAAGGTTCAAAGATGCGTCGATTAAATGAAA
  p-ddl-N315 (181) CATTAAAATGTGATACTATTAAGATTCAAAGATGCG---AATAAATCAAT
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             (251) 251        260        270        280        290        300
  p-ddl-8325 (228) TAACAATAGGACTAAATCAATATTA-ATTTATATTAAGGTAGCAAACCCT
  p-ddl-Mu50 (228) TAACAATAGGACTAAATCAATATTA-ATTTATATTAAGGTAGCAAACCCT
   p-ddl-MW2 (228) TAACAATAGGACTAAATCAATATTA-ATTTATATTAAGGTAGCAAACCCT
p-ddl-S.capitis (218) GCTATACATAATAAATAAAATATCACAATTATTAAACAGATAAATGGCAT
p-ddl-S.caprae (218) GCTATACATAATAAATAAAATATCACAATTATTAAACAGATAAATGGCAA
p-ddl-S.epidermidis (235) GTAGTAATAAAAGATCAATTAAACAATTACGTTAAAGA-AAAAGGC-T
p-ddl-S.pasteuri (229) AATACATATAATTAAAAGTAAATTT-TAAAATGATAAG-ACGTTATTCCA
p-ddl-S.warneri (229) AATACATATGATTAAAAGTAAATTT-TAAAATGATAAG-ACGTTATGCCA
 p-ddl-S.simiae (231) ATAATTAATAACCACATCAATTTTA-ATATATGATAGCTATGCTAT---T
  p-ddl-N315 (228) TAACAATAGGACTAAATCAATATTA-ATTTATATTAAGGTAGCAAACCCT
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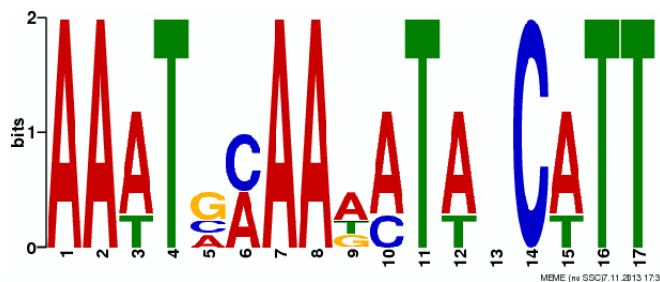
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             (301) 301        310        320    333
  p-ddl-8325 (277) GATATATCATTGGAGGAAAACGAA---------
  p-ddl-Mu50 (277) GATATATCATTGGAGGAAAACGAA---------
   p-ddl-MW2 (277) GATATATCATTGGAGGAAAACGAA---------
p-ddl-S.capitis (268) ATAAGCCGAGTAATTGTAATGGAGGAAAACGAA
p-ddl-S.caprae (268) ATAAGCCGAGTAATTGTAATGGAGGAAAACGAA
p-ddl-S.epidermidis (283) AAAAGAACTGTAATTGTA---------------
p-ddl-S.pasteuri (277) TAGCGTATATTGGAGGAAAACGAA---------
p-ddl-S.warneri (277) TAGCGTTTATTGGAGGAAAACGAA---------
 p-ddl-S.simiae (277) AATATATCATTGGAGGAAATTAAC---------
  p-ddl-N315 (277) GATATATCATTGGAGGAAAACGAA---------
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## Potential AirR binding sequence

Among the conservative regions of *ddl* promoter squared in red, only the sequence under blue line can be found in other AirR direct targets. The sequences was analyzed using MEME and listed below. The sequence conservation, measured in bits, in shown as the height of a stack of letters at each base position.



| Name | *p*-value | Sites |
|---|---|---|
| p-ddl | 2.52e-09 | GTTTTTA **AAATGCAAAATAGCATT** AAAATGTGAT |
| p-capA | 1.77e-07 | ATCAGTG **AAATCAAAGATATCATT** CAAACATCAT |
| p-pbp1 | 6.86e-07 | ACTTTCG **AAATACAATATTCCATT** AGAAAAGTG |
| p-lytM | 1.11e-06 | ACAGTTT **AATTGAAAACTAACTTT** AACTTTAATG |