

Supplementary material

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>extracted region of Acinetobacter sp. ADP1 genome from 17883 to 18443
Length of sequence-          561
Threshold for promoters -    0.20
Number of predicted promoters -      1
Promoter Pos:      321 LDF-    5.48
-10 box at pos.    306 GAGTAACAT Score    52
-35 box at pos.    287 TTGACT   Score    61

Oligonucleotides from known TF binding sites:

For promoter at      321:
  narP:  TTTAGAGT at position    302 Score -   8
  ompR:  GTAACATA at position    308 Score -  11
  fadR:  CCGACCTA at position    317 Score -  16
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Figure 2: Output of BPROM tool sited at SoftBerry.

TF	TF binding site	Position of TF binding site	Score	Reference	Function
narP	TTTAGAGT	302	8	Swiss-Prot entry P31802	This protein activates the expression of the nitrate reductase (narGHJI) and formate dehydrogenase-N (fdnGHI) operons and represses the transcription of the fumarate reductase (frdABCD) operon in response to a nitrate/nitrite induction signal transmitted by either the narX or narQ proteins.
ompR	GTAACATA	308	11	Swiss-Prot entry P0AA16	The N-terminus of this protein is required for the transcriptional expression of both major outer membrane protein genes ompF and ompC; its C-terminal moiety mediates the multimerization of the ompR protein. As a multimer, it turns on the expression of the ompC gene; as a monomer, it turns on the expression of the ompF gene.
fadR	CCGACCTA	317	16	Swiss-Prot entry A7ZKV8	Multifunctional regulator of fatty acid metabolism

Table 1: Details of Putative TF binding sites with sequence and function found in upstream region of *Acinetobacter* species 16S rRNA gene.