

1. The *cre* targets that were collected by Fujita in *B. subtilis* (1) to predict the *cre*-like sequences in the promoters of genes of *Bacillus thuringiensis* HD-789.

>amyE	TGTAAGCGTTAACA	Score : 12.97
>bglP	TGAAAGCGTTGACA	Score : 13.05
>cccA	TGTAAGCGTATACA	Score : 11.71
>citM	TGTAAGCGGATTCA	Score : 10.94
>ydbH	TGAAAACGCTATCA	Score : 13.28
>glpF	TGACACCGCTTTCA	Score : 11.57
>mala	TGTAAACGTTATCA	Score : 12.20
>gntR	TGAAAGTGTTTGCA	Score : 10.08
>kduI	TGAAACCGTTACCA	Score : 10.90
>phoP	TGAAAGCGCTATCA	Score : 14.62
>acoR	TGAAAGCGCTTTAT	Score : 11.85
>acuA	TGAAAACGCTTTAT	Score : 10.51
>mmgA	TGTAAGCGCTGTCT	Score : 12.67
>msmX	AGAAAGCGTTTACA	Score : 11.57
>xsa	TAAAAGCGCTTACA	Score : 11.69
>yxjC	TGTAAACGCTTTCT	Score : 12.31

2. The *dre* sequences of *nagA*, *nagP* and *chiB* in *Bacillus thuringiensis* HD-789 to predict the *dre*-like sequences in the promoters of genes of *Bacillus thuringiensis* HD-789

>nagA	GCACGAGTAGTTGTCT	Score : 11.72
>nagP	ACACATCTATACAAC	Score : 10.89
>chiB	AGACTTCGTGATGTCT	Score : 12.03

1. **Fujita Y.** 2009. Carbon catabolite control of the metabolic network in *Bacillus subtilis*. *Biosci Biotechnol Biochem* **73**:245-259.