CORRIGENDUM

A response-regulator-like activator of antibiotic synthesis from *Streptomyces coelicolor* A3(2) with an amino-terminal domain that lacks a phosphorylation pocket

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p. 732, Fig. 3 legend

The base change in the cloned **Pwb-6** mutant DNA is shown at nucleotide position 62.

should read

The base change in the cloned **Pwb-9** mutant DNA is shown at nucleotide position 62.

p. 735, first paragraph

Analysis of the sequence upstream of this from **Pwb-6** DNA revealed a base change in the –35 region of the *redZ* promoter (sequences upstream of the coding regions of *redZ* in **Pwb-9** and **Pwb-16** DNA have not yet been determined). This change caused a closer resemblance to the likely consensus –35 sequence for promoters presumed to be recognized by the major vegetative form of RNA polymerase holoenzyme:

TCTCCA **Pwb**⁺

TTTCCA **Pwb-6**

TTGACA –35 consensus

should read

Analysis of the sequence upstream of this from **Pwb-9** DNA revealed a base change in the –35 region of the *redZ* promoter (sequences upstream of the coding regions of *redZ* in **Pwb-6** and **Pwb-16** DNA have not yet been determined). This change caused a closer resemblance to the likely consensus –35 sequence for promoters presumed to be recognized by the major vegetative form of RNA polymerase holoenzyme:

TCTCCA **Pwb**⁺

TTTCCA **Pwb-9**

TTGACA –35 consensus