Erratum to: Transcriptome profiling of *degU* expression reveals unexpected regulatory patterns in *Bacillus megaterium* and discloses new targets for optimizing expression

Claudia Borgmeier · Rebekka Biedendieck ·
Kristina Hoffmann · Dieter Jahn · Friedhelm Meinhardt

Published online: 10 November 2011
© Springer-Verlag 2011

Erratum to: Appl Microbiol Biotechnol
DOI 10.1007/s00253-011-3575-x

In the original publication Figure 8 is erroneously identical to Figure 6. The correct Figure 8 is shown here.

The online version of the original article can be found at <http://dx.doi.org/10.1007/s00253-011-3575-x>.

C. Borgmeier · K. Hoffmann · F. Meinhardt (✉)
Institut für Molekulare Mikrobiologie und Biotechnologie,
Westfälische Wilhelms Universität,
Corrensstrasse 3,
48149, Münster, Germany
e-mail: meinhar@uni-muenster.de

R. Biedendieck · D. Jahn
Institut für Mikrobiologie, Technische Universität Braunschweig,
Braunschweig 38106 Niedersachsen, Germany

Present Address:
K. Hoffmann
Forschungszentrum Jülich,
Institut für Bio- und Geowissenschaften,
Jülich, Germany

Fig. 8 Extracellular protease activities from LB batch cultivation of DSM319 and MS071 (*degU32*) both carrying amylase expression-vector pBV1 with plasmid-encoded xylose-inducible expression of *degQ* (a, b) or *abba* (c, d) of *B. subtilis*. Protease activity was determined for noninduced (light grey) and induced (black, t+)

cultures at the end of exponential growth (t1) and 1 h after entry into the stationary phase (t2). Activity values refer to volumetric activity per OD_{546 nm} (a, c) and volumetric activity per μg total extracellular protein (b, d). Mean values were obtained from three independent experiments