

Structural and functional organization of the fengycin synthetase multienzyme system from *Bacillus subtilis* b213 and A1/3

Sigrid Steller, Dirk Vollenbroich, Frank Leenders, Torsten Stein, Birgit Conrad, Jürgen Hofemeister, Philippe Jacques, Philippe Thonart and Joachim Vater

Chemistry and Biology 1999, Vol 6 No 1:31–41

Errors were inadvertently introduced into Table 1 of this paper. Table 1 is correctly reprinted below.

Table 1

Amino-terminal sequence alignment of fengycin synthetase subunits from various *Bacillus* strains.

Gene product	<i>B. subtilis</i> strain	Amino-terminal sequence	Identity (%)	Homology (%)
Fen1	213	MENTVYSLTHAQ		
A1/3orf1	A1/3	MXNTVYSLTHAQRRVWFTELEPGTSICNL-30	100	100
Pps1	168	MSEHTYSLTHAQRRVWFTELEPDTSICNL	58	58
Fen2	213	TQATEIQDIY		
A1/3orf2	A1/3	MTQATEIQDIYPLSYMQEGMLFHSLLDSGS-30	100	100
Pps2	168	MAQSAQIQDIYPLSHMQEGMLFHSLLMDFSS	60	80
Fen3	213	QQPEIQDIYPLSFMQ		
A1/3orf3	A1/3	MGQQPEIQDIYPLSFMQEGMLFHSLLDHD-30	100	100
Pps3	168	MPQQPEIQDIYPLSFMQEGMLFHSLYDEQS	100	100
FenE	F29-3	MPQQPEIQDIYPLSFMQEGMLFHSLYDEQS	100	100
Fen4	213	TKKNAIQDIY		
A1/3orf4	A1/3	MTKKNAIQDIYPLSYMQEGMLFHSLLQKES-30	100	100
Pps4	168	MTKANSIQDIYPLSYMQEGMLFHSLLQKDS	80	90
FenA	F29-3	MTKANSIQDIYPLSYMQEGMLFHSLLQKDS	80	90
Fen5	213	MDKTKNQNY P		
A1/3orf5	A1/3	MDKTKNQNYPLSRMQEGMLFHSFLQKEG-30	100	100
Pps5	168	MNTIKKKNIPLSHMQEGMLFHSFLRKEE	58	75
FenB	F29-3	MVTKKKKNVYPLSHMQEGMLFHSFLHKEE	66	83