Corrections

The Nonribosomal Peptide Synthetase HMWP2 Forms a Thiazoline Ring during Biogenesis of Yersiniabactin, an Iron-Chelating Virulence Factor of *Yersinia pestis*, by Amy M. Gehring, Ichiro Mori, Robert D. Perry, and Christopher T. Walsh*, Volume 37, Number 33, August 18, 1998, pages 11637−11650.

Page 11649. In Table 3, bottom portion, the sequences appearing on lines 1, 3, and 4 are incorrect. A corrected table appears below. The Journal regrets introduction of these errors.

Table 3: Comparison of Core Motif 3 of Condensation Domains with the Same Region in the Putative Condensation/ Heterocyclization Domains of Thiazoline/Oxazoline Ring-Forming Synthetases

Enzyme	Organism	Position (aa)	Sequence
Domains catalyzing amide-bond formation[a]			
EntF	*Escherichia coli*	135	RY**HH**LLV**DG**F**S**FPAI
PvdD	*Pseudomonas aeruginosa*	171	VQ**HH**IVS**DG**W**S**MQVM
SnbC	*Streptomyces pristinaespiralis*	139	HV**HH**LLL**DG**YGFRLV
SrfA-A	*Bacillus subtilis*	1184	DM**HH**LIS**DG**V**S**IGIM
BA1 (BacA)	*Bacillus licheniformis*	1803	NF**HH**IIS**DG**V**S**QGIL
Domains catalyzing bond formation/heterocyclization[b]			
HMWP2	*Yersinia pestis/enterocolitica*	244	NI**D**LLIM**D**AS**S**FTLF
HMWP2	*Yersinia pestis/enterocolitica*	1618	CL**D**NLLL**DG**L**S**MQIL
HMWP1[c]	*Yersinia pestis/enterocolitica*	2047	NL**D**LLQF**D**VQ**S**FKVM
BA1	*Bacillus licheniformis*	764	NV**D**PLIC**D**DS**S**MKRL
AngR	*Vibrio anguillarum*	140	RFNSVVV**D**NP**S**VILF
MTCY22H8.02	*Mycobacterium tuberculosis*	228	DL**D**MQAA**D**AM**S**YRIL

[a] All sequences available in the GenBank, SwissProt, or EMBL databases. [b] *Y. pestis* sequences obtained from R. D. Perry (unpublished). All other sequences available in the GenBank, SwissProt, or EMBL databases. [c] Amino acid 2045 for the *Y. enterocolitica* sequence.

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