Correction to: Expanding tryptophan-containing cyclodipeptide synthase spectrum by identification of nine members from *Streptomyces* strains

Jing Liu¹ · Huili Yu¹ · Shu-Ming Li¹

Published online: 16 May 2018

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Correction to: Applied Microbiology and Biotechnology
<https://doi.org/10.1007/s00253-018-8908-6>

The original version of this article contained mistake. After careful re-examination of the LC-MS data, the products of CDPSs “WP_031028810” and “BAU83478” should be cFL instead of cPY. We apologize for any inconvenience that this may have caused.

Correct presentations given below:

The sixth sentence of the first paragraph in the **Discussion Section**:

“As shown in Fig. S10, WP_031028810 from *Streptomyces* sp. NRRL F-5639 and BAU83478 from *Streptomyces laurentii* DSM 41684 were proven to be responsible for the formation of *cyclo*-L-Pro-L-Tyr (cPY).”

should be changed to

“As shown in Fig. S10, WP_031028810 from *Streptomyces* sp. NRRL F-5639 and BAU83478 from *Streptomyces laurentii* DSM 41684 were proven to be responsible for the formation of *cyclo*-L-Phe-L-Leu (cFL).”

Jing Liu and Huili Yu contributed equally to this work.

The online version of the original article can be found at <https://doi.org/10.1007/s00253-018-8908-6>

✉ Shu-Ming Li
shuming.li@staff.uni-marburg.de

¹ Institut für Pharmazeutische Biologie und Biotechnologie,
Philipps-Universität Marburg, Robert-Koch-Straße 4,
35037 Marburg, Germany

Fig. 1 Phylogenetic analysis of CDPSs from actinobacteria. The main CDPS products are given in parenthesis. Enzymes investigated in this study are highlighted in red

Table 1 Information on CDPSs identified in this study

CDPS	Accession number	Protein length (aa)	Primer sequences (5'-3')	Cloning constructs in pGEM-T easy	Cloning sites in pET28a	Expression constructs
CWWS1 _{D46488}	WP_014141671	278	AACATATGCACGACAACGGTCATCGGCC <u>TTGGATCCTTACGTCACCGCT</u>	pHY02	<u>NdeI</u> <u>BamHI</u>	pHY34
CWWS2 _{D46488}	WP_014140974	234	GCCATATGCTGCATCGAACGTCCTT <u>TAGGATCCTCACGGCTCGGCGGGCAGTT</u>	pHY01	<u>NdeI</u> <u>BamHI</u>	pHY11
CWWS1 _{NB2774}	WP_078950527	265	CATATGACGATCACAGCTGACGCATCAITC <u>GGATCCTCAAGCTGCTCGACGCTCAT</u>	pHY72	<u>NdeI</u> <u>BamHI</u>	pHY82
CWWS1 _{NB5737}	WP_019889609	239	GCCATATGACTCTCATCGAAGACAC <u>GGATCCTCAAGCGGCTCGACGGTCAT</u>	pHY08	<u>NdeI</u> <u>BamHI</u>	pHY09
CWWS1 _{NB5414}	WP_063768158	273	CATATGAGGGCGATCACACAGGTGAC <u>GGATCCTCAAGCTGCTCGACGCTCAT</u>	pHY77	<u>NdeI</u> <u>BamHI</u>	pHY83
CWPS1 _{NS1868}	WP_078873129	241	CATATGAACACTTCCCTCGCTGC <u>GAATTCTCAGCGTTCGGCCGCCCGGTC</u>	pHY103	<u>NdeI</u> <u>EcoRI</u>	pHY107
CWLS1 _{NF5053}	WP_051847149	243	CATATGTGCGAGGGCGCGCATGTGC <u>GGATCCTCAGGATTCGTCCACCGG</u>	pJL03	<u>NdeI</u> <u>BamHI</u>	pJL26 ^a
CWPS1 _{NF5123}	WP_052397358	263	CATATGACCAGCAGGACCGAAAC <u>GAATTCTCACGGAAGCAGCCGGGGG</u>	pHY100	<u>NdeI</u> <u>EcoRI</u>	pHY105
CWXS1 _{NS1868}	WP_078872750	267	CATATGGCCACACACGCCTCCGC <u>GAATTCTCACTGCTGCTCACGTGGTC</u>	pHY101	<u>NdeI</u> <u>EcoRI</u>	pHY106
CWXS1 _{NB3589}	KOG90878	255	CATATGGGGGCCCGCAGCCC <u>GGATCCTCACGTCAAGTCCCTTCTCC</u>	pJL02	<u>NdeI</u> <u>BamHI</u>	pJL25
CWXS1 _{NB24309}	WP_078624487	282	GCGCATATGAGTGCATCGCAGGCTGTG <u>GGATCCTCACGTACGTCCCCCTGC</u>	pJL01	<u>NdeI</u> <u>BamHI</u>	pJL24 ^b
CFLS1 _{NF5639}	WP_031028810	278	CATATGAACCGCGCTGTTCTTCG <u>GGATCCTCATGCTCTGGGGCACTG</u>	pJL04	<u>NdeI</u> <u>BamHI</u>	pJL29
CFLS1 _{D41684}	BAU83478	224	CGCATATGAACCAAGTTCGACGTGCTGCC <u>GGATCCCGGACCACGAGGAAGCC</u>	pJL05	<u>NdeI</u> <u>BamHI</u>	pJL30 ^c

Restriction sites for cloning are underlined in primer sequences

a The 12 base pairs at the 5'-end of the sequence coding for WP_051847149 were not included in the expression construct pJL26

b The 96 base pairs at the 5'-end of the sequence coding for WP_078624487 were not included in the expression construct pJL24

c According to the annotation in database, BAU83478 comprises 484 amino acids and consists of CDPS sequence at its N-terminus and that for a putative methyltransferase at its C-terminus. The sequence coding for amino acids 1 - 224 of BAU83478 was cloned into pET28a generating pJL30