Supplementary Materials: Characterization of Enzymatic Activity of MlrB and MlrC Proteins Involved in Bacterial Degradation of Cyanotoxins Microcystins

Dariusz Dziga, Gabriela Zielinska, Benedykt Wladyka, Oliwia Bochenska, Anna Maksylewicz, Wojciech Strzalka and Jussi Meriluoto

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AAL10287	MRYLLTSSQITGLCYAVDLRGKVLFQGGFGLADLTTREPITPATRFEI	48
BAI47771	MTATKLFLALTAAMPMATSHVDPKELDAVFADIRPDQPGCAYAVDLRGKVLYQGGFGLADLATREPITTATRFEI	. 75
AGG86526	MTATKLFLALTVAMPMATSHVDPKELDAVFADIRPDQPGCAYAVDLRGKVLYQGGFGLADLATREPITPATRFEI	. 75
KR150744	MTATKLFLALTAAIPMATPQVDSRVLDAVFADIKPDEPGCAYAVDLRGKVLFQGGFGLADLTTREPITPATRFEI	. 75
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AAL10287	ASTSKQFTAALILILAQERRLRLTASIRTYLPDLPKVYEPVSVADLLHHTSGIREYFDAFRARGEEQSKSHSRE	E 123
BAI47771	ASTSKQFTAALILILAQERRLKLAASIRTYLPDLPKVYDSVTVADLLHHTSGIREYFDAFRTRGDDESKPHSRE	E 150
AGG86526	ASTSKQFTAALILILVQERRLKLAASIRTYLPDLPKVYDPVTVADLLHHTSGIREYFDAFRARGDDESKPHSRE	E 150
KR150744	ASTSKQFTAALILILAQERRLRLTASIRTYLPDLPKVYEPVSVADLLHHTSGIREYFDAFRARGEDESKSHSRE	E 150
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AAL10287	VLAFIKAQRGLDGPPGHRFSYVNTNYFLLAEIVERLIRKPFPDGARELLFIPAGMKETRATLDTTSLLAGDAHG	198 (
BAI47771	VLAFVKAQRGLDGPPGRRFSYVNTNYFLLAEIVERLTGKSFPDAARERLFIPAGMTETRATLDATSLIAGDARG	225
AGG86526	VLAFVKAQRGLDGPPGRRFSYVNTNYFLLAEIVERLTGKSFPDAARERLFIPAGMTETRATLDTTSLVAGDARG	225
KR150744	VLAFIKAQRGLDGPPGHRFSYVNTNYFLLAEIVERLIRKPFPDGARELLFIPAGMKETRATLDTTSLLAGDAHG	225
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AAL10287	QVTKDGKFAEAVWAWQGYGDRGVRTTVGDLAVWHGASLAATTGGQALEVARLANGKLRSGRPVDYAGGLFVDDRG	2 273
BAI47771	QIDKNGSFVSAAWTWQGYGDRGVRTTVGDLALWHGASLAATTGGEALKVARLANGKLRSGRSVDYAGGLFVDDRG	2 300
AGG86526	QIDKNGSFVSAAWTWQGYGDRGVRTNVGDLALWHGASLAATTGGEALEVARLANGKLRSGRSVDYAGGLFVDDRG	2 300
KR150744	QVTKDGKFAEAVWAWQGYGDRGVRTTVGDLAVWHGASLAATTGGQALEVARLANGKLRSGRPVDYAGGLFVDDRG	2 300
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Figure S1. Alignment of MIrB protein amino acid sequences from bacterial strains of *Sphingomonaceae* family (AAL10287–*Sphingomonas* sp. ACM-3962 (Bourne, 2001), BAI47771–*Sphingopyxis* sp. C-1, AGG86526–*Sphingomonas* sp. USTB-05, KR150744–*Sphingomonas* sp. ACM-3962) verified in the present study.





Figure S2. The examples of chromatograms indicating the formation of hexapeptides from different linearized MC variants by MIrC and the lack of degradation of linearized variants in the presence of extract of *E. coli* with empty plasmid pET21a (negative controls).





Figure S3. Cont.









Figure S3. Cont.



Figure S3. Cont.

hexaMC-RR:



Figure S3. MS² of the hexapeptides originated from other MC variants.

hexaMC-YR: