Supplementary Material

A new cyclopeptide metabolite of marine gut fungus from *Ligia oceanica*

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Abstract

Four amino acid derivatives, including a new cyclopeptide were isolated from marine-derived fungus *Aspergillus flavipes*, which was found in the gut of isopod *Ligia oceanica*. The novel peptide contains four amino acid units, proline, 5-methoxyanthranilic acid, isoleucine, and 3- aminoacrylic acid. Its structure was determined on the basis of NMR, HR-MS, and MSⁿ spectral data analysis. The two unusual amino acid residues, 5-methoxyanthranilic acid and 3-aminoacrylic acid, were first found in natural product. Known compound *N*-Benzoyl-phenylalanine methyl ester was first found as fungal metabolite.

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18S rDNA

GGTCGCATGTCTAGTATATGCACTTTATACCGTGAAACTGCGAATGGCTCATTAAATCAG
TTATCGTTTATTTGATAGTACCTTACTACATGGATACCTGTGGTAATTCTAGAGCTAATAC
ATGCTAAAAACCCGACTTCGGAAGGGGTGTATTTATTAGATAAAAAACCAATGCCCTT
CGGGGCTCCTTGGTGATTCATAATACTTAACGAATCGCATGGCCTTGCGCCGGCGATG
GTTCAATTCAAATTTCTGCCCTATCAACTTTTCGATGGTAGGATAGTGGCCTACCATGGTGG
CAACGGGTAAACGGGGAATTAGGGTTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTA
CCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTA
GTGACAATAAATACTGATACGGGGCTCTTTTGGGTCTCGTAATTGGAATGAGTACAATTT
AAATCCCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATT
CCAGCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTG
GGTCTGGCTGGCCGGTCCGCCTCACCGCGAGTACTGGTCCGGCTGGACCTTTCCTTCT
GGGGAATCCCATGGCCTTCACTGGCTGTGGGGGGAACCAGGACTTTTACTGTGAAAAA
ATTAGAGTGTTCAAAGCAGGCCTTTGCTCGAATACATTAGCATGGAATAATAGAATAGG
ACGTGCGGTTCTATTTTGTGGTTTCTAGGACCGCCGTAATGATTAATAGGGATAGTCCG
GGGCGTCAGTATTCAGCTGTCAGAGGTGAAATTCCTTGGATTTGCTGAAGACTAACTACT
GCGAAAGCATTCGCCAAGGATGTTTTTCATTAATCAGGGAACGAAAGTTAGGGGATCGA
AGACGATCAGATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGCGG
TGTTTCTATGATGACCCGCTCGGCACCTTACGAGAAATCAAAGTTTTTGGGTTCTGGGG
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AATAGCCCGGTCCGCATTTGCGGGCCGCTGGCTTCTTAGGGGGACTATCGGCTCAAGC
CGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGCCCTTAGATGTTCTGGGCCGCAC
GCGCGCTACACTGACAGGGTCAGCGAGTACATCACCTTGGCCGAGAGGTCTGGGTAAT
CTTGTTAAACCCTGTCGTGCTGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGA
ATGCCTAGTAGGCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACA
CCGCCCCGTCGCTACTACCGATTGAATGGCTCGGTGAGGCCTTCGGACTGGCTCAGGAG
GGTTGGCAACGACCCCCCAGAGCCGAAAGTTGGTCAAACCCGGTCATAGAGAAGAA
AGTATT