

Title	Identification of secondary metabolite gene clusters in the Pseudovibrio genus reveals encouraging biosynthetic potential toward the production of novel bioactive compounds
Author(s)	Naughton, Lynn M.; Romano, Stefano; O'Gara, Fergal; Dobson, Alan D. W.
Publication date	2017
Original citation	Naughton, L. M., Romano, S., O'Gara, F. and Dobson, A. D. W. (2017) 'Identification of secondary metabolite gene clusters in the Pseudovibrio genus reveals encouraging biosynthetic potential toward the production of novel bioactive compounds', <i>Frontiers in Microbiology</i> , 8, 1494 (15pp). doi: 10.3389/fmicb.2017.01494
Type of publication	Article (peer-reviewed)
Link to publisher's version	http://journal.frontiersin.org/article/10.3389/fmicb.2017.01494/full http://dx.doi.org/10.3389/fmicb.2017.01494 Access to the full text of the published version may require a subscription.
Rights	© 2017, Naughton, Romano, O'Gara and Dobson. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) or licensor are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms https://creativecommons.org/licenses/by/4.0/
Item downloaded from	http://hdl.handle.net/10468/4801

Downloaded on 2018-10-17T18:45:45Z

Supplementary Material

Identification of secondary metabolite gene clusters in the *Pseudovibrio* genus reveals a promising potential toward the discovery of novel bioactive compounds.

Lynn M. Naughton¹§, Stefano Romano²§, Fergal O’Gara^{3,4} and Alan D.W. Dobson^{1*}

* **Correspondence:** Professor Alan Dobson: a.dobson@ucc.ie

§ These authors contributed equally to this work



Supplementary Figure Legends

Figure S1. Maximum Likelihood tree performed for the AMP-binding domains of the NRPS biosynthetic gene clusters. *Pseudovibrio* sequences were combined with those of other bacterial BGCs present in the MIBiG database.

Figure S2. Maximum Likelihood tree performed for the KS domains of the PKS biosynthetic gene clusters. *Pseudovibrio* sequences were combined with those other bacterial BGCs present in the MIBiG database.

Figure S3. Sub-tree containing *Pseudovibrio* sequences extracted from the AMP-binding domains. The subtrees were recovered from the tree shown in Figure S1. Only support values higher than 0.5 are shown.

Figure S4. Sub-tree containing *Pseudovibrio* sequences extracted from the KS domains. The subtrees were recovered from the tree shown in Figure S2. Only support values higher than 0.5 are shown.