

Northumbria Research Link

Citation: Jones, Amanda, Fisher, Andrew, Mahida, Rahul, Gould, Kate, Perry, John, Hannan, Margaret, Judge, Eoin, Brown, Roselyn, Boagey, Kimberley and Goodfellow, Michael (2014) *Nocardia krogenstedtii* sp. nov., a novel actinomycete isolated from a lung transplant patient with a pulmonary infection. *International Journal of Systematic and Evolutionary Microbiology*, 64 (3). pp. 751-754. ISSN 1466-5026

Published by: Society for General Microbiology

URL: <http://dx.doi.org/10.1099/ijs.0.048330-0> <<http://dx.doi.org/10.1099/ijs.0.048330-0>>

This version was downloaded from Northumbria Research Link: <http://nrl.northumbria.ac.uk/15415/>

Northumbria University has developed Northumbria Research Link (NRL) to enable users to access the University's research output. Copyright © and moral rights for items on NRL are retained by the individual author(s) and/or other copyright owners. Single copies of full items can be reproduced, displayed or performed, and given to third parties in any format or medium for personal research or study, educational, or not-for-profit purposes without prior permission or charge, provided the authors, title and full bibliographic details are given, as well as a hyperlink and/or URL to the original metadata page. The content must not be changed in any way. Full items must not be sold commercially in any format or medium without formal permission of the copyright holder. The full policy is available online: <http://nrl.northumbria.ac.uk/policies.html>

This document may differ from the final, published version of the research and has been made available online in accordance with publisher policies. To read and/or cite from the published version of the research, please visit the publisher's website (a subscription may be required.)





Northumbria
University
NEWCASTLE

Fig. S2. Neighbour-joining tree based on nearly complete 16S rRNA gene sequences showing the position of strain N1286^T. Asterisks indicate branches of the tree that were also found with the maximum-likelihood and maximum-parsimony tree-making algorithms; L and M indicate branches found using the maximum-likelihood and maximum-parsimony methods, respectively. The numbers at the nodes indicate the levels of bootstrap support based on a neighbour-joining analysis of 1000 re-sampled datasets; only values above 50% are given. The scale bar indicates 10 substitutions per nucleotide position. ^T, type strain.

