CHAPTER 5

Polyphasic Characterisation of *Pantoea* Strains from Onion and Maize, and the Description of *Pantoea allii* sp. nov.

Abstract

Bacteria from the genus *Pantoea* have become increasingly important plant pathogens around the world. In South Africa, they cause diseases of two economically important crops, *Eucalyptus* and maize. The strains inducing center rot of onion have only been found in onion seed in this country, and have not yet been associated with any disease outbreak. The identity and taxonomic position of *Pantoea* isolates from onion and maize has not been fully determined. Forty-seven strains were subjected to a polyphasic study that included phenotypic characterisation, analysis of the F-AFLP patterns, rep-PCR genomic fingerprinting, 16S rDNA gene sequences and DNA-DNA hybridisation. The results revealed that the strains belong to three different species within the genus *Pantoea*. Majority of strains were identified as *P. ananatis*. Indole-negative strains from maize were identified as *P. vagens*. Some strains from onion, previously classified as *P. ananatis*, were shown to form a novel species. The name *Pantoea allii* sp. nov. is proposed for these strains (type strain BD 390^T) and the description of the species is presented.

INTRODUCTION

Bacteria belonging to the genus *Pantoea* are common on plant surfaces, in seeds, soil, and water and have been isolated from humans and animals (Gavini et al., 1989; Mergaert et al., 1993). Many microbiologists have studied the taxonomy of the genus. The studies included the numerical analysis of phenotypic characteristics (Verdonck et al., 1987), 16S rRNA gene sequence analysis (Hauben et al., 1998), fatty acid and protein profile analyses, DNA-DNA hybridisation (Brenner et al., 1984; Beji et al., 1988; Gavini et al., 1989, Mergaert et al., 1993) and AFLP fingerprints analysis (Brady, 2005). There are seven described species within the genus *Pantoea*: *P. agglomerans, P. ananatis, P. citrea, P. dispersa, P. punctata, P. terrea*, and *P. stewartii* containing two subspecies, *indologenes* and *stewartii.* There are also several hybridisation groups from a study by Brenner et al. (1984), and a protein profile group of Beji et al. (1988), that according to the latest edition of the Bergey's manual of systematic bacteriology belong to the genus *Pantoea* (Grimont and Grimont, 2005).

Plant pathogenic *Pantoea* species cause diseases on diverse crops, such as pineapple (Serrano, 1928; Kageyama et al., 1992), melons (Bruton et al., 1986; Wells et al., 1987), cantaloupe (Bruton et al., 1991) sudangrass (Azad et al., 2000), *Eucalyptus* (Coutinho et al., 2002), rice (Azegami et al., 1983; Cother et al., 2004), mandarin orange (Kageyama et al., 1992), sugarcane (Serrano, 1928), beets (Brown, 1928), *Gypsophila* (Brown, 1934), onion (Hattingh and Walters, 1981; Gitaitis and Gay, 1997; Schwartz and Otto, 2000; Goszczynska et al., 2006) and maize (Elliott, 1941; Paccola-Meirelles et al., 2001; Goszczynska et al., 2007). Disease symptoms are diverse and include galls, rots, wilt, leaf blights, necrosis and spots, dieback and stem necrosis (Grimont and Grimont, 2005).
However, not all *Pantoea* strains are plant pathogens, and some have been used for biological control of *Erwinia amylovora* (Beer et al., 1984) and *Xanthomonas albilineans* (Zhang and Birch, 1997). Some strains of *P. agglomerans* (Nunes et al., 2001) and *P. ananatis* (Torres et al., 2005) are effective for the biological control of post harvest pome fruit diseases caused by fungi.

Diseases of onion are characterised by leaf blight, central leaf rot, seed stalk necrosis and rot, and bulb decay and these symptoms can lead to economically significant loses (Hattingh and Walters, 1981; Walcott et al., 2002). These diseases are caused by *P. ananatis* (Gitaitis and Gay, 1997) and *P. agglomerans* (Hattingh and Walters, 1981). The strains of *P. ananatis*

inducing center rot of onion have only been found in onion seed in South Africa, and have not yet been associated with any disease outbreak (Goszczynska et al., 2006).

Brown stalk rot of maize was first observed in South Africa in 2004 and was caused by *P. ananatis* and an unknown *Pantoea* sp. similar phenotypically to *P. agglomerans* (Goszczynska et al., 2007). Affected plants were stunted, with a vertical crack at the first internode, surrounded by a dark brown, narrow lesion. Internal browning inside the stem extended upwards, reaching the top internode in some plants. Seed cobs were underdeveloped. Diseased plants were scattered over the fields and 10-70% of the crop was affected (Goszczynska et al., 2007).

The diseases of onion and maize caused by *Pantoea* species were recorded for the first time during the last decade. Their taxonomic position has not been fully clarified. Bacteria isolated from onion in the USA and South Africa was considered to be *P. ananatis*. This classification was based only on biochemical and physiological characteristics (Gitaitis and Gay, 1997; Schwartz and Otto, 2000; Walcott et al., 2002) and the analysis of the 16S rDNA sequences (Goszczynska et al., 2006). Such methods are often insufficient for species delineation according to the recommendation of Wayne et al. (1987) and Stackebrandt et al. (2002). *Pantoea* strains isolated from maize with brown stalk rot symptoms in South Africa were additionally examined by using fluorescent amplified fragment length polymorphism analysis (F-AFLP) (Goszczynska et al., 2007). The majority of strains isolated from diseased maize were *P. ananatis*. Several isolates, although similar to *P. agglomerans* on the basis on biochemical tests and 16S rDNA sequences, produced F-AFLP fingerprints that were distinctly different from that generated by *P. ananatis, P. agglomerans, P. dispersa, P. citrea, P. stewartii* subsp. *stewartii* and *P. stewartii* subsp. *indologenes*. The results indicated that these bacteria belong to a previously undescribed species of the genus *Pantoea* and their taxonomic status needed to be further investigated. Bacteria recently isolated from *Eucalyptus* in Uganda were proposed to form a new species within a genus *Pantoea*, *P. vagens* (unpublished results(Goszczynska et al., 2007).). The type strain of *P. vagens*, BCC 105^{T} was included in this study.

The present research was initiated to characterise a collection of *Pantoea* strains from onion and maize by a polyphasic approach based on analyses of carbon source utilisation,

physiological characteristics, 16S rRNA gene sequence analysis, DNA-DNA hybridisation and F-AFLP. Based on the results obtained, the new species *Pantoea allii* is proposed.

MATERIALS AND METHODS

Bacterial strains. Sixty-seven bacterial strains used in the study are listed in Table 1. Twenty-four strains were originally isolated from onion plants and seed in the USA and South Africa. Twenty-three strains were isolated from maize with brown stalk rot in South Africa. Twenty *Pantoea* strains, including the type strains of *P. ananatis*, *P. agglomerans, P. citrea, P. dispersa, P. vagens, P. stewartii* subsp. *indologenes* and *P. stewartii subsp. stewartii* were used as reference strains. The strains were routinely cultured on tryptone glucose extract agar (TGA) (Difco, Sparks, MD), at 26°C and preserved in milk glycerol liquid medium (10% skim milk, 15% glycerol in distilled water) at –20°C. All cultures were routinely checked for purity and colony characteristics on TGA.

Pathogenicity tests. Pathogenicity on onion cv. Granex 33 was determined in green house assays by using a stub inoculation test (Goszczynska et al., 2006). A sterile needle was dipped into the bacterial colony on TGA (24-48 hours growth) and then the needle was inserted under the epidermis of a leaf. At least two leaves were inoculated per isolate. Inoculated plants were incubated in a greenhouse with 27°C/23°C day/night temperatures and observed daily for the development of symptoms.

Pathogenicity on maize was determined in greenhouse assays on a susceptible maize cultivar SR 52 (Goszczynska et al., 2007). Nine-week-old plants were inoculated by injecting a few drops of bacterial suspensions into the first internode of the stem. Maize plants were maintained in a greenhouse with natural light and at temperatures and RH described above. At least two plants were inoculated with each bacterial strain per inoculation method. This experiment continued for ten weeks.
Three control plants in all experiments were inoculated with sterile distilled water.

Phenotypic methods

Morphological and physiological characteristics. Strains from onion and maize were characterised by colony morphology, pigment production on TGA, motility, cell

morphology, Gram-stain, oxidase reaction, catalase reaction, indole production, Hugh-Leifson oxidation/fermentation test, gas production from glucose, hydrogen sulphide production from cysteine, growth at different temperatures (4, 30, 37, 40 and 44°C), and tolerance to NaCl (Mergaert *et al.*, 1993). The tests were performed according to methods described by Fahy and Hayward (1983).

Utilisation of carbon sources. All strains listed in Table 1 were characterised phenotypically by the Biolog GN2 microplate system (Biolog, Inc., Hayward, CA), according to the manufacturer's instructions. The inoculated microplates were incubated at 30°C for 24 hours. Plates were then scored visually for carbon source utilisation patterns. The data was entered into the Bionumerics software (version 4.5, Applied Maths, Kortrijk, Belgium). Similarity matrixes were constructed using the Pearson coefficient. Groups of strains were defined by the unweighted pair group method (UPGMA) using the same software.

Biochemical tests. Biochemical characteristics of the strains listed in Table 1 were examined with the API 20E system (BioMérieux, La Balme les Grottes, Montalieu Vercieu, France), according to the procedure recommended by the manufacturers. Selected strains were also tested with the API 50CHE system. The results of the API 20E and API 50CHE tests were recorded after 24 and 48 hours of incubation at 30°C respectively.

Two cluster analyses were performed using the Bionumerics software. The first analysis was done with the API 20E data (21 characters) for all strains listed in Table 1 and the second analysis with the API 50CHE (49 characters) data for selected strains. Similarity matrixes were constructed with the Dice coefficient and cluster analyses were performed by the UPGMA method. The data was presented as UPGMA dendrograms.

Molecular methods

DNA extraction. Genomic DNA of bacterial strains (Table 1) was extracted by using the GenElute Bacterial Genomic DNA Kit (Sigma, Steinheim, Germany), according to the manufacturer's instructions. Purified DNA was quantified using a Dyna Quant 200 fluorometer (Hoefer, San Francisco, CA) and Hoescht H 33258 intercalating dye (Polysciences, Warrington, PA). The DNA was stored at –20^{o}C until further analysis.

Fluorescent amplified fragment length polymorphism (F-AFLP). All strains listed in Table 1 were examined by the fluorescent amplified fragment length polymorphism (F-AFLP)-based system for the identification of plant-associated species from the genus *Pantoea*, as described by Brady et al. (2006).

Genomic DNA, 50-100 ng from each isolate, was digested with *Eco*RI and *Mse*I (Roche, Mannheim, Germany) restriction enzymes, and then ligated to the respective adaptors. Pre-amplification PCR reactions were done with Eco-00 (5'-GAC TGC GTA CCA ATT C-3') and Mse-00 (5'-GAT GAG TCC TGA CTA A-3') primers. Selective PCR amplifications were performed with Mse-CG (5'-GAT GAG TCC TGA CTA ACG-3') and fluorescently labelled Eco-G (5'-GAC TGC GTA CCA ATT CG-3') primers. Amplifications were done at least twice for each strain in the Hybaid Omni Gene thermocycler (Teddington, England) according to the Brady (2005) specifications.

The selective amplification reactions (1 µl) were mixed with an equal volume of formamide loading buffer (95% formamide, 20 mM EDTA, bromophenol blue), heated for 3 min at 90^{o}C and then chilled on ice for 10 min. A volume of 0.5-0.8 µl of each mixture was loaded onto the gel. The AFLP products were separated in 8% Long Ranger (LI-COR Biosciences, Lincoln, NE) denaturing gels on a LI-COR IR automated sequencer. Electrophoresis was carried out for 4 hours at 1500 V in 0.8 x TBE buffer. Images were imported into BioNumerics software. Gels were standardized with a 50-700 bp sizing standard (LI-COR) and the bands between 50 and 700 bp were analysed (Brady, 2005).

Similarity of the AFLP fingerprints was calculated using the Dice correlation coefficient and the cluster analysis was performed using the unweighted pair group method (UPGMA). The results were presented as an UPGMA dendrogram.

Repetitive sequence based PCR genomic fingerprinting. Repetitive sequence based polymerase chain reaction (rep-PCR) genomic fingerprints were obtained for all strains listed in Table 1. PCR was performed in 10 µl volumes containing PCR buffer (10 mM Tris HCl, pH 9.0 at 25°C; 50 mM KCl; 0.1% Triton X-100); 3.5 mM $MgCl_2$; 150 µM dNTPs; 1.0 µM primer, 2.5% DMSO; Taq polymerase (Promega, Madison, WI) 0.15 units per reaction volume and 25-50 ng template µl $^{-1}$. Primers used in the PCR corresponded to the prokaryotic enterobacterial repetitive interogenic consensus (ERIC2) and the BOX1A subunit of the BOX element (Rademaker and de Bruijn, 1997). PCR reaction volumes were overlaid with 10 µl sterile mineral oil and PCR amplifications performed according to Rademaker and de Bruijn (1997) in a Hybaid Omni Gene thermocycler.

The rep-PCR products were separated in 1.5% agarose in 1 x TBE buffer at 80 V. Gels were stained in ethidium bromide (10 mg ml $^{-1}$) for 10 min and destained for 15 min in water. Images were imported into BioNumerics software. The similarity between strains was calculated using the Pearson's correlation coefficient applied to the entire densitometric curves of the gel tracks. Gels were standardized with DNA molecular weight marker VI (Roche, Steinheim, Germany). All PCR reactions were repeated at least twice. Cluster analysis was performed by the UPGMA method and the data presented as an UPGMA dendrogram.

16S rRNA gene sequence analysis. The 16S rRNA gene fragments of nine strains from onion and twelve strains from maize were amplified in previous studies (Goszczynska et al., 2006 and 2007). The GenBank accession numbers (National Center for Biotechnology Information, U.S. National Institute of Health, Bethesda, MD) are shown in Fig. 4. Ilse Cleenwerck (Ghent University, Belgium) provided the 16S rDNA sequences of *P. citrea, P. punctata* and *P. terrea*. Carrie Brady (University of Pretoria) supplied the sequence of *P. vagens* BD 105^T.

The 16S rDNA nucleotide sequences of strains from maize and onion were aligned with a selection of 16S rDNA sequences of *Pantoea* species from GenBank with the MAFFT software, ver. 5.743 (Katoh et al., 2002). Phylogenetic trees were constructed with the neighbor joining method (Saitou and Nei, 1987) and evolutionary distances calculated

according to the method of Kimura (1980), using the MEGA software package, version 3.1, Kumar, Tamura, Nei, 2004 (Kumar et al., 2004). Bootstrap analysis of the data, based on 1000 permutations was used to assess the stability of relationships.

DNA-DNA hybridisation. The DNA was extracted from the five strains from onion (BD 309, BD 310, BD 377, BD 390, PA 4) three strains from maize (BD 435, BD 442, BD 639), BCC 105 from *Eucalyptus*, and the type strains of *P. ananatis* LMG 2665^T, *P. agglomerans* LMG 1286^T, *P. stewartii* subsp. *stewartii* LMG 2715^T, *P. dispersa* LMG 2603^T and *P. vagens* BCC 105^T, using the method described by Wilson (1989) and modified by Cleenwerck et al (2002).

DNA-DNA hybridisations were performed with photo-biotin-labelled probes in microplate wells (Ezaki et al., 1989; Goris et al., 1998) as described by Cleenwerk et al. (2002). Fluorescent measurements were done with a HTS7000 BioAssay Reader (Perkin-Elmer Cetus, Norwalk, CT). The hybridisation temperature was 45^{o}C. Reciprocal experiments were performed for every pair of strains, and the means from reciprocal tests were presented.

RESULTS

Pathogenicity tests. All *Pantoea* strains isolated from onion induced identical symptoms on onion leaves cv. Granex 33 in pathogenicity tests. Two to four days after inoculation water soaked spots appeared on leaves that expanded into longitudinal, bleached-green lesions with chlorotic margins (Fig. 1).

All *Pantoea* from maize produced brown stalk rot symptoms within six to seven weeks (Fig. 2). Four to six days after inoculation, small, 2-4 mm, light brown or dark green lesions developed around the inoculation point. Additionally, drops of yellow liquid slowly oozed from the lesion for two to three days. After 6 to 7 weeks, a single, long, vertical crack appeared on the injected internode. A dark brown, narrow lesion was present in the internal stem tissue along the crack. The internal browning within the stem was also observed in upper internodes.

Morphological and physiological characteristics. The strains from onion and maize produced yellow colonies on TGA, were gram-negative rods (1.5-2.0 µm length and 0.5-0.75

µm width), motile, oxidase negative and catalase positive. All strains fermentatively utilised glucose. They did not produce gas from glucose nor hydrogen sulphide from cysteine. Majority of strains produced indole from tryptophane, with the exception of *Pantoea* sp. from maize. Cells grew on nutrient agar containing up to 6% NaCl.

Pantoea strains should be classified and identified mainly based on genotypic characteristics, as identification based on phenotypic tests does not always lead to clear results (Gavini et al., 1989, Mergaert et al., 1993). Thus, the results of molecular characterisation of the strains from onion and maize are presented first, followed by the phenotypic description.

Molecular characterisation

F-AFLP analysis. *Pantoea* strains used in the study generated complex DNA fingerprints from extracted genomic DNA (Fig. 3). The selective primers Eco-G/Mse-CG (Brady, 2005) yielded well-defined DNA fingerprints, with an average of 80 bands per isolate. Amplified DNA fragments ranged in size from approximately 50 bp to slightly greater than 700 bp. A total of 101 fragments were generated and all these fragments were polymorphic. Sixty-seven *Pantoea* strains formed seven clusters. Majority of strains from onion and maize clustered with *P. ananatis* type strain LMG 2665^T and *P. ananatis* reference strains. The similarity values among these strains were between 73 and 98%.

The strains from maize, classified as *Pantoea* sp. in a previous study (Goszczynska et al., 2006), formed a cluster with *P. vagens* BCC 105^T. The F-AFLP fingerprints obtained for these strains showed 87 to 94% similarity.

Five strains from onion, indistinguishable from *P. ananatis* by biochemical and morphological characteristics, generated F-AFLP patterns that were clearly different from those produced by other isolates used in the study, including the type strains of *P. ananatis*, *P. agglomerans*, *P. citrea*, *P. dispersa*, *P. vagens, P. stewartii* subsp. *stewartii* and *P. stewartii* subsp. *indologenes.* Fingerprints of BD 304, BD 309, BD 377, BD 380 and BD 390 were 70 to 92% similar to each other.

Rep-PCR genomic fingerprinting. The rep-PCR fragments amplified with the BOX1A and ERIC2 primers, ranged in size from approximately 230 bp to greater than 3 kb. The banding

pattern revealed a high degree of genetic diversity among the strains. Although significant differences were observed between the major groups, within each group of strains fingerprints were similar (Fig. 4). The groups of strains obtained by the analysis of the rep-PCR data were identical to that obtained by using the F-AFLP fingerprints.

The DNA fingerprint similarity among most of isolates from onion, maize, and *P. ananatis* reference strains ranged from 50% to 99% and all these strains clustered together on the rep-PCR dendrogram. The indole-negative strains from maize (Goszczynska et al., 2007) produced characteristic and unique rep-PCR fingerprints. BD 502 and BD 639 formed a separate cluster on the dendrogram with the type strain of *P. vagens*.

A group of five strains from onion (BD 304, BD 309, BD 377, BD 380 and BD 390), generated rep-PCR fingerprints that were similar to each other (50 to 80%), but distinctly different from other strains. The same five isolates also grouped together on the F-AFLP dendrogram.

16S rRNA gene sequence analysis. Figure 5 shows the phylogenetic relationship derived from a neighbor-joining analysis of the pairwise comparison among the 16S rDNA sequences of twelve strains from maize and nine strains from onion. The 16S rDNA sequences of fourteen *Pantoea* reference strains, including the type strains of seven described species within the genus were included in the analysis. The multiple sequence alignment of thirty-five 16S rDNA sequences used in the study is presented in Appendix A.

Phylogenetic evaluation confirmed the division of strains from maize and onion into three groups. Nine maize and five onion strains, that produced genomic fingerprints similar to *P. ananatis*, clustered with the 16S rDNA sequences of *P. ananatis*. Two indole negative isolates from maize grouped closely, at 62% confidence value, with *P. vagens* BCC 105^{T}. Although the sequences of three onion isolates, BD 309, BD 377 and BD 390 were more than 99% similar to that of *P. ananatis,* they formed a separate cluster in the tree, at a high, 81% confidence value.

DNA-DNA hybridisation. Between two and four strains from each F-AFLP and rep-PCR cluster were selected for the DNA-DNA hybridisation. The results of DNA-DNA hybridisations of all examined strains are shown in Table 2.

DNA-DNA binding values obtained for four indole positive strains, BD 310 and PA 4 from onion and BD 435 and BD 442 from maize and *P. ananatis* LMG 2665^T, varied between 90 and 100%. Since 70% DNA binding value was recommended as the minimum level of genotypic relatedness within a species (Wayne et al., 1987), these four isolates were identified as *P. ananatis*.

Strain BD 639 showed 89% DNA relatedness to BCC 105^T. These two strains displayed an intermediate level of DNA similarity, 63 to 65%, to the type strain of *P. agglomerans*, and low levels to the known *Pantoea* species. Therefore, BD 639, and two indole negative strains, BD 500 and BD 502 (Goszczynska et al., 2007) that grouped with BCC 105^T in the F-AFLP, rep-PCR and 16S rDNA dendrograms, were identified as *P. vagens*.
DNA-DNA hybridisation data revealed that three strains from onion, BD 309, BD 377 and BD 390 displayed a high level of DNA relatedness, 90 to 100%, and low levels of relatedness to the known *Pantoea* species and *P. vagens*. The name *Pantoea allii* sp. nov. is proposed for this taxon.

Phenotypic characteristics

Utilisation of carbon sources. On the UPGMA dendrogram of the Biolog data (Fig. 6), the strains used in the study formed four clusters. The biggest group consisted of 54 strains and included all strains identified as *P. ananatis* by molecular fingerprinting, *P. stewartii* subsp. *indologenes* and *P. allii* sp. nov. There was consistency in utilisation of 69 substrates on the GN2 plates among these strains, 41 positive and 28 negative reactions. No single test was able to differentiate between *P. ananatis* and *P. allii*. *P. stewartii* subsp. *indologenes*, however, could be distinguished from these two other species by its inability to utilise L-rhamnose, L-histidine and D,L,α-glycerol phosphate.

The *P. vagens* strains from maize and the *P. vagens* type strain BCC 105^T clustered with *P. agglomerans*. The isolates within a cluster gave 41 positive and 27 negative reactions in Biolog GN2 plates. *P. vagens* differed from *P. agglomerans* by its ability to utilise nine substrates: D-melibiose, turanose, L-ornithine, D-serine, L-threonine and four acids, formic, α-hydroxybutyric, α-ketoglutaric and succinamic.

API 20E. The results of physiological and biochemical tests using the API 20E system separated 67 strains (Table 1) into six groups (Fig. 7). All *P. ananatis* and *P. allii* fell within a single cluster. These two species could not be distinguished from each other based on API 20E tests. Five *P. ananatis* strains isolated from onion seed did not produce acid from sucrose, unlike the other *P. ananatis* used in the study and 18 strains of *P. ananatis* studied by Mergaert et al. (1993).

Three strains of *P. vagens* formed a separate group in the dendrogram (Fig. 7). They gave positive reactions in the following tests: β-galactosidase, acetoin, gelatinase and produced acid from D-glucose, D-mannitol, inositol, L-rhamnose, D-sucrose, D-melibiose, and L-arabinose. They did not produce acid from D-sorbitol and amygdalin, indole from tryptophane, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, citrate, H_2S and urease. Although in another study (Goszczynska et al., 2007) three strains from maize differed from other *Pantoea* species by giving a positive reaction in tryptophane deaminase test, the type strain of *P. vagens*, BCC 105^T, was negative for this test. In contrast to other indole negative *Pantoea* species, *P. vagens* did not produce acid from amygdalin, and could be distinguished by that characteristic.

API 50CHE. Thirty-three strains were examined by the analysis of anaerobic acid production from 48 substrates and the ability to hydrolyse esculin in the API 50CHE strips.

Contrary to Biolog and API 20E, *P. allii* could be differentiated from *P. ananatis* and other *Pantoea* species by the API 50CHE tests (Fig. 7). Five *P. allii* strains produced acid from at least one of the following compounds; D-adonitol, methyl-β-D-xylopyranoside, L-sorbose, inulin and xylitol, while all other *Pantoea* isolates did not. Production of acid from D-adonitol, methyl-ß-D-xylopyranoside, L-sorbose and inulin, were not reported for members of the genus (Gavini et al., 1989; Mergaert et al., 1993).

Biochemical characteristics of *P. vagens* were additionally defined by the API 50CHE. The isolates produced acid from D-fucose, unlike other strains used in the study.

DISCUSSION

Diseases caused by bacteria belonging to the genus *Pantoea* are emerging diseases in South Africa, and may have an increasing economic impact in the future. The causal agents, isolated from onion (Hattingh and Walters, 1981), *Eucalyptus* (Coutinho et al., 2002), onion seed (Goszczynska et al., 2006) and most recently from maize (Goszczynska et al., 2007), have been described as *P. agglomerans, P. ananatis* and *Pantoea* sp. closely related to *P. agglomerans*, respectively. The species allocation, with the exception *P. ananatis* from *Eucalyptus*, was based on a biochemical and physiological characterisation, analysis of the 16S rDNA sequences and, in the case of maize pathogens, F-AFLP genomic fingerprinting. Such a taxonomic system is insufficient for species delineation according to the recommendation of Wayne et al. (1987) and Stackebrandt et al. (2002). This study was performed to determine the accurate taxonomic position of bacteria from onion and maize in the genus *Pantoea*. To achieve this, a collection of strains from South African maize and strains pathogenic to onion isolated in South Africa and the USA were examined using a variety of methods, recommended for the taxonomic description of bacterial species (Stackebrandt et al., 2002).

Phenotypic characterisation confirmed that strains from maize and onion belong to the genus *Pantoea* and indicated, as expected, that at least two bacterial species were present. The 16S rDNA sequence analysis, however, revealed that three species could be present, as some strains from onion, thought to be *P. ananatis*, formed a separate cluster in the 16S rDNA tree (Fig. 5). However, 16S rDNA sequence analysis is known to be of limited value in terms of taxonomic resolution at the species level for members of *Enterobacteriaceae,* due to possible lateral transfers within the gene (Rayssiguier et al., 1989) and multiple copies of the 16S rRNA gene (Cillia et al., 1996).

Taxonomic relationships at the species level were assessed by rep-PCR and F-AFLP genomic fingerprints analysis and DNA-DNA hybridisation. All indole positive *Pantoea* from maize and the majority of strains from onion generated genomic fingerprints that were similar to that produced by the reference strains of *P. ananatis* (Fig. 3, Fig. 4). Four strains of that group, two from onion and two from maize, showed 90-100% DNA binding to *P. ananatis* type strain LMG 2665^{T} (Table 2). As strains with similar genomic fingerprints are

genomically closely related (Gavini et al., 1989; Rademaker et al., 2000), all strains within *P. ananatis* rep-PCR and F-AFLP clusters are thus identified as *P. ananatis*.

The indole negative strains from maize, although similar to *P. agglomerans* by phenotypic tests and the 16S rDNA sequences, produced genomic fingerprints that clustered with *P. vagens* BCC 105^T (Fig. 3, Fig. 4). BD 639 showed a high level, 89%, of DNA relatedness to BCC 105^T. Although DNA biding ratios of these two strains to *P. agglomerans* were between 63 and 65%, they should not be classified as a subspecies of *P. agglomerans*. The fingerprints of *P. vagens* were distinctly different from that of *P. agglomerans*, further supporting the establishment of a separate species to contain them.

The strains BD 390 and BD 309 were identified in a previous study as *P. ananatis* (Goszczynska et al., 2006). However, the genomic fingerprints generated by BD 309, BD 390 and three other isolates from onion, did not resemble that produced by *P. ananatis*, and formed a separate cluster in the F-AFLP and rep-PCR dendrograms (Fig. 3, Fig. 4). The DNA-DNA hybridisation values among three strains of this cluster were between 90 and 100%, confirming that they belong to a single species. The most closely related type strain was *P. ananatis* with 44 to 57% DNA reassociation, below the 70% threshold allowed for species delineation (Wayne et al., 1987). The name *Pantoea allii* sp. nov. is proposed for this species.

Table 3 gives phenotypic characteristics useful in the differentiation of the species of the genus *Pantoea*. *P. vagens* could not be easily differentiated from *P. agglomerans* and *P. allii* from *P. ananatis* by an exclusive biochemical or physiological tests. A similar problem was reported by Gavini et al. (1989) with *P. agglomerans* versus *P. dispersa* and by Mergaert et al. (1993) concerning *P. ananatis* versus *P. stewartii* subsp. *indologenes*.
Pantoea strains should be classified and identified mainly based on genotypic characteristics, as identification based on phenotypic tests does not always lead to clear results (Gavini et al., 1989, Mergaert et al., 1993).

Description of *Pantoea allii* sp. nov.

Pantoea allii [al'li.i. N.L. adj. *allii* from *Allium*, the genus of onion (*Allium cepa* L.).

The description below is based on the data obtained for the five strains, BD 304, BD 309, BD 377, BD 380 and BD 390, isolated from onion plants with centre rot symptoms in the USA and from onion seed in South Africa. In pathogenicity tests, strains induce symptoms identical to those caused by *P. ananatis* on onion plants.

Gram-negative, non-capsulated, non-spore forming straight rods, motile. Colonies on nutrient agar and TGA are yellow, smooth, round, and convex with entire margins. They are facultatively anaerobic, oxidase negative and catalase positive. Cells tolerate up to 6% NaCl and grow at 30°C, 37°C and 40°C, but not at 4°C and 44°C.

P. allii does not produce arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, H_2S, urease, tryptophane deaminase and gas from glucose. Citrate is utilised. Indole, acetoin, and β-galactosidase are produced.

P. allii strains produce acid from at least one of the following carbon sources: D-adonitol, methyl-β-D-xylopyranoside, L-sorbose, inulin and xylitol, while *P. ananatis* do not produce acid from this compounds. Other biochemical characteristics of *P. allii* at 30°C are shown in Table 3.

The following carbon sources are utilised at 30°C (as assessed by Biolog GN microplates), by 100% of strains: dextrin, tween 40, tween 80, N-acetyl-D-glucosamine, L-arabinose, D-arabitol, D-cellobiose, D-fructose, D-galactose, gentiobiose, α-D-glucose, inositol, α-D-lactose, lactulose, D-mannitol, D-mannose, D-melibiose, β-methyl-D-glucoside, D-raffinose, L-rhamnose, sucrose, D-trehalose, pyruvic acid methyl ester, succinic acid mono-methyl ester, acetic acid, cis-aconitic acid, citric acid, D-galacturonic acid, D-gluconic acid, D-glucosaminic acid, D-glucuronic acid, D,L-lactic acid, quinic acid, D-saccharic acid, succinic acid, bromosuccinic acid, D-alanine, L-alanine, L-alanyl-glutamic acid, L-histidine, L-proline, L-serine, urocanic acid, inosine, thymidine, glycerol, D,L,α-glycerol phosphate, α-D-glucose-1-phosphate and D-glucose-6-phosphate. The following carbon substrates are not utilised: α-cyclodextrin, N-acetyl-D-galactosamine, erythitol, L-fucose, turanose, xylitol, D-galactonic acid lactone, β-hydroxybutyric acid, p-hydroxyphenylacetic acid, itaconic acid, α-ketobutyric acid, α-ketoglutaric acid, α-ketovaleric acid, malonic acid, propionic acid, sebacic acid, L-alaninamide, hydroxy-L-proline, L-leucine, L-phenylalanine, L-pyroglutamic acid, L-threonine, D,L-carnitine, γ-aminobutyric acid, phenylethylamine, putrescine, 2-

aminoethanol and 2,3-butanediol. *P. allii* varies in the utilisation of the following carbon sources in the Biolog GN plates: glycogen, adonitol, maltose, D-psicose, D-sorbitol, formic acid, α-hydroxybutyric acid, γ-hydroxybutyric acid, succinamic acid, glucuronamide, L-ornithine and D-serine.

The proposed type strain is BD 390, isolated from onion seed in South Africa.

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LITERATURE CITED

Azad, H. R., Holmes, G. J. & Cooksey, D. A. (2000). A new leaf blotch disease of sudangrass caused by *Pantoea ananatis* and *Pantoea stewartii*. *Plant Dis* **84**, 973-979.

Azegami, K., Ozaki, K. & Matsuda, A. (1983). Bacterial palea browning, a new disease of rice caused by *Erwinia herbicola. Bull Nat Inst Agri Sci Ser C* **39**, 1-12.

Beer, S. V., Rundle, J. R. & Wodzinski, R. S. (1984). Interaction between *E. amylovora* and *E. herbicola* "in vitro", in immature pear fruits and in apple blossoms. *Acta Horticult* **151**, 203-204.

Beji, A., Mergaert, J., Gavini, F., Izard, D., Kersters, K., Leclerc, H. & De Ley, J. (1988). Subjective synonymy of *Erwinia herbicola*, *Erwinia milletiae*, and *Enterobacter agglomerans* and redefinition of the taxon by genotypic and phenotypic data. *Intern J Syst Bacteriol* **38**, 77-88.

Brady, C. L. (2005). Taxonomy of *Pantoea* associated with bacterial blight of *Eucalyptus*. Master Thesis. The Faculty of Natural and Agricultural Sciences, Department of Microbiology and Plant Pathology, University of Pretoria, Pretoria, South Africa.

Brenner, D. J., Fanning, G. R., Knutson, J. K. L., Steigerwalt, A. G. & Krichevsky, M. I. (1984). Attempts to classify Herbicola group-Enterobacter agglomerans strains by deoxyribonucleic acid hybridisation and phenotypic tests. *Int J Syst.Bacteriol* **34**, 45-55.

Brown, N. A. (1928). Bacterial pocket disease of the sugar beet. *J Agric Res* **37**, 155-168.

Brown, N. A. (1934). A gall similar to crown gall, produced on *Gypsophila* by a new bacterium. *J Agric Res* **48**, 1099-1112.

Bruton, B. D., Wells, J. M. & Lester, G. E. (1986). Pathogenicity of *Erwinia ananas* to muskmelons in Texas. *Phytopathology* **76**, 1136.

Bruton, B. D., Wells, J. M., Lester, G. E. & Patterson, C. L. (1991). Pathogenicity and characterization of *Erwinia ananas* causing a postharvest disease of cantaloup fruit. *Plant Dis* **75**, 180-183.

Cillia, V., Lafay, B. & Christen, R (1996). Sequence heterogeneities among 16S ribosomal RNA sequences, and their effect on phylogenetic analyses at the species level. *Mol Biol Evol* **13**, 451-461.

Cleenwerck, I., Vandemeulebroecke, K., Janssens, D. & Swings, J. (2002). Re-examination of the genus *Acetobacter*, with description of *Acetobacter cerevisiae* sp. nov. and *Acetobacter malorum* sp. nov. *Int J Syst Bacteriol* **52**, 1551-1558.

Cother, E. J., Reinke, R., McKenzie, C., Lanoiselet, V. M. & Noble, D. H. (2004). An unusual stem necrosis of rice caused by *Pantoea ananas* and the first record of this pathogen on rice in Australia. *Austral Plant Pathol* **33**, 494-503.

Coutinho, T.A., Preisig, O., Mergaert, J., Cnockaert, M. C., Riedel, K.-H., Swings, J. & Wingfield, M. J. (2002). Bacterial blight and dieback of *Eucalyptus* species, hybrids and clones in South Africa. *Plant Dis* **86**, 20-25.

Elliott, C. (1941). Bacterial wilt of dent corn inbreds. *Phytopathology* **32**, 262-265.

Ezaki, T., Hashimoto, Y. & Yabuuchi, E. (1989). Fluorometric deoxyribonucleic acid-deoxyribonucleic acid hybridisation in microdilution wells as an alternative to memrane filter hybridisation in which radioisotopes are used to determine genetic relatedness among bacterial strains. *Int J Syst Bacteriol* **39**, 224-229.

Fahy, P. C. & Hayward, A. C. (1983). Media and methods for isolation and diagnostic tests. In *Plant bacterial diseases, a diagnostic guide*. (eds. Fahy, P. C., and Persley, G. J.), pp. 337-378, Academic Press Australia.

Gavini, F., Mergaert, J., Beji, A., Mielcarek, C., Izard, D., Kersters, K. & De Ley, J. (1989). Transfer of *Enterobacter agglomerans* (Beijerinck 1888) Ewing and Fife 1972 to *Pantoea* gen. Nov. as *Pantoea agglomerans* comb. Nov. and description of *Pantoea dispersa* sp. nov. *Intern J Syst Bacteriol* **39**, 337-345.

Gitaitis, R. D. & Gay, J. D. (1997). First report of a leaf blight, seed stalk rot, and bulb decay of onion by *Pantoea ananas* in Georgia. *Plant Dis* 8, 1096.

Goris, J., Suzuki, K.-I., De Vos, P., Nakase, T. & Kersters, K. (1998). Evaluation of a microplate DNA-DNA hybridisation method compared with the initial renaturation method. *Can J Microbiol* **44**, 1184-1153.

Goszczynska, T., Moloto, V. M., Venter, S. N. & Coutinho, T. A. (2006). Isolation and identification of P*antoea ananatis* from onion seed in South Africa. *Seed Sci & Tech* **34**, 677-690.

Goszczynska, T., Botha, W.J., Venter, S. N. & Coutinho, T. A. (2007). Isolation and identification of the causal agent of brown stalk rot, a new disease of maize in South Africa. *Plant Dis* **91**, 711-718.

Grimont, P. A. D. & Grimont, F. (2005). Genus XXIII. Pantoea Gavini, Mergaert, Beji, Mielcarek, Izarc, Kersters and De Ley 1989b, 343^{VP} emend. Mergaert, Verdonck and Kersters 1993, 172. Pages 713-721 in: Bergey's manual of systematic bacteriology, Volume two, Part B. D. J. Brenner, N. J. Krieg, J. T. Staley and G. M. Garrity, eds. Springer.

Hattingh, M. J. & Walters, D. F. (1981). Stalk and leaf necrosis of onion caused by *Erwinia herbicola*. *Plant Dis* **65**, 615-618.

Hauben, l., Moore, E. R. B., Vauterin, L., Steenackers, M., Mergaert, J., Verdonck, L. & Swings, J. (1998). Phylogenetic position of phytopatogens within the *Enterobacteriaceae. System Appl Microbiol* **21**, 384-397.

Kageyama, B., Nakae, M., Yagi, S. & Sonoyama, T. (1992). *Pantoea punctata* sp. nov., *Pantoea citrea* sp. nov., and *Pantoea terrea* sp. nov. isolated from fruit and soil samples. *Int J Syst Bacteriol* **42**, 203-210.

Katoh, K., Kuma, K., Toh, H. & Miyata, T. (2002). MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucl Acids Res* **30**, 3059-3066.

Kimura, M. (1980). A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *J Molec Evol* **16**, 111-120.

Kumar, S., Tamura, K. & Nei, M. (2004). MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. *Brief Bioinformatics* 5, 150-163.

Mergaert, J., Verdonck, L. & Kersters, K. (1993). Transfer of *Erwinia ananas* (synonym, *Erwinia uredovora*) and *Erwinia stewartii* to the genus *Pantoea* emend. as *Pantoea ananas* (Serrano 1928) comb. Nov. and *Pantoea stewartii* (Smith 1898) comb. nov., respectively, and description of *Pantoea stewartii* subsp. *indologenes* subsp. nov. *Int J Syst Bacteriol* **43**, 162-173.

Nunes, C., Usall, J., Teixido, N. & Vinas, I. (2001). Biological control of postharvest pear diseases using a bacterium, *Pantoea agglomerans* CPA-2. *Int J Food Microbiol* **70**, 53-61.

Paccola-Meirelles, L. D., Ferreira, A. S., Merelles, W. F., Marriel, I. E. & Casela, C. R. (2001). Detection of bacterium associated with a leaf spot disease of maize in Brazil. *J Phytopathology* **149**, 275-279.

Rademaker, J. L. W. & de Bruijn, F. J. (1997). Characterisation and classification of microbes by Rep-PCR genomic fingerprinting and computer-assisted pattern analysis. Pages 51-171 in: DNA markers: Protocols, applications and overviews. G. Caetano-Annolles and P. M. Gresshoff, eds. Wiley, New York.

Rademaker, J. L. W., Hoste, B., Louws, F. J., Kersters, K., Swings, J., Vauterin, L., Vauterin, P. & de Bruijn, F. J. (2000). Comparision of AFLP and rep-PCR genomic fingerprinting with DNA-DNA homology studies: *Xanthomonas* as a model system. *Int J Syst Evol Microbiol* **50**, 665-677.

Rayssiguier, C., Thaller, D. S. & Radman, M. (1989). The barrier to recombination between *Escherichia coli* and *Salmonella typhimurium* is disrupted in mismatch repair mutants. *Nature* **342**, 396-401.

Saitou, N. & Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molec Biol Evol*, **4**, 406-425.

Schwartz, H. F. & Otto, K. (2000). First report of a leaf blight and bulb decay of onion by *Pantoea ananatis* in Colorado. *Plant Dis* **84**, 808.

Serrano, F. B. (1928). Bacterial fruitlet brown-rot of pineapple in the Philippines. *Philippine J Sci* **36**, 271-305.

Stackebrandt, E., Frederiksen, W., Garrity, G. M. & 10 other authors (2002). Report of the ad-hoc committee for the re-evaluation of the species definition in bacteriology. *Int J Syst Evol Microbiol* **52**, 1043-1047.

Torres, R., Teixidó, N., Ussal, J., Abadias, M. & Viñas, I. (2005). Post-harvest control of Penicillium expansum on pome fruits by the bacterium Pantoea ananatis CPA-3. *The J Hort Sci Biotech* **80**, 75-81.

Verdonck, L., Mergaert, J., Rijckaert, C., Swings, J., Kersters, K. & De Ley, J. (1987). Genus *Erwinia*: Numerical analysis of phenotypic features. *Int J Syst Bacteriol* **37**, 4-18.

Walcott, R. R., Gitaitis, R. D., Castro, A. C., Sanders Jr., F. H. & Diaz-Perez, J. C. (2002). Natural infestation of onion seed by *Pantoea ananatis*, causal agent of center rot. *Plant Dis* **86**, 106-111.

Wayne, L. G., Brenner, D. J., Colwell, R. R., Grimont, P. A. D., Kandler, O., Krichevsky, M. I., Moore, W. E. C., Murray, R. G. E., Stackebrandt, E., Starr, M. P. & Trüper, H. G. (1987). Report on the Ad Hoc Committee on Reconciliation of Approaches to Bacterial Systematics. *Int J Syst Bacteriol* **37**, 463-464.

Wells, J. M., Sheng, W. S., Ceponis, M. J. & Chen, T. A. (1987). Isolation and characterization of strains of *Erwinia ananas* from honeydew melons. *Phytopathology* **77**, 511-514.

Wilson, K. (1989). Preparation of genomic DNA from bacteria. Pages 241-245 in: Current protocols in molecular biology. F. M. Ausubel, R. Brent, R. E. Kimston, D. D. Moore, J. G. Seidman, J. A. Smith and K. Sthrul, eds. John Wiley & Sons, Inc, New York, N. Y.

Zhang, L. & Birch, R. G. (1997). Mechanism of biocontrol by *Pantoea dispersa* of sugar cane leaf scald disease caused by *Xanthomonas albilineans*. *J Appl Microbiol* **82**, 448-454.

Table 1. *Pantoea* strains used in this study.

Strain	Other strain designations	Species (as received)	Host	Location	Source
0197-28		*P. ananatis*	*Sorghum sudanense*	USA, California	D. Azad
BCC 105^{T}		*Pantoea vagens.*	*Eucalyptus*	Uganda	T. A. Coutinho
BD 250	98-1	*P. ananatis*	*Allium cepa*	USA	R. Gitaitis
BD 287	SUH 2	*P. agglomerans*	*Allium cepa*	South Africa	PPPPB
BD 295	ATCC BAA 517	*P. ananatis*	*Allium cepa*	USA, Colorado	ATCC
BD 296	ATCC BAA 516	*P. ananatis*	*Allium cepa*	USA, Colorado	ATCC
BD 301	Blackshank 15	*P. ananatis*	*Allium cepa*	USA, Georgia	R. Walcott
BD 304	Blackshank 24	*P. ananatis*	*Allium cepa*	USA, Georgia	R. Walcott
BD 305	Blackshank 30	*P. ananatis*	*Allium cepa*	USA, Georgia	R. Walcott
BD 309	Hort. Hill 24	*P. ananatis*	*Allium cepa*	USA, Georgia	R. Walcott
BD 310	Hort. Hill 31	*P. ananatis*	*Allium cepa*	USA, Georgia	R. Walcott
BD 311	Hort. Hill 32	*P. ananatis*	*Allium cepa*	USA, Georgia	R. Walcott
BD 312	Pans	*P. ananatis*	*Allium cepa*	USA, Georgia	R. Walcott
BD 315	Pans 2002-2	*P. ananatis*	*Allium cepa*	USA, Georgia	R. Walcott
BD 317	Pans	*P. ananatis*	*Allium cepa*	USA, Georgia	R. Walcott
BD 325		*P. ananatis*	*Allium cepa*	South Africa	R. Walcott
BD 326		*P. ananatis*	*Allium cepa*	South Africa	PPPPB
BD 331		*P. ananatis*	*Allium cepa*	South Africa	PPPPB

Strain	Other strain designations	Species (as received)	Host	Location	Source
BD 333		*P. ananatis*	*Allium cepa*	South Africa	PPPPB
BD 334		*P. ananatis*	*Allium cepa*	South Africa	PPPPB
BD 335		*P. ananatis*	*Allium cepa*	South Africa	PPPPB
BD 336		*P. ananatis*	*Allium cepa*	South Africa	PPPPB
BD 377		*P. ananatis*	*Allium cepa*	South Africa	PPPPB
BD 380		*P. ananatis*	*Allium cepa*	South Africa	PPPPB
BD 390		*P. ananatis*	*Allium cepa*	South Africa	PPPPB
BD 435		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 442		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 478		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 494		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 515		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 527		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 541		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 543		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 551		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 556		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 561		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 577		*P. ananatis*	*Zea mays*	South Africa	PPPPB

Strain	Other strain designations	Species (as received)	Host	Location	Source
BD 588		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 596		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 602		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 614		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 620		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 622		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 629		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 639		*Pantoea* sp.	*Zea mays*	South Africa	PPPPB
BD 640		*P. ananatis*	*Zea mays*	South Africa	PPPPB
BD 647		*P. ananatis*	*Zea mays*	South Africa	PPPPB
CTB 1061		*P. ananatis*	*Oryza sativa*	Japan	CTB
CTB 1135		*P. ananatis*	*Oryza sativa*	Japan	CTB
DAR 49828		*P. agglomerans*	*Pyrrus communis*	Australia	ACPPB
DAR 72041		*P. agglomerans*	*Allium cepa*	Australia	ACPPB
LMG 1286T		*P. agglomerans*	Human	Zimbabwe	BCCM/LMG
LMG 20103		*P. ananatis*	*Eucalyptus*	South Africa	BCCM/LMG
LMG 20104		*P. ananatis*	*Eucalyptus*	South Africa	BCCM/LMG
LMG 22049T		*P. citrea*	Mandarin orange	Japan	BCCM/LMG
LMG 2565		*P. agglomerans*	Cereals	Canada	BCCM/LMG

Strain	Other strain designations	Species (as received)	Host	Location	Source
LMG 2603T		*P. dispersa*	Soil	Japan	BCCM/LMG
LMG 2632		*P. stewartii* subsp. *indologenes*	*Setaria italica*	India	BCCM/LMG
LMG 2665T		*P. ananatis*	*Ananas cosmosus*	Hawaii	BCCM/LMG
LMG 2671		*P. stewartii* subsp. *indologenes*	*Ananas cosmosus*	Hawaii	BCCM/LMG
LMG 2676		*P. ananatis*	*Puccinia graminis*	USA	BCCM/LMG
LMG 2713		*P. stewartii* subsp. *stewartii*	*Zea mays*	USA	BCCM/LMG
LMG 2715T		*P. stewartii* subsp. *stewartii*	*Zea mays*	USA	BCCM/LMG
LMG 2749		*P. dispersa*	Human		BCCM/LMG
PA 3		*P. ananatis*	*Allium cepa*	South Africa	PPPPB
PA 4		*P. ananatis*	*Allium cepa*	South Africa	PPPPB

BCCM/LMG Culture Collection: Universiteit Gent, Belgium; ATCC: American Type Culture Collection, Manassas, VA; ACPPB: Australian Collection of Plant Pathogenic Bacteria, Orange; PPPPB: Plant Pathogenic and Plant Protecting Bacteria, ARC-PPRI, South Africa; R. Walcott: Department of Plant Pathology, University of Georgia, Athens; T. A. Coutinho: Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa; R. Gitaitis: Department of Plant Pathology, University of Georgia; CTB: Centre Technique du Bois, Paris, France.

Table 2. DNA binding values of examined *Pantoea* strains. The tests were performed at the University of Ghent, Belgium.

	Strain	1	2	3	4	5	6	7	8	9	10	11	12	13
	P. ananatis													
1	LMG 2665^T	100												
2	BD 310	90	100											
3	BD 442	93	100	100										
4	BD 435	90	87	91	100									
5	PA 4	92	97	99	92	100								
	***P. allii* sp. nov.**													
6	BD 377	44					100							
7	BD 390T	55					99	100						
8	BD 309	57					90	99	100					
	P. agglomerans													
9	LMG 1286^T	21						26		100				
	P. vagens													
10	BCC 105^T	20						24		65	100			
11	BD 639									63	89	100		
	P. stewartii* subsp. *stewartii													
12	LMG 2715^T	20						18		6	9		100	
	P. dispersa													
13	LMG 2603^T	20						22		24	19		22	100

Table 3. Differential characteristics of *Pantoea allii* and some biochemically similar species within the genus *Pantoea*.

Characteristic	**1**	**2**	**3**	**4**	**5**	**6**
API 20E tests						
Citrate utilisation	+	+	+	-	-	-
Tryptophane deaminase	-	-	-	d	-	-
Indole	+	+	+	-	-	-
Gelatinase	+	d	-	+	d	-
Acid from:						
Inositol	d	d	-	+	d	-
D-sorbitol	+	d	-	-	-	-
L-rhamnose	+	d	d	+	+	d
D-sucrose	+	d	+	+	+	+
Amygdalin	+	+	+	-	+	d
API 50CHE tests						
Esculin hydrolysis	+	d	d	d	+	-
Acid from:						
D-adonitol	d	-	-	-	-	-
Methyl-β-D-xylopyranoside	d	-	-	-	-	-
L-sorbose	d	-	-	-	-	-
Inositol	+	+	+	+	d	+
D-sorbitol	+	d	-	-	-	-
Amygdalin	+	d	-	-	-	-
D-lactose	+	+	+	-	-	-
Inulin	d	-	-	-	-	-
Starch	-	-	-	d	-	-
Glycogen	-	-	-	d	-	-
Xylitol	+	-	-	-	-	-
D-fucose	-	-	-	+	-	-

+ , positive reaction for at least 90% of the strains; – ,negative reaction for at least 90 % of the strains; d, 11-89% strains positive. 1, *Pantoea allii*; 2, *P. ananatis*; 3, *P. stewartii* subsp. *indologenes*; 4, *P. vagens*; 5, *P. agglomerans*; 6, *P. dispersa*

Data for *P. ananatis* and *P. stewartii* subsp. *indologenes* are from this study and Mergaert et al. (1993); for *P. agglomerans* and *P. dispersa* are from this study and Gavini et al. (1989).

Fig. 1. The symptoms induced by *Pantoea ananatis* (A) and *P. allii* (B) strains isolated from onion on onion leaves in pathogenicity tests. Two to four days after inoculation water soaked spots appeared on leaves that expanded into longitudinal, bleached-green lesions with chlorotic margins.

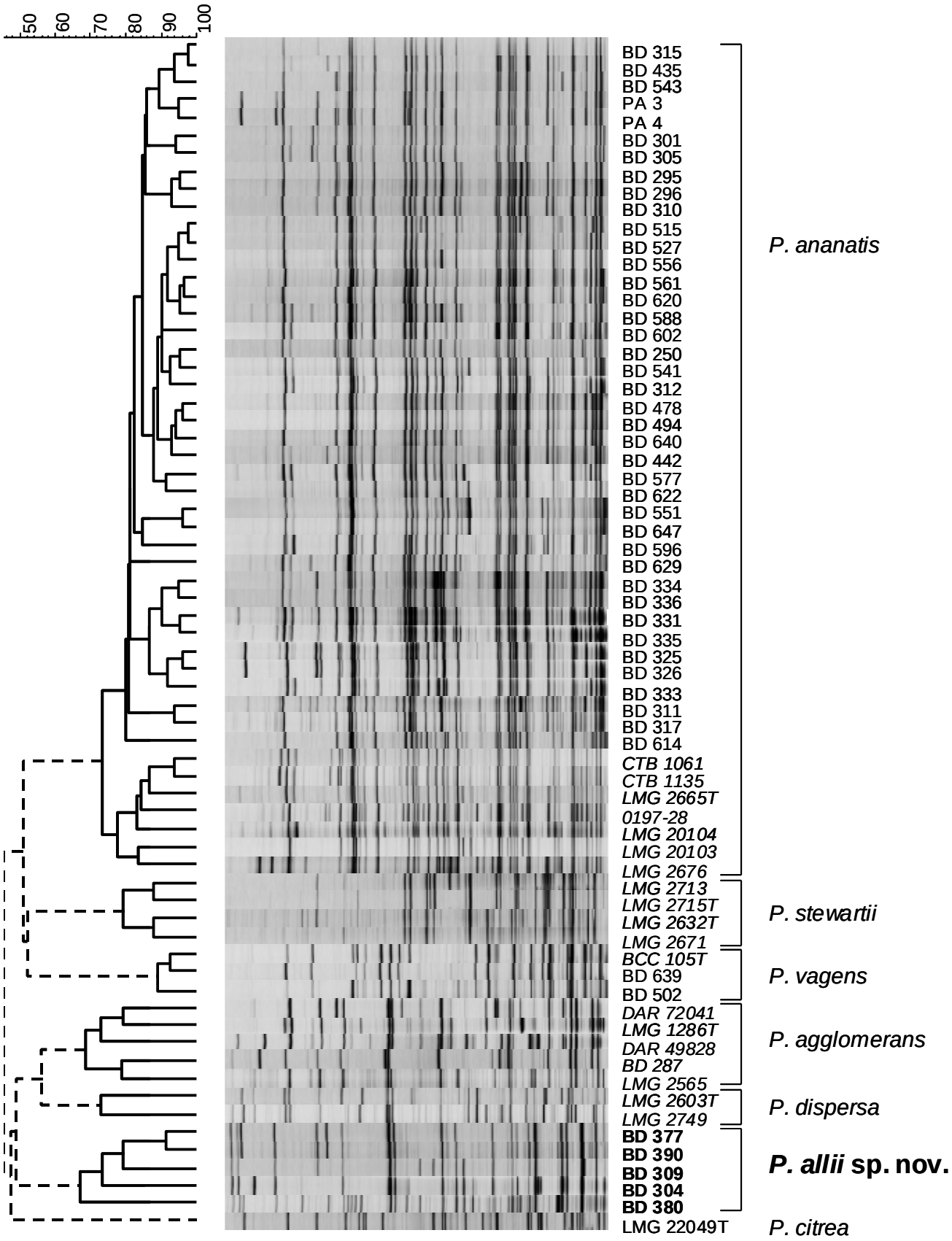
Fig. 1

Fig. 2. The symptoms produced by *P. ananatis* isolated from maize with brown stalk rot on maize SR 52. A, Four to six days after inoculation, small, 2-4 mm, light brown or dark green lesions developed around the inoculation point. Additionally, drops of yellow liquid slowly oozed from the lesion for two to three days. B, after 6 to 7 weeks, a single, long, vertical crack appeared on the injected internode. C, A dark brown, narrow lesion was present in an internal stem tissue along the crack. D, Browning of the internal tissue in an upper internode. The symptoms induced by *P. vagens* were indistinguishable from those induced by *P. ananatis*.

Fig. 2

Fig. 2

Fig. 3. A dendrogram showing the relationships between *Pantoea* strains used in the study based on F-AFLP fingerprints. *P. allii* strains are highlighted in bold. Reference strains, including the type strains of *Pantoea* species, are in italics.


F-AFLP
50
60
70
80
90
100
BD 315
BD 435
BD 543
PA 3
PA 4
BD 301
BD 305
BD 295
BD 296
BD 310
BD 515
BD 527
BD 556
BD 561
BD 620
BD 588
BD 602
BD 250
BD 541
BD 312
BD 478
BD 494
BD 640
BD 442
BD 577
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BD 647
BD 596
BD 629
BD 334
BD 336
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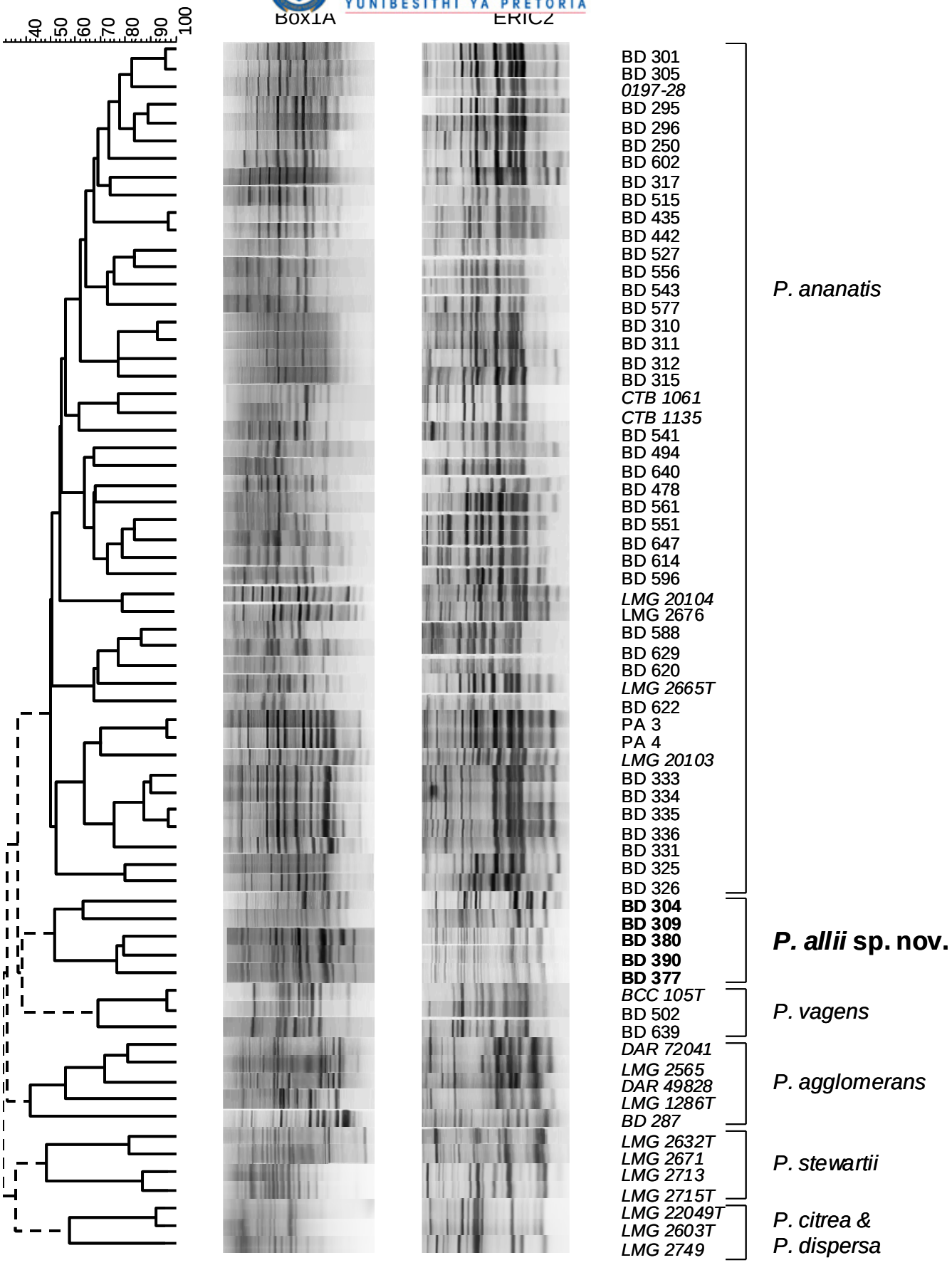
BD 335
BD 325
BD 326
BD 333
BD 311
BD 317
BD 614
CTB 1061
CTB 1135
LMG 2665T
0197-28
LMG 20104
LMG 20103
LMG 2676
LMG 2713
LMG 2715T
LMG 2632T
LMG 2671
BCC 105T
BD 639
BD 502
DAR 72041
LMG 1286T
DAR 49828
BD 287
LMG 2565
LMG 2603T
LMG 2749
BD 377
BD 390
BD 309
BD 304
BD 380
LMG 22049T
P. ananatis
P. stewartii
P. vagens
P. agglomerans
P. dispersa
P. allii sp. nov.
P. citrea

Fig. 4. A dendrogram showing the relationships between the *Pantoea* strains used in the study based on the rep-PCR fingerprints. ***P. allii*** are highlighted in bold. Reference strains, including the type strains of *Pantoea* species, are in italics.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60
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80
90
100
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ERIC2
BD 301
BD 305
0197-28
BD 295
BD 296
BD 250
BD 602
BD 317
BD 515
BD 435
BD 442
BD 527
BD 556
BD 543
BD 577
BD 310
BD 311
BD 312
BD 315
CTB 1061
CTB 1135
BD 541
BD 494
BD 640
BD 478
BD 561
BD 551
BD 647
BD 614
BD 596
LMG 20104
LMG 2676
BD 588
BD 629
BD 620
LMG 2665T
BD 622
PA 3
PA 4
LMG 20103
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DAR 49828
LMG 1286T
BD 287
LMG 2632T
LMG 2671
LMG 2713
LMG 2715T
LMG 22049T
LMG 2603T
LMG 2749
P. ananatis
P. allii sp. nov.
P. vagens
P. agglomerans
P. stewartii
P. citrea &
P. dispersa

Fig. 5. Neighbour-joining tree reflecting the phylogenetic position of *Pantoea* strains from maize and onion based on 16S rDNA sequences. Numbers at branching points indicate bootstrap values derived from 1000 samples. The bar represents genetic distance. *P. allii* strains are highlighted in bold. Reference strains, including the type strains of *Pantoea* species, are in italics.

The 16S rDNA accession numbers of maize and onion strains:

Maize: BD 602, DQ195522; BD 647, DQ195525; BD 435, AY89864; BD 442, AY898643; BD 640, DQ195524; BD 588, DQ133548BD 561, DQ133546; BD 622, DQ195523; BD 577, DQ133547; BD 639, DQ512489; BD 500, DQ849042; BD 502, DQ849043.Onion: BD 309, AY579210; BD 390, AY530795; BD 377, DQ512491; BD 310, AY579211; BD 301, AY579209; BD 315, AY579212; PA 4, AY530796; BD 336, AY530794; BD 287, AY530797.

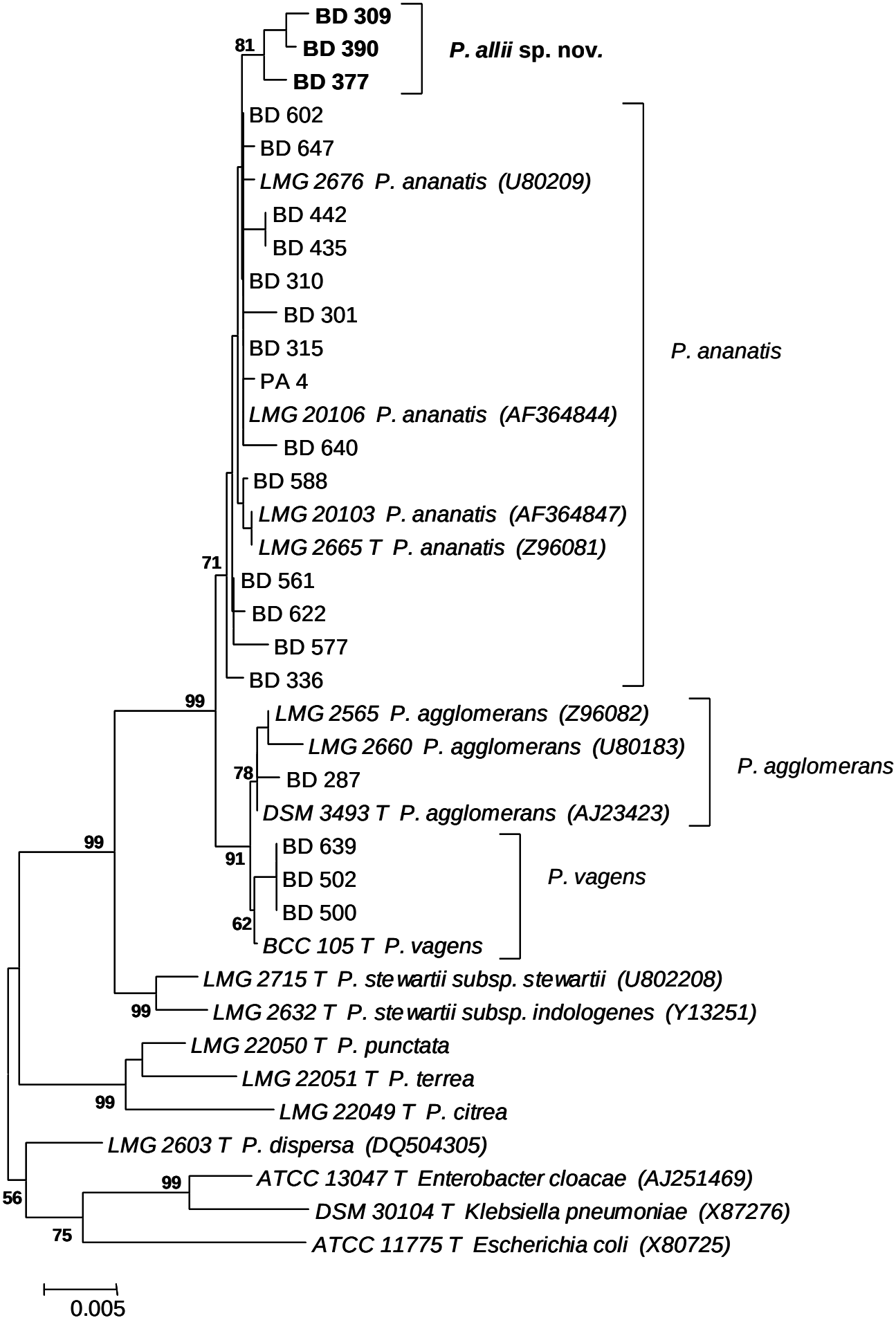

BD 309
BD 390
BD 377
P. allii sp. nov.
81
BD 602
BD 647
LMG 2676 P. ananatis (U80209)
BD 442
BD 435
BD 310
BD 301
BD 315
PA 4
LMG 20106 P. ananatis (AF364844)
BD 640
BD 588
LMG 20103 P. ananatis (AF364847)
LMG 2665 T P. ananatis (Z96081)
71
BD 561
BD 622
BD 577
BD 336
P. ananatis
99
LMG 2565 P. agglomerans (Z96082)
LMG 2660 P. agglomerans (U80183)
78
BD 287
DSM 3493 T P. agglomerans (AJ23423)
P. agglomerans
99
91
BD 639
BD 502
BD 500
62
BCC 105 T P. vagens
P. vagens
LMG 2715 T P. stewartii subsp. stewartii (U802208)
99
LMG 2632 T P. stewartii subsp. indologenes (Y13251)
LMG 22050 T P. punctata
LMG 22051 T P. terrea
99
LMG 22049 T P. citrea
LMG 2603 T P. dispersa (DQ504305)
99
ATCC 13047 T Enterobacter cloacae (AJ251469)
56
DSM 30104 T Klebsiella pneumoniae (X87276)
75
ATCC 11775 T Escherichia coli (X80725)
0.005

Fig. 6. Relationships among 67 *Pantoea* strains, including strains isolated from onion and maize, based on Biolog GN microplate substrate utilisation patterns. *P. allii* strains are highlighted in bold. Reference strains, including the type strains of *Pantoea* species, are in italics.

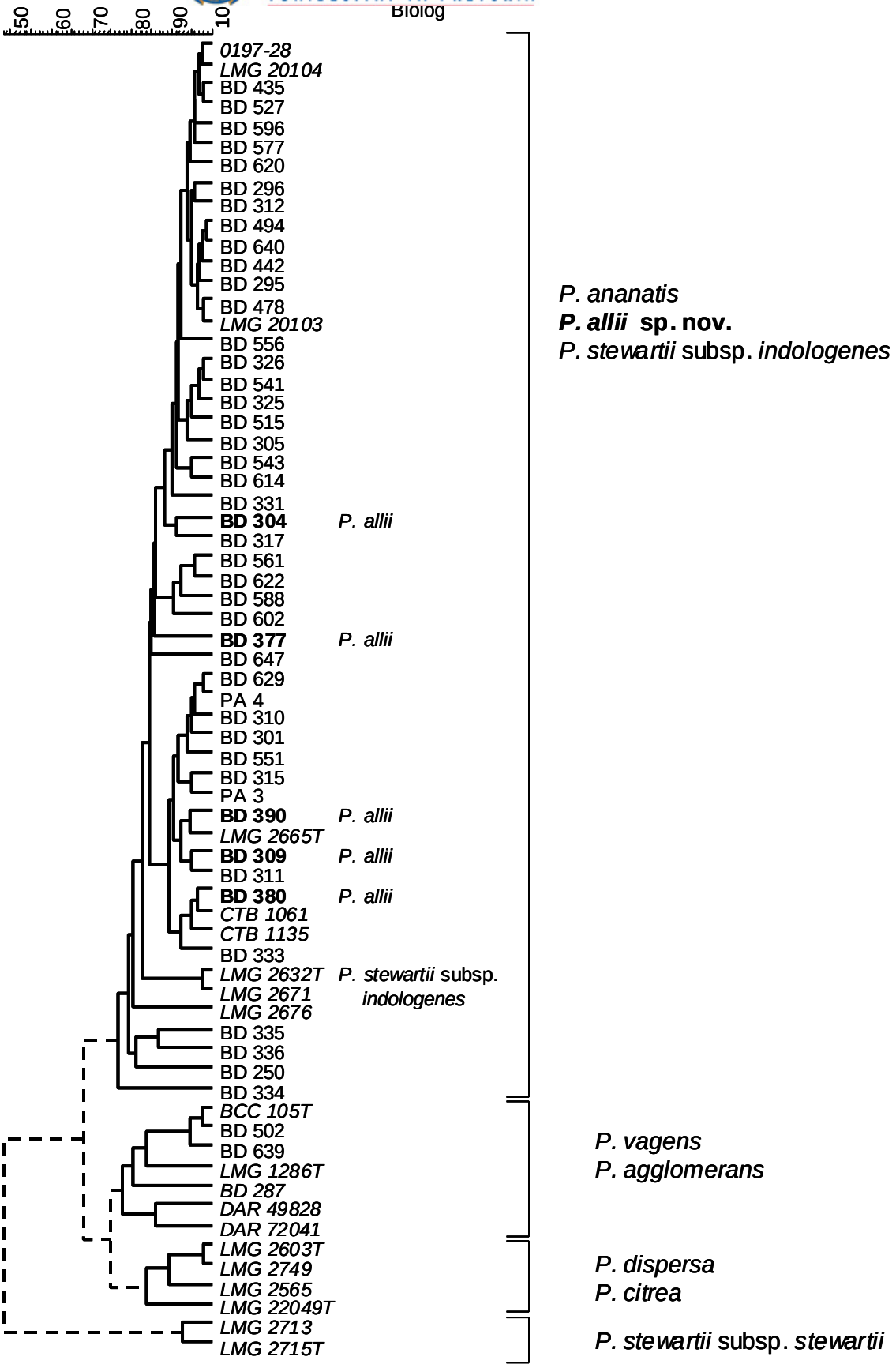
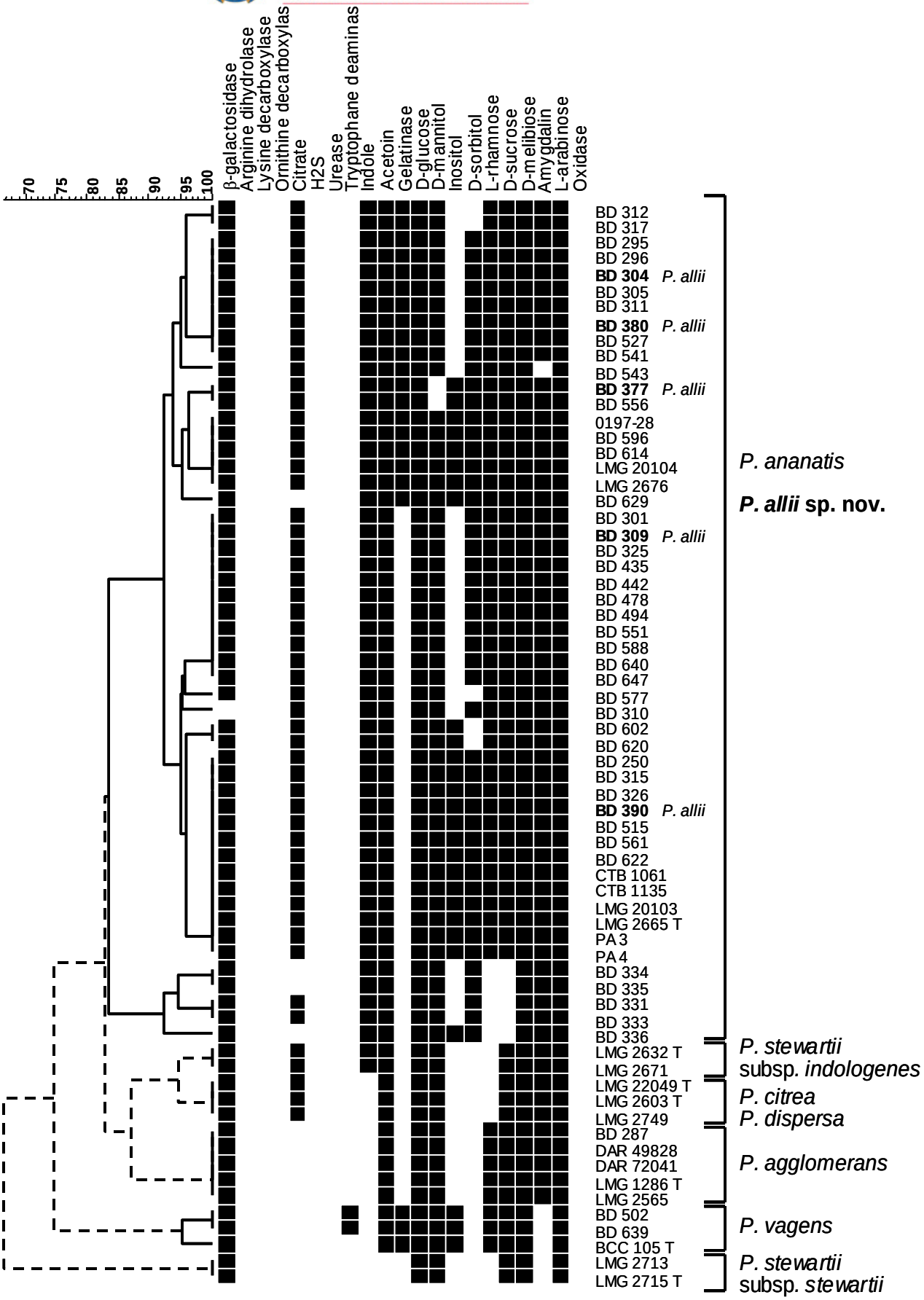

Biolog
50
60
70
80
90
100
0197-28
LMG 20104
BD 435
BD 527
BD 596
BD 577
BD 620
BD 296
BD 312
BD 494
BD 640
BD 442
BD 295
BD 478
LMG 20103
BD 556
BD 326
BD 541
BD 325
BD 515
BD 305
BD 543
BD 614
BD 331
BD 304
P. allii
BD 317
BD 561
BD 622
BD 588
BD 602
BD 377
P. allii
BD 647
BD 629
PA 4
BD 310
BD 301
BD 551
BD 315
PA 3
BD 390
P. allii
LMG 2665T
BD 309
P. allii
BD 311
BD 380
P. allii
CTB 1061
CTB 1135
BD 333
LMG 2632T
P. stewartii subsp. indologenes
LMG 2671
LMG 2676
BD 335
BD 336
BD 250
BD 334
BCC 105T
BD 502
BD 639
LMG 1286T
BD 287
DAR 49828
DAR 72041
LMG 2603T
LMG 2749
LMG 2565
LMG 22049T
LMG 2713
LMG 2715T
P. ananatis
P. allii sp. nov.
P. stewartii subsp. indologenes
P. vagens
P. agglomerans
P. dispersa
P. citrea
P. stewartii subsp. stewartii

Fig. 7. Relationships among 67 *Pantoea* strains, including strains isolated from onion and maize, based on API 20E tests. ***P. allii*** strains are highlighted in bold. Reference strains, including the type strains of *Pantoea* species, are in italics. A black rectangle indicates a positive reaction in the test while a white rectangle indicates a negative reaction in the test.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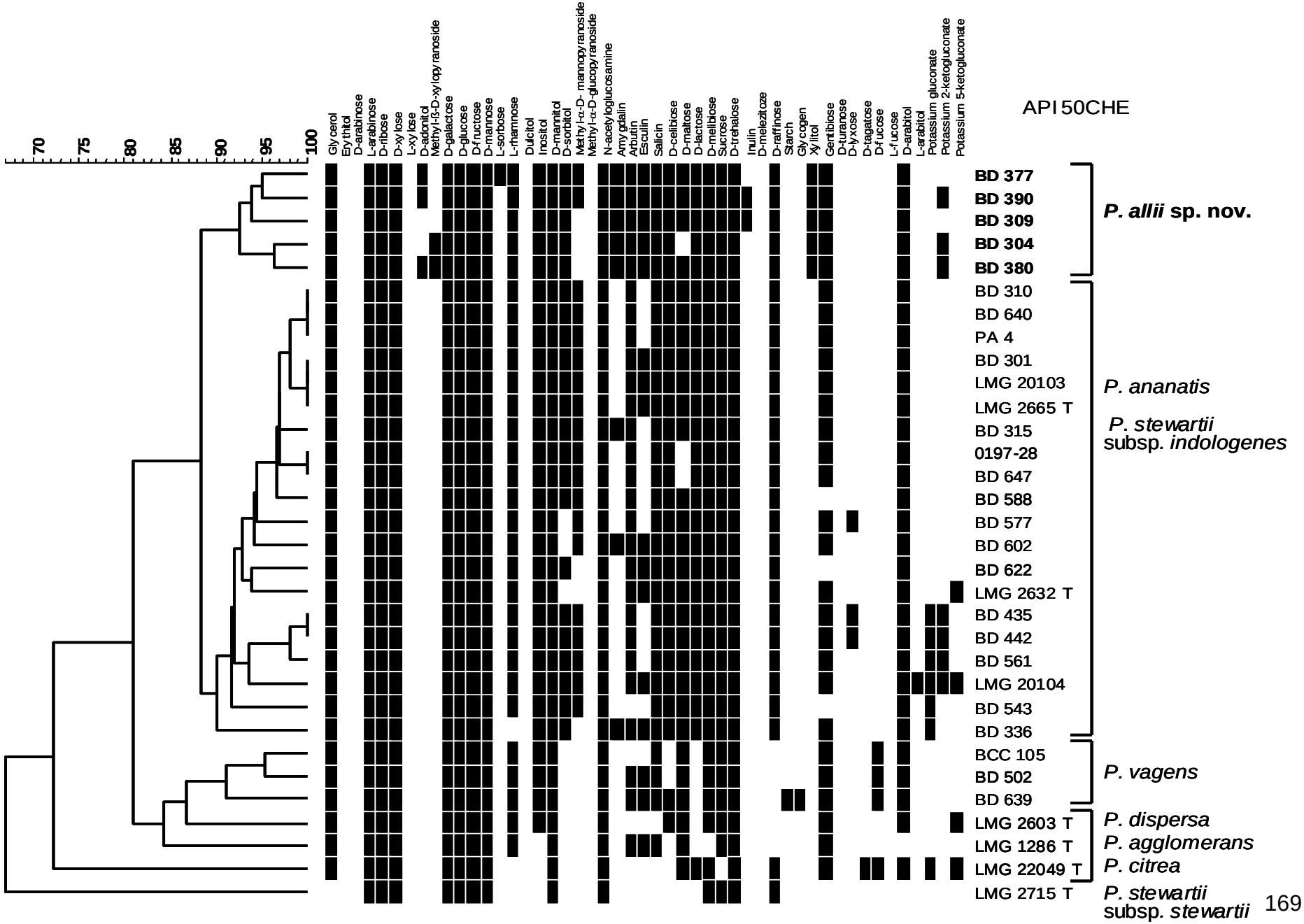
75
80
85
90
95
100
β-galactosidase
Arginine dihydrolase
Lysine decarboxylase
Ornithine decarboxylase
Citrate
H2S
Urease
Tryptophane deaminase
Indole
Acetoin
Gelatinase
D-glucose
D-mannitol
Inositol
D-sorbitol
L-rhamnose
D-sucrose
D-melibiose
Amygdalin
L-arabinose
Oxidase
BD 312
BD 317
BD 295
BD 296
BD 304 P. allii
BD 305
BD 311
BD 380 P. allii
BD 527
BD 541
BD 543
BD 377 P. allii
BD 556
0197-28
BD 596
BD 614
LMG 20104
LMG 2676
BD 629
BD 301
BD 309 P. allii
BD 325
BD 435
BD 442
BD 478
BD 494
BD 551
BD 588
BD 640
BD 647
BD 577
BD 310
BD 602
BD 620
BD 250
BD 315
BD 326
BD 390 P. allii
BD 515
BD 561
BD 622
CTB 1061
CTB 1135
LMG 20103
LMG 2665 T
PA 3
PA 4
BD 334
BD 335
BD 331
BD 333
BD 336
LMG 2632 T
LMG 2671
LMG 22049 T
LMG 2603 T
LMG 2749
BD 287
DAR 49828
DAR 72041
LMG 1286 T
LMG 2565
BD 502
BD 639
BCC 105 T
LMG 2713
LMG 2715 T
P. ananatis
P. allii sp. nov.
P. stewartii subsp. indologenes
P. citrea
P. dispersa
P. agglomerans
P. vagens
P. stewartii subsp. stewartii

Fig. 8. Relationships among 33 selected *Pantoea* strains, based on API 50CHE tests. *P. allii* strains are highlighted in bold. Reference strains, including the type strains of *Pantoea* species, are in italics. A black rectangle indicates a positive reaction in the test while a white rectangle indicates a negative reaction in the test.


API 50CHE
70
75
80
85
90
95
100
Gly cerol
Ery thitol
D-arabinose
L-arabinose
D-ribose
D-xy lose
L-xy lose
D-adonitol
Methyl-ß-D-xy lopy ranoside
D-galactose
D-glucose
D-fructose
D-mannose
L-sorbose
L-rhamnose
Dulcitol
Inositol
D-mannitol
D-sorbitol
Methyl-α-D- mannopy ranoside
Methyl-α-D-glucopy ranoside
N-acetyloglucosamine
Amy gdalin
Arbutin
Esculin
Salicin
D-celibiose
D-maltose
D-lactose
D-melibiose
Sucrose
D-trehalose
Inulin
D-melezitoze
D-raffinose
Starch
Gly cogen
Xy litol
Gentibiose
D-turanose
D-lyxose
D-tagatose
D-fucose
L-fucose
D-arabitol
L-arabitol
Potassium gluconate
Potassium 2-ketogluconate
Potassium 5-ketogluconate
BD 377
BD 390
BD 309
BD 304
BD 380
BD 310
BD 640
PA 4
BD 301
LMG 20103
LMG 2665 T
BD 315
0197-28
BD 647
BD 588
BD 577
BD 602
BD 622
LMG 2632 T
BD 435
BD 442
BD 561
LMG 20104
BD 543
BD 336
BCC 105
BD 502
BD 639
LMG 2603 T
LMG 1286 T
LMG 22049 T
LMG 2715 T
P. allii sp. nov.
P. ananatis
P. stewartii subsp. indologenes
P. vagens
P. dispersa
P. agglomerans
P. citrea
P. stewartii subsp. stewartii

APPENDIX A: Multiple Sequence Alignment, 16S rDNA sequences of *P. allii, P. ananatis, P. agglomerans, P. vagens, P. stewartii* subsp. *stewartii, P. stewartii* subsp. *indologenes, P. punctata, P. terrea, P. citrea, P. dispersa, Enterobacter cloacae, Klebsiella pneumoniae* and *Escherichia coli***.**Number of sequences: 38

Maximum length: 1560

Strains:

P. allii: BD 309, BD 390, BD 377

P. ananatis: BD 301, BD 315, LMG 20106, BD 442, BD 435, BD 310, LMG 2676, BD 647, PA 4, BD 602, BD 640, BD 588, LMG 20103, LMG 2665T, BD 561, BD 622, BD 577, BD 336

P. agglomerans: LMG 2565, LMG 2660, BB 287, DSM 3493 T (= LMG 1286 T)

P. vagens: BCC 105 T, BD 500, BD 502, BD 639

P. stewartii subsp. *stewartii*: LMG 2715 T; *P. stewartii* subsp. *indologenes*: LMG 2632 T; *P. punctata*: LMG 22050 T; *P. terrea*: LMG 22051 T; *P. citrea*: LMG 22049 T; *P. dispersa* LMG 2603 T

Enterobacter cloacae: ATCC 13047 T*; Klebsiella pneumoniae*: DSM 30104 T*; Escherichia coli* ATCC 11775 T

The differences in nucleotides between *P. allii* and *P. ananatis* are marked in green: BD 309 nucleotide numbering, position 378-179.

The differences in nucleotides between *P. vagens* and *P. agglomerans* are marked in blue: BCC 105 nucleotide numbering, position 375-376.

Upper line in the alignment:

symbol " - " indicates sites excluded from the construction of phylogenetic tree (Fig. 3).

Symbol " * "indicates sites included in the construction of phylogenetic tree (Fig. 3).

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                ------------------------------------------------------------
BD 309          ............................................................  0
BD 390          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
BD 377          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
BD 602          .agagtttgatcctggctcagattgaacg.ccggcggcaggcctaacacat.gcaagtcg  57
BD 647          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
LMG 2676        ........................................aacacat.gcaagtcg  15
BD 442          ............................................................  0
BD 435          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
BD 310          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
BD 301          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
BD 315          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
PA 4            .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacattgcaagtcg  58
LMG 20106       ...agtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  55
BD 640          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
BD 588          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
LMG 20103       .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
LMG 2665 T      ..................agtgaacg.ctggcggcagccctaacacat.gcaagtcg  37
BD 561          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
BD 622          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
BD 577          .agagtttgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
BD 336          ................tcaagatgaacg..ctgcggcaggcctaacacat.gcaagtcg  40
LMG 2565        ..................attgaacg.ctggcggcaggcctaacacat.gcaagtcg  37
LMG 2660        ........................................aacacat.gcaagtcg  15
BD 287          .agagtttgatcctggctcagattgaacgnctggcggcaggcctaacacat.gcaagtcg  58
LMG 1286 T      ....................................ggcctaacacat.gcaagtct  20
BD 639          ............................................................  0
BD 502          ............................................................  0
BD 500          ............................................................  0
BCC 105 T       ............................................................  0
LMG 2715 T      ........................................aacacat.gcaagtcg  15
LMG 2632 T      tagagtntgatcctggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  58
LMG 22050 T     ..................attgaacg.ctggcggcaggcctaacacat.gcaagtcg  37
LMG 22051 T     ..................attgaacg.ctggcggcaggcctaacacat.gcaagtcg  37
LMG 22049 T     ..................attgaacg.ctggcggcaggcctaacacat.gcaagtcg  37
LMG 2603 T      ............................................................  0
ATCC 13047 T    ....................tgaacg.ctggcggcaggcctaacacat.gcaagtcg  35
DSM 30104 T     .agagtttgatnntggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  57
ATCC 11775 T    ...agtttgatcatggctcagattgaacg.ctggcggcaggcctaacacat.gcaagtcg  55
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BD 309          .............GGGAGCTTGCTCCTCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     46
BD 390          gacggtagcacagaG.AGCTTGCTCt.CGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    114
BD 377          gacggtagcacagaG.AGCTTGCTCt.CGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    114
BD 602          gacggtagcacagaG.AGCTTGCTC.TCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    114
BD 647          gacggtagcacagaG.AGCTTGCTC.TCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    114
LMG 2676        gacggtagcacagaG.AGCTTGCTCt.CGtGTGACGAGTGGCGGACGGGTGAGTAATGT.     72
BD 442          ...ggtagcacagaG.AGCTTGCTC.TCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     54
BD 435          gacggtagcacagaG.AGCTTGCTC.TCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    114
BD 310          gacggtagcacagaGGAGCTTGCTCCTCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    116
BD 301          gacggtagcacagaGGAGCTTGCTCCTCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    116
BD 315          gacggtagcacagaGGAGCTTGCTCCTCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    116
PA 4            gacggtagcacagaG.AGCTTGCTCt.CGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    115
LMG 20106       gacggtagcacagGGGAGCTTGCTCCTCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    114
BD 640          gacggtagcacagaG.AGCTTGCTCt.CGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    114
BD 588          gacggtagcacagaGGAGCTTGCTCCTCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    116
LMG 20103       gacggtagcacagaG.AGCTTGCTCt.CGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    114
LMG 2665 T      ggcggtagcacagaG.AGCTTcCTC.TCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     94
BD 561          gacggtagcacagaGGAGCTTGCTCCTCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    116
BD 622          gacggtagcacagaG.AGCTTGCTCt.CGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    114
BD 577          gacggtagcacagaG.AGCTTGCTCt.CGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    114
BD 336          gacg.tagcacagaG.AGCTTGCTnt.CGGGTGACGA.TtGCGGACGGGTGAGTAATGTt     96
LMG 2565        gacggtancacagaG.AGnTTGtTCt.nGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     94
LMG 2660        gacggtagcacagaGGAGCTTGCTCtctGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     74
BD 287          gacggtagcacagaG.AGCTTGCTCt.tGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    115
LMG 1286 T      gacggtagcacagaGGAGCTTGCTCCTtGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     79
BD 639          ........................CTtGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     34
BD 502          ........................CTtGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     34
BD 500          ......................CCTtGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     35
BCC 105 T       ............................GGGTGACGAGTGGCGGACGGGTGAGTAATGT.     31
LMG 2715 T      gacggtagcacagaGGAGCTTGCTC.TCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     73
LMG 2632 T      gacggtagcacagaGGAGCTTGCTCCTCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.    117
LMG 22050 T     aacggtagcacagGGGAGCTTGCTCCcCGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     96
LMG 22051 T     aacggtagcacagaGGAGCTTGCTCCTtGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     96
LMG 22049 T     aacggtagcacagaGGAGCTTGCTCCTtGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     96
LMG 2603 T      ........................................GGACGGGTGAGTAATGT.     17
ATCC 13047 T    aacggtagcacagaG.AGCTTGCTCt.CGGGTGACGAGTGGCGGACGGGTGAGTAATGT.     92
DSM 30104 T     agcggtagcacagaG.AGCTTGCTCt.CGGGTGACGAGcGGCGGACGGGTGAGTAATGT.    114
ATCC 11775 T    aacggtaacaggaaGcAGCTTGCTgCTttGcTGACGAGTGGCGGACGGGTGAGTAATGT.    114
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BD 309          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    106
BD 390          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    174
BD 377          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    174
BD 602          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    174
BD 647          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    174
LMG 2676        CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    132
BD 442          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    114
BD 435          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    174
BD 310          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    176
BD 301          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    176
BD 315          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    176
PA 4            CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    175
LMG 20106       CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    174
BD 640          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    174
BD 588          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    176
LMG 20103       CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    174
LMG 2665 T      CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    154
BD 561          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    176
BD 622          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    174
BD 577          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    174
BD 336          CTGGGnATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    156
LMG 2565        CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    154
LMG 2660        CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    134
BD 287          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    175
LMG 1286 T      CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC    139
BD 639          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC     94
BD 502          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC     94
BD 500          CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC     95
BCC 105 T       CTGGGGATCTGCCCGATAGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAAC     91
LMG 2715 T      CTGGGaAaCTGCCCGATgGAGGGGGATAACtACTGGAAACGGTaGCTAATACCGCATAAC    133
LMG 2632 T      nTGGGaAaCTGCCCGATgGAGGGGGATAACtACTGGAAACGGTaGCTAATACCGCATAAC    177
LMG 22050 T     CTGGGaAaCTGCCtGATgGAGGGGGATAACtACTGGAAACGGTaGCTAATACCGCATAAt    156
LMG 22051 T     CTGGGaAaCTGCCtGATgGAGGGGGATAACtACTGGAAACGGTaGCTAATACCGCATAAn    156
LMG 22049 T     CTGGGaAaCTGCCtGATgGnGGGGGATAACtACTGGAAACGGTaGCTAATACCGCATAAC    156
LMG 2603 T      CTGGGaAaCTGCCCGATgGAGGGGGATAACtACTGGAAACGGTaGCTAATACCGCATAAC     77
ATCC 13047 T    CTGGGaAaCTGCCtGATgGAGGGGGATAACtACTGGAAACGGTaGCTAATACCGCATAAn    152
DSM 30104 T     CTGGGaAaCTGCCtGATgGAGGGGGATAACtACTGGAAACGGTaGCTAATACCGCATAAC    174
ATCC 11775 T    CTGGGaAaCTGCCtGATgGAGGGGGATAACtACTGGAAACGGTaGCTAATACCGCATAAC    174
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BD 309          GTCGCAAGACCAAAGAGGGGGACCTTAGGGCCTCTCACTATCGGATGAACCCAGATGGGA   166
BD 390          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   234
BD 377          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   234
BD 602          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   234
BD 647          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   234
LMG 2676        GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   192
BD 442          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   174
BD 435          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   234
BD 310          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   236
BD 301          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   236
BD 315          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   236
PA 4            GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   235
LMG 20106       GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   234
BD 640          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   234
BD 588          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   236
LMG 20103       GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   234
LMG 2665 T      GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   214
BD 561          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   236
BD 622          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   234
BD 577          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   234
BD 336          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   216
LMG 2565        GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   214
LMG 2660        GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   194
BD 287          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   235
LMG 1286 T      GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   199
BD 639          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   154
BD 502          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   154
BD 500          GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   155
BCC 105 T       GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTCACTATCGGATGAACCCAGATGGGA   151
LMG 2715 T      GTCGCAAGACCAAAGtGGGGGACCTccGGGCCTCaCACCcATCGGATGtgCCCAGATGGGA   193
LMG 2632 T      GTCGCAAGACCAAAGtGGGGGACCTTcGGGCCTCaCACCcATCGGATGtgCCCAGATGGGA   237
LMG 22050 T     GTCGCAAGACCAAAGcGGGGGACCTTcGGGCCTCgCACcATCGGATGtgCCCAGATGGGA   216
LMG 22051 T     GTCGCAAGACCAAAGtGGGGGACCTTcGGGCCTCaCACcATCGGATGtgCCCAGATGGGA   216
LMG 22049 T     GTCGCAAGACCAAAGtGGGGGACCTTcGGGCCTCaCACcATCGGATGtgCCCAGATGGGA   216
LMG 2603 T      GTCGCnAGACCAAAGtGGGGGACCTTcGGGCCTCaCACcATCGGATGtgCCCAGATGGGA   137
ATCC 13047 T    GTCGCAAGACCAAAGAGGGGGACCTTcGGGCCTCTtgCcATCaGATGtgCCCAGATGGGA   212
DSM 30104 T     GTCGCAAGACCAAAGtGGGGGACCTTcGGGCCTCatgCcATCaGATGtgCCCAGATGGGA   234
ATCC 11775 T    GTCGCAAGcaCAAAGAGGGGGACCTTAGGGCCTCTtgCcATCGGATGtgCCCAGATGGGA   234
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BD 309          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    226
BD 390          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
BD 377          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
BD 602          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
BD 647          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
LMG 2676        TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    252
BD 442          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    234
BD 435          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
BD 310          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    296
BD 301          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    296
BD 315          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    296
PA 4            TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGtTCCCTAGCTGGTCTGAGAGGA    295
LMG 20106       TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
BD 640          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
BD 588          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    296
LMG 20103       TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
LMG 2665 T      TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    274
BD 561          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    296
BD 622          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
BD 577          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
BD 336          TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    276
LMG 2565        TTAGCTAGTAGGCGGGGTAAtGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    274
LMG 2660        TTAGCTAGTAGGCGGGGTAAtGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGgGGA    254
BD 287          TTAGCTAGTAGGCGGGGTAAtGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    295
LMG 1286 T      TTAGCTAGTAGGCGGGGTAAtGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    259
BD 639          TTAGCTAGTAGGCGGGGTAAtGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    214
BD 502          TTAGCTAGTAGGCGGGGTAAtGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    214
BD 500          TTAGCTAGTAGGCGGGGTAAtGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    215
BCC 105 T       TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    211
LMG 2715 T      TTAGCTAGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    253
LMG 2632 T      TTAGCTtGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCCCTAGCTGGTnTGAGAGGA    297
LMG 22050 T     TTAGCTAGTAGGtGGGGTAAtGGCtCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    276
LMG 22051 T     TTAGCTAGTAGGtGGGGTAAtGGCtCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    276
LMG 22049 T     TTAGCTAGTAGGtGGGGTAACGGCtCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    276
LMG 2603 T      TTAGCTAGTAGGtGGGGTAAtGGCtCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    197
ATCC 13047 T    TTAGCTAGTAGGtGGGGTAACGGCtCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    272
DSM 30104 T     TTAGCTAGTAGGtGGGGTAACGGCtCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
ATCC 11775 T    TTAGCTAGTAGGtGGGGTAACGGCtCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGA    294
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BD 309            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGAGA    286
BD 390            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    354
BD 377            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACcCCTACGGGAGGCAGCAGTGGgGA    354
BD 602            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    354
BD 647            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    354
LMG 2676          TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    312
BD 442            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    294
BD 435            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    354
BD 310            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    356
BD 301            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    356
BD 315            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    356
PA 4              TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    355
LMG 20106         TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    354
BD 640            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    354
BD 588            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    356
LMG 20103         TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    354
LMG 2665 T        TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    334
BD 561            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    356
BD 622            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    354
BD 577            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    354
BD 336            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    336
LMG 2565          TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    334
LMG 2660          TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTC.TACGGGAGGCAGCAGTGGgGA    313
BD 287            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    355
LMG 1286 T        TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    319
BD 639            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    274
BD 502            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    274
BD 500            TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    275
BCC 105 T         TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    271
LMG 2715 T        TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    313
LMG 2632 T        TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    357
LMG 22050 T       TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    336
LMG 22051 T       TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    336
LMG 22049 T       TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    336
LMG 2603 T        TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    257
ATCC 13047 T      TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    332
DSM 30104 T       TGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    354
ATCC 11775 T      TGACCAGCaACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGgGA    354
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BD 309            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    345
BD 390            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    413
BD 377            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    413
BD 602            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    413
BD 647            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    413
LMG 2676          ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    371
BD 442            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    353
BD 435            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    413
BD 310            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    415
BD 301            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAgGAAGGCCTTC    415
BD 315            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    415
PA 4              ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    414
LMG 20106         ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    413
BD 640            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    413
BD 588            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    415
LMG 20103         ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    413
LMG 2665 T        ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    393
BD 561            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    415
BD 622            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    413
BD 577            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCcTC    413
BD 336            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    395
LMG 2565          ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    393
LMG 2660          ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    372
BD 287            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGaCGTGTATGAAGAAGGCCTTC    415
LMG 1286 T        ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    378
BD 639            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    333
BD 502            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    333
BD 500            ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    334
BCC 105 T         ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    330
LMG 2715 T        ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    372
LMG 2632 T        ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    416
LMG 22050 T       ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    395
LMG 22051 T       ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    395
LMG 22049 T       ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    395
LMG 2603 T        ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    316
ATCC 13047 T      ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTATGAAGAAGGCCTTC    391
DSM 30104 T       ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCG.CGTGTgTGAAGAAGGCCTTC    413
ATCC 11775 T      ATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCnG.CGTGTATGAAGAAGGCCTTC    413
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BD 309 T          GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCATTGTGGTTAATAACCGCAGTGATTGA    405
BD 390            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCATTGTGGTTAATAACCGCAGTGATTGA    473
BD 377            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCATTGTGGTTAATAACCGCAtTGATTGA    473
BD 602            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCAtTGATTGA    473
BD 647            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCAtTGATTGA    473
LMG 2676          GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCAtTGATTGA    431
BD 442            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCAtTGATTGA    413
BD 435            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCAtTGATTGA    473
BD 310            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCAtTGATTGA    475
BD 301            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCAtTGATTGA    475
BD 315            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCnCAtTGATTGA    475
PA 4              GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCAtTGATTGA    474
LMG 20106         GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCAtTGATTGA    473
BD 640            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCAtTGAcTGA    473
BD 588            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCAtTGATTGA    475
LMG 20103         GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCgtcGATTGA    473
LMG 2665 T        GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTnTGGTTAATAACCnngtcGATTGA    453
BD 561            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCgtcGATTGA    475
BD 622            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCttgtcGATTGA    473
BD 577            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCgtcGATTGA    473
BD 336            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTaaGGcTAATAACCttgtcGATTGA    455
LMG 2565          GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgacGgGGTTAATAACCctgtcGATTGA    453
LMG 2660          GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgacGgG.TTAATAACCctgtcGATTGA    431
BD 287            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGgGGTTAATAACCctgtcGATTGA    475
LMG 1286 T        GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGgGGTTAATAACCttgtcGATTGA    438
BD 639            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCggTGcGGTTAATAACCGCgccGATTGA    393
BD 502            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCggTGcGGTTAATAACCGCgccGATTGA    393
BD 500            GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCggTGcGGTTAATAACCGCgccGATTGA    394
BCC 105 T         GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCgaTGTGGTTAATAACCGCgtcGATTGA    390
LMG 2715 T        GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGtggTGaGGTTAATAACCtCAtcaATTGA    432
LMG 2632 T        GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGtggTGaGGTTAATAACCtCAtcaATTGA    476
LMG 22050 T       GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCATTGcGGTTAATAACCGCAGTGATTGA    455
LMG 22051 T       GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCAgTcgtGTTAATAgCacgncTGATTGA    455
LMG 22049 T       GGGTTGTAAAGTACTTTCAGtcaGGAGGAAGGgtgTagtcTTAATAcggctAtgcATTGA    455
LMG 2603 T        GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCggTGaGGTTAATAACCtngccGATTGA    376
ATCC 13047 T      GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGtgTTGTGGTTAATAACCGCAGcaATTGA    451
DSM 30104 T       GGGTTGTAAAGcACTTTCAGCGGGGAGGAAGGCgaTGaGGTTAATAACCtCAtcGATTGA    473
ATCC 11775 T      GGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGgAgTaaaGTTAATAcCtttgcTcATTGA    473
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BD 309          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    463
BD 390          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    531
BD 377          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    531
BD 602          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    531
BD 647          CGTTACCC.GCAGAAGAgGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    531
LMG 2676        CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    489
BD 442          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    471
BD 435          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    531
BD 310          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGnCAGCAGCCGCGGnTAATACGGAG    534
BD 301          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    533
BD 315          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    533
PA 4            CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    532
LMG 20106       CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    531
BD 640          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    531
BD 588          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    533
LMG 20103       CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    531
LMG 2665 T      CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    511
BD 561          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    533
BD 622          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    531
BD 577          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    531
BD 336          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    513
LMG 2565        CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    511
LMG 2660        CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    489
BD 287          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGnCGCGG.TAATACGGAG    533
LMG 1286 T      CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    496
BD 639          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    451
BD 502          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    451
BD 500          CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    452
BCC 105 T       CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    448
LMG 2715 T      CaTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    490
LMG 2632 T      CGTTACnC.GCAnAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    534
LMG 22050 T     CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    513
LMG 22051 T     CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    513
LMG 22049 T     CGTTACtg.aCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    513
LMG 2603 T      CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    434
ATCC 13047 T    CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    509
DSM 30104 T     CGTTACCCtGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    532
ATCC 11775 T    CGTTACCC.GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGG.TAATACGGAG    531
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BD 309          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    523
BD 390          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    591
BD 377          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    591
BD 602          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    591
BD 647          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    591
LMG 2676        GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    549
BD 442          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    531
BD 435          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    591
BD 310          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAaCGCACGCAGGCGGTCTGTTAAGTCA    594
BD 301          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    593
BD 315          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    593
PA 4            GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    592
LMG 20106       GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    591
BD 640          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    591
BD 588          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    593
LMG 20103       GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    591
LMG 2665 T      GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    571
BD 561          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    593
BD 622          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    591
BD 577          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    591
BD 336          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    573
LMG 2565        GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    571
LMG 2660        GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    549
BD 287          GGTGCAAGCGTnAATCGGAATTACTGGGCGTAAcGCGCACGCAGGCGGTCTGTTAAGTCA    593
LMG 1286 T      GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    556
BD 639          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    511
BD 502          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    511
BD 500          GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    512
BCC 105 T       GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    508
LMG 2715 T      GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    550
LMG 2632 T      GGTGCAAGCGTTAATCGGAATTACnGGGCGTAAAnCGCACGCAGGCGGTCTGTTAAGTCA    594
LMG 22050 T     GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTcAAGTCg    573
LMG 22051 T     GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTcAAGTCg    573
LMG 22049 T     GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTcAAGTCg    573
LMG 2603 T      GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCA    494
ATCC 13047 T    GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTcAAGTCg    569
DSM 30104 T     GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTcAAGTCg    592
ATCC 11775 T    GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTtTGTTAAGTCA    591
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BD 309          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    582
BD 390          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    650
BD 377          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTcGAAACTGGCAGGCTTGAGTCT    650
BD 602          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    650
BD 647          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    650
LMG 2676        GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    608
BD 442          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    590
BD 435          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    650
BD 310          GATGnnnAAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    654
BD 301          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    652
BD 315          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    652
PA 4            GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    651
LMG 20106       GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    650
BD 640          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCgGGCTTGAGTCT    650
BD 588          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    652
LMG 20103       GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    650
LMG 2665 T      GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    630
BD 561          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    652
BD 622          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    650
BD 577          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    650
BD 336          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    632
LMG 2565        nATGTG.AAAnCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    630
LMG 2660        GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    608
BD 287          GATGTG.AAAnCCCnnGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    652
LMG 1286 T      GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    615
BD 639          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    570
BD 502          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    570
BD 500          GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    571
BCC 105 T       GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    567
LMG 2715 T      GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    609
LMG 2632 T      GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAnTCT    653
LMG 22050 T     GATGTG.AAATCCCCGGGCTcAACCcGGGAACTGCATTcGAAACTGGCAGaCTaGAGTCT    632
LMG 22051 T     GATGTG.AAATCCCCGGGCTcAACCcGGGAACTGCATTcGAAACTGGCAGaCTaGAGTCT    632
LMG 22049 T     GATGTG.AAATCCCCGGGCTcAACCcGGGAACTGCATTcGAAACTGGCAGGCTaGAGTCT    632
LMG 2603 T      GATGTG.AAATCCCCGGGCTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCT    553
ATCC 13047 T    GATGTG.AAATCCCCGGGCTcAACCTGGGAACTGCATTcGAAACTGGCAGGCTgGAGTCT    628
DSM 30104 T     GATGTG.AAATCCCCGGGCTcAACCTGGGAACTGCATTcGAAACTGGCAGGCTaGAGTCT    651
ATCC 11775 T    GATGTG.AAATCCCCGGGCTcAACCTGGGAACTGCATcTGAtACTGGCAaGCTTGAGTCT    650
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BD 309            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    641
BD 390            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    709
BD 377            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    709
BD 602            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    709
BD 647            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    709
LMG 2676          CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    667
BD 442            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    649
BD 435            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    709
BD 310            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    713
BD 301            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    711
BD 315            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    711
PA 4              CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    710
LMG 20106         CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    709
BD 640            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    709
BD 588            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    711
LMG 20103         CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    709
LMG 2665 T        CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    689
BD 561            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    711
BD 622            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    709
BD 577            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    709
BD 336            CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATn    691
LMG 2565          tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    689
LMG 2660          tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    667
BD 287            tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAAaTGCGnnnnGATCTGGAGGAATA    712
LMG 1286 T        tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    674
BD 639            tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    629
BD 502            tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    629
BD 500            tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    630
BCC 105 T         CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    626
LMG 2715 T        CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    668
LMG 2632 T        CGTAGAGGGGGGTAGAATTCCAnGTGTAGCGGTGAAA.TGCGTAnAGATCTGGAGGAATA    712
LMG 22050 T       tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    691
LMG 22051 T       tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    691
LMG 22049 T       tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    691
LMG 2603 T        CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    612
ATCC 13047 T      tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    687
DSM 30104 T       tGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    710
ATCC 11775 T      CGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA.TGCGTAGAGATCTGGAGGAATA    709
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BD 309      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  700
BD 390      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  768
BD 377      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  768
BD 602      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  768
BD 647      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  768
LMG 2676    CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  726
BD 442      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  708
BD 435      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  768
BD 310      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  772
BD 301      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  770
BD 315      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  770
PA 4        CCGGTGGCGAAGaGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  770
LMG 20106   CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  768
BD 640      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  768
BD 588      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  770
LMG 20103   CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  768
LMG 2665 T  CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  748
BD 561      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  770
BD 622      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  768
BD 577      CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  768
BD 336      nCnGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  750
LMG 2565    CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  748
LMG 2660    CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  726
BD 287      CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  771
LMG 1286 T  CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  733
BD 639      CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  688
BD 502      CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  688
BD 500      CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  689
BCC 105 T   CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  685
LMG 2715 T  CCGGTGGCGAAG.GCGGtCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  727
LMG 2632 T  CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  771
LMG 22050 T CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  750
LMG 22051 T CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  750
LMG 22049 T CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  750
LMG 2603 T  CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  671
ATCC 13047 T CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  746
DSM 30104 T CCGGTGGCGAAG.GCGGCCCCCTGGACaAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  769
ATCC 11775 T CCGGTGGCGAAG.GCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  768
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                ************************************************************
BD 309          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    760
BD 390          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    828
BD 377          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    828
BD 602          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    828
BD 647          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    828
LMG 2676        GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    786
BD 442          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGgGGTTGT    768
BD 435          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGgGGTTGT    828
BD 310          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTnGACTTGGAGGTTGT    832
BD 301          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    830
BD 315          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    830
PA 4            GCAAACAGGATTAGATACCCTGGTAnTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    830
LMG 20106       GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    828
BD 640          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    828
BD 588          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    830
LMG 20103       GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    828
LMG 2665 T      GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    808
BD 561          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    830
BD 622          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    828
BD 577          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    828
BD 336          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    810
LMG 2565        GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    808
LMG 2660        GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    786
BD 287          GCAAACAGGATTAGATACCCTGGTAnTCCgCGCCGTAAACGATGTCGACTTGGAGGTTGT    831
LMG 1286 T      GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    793
BD 639          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    748
BD 502          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    748
BD 500          GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    749
BCC 105 T       GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    745
LMG 2715 T      GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    787
LMG 2632 T      GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    831
LMG 22050 T     GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGcTGT    810
LMG 22051 T     GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGcTGT    810
LMG 22049 T     GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    810
LMG 2603 T      GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    731
ATCC 13047 T    GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGAtTTGGAGGTTGT    806
DSM 30104 T     GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGAtTTGGAGGTTGT    829
ATCC 11775 T    GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGT    828
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BD 309          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    820
BD 390          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    888
BD 377          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    888
BD 602          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    888
BD 647          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    888
LMG 2676        TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    846
BD 442          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    828
BD 435          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    888
BD 310          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    892
BD 301          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    890
BD 315          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    890
PA 4            TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    890
LMG 20106       TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    888
BD 640          TCCCTTGAaGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    888
BD 588          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    890
LMG 20103       TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    888
LMG 2665 T      TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    868
BD 561          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    890
BD 622          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    888
BD 577          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCcTTAAGTCGACCGCCTGGGGAGTACGGCC    888
BD 336          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    870
LMG 2565        TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    868
LMG 2660        TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    846
BD 287          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGnGGAGTACGGCC    891
LMG 1286 T      TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    853
BD 639          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    808
BD 502          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    808
BD 500          TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    809
BCC 105 T       TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    805
LMG 2715 T      TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    847
LMG 2632 T      TCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    891
LMG 22050 T     gCCCTTGAGGcGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    870
LMG 22051 T     TCCCnTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    870
LMG 22049 T     gCCCTTGAGGnGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    870
LMG 2603 T      gCCCTTGAGGnGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    791
ATCC 13047 T    gCCCTTGAGGcGTGGCTTCCGGAGCTAACGCGTTAAaTCGACCGCCTGGGGAGTACGGCC    866
DSM 30104 T     gCCCTTGAGGcGTGGCTTCCGGAGCTAACGCGTTAAaTCGACCGCCTGGGGAGTACGGCC    889
ATCC 11775 T    gCCCTTGAGGcGTGGCTTCCGGAnnTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCC    888
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                **********************************************************
BD 309          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    880
BD 390          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    948
BD 377          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    948
BD 602          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    948
BD 647          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    948
LMG 2676        GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATaTGGTTT    906
BD 442          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    888
BD 435          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    948
BD 310          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    952
BD 301          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGcGGAGCATGTGGTTT    950
BD 315          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    950
PA 4            GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    950
LMG 20106       GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    948
BD 640          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    948
BD 588          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    950
LMG 20103       GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    948
LMG 2665 T      GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    928
BD 561          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    950
BD 622          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    948
BD 577          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    948
BD 336          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    930
LMG 2565        GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    928
LMG 2660        GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    906
BD 287          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    951
LMG 1286 T      GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    913
BD 639          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    868
BD 502          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    868
BD 500          GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    869
BCC 105 T       GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    865
LMG 2715 T      GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    907
LMG 2632 T      GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    951
LMG 22050 T     GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    930
LMG 22051 T     GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    930
LMG 22049 T     GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    930
LMG 2603 T      GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    851
ATCC 13047 T    GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    926
DSM 30104 T     GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT    949
ATCC 11775 T    GCAAGGTTAAAACTCAAATGAATTGACGGGGGCC.GCACAAGCGGTGGAGCATGTGGTTT    947
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BD 309          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCACGGAATTCGGCAGAG    938
BD 390          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG   1006
BD 377          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG   1006
BD 602          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCACGGAATTtGGCAGAG   1006
BD 647          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCACGGAATTtGGCAGAG   1006
LMG 2676        AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG    964
BD 442          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAATTtaGCAGAG    946
BD 435          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCACGGAATTtGGCAGAG   1006
BD 310          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTGgACATCCAgaGAAcTtaGCAGAG   1011
BD 301          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG   1008
BD 315          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG   1008
PA 4            AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG   1008
LMG 20106       AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG   1006
BD 640          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG   1006
BD 588          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG   1008
LMG 20103       AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG   1006
LMG 2665 T      AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtGGCAGAG    986
BD 561          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCACGGAATTCGGCAGAG   1008
BD 622          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG   1006
BD 577          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG   1006
BD 336          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCACGGAATTCGGCAGAG    988
LMG 2565        AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCACGGAATTtGGCAGAG    986
LMG 2660        AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCACGGAATTtGGCAGAG    964
BD 287          AATTCGATGCAACGCGAAGAAgCCTTACCTACTCTTG.ACATCCACGGAATTtGGCAGAG   1010
LMG 1286 T      AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCACGGAATTtGGCAGAG    971
BD 639          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAnnGAAnTnnGCAGAG    926
BD 502          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAnnGAAnTnGGCAGAG    926
BD 500          AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCACnGAAnTnnGCAGAG    927
BCC 105 T       AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG    923
LMG 2715 T      AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgcGAAcTtGGCAGAG    965
LMG 2632 T      AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgcGAAcTttnCAGAG   1009
LMG 22050 T     AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG    988
LMG 22051 T     AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTttcCAGAG    988
LMG 22049 T     AATTCGATGCAACGCGAAGAA.CCTTACCTACTCTTG.ACATCCAgaGAAcTtaGCAGAG    988
LMG 2603 T      AATTCGATGCAACGCGAAGAA.CCTTACCTggcCTTG.ACATCCAgaGAAcTtaGCAGAG    909
ATCC 13047 T    AATTCGATGCAACGCGAAGAA.CCTTACCTggTCTTG.ACATCCACaGAAcTttcCAGAG    984
DSM 30104 T     AATTCGATGCAACGCGAAGAA.CCTTACCTggTCTTG.ACATCCACaGAAcTttcCAGAG   1007
ATCC 11775 T    AATTCGATGCAACGCGAAGAA.CCTTACCTggTCTTG.ACATCCACGGAAgTtttCAGAG   1005
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BD 309          ATGCCTTAGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT    998
BD 390          ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1066
BD 377          ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1066
BD 602          ATGCCTTAGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1066
BD 647          ATGCCTTAGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1066
LMG 2676        ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1024
BD 442          ATGCgTTgGTGCCTTCGGGAACCcTGAGACAGGTGCTGCATGGCTGTtGTCAGCTCGTGT   1006
BD 435          ATGCgTTAGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTtGTCAGCTCGTGT   1066
BD 310          ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1071
BD 301          ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1068
BD 315          ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1068
PA 4            ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1068
LMG 20106       ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1066
BD 640          ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1066
BD 588          ATGCtTTgGTGCCTTCGGGAgCtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1068
LMG 20103       ATGCtTTgGTGCCTTCGGGAgCtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1066
LMG 2665 T      ATGCtTTgGTGCCTTCGGGAgCCcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1046
BD 561          ATGCCTTAGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1068
BD 622          ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1066
BD 577          ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1066
BD 336          ATGCCTTAGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1048
LMG 2565        ATGCCTTAGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1046
LMG 2660        ATGCCTTAGTGCCTTCGGGgACCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1024
BD 287          ATGCCTTAGTGCCTTCGGGAACCGTGAnACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1070
LMG 1286 T      ATGCCTTAGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1031
BD 639          ATGCnTTnGTGCCTTCGGGAACnnTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT    986
BD 502          ATGCCTTnGTGCCTTCGGGAACnnTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT    986
BD 500          ATGCnTTnGTGCCTTCGGGAACnnTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT    987
BCC 105 T       ATGCtTTgGTGCCTTCGGGAACCcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT    983
LMG 2715 T      ATGCCTTgGTGCCTTCGGGAACgcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1025
LMG 2632 T      ATGgaTTgGTGCCTTCGGGAACgcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1069
LMG 22050 T     ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1048
LMG 22051 T     ATGgaTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1048
LMG 22049 T     ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1048
LMG 2603 T      ATGCtTTgGTGCCTTCGGGAACtcTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT    969
ATCC 13047 T    ATGgaTTgGTGCCTTCGGGAACtGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1044
DSM 30104 T     ATGgaTTgGTGCCTTCGGGAACtGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1067
ATCC 11775 T    ATGagaatGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGT   1065
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BD 309          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1058
BD 390          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1126
BD 377          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1126
BD 602          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1126
BD 647          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1126
LMG 2676        TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1084
BD 442          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1066
BD 435          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1126
BD 310          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1131
BD 301          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1128
BD 315          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1128
PA 4            TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1128
LMG 20106       TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1126
BD 640          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1126
BD 588          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1128
LMG 20103       TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1126
LMG 2665 T      TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1106
BD 561          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1128
BD 622          TGTGAAATGTTGGGTTAAGTCCtGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1126
BD 577          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1126
BD 336          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1108
LMG 2565        TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1106
LMG 2660        TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1084
BD 287          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1130
LMG 1286 T      TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1091
BD 639          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1046
BD 502          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1046
BD 500          TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1047
BCC 105 T       TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1043
LMG 2715 T      TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1085
LMG 2632 T      TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGAT   1129
LMG 22050 T     TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCcTATCCTTTGTTGCCAGCGAT   1108
LMG 22051 T     TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCcTATCCTTTGTTGCCAGCGAT   1108
LMG 22049 T     TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCcTATCCTTTGTTGCCAGCGAT   1108
LMG 2603 T      TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGgn   1029
ATCC 13047 T    TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGgT   1104
DSM 30104 T     TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGgT   1127
ATCC 11775 T    TGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGgT   1125
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BD 309          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1118
BD 390          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1186
BD 377          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1186
BD 602          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1186
BD 647          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1186
LMG 2676        TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1144
BD 442          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1126
BD 435          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1186
BD 310          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1191
BD 301          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1188
BD 315          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1188
PA 4            TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1188
LMG 20106       TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1186
BD 640          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1186
BD 588          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1188
LMG 20103       TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1186
LMG 2665 T      TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1166
BD 561          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1188
BD 622          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1186
BD 577          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1186
BD 336          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1168
LMG 2565        TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1166
LMG 2660        TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1144
BD 287          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1190
LMG 1286 T      TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1151
BD 639          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1106
BD 502          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1106
BD 500          TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1107
BCC 105 T       TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1103
LMG 2715 T      TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1145
LMG 2632 T      TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1189
LMG 22050 T     TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1168
LMG 22051 T     TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1168
LMG 22049 T     TCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1168
LMG 2603 T      TCGGcCGGGAACTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGACGTC   1089
ATCC 13047 T    cCGGcCGGGAACTCAAAGGAGACTGCCaGTGATAAACtGGAGGAAGGTGGGGATGACGTC   1164
DSM 30104 T     TaGGcCGGGAACTCAAAGGAGACTGCCaGTGATAAACtGGAGGAAGGTGGGGATGACGTC   1187
ATCC 11775 T    cCGGcCGGGAACTCAAAGGAGACTGCCaGTGATAAACtGGAGGAAGGTGGGGATGACGTC   1185
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BD 309          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1178
BD 390          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1246
BD 377          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1246
BD 602          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1246
BD 647          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1246
LMG 2676        AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1204
BD 442          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1186
BD 435          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1246
BD 310          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1251
BD 301          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1248
BD 315          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1248
PA 4            AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1248
LMG 20106       AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1246
BD 640          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1246
BD 588          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1248
LMG 20103       AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1246
LMG 2665 T      AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1226
BD 561          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1248
BD 622          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1246
BD 577          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1246
BD 336          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1228
LMG 2565        AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1226
LMG 2660        AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1204
BD 287          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1250
LMG 1286 T      AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1211
BD 639          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1166
BD 502          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1166
BD 500          AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1167
BCC 105 T       AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1163
LMG 2715 T      AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1205
LMG 2632 T      AAGTCATCATGGCCCTTACcAGTAnGGCTACACACnTGCTACAATGGCGCATACAAnGAG   1249
LMG 22050 T     AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1228
LMG 22051 T     AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGtATACAAAGAG   1228
LMG 22049 T     AAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1228
LMG 2603 T      AAGTCATCATGGCCCTTACGgccAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1149
ATCC 13047 T    AAGTCATCATGGCCCTTACGAccAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1224
DSM 30104 T     AAGTCATCATGGCCCTTACGAccAGGGCTACACACGTGCTACAATGGCatATACAAAGAG   1247
ATCC 11775 T    AAGTCATCATGGCCCTTACGAccAGGGCTACACACGTGCTACAATGGCGCATACAAAGAG   1245
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BD 309          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1238
BD 390          AAGCGACCTCGCGAGAGCAAGCGGACCTCAcAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1306
BD 377          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1306
BD 602          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1306
BD 647          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1306
LMG 2676        AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1264
BD 442          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1246
BD 435          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1306
BD 310          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1311
BD 301          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1308
BD 315          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1308
PA 4            AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1308
LMG 20106       AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1306
BD 640          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1306
BD 588          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1308
LMG 20103       AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1306
LMG 2665 T      AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1286
BD 561          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1308
BD 622          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1306
BD 577          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1306
BD 336          AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1288
LMG 2565        AAGCGACCTCGCGAGAGCAAGCGGACCTCAcAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1286
LMG 2660        AAGCaACCTCGCGAGAGCAAGCGGACCTCAcAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1264
BD 287          AAGCGACCTCGCGAGAGCAAGCGGACCTCAcAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1310
LMG 1286 T      AAGCGACCTCGCGAGAGCAAGCGGACCTCAcAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1271
BD 639          AAGCGACCTCGCGAGAGCAAGCGGACCTCAcAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1226
BD 502          AAGCGACCTCGCGAGAGCAAGCGGACCTCAcAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1226
BD 500          AAGCGACCTCGCGAGAGCAAGCGGACCTCAcAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1227
BCC 105 T       AAGCGACCTCGCGAGAGCAAGCGGACCTCAcAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1223
LMG 2715 T      AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1265
LMG 2632 T      AAGCGACCTCGCGAGAnCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATCGGAGTCT   1309
LMG 22050 T     AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATtGGAGTCT   1288
LMG 22051 T     AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTaCGTCGTAGTCCGGATtGGAGTCT   1288
LMG 22049 T     AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATtGGAGTCT   1288
LMG 2603 T      AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATtGGAGTCT   1209
ATCC 13047 T    AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATtGGAGTCT   1284
DSM 30104 T     AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTatGTCGTAGTCCGGATtGGAGTCT   1307
ATCC 11775 T    AAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATtGGAGTCT   1305
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BD 309            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1297
BD 390            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCtGTGGATCAGAATGCCACGGTGA   1366
BD 377            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1365
BD 602            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1365
BD 647            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1365
LMG 2676          GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1323
BD 442            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1305
BD 435            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1365
BD 310            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGnCACGGTGA   1370
BD 301            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATt.GTGGATCAGAATGCCACGGTGA   1367
BD 315            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGnCACGGTGA   1367
PA 4              GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1367
LMG 20106         GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1365
BD 640            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1365
BD 588            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1367
LMG 20103         GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1365
LMG 2665 T        GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1345
BD 561            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1367
BD 622            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1365
BD 577            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTgATC.GTGGATCAGAATGCCACGGTGA   1365
BD 336            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1347
LMG 2565          GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1345
LMG 2660          GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1323
BD 287            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1369
LMG 1286 T        GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1330
BD 639            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1285
BD 502            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1285
BD 500            GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1286
BCC 105 T         GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1282
LMG 2715 T        GCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1324
LMG 2632 T        GCAACTCnACTCCGTGAAGTCGGAATCGCTAGTAATC.GTGGATCnnAATGCCACnGTGA   1368
LMG 22050 T       GCAACTCGACTCCaTGAAGTCGGAATCGCTAGTAATC.GTaGATCAGAATGCtACGGTGA   1347
LMG 22051 T       GCAACTCGACTCCaTGAAGTCGGAATCGCTAGTAATC.GTaGATCAGAATGCtACGGTGA   1347
LMG 22049 T       GCAACTCGACTCCaTGAAGTCGGAATCGCTAGTAATC.GTaGATCAGAATGCtACGGTGA   1347
LMG 2603 T        GCAACTCGACTCCaTGAAGTCGGAATCGCTAGTAATC.GTaGATCAGAATGCtACGGTGA   1268
ATCC 13047 T      GCAACTCGACTCCaTGAAGTCGGAATCGCTAGTAATC.GTaGATCAGAATGCtACGGTGA   1343
DSM 30104 T       GCAACTCGACTCCaTGAAGTCGGAATCGCTAGTAATC.GTaGATCAGAATGCtACGGTGA   1366
ATCC 11775 T      GCAACTCGACTCCaTGAAGTCGGAATCGCTAGTAATC.GTGGATCAGAATGCCACGGTGA   1364
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BD 309          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1357
BD 390          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1426
BD 377          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1425
BD 602          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1425
BD 647          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1425
LMG 2676        ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1383
BD 442          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1365
BD 435          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1425
BD 310          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1430
BD 301          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1427
BD 315          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1427
PA 4            ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1427
LMG 20106       ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1425
BD 640          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1425
BD 588          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1427
LMG 20103       ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1425
LMG 2665 T      ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1405
BD 561          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1427
BD 622          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1425
BD 577          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1425
BD 336          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1407
LMG 2565        ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAnAA   1405
LMG 2660        ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1383
BD 287          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1429
LMG 1286 T      ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1390
BD 639          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1345
BD 502          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1345
BD 500          ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1346
BCC 105 T       ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG.................   1325
LMG 2715 T      ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1384
LMG 2632 T      ATnCGTTCCCGGGCCTTGTACACACnGCCCGTCACnCCATGGGAGTGGGTTGCAnAAGAA   1428
LMG 22050 T     ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1407
LMG 22051 T     ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1407
LMG 22049 T     ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1407
LMG 2603 T      ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1328
ATCC 13047 T    ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1403
DSM 30104 T     ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1426
ATCC 11775 T    ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAA   1424
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BD 309          GTAGGTAGCTTAACCTCCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1417
BD 390          GTAGGTAGCTTAACCTCCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1486
BD 377          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1485
BD 602          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1485
BD 647          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1485
LMG 2676        GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1443
BD 442          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATcCATGACTGGGGTGAAG   1425
BD 435          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATcCATGACTGGGGTGAAG   1485
BD 310          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1490
BD 301          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1487
BD 315          GTAGGTAGCTTAACCTtCGGGgGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1487
PA 4            GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1487
LMG 20106       GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1485
BD 640          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTcGTGATTCATGACTGGGGTGAAG   1485
BD 588          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1487
LMG 20103       GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1485
LMG 2665 T      GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1465
BD 561          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1487
BD 622          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1485
BD 577          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1485
BD 336          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1467
LMG 2565        GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCAC.........................   1440
LMG 2660        GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1443
BD 287          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1489
LMG 1286 T      GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1450
BD 639          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1405
BD 502          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1405
BD 500          GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGG.....   1401
BCC 105 T       ............................................................   1325
LMG 2715 T      GTAGGTAGCTTAACCctCGGGAGGGCGCTTACtACTTTGTGATTCATGACTGGGGTGAAG   1444
LMG 2632 T      GTnnGTAGCTTAACCaCCGGGAGGGCGCTTACCAnTTTGTGATTCnnGACTGGGGTnAAG   1488
LMG 22050 T     GTAGaTAGCTTAACCTtCGGGAGGGCGtTTACCACTTTGTGATTCATGACTGGGGTGAAG   1467
LMG 22051 T     GTAGaTAGCTTAACCTtCGGGAGGGCGtTTACCACTTTGTGATTCATGACTGGGGTGAAG   1467
LMG 22049 T     GTAGaTAGCTTAACCTtCGGGAGGGCGtTTACCACTTTGTGATTCATGACTGGGGTGAAG   1467
LMG 2603 T      GTAGGTAGCTTAACCTtCG..........................................   1347
ATCC 13047 T    GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1463
DSM 30104 T     GTAGGTAGCTTAACCTtCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAG   1486
ATCC 11775 T    GTAGGTAGCTTAAC.TtCGGGAGGGCG.................................   1450
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BD 309          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1464
BD 390          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1533
BD 377          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1532
BD 602          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1532
BD 647          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1532
LMG 2676        TCGTAACAAGGT.................................       1455
BD 442          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1472
BD 435          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1532
BD 310          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1537
BD 301          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1534
BD 315          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTTa    1535
PA 4            TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1534
LMG 20106       TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1532
BD 640          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1532
BD 588          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1534
LMG 20103       TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1532
LMG 2665 T      TCGTAACAAGGTAACCGcAGGGGAACCTGC...............       1495
BD 561          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1534
BD 622          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1532
BD 577          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1532
BD 336          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1514
LMG 2565        .............................................       1440
LMG 2660        TCGTAACAAGGT.................................       1455
BD 287          TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTT.    1536
LMG 1286 T      TCGTAACAAGGTAACCGTAGGGG.....................        1473
BD 639          TCGTAACAAGGTAACCGTAGGGGAACC..................       1432
BD 502          TCGT.........................................       1409
BD 500          .............................................       1401
BCC 105 T       .............................................       1325
LMG 2715 T      TCGTAACAAGGT.................................       1456
LMG 2632 T      TCGTnnCAAGG..................................       1499
LMG 22050 T     TCGTAACAAGGTAACCGTAGGGGAACC..................       1494
LMG 22051 T     TCGTAACAAGGTAACCGTAGGGGAACC..................       1494
LMG 22049 T     TCGTAACAAGGTAACCGTAGGGGAACC..................       1494
LMG 2603 T      .............................................       1347
ATCC 13047 T    TCGTAACAAGGTAACCGTAGGGGAACCTGCGGCTGGATCACCTCCTTg    1511
DSM 30104 T     TCGTAACAAGGTAACCGTAGGGGAACCTGCGGtTGGATCACCTCCTTt    1534
ATCC 11775 T    .............................................       1450
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