**full_name_ltp**
Corrected species names according to Validation Lists and Notification Lists (IJSEM).

**rel_ltp**
Name of the LTP release where the sequence (acc) first appeared.

**hi_tax_ltp**
Name of the family or given taxon above genus. Unclassified taxa are explicitly labeled as 'Unclassified'.

**type_ltp**
Every type species receives the label 'type sp.'

**riskgroup_ltp**
Information inherited from DSMZ's nomenclature-up-to-date in September 2017. Directive 2000/54/EC and Directive 90/679/EEC (adopted 20 November, 1990; revised 18 September 2000) on the protection of workers from risks related to exposure to biological agents at work provides for the Classification of biological agents into four infection risk groups on the basis of the following criteria: Group 1 biological agent means one that is unlikely to cause human disease. Group 2 biological agent means one that can cause human disease and might be a hazard to workers; it is unlikely to spread to the community; there is usually effective prophylaxis or treatment available. Group 3 biological agent means one that can cause severe human disease and present a serious hazard to workers; it may present a risk of spreading to the community, but there is usually effective prophylaxis or treatment available. Group 4 biological agent means one that causes severe human disease and is a serious hazard to workers; it may present a high risk of spreading to the community; there is usually no effective prophylaxis or treatment available.

**tax_ltp**
Last update of the accepted taxonomy according to Validation and Notification Lists in IJSEM.

**phylo_ltp**
*Phylogenetic path according to the LTP trees.* Monophyletic branches with taxonomic coherence are clustered and named in the LTP tree. This field compiles the phylogenetic affiliation of each sequence as induced from the LTP tree by listing the names of clusters a sequence is within. It starts at the domain level and can end at the family rank, genera are not clustered in the tree. By comparing the taxonomic path (field “tax_ltp”) and the phylogenetic path (field “phylo_ltp”) assigned to a sequence it will be easier to detect incongruencies between type strains' taxonomy (i.e. accepted nomenclature) and our phylogeny of the 16S rRNA. For the LSU database this field will be implemented in the next release. The tree topology was last updated in release s108. Therefore, the level of confidence in this phylogenetic path must not be high but orientative, which is fine for its purpose.

**url_lpsn_ltp**
It contains the variable part of the URLs leading to the LPSN's species files (http://www.bacterio.net) To use the www-interface in ARB write: readdb (url_lpsn_ltp) on an available slot of the application "search world wide web (WWW)" window.

**NJ_support_pk4_ltp**
Selection of 757 reference sequences to stabilize Neighbour-joining reconstructions. Available in the SSU database only. This methodology was developed to harmonize trees in The Prokaryotes fourth edition (pk4) and more information can be found in its chapter ‘Harmonized Phylogenetic Trees for The Prokaryotes’ (Raul Munoz et al. 2014. DOI 10.1007/978-3-642-30138-4_415, © Springer-Verlag Berlin Heidelberg.)