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**Title:** Complete genome sequence of *Planctomyces brasiliensis* type strain (DSM 5305(T)), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of *Gimesia* gen. nov., *Planctopirus* gen. nov and *Rubinisphaera* gen. nov and emended descriptions of the order Planctomycetales and the family Planctomycetaceae

**Author(s):** Scheuner, C (Scheuner, Carmen); Tindall, BJ (Tindall, Brian J.); Lu, M (Lu, Megan); Nolan, M (Nolan, Matt); Lapidus, A (Lapidus, Alla); Cheng, JF (Cheng, Jan-Fang); Goodwin, L (Goodwin, Lynne); Pitluck, S (Pitluck, Sam); Huntemann, M (Huntemann, Marcel); Liolios, K (Liolios, Konstantinos); Pagani, I (Pagani, Ioanna); Mavromatis, K (Mavromatis, Konstantinos); Ivanova, N (Ivanova, Natalia); Pati, A (Pati, Amrita); Chen, A (Chen, Amy); Palaniappan, K (Palaniappan, Krishna); Jeffries, CD (Jeffries, Cynthia D.); Hauser, L (Hauser, Loren); Land, M (Land, Miriam); Mwirichia, R (Mwirichia, Romano); Rohde, M (Rohde, Manfred); Abt, B (Abt, Birte); Detter, JC (Detter, John C.); Woyke, T (Woyke, Tanja); Eisen, JA (Eisen, Jonathan A.); Markowitz, V (Markowitz, Victor); Hugenholtz, P (Hugenholtz, Philip); Goker, M (Goeker, Markus); Kyrpidis, NC (Kyrpidis, Nikos C.); Klenk, HP (Klenk, Hans-Peter)

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**Abstract:** *Planctomyces brasiliensis* Schlesner 1990 belongs to the order Planctomycetales, which differs from other bacterial taxa by several distinctive features such as internal cell compartmentalization, multiplication by forming buds directly from the spherical, ovoid or pear-shaped mother cell and a cell wall consisting of a proteinaceous layer rather than a peptidoglycan layer. The first strains of *P. brasiliensis*, including the type strain IFAM 1448(T), were isolated from a water sample of Lagoa Vermelha, a salt pit near Rio de Janeiro, Brasil. This is the second completed genome sequence of a type strain of the genus *Planctomyces* to be published and the sixth type strain genome sequence from the family Planctomycetaceae. The 6,006,602 bp long genome with its 4,811 protein-coding and 54 RNA genes is a part of the Genomic Encyclopedia of Bacteria and Archaea project. Phylogenomic analyses indicate that the classification within the Planctomycetaceae is partially in conflict with its evolutionary history, as the positioning of *Schlesneria* renders the genus *Planctomyces* paraphyletic. A re-analysis of published fatty-acid measurements also does not support the current arrangement of the two genera. A quantitative comparison of phylogenetic and phenotypic aspects indicates that the three *Planctomyces* species with type strains available in public culture collections should be placed in separate genera. Thus the genera *Gimesia*, *Planctopirus* and *Rubinisphaera* are proposed to accommodate *P. maris*, *P. limnophilus* and *P. brasiliensis*, respectively. Pronounced differences between the reported G + C content of *Gemmata obscuriglobus*, *Singulisphaera acidiphila* and *Zavarzinella formosa* and G + C content calculated from their genome sequences call for emendation of their species descriptions. In addition to other features, the range of G + C values reported for the genera within the Planctomycetaceae indicates that the descriptions of the family and the order should be emended.

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**Addresses:** [Scheuner, Carmen; Tindall, Brian J.; Abt, Birte; Goeker, Markus; Klenk, Hans-Peter] DSMZ German Collect Microorganisms & Cell Culture, Braunschweig, Germany.

[Lu, Megan; Nolan, Matt; Lapidus, Alla; Cheng, Jan-Fang; Goodwin, Lynne; Pitluck, Sam; Huntemann, Marcel; Liolios, Konstantinos; Pagani, Ioanna; Mavromatis, Konstantinos; Ivanova, Natalia; Pati, Amrita; Jeffries, Cynthia D.; Hauser, Loren; Land, Miriam; Detter, John C.; Woyke, Tanja; Eisen, Jonathan A.; Hugenholtz, Philip; Kyrpidis, Nikos C.] DOE Joint Genome Inst, Walnut Creek, CA USA.

[Lu, Megan; Goodwin, Lynne; Detter, John C.] Los Alamos Natl Lab, Biosci Div, Los Alamos, NM USA.

[Chen, Amy; Palaniappan, Krishna; Markowitz, Victor] Lawrence Berkeley Natl Lab, Biol Data Management & Technol Ctr, Berkeley, CA USA.

[Jeffries, Cynthia D.; Hauser, Loren; Land, Miriam] Oak Ridge Natl Lab, Oak Ridge, TN USA.

[Mwirichia, Romano] Jomo Kenyatta Univ Agr & Technol, Juja, Kenya.

[Rohde, Manfred] HZI Helmholtz Ctr Infect Res, Braunschweig, Germany.

[Eisen, Jonathan A.] Univ Calif Davis, Genome Ctr, Davis, CA 95616 USA.

[Hugenholtz, Philip] Univ Queensland, Australian Ctr Ecogen, Sch Chem & Mol Biosci, Brisbane, Qld, Australia.

[Kyrpidis, Nikos C.] King Abdulaziz Univ, Dept Biol Sci, Jeddah, Saudi Arabia.

**Reprint Address:** Goker, M (reprint author), DSMZ German Collect Microorganisms & Cell Culture, Braunschweig, Germany.

**E-mail Addresses:** markus.goeker@dsMZ.de

**Author Identifiers:**

Author	ResearcherID Number	ORCID Number
Land, Miriam	A-6200-2011	0000-0001-7102-0031
Kyrpidis, Nikos	A-6305-2014	0000-0002-6131-0462
Lapidus, Alla	I-4348-2013	0000-0003-0427-8731
Fac Sci, KAU, Biol Sci Dept	L-4228-2013	

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