

Complete genome sequence of the filamentous gliding predatory bacterium *Herpetosiphon aurantiacus* type strain (114-95(T)).

Kiss H, Nett M, Domin N, Martin K, Maresca JA, Copeland A, Lapidus A, Lucas S, Berry KW, Glavina Del Rio T, Dalin E, Tice H, Pitluck S, Richardson P, Bruce D, Goodwin L, Han C, Detter JC, Schmutz J, Brettin T, Land M, Hauser L, Kyrpides NC, Ivanova N, Göker M, Woyke T, Klenk HP, Bryant DA (2011) Complete genome sequence of the filamentous gliding predatory bacterium *Herpetosiphon aurantiacus* type strain (114-95(T)). *Stand Genomic Sci* 5(3), 356-370.

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Abstract

Herpetosiphon aurantiacus Holt and Lewin 1968 is the type species of the genus *Herpetosiphon*, which in turn is the type genus of the family *Herpetosiphonaceae*, type family of the order *Herpetosiphonales* in the phylum *Chloroflexi*. *H. aurantiacus* cells are organized in filaments which can rapidly glide. The species is of interest not only because of its rather isolated position in the tree of life, but also because *Herpetosiphon* spp. were identified as predators capable of facultative predation by a wolf pack strategy and of degrading the prey organisms by excreted hydrolytic enzymes. The genome of *H. aurantiacus* strain 114-95(T) is the first completely sequenced genome of a member of the family *Herpetosiphonaceae*. The 6,346,587 bp long chromosome and the two 339,639 bp and 99,204 bp long plasmids with a total of 5,577 protein-coding and 77 RNA genes was sequenced as part of the DOE Joint Genome Institute Program

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