



Is your gut flora “in balance”?

RIDA®GENE Gut Balance

Besides a variety of different species of bacteria, 90 % of the normal human gut flora is populated by two phylogenetic groups which exist in a symbiotic balance: *Bacteroides* and *Firmicutes*. *Bacteroides* are anaerobic, gram-negative bacteria and in the large intestine, approximately 10^{11} *Bacteroides*/g stool exist. Therefore, *Bacteroides* are the dominant bacteria in terms of numbers. The second phylogenetic group is the *firmicutes*. *Clostridium* Cluster XIVa are a class of *firmicutes* to which, besides others, *Eubacterium* spp. and *Roseburia* spp. belong.

External factors such as stress and diet can influence this balance of gut bacteria and hence have severe

consequences on the human organism.

Firmicutes are fatty acid producers which are able to impact the energy balance. This is reflected in the fact that the presence of decreased *Bacteroides* and increased *Firmicutes* is often described in obese patients.^{1,2,3,4} Obesity is one of the major problems of the westernized countries and in Germany approximately 20 % of the population suffers from obesity and 30 % are in a pre-condition to obesity.

With the RIDA®GENE Gut Balance real-time PCR assay the ratio of *Bacteroides* and *Clostridium* Cluster XIVa can be determined.

RIDA®GENE Gut Balance Art. No. PG0105



- Real-time multiplex PCR
- Quantitative – Standard DNA included
- Detection and differentiation of *Bacteroides* and *Clostridium* Cluster XIVa in human stool samples
- **Flexible** – The assay can be run on the commonly used real-time PCR instruments, such as the Mx3005P, LightCycler® 480II, SmartCycler®, ABI 7500, m2000rt, CFX96 or Rotor-Gene Q
- **Reliable** – An included extraction control (Internal control DNA, ICD) detects PCR inhibition, monitors reagent integrity and confirms that nucleic acid extraction was sufficient

Ordering information

Product	Description	Tests	Matrix	Art. No.
RIDA® GENE	Real-time PCR			
Gut Balance	Real-time PCR for the direct qualitative or quantitative detection and differentiation of <i>Bacteroides</i> and <i>Clostridium</i> Cluster XIVa from human stool samples	100	Stool	PG0105



For detailed
information on
Gut balance
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¹. Max Rubner Institut: Nationale Verzehrs-Studie II.

². Ley, RE et al. Microbial ecology: human gut microbes associated with obesity. Nature 2006, 444(7122):1022-1030.

³. Turnbaugh P et al. A core gut microbiome in obese and lean twins. Nature 2009, 457(7228): 480 – 484.

⁴. Vaarala O. Gut Microbiota and Type 1 Diabetes. Rev. Diab. Stud. 2013, 9(4): 251 -259.