

A snapshot of the microbiome field

A survey of leading scientists from academia and industry highlights notable papers that have garnered momentum in microbiome research.

Nature Biotechnology sent a survey to 55 prominent researchers in the microbiome field and asked them to identify and comment on what they thought were the most influential papers since the field's inception. The results received from 17 of these researchers are presented in this article. Perhaps the most striking finding was

that a handful of papers dominated their selections.

We present the top five papers selected most often (all were selected by three or more scientists), together with comments from experts to illustrate why each paper was chosen. All but one of the selected papers focus on the microbiota of the gut, probably because this niche is

where most of the approximately 100 trillion microbes in the human body reside. Only one of the top five papers used an animal model, and was selected because it provided the first evidence of a mechanistic link between the complement (and functioning) of gut microbes and obesity. The bulk of the selected papers catalog the membership of the microbiome, because that has been the main focus of much of the research effort. Moving forward, a panel of experts contacted by *Nature Biotechnology* (Feature p. 304) identify function as the next hurdle in this field. So expect to see studies on microbiome metabolomes, integrated views of host and microbial genotypes and phenotypes, and RNA-seq analyses dominating the future research landscape.

Susan Jones

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Ranked 1st



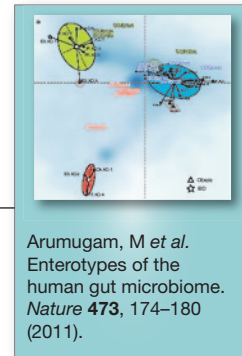
Qin, J. *et al.* A human gut microbial gene catalogue established by metagenomic sequencing. *Nature* 464, 59–65 (2010).



“The first gene catalog of the human microbiome, demonstrating that the [gut microbiome] metagenome contains 150-fold more genes than our own genome.” **Frederik Bäckhed**, University of Gothenburg, Sweden.

“Stirred up discussions but indicates high-level clustering that will be useful to provide further segmentation.” **Willem de Vos**, Wageningen University, The Netherlands.

Ranked 2nd

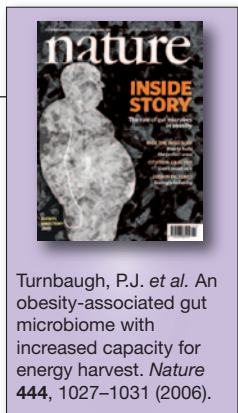


Arumugam, M *et al.* Enterotypes of the human gut microbiome. *Nature* 473, 174–180 (2011).



“Demonstrated in rodents that an obese phenotype could be transferred or reversed by fecal transplant of the microbiota.” **Peter DiStefano**, Second Genome, San Bruno, California, USA.

Ranked 3rd



Turnbaugh, P.J. *et al.* An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature* 444, 1027–1031 (2006).



“The authors showed that the microbiome could actively shape disease susceptibility. All the ingredients of microbiome research (germ-free mice, next-generation sequencing and fecal transplantation) are included in this paper. The study has trail-blazed this field of research and provided a template for investigation of the impact of the microbiome on diseases and health such as cancer, diabetes, behavior and colitis.” **Christian Jobin**, University of North Carolina at Chapel Hill, USA.

Susan Jones, Senior Editor, *Nature Biotechnology*

Ranked
4th

Yatsunenko, T. *et al.* Human gut microbiome viewed across age and geography. *Nature* **486**, 222–227 (2012).



“Demonstrates differences in microbiomes between the US, South America and Africa. Shows that microbiota of many human populations still need to be studied.” **Erwin Zoetendahl**, Wageningen University, The Netherlands.

Ranked
5th

Eckburg, P.B. *et al.* Diversity of the human intestinal microbial flora. *Science* **308**, 1635–1638 (2005).

Huttenhower, C. *et al.* Structure, function and diversity of the healthy human microbiome. *Nature* **486**, 207–214 (2012).



“Its impact stemmed from integration of emerging insights and approaches [in environmental microbiology and bacterial diversity, concepts in ecology] and long-standing interest among clinicians and clinical microbiologists in the possible roles of the human microbiome in health and disease. This near-full-length 16S-rRNA gene-based survey of the healthy human distal gut was the most extensive sequence-based survey of any environment at that time (to my knowledge).” **David Relman**, Stanford University and the Veterans Affairs Palo Alto Health Care System, Palo Alto, California, USA.



“Crucial, as (together with other papers), it laid the foundations for mapping the phylogenetic and genetic makeup of the human microbiome.” **Jeroen Raes**, Flanders Institute for Biotechnology, Belgium.