

## PUBLICATIONS AND COMMUNICATIONS

Main publications from Joël Doré, Scientific Advisor and Co-founder of MaaT Pharma.  
In **bold** are the most relevant publications with regards to MaaT Pharma technologie

1. B. Poutrel and J. Doré. 1985. Virulence of human and bovine isolates of group B streptococci (type Ia and III) in experimental pregnant mouse models. *Infect Immun.* 47:94-97.
2. J. Doré and M.P. Bryant. 1989. Lipid growth requirement and the influence of the lipid supplement on the fatty acid and aldehyde composition of *Syntrophococcus sucromutans*. *Appl. Environ. Microbiol.* 55:927-933.
3. J. Doré and M.P. Bryant. 1990. Metabolism of one-carbon compounds by the ruminal acetogen *Syntrophococcus sucromutans*. *Appl. Environ. Microbiol.* 56:984-989.
4. [\*] J. Doré and D.A. Stahl. 1991. Phylogeny of anaerobic rumen Chytridiomycetes inferred from small subunit ribosomal RNA sequence comparisons. *Can J. Botany* 69:1964-1971.
5. P. Pochart, J. Doré, F. Lémann, I. Goderel and J-C Rambaud. 1992. Interrelations between populations of methanogenic archaea and sulfate reducing bacteria in the human colon. *FEMS Microbiol. Letters.* 98:225-228.
6. [\*] B. Morvan, J. Doré, F. Rieu-Lesme, L. Foucat, G. Fonty and P. Gouet. 1994. Establishment of hydrogen-utilizing bacteria in the rumen of the newborn lamb. *FEMS Microbiol. Letters.* 117:249-256.
7. F. Rieu-Lesme, G. Fonty and J. Doré. 1995. Isolation and characterization of a new hydrogen-utilizing bacterium from the rumen. *FEMS Microbiol. Letters.* 125:77-82.
8. M.A. Bernard-Vailhé, J.M. Besle and J. Doré. 1995. Transformation of <sup>14</sup>C-lignin-labeled cell walls of wheat by *Syntrophococcus sucromutans*, *Eubacterium oxidoreducens*, and *Neocallimastix frontalis*. *Appl. Environ. Microbiol.* 61:379-381.
9. J. Doré, B. Morvan, F. Rieu-Lesme, I. Goderel, P. Gouet and P. Pochart. 1995. Most probable number enumeration of H<sub>2</sub>-utilizing acetogenic bacteria from the digestive tract of animals and man. *FEMS Microbiol. Letters.* 130:7-12.
10. J. Doré, P. Pochart, A. Bernalier, I. Goderel, B. Morvan and J-C Rambaud. 1995. Enumeration of H<sub>2</sub>-utilizing methanogenic archaea, acetogenic and sulfate-reducing bacteria from human feces. *FEMS Microbiol. Ecol.* 17:279-284.
11. F. Rieu-Lesme, C. Dauga, B. Morvan, O.M.M. Bouvet, P.A.D. Grimont and J. Doré. 1996. Acetogenic coccoid spore-forming bacteria isolated from the rumen. *Res. Microbiol.* 147:753-764.
12. A. Bernalier, V. Rochet, M. Leclerc, J. Doré and P. Pochart. 1996. Diversity of H<sub>2</sub>/CO<sub>2</sub>-utilizing acetogenic bacteria from feces of non-methane-producing humans. *Current Microbiol.* 33:94-99.
13. G.J. Faichney, C. Poncet, B. Lassalas, J-P. Jouany, L. Millet, J. Doré and A. Brownlee. 1997. Effect of concentrate in a hay diet on the contribution of anaerobic fungi, protozoa and bacteria to nitrogen in rumen and duodenal digesta in sheep. *Animal Feed Science and Technology.* 64:193-213.
14. [\*] J. Doré, A. Sghir, G. Hannequart-Gramet, G. Corthier and P. Pochart. 1998. Design and evaluation of a 16S rRNA-targeted oligonucleotide probe for specific detection and quantitation of human faecal *Bacteroides* populations. *Syst. Appl. Microbiol.* 21:65-71.
15. J. Doré, G. Gramet, I. Goderel and P. Pochart. 1998. Culture independent characterisation of human fecal flora using rRNA-targeted hybridisation probes. *Genet. Select. Evol.*30(Suppl.1): 287-296.
16. N. Fontaine, J-C. Meslin and J. Doré. 1998. Selective in vitro degradation of the sialylated fraction of germ-free rat mucins by the caecal flora of the rat. *Reprod. Nutr. Dev.* 38:289-296.
17. [\*] C. Vetriani, A-L. Reysenbach and J. Doré. 1998. Recovery and phylogenetic analysis of archaeal rRNA sequences from continental shelf sediments. *FEMS Microbiol Letters.* 161:83-88.
18. F. Rieu-Lesme, C. Dauga, G. Fonty and J. Doré. 1998. Isolation from the rumen of a new acetogenic bacterium phylogenetically closely related to *Clostridium difficile*. *Anaerobe* 4:89-94.
19. A. Bernalier, J. Doré, M. Durand. 1999. Biochemistry of fermentation. In G.R. Gibson and M.B. Roberfroid (eds), *Colonic Microbiota, Nutrition and Health*. Kluwer Academic Press. pp37-53.
20. [\*] A. Suau, R. Bonnet, M. Sutren, J-J. Godon, G.R. Gibson, M.D. Collins and J. Doré. 1999. Direct analysis of genes encoding 16S rRNA from complex communities reveals many novel

- molecular species within the human gut. *Appl Environ Microbiol.* 65:4799-807.
21. [\*] A. Sghir, G. Gramet, A. Suau, V. Rochet, P. Pochart and J. Doré. 2000. Quantification of bacterial groups within human fecal flora by oligonucleotide probe hybridization. *Appl Environ Microbiol.* 66:2263-2266.
  22. [\*] T. Bouchez, D. Patureau, P. Dabert, S. Juretschko, J. Doré, P. Delgenes, R. Moletta and M. Wagner. 2000. Ecological study of a bioaugmentation failure. *Environ. Microbiol.* 2:179-190.
  23. V. Rochet, L. Rigottier-Gois, F. Béguet and J. Doré. 2001. Composition of Human Intestinal Flora Analysed by Fluorescent In Situ Hybridisation using Group-Specific 16S rRNA-Targeted Oligonucleotide Probes. *Genet. Select. and Evol.* (in Press).
  24. [\*] A. Brauman, J. Doré, P. Eggleton, D. Bignell, J.A. Breznak and M.D. Kane. 2001. Molecular phylogenetic profiling of prokaryotic communities in guts of termites with different feeding habits. *FEMS Microbiol. Ecol.* 35 :27-36.
  25. [\*] A. Suau, V. Rochet, A. Sghir, G. Gramet, S. Brewaeys, M. Sutren, L. Rigottier-Gois and J. Doré. 2001. *Fusobacterium prausnitzii* and related species represent a dominant group within the human faecal flora. *Syst. Appl. Microbiol.* 24 :139-145.
  26. [\*] Ph. Marteau, Ph. Pochart, J. Doré, C. Mailliet, A. Bernalier, G. Corthier. 2001. Comparative study of the human cecal and fecal flora. *Appl. Environ. Microbiol.* 67 :4939-4942.
  27. [\*] Blaut M, Collins MD, Welling GW, Doré J, Van Loo J, de Vos WM. 2002. Molecular biological methods for studying the gut microbiota: the EU human gut flora project. *British Journal of Nutrition.* 87 (Suppl.2): S203-S211.
  28. Bonnet R, Suau A, Doré J, Gibson GR, Collins MD. 2002. Differences in rRNA faecal bacterial communities derived from 10- and 25-cycle PCR. *Int J Syst Evol Microbiol* 52: 757-763.
  29. de la Cochetière M-F, Michel C, Cherbut C, Galmiche J-P and Doré J. 2002. Molecular monitoring of bacterial populations during induced colitis in rats reveals changes in dominant faecal microbiota. *Microecol Therapy* 29: 23-35.
  30. [\*] Hur HG, Beger RD, Heinze TM, Lay JO Jr, Freeman JP, Dore J, Rafii F. 2002. Isolation of an anaerobic intestinal bacterium capable of cleaving the C-ring of the isoflavonoid daidzein. *Arch Microbiol* 178: 8-12. Erratum in: *Arch Microbiol* 2002 Jul;178(1):75
  31. Mangin I, Bouhnik Y, Suau A, Rochet V, Raskine L, Crenn P, Dyard F, Rambaud JC and Doré J. 2002. Molecular analysis of the intestinal microbiota composition to evaluate the effect of PEG and lactulose laxatives in humans. *Microb Ecol Health Dis* 14: 54-62.
  32. Mathlouthi N, Lalles J-P, Lepercq P, Juste C, Larbier M. 2002. Xylanase and beta-glucanase supplementation improve conjugated bile acid fraction in intestinal contents and increase villus size of small intestine wall in broiler chickens fed a rye-based diet. *Journal of Animal Science* 80: 2773-2779.
  33. Mattila-Sandholm T, Blaut M, Daly C, Doré J, Gibson G, Goossens H, Knorr D, Lucas J, Lähteenmaki L, A. Mercenier, Saarela M, Shanahan F, and De Vos WM. 2002. Food, GI-tract functionality and human health cluster : PROEUHEALTH. *Microb Ecol Health Dis* 14: 65-74.
  34. Satokari RM, Vaughan EE, Doré J and de Vos WM. 2002. Diversity of Bifidobacterium and Lactobacillus spp. in breast-fed and formula-fed infants as assessed by 16S rDNA sequence differences. *Microb Ecol Health Dis* 14: 97-105.
  35. Stebbings S, Munro K, Simon MA, Tannock G, Highton J, Harmsen H, Welling G, Seksik P, Doré J, Gramet G and Tilsala-Timisjarvi . 2002. Comparison of the faecal microflora of patients with ankylosing spondylitis and controls using molecular methods of analysis. *Rheumatology.* 41:1 395-1401.
  36. Thomas V, Rochet V, Boureau H, Ekstrand C, Bulteau S, Doré J, Collignon A, Bourlioux P. 2002. Molecular characterization and spatial analysis of a simplified gut microbiota displaying colonization resistance against *Clostridium difficile*. *Microb Ecol Health Dis* 14: 203-210.
  37. Edwards CA, Rumney C, Davies M, Parrett AM, Doré J, Martin F, Schmitt J, Stahl B, Norin E, Midtvedt T, Rowland IR, Heavey P, Köhler H, Stocks B, Schrotten H. 2003. A human flora-associated rat model of the breast-fed infant gut. *J Pediatr Gastroenterol Nutr* 37: 168-177.
  38. Leplingard A, Oozeer R, Michelin R, Mogenet A, Seksek I, Diop L, Dore J, Bresson J-L, Corthier G. 2003. Persistence of living *Lactobacillus casei* in human stools after regular ingestion of fermented milk. *Ann Nutr Metab*
  39. [\*] Rigottier-Gois L, Le Bourhis AG, Gramet G, Rochet V and Doré J. 2003. Fluorescent in situ hybridisation combined with flow cytometry and hybridisation of total RNA to analyse the composition of microbial communities in human feces using 16S rRNA probes. *FEMS Microbiology Ecology* 43: 237-245.

40. [\*] Rigottier-Gois L, Rochet V, Garrec N, Suau A and Doré J. 2003. Enumeration of *Bacteroides* species in human feces by fluorescent in situ hybridisation combined with flow cytometry using 16S rRNA probes. *Syst Appl Microbiol* 26: 110-118.
41. [\*] Seksik P, Rigottier-Gois L, Gramet G, Sutren M, Pochart Ph, Marteau Ph, Doré J. 2003. Alterations of the dominant faecal bacterial groups in patients with Crohn's disease of the colon. *Gut* 52: 237-242.
42. Barc M.C, Bourlioux F, Rigottier-Gois L, Charrin-Sarnel C, Janoir C, Bureau H, Doré J and Collignon A. 2004. Effect of Amoxicillin-Clavulanic Acid on Human Fecal Flora in a Gnotobiotic Mouse Model Assessed with Fluorescence Hybridization Using Group-Specific 16S rRNA Probes in Combination with Flow Cytometry. *Antimicrob Agents Chemother* 48: 1365-1368.
43. Cibik R, Marcille F, Corthier G, Doré J. 2004. Bacterial intestinal flora: development, characteristics and influence of the type of feeding. *Arch Pediatr* 11: 573-575.
44. Lay C, Sutren M, Lepercq P, Juste C, Rigottier-Gois L, Lhoste E, Lemée R, Le Ruyet P, Doré J and Andrieux C. 2004. Influence of Camembert consumption on the composition and metabolism of intestinal microbiota: study in human microbiota associated rats. *Br J Nutr* 92: 429-438.
45. [\*] Mangin I, Bonnet R, Seksik P, Rigottier-Gois L, Sutren M, Bouhnik Y, Neut C, Collins MD, Colombel JF, Marteau P, and Dore J. 2004. Molecular inventory of faecal microflora in patients with Crohn's disease. *FEMS Microbiology Ecology* 50: 25-36.
46. [\*] Marteau Ph, Lepage P, Mangin I, et al. 2004. Review article: gut flora and inflammatory bowel disease. *Aliment Pharm Therap.* 20:18-23. [cited 67]
47. Rochet V, Rigottier-Gois L, Rabot S, and Doré J. 2004. Validation of fluorescent in situ hybridization combined with flow cytometry for assessing interindividual variation in the composition of human fecal microflora during long-term storage of samples. *Journal of Microbiological Methods.* 59: 263-270.
48. Zunft HJ, Hanish C, Mueller S, Koebnick C, Blaut M, Dore J. 2004. Symbiotic containing *Bifidobacterium animalis* and inulin increases stool frequency in elderly healthy people. *Asia Pac J Clin Nutr* 13(Suppl): S112.
49. [\*] Clavel T, Henderson G, Alpert CA, Philippe C, Rigottier-Gois L, Doré J and Blaut M. 2005. Intestinal bacterial communities that produce the active estrogen-like compounds enterodiol and enterolactone in humans. *Appl Environ Microbiol* 71:6077-6085.
50. Clavel T, Fallani M, Lepage P, Levenez F, Mathey J, Rochet V, Sérézat M, Sutren M, Henderson G, Bennetau-Pelissero C, Tondou F, Blaut M, Doré J, Coxam. V. 2005. Isoflavones and functional foods alter the dominant intestinal microbiota in postmenopausal women. *J Nutr* 135:2786-2792.
51. Dauga C, Doré J, Sghir A. 2005. Identification des bactéries non ou difficilement cultivables en clinique et dans l'environnement : une diversité insoupçonnée de monde microbien. *Medecine Science* 21:1-7
52. [\*] De la Cochetière MF, Durand T, Lepage P, Boureille A, Galmiche JP, Doré J. 2005. Resilience of the dominant human fecal microbiota upon short-course antibiotic challenge. *J Clin Microbiol* 43:5588-5592. [cited 75]
53. Humblot C, Bruneau A, Sutren M, Lhoste E.F, Doré J, Andrieux C, Rabot S. 2005. Brussels sprouts, inulin and fermented milk alter the faecal microbiota of human microbiota-associated rats as shown by PCR-TTGE using universal, *Lactobacillus* and *Bifidobacterium* 16S rRNA gene primers. *Br J Nutr* 93:677-684.
54. [\*] Lay C, Rigottier-Gois L, Holmstrom K, Rajilic M, Vaughan E, De Vos WM, Collins M-D, Thiel R, Namsollock P, Blaut M, Doré J. 2005. Colonic microbiota signatures across five northern european countries. *Appl Environ Microbiol* 71:4153-4155.
55. [\*] Lay C, Sutren M, Rochet V, Saunier K, Dore J, Rigottier-Gois L. 2005. Design and validation of 16S rRNA probes to enumerate members of the *Clostridium leptum* subgroup in human faecal microbiota. *Environ Microbiol* 7:933-946. [cited 74]
56. Le Bourhis AG, Saunier K, Doré J, Carlier JP, Chamba JF, Popoff MR, Tholozan JL. 2005. Development and validation of PCR primers to assess the diversity of *Clostridium* spp. in cheese by temporal temperature gradient gel electrophoresis. *Appl Environ Microbiol* 71:29-38.
57. [\*] Lepage P, Seksik P, Sutren M, de la Cochetiere MF, Jian R, Marteau P, Dore J. 2005. Biodiversity of the mucosa-associated microbiota is stable along the distal digestive tract in healthy individuals and patients with IBD. *Inflamm Bowel Dis* 11:473-480.
58. Saunier K, Rougé C, Lay C, Rigottier-Gois L, Doré J. 2005. Enumeration of bacteria from the *Clostridium leptum* subgroup in human faecal microbiota using Clep1156 16S rRNA probe in combination with helper and competitor oligonucleotides. *Syst Appl Microbiol* 28:454-64.

59. [\*] Seksik P, Lepage P, de la Cochetiere MF, Boureille A, Sutren M, Galmiche JP, Dore J, Marteau P. 2005. Search for localized dysbiosis in Crohn's disease ulcerations by temporal temperature gradient gel electrophoresis of 16S rRNA. *J Clin Microbiol* 43:4654-8.
60. [\*] Clavel T, Borrmann D, Braune A, Doré J, Blaut M. 2006. Occurrence and activity of human intestinal bacteria involved in the conversion of dietary lignans. *Anaerobe* 12:140-147.
61. [\*] Clavel T, Henderson G, Engst W, Doré J, Blaut M. 2006. Phylogeny of human intestinal bacteria that activate the dietary lignan secoisolariciresinol diglucoside. *FEMS Microbiol Ecol* 55:471-478.
62. Fallani L, Rigottier-Gois L, Aguilera M, Bridonneau C, Collignon A, Edwards CA, Corthier G, Doré J. 2006. *Clostridium difficile* and *Clostridium perfringens* species detected in infant faecal microbiota using 16S rRNA targeted probes. *J Microbiol Methods* 67:150-161.
63. [\*] Manichanh C, Rigottier-Gois L, Bonnaud E, Gloux K, Pelletier E, Frangeul L, Nalin R, Jarrin C, Chardon P, Marteau P, Roca J, Doré J. 2006. Reduced diversity of faecal microbiota in Crohn's disease revealed by a metagenomic approach. *Gut* 55:205-211.
64. [\*] Mueller S, Saunier K, Hanisch C, Norin E, Alm L, Midtvedt T, Cresci A, Silvi S, Orpianesi C, Verdenelli MC, Clavel T, Koebnick C, Zunft HJ, Doré J, Blaut M. 2006. Differences in fecal microbiota in different European study populations in relation to age, gender, and country: a cross-sectional study. *Appl Environ Microbiol* 72:1027-33.
65. Oozeer R, Leplingard A, Mater DD, Mogenet A, Michelin R, Seksek I, Marteau P, Dore J, Bresson JL, Corthier G. 2006. Survival of *Lactobacillus casei* in the human digestive tract after consumption of fermented milk. *Appl Environ Microbiol* 72:5615-5617.
66. Rochet V, Rigottier-Gois L, Sutren M, Kremetscki MN, Andrieux C, Furet JP, Taillez P, Levenez F, Mogenet A, Bresson JL, Meance S, Cayuela C, Leplingard A, Doré J. 2006. Effects of orally administered *Lactobacillus casei* DN-114 001 on the composition or activities of the dominant faecal microbiota in healthy humans. *Br J Nutr* 95:421-429.
67. Rochet V, Rigottier-Gois L, Ledaire A, Andrieux C, Sutren M, Rabot S, Mogenet A, Bresson JL, Cools S, Picard C, Goupil-Feuillerat N, Doré J. Survival of *Bifidobacterium animalis* DN-173 010 in the faecal microbiota after administration in lyophilised form or in fermented product - a randomised study in healthy adults. *Accepté J Mol Micobiol Biothech* le 23/10/2006
68. [\*] Sokol H, Seksik P, Rigottier-Gois L, Lay C, Lepage P, Podglajen I, Marteau P, Doré J. 2006. Specificities of the fecal microbiota in inflammatory bowel disease. *Inflamm Bowel Dis* 12:106-111.
69. [\*] Sokol H, Lepage P, Seksik P, Dore J, Marteau P. 2006. Temperature gradient gel electrophoresis of fecal 16S rRNA reveals active *Escherichia coli* in the microbiota of patients with ulcerative colitis. *J Clin Microbiol* 44:3172-3177.
70. Sokol H, Lepage P, Seksik Ph, Dore J, Marteau Ph. 2006. Molecular comparison of dominant microbiota associated with injured versus healthy mucosa in ulcerative colitis. *Gut* in press
71. [\*] Seksik Ph, Sokol H, Lepage P, 2006. Review article: the role of bacteria in onset and perpetuation of inflammatory bowel disease. *Aliment Pharm Therap.* 24:11-18. [cited 77]
72. Vasquez N, Mangin I, Lepage P, Seksik P, Duong JP, Blum S, Schiffrin E, Suau A, Allez M, Vernier G, Tréton X, Doré J, Marteau P, Pochart P. 2006. Patchy distribution of mucosal lesions in ileal Crohn's disease is not linked to differences in the dominant mucosa-associated bacteria: A study using fluorescence *in situ* hybridization and temporal temperature gradient gel electrophoresis. *Inflamm Bowel Dis*. Dec 19.
73. Spehlmann M, Begun A, Burghardt J, Lepage P, Raedler A, Schreiber S. 2007. Epidemiology of inflammatory bowel disease in a german twin cohort: results of a nationwide study. *Inflam Bowel Dis*, In press.
74. Alvaro E, Andrieux C, Rochet V, Rigottier-Gois L, Lepercq P, Sutren M, Galan P, Duval Y, Juste C, Doré J. 2007. Composition and metabolism of the intestinal microbiota in consumers and non-consumers of yogurt. *Br J Nutr* 97:126-133.
75. Clavel T, Lippman R, Gavini F, Dore J, Blaut M. 2007. *Clostridium saccharogumia* sp. nov. and *Lactonifactor longoviformis* gen. nov., sp. nov., two novel human faecal bacteria involved in the conversion of the dietary phytoestrogen secoisolariciresinol diglucoside. *Syst Appl Microbiol* 30:16-26.
76. Gill CI, Heavey P, McConville E, Bradbury I, Fassler C, Mueller S, Cresci A, Doré J, Norin E, Rowland I. 2007. Effect of fecal water on an in vitro model of colonic mucosal barrier function. *Nutr Cancer* 57:59-65.
77. Gloux K, Leclerc M, Iliozier H, L'haridon R, Manichanh C, Corthier G, Nalin R, Blottière HM, Doré J. 2007. Development of high-throughput phenotyping of metagenomic clones from the human gut microbiome for modulation of eukaryotic cell growth. *Appl Envir Microbiol* 73:3734-3737.

78. Leclerc M, Juste C, Blottière H, Doré J. 2007. Le microbiote : un monde polymorphe aux fonctions multiples. Microbiote intestinal : un univers méconnu. *Cah Nutr Diét* 42, Hors-série 2.
79. Lay C, Dore J, Rigottier-Gois L. 2007. Separation of bacteria of the *Clostridium leptum* subgroup from the human colonic microbiota by fluorescence activated cell sorting or group-specific PCR using 16S rRNA gene oligonucleotides. *FEMS Microbiol Ecol* 60:513-520.
80. [\*] Perez PF, Dore J, Leclerc M, Levenez F, Benyacoub J, Serrant P, Segura-Roggero I, Schiffrin EJ, Donnet-Hughes A. 2007. Bacterial imprinting of the neonatal immune system: lessons from maternal cells. *Pediatrics* 119:724-32.
81. Sokol H, Lepage P, Seksik Ph, Doré J, Marteau Ph. 2007. Molecular comparison of dominant microbiota associated with injured versus healthy mucosa in ulcerative colitis. *Gut* 56:152-154.
82. Barc MC, Charrin-Sarnel C, Rochet V, Bourlioux F, Sandré C, Boureau H, Doré J, Collignon A. Molecular analysis of the digestive microbiota in a gnotobiotic mouse model during antibiotic treatment: Influence of *Saccharomyces boulardii*. *Anaerobe*, 2008, 14:229-33 (FI 1.352)
83. Firmesse O, Alvaro E, Mogenet A, Bresson JL, Lemée R, Le Ruyet P, Bonhomme C, Lambert D, Andrieux C, Doré J, Corthier G, Furet JP, Rigottier-Gois L. Fate and effects of Camembert cheese micro-organisms in the human colonic microbiota of healthy volunteers after regular Camembert consumption. *Int J Food Microbiol*, 2008, 125:176-81
84. [\*] Guigoz Y, Dore J, Schiffrin E. The inflammatory status of old age can be nurtured from the intestinal environment. *Current Opinion in Clinical Nutrition and Metabolic Care*, 2008, 11:13-20 (FI 2.930) [Review]
85. Kuehbach T, Rehman A, Lepage P, Hellmig S, Fölsch UR, Schreiber S, Ott SJ. Intestinal TM7 bacterial phylogenies in active inflammatory bowel disease. *J Med Microbiol* 2008 Dec;57(Pt 12):1569-76. PubMed PMID: 19018031
86. Lepage P, Colombet J, Marteau P, Sime-Ngando T, Doré J, Leclerc M. Dysbiosis in inflammatory bowel disease : a role for bacteriophages. *Gut*, 2008, 57:424-5 (FI 10.015)
87. Manichanh C, Varela E, Martinez C, Antolin M, Llopis M, Doré J, Giralt J, Guarner F, Malagelada J-R. 2008. The gut microbiota predispose to the pathophysiology of acute post-radiotherapy diarrhea. *Am J Gastroenterol*. 103:1754-61.
88. Manichanh C, Chapple CE, Frangeul L, Gloux K, Guigo R, Dore J. 2008. Estimating the biodiversity of a metagenomic library by random. Sequence reads compared with 16S rDNA sequences. *Nucleic Acids Res* 36:5180-8.
89. Rochet V, Rigottier-Gois L, Ledaire A, Andrieux C, Sutren M, Rabot S, Mogenet A, Bresson JL, Cools S, Picard C, Goupil-Feuillerat N, Doré J. Survival of *Bifidobacterium animalis* DN-173010 in the faecal microbiota after administration in lyophilised form or in fermented product - A randomised study in healthy adults. *Journal of Molecular Microbiology and Biotechnology*, 2008, 14:128-36 (FI 2.588)
90. Rochet V, Rigottier-Gois L, Levenez F, Cadiou J, Marteau P, Bresson JL, Goupil-Feuillerat N, Doré J. Modulation of *Lactobacillus casei* in ileal and fecal samples from healthy volunteers after consumption of a fermented milk containing *Lactobacillus casei* DN-114 001Rif. *Can J Microbiol*, 2008 54:660-7
91. Spehlmann ME, Begun AZ, Burghardt J, Lepage P, Raedler A, Schreiber S. Epidemiology of inflammatory bowel disease in a German twin cohort: Results of a nationwide study. *Inflammatory Bowel Diseases*, 2008, 14:968-76 (FI 4.705)
92. [\*] Sokol H, Pigneur B, Watterlot L, Lakhdari O, Bermudez-Humaran LG, Gratadoux J-J, Blugeon S, Bridonneau C, Furet J-P, Corthier G, Grangette C, Vasquez N, Pochart Ph, Trugnan G, Thomas G, Blottière HM, Doré J, Marteau P, Seksik P & Langella P. *Faecalibacterium prausnitzii* is an anti-inflammatory commensal bacterium identified by gut microbiota analysis of Crohn's disease patients. *Proceedings of the National Academy of Sciences of the United States of America*, 2008, 105:16731-6 (FI 9.598)
93. [\*] Furet JP, Firmesse O, Gourmelon M, Bridonneau C, Tap J, Mondot S, Doré J, Corthier G. Comparative assessment of human and farm animal faecal microbiota using real-time quantitative PCR. *FEMS Microbiol Ecol* 2009, 68, 351-362
94. [\*] Mariat D, Firmesse O, Levenez F, Guimarães V, Sokol H, Doré J, Corthier G, Furet JP. (2009) The Firmicutes/Bacteroidetes ratio of the human microbiota changes with age. *BMC Microbiol* 9:123 doi:10.1186/1471-2180-9-123
95. [\*] Sokol H, Seksik P, Furet JP, Firmesse O, Nion-larmurier I, Beaugerie L, Cosnes J, Corthier G, Marteau P, Doré J. (2009) Low counts of *Faecalibacterium prausnitzii* in Colitis Microbiota. *Inflamm Bowel Dis* 15, 1183-1189

96. [\*] Tap J, Mondot S, Levenez F, Pelletier E, Caron C, Furet JP, Ugarte E, Muñoz-Tamayo R, Le Paslier D, Nalin R, Dore J, Leclerc M. (2009) Towards the human intestinal microbiota phylogenetic core. *Environ Microbiol* 11, 2574–2584
97. Derrien M, El Aidy S, Rajilic-Stojanovic M, Molenaar D, Levenez F, Zoetendal EG, Dore J, Kleerebezem M. 2009. Spatial And Temporal Analysis Of Intestinal Microbiota In Conventionalized Germ Free Mice In Correlation With The Host Responses, Using A High-Throughput Phylogenetic Microarray. *Microbial Ecol* 57:566-567.
98. Oozeer R, Rescigno M, Ross RP, Knol J, Blaut M, Khlebnikov A, Dore J. 2010. Gut health: predictive biomarkers for preventive medicine and development of functional foods. *Brit J Nutr* 103:1539-1544.
99. Corthier G, Dore J. 2010. A new era in gut research concerning interactions between microbiota and human health. *Gastroenterol Clin Biol* 34 Suppl.1:1-6. [Review]
100. Dore J, Corthier G. 2010. The human intestinal microbiota. *Gastroenterol Clin Biol* 34 Suppl.1:7-16. [Review]
101. Donnet-Hughes A, Perez PF, Doré J, Leclerc M, Levenez F, Benyacoub J, Serrant P, Segura-Roggero I, Schiffrin EJ. Potential role of the intestinal microbiota of the mother in neonatal immune education. *Proc Nutr Soc* 2010 69:407-15
102. Ehrlich SD, MetaHIT consortium. Metagenomics of the intestinal microbiota: potential applications. *Gastroenterol Clin Biol* 2010 34 Suppl 1:S23-8. [Review]
103. [\*] Fallani M, Young D, Scott J, Norin E, Amarri S, Rüdiger A, Aguilera M, Khanna S, Gil A, Edwards CA, and Doré J, and other members of the INFABIO team. 2010. The intestinal microbiota of 6-week old infants across Europe: geographic influence beyond delivery mode, breast-feeding and antibiotics. *J Pediatr Gastroenterol Nutr.* Jul;51(1):77-84. doi: 10.1097/MPG.0b013e3181d1b11e.
104. [\*] Furet JP, Kong LC, Tap J, Poitou C, Basdevant A, Bouillot JL, Mariat D, Corthier G, Doré J, Henegar C, Rizkalla S, Clément K. Differential adaptation of human gut microbiota to bariatric surgery–induced weight loss ; Links with metabolic and low-grade inflammation markers. *Diabetes* 2010, 59:3049-3057
105. [\*] Kang S, Denman S, Morrison M, Yu Z, Dore J, Leclerc M and Mcsweeney C. 2010. Dysbiosis of faecal microbiota in Crohn's disease patients as revealed by a custom phylogenetic microarray. *Inflammatory Bowel Disease*, 16, 2034-2042.
106. Lakhdari O, Cultrone A, Tap J, Gloux K, Bernard F, Ehrlich SD, Lefèvre F, Doré J, Blottière HM (2010) Functional metagenomics: a high throughput screening method to decipher microbiota-driven NF-κB modulation in the human gut. *PLoS One* 2010 Sep 30;5(9). pii: e13092. Erratum in: *PLoS One* 2010;5(10). doi:10.1371/journal.pone.0013092
107. Madi A, Lakhdari O, Blottière HM, Guyard M, Le Roux K, Svinareff P, Doré J, Orange N, Feuilleley MGJ and Connil N (2010) The clinical *Pseudomonas fluorescens* MFN1032 strain exerts cytotoxic effect on epithelial intestinal cells and induces Interleukin-8 via the AP-1 signaling pathway. *BMC Microbiol*, 10:215
108. Muñoz-Tamayo R, Laroche B, Walter E, Doré J, Leclerc M. Mathematical modelling of carbohydrate degradation by human colonic microbiota. *J Theor Biol* 2010 266:189-201. Epub 2010 Jun 16
109. [\*] Qin J, Ruiqiang L, Raes J, Arumugam M, Solvsten K, Burgdorf, Manichanh C, Nielsen T, Pons N, Levenez F, Yamada T, Mende D, Li J, Xu J, Li S, Li D, Cao J, Wang B, Liang H, Zheng H, Xie Y, Tap J, Lepage P, Bertalan M, Batto JM, Hansen T, Le Paslier D, Linneberg A, Nielsen HB, Pelletier E, Renault P, Sicheritz-Ponten T, Turner K, Zhu H, Yu C, Li S, Jian M, Zhou Y, Zhang X, Li S, Yang H, Wang J, Brunak S, Doré J, Guarner F, Kristiansen K, Pedersen O, Parkhill J, Weissenbach J, MetaHIT Consortium, Bork P, Ehrlich SD and Wang J. (2010) A human gut microbial gene catalog established by deep metagenomic sequencing. *Nature* 464, 59-65
110. [\*] Sun L, Yu Z, Ye X, Zou S, Li H, Yu D, Wu H, Chen Y, Dore J, Clément K, Hu FB, Lin X. A marker of endotoxemia is associated with obesity and related metabolic disorders in apparently healthy Chinese. *Diabetes Care*. 2010 33:1925-32. Epub 2010 Jun 8
111. [\*] Tasse L, Bercovici J, Pizzut-Serin S, Robe P, Tap J, Klopp C, Cantarel BL, Coutinho PM, Henrissat B, Leclerc M, Doré J, Monsan P, Remaud-Simeon M, Potocki-Veronese G. Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. *Genome Res* 2010 20:1605-12. Epub 2010 Sep 14
112. Mihajlovski A, Dore J, Levenez F, Alric M, Brugere JF. 2010. Molecular evaluation of the human gut methanogenic archaeal microbiota reveals an age-associated increase of the diversity. *Environ Microbiol Reports* 2:272-280.

113. [\*] Mondot S, Kang S, Furet, JP, Aguirre de Carcer D, McSweeney C, Morrison M, Marteau P, Dore J and Leclerc M. Highlighting new phylogenetic specificities of Crohn's disease microbiota. *Inflamm Bowel Dis* 2010, 17:185-192.
114. [\*] Amar J, Serino M, Lange C, Chabo C, Iacovoni J, Mondot S, Lepage P, Klopp C, Mariette J, Bouchez O, Perez L, Courtney M, Marre M, Klopp P, Lantieri O, Doré J, Charles M, Balkau B, Burcelin R; D.E.S.I.R. Study Group. Involvement of tissue bacteria in the onset of diabetes in humans: evidence for a concept. *Diabetologia*. 2011 Dec;54(12):3055-61. doi: 10.1007/s00125-011-2329-8.
115. Kong I, Wuillemin P, Hajduch F, Bastard J, Fellahi S, Basdevant A, Zucker J-D, Dore J, Rizkalla S, Clement K. Insulinemia and inflammatory markers might predict different responses of obese subjects under the same hypocaloric diet intervention. *Annals Nutr Metabol*. 58 Suppl.3:75-76.
116. Dore J. 2011. Normal Intestinal Microbiota?. *Bull Acad Nat Med* 195 :1291-1293. [Review]
117. Gloux K, Berteau O, El Oumami H, Béguet F, Leclerc M, and Dore J. (2010) A metagenomic  $\beta$ -glucuronidase uncovers a core adaptive function of the human intestinal microbiome. *Proc Natl Acad Sci U S A* [www.pnas.org/cgi/doi/10.1073/pnas.1000066107](http://www.pnas.org/cgi/doi/10.1073/pnas.1000066107)
118. [\*] van Duynhoven J, Vaughan EE, Jacobs DM, Kemperman RA, van Velzen EJJ, Gross G, Roger LC, Possemiers S, Smilde AK, Doré J, Westerhuis JA, Van de Wiele T. Metabolic fate of polyphenols in the human superorganism. *Proc Natl Acad Sci U S A* 2011 108 Suppl 1:4531-8. Epub 2010 Jun 25. [Review]
119. [\*] Arumugam M, Raes J, Pelletier E, Le Paslier D, Yamada T, Mende DR, Fernandes GR, Tap J, Bruls T, Batto JM, Bertalan M, Borruel N, Casellas F, Fernandez L, Gautier L, Hansen T, Hattori M, Hayashi T, Kleerebezem M, Kurokawa K, Leclerc M, Levenez F, Manichanh C, Nielsen HB, Nielsen T, Pons N, Poulain J, Qin J, Sicheritz-Ponten T, Tims S, Torrents D, Ugarte E, Zoetendal EG, Wang J, Guarner F, Pedersen O, de Vos WM, Brunak S, Doré J; MetaHIT Consortium, Antolín M, Artiguenave F, Blottiere HM, Almeida M, Brechot C, Cara C, Chervaux C, Cultrone A, Delorme C, Denariac G, Dervyn R, Foerstner KU, Friss C, van de Guchte M, Guedon E, Haimet F, Huber W, van Hylckama-Vlieg J, Jamet A, Juste C, Kaci G, Knol J, Lakhdari O, Layec S, Le Roux K, Maguin E, Mérieux A, Melo Minardi R, M'rini C, Muller J, Oozeer R, Parkhill J, Renault P, Rescigno M, Sanchez N, Sunagawa S, Torrejon A, Turner K, Vandemeulebrouck G, Varela E, Winogradsky Y, Zeller G, Weissenbach J, Ehrlich SD, Bork P. **Enterotypes of the human gut microbiome. *Nature* 2011 473:174–180**
120. Dumetz F, Jouvion G, Khun H, Glomski IJ, Corre JP, Rougeaux C, Tang WJ, Mock M, Huerre M, Goossens PL. Noninvasive imaging technologies reveal edema toxin as a key virulence factor in anthrax. *Am J Pathol*. 2011 Jun;178(6):2523-35.
121. Fallani M, Amari S, Uusijarvi A, Adam R, Khanna S, Aguilera M, Gil A, Vieites JM, Norin E, Young D, Scott JA, Doré J, Edwards CA; INFABIO team. Determinants of the human infant intestinal microbiota after the introduction of first complementary foods in infant samples from five European centres. *Microbiology* 2011 157:1385-92.
122. Kaci G, Lakhdari O, Doré J, Ehrlich SD, Renault P, Blottière HM, Delorme C. Inhibition of the NF- $\kappa$ B pathway in human intestinal epithelial cells by commensal *Streptococcus salivarius*. *Appl Environ Microbiol* 2011 77:4681-4684
123. Lakhdari O, Tap J, Béguet-Crespel F, Le Roux K, deWouters T, Cultrone A, Nepelska M, Lefèvre F, Doré J, Blottière HM. Identification of NF- $\kappa$ B modulation capabilities within human intestinal commensal bacteria. *Journal of Biomedicine and Biotechnology* 2011, Article ID 282356, doi:10.1155/2011/282356
124. [\*] Lepage P, Häsler R,\* Spehlmann ME, Rehman A, Zvirbliene A, Begun A, Ott S, Kupcinskas L, Doré J, Raedler A, Schreiber S. Twin study indicates loss of interaction between microbiota and mucosa of patients with ulcerative colitis. *Gastroenterology* 2011 141:227-236
125. Muñoz-Tamayo R, Laroche B, Walter E, Doré J, Duncan SH, Flint HJ, Leclerc M. Kinetic modelling of lactate utilization and butyrate production by key human colonic bacterial species. *FEMS Microbiol Ecol* 2011 76:615-624
126. Rooijers K, Kolmeder C, Juste C, Doré J, de Been M, Boeren S, Galan P, Beauvallet C, de Vos WM, Schaap PJ. An iterative workflow for mining the human intestinal metaproteome. *BMC Genomics*. 2011 Jan 5;12:6. doi: 10.1186/1471-2164-12-6.
127. Thompson-Chagoyan OC, Fallani M, Maldonado J, Vieites JM, Khanna S, Edwards C, Doré J, Gil A. Faecal Microbiota and short-chain fatty acid levels in faeces from infants with cow's milk protein allergy. *Int Arch Allergy Immunol* 2011 156:325-332
128. Rousseau C, Levenez F, Fouqueray C, Doré J, Collignon A, Lepage P. *Clostridium difficile* colonization in early infancy is accompanied by changes in intestinal microbiota composition. *Journal of Clinical Microbiology* 2011, 49:858–865

129. Aron-Wisnewsky J, Doré J, Clement K. The importance of the gut microbiota after bariatric surgery. *Nat Rev Gastroenterol Hepatol*. 2012 Oct;9(10):590-8. doi: 10.1038/nrgastro.2012.161. Epub 2012 Aug 28. [Review]
130. Candela T, Dumetz F, Tosi-Couture E, Mock M, Goossens PL, Fouet A. Cell-wall preparation containing poly- $\gamma$ -D-glutamate covalently linked to peptidoglycan, a straightforward extractable molecule, protects mice against experimental anthrax infection. *Vaccine*. 2012 Dec 17;31(1):171-5.
131. Cardona S, Eck A, Cassellas M, Gallart M, Alastrue C, Dore J, Azpiroz F, Roca J, Guarner F, Manichanh C. Storage conditions of intestinal microbiota matter in metagenomic analysis. *BMC Microbiol*. 2012 Jul 30;12:158. doi: 10.1186/1471-2180-12-158.
132. El Aidy S, Merrifield CA, Derrien M, van Baarlen P, Hooiveld G, Levenez F, Doré J, Dekker J, Holmes E, Claus SP, Reijngoud DJ, Kleerebezem M. The gut microbiota elicits a profound metabolic reorientation in the mouse jejunal mucosa during conventionalisation. *Gut*. 2012 Jun 21. Gut doi:10.1136/gutjnl-2011-301955
133. El Aidy S, van Baarlen P, Derrien M, Lindenbergh-Kortleve DJ, Hooiveld G, Levenez F, Doré J, Dekker J, Samsom JN, Nieuwenhuis EE, Kleerebezem M. Temporal and spatial interplay of microbiota and intestinal mucosa drive establishment of immune homeostasis in conventionalized mice. *Mucosal Immunol*. 2012 Sep;5(5):567-79. doi: 10.1038/mi.2012.32. Epub 2012 May
134. Mondot S, Barreau F, Al Nabhani Z, Dussaillant M, Le Roux K, Doré J, Leclerc M, Hugot JP, Lepage P. Altered gut microbiota composition in immune-impaired Nod2(-/-) mice. *Gut*. 2012 Apr;61(4):634-5. doi: 10.1136/gutjnl-2011-300478. Epub 2011 Aug 25.
135. Nepelska M, Cultrone A, Béguet-Crespel F, Le Roux K, Doré J, Arulampalam V, Blottière HM. Butyrate produced by commensal bacteria potentiates phorbol esters induced AP-1 response in human intestinal epithelial cells. *PLoS One*. 2012 ;7(12):e52869. doi: 10.1371/journal.pone.0052869. Epub 2012 Dec 27.
136. Santos Rocha C, Lakhdari O, Blottière HM, Blugeon S, Sokol H, Bermúdez-Humarán LG, Azevedo V, Miyoshi A, Doré J, Langella P, Maguin E, van de Guchte M. Anti-inflammatory properties of dairy lactobacilli. *Inflamm Bowel Dis*. 2012 Apr;18(4):657-66. doi: 10.1002/ibd.21834. Epub 2011 Aug 11.
137. de Wouters T, Doré J, Lepage P. Does our food (environment) change our gut microbiome ('in-vi-environment'): a potential role for inflammatory bowel disease? *Dig Dis*. 2012;30 Suppl 3:33-9. doi: 10.1159/000342595. Epub 2013 Jan 3. [Review]
- Patent # 12306285.3 Prognostic of diet impact on obesity-related co-morbidities ; INRA/UPMC ; EP 17/10/2012
138. Aziz Q, Doré J, Emmanuel A, Guarner F, Quigley EM. Gut microbiota and gastrointestinal health: current concepts and future directions. *Neurogastroenterol Motil*. 2013 Jan; 25(1):4-15. doi: 10.1111/nmo.12046. [Review]
139. Cotillard A, Kennedy SP, Kong LC, Prifti E, Pons N, Le Chatelier E, Almeida M, Quinquis B, Levenez F, Galleron N, Gougis S, Rizkalla S, Batto JM, Renault P, ANR MicroObes consortium, Doré J, Zucker JD, Clément K, Ehrlich SD. Dietary intervention impact on gut microbial richness. *Nature*. 2013, 500:585-588. doi:10.1038/nature12480
140. Blottière HM, deVos WM, Ehrlich SD, Doré J. Human intestinal metagenomics – state of the art and future. *Curr Opin Microbiol* 2013, in press. [Review]
141. Brown J, de Vos WM, DiStefano PS, Doré J, Huttenhower C, Knight R, Lawley TD, Raes J, Turnbaugh P. Translating the human microbiome. *Nat Biotechnol*. 2013 Apr; 31(4):304-8. doi: 10.1038/nbt.2543. [Review]
142. Cultrone A, de Wouters T, Lakhdari O, Kelly D, Mulder I, Logan E, Lapaque N, Doré J, Blottière HM. The NF- $\kappa$ B binding site located in the proximal region of the TSLP promoter is critical for TSLP modulation in human intestinal epithelial cells. *Eur J Immunol*. 2013 Apr;43(4):1053-62. doi: 10.1002/eji.201142340. Epub 2013 Feb 11.
143. Doré J, Simrén M, Buttle L, Guarner F. Hot topics in gut microbiota. *United European Gastroenterology Journal*. 2013 doi: 10.1177/2050640613502477 [Review]
144. El Aidy S, Derrien M, Merrifield CA, Levenez F, Doré J, Boekschoten MV, Dekker J, Holmes E, Zoetendal EG, van Baarlen P, Claus SP, Kleerebezem M. Gut bacteria-host metabolic interplay during conventionalisation of the mouse germfree colon. *ISME J*. 2013 Apr;7(4):743-55. doi: 10.1038/ismej.2012.142. Epub 2012 Nov 22.
145. Korecka A, de Wouters T, Cultrone A, Lapaque N, Pettersson S, Doré J, Blottière HM, Arulampalam V. ANGPTL4 expression induced by butyrate and rosiglitazone in human intestinal epithelial cells utilize independent pathways. *Am J Physiol Gastrointest Liver Physiol*. 2013 Mar 21. [Epub ahead of print]



146. [\*] Le Chatelier E, Nielsen T, Qin J, Prifti E, Hildebrand F, Falony G, Almeida M, Arumugam M, Batto JM, Kennedy S, Leonard P, Li J, Burgdorf K, Grarup N, Jørgensen T, Brandslund I, Nielsen HB, Juncker AS, Bertalan M, Levenez F, Pons N, Rasmussen S, Sunagawa S, Tap J, Tims S, Zoetendal EG, Brunak S, Clément K, Doré J, Kleerebezem M, Kristiansen K, Renault P, Sicheritz-Ponten T, de Vos WM, Zucker JD, Raes J, Hansen T, MetaHIT consortium, Bork P, Wang J, Ehrlich SD, Pedersen O. Richness of human gut microbiome correlates with metabolic markers. *Nature*. 2013, 500:541-546 doi:10.1038/nature12506
147. [\*] Lepage P, Leclerc M, Joossens M, Mondot S, Blottière HM, Raes J, Ehrlich SD, Doré J. A metagenomic insight into our gut's microbiome. *Gut*. 2013 Jan;62(1):146-58. doi: 10.1136/gutjnl-2011-301805. Epub 2012 Apr 23. [Review]
148. de Wouters T, Lapaque N, Maguin E, Doré J, Blottière HM. Functional Metagenomics of Bacterial-Cell crosstalk. *Encyclopedia of Metagenomics*, SpringerReference, in press, 2013. [Review]
149. Kong L-C, Tap J, Aron-Wisniewsky J, Pelloux V, Basdevant A, Bouillot J-L, Zucker J-D, Dore J and Clement K. 2013. Gut microbiota after gastric bypass in human obesity: increased richness and associations of bacterial genera with adipose tissue genes. *Am J Clin Nutr* 98:16-24 DOI: 10.3945/ajcn.113.058743
150. Kong LC, Wuillemin PH, Bastard JP, Sokolovska N, Gougis S, Fellahi S, Darakhshan F, Bonnefont-Rousselot D, Bittar R, Dore J, Zucker JD, Clement K, Rizkalla S. 2013. Insulin resistance and inflammation predict kinetic body weight changes in response to dietary weight loss and maintenance in overweight and obese subjects by using a Bayesian network approach. *Am J Clin Nutr* 98:1385-1394 DOI: 10.3945/ajcn.113.058099
151. [\*] **Viaud S, Saccheri F, Mignot G, Yamazaki T, Daillere R, Hannani D, Enot DP, Pfirschke C, Engblom C, Pittet MJ, Schlitzer A, Ginhoux F, Apetoh L, Chachaty E, Woerther PL, Eberl G, Berard M, Ecobichon C, Clermont D, Bizet C, Gaboriau-Routhiau V, Cerf-Bensussan N, Opolon P, Yessaad N, Vivier E, Ryffel B, Elson CO, Dore J, Kroemer G, Lepage P, Boneca IG, Ghiringhelli F, Zitvogel L. 2013. The Intestinal Microbiota Modulates the Anticancer Immune Effects of Cyclophosphamide. *Science* 342:971-976. DOI: 10.1126/science.1240537**
152. Kaci G, Goudercourt D, Dennin V, Pot B, Doré J, Ehrlich SD, Renault P, Blottière HM, Daniel C, Delorme C. 2013 Anti-inflammatory properties of *Streptococcus salivarius* a commensal bacterium of the oral cavity and digestive tract. *Appl Environ Microbiol*. Nov 22. [Epub ahead of print]
153. Sunagawa S, Mende DR, Zeller G, Izquierdo-Carrasco F, Berger SA, Roat Kultima J, Arumugam M, Tap J, Bjørn Nielsen H, Rasmussen S, Pedersen O, Guarner F, de Vos WM, Wang J, Li J, Doré J, Ehrlich SD, Stamatakis A & Bork P. 2013. Metagenomic species profiling using universal phylogenetic marker genes. *Nature Methods* 10:1196- . DOI: 10.1038/NMETH.2693
154. Cecchini DA, Laville E, Laguerre S, Robe P, Leclerc M, Doré J, Henrissat B, Remaud-Siméon M, Monsan P, Potocki-Véronèse G. 2013. Functional metagenomics reveals novel pathways of prebiotic breakdown by human gut bacteria. *PLoS One*. 2013 Sep 16;8(9):e72766. doi: 10.1371/journal.pone.0072766.
155. Mondot S, de Wouters T, Doré J, Lepage P. 2013. The human gut microbiome and its dysfunctions. *Dig Dis*.
- Patent#13 53600: Souche de *Lactobacillus* spp régulatrice du métabolisme lipidique ; INRA/Danone ; FR 19/04/2013
156. Juste C, Kreil DP, Beauvallet C, Guillot A, Vaca S, Carapito C, Mondot S, Sykacek P, Sokol H, Blon F, Lepercq P, Levenez F, Valot B, Carré W, Loux V, Pons N, David O, Schaeffer B, Lepage P, Martin P, Monnet V, Seksik P, Beaugerie L, Ehrlich SD, Gibrat J-F, Van Dorsselaer A, Doré J. 2013. Bacterial protein signals are associated with Crohn's disease. *Gut* [Epub ahead of print]
157. Doré J, Clément K. 2014. Reply to C Matuchansky. *AmJClinNutr\_Reply*
158. Mach N, Berri M, Esquerré D, Chevaleyre C, Lemonnier G, Billon Y, Lepage L, Oswald IP, Doré J, Rogel-Gaillard C, Estellé J. 2014. Extensive expression differences along porcine small intestine evidenced by transcriptome sequencing. *PLoS One* 9: e88515
159. Santiago, A, Panda, S, Mengels, G, Martinez, X, Azpiroz, F, Dore, J, Guarner, F, Manichanh, C. 2014. Processing faecal samples: a step forward for standards in microbial community analysis. *BMC MICROBIOLOGY*. 14: DOI: 10.1186/1471-2180-14-112  
Patent #1456674 Système de collecte d'échantillons de matière fécale. Enterome ; INRA 10/07/2014  
Patent #1462867 Marqueurs diagnostiques de la maladie de Crohn : INRA 19/12/2014
160. El Aidy, S, Derrien, M, Aardema, R, Hooiveld, G, Richards, SE, Dane, A, Dekker, J, Vreeken, R, Levenez, F, Dore, J, Zoetendal, EG, van Baarlen, P, Kleerebezem, M. Transient inflammatory-

- like state and microbial dysbiosis are pivotal in establishment of mucosal homeostasis during colonisation of germ-free mice. **BENEFICIAL MICROBES**. 5:67-77
161. Kaci 2014. Anti-inflammatory properties of *Streptococcus salivarius*, a commensal bacterium of the oral cavity and digestive tract. *Appl Environ Microbiol*. 80:928-934.
  162. Slezak K, Krupova Z, Rabot S, Loh G, Levenez F, Descamps A, Lepage P, Doré J, Bellier S, Blaut M. 2014. Association of germ-free mice with a simplified human intestinal microbiota results in a shortened intestine. *Gut Microbes* 5:1-7.
  163. Nielsen H, Almeida M, ... Casellas F, Doré J, Dworzynski P, Guarner F, Hansen T, ..., MetaHIT Consortium, Renault P, Sicheritz-Ponten T, Bork P, Wang J, Brunak S, Ehrlich SD. 2014. Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. *Nature Biotech*. 32:822–828.
  164. Li J, Jia H, Cai X, ... Pedersen O, Doré J, Ehrlich SD, MetaHIT Consortium, Bork P, Wang J. **An integrated reference gene catalog of the human gut microbiome. *Nature Biotech*. 32:834-841. 2014**
  165. de Wouters T, Ledue F, Nepelska M, Dore J, Blottiere HM, Lapaque N. 2015. A robust and adaptable high throughput screening method to study host-microbiota interactions in the human intestine. *PLOS One*. 9:e105598
  166. Kong LC, Holmes BA, Cotillard A, Habi-Rachedi F, Brazeilles R, Gougis S, Gausseres N, Cani PD, Fellahi S, Bastard JP, Kennedy SP, Dore J, Ehrlich SD, Zucker JD, Rizkalla SW, Clement K. 2015. Dietary Patterns Differently Associate with Inflammation and Gut Microbiota in Overweight and Obese Subjects. *PLOS One*. 9:e109434.
  167. Larraufie P, de Wouters P, Potocki-Veronese G, Blottière HM, Doré J. 2015. Functional metagenomics to decipher food–microbe–host crosstalk. *Proceedings of the Nutrition Society*. 74:1–4.
  168. Plaza Onate, F, Batto, J-M, Juste, C, Fadlallah, J, Fougeroux, C, Gouas, D, Pons, N, Kennedy, S, Levenez, F, Dore, J, Ehrlich, SD, Gorochov, G, Larsen, M. Quality control of microbiota metagenomics by k-mer analysis. *BMC genomics*. 16:1406
  169. Patent #1553716 Procédé de préparation d'un échantillon de microbiote fécal : MaaT Pharma ; INRA 24/04/2015
  170. Patent #1553721 Dispositif de prélèvement de micro-organismes, kit de prélèvement comprenant un tel dispositif et procédé de prélèvement mettant en oeuvre un tel dispositif : MaaT Pharma ; INRA 24/04/2015
  171. Patent #FR1562750 Procédé de lyophilisation d'un échantillon de microbiote : MaaT Pharma ; INRA 18/12/2015
  172. Patent #FR1562748 Procédé de purification d'un échantillon de microbiote : MaaT Pharma ; INRA 18/12/2015
  173. Shoaie, S, Ghaffari, P, Kovatcheva-Datchary, P, Mardinoglu, A, Sen, P, Pujos-Guillot, E, de Wouters, T, Juste, C, Rizkalla, S, Chilloux, J, Hoyles, L, Nicholson, JK, Dore, J, Dumas, ME, Clement, K, Backhed, F, Nielsen, J & MICRO-Obes Consortium. 2015. Quantifying Diet-Induced Metabolic Changes of the Human Gut Microbiome . *Cell Metabol*. 22:320-331
  174. Mach, N, Berri, M, Estelle, J, Levenez, F, Lemonnier, G, Denis, C, Leplat, JJ, Chevalleyre, C, Billon, Y, Dore, J, Rogel-Gaillard, C, Lepage, P. 2015. Early-life establishment of the swine gut microbiome and impact on host phenotypes. *Environ Microbiol Reports*. 7:554-569
  175. Couvigny, B, de Wouters, T, Kaci, G, Jacouton, E, Delorme, C, Dore, J, Renault, P, Blottiere, HM, Guedon, E, Lapaque, N. 2015. Commensal *Streptococcus salivarius* modulates PPAR gamma transcriptional activity in human intestinal epithelial cells. *PLOS One* 10: e0125371
  176. Dore, J and Blottiere, H. 2015. The influence of diet on the gut microbiota and its consequences for health. *Curr Opin Biotechnol*.. 32:195-199
  177. Jacouton,E.; Mach,N.; Cadiou,J.; Lapaque,N.; Clement,K.; Dore,J.; Vlieg,JETV.; Smokvina,T.; Blottiere,HM. 2015. *Lactobacillus rhamnosus* CNCMI-4317 Modulates Fiaf/Angptl4 in Intestinal Epithelial Cells and Circulating Level in Mice *PLOS ONE*
  178. Zhang C, Yin A, Li H, Wang R, Wu G, Shen J, Zhang M, Wang L, Hou Y, Ouyang H, Zhang Y, Zheng Y, Wang J, Lv X, Wang Y, Zhang F, Zeng B, Li W, Yan F, Zhao Y, Pang X, Zhang X, Fu H, Chen F, Zhao N, Hamaker BR, Bridgewater LC, Weinkove D, Clement K, Dore J, Holmes E, Xiao H, Zhao G, Yang S, Bork P, Nicholson JK, Wei H, Tang H, Zhang X, Zhao L. Dietary Modulation of Gut Microbiota Contributes to Alleviation of Both Genetic and Simple Obesity in Children. *EBIOMEDICINE*
  179. Cultrone,A.; Tap,J.; Lapaque,N.; Dore,J.; Blottiere,HM Metagenomics of the human intestinal tract: from who is there to what is done there? *Curr Opin Food Sci*

180. Thomas, V.; Clark, J.; Doré, J. Fecal microbiota analysis: an overview of sample collection methods and sequencing strategies. *Future Microbiol*
181. Tap, J.; Furet, J-P.; Bensaada, M.; Philippe, C.; Roth, H.; Rabot, S.; Lakhdari, O.; Lombard, V.; Henrissat, B.; Corthier, G.; Fontaine, E.; Doré, J.; Leclerc, M. 2015. Gut microbiota richness promotes its stability upon increased dietary fiber intake in healthy adults. *Environ Microbiol* 17, 4954–4964
182. Dao, M.C.; Everard, A.; Aron-Wisnewsky, J.; Sokolovska, N.; Prifti, E.; Verger, E.O.; Kayser, B.D.; Levenez, F.; Chilloux, J.; Hoyles, L.; MICRO-Obes Consortium; Dumas, M-E.; Rizkalla, S.W.; Doré, J.; Cani, P.D.; Clément, K. **Akkermansia muciniphila and improved metabolic health during a dietary intervention in obesity: relationship with gut microbiome richness and ecology, Gut**
183. K. Forslund, F. Hildebrand, T. Nielsen, G. Falony, E. Le Chatelier, S. Sunagawa, E. Prifti, S. Vieira-Silva, V. Gudmundsdottir, H. K. Pedersen, M. Arumugam, K. Kristiansen, A. Y. Voigt, H. Vestergaard, R. Herczeg, P.I. Costea, J. R. Kultima, J. Li, T. Jørgensen, F. Levenez, J. Dore, MetaHIT consortium, H. B. Nielsen, S. Brunak, J. Raes, T. Hansen, J. Wang, S.D. Ehrlich, P. Bork, O. Pedersen (2015) **Disentangling the effects of type 2 diabetes and metformin on the human gut microbiota. Nature, on line 2 December 2015. doi: 10.1038/nature15766**
184. Mondot S, Lepage P, Seksik P, Allez M, Treton X, Bouhnik Y, Colombel JF, Leclerc M, Pochart P, Dore J, Marteau P; GETAID. Structural robustness of the gut mucosal microbiota is associated with Crohn's disease remission after surgery. *Gut*. 2016 Jun;65(6):954-62
185. **Sokolovska N, Teytaud O, Rizkalla S; MicroObese consortium, Clément K, Zucker JD. Sparse Zero-Sum Games as Stable Functional Feature Selection. PLoS One**
186. L. Xiao, Q. Feng, S. Liang, S. B. Sonne, Z. Xia, X. Qiu, X. Li, H. Long, J. Zhang, D. Zhang, C. Liu, Z. Fang, J. Chou, J. Glanville, Q. Hao, D. Kotowska, C. Colding, T.R. Licht, D. Wu, J. Yu, J.J.Y. Sung, Q. Liang, J. Li, H. Jia, Z. Lan, V. Tremaroli, P. Dworkowski, H.B. Nielsen, F. Bäckhed, J. Doré, E. Le Chatelier, S.D. Ehrlich, J.C. Lin, M. Arumugam, J. Wang, L. Madsen, K. Kristiansen (2015) **A Catalogue of the mouse gut metagenome. Nature Biotech 33:1103-1108. doi:10.1038/nbt.3353**
187. N. Qin, B. Zheng, J. Yao, L. Guo, J. Zuo, L. Wu, J. Zhou, L. Liu, J. Guo, S. Ni, A. Li, Y. Zhu, W. Liang, Y. Xiao, S.D. Ehrlich, L. Li (2015) **Influence of H7N9 virus infection and associated treatment on human gut microbiota. Scientific Reports 5:14771. doi: 10.1038/srep14771**
188. H. Krogh Pedersen, V. Gudmundsdottir, H. B. Nielsen, T. Hyötyläinen, T. Nielsen, B.A. H. Jensen, K. Forslund, F. Hildebrand, E. Prifti, G. Falony, E. Le Chatelier, F. Levenez, J. Doré, I. Mattila, Damian R. Plichta, P. Pöhö, L.I. Hellgren, M. Arumugam, S. Sunagawa, S. Vieira-Silva, T. Jørgensen, J. Bak Holm, K. Trošt, MetaHit consortium, K. Kristiansen, S.B. Pedersen, J. Raes, J. Wang, T. Hansen, P. Bork, S. Brunak, M. Oresic, S.D. Ehrlich and O. Pedersen (2016) **Human gut microbiome impacts the serum metabolome and contributes to insulin resistance. Nature 535, 376-381. doi: 10.1038/nature18646**
189. **Identification of an Intestinal Microbiota Signature Associated With Severity of Irritable Bowel Syndrome.** Tap J, Derrien M, Törnblom H, Brazeilles R, Cools-Portier S, Doré J, Störsrud S, Le Nevé B, Öhman L, Simrén M. *Gastroenterology*. 2017 Jan;152(1):111-123.e8. doi: 10.1053/j.gastro.2016.09.049. Epub 2016 Oct 7.
190. D.R. Plichta, A.S. Juncker, M. Bertalan, E. Rettedal, L. Gautier, E. Varela, C. Manichanh, C. Fouqueray, F. Levenez, T. Nielsen, J. Doré, A. M. Dantas Machado, M.C. Rodriguez de Evgrafov, T. Hansen, T. Jørgensen, P. Bork, F. Guarner, O. Pedersen, Metagenomics of the Human Intestinal Tract (MetaHIT) Consortium, M.O.A. Sommer, S.D. Ehrlich, T. Sicheritz-Pontén, S. Brunak and H. B Nielsen (2016) **Transcriptional interactions suggest niche segregation among microorganisms in the human gut. Nature Microbiol. in press.**
191. L. Xiao, J. Estellé, P. Kiilerich, Y. Ramayo-Caldas, Z. Xia, Q. Feng, S. Liang, A.Ø. Pedersen, N.J. Kjeldsen, C. Liu, E. Maguin, J. Doré, N. Pons, E. Le Chatelier, E. Prifti, J. Li, H. Jia, X. Liu, X. Xu, S.D. Ehrlich, L. Madsen, K. Kristiansen, C. Rogel-Gaillard, J. Wang (2016) **A reference gene catalogue of the pig gut microbiome. Nature Microbiol. In press.**
192. **The human gut microbiome as source of innovation for health: Which physiological and therapeutic outcomes could we expect?**  
Doré J, Multon MC, Béhier JM; participants of Giens XXXII, Round Table No. 2. *Thérapie*. 2017 Feb;72(1):21-38. doi: 10.1016/j.therap.2016.12.007. Epub 2017 Jan 3. PMID: 28131442
- 193.