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Metagenomic biomarker discovery and explanation

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2275	The genome of th17 cell-inducing segmented filamentous bacteria reveals extensive auxotrophy and adaptations to the intestinal environment. 2011 , 10, 260-72		142
2274	Toward an efficient method of identifying core genes for evolutionary and functional microbial phylogenies. 2011 , 6, e24704		67
2273	Metabolic reconstruction for metagenomic data and its application to the human microbiome. 2012 , 8, e1002358		730
2272	Therapeutic helminth infection of macaques with idiopathic chronic diarrhea alters the inflammatory signature and mucosal microbiota of the colon. 2012 , 8, e1003000		157
2271	Effects of the UK Biobank collection protocol on potential biomarkers in saliva. 2012 , 41, 1786-97		25
2270	Human intestinal lumen and mucosa-associated microbiota in patients with colorectal cancer. 2012 , 7, e39743		553
2269	Bioinformatic approaches for functional annotation and pathway inference in metagenomics data. 2012 , 13, 696-710		60
2268	Colonic mucosal microbiome differs from stool microbiome in cirrhosis and hepatic encephalopathy and is linked to cognition and inflammation. 2012 , 303, G675-85		331
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2265	Composition of the adult digestive tract bacterial microbiome based on seven mouth surfaces, tonsils, throat and stool samples. <i>Genome Biology</i> , 2012 , 13, R42	18.3	572
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